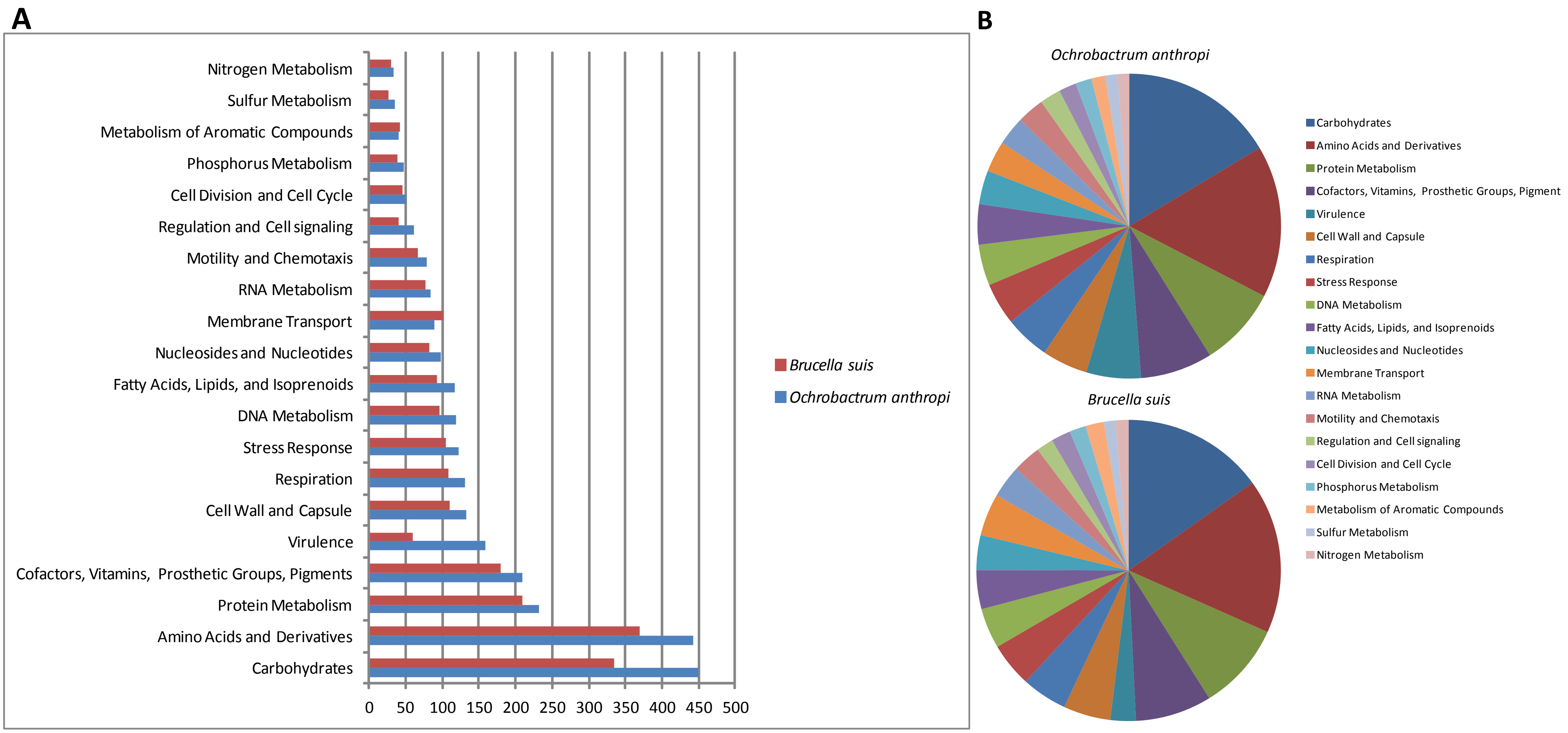
A
Nitrogen Metabolism
Sulfur Metabolism
Metabolism of Aromatic Compounds
Phosphorus Metabolism
Cell Division and Cell Cycle
Regulation and Cell signaling
Motility and Chemotaxis
RNA Metabolism
Membrane Transport
Nucleosides and Nucleotides
Fatty Acids, Lipids, and Isoprenoids
DNA Metabolism
Stress Response
Respiration
Cell Wall and Capsule
Virulence
Cofactors, Vitamins, Prosthetic Groups, Pigments
Protein Metabolism
Amino Acids and Derivatives
Carbohydrates
0
50
100
150
200
250
300
350
400
450
500
Brucella suis
Ochrobactrum anthropi
B
Ochrobactrum anthropi
Brucella suis
Carbohydrates
Amino Acids and Derivatives
Protein Metabolism
Cofactors, Vitamins, Prosthetic Groups, Pigment
Virulence
Cell Wall and Capsule
Respiration
Stress Response
DNA Metabolism
Fatty Acids, Lipids, and Isoprenoids
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RNA Metabolism
Motility and Chemotaxis
Regulation and Cell signaling
Cell Division and Cell Cycle
Phosphorus Metabolism
Metabolism of Aromatic Compounds
Sulfur Metabolism
Nitrogen Metabolism

Table S1. Isolate descriptions, sources, and genomic data for *Brucella* and *Ochrobactrum* species used in genomic analyses.

Species	ID	Biovar	Host	Host species	Genome size (nt)	Contigs	CDS	Genes
B. abortus	NCTC 8038	-	Bovine	*Bos primigenius*	3276866	16	3439	3538
B. abortus	S19	-	Bovine	*Bos primigenius*	3283936	2	3476	3591
B. abortus	2308A	-	Bovine	*Bos primigenius*	3277197	9	3473	3580
B. abortus	2308	-	Bovine	*Bos primigenius*	3278307	2	3467	3578
B. abortus	86/8/59	2	Bovine	*Bos primigenius*	3294912	21	3574	3670
B. abortus	9-941	1	Bovine	*Bos primigenius*	3286445	2	3476	3587
B. abortus	292	4	Bovine	*Bos primigenius*	3272945	12	3429	3567
B. abortus	C68	9	Bovine	*Bos primigenius*	3269576	13	3406	3501
B. abortus	B3196	5	Bovine	*Bos primigenius*	3343441	48	3473	3567
B. abortus	870	6	Bovine	*Bos primigenius*	3270344	13	3435	3488
B. abortus	Tulya	3	Human	*Homo sapiens*	3282764	13	3521	3614
B. melitensis	16M	1	Caprine	*Capra hircus*	3294931	2	3499	3598
B. melitensis	16MWGS	1	Caprine	*Capra hircus*	3291248	15	3538	3624
B. melitensis	REV1	-	Caprine	*Capra hircus*	3305822	26	3440	3528
B. melitensis	ATCC 23457	2	Caprine	*Capra hircus*	3311219	2	3486	3590
B. melitensis	63/9	2	Caprine	*Capra hircus*	3284951	60	3447	3533
B. melitensis	Ether	3	Caprine	*Capra hircus*	3308792	13	3457	3548
B. ovis	ATCC 25840	-	Ovine	*Ovis aries*	3275590	2	3543	3656
Brucella sp.	NVSL 07-0026	-	Baboon	*Papio sp.*	3297137	17	3531	3645
B. ceti	M490/95/1	-	Common seal	*Phoca vitulina*	3345471	17	3386	3460
B. ceti	B1/94	-	Harbor porpoise	*Phocoena phocoena*	3337159	14	3386	3465
B. ceti	F5/99	-	Bottlenose dolphin	*Tursiops truncatus*	3336716	18	3359	3433
B. ceti	Cudo	-	Bottlenose dolphin	*Tursiops truncatus*	3389269	7	3610	3709
B. pinnipedialis	B2/94	-	Common seal	*Phoca vitulina*	3398674	19	3425	3502
B. pinnipedialis	M292/94/1	-	Common seal	*Phoca vitulina*	3373519	15	3399	3470
B. pinnipedialis	M163/99/10	-	Hooded seal	*Cystophora cristata*	3404050	89	3453	3541
B. ceti	M13/05/01	-	Striped dolphin	*Stenella coeruleoalba*	3334689	17	3414	3496
B. ceti	M644/93/1	-	Common dolphin	*Delphinus delphis*	3337230	22	3406	3491
B. canis	RM6/66	-	Dog	*Canis domesticus*	3312769	2	3435	3523
B. suis	40	4	Reindeer	*Rangifer tarandus*	3307260	12	3388	3470
B. suis	686	3	Swine	*Sus scrofa*	3298529	23	3515	3593
B. suis	1330	1	Swine	*Sus scrofa*	3315175	2	3432	3521
B. suis	Thomsen	2	Swine	*Sus scrofa*	3324607	2	3591	3681
B. suis	513	5	Rodent	Rodentia	3323676	19	3377	3430
B. neotomae	5K33	-	Desert woodrat	*Neotoma lepida*	3329623	11	3434	3509
B. microti	CCM 4915	-	Common vole	*Microtus arvalis*	3337369	2	3410	3490
Brucella sp.	NF2653	-	Australian rodents	Rodentia	3110281	113	3167	3239
Brucella sp.	83/13	-	Australian rodents	Rodentia	3153851	20	3167	3235
B. inopinata	BO1	-	Human	*Homo sapiens*	3366774	55	3330	3390
B. inopinata	BO2	-	Human	*Homo sapiens*	3305941	174	3251	3311
O. anthropi	LMG3331	-	Human	*Homo sapiens*	5205777	6	5025	5095
O. intermedium	LMG3301	-	Human	*Homo sapiens*	4725392	4	4533	4617

Table S2. *Ochrobactrum anthropi* ortholog groups that are not present in *Brucella*.

Ochrobactrum intermedium LMG 3301	*Bartonella quintana* str. Toulouse	*Mesorhizobium loti* MAFF303099	*Agrobacterium tumefaciens* str. C58	*Ochrobactrum anthropi* ATCC 49188 PATRIC locus tag	*Ochrobactrum anthropi* ATCC 49188 RefSeq locus tag	**Product**
√		√	√	VBIOchAnt73124_0007	Oant_0007	PUTATIVE ACETYLTRANSFERASE PROTEIN(EC:2.3.1.-)
√		√	√	VBIOchAnt73124_0008	Oant_0008	hypothetical protein
√				VBIOchAnt73124_0062	Oant_0060	Glucose-methanol-choline (GMC) oxidoreductase:NAD binding site
√				VBIOchAnt73124_0063	Oant_0061	Tat (Twin-arginine translocation) pathway signal sequence domain protein
√		√	√	VBIOchAnt73124_0068	Oant_0066	Transcriptional regulator, AraC family
√		√	√	VBIOchAnt73124_0069	Oant_0067	Uncharacterized protein conserved in bacteria
√		√	√	VBIOchAnt73124_0070	Oant_0068	Transcriptional regulator FrcR for fructose utilization, ROK family
√		√	√	VBIOchAnt73124_0071	Oant_0069	Fructose ABC transporter, substrate-binding component FrcB
√		√	√	VBIOchAnt73124_0072	Oant_0070	Fructose ABC transporter, permease component FrcC
√				VBIOchAnt73124_0084	Oant_0082	hypothetical protein
√				VBIOchAnt73124_0085	Oant_0083	Transcriptional regulator, MarR family
√				VBIOchAnt73124_0086	Oant_0084	hypothetical protein
√				VBIOchAnt73124_0087	Oant_0085	Methionine aminopeptidase
√		√		VBIOchAnt73124_0089	Oant_0087	Antibiotic biosynthesis monooxygenase
√				VBIOchAnt73124_0096	Oant_0093	hypothetical protein
√				VBIOchAnt73124_0123	Oant_0116	hypothetical protein
√		√	√	VBIOchAnt73124_0136	Oant_0128	RhtB family transporter
√		√	√	VBIOchAnt73124_0142	Oant_0134	hypothetical protein
√		√	√	VBIOchAnt73124_0149	Oant_0140	small molecule metabolism
√			√	VBIOchAnt73124_0155	Oant_0146	hypothetical protein
√		√		VBIOchAnt73124_0215	Oant_0203	Integrase
√				VBIOchAnt73124_0264	Oant_0247	hypothetical protein
√		√	√	VBIOchAnt73124_0295	Oant_0275	Cyclic beta-1,2-glucan modification transmembrane protein
√		√	√	VBIOchAnt73124_0309	Oant_0288	6-phosphofructokinase, PF08013 family
√		√	√	VBIOchAnt73124_0310	Oant_0289	Fructokinase
√		√		VBIOchAnt73124_0311	Oant_0290	Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1)

√			VBIOchAnt73124_0312	Oant_0291	Putative ribose/galactose/methyl galactoside import ATP-binding protein 1
√	√	√	VBIOchAnt73124_0313	Oant_0292	Ribose/xylose/arabinose/galactoside ABC-type transport systems, substrate-binding component
			VBIOchAnt73124_0314		hypothetical protein
√	√	√	VBIOchAnt73124_0315	Oant_0293	Ribose operon repressor
√	√	√	VBIOchAnt73124_0316	Oant_0294	Glucose dehydrogenase, PQQ-dependent
√	√	√	VBIOchAnt73124_0342	Oant_0320	hypothetical protein
√			VBIOchAnt73124_0351		hypothetical protein
√	√	√	VBIOchAnt73124_0352	Oant_0330	cytochrome c oxidase subunit I
√	√	√	VBIOchAnt73124_0355	Oant_0333	Urease accessory protein UreD
√	√	√	VBIOchAnt73124_0361	Oant_0339	Deoxyribodipyrimidine photolyase
√			VBIOchAnt73124_0363		hypothetical protein
√	√	√	VBIOchAnt73124_0366	Oant_0343	Pyrimidine ABC transporter, substrate-binding component
√	√	√	VBIOchAnt73124_0367	Oant_0344	Pyrimidine ABC transporter, transmembrane component 2
√	√	√	VBIOchAnt73124_0368	Oant_0345	Pyrimidine ABC transporter, transmembrane component 1
√	√	√	VBIOchAnt73124_0369	Oant_0346	Pyrimidine ABC transporter, ATP-binding protein
√		√	VBIOchAnt73124_0374	Oant_0351	Maltose/maltodextrin transport ATP-binding protein MalK
√	√	√	VBIOchAnt73124_0376	Oant_0353	ABC-type sugar transport systems, permease components
√	√	√	VBIOchAnt73124_0377	Oant_0354	Sugar ABC transporter, periplasmic sugar-binding protein
√	√	√	VBIOchAnt73124_0378	Oant_0355	Cystathionine gamma-synthase
√	√	√	VBIOchAnt73124_0379	Oant_0356	Transcriptional regulator, GntR family
√	√	√	VBIOchAnt73124_0380	Oant_0357	L-fuco-beta-pyranose dehydrogenase
√	√	√	VBIOchAnt73124_0381	Oant_0358	Ribokinase
√		√	VBIOchAnt73124_0382	Oant_0359	Dihydrodipicolinate synthase
√	√	√	VBIOchAnt73124_0383	Oant_0360	Transcriptional regulator, GntR family
√	√	√	VBIOchAnt73124_0384	Oant_0361	Sugar ABC transporter, periplasmic sugar-binding protein
√	√	√	VBIOchAnt73124_0385	Oant_0362	ABC-type sugar transport systems, permease components
√		√	VBIOchAnt73124_0386	Oant_0363	Maltose/maltodextrin ABC transporter, permease protein MalG
√	√	√	VBIOchAnt73124_0387	Oant_0364	Maltose/maltodextrin transport ATP-binding protein MalK
√	√	√	VBIOchAnt73124_0390	Oant_0367	carbon monoxide dehydrogenase G protein
√	√		VBIOchAnt73124_0406	Oant_0382	hypothetical protein
√		√	VBIOchAnt73124_0407	Oant_0383	glycosyl transferase, family 2
√			VBIOchAnt73124_0408	Oant_0384	hypothetical protein
√	√	√	VBIOchAnt73124_0409	Oant_0385	conserved hypothetical membrane protein
√		√	VBIOchAnt73124_0411	Oant_0386	putative cell-surface polysaccharide exporter protein, PST family
√	√		VBIOchAnt73124_0412	Oant_0387	succinoglycan biosynthesis transport protein
√	√	√	VBIOchAnt73124_0437	Oant_0411	Aspartate aminotransferase
√			VBIOchAnt73124_0439	Oant_0413	hypothetical protein
√			VBIOchAnt73124_0442	Oant_0416	hypothetical protein

√				VBIOchAnt73124_0444	Oant_0418	protein of unknown function DUF1127
√			√	VBIOchAnt73124_0450	Oant_0423	Glyoxalase family protein
√		√		VBIOchAnt73124_0451	Oant_0424	Glyoxalase family protein
√		√	√	VBIOchAnt73124_0455	Oant_0428	Predicted NAD regulator in Alphaproteobacteria
√		√	√	VBIOchAnt73124_0456	Oant_0429	Quinolinate synthetase
√		√	√	VBIOchAnt73124_0457	Oant_0430	L-aspartate oxidase
√		√	√	VBIOchAnt73124_0458	Oant_0431	Quinolinate phosphoribosyltransferase [decarboxylating]
√				VBIOchAnt73124_0460		hypothetical protein
√		√		VBIOchAnt73124_0461	Oant_0432	Transcriptional regulator, TetR family
√				VBIOchAnt73124_0463	Oant_0434	Superoxide dismutase [Fe]
√				VBIOchAnt73124_0464	Oant_0435	hypothetical protein
√	√	√	√	VBIOchAnt73124_0465	Oant_0436	Putative transport protein
√				VBIOchAnt73124_0476	Oant_0447	ATP/GTP-binding site motif A (P-loop) :Porin, alpha proteobacteria type
√				VBIOchAnt73124_0479	Oant_0450	Transthyretin family protein
√		√	√	VBIOchAnt73124_0486	Oant_0457	Negative regulator of allantoin and glyoxylate utilization operons
√		√		VBIOchAnt73124_0487	Oant_0458	Glyoxylate carboligase
√		√		VBIOchAnt73124_0490	Oant_0460	2-hydroxy-3-oxopropionate reductase
√				VBIOchAnt73124_0498		hypothetical protein
√				VBIOchAnt73124_0503	Oant_0472	Cytochrome c-type biogenesis protein DsbD, protein-disulfide reductase
√			√	VBIOchAnt73124_0505	Oant_0473	hypothetical protein
√		√		VBIOchAnt73124_0509	Oant_0477	hypothetical protein
√			√	VBIOchAnt73124_0513	Oant_0481	hypothetical protein
√		√	√	VBIOchAnt73124_0514	Oant_0482	Transcriptional regulator, ArsR family
√		√	√	VBIOchAnt73124_0516	Oant_0483	hypothetical protein
√		√	√	VBIOchAnt73124_0522	Oant_0489	Probable signal peptide protein
√				VBIOchAnt73124_0527	Oant_0494	hypothetical protein
√		√		VBIOchAnt73124_0530	Oant_0497	Gfa-like protein
√				VBIOchAnt73124_0531		hypothetical protein
√		√	√	VBIOchAnt73124_0539	Oant_0505	Transcriptional regulator, AsnC family
√		√	√	VBIOchAnt73124_0540	Oant_0506	L-lysine permease
√				VBIOchAnt73124_0542		hypothetical protein
√				VBIOchAnt73124_0546	Oant_0511	hypothetical protein
√				VBIOchAnt73124_0551	Oant_0516	hypothetical protein
√				VBIOchAnt73124_0556		hypothetical protein
√				VBIOchAnt73124_0559	Oant_0523	hypothetical protein
√				VBIOchAnt73124_0569	Oant_0532	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)
√		√	√	VBIOchAnt73124_0574	Oant_0537	hypothetical protein
√		√	√	VBIOchAnt73124_0587	Oant_0550	Aspartate racemase
√		√		VBIOchAnt73124_0591	Oant_0554	transcriptional regulator, ArsR family

√		√	√	VBIOchAnt73124_0596	Oant_0558	hypothetical protein
√				VBIOchAnt73124_0617		hypothetical protein
√		√	√	VBIOchAnt73124_0649	Oant_0610	dTDP-glucose 4,6-dehydratase
√	√		√	VBIOchAnt73124_0685	Oant_0647	Type IV secretion system protein VirD4
√		√	√	VBIOchAnt73124_0687	Oant_0650	hypothetical protein
√			√	VBIOchAnt73124_0709	Oant_0672	hypothetical protein
√	√		√	VBIOchAnt73124_0711	Oant_0675	Major pilus subunit of type IV secretion complex (VirB2)
√	√		√	VBIOchAnt73124_0712	Oant_0676	Inner membrane protein forms channel for type IV secretion of T-DNA complex (VirB3)
√			√	VBIOchAnt73124_0714	Oant_0678	Minor pilin of type IV secretion complex (VirB5)
√	√		√	VBIOchAnt73124_0716	Oant_0680	Integral inner membrane protein of type IV secretion complex (VirB6)
√	√	√	√	VBIOchAnt73124_0719	Oant_0683	secretin-like domain, VirB9
√				VBIOchAnt73124_0725	Oant_0689	Putative diheme cytochrome c-553
√				VBIOchAnt73124_0748	Oant_0710	IS66 Orf2 family protein
√				VBIOchAnt73124_0749	Oant_0711	Transposase
√		√	√	VBIOchAnt73124_0755	Oant_0717	hypothetical protein
√		√	√	VBIOchAnt73124_0756	Oant_0718	Similar to TadZ/CpaE, associated with Flp pilus assembly
√		√	√	VBIOchAnt73124_0757	Oant_0719	Similar to secretin RcpA/CpaC, associated with Flp pilus assembly
√				VBIOchAnt73124_0758	Oant_0720	Flp/Fap pilin component
√		√	√	VBIOchAnt73124_0760	Oant_0721	Type IV prepilin peptidase TadV/CpaA
√		√	√	VBIOchAnt73124_0761	Oant_0722	Flp pilus assembly protein RcpC/CpaB
√		√	√	VBIOchAnt73124_0763	Oant_0723	Type II/IV secretion system secretin RcpA/CpaC, associated with Flp pilus assembly
√		√	√	VBIOchAnt73124_0764	Oant_0724	Flp pilus assembly protein CpaD
√		√	√	VBIOchAnt73124_0765	Oant_0725	Type II/IV secretion system ATPase TadZ/CpaE, associated with Flp pilus assembly
√		√	√	VBIOchAnt73124_0766	Oant_0726	Type II/IV secretion system ATP hydrolase TadA/VirB11/CpaF, TadA subfamily
√		√	√	VBIOchAnt73124_0767	Oant_0727	Flp pilus assembly protein TadB
√		√	√	VBIOchAnt73124_0768	Oant_0728	Type II/IV secretion system protein TadC, associated with Flp pilus assembly
√		√	√	VBIOchAnt73124_0769	Oant_0729	Flp pilus assembly protein TadD, contains TPR repeat
√				VBIOchAnt73124_0775		hypothetical protein
√				VBIOchAnt73124_0809		hypothetical protein
√		√		VBIOchAnt73124_0819	Oant_0776	Ribosomal protein S6 glutaminyl transferase
√		√		VBIOchAnt73124_0822	Oant_0779	Glyoxalase/bleomycin resistance protein/dioxygenase
√		√		VBIOchAnt73124_0830	Oant_0787	NADPH:quinone oxidoreductase
√		√		VBIOchAnt73124_0836	Oant_0792	hypothetical protein
√		√	√	VBIOchAnt73124_0838	Oant_0794	Aldo-keto reductase
√				VBIOchAnt73124_0839	Oant_0795	hypothetical protein
√				VBIOchAnt73124_0840	Oant_0796	Transcriptional regulator, TetR family
√				VBIOchAnt73124_0868	Oant_0823	Glutamate racemase
√				VBIOchAnt73124_0876	Oant_0831	hypothetical protein
√		√	√	VBIOchAnt73124_0885	Oant_0840	hypothetical protein

√				VBIOchAnt73124_0912		hypothetical protein
√			√	VBIOchAnt73124_0960	Oant_0916	Oxidoreductase, short-chain dehydrogenase/reductase family
√				VBIOchAnt73124_0984	Oant_0940	hypothetical protein
√		√		VBIOchAnt73124_0989	Oant_0945	hypothetical protein
√				VBIOchAnt73124_0994	Oant_0949	hypothetical protein
√		√		VBIOchAnt73124_1001	Oant_0956	osmotically inducible protein C, putative ATP/GTP binding protein
√			√	VBIOchAnt73124_1009	Oant_0963	hypothetical protein
√				VBIOchAnt73124_1013	Oant_0967	Xanthine permease
√				VBIOchAnt73124_1030	Oant_0983	hypothetical protein
√		√	√	VBIOchAnt73124_1049	Oant_1001	Homoserine/homoserine lactone efflux protein
√		√	√	VBIOchAnt73124_1052	Oant_1003	Permease of the drug/metabolite transporter (DMT) superfamily
√		√	√	VBIOchAnt73124_1069	Oant_1020	similar to polysaccharide biosynthesis related protein
√		√	√	VBIOchAnt73124_1092	Oant_1044	Na+-driven multidrug efflux pump
√		√	√	VBIOchAnt73124_1093	Oant_1045	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)
√			√	VBIOchAnt73124_1094	Oant_1046	conserved hypothetical protein
√			√	VBIOchAnt73124_1095	Oant_1047	Ribosomal large subunit pseudouridine synthase A
√		√	√	VBIOchAnt73124_1112	Oant_1063	Possible divergent polysaccharide deacetylase
√			√	VBIOchAnt73124_1118	Oant_1069	hypothetical protein
√		√		VBIOchAnt73124_1119	Oant_1070	Putative oxidoreductase YncB
√		√		VBIOchAnt73124_1122	Oant_1073	hypothetical protein
√				VBIOchAnt73124_1148	Oant_1098	putative RecF protein
√		√	√	VBIOchAnt73124_1174	Oant_1124	MFS permease protein
√		√		VBIOchAnt73124_1175	Oant_1125	Transcriptional regulator, HxlR family
√				VBIOchAnt73124_1182		hypothetical protein
√				VBIOchAnt73124_1183		hypothetical protein
√		√	√	VBIOchAnt73124_1199	Oant_1146	Oxidoreductase
√				VBIOchAnt73124_1235	Oant_1182	3-oxoacyl-[acyl-carrier protein] reductase
√	√	√	√	VBIOchAnt73124_1238	Oant_1185	Fructose-bisphosphate aldolase class I
√		√	√	VBIOchAnt73124_1239	Oant_1186	PQQ-dependent oxidoreductase, gdhB family
√		√		VBIOchAnt73124_1241	Oant_1188	conserved hypothetical protein
√				VBIOchAnt73124_1246	Oant_1193	hypothetical protein
√			√	VBIOchAnt73124_1306	Oant_1247	hypothetical protein
√				VBIOchAnt73124_1313		hypothetical protein
√		√	√	VBIOchAnt73124_1321	Oant_1260	HYPOTHETICAL SIGNAL PEPTIDE PROTEIN
√		√	√	VBIOchAnt73124_1322	Oant_1261	hypothetical protein
√		√	√	VBIOchAnt73124_1339	Oant_1278	Aldo/keto reductase
√		√	√	VBIOchAnt73124_1340	Oant_1279	polysaccharide deacetylase
√				VBIOchAnt73124_1343	Oant_1281	Cyanate transport protein CynX
√				VBIOchAnt73124_1344	Oant_1282	Probable deaminase

√	√	√	VBIOchAnt73124_1345	Oant_1283	Ankyrin
√	√	√	VBIOchAnt73124_1346	Oant_1284	Transcriptional regulator, LysR family
√	√	√	VBIOchAnt73124_1373	Oant_1313	GCN5-related N-acetyltransferase
√	√	√	VBIOchAnt73124_1375	Oant_1315	hypothetical protein
√			VBIOchAnt73124_1400	Oant_1335	Bicyclomycin resistance protein
√			VBIOchAnt73124_1412	Oant_1347	Quinone oxidoreductase
√		√	VBIOchAnt73124_1422	Oant_1356	protein of unknown function DUF817
√	√		VBIOchAnt73124_1425	Oant_1359	contains type I hydrophobic transmembrane region and ATP/GTP binding motif
√	√	√	VBIOchAnt73124_1431	Oant_1364	hypothetical protein
√		√	VBIOchAnt73124_1484	Oant_1415	Putative sugar ABC transport system, permease protein YjfF
√		√	VBIOchAnt73124_1485	Oant_1416	Putative sugar ABC transport system, permease protein YtfT
√		√	VBIOchAnt73124_1486	Oant_1417	Putative sugar ABC transport system, ATP-binding protein YtfR
√		√	VBIOchAnt73124_1487	Oant_1418	Putative sugar ABC transport system, periplasmic binding protein YtfQ precursor
√			VBIOchAnt73124_1533		hypothetical protein
√	√	√	VBIOchAnt73124_1534	Oant_1463	ABC transporter, substrate binding protein
√	√	√	VBIOchAnt73124_1535	Oant_1464	Ferric iron ABC transporter, permease protein
√	√	√	VBIOchAnt73124_1536	Oant_1465	Putrescine transport ATP-binding protein PotA (TC 3.A.1.11.1)
√		√	VBIOchAnt73124_1543	Oant_1472	hypothetical protein
√		√	VBIOchAnt73124_1544	Oant_1473	Beta-mannosidase
√		√	VBIOchAnt73124_1545	Oant_1474	hypothetical protein
√		√	VBIOchAnt73124_1546	Oant_1475	Archaeal seryl-tRNA synthetase-related sequence
√		√	VBIOchAnt73124_1547	Oant_1476	Acyl-CoA dehydrogenase
√		√	VBIOchAnt73124_1548	Oant_1477	Acyl carrier protein
√		√	VBIOchAnt73124_1550	Oant_1479	hypothetical protein
√		√	VBIOchAnt73124_1551	Oant_1480	hypothetical protein
√	√		VBIOchAnt73124_1555	Oant_1484	hypothetical protein
√			VBIOchAnt73124_1562	Oant_1492	hypothetical protein
√			VBIOchAnt73124_1563	Oant_1493	hypothetical protein
√			VBIOchAnt73124_1566	Oant_1496	conserved hypothetical protein
√			VBIOchAnt73124_1567	Oant_1497	hypothetical protein
√			VBIOchAnt73124_1568	Oant_1498	Baseplate assembly protein J
√		√	VBIOchAnt73124_1571	Oant_1500	Phage-related baseplate assembly protein V
√	√		VBIOchAnt73124_1593	Oant_1519	hypothetical protein
√			VBIOchAnt73124_1604		hypothetical protein
√			VBIOchAnt73124_1649	Oant_1566	PhnB protein; putative DNA binding 3-demethylubiquinone-9 3-methyltransferase domain protein
√	√	√	VBIOchAnt73124_1650	Oant_1567	Putative transport protein
√	√		VBIOchAnt73124_1654	Oant_1570	response regulator receiver domain protein
√			VBIOchAnt73124_1665		Signal transduction histidine kinase

√				VBIOchAnt73124_1677	Oant_1592	LysR family transcriptional regulator STM2281
√		√		VBIOchAnt73124_1678	Oant_1593	hypothetical protein
√		√	√	VBIOchAnt73124_1701	Oant_1614	hypothetical protein
√		√		VBIOchAnt73124_1721	Oant_1633	Chromate transport protein ChrA
√	√	√		VBIOchAnt73124_1734	Oant_1646	Branched-chain amino acid aminotransferase
√				VBIOchAnt73124_1761		hypothetical protein
√		√		VBIOchAnt73124_1766	Oant_1675	Integral membrane protein
√				VBIOchAnt73124_1782	Oant_1690	conserved hypothetical protein
√			√	VBIOchAnt73124_1791	Oant_1698	UPF0337 protein RB0906
√				VBIOchAnt73124_1795	Oant_1701	hypothetical protein
√				VBIOchAnt73124_1803	Oant_1708	probable membrane protein YPO0899
√		√	√	VBIOchAnt73124_1825	Oant_1727	Mlr1575 protein
√		√	√	VBIOchAnt73124_1826	Oant_1728	S-adenosylmethionine:diacylglycerol 3-amino-3-carboxypropyl transferase
√				VBIOchAnt73124_1827	Oant_1756	hypothetical protein
√		√	√	VBIOchAnt73124_1857		conserved hypothetical protein
√		√	√	VBIOchAnt73124_1858	Oant_1757	hypothetical protein
√		√	√	VBIOchAnt73124_1900	Oant_1799	Acetyltransferase
√		√		VBIOchAnt73124_1903	Oant_1802	FOG: GGDEF domain
√		√	√	VBIOchAnt73124_1904	Oant_1803	Nucleotidyltransferase
√	√		√	VBIOchAnt73124_1936	Oant_1835	conserved hypothetical protein
√				VBIOchAnt73124_1937		hypothetical protein
√		√		VBIOchAnt73124_1938	Oant_1836	Phosphonate monoester hydrolase
√		√	√	VBIOchAnt73124_1939	Oant_1837	cell processes; transport of small molecules; amino acids, amines, peptides
√			√	VBIOchAnt73124_1942	Oant_1840	cell processes; transport of small molecules; amino acids, amines, peptides
√		√	√	VBIOchAnt73124_1943	Oant_1841	cell processes; transport of small molecules; amino acids, amines, peptides
√				VBIOchAnt73124_1969	Oant_1869	glycosyl transferase family 39
√		√		VBIOchAnt73124_1983	Oant_1883	probable major facilitator superfamily (MFS) transporter
√			√	VBIOchAnt73124_1984	Oant_1884	Transcriptional regulator, TetR family
√			√	VBIOchAnt73124_2001	Oant_1901	iron-chelator utilization protein
√		√	√	VBIOchAnt73124_2002	Oant_1902	Dipeptide transport ATP-binding protein DppF (TC 3.A.1.5.2)
√	√	√	√	VBIOchAnt73124_2003	Oant_1903	Dipeptide transport ATP-binding protein DppD (TC 3.A.1.5.2)
√		√	√	VBIOchAnt73124_2005	Oant_1905	Dipeptide transport system permease protein DppB (TC 3.A.1.5.2)
√		√	√	VBIOchAnt73124_2006	Oant_1906	Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)
√			√	VBIOchAnt73124_2007	Oant_1907	Microsomal dipeptidase
√		√	√	VBIOchAnt73124_2019	Oant_1918	ATP-binding protein of ABC transporter
√				VBIOchAnt73124_2030	Oant_1929	hypothetical protein
√		√	√	VBIOchAnt73124_2033	Oant_1932	hypothetical protein
√		√	√	VBIOchAnt73124_2037	Oant_1935	hypothetical protein

√	√	√	VBIOchAnt73124_2093	Oant_1991	Glutathione S-transferase
√	√	√	VBIOchAnt73124_2099	Oant_1997	Oxidoreductase, aldo/keto reductase family
√	√		VBIOchAnt73124_2100	Oant_1998	hypothetical protein
√	√	√	VBIOchAnt73124_2101	Oant_1999	protein of unknown function DUF1452
√	√	√	VBIOchAnt73124_2112	Oant_2009	hypothetical protein
√		√	VBIOchAnt73124_2127	Oant_2023	hypothetical protein
√	√		VBIOchAnt73124_2163	Oant_2057	RNA signal recognition particle 4.5S RNA
√	√		VBIOchAnt73124_2179	Oant_2073	hypothetical protein
√	√		VBIOchAnt73124_2180	Oant_2074	Transcription regulator [contains diacylglycerol kinase catalytic domain]
√	√	√	VBIOchAnt73124_2206	Oant_2101	3-oxoacyl-[acyl-carrier protein] reductase
√	√	√	VBIOchAnt73124_2207	Oant_2102	Citrate synthase (si)
√	√	√	VBIOchAnt73124_2208	Oant_2103	Citrate synthase (si)
√	√	√	VBIOchAnt73124_2209	Oant_2104	Ser/Thr protein phosphatase family protein, UDP-2,3-diacylglucosamine hydrolase homolog
√	√	√	VBIOchAnt73124_2210	Oant_2105	Glycosyltransferase
√		√	VBIOchAnt73124_2233	Oant_2126	Probable transmembrane protein
√	√		VBIOchAnt73124_2234	Oant_2127	putative oxidoreductase
√	√	√	VBIOchAnt73124_2253	Oant_2145	hypothetical protein
√	√	√	VBIOchAnt73124_2294	Oant_2184	Phosphonate ABC transporter permease protein phnE1 (TC 3.A.1.9.1)
√	√	√	VBIOchAnt73124_2295	Oant_2185	Phosphonate ABC transporter permease protein phnE2 (TC 3.A.1.9.1)
√	√	√	VBIOchAnt73124_2296	Oant_2186	Phosphonate ABC transporter phosphate-binding periplasmic component (TC 3.A.1.9.1)
√	√	√	VBIOchAnt73124_2297	Oant_2187	Phosphonate ABC transporter ATP-binding protein (TC 3.A.1.9.1)
√	√	√	VBIOchAnt73124_2301	Oant_2191	Phosphonates transport ATP-binding protein PhnL
√	√	√	VBIOchAnt73124_2302	Oant_2192	Phosphonates transport ATP-binding protein PhnK
√	√	√	VBIOchAnt73124_2303	Oant_2193	PhnJ protein
√	√	√	VBIOchAnt73124_2304	Oant_2194	PhnI protein
√	√	√	VBIOchAnt73124_2305	Oant_2195	PhnH protein
√	√	√	VBIOchAnt73124_2306	Oant_2196	PhnG protein
√	√	√	VBIOchAnt73124_2328	Oant_2217	ATP-binding protein of ABC transporter
√			VBIOchAnt73124_2329	Oant_2218	Lipoate-protein ligase A
√	√		VBIOchAnt73124_2332	Oant_2219	hypothetical protein
√			VBIOchAnt73124_2335	Oant_2221	ATP/GTP-binding site motif A (P-loop) :Porin, alpha proteobacteria type
√		√	VBIOchAnt73124_2338	Oant_2223	hypothetical protein
√	√	√	VBIOchAnt73124_2347	Oant_2232	protein of unknown function DUF6 transmembrane
√	√	√	VBIOchAnt73124_2382	Oant_2264	Membrane proteins related to metalloendopeptidases
√			VBIOchAnt73124_2459	Oant_2329	Site-specific recombinase, phage integrase family
√			VBIOchAnt73124_2518	Oant_2387	hypothetical protein
√	√	√	VBIOchAnt73124_2519	Oant_2388	Transcriptional regulator, GntR family domain / Aspartate aminotransferase
√	√	√	VBIOchAnt73124_2530	Oant_2400	Transcriptional regulator, HxlR family

√	√	√	VBIOchAnt73124_2531	Oant_2401	Rrf2-linked NADH-flavin reductase
√	√	√	VBIOchAnt73124_2553	Oant_2421	Gfa-like protein
√			VBIOchAnt73124_2557	Oant_2425	Mll0159 protein
√	√	√	VBIOchAnt73124_2560	Oant_2426	Transcriptional regulator, TetR family
√	√		VBIOchAnt73124_2561	Oant_2427	Probable glutathione S-transferase-related transmembrane protein
√			VBIOchAnt73124_2566	Oant_2431	Proteinase inhibitor I11, ecotin precursor
√	√		VBIOchAnt73124_2570	Oant_2435	hypothetical protein
√			VBIOchAnt73124_2572	Oant_2437	D-beta-hydroxybutyrate permease
√	√		VBIOchAnt73124_2582	Oant_2448	lipoprotein, putative
√	√		VBIOchAnt73124_2583	Oant_2449	hypothetical protein
√			VBIOchAnt73124_2584	Oant_2450	Prolidase
√	√	√	VBIOchAnt73124_2585	Oant_2452	Lipopolysaccharide biosynthesis protein-like protein
√		√	VBIOchAnt73124_2609	Oant_2477	Ribokinase
√		√	VBIOchAnt73124_2612	Oant_2481	SN-glycerol-3-phosphate transport ATP-binding protein UgpC (TC 3.A.1.1.3)
√		√	VBIOchAnt73124_2613	Oant_2482	Argininosuccinate lyase
√	√	√	VBIOchAnt73124_2614	Oant_2483	N-Acetyl-D-glucosamine ABC transport system, permease protein 2
√		√	VBIOchAnt73124_2615	Oant_2484	N-Acetyl-D-glucosamine ABC transport system, permease protein 1
√		√	VBIOchAnt73124_2616	Oant_2485	hypothetical protein
√		√	VBIOchAnt73124_2620	Oant_2487	hypothetical protein
√			VBIOchAnt73124_2621	Oant_2488	hypothetical protein
√	√	√	VBIOchAnt73124_2622	Oant_2489	Flp pilus assembly protein, pilin Flp
√	√	√	VBIOchAnt73124_2624	Oant_2491	protein
√	√	√	VBIOchAnt73124_2626	Oant_2493	Succinyl-CoA synthetase, alpha subunit-related enzymes
√			VBIOchAnt73124_2630	Oant_2497	Outer membrane lipoprotein e (P4) / NMN 5'-nucleotidase, extracellular
√			VBIOchAnt73124_2631	Oant_2498	hypothetical protein
√	√	√	VBIOchAnt73124_2634	Oant_2501	hypothetical protein
√	√	√	VBIOchAnt73124_2637	Oant_2504	hypothetical protein
√	√	√	VBIOchAnt73124_2640	Oant_2507	Glycosyltransferase
√			VBIOchAnt73124_2642		hypothetical protein
√	√	√	VBIOchAnt73124_2644	Oant_2510	hypothetical protein
√	√	√	VBIOchAnt73124_2645	Oant_2511	Protein of unknown function UPF0060
√	√		VBIOchAnt73124_2646	Oant_2512	3-oxoacyl-[acyl-carrier protein] reductase
√	√	√	VBIOchAnt73124_2647	Oant_2513	Metallo-beta-lactamase family protein
√			VBIOchAnt73124_2648	Oant_2514	ATP synthase A chain
√			VBIOchAnt73124_2667	Oant_2533	CopG protein
√	√	√	VBIOchAnt73124_2682	Oant_2547	DNA-binding protein
√	√	√	VBIOchAnt73124_2683	Oant_2548	Glyoxalase family protein
√	√		VBIOchAnt73124_2684	Oant_2549	putative transcriptional regulator
√	√		VBIOchAnt73124_2685	Oant_2550	conserved hypothetical protein

√	√		VBIOchAnt73124_2686	Oant_2551	Transcriptional regulator, ArsR family
√	√		VBIOchAnt73124_2687	Oant_2552	GCN5-related N-acetyltransferase
√	√		VBIOchAnt73124_2697	Oant_2560	hypothetical protein
√			VBIOchAnt73124_2698	Oant_2561	extracellular solute-binding protein, family 3
√	√	√	VBIOchAnt73124_2707	Oant_2570	hypothetical protein
√		√	VBIOchAnt73124_2724	Oant_2585	Beta-lactamase
√	√	√	VBIOchAnt73124_2725	Oant_2586	HTH-type transcriptional activator ampR
√			VBIOchAnt73124_2738	Oant_2597	hypothetical protein
√	√	√	VBIOchAnt73124_2752	Oant_2610	Gfa-like protein
√		√	VBIOchAnt73124_2760	Oant_2618	Transcriptional regulator, AraC family
√		√	VBIOchAnt73124_2761	Oant_2619	probable hydrolase
√	√		VBIOchAnt73124_2762	Oant_2620	uncharacterized conserved protein, YciI family
√			VBIOchAnt73124_2789		hypothetical protein
√			VBIOchAnt73124_2795		hypothetical protein
√	√	√	VBIOchAnt73124_2839	Oant_2693	Long-chain-fatty-acid--CoA ligase
√	√	√	VBIOchAnt73124_2841	Oant_2695	cytochrome c556
√	√	√	VBIOchAnt73124_2842	Oant_2696	Putative diheme cytochrome c-553
√	√		VBIOchAnt73124_2862	Oant_2713	Alpha,alpha-trehalose-phosphate synthase [UDP-forming]
√	√		VBIOchAnt73124_2863	Oant_2714	Trehalose-6-phosphate phosphatase
√			VBIOchAnt73124_2872	Oant_2724	transposase IS3/IS911 family protein
√			VBIOchAnt73124_2900	Oant_2761	Inosine-uridine preferring nucleoside hydrolase
√	√	√	VBIOchAnt73124_2907	Oant_2768	hypothetical protein
√			VBIOchAnt73124_2908	Oant_2769	Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OppA (TC 3.A.1.5.1)
√			VBIOchAnt73124_2909	Oant_2770	binding-protein-dependent transport systems inner membrane component
√			VBIOchAnt73124_2910	Oant_2771	binding-protein-dependent transport systems inner membrane component
√			VBIOchAnt73124_2911	Oant_2772	ABC transporter, ATP-binding protein
√			VBIOchAnt73124_2912	Oant_2773	ABC transporter related
√		√	VBIOchAnt73124_2916	Oant_2777	hypothetical protein
√		√	VBIOchAnt73124_2917	Oant_2778	Ferric hydroxamate ABC transporter (TC 3.A.1.14.3), permease component FhuB
√	√		VBIOchAnt73124_2918	Oant_2779	transcriptional regulator, LysR family
√			VBIOchAnt73124_2919	Oant_2780	hypothetical protein
√	√	√	VBIOchAnt73124_2921	Oant_2781	ABC transporter, substrate binding protein
√	√	√	VBIOchAnt73124_2922	Oant_2782	ABC transporter, permease protein
√	√	√	VBIOchAnt73124_2923	Oant_2783	Dipeptide transport system permease protein DppC (TC 3.A.1.5.2)
√	√	√	VBIOchAnt73124_2924	Oant_2784	Alpha-glucoside transport ATP-binding protein AglK
√	√		VBIOchAnt73124_2925	Oant_2785	Mll5128 protein
√	√	√	VBIOchAnt73124_2926	Oant_2786	Alkaline phosphatase
√		√	VBIOchAnt73124_2942	Oant_2800	Lysine-arginine-ornithine-binding periplasmic protein precursor (TC 3.A.1.3.1)

√				VBIOchAnt73124_2949	Oant_2807	Ribose ABC transport system, periplasmic ribose-binding protein RbsB (TC 3.A.1.2.1)
√				VBIOchAnt73124_2950	Oant_2808	Ribose ABC transport system, ATP-binding protein RbsA (TC 3.A.1.2.1)
√				VBIOchAnt73124_2951	Oant_2809	Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1)
√			√	VBIOchAnt73124_2960	Oant_2818	Oxidoreductase-related protein
√				VBIOchAnt73124_2967	Oant_2825	ABC-type Fe3+-siderophore transport system, permease 2 component
√			√	VBIOchAnt73124_2968	Oant_2826	ABC-type Fe3+-siderophore transport system, permease component
√			√	VBIOchAnt73124_2969	Oant_2827	putative lipoprotein
√				VBIOchAnt73124_2973		Ferrichrome-iron receptor
√		√		VBIOchAnt73124_2974	Oant_2830	Transcriptional regulator, AraC family
√		√		VBIOchAnt73124_2975	Oant_2831	hypothetical protein
√				VBIOchAnt73124_2976	Oant_2832	Ferric iron ABC transporter, permease protein
√				VBIOchAnt73124_2977	Oant_2833	Ferric iron ABC transporter, iron-binding protein
√				VBIOchAnt73124_2978	Oant_2834	ABC transporter related
√				VBIOchAnt73124_2979	Oant_2835	Lipoprotein Blc
√		√	√	VBIOchAnt73124_2980	Oant_2836	Aldehyde dehydrogenase
√		√	√	VBIOchAnt73124_2981	Oant_2837	Deoxyribose-phosphate aldolase
√			√	VBIOchAnt73124_2983	Oant_2839	Putative uncharacterized protein STY3991
√			√	VBIOchAnt73124_2984	Oant_2840	Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1)
√			√	VBIOchAnt73124_2985	Oant_2841	Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1)
√			√	VBIOchAnt73124_2986	Oant_2842	Ribose ABC transport system, ATP-binding protein RbsA (TC 3.A.1.2.1)
√			√	VBIOchAnt73124_2987	Oant_2843	Ribose ABC transport system, periplasmic ribose-binding protein RbsB (TC 3.A.1.2.1)
√		√	√	VBIOchAnt73124_2988	Oant_2844	Deoxyribose operon repressor, DeoR family
√		√	√	VBIOchAnt73124_2989	Oant_2845	Transcriptional regulator, TetR family
√		√	√	VBIOchAnt73124_2990	Oant_2846	ABC transporter, permease protein
√				VBIOchAnt73124_2991	Oant_2847	Transcriptional regulator, LysR family
√				VBIOchAnt73124_2992	Oant_2848	Amino acid ABC transporter, periplasmic amino acid-binding protein
√				VBIOchAnt73124_2993	Oant_2849	Putative transport system permease protein
√				VBIOchAnt73124_2995	Oant_2851	Glutamate transport ATP-binding protein
√		√		VBIOchAnt73124_2997	Oant_2853	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
√		√		VBIOchAnt73124_2998	Oant_2854	hypothetical protein
√		√	√	VBIOchAnt73124_2999	Oant_2855	GCN5-related N-acetyltransferase
√		√		VBIOchAnt73124_3000	Oant_2856	Acetylpolyamine aminohydrolase
√				VBIOchAnt73124_3002	Oant_2857	thioesterase superfamily protein
√				VBIOchAnt73124_3005	Oant_2860	Selenide,water dikinase
√				VBIOchAnt73124_3006	Oant_2861	transglutaminase domain protein
√				VBIOchAnt73124_3008	Oant_2863	Formate dehydrogenase O alpha subunit @ selenocysteine-containing
√				VBIOchAnt73124_3009	Oant_2864	Formate dehydrogenase O beta subunit
√				VBIOchAnt73124_3010	Oant_2865	Formate dehydrogenase O gamma subunit
√	√			VBIOchAnt73124_3011	Oant_2866	formate dehydrogenase formation protein FdhE

√			VBIOchAnt73124_3012	Oant_2867	L-seryl-tRNA(Sec) selenium transferase
√	√		VBIOchAnt73124_3013	Oant_2868	hypothetical protein
√			VBIOchAnt73124_3014	Oant_2869	Selenocysteine-specific translation elongation factor
√			VBIOchAnt73124_3018	Oant_2873	response regulator receiver protein
√			VBIOchAnt73124_3019	Oant_2874	two-component sensor histidine kinase
√			VBIOchAnt73124_3020	Oant_2875	hypothetical protein
√	√	√	VBIOchAnt73124_3021	Oant_2876	putative autotransporter protein
√			VBIOchAnt73124_3022		hypothetical protein
√	√	√	VBIOchAnt73124_3025	Oant_2879	Esterase/lipase
√		√	VBIOchAnt73124_3026	Oant_2880	Transcriptional regulator, LysR family
√			VBIOchAnt73124_3027	Oant_2881	hypothetical protein
√			VBIOchAnt73124_3028	Oant_2882	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase
√			VBIOchAnt73124_3029	Oant_2883	Putative lipase in cluster with Phosphatidate cytidylyltransferase
√			VBIOchAnt73124_3030	Oant_2884	Ser/Thr and Tyr protein phosphatase (dual specificity)
√			VBIOchAnt73124_3031	Oant_2885	hypothetical protein
√			VBIOchAnt73124_3032	Oant_2886	1-acyl-sn-glycerol-3-phosphate acyltransferase
√			VBIOchAnt73124_3033	Oant_2887	Phosphatidate cytidylyltransferase
√	√	√	VBIOchAnt73124_3034	Oant_2888	hypothetical protein
√			VBIOchAnt73124_3049	Oant_2902	Transketolase
√		√	VBIOchAnt73124_3065	Oant_2917	Erythritol kinase EryA
√		√	VBIOchAnt73124_3066	Oant_2918	Glycerol-3-phosphate dehydrogenase
√			VBIOchAnt73124_3068	Oant_2920	L-proline glycine betaine binding ABC transporter protein ProX (TC 3.A.1.12.1)
√	√		VBIOchAnt73124_3069	Oant_2921	transcription regulator
√	√	√	VBIOchAnt73124_3070	Oant_2922	hypothetical protein
√	√	√	VBIOchAnt73124_3071	Oant_2923	3-hydroxyacyl-CoA dehydrogenase
√	√	√	VBIOchAnt73124_3076	Oant_2928	Putative drug efflux protein
√	√	√	VBIOchAnt73124_3078	Oant_2930	Transcriptional regulator, LysR family
√			VBIOchAnt73124_3082	Oant_2934	putative methylisocitrate lyase
√			VBIOchAnt73124_3085	Oant_2937	Transcriptional regulator, GntR family
√		√	VBIOchAnt73124_3086	Oant_2938	Cobalt-zinc-cadmium resistance protein
√			VBIOchAnt73124_3094	Oant_2946	hypothetical protein
√		√	VBIOchAnt73124_3095	Oant_2947	Alcohol dehydrogenase
√		√	VBIOchAnt73124_3097	Oant_2949	hypothetical protein
√	√	√	VBIOchAnt73124_3098	Oant_2950	Redox-sensitive transcriptional activator SoxR
√			VBIOchAnt73124_3099	Oant_2951	short-chain dehydrogenase/reductase SDR
√			VBIOchAnt73124_3106	Oant_2956	Deblocking aminopeptidase @ Cyanophycinase 2
√	√		VBIOchAnt73124_3107	Oant_2957	Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)
√			VBIOchAnt73124_3109	Oant_2959	Probable oligopeptide ABC transporter, ATP-binding protein

√				VBIOchAnt73124_3110	Oant_2960	Dipeptide transport ATP-binding protein DppF (TC 3.A.1.5.2)
√				VBIOchAnt73124_3111	Oant_2961	Transcriptional regulator, GntR family
√		√		VBIOchAnt73124_3112	Oant_2962	Asparagine synthetase [glutamine-hydrolyzing]
√		√		VBIOchAnt73124_3113	Oant_2963	Cyanophycin synthase
√			√	VBIOchAnt73124_3125	Oant_2974	Transcriptional regulator, LysR family
√				VBIOchAnt73124_3127	Oant_2976	5-FCL-like protein
√				VBIOchAnt73124_3128	Oant_2977	putative ABC transporter, permease protein
√				VBIOchAnt73124_3129	Oant_2978	Pyrimidine ABC transporter, ATP-binding protein
√				VBIOchAnt73124_3130	Oant_2979	Hydroxymethylpyrimidine ABC transporter, substrate-binding component
√				VBIOchAnt73124_3131	Oant_2980	5-FCL-like protein
√				VBIOchAnt73124_3132	Oant_2981	transcriptional regulator, RpiR family
√			√	VBIOchAnt73124_3133	Oant_2982	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases
√		√	√	VBIOchAnt73124_3136	Oant_2985	Binding-protein-dependent transport systems inner membrane component precursor
√		√	√	VBIOchAnt73124_3138	Oant_2987	Metallo-dependent hydrolases, subgroup B
√		√	√	VBIOchAnt73124_3139	Oant_2988	Putative translation initiation inhibitor, yjgF family
√		√	√	VBIOchAnt73124_3141	Oant_2990	L-seryl-tRNA(Sec) selenium transferase-related protein
√		√	√	VBIOchAnt73124_3142	Oant_2991	Putative glutathione transporter, ATP-binding component
√			√	VBIOchAnt73124_3144	Oant_2993	Integral membrane protein TerC
√				VBIOchAnt73124_3148	Oant_2997	hypothetical protein
√		√	√	VBIOchAnt73124_3157	Oant_3006	serine/threonine protein phosphatase
√			√	VBIOchAnt73124_3159	Oant_3008	hypothetical protein
√		√		VBIOchAnt73124_3175	Oant_3024	NADPH-dependent FMN reductase
√		√		VBIOchAnt73124_3176	Oant_3025	Transcriptional regulator, HxlR family
√		√	√	VBIOchAnt73124_3179	Oant_3028	hypothetical protein
√		√	√	VBIOchAnt73124_3182	Oant_3031	hypothetical protein
√		√		VBIOchAnt73124_3210	Oant_3059	hypothetical protein
√		√	√	VBIOchAnt73124_3211	Oant_3060	putative GFO/IDH/MocA family oxidoreductase
√		√		VBIOchAnt73124_3214	Oant_3063	putative lipoprotein
√		√		VBIOchAnt73124_3216	Oant_3065	Putative oxidoreductase
√		√		VBIOchAnt73124_3218	Oant_3067	similar to ribulose-1,5-bisphosphate carboxylase, Type III
√		√		VBIOchAnt73124_3219	Oant_3068	Transcriptional regulator, GntR family
√		√		VBIOchAnt73124_3231	Oant_3080	Cyclopropane-fatty-acyl-phospholipid synthase
√				VBIOchAnt73124_3232	Oant_3081	hypothetical protein
√			√	VBIOchAnt73124_3234	Oant_3084	Isoaspartyl aminopeptidase @ Asp-X dipeptidase
√				VBIOchAnt73124_3235	Oant_3085	Proline iminopeptidase
√			√	VBIOchAnt73124_3236	Oant_3086	prolyl oligopeptidase family protein
√		√		VBIOchAnt73124_3237	Oant_3087	Catalyzes the cleavage of p-aminobenzoyl-glutamate to p-aminobenzoate and glutamate, subunit B
√	√			VBIOchAnt73124_3238	Oant_3088	Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)

√			√	VBIOchAnt73124_3239	Oant_3089	Dipeptide transport system permease protein DppB (TC 3.A.1.5.2)
√	√			VBIOchAnt73124_3242	Oant_3092	Oligopeptide transport ATP-binding protein OppF (TC 3.A.1.5.1)
√			√	VBIOchAnt73124_3243	Oant_3093	Beta-lactamase class C and other penicillin binding proteins
√		√	√	VBIOchAnt73124_3244	Oant_3094	hypothetical protein
√				VBIOchAnt73124_3245	Oant_3095	Transcriptional regulator
√				VBIOchAnt73124_3246	Oant_3096	Transcriptional regulator associated with Tricarboxylic transport
√				VBIOchAnt73124_3247	Oant_3097	4-hydroxythreonine-4-phosphate dehydrogenase
√				VBIOchAnt73124_3248	Oant_3098	Tricarboxylate transport protein TctC
√				VBIOchAnt73124_3249	Oant_3099	Tricarboxylate transport protein TctB
√				VBIOchAnt73124_3250	Oant_3100	Tricarboxylate transport membrane protein TctA
√				VBIOchAnt73124_3251	Oant_3101	hypothetical protein
√		√	√	VBIOchAnt73124_3252	Oant_3102	Dihydroxyacetone kinase, ATP-dependent
√				VBIOchAnt73124_3253	Oant_3103	hypothetical protein
√				VBIOchAnt73124_3262	Oant_3112	periplasmic sensor signal transduction histidine kinase
√				VBIOchAnt73124_3263	Oant_3113	C4-dicarboxylate transport transcriptional regulatory protein
√				VBIOchAnt73124_3271	Oant_3121	hypothetical protein
√		√		VBIOchAnt73124_3272	Oant_3122	Sialic acid utilization regulator, RpiR family
√		√		VBIOchAnt73124_3275	Oant_3125	N-acetylmuramic acid 6-phosphate etherase
√		√		VBIOchAnt73124_3276	Oant_3126	Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)
√		√	√	VBIOchAnt73124_3278	Oant_3128	Dipeptide transport system permease protein DppC (TC 3.A.1.5.2)
√		√		VBIOchAnt73124_3279	Oant_3129	Oligopeptide transport ATP-binding protein OppD (TC 3.A.1.5.1)
√		√		VBIOchAnt73124_3280	Oant_3130	Beta-lactamase class C and other penicillin binding proteins
√			√	VBIOchAnt73124_3282	Oant_3132	hypothetical protein
√			√	VBIOchAnt73124_3283	Oant_3133	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)
√			√	VBIOchAnt73124_3284	Oant_3134	Methyltransferase, FkbM family
√		√	√	VBIOchAnt73124_3293	Oant_3144	conserved hypothetical protein
√		√	√	VBIOchAnt73124_3312	Oant_3160	Mercuric ion reductase
√			√	VBIOchAnt73124_3352	Oant_3197	Arsenic resistance protein ArsH
√			√	VBIOchAnt73124_3353	Oant_3198	Arsenical-resistance protein ACR3
√		√	√	VBIOchAnt73124_3356	Oant_3201	Transcriptional regulator, ArsR family
√		√	√	VBIOchAnt73124_3376	Oant_3221	Conjugative transfer protein TrbI
√			√	VBIOchAnt73124_3417	Oant_3259	AmpG permease
√				VBIOchAnt73124_3423	Oant_3265	cell processes; transport of small molecules; amino acids, amines, peptides
√				VBIOchAnt73124_3424	Oant_3266	Putative translation initiation inhibitor, yjgF family
√		√	√	VBIOchAnt73124_3425	Oant_3267	drug resistance transporter, EmrB/QacA family
√			√	VBIOchAnt73124_3453	Oant_3298	hypothetical protein
√		√		VBIOchAnt73124_3461	Oant_3306	Uncharacterized ABC-type transport system, permease component
√		√		VBIOchAnt73124_3462	Oant_3307	Sugar ABC transporter, permease protein

√	√		VBIOchAnt73124_3463	Oant_3308	Sugar ABC transporter, ATP-binding protein
√	√		VBIOchAnt73124_3464	Oant_3309	hypothetical protein
√	√		VBIOchAnt73124_3465	Oant_3310	Bmp family protein
√	√		VBIOchAnt73124_3466	Oant_3311	Cytosine deaminase
√		√	VBIOchAnt73124_3468	Oant_3313	FOG: PAS/PAC domain
√			VBIOchAnt73124_3469	Oant_3314	N-acetyl-L,L-diaminopimelate deacetylase
√			VBIOchAnt73124_3470	Oant_3315	L-2-amino-thiazoline-4-carboxylic acid hydrolase
√	√		VBIOchAnt73124_3471	Oant_3316	FAD dependent oxidoreductase
√		√	VBIOchAnt73124_3472	Oant_3317	Putative glutathione transporter, ATP-binding component
√		√	VBIOchAnt73124_3473	Oant_3318	Dipeptide transport system permease protein DppC (TC 3.A.1.5.2)
√			VBIOchAnt73124_3474	Oant_3319	Oligopeptide transport system permease protein OppB (TC 3.A.1.5.1)
√			VBIOchAnt73124_3475	Oant_3320	InterPro IPR000914 COGs COG0747
√		√	VBIOchAnt73124_3476	Oant_3321	putative short-chain alcohol dehydrogenase
√	√	√	VBIOchAnt73124_3477	Oant_3322	Bll2707 protein
√	√	√	VBIOchAnt73124_3478	Oant_3323	Choline-sulfatase
√		√	VBIOchAnt73124_3479	Oant_3324	L-proline glycine betaine binding ABC transporter protein ProX (TC 3.A.1.12.1)
√		√	VBIOchAnt73124_3480	Oant_3325	Transcriptional regulator, LysR family
√		√	VBIOchAnt73124_3481	Oant_3326	hypothetical protein
√	√	√	VBIOchAnt73124_3484	Oant_3329	Glyoxalase family protein
√	√	√	VBIOchAnt73124_3485	Oant_3330	Carboxylesterase
√	√	√	VBIOchAnt73124_3489	Oant_3334	ABC transporter, nucleotide binding/ATPase protein
√			VBIOchAnt73124_3490	Oant_3335	transcriptional regulator, GntR family
√		√	VBIOchAnt73124_3491	Oant_3336	Dihydrodipicolinate synthase
√			VBIOchAnt73124_3496	Oant_3341	Gluconate dehydratase
√	√	√	VBIOchAnt73124_3497	Oant_3342	conserved hypothetical protein
√	√	√	VBIOchAnt73124_3498	Oant_3343	Dehydratase, IlvD/Edd family
√	√	√	VBIOchAnt73124_3499	Oant_3344	Demethylmenaquinone methyltransferase
√	√	√	VBIOchAnt73124_3500	Oant_3345	Ribose ABC transporter, periplasmic ribose-binding protein RbsB (TC 3.A.1.2.1)
√		√	VBIOchAnt73124_3502	Oant_3347	Putative ribose/galactose/methyl galactoside import ATP-binding protein 1
√	√	√	VBIOchAnt73124_3503	Oant_3348	Hemolysins and related proteins containing CBS domains
√			VBIOchAnt73124_3505	Oant_3349	diguanylate cyclase/phosphodiesterase
√			VBIOchAnt73124_3506	Oant_3350	hypothetical protein
√	√		VBIOchAnt73124_3507	Oant_3351	hypothetical protein
√	√	√	VBIOchAnt73124_3508	Oant_3352	hypothetical protein
√	√	√	VBIOchAnt73124_3514	Oant_3358	D-serine dehydratase transcriptional activator
√			VBIOchAnt73124_3515	Oant_3359	Permease of the drug/metabolite transporter (DMT) superfamily
√	√	√	VBIOchAnt73124_3516	Oant_3360	COG1309: Transcriptional regulator
√	√		VBIOchAnt73124_3518	Oant_3362	GGDEF:GAF
√	√	√	VBIOchAnt73124_3553	Oant_3396	Orf21; putative lipoprotein

√		√	VBIOchAnt73124_3554	Oant_3397	RNA polymerase sigma-54 factor RpoN
√	√	√	VBIOchAnt73124_3555	Oant_3398	Transmembrane regulator protein PrtR
√		√	VBIOchAnt73124_3559	Oant_3401	transcriptional regulator, FadR/GntR family
√			VBIOchAnt73124_3560	Oant_3402	hypothetical protein
√		√	VBIOchAnt73124_3563	Oant_3405	UDP-glucose 4-epimerase
√		√	VBIOchAnt73124_3579	Oant_3421	Tricarboxylate transport membrane protein TctA
√		√	VBIOchAnt73124_3580	Oant_3422	Tricarboxylate transport protein TctB
√		√	VBIOchAnt73124_3581	Oant_3423	Tricarboxylate transport protein TctC
√	√	√	VBIOchAnt73124_3584	Oant_3426	Probable transmembrane protein
√			VBIOchAnt73124_3586	Oant_3428	hypothetical protein
√			VBIOchAnt73124_3587	Oant_3429	STRUCTURAL ELEMENTS; Cell Exterior; surface polysaccharides/antigens
√			VBIOchAnt73124_3588	Oant_3430	STRUCTURAL ELEMENTS; Cell Exterior; surface polysaccharides/antigens
√			VBIOchAnt73124_3589	Oant_3431	STRUCTURAL ELEMENTS; Cell Exterior; surface polysaccharides/antigens
√			VBIOchAnt73124_3590	Oant_3432	STRUCTURAL ELEMENTS; Cell Exterior; surface polysaccharides/antigens
√			VBIOchAnt73124_3591	Oant_3433	STRUCTURAL ELEMENTS; Cell Exterior; surface polysaccharides/antigens
√	√	√	VBIOchAnt73124_3592	Oant_3434	STRUCTURAL ELEMENTS; Cell Exterior; surface polysaccharides/antigens
√	√	√	VBIOchAnt73124_3595	Oant_3436	STRUCTURAL ELEMENTS; Cell Exterior; surface polysaccharides/antigens
√	√	√	VBIOchAnt73124_3596	Oant_3437	STRUCTURAL ELEMENTS; Cell Exterior; surface polysaccharides/antigens
√			VBIOchAnt73124_3597	Oant_3438	transcriptional activator of exopolysaccharide II synthesis, MarR family protein
√			VBIOchAnt73124_3598	Oant_3439	Probable glycosyltransferase
√			VBIOchAnt73124_3599	Oant_3440	STRUCTURAL ELEMENTS; Cell Exterior; surface polysaccharides/antigens
√			VBIOchAnt73124_3600	Oant_3441	STRUCTURAL ELEMENTS; Cell Exterior; surface polysaccharides/antigens
√			VBIOchAnt73124_3601	Oant_3442	STRUCTURAL ELEMENTS; Cell Exterior; surface polysaccharides/antigens
√			VBIOchAnt73124_3602	Oant_3443	STRUCTURAL ELEMENTS; Cell Exterior; surface polysaccharides/antigens
√			VBIOchAnt73124_3603	Oant_3444	putative protein, probably exported to periplasma
√			VBIOchAnt73124_3604	Oant_3445	hypothetical protein
√	√	√	VBIOchAnt73124_3605	Oant_3446	Multimodular transpeptidase-transglycosylase
√	√	√	VBIOchAnt73124_3606	Oant_3447	PAN domain protein
√	√		VBIOchAnt73124_3607	Oant_3448	Enoyl-[acyl-carrier-protein] reductase [NADPH]
√	√	√	VBIOchAnt73124_3608	Oant_3449	Transcriptional regulator, LysR family
√		√	VBIOchAnt73124_3611	Oant_3452	hypothetical protein
√		√	VBIOchAnt73124_3612	Oant_3453	Threonine dehydrogenase and related Zn-dependent dehydrogenases
√	√	√	VBIOchAnt73124_3616	Oant_3457	cell processes; transport of small molecules
√	√	√	VBIOchAnt73124_3617	Oant_3458	Sugar phosphate isomerases/epimerases
√	√	√	VBIOchAnt73124_3618	Oant_3459	PUTATIVE OXIDOREDUCTASE PROTEIN
√	√	√	VBIOchAnt73124_3619	Oant_3460	transcription regulator
√	√	√	VBIOchAnt73124_3620	Oant_3461	Transcriptional regulator GabR of GABA utilization (GntR family with aminotransferase-like domain)
√		√	VBIOchAnt73124_3621	Oant_3462	amino acid ABC transporter, ATP-binding protein

√	√	√	VBIOchAnt73124_3623	Oant_3464	amino acid ABC transporter, permease protein
√	√	√	VBIOchAnt73124_3624	Oant_3465	ABC transporter, substrate binding protein [amino acid]
√	√	√	VBIOchAnt73124_3625	Oant_3466	succinate dehydrogenase subunit
√	√	√	VBIOchAnt73124_3626	Oant_3467	Xaa-Pro aminopeptidase
√	√	√	VBIOchAnt73124_3627	Oant_3468	Ornithine cyclodeaminase
√	√	√	VBIOchAnt73124_3628	Oant_3469	Threonine dehydratase, catabolic
√	√	√	VBIOchAnt73124_3629	Oant_3470	Leucine-responsive regulatory protein, regulator for leucine (or lrp) regulon and high-affinity branched-chain amino acid transport system
√	√	√	VBIOchAnt73124_3630	Oant_3471	Succinate-semialdehyde dehydrogenase [NADP+]
√	√	√	VBIOchAnt73124_3631	Oant_3472	Gamma-aminobutyrate:alpha-ketoglutarate aminotransferase
√		√	VBIOchAnt73124_3633	Oant_3474	Ferrichrome-iron receptor
√	√	√	VBIOchAnt73124_3634	Oant_3475	transcriptional regulatory protein
√		√	VBIOchAnt73124_3635	Oant_3476	Ferric hydroxamate ABC transporter (TC 3.A.1.14.3), ATP-binding protein FhuC
√	√		VBIOchAnt73124_3636	Oant_3477	Glutathione S-transferase, N-terminal domain
√	√	√	VBIOchAnt73124_3637	Oant_3478	C4-dicarboxylate transport transcriptional regulatory protein dctD
√	√	√	VBIOchAnt73124_3638	Oant_3479	Signal transduction histidine kinase regulating C4-dicarboxylate transport system
√	√	√	VBIOchAnt73124_3639	Oant_3480	C4-dicarboxylate transport protein
√	√	√	VBIOchAnt73124_3644	Oant_3485	Uncharacterized protein conserved in bacteria
√		√	VBIOchAnt73124_3646	Oant_3487	N-acetylmannosamine kinase
√	√	√	VBIOchAnt73124_3647	Oant_3488	Cytoplasmic copper homeostasis protein cutC
√	√		VBIOchAnt73124_3650	Oant_3492	Transcriptional regulator, GntR family domain / Aspartate aminotransferase
√	√		VBIOchAnt73124_3651	Oant_3493	Pyridoxamine 5'-phosphate oxidase-related, FMN-binding
√			VBIOchAnt73124_3652	Oant_3494	putative transcriptional regulator, asnC family
√			VBIOchAnt73124_3653	Oant_3496	Amino acid ABC transporter, periplasmic amino acid-binding protein
√			VBIOchAnt73124_3654	Oant_3497	Putative transport system permease protein
√			VBIOchAnt73124_3655	Oant_3498	ABC-type amino acid transport system, permease component
√		√	VBIOchAnt73124_3656	Oant_3499	Glutamate transport ATP-binding protein
√			VBIOchAnt73124_3657	Oant_3500	Arginine utilization protein RocB
√			VBIOchAnt73124_3658	Oant_3501	Phosphate acetyltransferase
√			VBIOchAnt73124_3659	Oant_3502	Sulfoacetaldehyde acetyltransferase
√			VBIOchAnt73124_3660	Oant_3503	Oxidoreductase
√	√		VBIOchAnt73124_3661	Oant_3504	Ketosteroid isomerase-related protein
√	√		VBIOchAnt73124_3665	Oant_3508	Transcriptional regulator, MocR family, putative Taurine regulator tauR
√	√	√	VBIOchAnt73124_3666	Oant_3509	hypothetical protein
√			VBIOchAnt73124_3668	Oant_3511	hypothetical protein
√	√		VBIOchAnt73124_3669	Oant_3512	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components
√	√		VBIOchAnt73124_3670	Oant_3513	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component
√	√		VBIOchAnt73124_3671	Oant_3514	ABC-type nitrate/sulfonate/bicarbonate transport system, permease component
√	√	√	VBIOchAnt73124_3672	Oant_3515	hypothetical protein

√		√	√	VBIOchAnt73124_3673	Oant_3516	two-component response regulator
√				VBIOchAnt73124_3674	Oant_3517	hypothetical protein
√			√	VBIOchAnt73124_3676	Oant_3518	Catalyzes the cleavage of p-aminobenzoyl-glutamate to p-aminobenzoate and glutamate, subunit B
√		√	√	VBIOchAnt73124_3677	Oant_3519	hypothetical protein
√		√	√	VBIOchAnt73124_3678	Oant_3520	octopine transport system permease protein
√		√	√	VBIOchAnt73124_3680	Oant_3522	Amino acid ABC transporter, periplasmic amino acid-binding protein
√		√	√	VBIOchAnt73124_3682	Oant_3524	Protein containing domains DUF404, DUF407
√		√	√	VBIOchAnt73124_3683	Oant_3525	Protein containing domains DUF403
√		√	√	VBIOchAnt73124_3684	Oant_3526	Protein containing transglutaminase-like domain, putative cysteine protease
√		√		VBIOchAnt73124_3685	Oant_3527	hypothetical protein
√				VBIOchAnt73124_3718	Oant_3559	Macrolide-specific efflux protein MacA
√	√		√	VBIOchAnt73124_3719	Oant_3560	hypothetical protein
√				VBIOchAnt73124_3721	Oant_3562	D-alanine aminotransferase
√			√	VBIOchAnt73124_3723	Oant_3563	putative transcriptional regulator
√		√	√	VBIOchAnt73124_3736	Oant_3576	probable dehydrogenase
√				VBIOchAnt73124_3737	Oant_3577	Putrescine transport ATP-binding protein PotA (TC 3.A.1.11.1)
√				VBIOchAnt73124_3738	Oant_3578	Spermidine/putrescine-binding periplasmic protein
√		√		VBIOchAnt73124_3739	Oant_3579	ABC transporter permease protein
√				VBIOchAnt73124_3740	Oant_3580	putative ABC transporter, permease
√		√		VBIOchAnt73124_3741	Oant_3581	Histidinol dehydrogenase
√		√	√	VBIOchAnt73124_3742	Oant_3582	hypothetical protein
√			√	VBIOchAnt73124_3744	Oant_3584	Rrf2 family transcriptional regulator, group III
√			√	VBIOchAnt73124_3745	Oant_3585	Thioredoxin reductase
√		√		VBIOchAnt73124_3746	Oant_3586	putative transmembrane protein
√			√	VBIOchAnt73124_3747	Oant_3587	hypothetical protein
√		√	√	VBIOchAnt73124_3748	Oant_3588	Transcriptional regulator, LysR family
√				VBIOchAnt73124_3756	Oant_3596	Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OppA (TC 3.A.1.5.1)
√				VBIOchAnt73124_3757	Oant_3597	ATP/GTP-binding site motif A (P-loop) :Porin, alpha proteobacteria type
√		√	√	VBIOchAnt73124_3763	Oant_3603	putative two-component response regulator with GGDEF sensory box protein
√			√	VBIOchAnt73124_3765	Oant_3605	Alcohol dehydrogenase
√		√	√	VBIOchAnt73124_3767	Oant_3606	Transcriptional regulator, AraC family
√				VBIOchAnt73124_3768	Oant_3607	Gluconate 2-dehydrogenase, membrane-bound, cytochrome c
√				VBIOchAnt73124_3769	Oant_3608	Gluconate 2-dehydrogenase, membrane-bound, flavoprotein
√				VBIOchAnt73124_3770	Oant_3609	Gluconate 2-dehydrogenase, membrane-bound, gamma subunit
√		√	√	VBIOchAnt73124_3772	Oant_3611	hypothetical protein
√		√		VBIOchAnt73124_3776	Oant_3615	Bll4831 protein
√	√	√	√	VBIOchAnt73124_3781	Oant_3620	Periplasmic hemin-binding protein

√	√	√		VBIOchAnt73124_3782	Oant_3621	Hemin transport protein HmuS
√		√		VBIOchAnt73124_3783	Oant_3622	hypothetical protein
√		√	√	VBIOchAnt73124_3789	Oant_3628	putative acetyltransferase
√		√	√	VBIOchAnt73124_3811	Oant_3649	hypothetical protein
√		√		VBIOchAnt73124_3812	Oant_3650	hypothetical protein
√			√	VBIOchAnt73124_3815	Oant_3653	hypothetical protein
√		√	√	VBIOchAnt73124_3816	Oant_3654	Putative Heme-regulated two-component response regulator
√			√	VBIOchAnt73124_3821	Oant_3659	putative acetyltransferase
√		√	√	VBIOchAnt73124_3823	Oant_3661	acetyl transferase
√				VBIOchAnt73124_3833	Oant_3670	hypothetical protein
√	√	√	√	VBIOchAnt73124_3862	Oant_3698	Manganese ABC transporter, periplasmic-binding protein SitA
√	√		√	VBIOchAnt73124_3863	Oant_3699	Manganese ABC transporter, ATP-binding protein SitB
√	√		√	VBIOchAnt73124_3864	Oant_3700	Manganese ABC transporter, inner membrane permease protein SitC
√	√		√	VBIOchAnt73124_3865	Oant_3701	Manganese ABC transporter, inner membrane permease protein SitD
√				VBIOchAnt73124_3866	Oant_3702	SN-glycerol-3-phosphate transport ATP-binding protein UgpC (TC 3.A.1.1.3)
√				VBIOchAnt73124_3867	Oant_3703	ABC transporter periplasmic binding protein
√			√	VBIOchAnt73124_3868	Oant_3704	hypothetical protein
√			√	VBIOchAnt73124_3869	Oant_3705	ABC transporter permease protein
√				VBIOchAnt73124_3870	Oant_3706	Transcriptional regulator, LacI family
√		√	√	VBIOchAnt73124_3872	Oant_3708	Oxidoreductase, aldo/keto reductase family
√			√	VBIOchAnt73124_3900	Oant_3736	D-alanyl-D-alanine carboxypeptidase
√			√	VBIOchAnt73124_3901	Oant_3737	Oligopeptide transport ATP-binding protein OppF (TC 3.A.1.5.1)
√			√	VBIOchAnt73124_3902	Oant_3738	Dipeptide transport ATP-binding protein DppD (TC 3.A.1.5.2)
√				VBIOchAnt73124_3903	Oant_3739	Dipeptide transport system permease protein DppC (TC 3.A.1.5.2)
√			√	VBIOchAnt73124_3904	Oant_3740	Dipeptide transport system permease protein DppB (TC 3.A.1.5.2)
√			√	VBIOchAnt73124_3905	Oant_3741	Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)
√			√	VBIOchAnt73124_3907	Oant_3743	hypothetical protein
√			√	VBIOchAnt73124_3908	Oant_3744	D-3-phosphoglycerate dehydrogenase
√				VBIOchAnt73124_3909	Oant_3745	putative ABC transporter ATP-binding protein
√		√	√	VBIOchAnt73124_3910	Oant_3746	hypothetical protein
√		√	√	VBIOchAnt73124_3911	Oant_3747	putative ABC transporter permease
√			√	VBIOchAnt73124_3912	Oant_3748	putative ABC transporter permease
√				VBIOchAnt73124_3913	Oant_3749	putative LacI-family transcriptional regulator
√		√	√	VBIOchAnt73124_3919	Oant_3755	Gluconokinase
√		√	√	VBIOchAnt73124_3920	Oant_3756	5-keto-D-gluconate 5-reductase
√		√	√	VBIOchAnt73124_3922	Oant_3758	D-2-hydroxyglutarate dehydrogenase
√			√	VBIOchAnt73124_3924	Oant_3760	2-hydroxy-3-oxopropionate reductase
√		√	√	VBIOchAnt73124_3925	Oant_3761	Gluconate dehydratase

√	√	√	VBIOchAnt73124_3926	Oant_3762	Fumarylacetoacetate hydrolase family protein
√		√	VBIOchAnt73124_3927	Oant_3763	TRAP-type transport system, small permease component, predicted N-acetylneuraminate transporter
√		√	VBIOchAnt73124_3928	Oant_3764	TRAP-type C4-dicarboxylate transport system, large permease component
√		√	VBIOchAnt73124_3929	Oant_3765	TRAP-type C4-dicarboxylate transport system, periplasmic component
√		√	VBIOchAnt73124_3930	Oant_3766	Sugar phosphate isomerases/epimerases
√	√	√	VBIOchAnt73124_3939	Oant_3776	Potassium-transporting ATPase A chain (TC 3.A.3.7.1)
√	√	√	VBIOchAnt73124_3941	Oant_3777	Potassium-transporting ATPase B chain (TC 3.A.3.7.1)
√	√	√	VBIOchAnt73124_3942	Oant_3778	Potassium-transporting ATPase C chain (TC 3.A.3.7.1)
√	√	√	VBIOchAnt73124_3943	Oant_3779	Osmosensitive K+ channel histidine kinase KdpD
√	√	√	VBIOchAnt73124_3944	Oant_3780	DNA-binding response regulator KdpE
√	√		VBIOchAnt73124_3954	Oant_3789	2-Oxobutyrate oxidase, putative
√			VBIOchAnt73124_3956	Oant_3791	Methionine ABC transporter ATP-binding protein
√			VBIOchAnt73124_3957	Oant_3792	Methionine ABC transporter substrate-binding protein
√			VBIOchAnt73124_3958	Oant_3793	Aspartate/tyrosine/aromatic aminotransferase
√	√	√	VBIOchAnt73124_3959	Oant_3794	hypothetical protein
√	√	√	VBIOchAnt73124_3960	Oant_3795	TonB-dependent receptor; Outer membrane receptor for ferrienterochelin and colicins
√		√	VBIOchAnt73124_3966	Oant_3801	hypothetical protein
√		√	VBIOchAnt73124_3967	Oant_3802	Dipeptide transport system permease protein DppC (TC 3.A.1.5.2)
√	√	√	VBIOchAnt73124_3969	Oant_3804	Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)
√		√	VBIOchAnt73124_3970	Oant_3805	Dipeptide transport ATP-binding protein DppD (TC 3.A.1.5.2)
√	√	√	VBIOchAnt73124_4016	Oant_3848	Multiple polyol-specific dehydrogenase
√	√	√	VBIOchAnt73124_4017	Oant_3849	Sorbitol dehydrogenase
√	√	√	VBIOchAnt73124_4020	Oant_3852	Various polyols ABC transporter, permease component 2
√	√	√	VBIOchAnt73124_4021	Oant_3853	Various polyols ABC transporter, permease component 1
√	√	√	VBIOchAnt73124_4022	Oant_3854	Various polyols ABC transporter, periplasmic substrate-binding protein
√			VBIOchAnt73124_4024	Oant_3856	Ferrous iron transport periplasmic protein EfeO, contains peptidase-M75 domain and (frequently) cupredoxin-like domain
√			VBIOchAnt73124_4025	Oant_3857	Ferrous iron transport peroxidase EfeB
√			VBIOchAnt73124_4026	Oant_3858	Ferrous iron transport periplasmic protein EfeO, contains peptidase-M75 domain and (frequently) cupredoxin-like domain
√	√		VBIOchAnt73124_4035	Oant_3867	hypothetical protein
√			VBIOchAnt73124_4037	Oant_3869	Creatinine amidohydrolase
√	√		VBIOchAnt73124_4038	Oant_3870	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component
√	√		VBIOchAnt73124_4039	Oant_3871	Hydroxymethylpyrimidine ABC transporter, transmembrane component
√	√		VBIOchAnt73124_4040	Oant_3872	Cytosine deaminase
√	√		VBIOchAnt73124_4041	Oant_3873	FAD/FMN-containing dehydrogenase
√	√	√	VBIOchAnt73124_4042	Oant_3874	Hydroxymethylpyrimidine ABC transporter, substrate-binding component
√			VBIOchAnt73124_4043	Oant_3875	transcriptional regulator, TetR family

√			VBIOchAnt73124_4047	Oant_3878	TRAP-type C4-dicarboxylate transport system, small permease component
√			VBIOchAnt73124_4048	Oant_3879	TRAP-type C4-dicarboxylate transport system, large permease component
√			VBIOchAnt73124_4049	Oant_3880	TRAP-type C4-dicarboxylate transport system, periplasmic component
√	√	√	VBIOchAnt73124_4051	Oant_3882	aldehyde dehydrogenase)
√			VBIOchAnt73124_4069	Oant_3900	TRAP dicarboxylate transporter, DctM subunit, unknown substrate 8
√			VBIOchAnt73124_4070	Oant_3901	TRAP dicarboxylate transporter, DctQ subunit, unknown substrate 8
√		√	VBIOchAnt73124_4071	Oant_3902	TRAP transporter solute receptor, unknown substrate 8
√	√	√	VBIOchAnt73124_4072	Oant_3903	Sorbitol dehydrogenase
√		√	VBIOchAnt73124_4075	Oant_3906	Altronate oxidoreductase
√		√	VBIOchAnt73124_4076	Oant_3907	DNA-binding response regulator, LuxR family
√		√	VBIOchAnt73124_4077	Oant_3908	Miscellaneous; Not classified regulator
√	√	√	VBIOchAnt73124_4079	Oant_3910	Ribose ABC transport system, ATP-binding protein RbsA (TC 3.A.1.2.1)
√	√	√	VBIOchAnt73124_4080	Oant_3911	Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1)
√	√	√	VBIOchAnt73124_4082	Oant_3913	Gluconolactonase
√			VBIOchAnt73124_4087		hypothetical protein
√		√	VBIOchAnt73124_4088	Oant_3917	Tricarboxylate transport protein TctC
√		√	VBIOchAnt73124_4089	Oant_3918	tricarboxylate transport protein TctB, putative
√		√	VBIOchAnt73124_4090	Oant_3919	Tricarboxylate transport membrane protein TctA
√		√	VBIOchAnt73124_4091		hypothetical protein
√		√	VBIOchAnt73124_4093	Oant_3921	MgtC/SapB transporter
√		√	VBIOchAnt73124_4094	Oant_3922	hypothetical protein
√	√		VBIOchAnt73124_4107	Oant_3935	hypothetical protein
√		√	VBIOchAnt73124_4113	Oant_3941	Cobalt-zinc-cadmium resistance protein CzcD
√		√	VBIOchAnt73124_4114	Oant_3942	protein of unknown function DUF156
√			VBIOchAnt73124_4115	Oant_3943	Prephenate and/or arogenate dehydrogenase (unknown specificity)
√	√	√	VBIOchAnt73124_4120	Oant_3948	DNA-directed RNA polymerase specialized sigma subunit, sigma24-like
√	√		VBIOchAnt73124_4121	Oant_3949	4-carboxymuconolactone decarboxylase domain/alkylhydroperoxidase AhpD family core domain protein
√	√	√	VBIOchAnt73124_4122	Oant_3950	probable gst14 glutatione S-transferase(EC:2.5.1.18)
√	√	√	VBIOchAnt73124_4123	Oant_3951	Glycine cleavage system transcriptional activator GcvA
√	√	√	VBIOchAnt73124_4125	Oant_3952	Transcriptional regulator, GntR family
√		√	VBIOchAnt73124_4127	Oant_3954	metal-dependent phosphohydrolase
√			VBIOchAnt73124_4133	Oant_3960	hypothetical protein
√			VBIOchAnt73124_4134	Oant_3961	Hydrolase (HAD superfamily)
√	√	√	VBIOchAnt73124_4151	Oant_3977	SN-glycerol-3-phosphate transport ATP-binding protein UgpC (TC 3.A.1.1.3)
√	√	√	VBIOchAnt73124_4152	Oant_3978	SN-glycerol-3-phosphate transport ATP-binding protein UgpC (TC 3.A.1.1.3)
√	√	√	VBIOchAnt73124_4153	Oant_3979	SN-glycerol-3-phosphate transport system permease protein UgpA (TC 3.A.1.1.3)
√	√	√	VBIOchAnt73124_4154	Oant_3980	SN-glycerol-3-phosphate transport system permease protein UgpE (TC 3.A.1.1.3)
√	√	√	VBIOchAnt73124_4156	Oant_3982	SN-glycerol-3-phosphate transport system permease protein UgpA (TC 3.A.1.1.3)

√	√		VBIOchAnt73124_4164	Oant_3990	Membrane fusion component of tripartite multidrug resistance system
√	√		VBIOchAnt73124_4200	Oant_4024	extracellular solute-binding protein, family 3
√	√	√	VBIOchAnt73124_4210	Oant_4035	hypothetical protein
√			VBIOchAnt73124_4213	Oant_4038	hypothetical protein
√	√	√	VBIOchAnt73124_4218	Oant_4043	mRNA 3-end processing factor
√	√	√	VBIOchAnt73124_4219	Oant_4044	ATP-dependent DNA ligase LigC
√			VBIOchAnt73124_4233	Oant_4059	Putative transcriptional regulatory protein
√			VBIOchAnt73124_4234	Oant_4060	Ribokinase
√			VBIOchAnt73124_4235	Oant_4061	Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1)
√			VBIOchAnt73124_4236	Oant_4062	Ribose ABC transport system, ATP-binding protein RbsA (TC 3.A.1.2.1)
√			VBIOchAnt73124_4237	Oant_4063	Ribose ABC transport system, periplasmic ribose-binding protein RbsB (TC 3.A.1.2.1)
√			VBIOchAnt73124_4238	Oant_4064	Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1)
√			VBIOchAnt73124_4247	Oant_4073	blr6818; hypothetical protein
√		√	VBIOchAnt73124_4255	Oant_4081	COG0028: Thiamine pyrophosphate-requiring enzymes
√		√	VBIOchAnt73124_4261	Oant_4087	Outer membrane receptor proteins, mostly Fe transport
√			VBIOchAnt73124_4262	Oant_4088	Nitrilotriacetate monooxygenase
√			VBIOchAnt73124_4272	Oant_4099	DUF1850 domain-containing protein
√			VBIOchAnt73124_4273	Oant_4100	TRAP transporter, 4TM/12TM fusion protein, unknown substrate 1
√			VBIOchAnt73124_4274	Oant_4101	TRAP transporter solute receptor, unknown substrate 1
√	√		VBIOchAnt73124_4280	Oant_4107	hypothetical protein
√	√		VBIOchAnt73124_4281	Oant_4108	hypothetical protein
√	√		VBIOchAnt73124_4282	Oant_4109	PTS system, glucitol/sorbitol-specific IIC component
√	√		VBIOchAnt73124_4283	Oant_4110	PTS system, glucitol/sorbitol-specific IIB component and second of two IIC components
√	√		VBIOchAnt73124_4284	Oant_4111	hypothetical protein
√	√		VBIOchAnt73124_4285	Oant_4112	Phosphoenolpyruvate-protein phosphotransferase of PTS system
√	√		VBIOchAnt73124_4286	Oant_4113	hypothetical protein
√	√	√	VBIOchAnt73124_4287	Oant_4114	transcriptional regulator
√	√		VBIOchAnt73124_4289	Oant_4116	Acetoin dehydrogenase E1 component beta-subunit
√	√		VBIOchAnt73124_4290	Oant_4117	Acetoin dehydrogenase E1 component alpha-subunit
√			VBIOchAnt73124_4292	Oant_4119	PTS system, galactitol-specific IIC component
√			VBIOchAnt73124_4293	Oant_4120	PTS system, galactitol-specific IIA component
√			VBIOchAnt73124_4294	Oant_4121	phosphotransferase system, lactose/cellobiose-specific IIB subunit
√			VBIOchAnt73124_4295	Oant_4122	tail-specific protease
√		√	VBIOchAnt73124_4296	Oant_4125	(Y14336) putative extracellular protein containing predicted 35aa signal peptide
√		√	VBIOchAnt73124_4297	Oant_4126	Transcriptional regulatory protein fixJ
√	√	√	VBIOchAnt73124_4298	Oant_4127	hypothetical protein
√			VBIOchAnt73124_4304	Oant_4135	Ferric hydroxamate outer membrane receptor FhuA
√		√	VBIOchAnt73124_4311	Oant_4142	putative membrane protein
√	√	√	VBIOchAnt73124_4319	Oant_4149	putative transcriptional regulator,lysR family

√			√	VBIOchAnt73124_4320	Oant_4150	Demethylmenaquinone methyltransferase
√				VBIOchAnt73124_4321	Oant_4151	Predicted amidohydrolase
√				VBIOchAnt73124_4322	Oant_4152	HpcH/HpaI aldolase
√				VBIOchAnt73124_4323	Oant_4153	binding-protein-dependent transport systems inner membrane component
√		√	√	VBIOchAnt73124_4324	Oant_4154	Spermidine Putrescine ABC transporter permease component PotB (TC 3.A.1.11.1)
√				VBIOchAnt73124_4325	Oant_4155	spermidine/putrescine ABC transporter ATPase subunit
√				VBIOchAnt73124_4326	Oant_4156	ABC opine/polyamine transporter, periplasmic binding protein
√		√	√	VBIOchAnt73124_4328	Oant_4157	Glutamine synthetase type II, eukaryotic
√				VBIOchAnt73124_4334	Oant_4162	protein tyrosine phosphatase-like
√				VBIOchAnt73124_4346	Oant_4175	Additional periplasmic component NikK of nickel ECF transporter
√				VBIOchAnt73124_4404		hypothetical protein
√		√		VBIOchAnt73124_4405	Oant_4234	Uncharacterized protein conserved in bacteria
√	√	√	√	VBIOchAnt73124_4415	Oant_4244	Acetyltransferase
√				VBIOchAnt73124_4444	Oant_4271	Low-affinity gluconate/H+ symporter GntU
√				VBIOchAnt73124_4462		hypothetical protein
√				VBIOchAnt73124_4463	Oant_4286	hypothetical protein
√		√		VBIOchAnt73124_4465		hypothetical protein
√				VBIOchAnt73124_4468	Oant_4290	conserved hypothetical protein
√		√		VBIOchAnt73124_4471	Oant_4293	hypothetical protein
√				VBIOchAnt73124_4472		hypothetical protein
√				VBIOchAnt73124_4473	Oant_4294	hypothetical protein
√		√	√	VBIOchAnt73124_4474	Oant_4295	Protein yciF
√				VBIOchAnt73124_4475	Oant_4296	hypothetical protein
√		√	√	VBIOchAnt73124_4476	Oant_4298	hypothetical protein
√		√	√	VBIOchAnt73124_4477	Oant_4299	hypothetical protein
√			√	VBIOchAnt73124_4482	Oant_4302	DNA-directed RNA polymerase specialized sigma subunit, sigma24-like
√				VBIOchAnt73124_4483	Oant_4303	hypothetical protein
√		√	√	VBIOchAnt73124_4485	Oant_4305	hypothetical protein
√		√	√	VBIOchAnt73124_4487	Oant_4307	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases
√				VBIOchAnt73124_4488		hypothetical protein
√			√	VBIOchAnt73124_4490	Oant_4311	sensor histidine kinase/response regulator
√		√	√	VBIOchAnt73124_4493	Oant_4313	DNA topoisomerase IB (poxvirus type)
√			√	VBIOchAnt73124_4494	Oant_4314	Ku domain protein
√		√	√	VBIOchAnt73124_4495	Oant_4315	ATP-dependent DNA ligase clustered with Ku protein, LigD
√		√	√	VBIOchAnt73124_4496	Oant_4316	Ku domain protein
√			√	VBIOchAnt73124_4522	Oant_4348	2-hydroxychromene-2-carboxylate isomerase
√			√	VBIOchAnt73124_4523	Oant_4349	Periplasmic binding protein
√				VBIOchAnt73124_4524	Oant_4350	Periplasmic binding protein

√			√	VBIOchAnt73124_4526	Oant_4352	Acetyltransferase
√			√	VBIOchAnt73124_4527	Oant_4353	Peptidase M20D, amidohydrolase
√			√	VBIOchAnt73124_4528	Oant_4354	Nitrilotriacetate monooxygenase component A
√				VBIOchAnt73124_4529	Oant_4355	hypothetical protein
√		√	√	VBIOchAnt73124_4531	Oant_4357	4-hydroxyphenylacetate 3-monooxygenase, reductase component
√			√	VBIOchAnt73124_4532	Oant_4358	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductases
√				VBIOchAnt73124_4533	Oant_4359	probable acetyltransferase protein
√			√	VBIOchAnt73124_4534	Oant_4360	Bacterial luciferase family protein YtmO, in cluster with L-cystine ABC transporter
√				VBIOchAnt73124_4535	Oant_4361	hypothetical protein
√				VBIOchAnt73124_4536	Oant_4362	hypothetical protein
√				VBIOchAnt73124_4537	Oant_4363	N-acylamino acid racemase
√		√		VBIOchAnt73124_4538	Oant_4364	hypothetical protein
√				VBIOchAnt73124_4539	Oant_4365	Amino acid ABC transporter, periplasmic amino acid-binding protein
√				VBIOchAnt73124_4540	Oant_4366	Transcriptional activator ampR family
√				VBIOchAnt73124_4581	Oant_4405	Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)
√				VBIOchAnt73124_4582	Oant_4406	Tripeptide aminopeptidase
√		√	√	VBIOchAnt73124_4583	Oant_4407	Gamma-glutamyltranspeptidase
√		√	√	VBIOchAnt73124_4596	Oant_4419	Hydantoin racemase
√			√	VBIOchAnt73124_4603	Oant_4426	Quinate/shikimate 5-dehydrogenase I delta
√			√	VBIOchAnt73124_4604	Oant_4427	Transcriptional regulator, TetR family
√		√	√	VBIOchAnt73124_4605	Oant_4428	4-hydroxyphenylpyruvate dioxygenase
√		√		VBIOchAnt73124_4606	Oant_4429	TRAP-type C4-dicarboxylate transport system, periplasmic component
√				VBIOchAnt73124_4607	Oant_4430	TRAP-type C4-dicarboxylate transport system, large permease component
√				VBIOchAnt73124_4608	Oant_4431	TRAP-type transport system, small permease component, predicted N-acetylneuraminate transporter
√				VBIOchAnt73124_4610	Oant_4433	Spermidine/putrescine-binding periplasmic protein
√		√		VBIOchAnt73124_4611	Oant_4434	Sarcosine oxidase beta subunit
√		√	√	VBIOchAnt73124_4612	Oant_4435	Opine oxidase subunit A
√		√		VBIOchAnt73124_4613	Oant_4436	hypothetical protein
√		√	√	VBIOchAnt73124_4614	Oant_4437	ABC-type spermidine/putrescine transport system, permease component II
√				VBIOchAnt73124_4615	Oant_4438	ABC-type spermidine/putrescine transport system, permease component I
√				VBIOchAnt73124_4616	Oant_4439	ABC-type spermidine/putrescine transport systems, ATPase components
√			√	VBIOchAnt73124_4625	Oant_4448	putative exported protein
√		√	√	VBIOchAnt73124_4626	Oant_4449	Putative phosphatase
√		√	√	VBIOchAnt73124_4627	Oant_4451	major facilitator superfamily MFS_1
√				VBIOchAnt73124_4628	Oant_4452	Adenosylcobinamide amidohydrolase
√	√		√	VBIOchAnt73124_4658	Oant_4484	3-oxoacyl-[acyl-carrier protein] reductase
√		√	√	VBIOchAnt73124_4681	Oant_4508	D-alanine aminotransferase

√		√	VBIOchAnt73124_4783	Oant_4611	Oligopeptide/dipeptide ABC transporter, ATP-binding protein
√	√		VBIOchAnt73124_4784	Oant_4612	Oligopeptide transport ATP-binding protein OppD (TC 3.A.1.5.1)
√	√	√	VBIOchAnt73124_4788	Oant_4616	Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OppA (TC 3.A.1.5.1)
√	√		VBIOchAnt73124_4789		putative LysR-family transcriptional regulator
√			VBIOchAnt73124_4806	Oant_4634	hypothetical protein
√	√		VBIOchAnt73124_4807	Oant_4635	Small heat shock protein
√	√	√	VBIOchAnt73124_4808	Oant_4636	Small heat shock protein
√	√	√	VBIOchAnt73124_4820	Oant_4742	hypothetical protein
√	√	√	VBIOchAnt73124_4824	Oant_4746	Transcriptional regulator, HxlR family
√	√	√	VBIOchAnt73124_4862	Oant_4781	signal transduction histidine kinase
√		√	VBIOchAnt73124_4876	Oant_4795	Dipeptide transport system permease protein DppB (TC 3.A.1.5.2)
√			VBIOchAnt73124_4882	Oant_4800	Catalase
√		√	VBIOchAnt73124_4908	Oant_4642	IS426 transposase
√		√	VBIOchAnt73124_4909	Oant_4643	IS426 transposase
√	√		VBIOchAnt73124_4922	Oant_4656	Lead, cadmium, zinc and mercury transporting ATPase; Copper-translocating P-type ATPase
√	√	√	VBIOchAnt73124_4952	Oant_4689	Sigma-fimbriae chaperone protein
√	√	√	VBIOchAnt73124_4953	Oant_4690	Sigma-fimbriae tip adhesin
√		√	VBIOchAnt73124_4958	Oant_4695	ABC-type amino acid transport system, permease component
√	√	√	VBIOchAnt73124_4960	Oant_4697	Aldehyde dehydrogenase
√		√	VBIOchAnt73124_4980	Oant_4719	protein of unknown function DUF1612
√	√		VBIOchAnt73124_4984	Oant_4725	putative transposase
√	√		VBIOchAnt73124_4990	Oant_4827	Putative oxidoreductase
√			VBIOchAnt73124_5000	Oant_4837	Amino acid ABC transporter, ATP-binding protein
√	√		VBIOchAnt73124_5001	Oant_4838	ABC-type amino acid transport system, permease component
√	√	√	VBIOchAnt73124_5005	Oant_4842	hypothetical protein
√			VBIOchAnt73124_5007	Oant_4845	hypothetical protein
√			VBIOchAnt73124_5008	Oant_4846	Inter-alpha-trypsin inhibitor domain protein
√			VBIOchAnt73124_5009	Oant_4847	LPXTG-site transpeptidase family protein

Table S3. Comparison of metabolic reconstruction of *Ochrobactrum anthropi* and *Brucella suis* 1330.

Category	Subcategory	Subsystem	Role	*O. anthropi* Features PubSeed locus tags	*B. suis* 1330 Features PubSeed locus tags
	Alanine, serine, and glycine	Alanine biosynthesis	Alanine racemase (EC 5.1.1.1)	fig|439375.7.peg.1514	fig|204722.5.peg.3140
			Branched-chain amino acid aminotransferase (EC 2.6.1.42)	fig|439375.7.peg.1734, fig|439375.7.peg.3936	fig|204722.5.peg.2880, fig|204722.5.peg.2881
			Cysteine desulfurase (EC 2.8.1.7)	fig|439375.7.peg.2375, fig|439375.7.peg.4198	fig|204722.5.peg.945
			Cysteine desulfurase (EC 2.8.1.7), SufS subfamily	fig|439375.7.peg.2370	fig|204722.5.peg.949
		Glycine and Serine Utilization	Aminomethyltransferase (glycine cleavage system T protein) (EC 2.1.2.10)	fig|439375.7.peg.4031	fig|204722.5.peg.2942
			Cystathionine gamma-lyase (EC 4.4.1.1)	fig|439375.7.peg.4548	■
			D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	fig|439375.7.peg.10, fig|439375.7.peg.1286, fig|439375.7.peg.1445, fig|439375.7.peg.3254, fig|439375.7.peg.3908, fig|439375.7.peg.4999	fig|204722.5.peg.6, fig|204722.5.peg.1712, fig|204722.5.peg.2671, fig|204722.5.peg.3205
			D-serine dehydratase transcriptional activator	fig|439375.7.peg.3514	■
			D-serine/D-alanine/glycine transporter	fig|439375.7.peg.4448	fig|204722.5.peg.2276
			Glycine cleavage system H protein	fig|439375.7.peg.4030	fig|204722.5.peg.2941
			Glycine dehydrogenase [decarboxylating] (glycine cleavage system P protein) (EC 1.4.4.2)	fig|439375.7.peg.4029	fig|204722.5.peg.2940
			L-serine dehydratase (EC 4.3.1.17)	fig|439375.7.peg.2120	fig|204722.5.peg.1194
			Phosphoserine aminotransferase (EC 2.6.1.52)	fig|439375.7.peg.1285	fig|204722.5.peg.1714
			Phosphoserine phosphatase (EC 3.1.3.3)	fig|439375.7.peg.1901	fig|204722.5.peg.1417
			Serine hydroxymethyltransferase (EC 2.1.2.1)	fig|439375.7.peg.2664	fig|204722.5.peg.776
			Seryl-tRNA synthetase (EC 6.1.1.11)	fig|439375.7.peg.2472	fig|204722.5.peg.896
			Threonine dehydratase, catabolic (EC 4.3.1.19)	fig|439375.7.peg.1908, fig|439375.7.peg.3628	■
		Glycine Biosynthesis	Low-specificity L-threonine aldolase (EC 4.1.2.5)	fig|439375.7.peg.4452	fig|204722.5.peg.2273
			Serine hydroxymethyltransferase (EC 2.1.2.1)	fig|439375.7.peg.2664	fig|204722.5.peg.776
		Glycine cleavage system	Aminomethyltransferase (glycine cleavage system T protein) (EC 2.1.2.10)	fig|439375.7.peg.4031	fig|204722.5.peg.2942
			Glycine cleavage system H protein	fig|439375.7.peg.4030	fig|204722.5.peg.2941
			Glycine cleavage system transcriptional activator GcvA	fig|439375.7.peg.2705, fig|439375.7.peg.4123, fig|439375.7.peg.4254	▨
			Glycine dehydrogenase [decarboxylating] (glycine cleavage system P protein) (EC 1.4.4.2)	fig|439375.7.peg.4029	fig|204722.5.peg.2940
		Serine Biosynthesis	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	fig|439375.7.peg.10, fig|439375.7.peg.1286, fig|439375.7.peg.1445, fig|439375.7.peg.3254, fig|439375.7.peg.3908, fig|439375.7.peg.4999	fig|204722.5.peg.6, fig|204722.5.peg.1712, fig|204722.5.peg.2671, fig|204722.5.peg.3205
			Phosphoserine aminotransferase (EC 2.6.1.52)	fig|439375.7.peg.1285	fig|204722.5.peg.1714

		Phosphoserine phosphatase (EC 3.1.3.3)	fig|439375.7.peg.1901	fig|204722.5.peg.1417
		Serine hydroxymethyltransferase (EC 2.1.2.1)	fig|439375.7.peg.2664	fig|204722.5.peg.776
Amino Acids and Derivatives	Creatine and Creatinine Degradation	Creatinine amidohydrolase (EC 3.5.2.10)	fig|439375.7.peg.1442, fig|439375.7.peg.4037	fig|204722.5.peg.3210
		Cytosine deaminase (EC 3.5.4.1)	fig|439375.7.peg.3466, fig|439375.7.peg.4040	
		N-methylhydantoinase A (EC 3.5.2.14)	fig|439375.7.peg.4751	
		N-methylhydantoinase B (EC 3.5.2.14)	fig|439375.7.peg.4752	
	L-2-amino-thiazoline-4-carboxylic acid-Lcysteine conversion	Beta-ureidopropionase (EC 3.5.1.6)	fig|439375.7.peg.371	fig|204722.5.peg.292
		L-2-amino-thiazoline-4-carboxylic acid hydrolase (EC 3.5.2.-)	fig|439375.7.peg.3470	
	Arginine and Ornithine Degradation	Agmatinase (EC 3.5.3.11)	fig|439375.7.peg.2632, fig|439375.7.peg.4682	fig|204722.5.peg.799
		Agmatine deiminase (EC 3.5.3.12)	fig|439375.7.peg.1096	
		Arginase (EC 3.5.3.1)	fig|439375.7.peg.1541	fig|204722.5.peg.3118
		Arginine ABC transporter, permease protein ArtQ	fig|439375.7.peg.2351	fig|204722.5.peg.967
		Arginine decarboxylase (EC 4.1.1.19)	fig|439375.7.peg.4417	fig|204722.5.peg.2320
		Arginine deiminase (EC 3.5.3.6)	fig|439375.7.peg.4912	
		Arginine utilization protein RocB	fig|439375.7.peg.3657	
		Arginine/ornithine antiporter ArcD	fig|439375.7.peg.4911	
		Carbamate kinase (EC 2.7.2.2)	fig|439375.7.peg.4914	
		Delta-1-pyrroline-5-carboxylate dehydrogenase (EC 1.5.1.12)	fig|439375.7.peg.4014	fig|204722.5.peg.2937
		Histidine ABC transporter, ATP-binding protein HisP (TC 3.A.1.3.1)	fig|439375.7.peg.3679	fig|204722.5.peg.2937
		Lysine-arginine-ornithine-binding periplasmic protein precursor (TC 3.A.1.3.1)	fig|439375.7.peg.2942	
		NADP-specific glutamate dehydrogenase (EC 1.4.1.4)	fig|439375.7.peg.322, fig|439375.7.peg.4768	fig|204722.5.peg.234
		Ornithine aminotransferase (EC 2.6.1.13)	fig|439375.7.peg.3118	fig|204722.5.peg.3067
		Ornithine carbamoyltransferase (EC 2.1.3.3)	fig|439375.7.peg.421, fig|439375.7.peg.4913	fig|204722.5.peg.315
		Ornithine cyclodeaminase (EC 4.3.1.12)	fig|439375.7.peg.1542, fig|439375.7.peg.3627, fig|439375.7.peg.4765, fig|439375.7.peg.4789	fig|204722.5.peg.3117
		Ornithine decarboxylase (EC 4.1.1.17)	fig|439375.7.peg.4417	fig|204722.5.peg.2320
		Succinylornithine transaminase (EC 2.6.1.81)	fig|439375.7.peg.3118	fig|204722.5.peg.3067
	Arginine Biosynthesis extended	Acetylglutamate kinase (EC 2.7.2.8)	fig|439375.7.peg.1424, fig|439375.7.peg.3451	fig|204722.5.peg.3102, fig|204722.5.peg.3250
		Acetylornithine aminotransferase (EC 2.6.1.11)	fig|439375.7.peg.420, fig|439375.7.peg.3118, fig|439375.7.peg.4667	fig|204722.5.peg.314, fig|204722.5.peg.3067
		Acetylornithine deacetylase (EC 3.5.1.16)	fig|439375.7.peg.4681	
		Argininosuccinate lyase (EC 4.3.2.1)	fig|439375.7.peg.1047, fig|439375.7.peg.2613	fig|204722.5.peg.2018
		Argininosuccinate synthase (EC 6.3.4.5)	fig|439375.7.peg.88	fig|204722.5.peg.77
		Glutamate N-acetyltransferase (EC 2.3.1.35)	fig|439375.7.peg.1073	fig|204722.5.peg.1975

	Arginine; urea cycle, polyamines		N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38)	fig|439375.7.peg.2633	fig|204722.5.peg.798
			N-acetylglutamate synthase (EC 2.3.1.1)	fig|439375.7.peg.1073	fig|204722.5.peg.1975
			N-succinyl-L,L-diaminopimelate desuccinylase (EC 3.5.1.18)	fig|439375.7.peg.1415	fig|204722.5.peg.3256
			Ornithine carbamoyltransferase (EC 2.1.3.3)	fig|439375.7.peg.421, fig|439375.7.peg.4913	fig|204722.5.peg.315
		Arginine Deiminase Pathway	Arginine deiminase (EC 3.5.3.6)	fig|439375.7.peg.4912	■
			Arginine/ornithine antiporter ArcD	fig|439375.7.peg.4911	■
			Carbamate kinase (EC 2.7.2.2)	fig|439375.7.peg.4914	■
			Ornithine carbamoyltransferase (EC 2.1.3.3)	fig|439375.7.peg.421, fig|439375.7.peg.4913	fig|204722.5.peg.315
		Cyanophycin Metabolism	Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4)	fig|439375.7.peg.3112	■
			Cyanophycin synthase (EC 6.3.2.29)(EC 6.3.2.30)	fig|439375.7.peg.3113	■
			Cyanophycinase 2 (EC 3.4.15.6)	fig|439375.7.peg.3106	■
		Polyamine Metabolism	4-aminobutyraldehyde dehydrogenase (EC 1.2.1.19)	fig|439375.7.peg.2932	■
			5'-methylthioadenosine nucleosidase (EC 3.2.2.16)	fig|439375.7.peg.3208	fig|204722.5.peg.2574
			ABC transporter, periplasmic spermidine putrescine-binding protein PotD (TC 3.A.1.11.1)	fig|439375.7.peg.2928, fig|439375.7.peg.2944, fig|439375.7.peg.3881, fig|439375.7.peg.5015	fig|204722.5.peg.2542, fig|204722.5.peg.3329, fig|204722.5.peg.3330
			Agmatinase (EC 3.5.3.11)	fig|439375.7.peg.2632, fig|439375.7.peg.4682	fig|204722.5.peg.799
			Agmatine deiminase (EC 3.5.3.12)	fig|439375.7.peg.1096	■
			Arginine decarboxylase (EC 4.1.1.19)	fig|439375.7.peg.4417	fig|204722.5.peg.2320
			Arginine/ornithine antiporter ArcD	fig|439375.7.peg.4911	■
			Carbamate kinase (EC 2.7.2.2)	fig|439375.7.peg.4914	■
			Carboxynorspermidine decarboxylase, putative (EC 4.1.1.-)	fig|439375.7.peg.466	fig|204722.5.peg.347
			Carboxynorspermidine dehydrogenase, putative (EC 1.1.1.-)	fig|439375.7.peg.467	fig|204722.5.peg.349
			Ornithine decarboxylase (EC 4.1.1.17)	fig|439375.7.peg.4417	fig|204722.5.peg.2320
			Putrescine ABC transporter putrescine-binding protein PotF (TC 3.A.1.11.2)	fig|439375.7.peg.4100	fig|204722.5.peg.1638
			Putrescine transport ATP-binding protein PotA (TC 3.A.1.11.1)	fig|439375.7.peg.1536, fig|439375.7.peg.2929, fig|439375.7.peg.2945, fig|439375.7.peg.3737, fig|439375.7.peg.3880, fig|439375.7.peg.5016	fig|204722.5.peg.2543, fig|204722.5.peg.3333, fig|204722.5.peg.3334
			Putrescine transport ATP-binding protein PotG (TC 3.A.1.11.2)	fig|439375.7.peg.3981, fig|439375.7.peg.4099	fig|204722.5.peg.1637, fig|204722.5.peg.2901, fig|204722.5.peg.2902
			Putrescine transport system permease protein PotH (TC 3.A.1.11.2)	fig|439375.7.peg.4098	fig|204722.5.peg.1636
			Putrescine transport system permease protein PotI (TC 3.A.1.11.2)	fig|439375.7.peg.4097	fig|204722.5.peg.1635
			Spermidine Putrescine ABC transporter permease component PotB (TC 3.A.1.11.1)	fig|439375.7.peg.2930, fig|439375.7.peg.2946, fig|439375.7.peg.3879, fig|439375.7.peg.4324, fig|439375.7.peg.5014	fig|204722.5.peg.2544, fig|204722.5.peg.3332

	Spermidine Putrescine ABC transporter permease component potC (TC_3.A.1.11.1)	fig|439375.7.peg.2931, fig|439375.7.peg.2947, fig|439375.7.peg.3878, fig|439375.7.peg.5013	fig|204722.5.peg.2545, fig|204722.5.peg.3331
Putrescine utilization pathways	4-aminobutyraldehyde dehydrogenase (EC 1.2.1.19)	fig|439375.7.peg.2932	■
	Gamma-aminobutyrate:alpha-ketoglutarate aminotransferase (EC 2.6.1.19)	fig|439375.7.peg.3631	■
	Putrescine utilization regulator	fig|439375.7.peg.1512	■
Urea decomposition	Eukaryotic-type low-affinity urea transporter	fig|439375.7.peg.2575	fig|204722.5.peg.1385
	HupE-UreJ family metal transporter	fig|439375.7.peg.355, fig|439375.7.peg.2573	■
	Urea ABC transporter, ATPase protein UrtD	fig|439375.7.peg.4175, fig|439375.7.peg.4574	■
	Urease accessory protein UreD	fig|439375.7.peg.353, fig|439375.7.peg.2579	fig|204722.5.peg.280, fig|204722.5.peg.1384
	Urease accessory protein UreE	fig|439375.7.peg.358	fig|204722.5.peg.285, fig|204722.5.peg.1381
	Urease accessory protein UreF	fig|439375.7.peg.359, fig|439375.7.peg.2574	fig|204722.5.peg.286, fig|204722.5.peg.1382
	Urease accessory protein UreG	fig|439375.7.peg.360	fig|204722.5.peg.287, fig|204722.5.peg.1383
	Urease alpha subunit (EC 3.5.1.5)	fig|439375.7.peg.357, fig|439375.7.peg.2576	fig|204722.5.peg.284, fig|204722.5.peg.1380
	Urease beta subunit (EC 3.5.1.5)	fig|439375.7.peg.356, fig|439375.7.peg.2577	fig|204722.5.peg.283, fig|204722.5.peg.1379
	Urease gamma subunit (EC 3.5.1.5)	fig|439375.7.peg.354, fig|439375.7.peg.2578	fig|204722.5.peg.281, fig|204722.5.peg.1378
Aromatic amino acid degradation	2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase (EC 4.1.2.-)	■	fig|204722.5.peg.3387
	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (EC 5.3.3.-)	■	fig|204722.5.peg.3389
	2-oxo-hepta-3-ene-1,7-dioic acid hydratase (EC 4.2.-.-)	■	fig|204722.5.peg.3388
	5-carboxymethyl-2-hydroxymuconate delta-isomerase (EC 5.3.3.10)	■	fig|204722.5.peg.3393
	5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase (EC 1.2.1.60)	■	fig|204722.5.peg.3392
	5-carboxymethyl-2-oxo-hex-3- ene-1,7-dioate decarboxylase (EC 4.1.1.68)	■	fig|204722.5.peg.3389
	Homoprotocatechuate degradative operon repressor	■	fig|204722.5.peg.3394
Chorismate Synthesis	2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase II (EC 2.5.1.54)	fig|439375.7.peg.2201	fig|204722.5.peg.1024
	3-dehydroquinate dehydratase II (EC 4.2.1.10)	fig|439375.7.peg.2392	fig|204722.5.peg.922
	3-dehydroquinate synthase (EC 4.2.3.4)	fig|439375.7.peg.952	fig|204722.5.peg.2063
	5-Enolpyruvylshikimate-3-phosphate synthase (EC 2.5.1.19)	fig|439375.7.peg.32	fig|204722.5.peg.28
	Chorismate mutase I (EC 5.4.99.5)	fig|439375.7.peg.1127	fig|204722.5.peg.1855
	Chorismate synthase (EC 4.2.3.5)	fig|439375.7.peg.576	fig|204722.5.peg.443
	Cyclohexadienyl dehydrogenase (EC 1.3.1.12)(EC 1.3.1.43)	fig|439375.7.peg.1040	fig|204722.5.peg.2025
	Prephenate and/or arogenate dehydrogenase (unknown specificity) (EC 1.3.1.12)(EC 1.3.1.43)	fig|439375.7.peg.4115	■
	Prephenate dehydratase (EC 4.2.1.51)	fig|439375.7.peg.18	fig|204722.5.peg.41
	Quinate/shikimate 5-dehydrogenase I delta (EC 1.1.1.25)	fig|439375.7.peg.4603	■

	Aromatic amino acids and derivatives		Shikimate 5-dehydrogenase I alpha (EC 1.1.1.25)	fig|439375.7.peg.896	fig|204722.5.peg.2104, fig|204722.5.peg.2256, fig|204722.5.peg.2610
			Shikimate kinase I (EC 2.7.1.71)	fig|439375.7.peg.951	fig|204722.5.peg.2064
		Chorismate: Intermediate for synthesis of PAPA antibiotics, PABA, anthranilate, 3-hydroxyanthranilate and more.	Aminodeoxychorismate lyase (EC 4.1.3.38)	fig|439375.7.peg.4435	fig|204722.5.peg.2299
			Anthranilate synthase, amidotransferase component (EC 4.1.3.27)	fig|439375.7.peg.1682	fig|204722.5.peg.1596
			Anthranilate synthase, aminase component (EC 4.1.3.27)	fig|439375.7.peg.1682	fig|204722.5.peg.1596
			Isochorismatase (EC 3.3.2.1) of siderophore biosynthesis		fig|204722.5.peg.2236
			Isochorismate synthase (EC 5.4.4.2) of siderophore biosynthesis		fig|204722.5.peg.2238
			Para-aminobenzoate synthase, amidotransferase component (EC 2.6.1.85)	fig|439375.7.peg.1682	fig|204722.5.peg.1596
			Para-aminobenzoate synthase, aminase component (EC 2.6.1.85)	fig|439375.7.peg.4434	fig|204722.5.peg.2300
		Common Pathway For Synthesis of Aromatic Compounds (DAHP synthase to chorismate)	2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase II (EC 2.5.1.54)	fig|439375.7.peg.2201	fig|204722.5.peg.1024
			3-dehydroquinate dehydratase II (EC 4.2.1.10)	fig|439375.7.peg.2392	fig|204722.5.peg.922
			3-dehydroquinate synthase (EC 4.2.3.4)	fig|439375.7.peg.952	fig|204722.5.peg.2063
			5-Enolpyruvylshikimate-3-phosphate synthase (EC 2.5.1.19)	fig|439375.7.peg.32	fig|204722.5.peg.28
			Chorismate synthase (EC 4.2.3.5)	fig|439375.7.peg.576	fig|204722.5.peg.443
			Quinate/shikimate 5-dehydrogenase I delta (EC 1.1.1.25)	fig|439375.7.peg.4603	
			Shikimate 5-dehydrogenase I alpha (EC 1.1.1.25)	fig|439375.7.peg.896	fig|204722.5.peg.2104, fig|204722.5.peg.2256, fig|204722.5.peg.2610
			Shikimate kinase I (EC 2.7.1.71)	fig|439375.7.peg.951	fig|204722.5.peg.2064
		Phenylalanine and Tyrosine Branches from Chorismate	Biosynthetic Aromatic amino acid aminotransferase beta (EC 2.6.1.57)	fig|439375.7.peg.1041, fig|439375.7.peg.2792, fig|439375.7.peg.3735	fig|204722.5.peg.651, fig|204722.5.peg.2024
			Chorismate mutase I (EC 5.4.99.5)	fig|439375.7.peg.1127	fig|204722.5.peg.1855
			Cyclohexadienyl dehydrogenase (EC 1.3.1.12)(EC 1.3.1.43)	fig|439375.7.peg.1040	fig|204722.5.peg.2025
			Prephenate and/or arogenate dehydrogenase (unknown specificity) (EC 1.3.1.12)(EC 1.3.1.43)	fig|439375.7.peg.4115	
			Prephenate dehydratase (EC 4.2.1.51)	fig|439375.7.peg.18	fig|204722.5.peg.41
		Tryptophan synthesis	Anthranilate phosphoribosyltransferase (EC 2.4.2.18)	fig|439375.7.peg.2154	fig|204722.5.peg.1160
			Anthranilate synthase, amidotransferase component (EC 4.1.3.27)	fig|439375.7.peg.1682	fig|204722.5.peg.1596
			Anthranilate synthase, aminase component (EC 4.1.3.27)	fig|439375.7.peg.1682	fig|204722.5.peg.1596
			Indole-3-glycerol phosphate synthase (EC 4.1.1.48)	fig|439375.7.peg.2153	fig|204722.5.peg.1161
			Para-aminobenzoate synthase, amidotransferase component (EC 2.6.1.85)	fig|439375.7.peg.1682	fig|204722.5.peg.1596
			Phosphoribosylanthranilate isomerase (EC 5.3.1.24)	fig|439375.7.peg.854	fig|204722.5.peg.2148
			Tryptophan synthase alpha chain (EC 4.2.1.20)	fig|439375.7.peg.857	fig|204722.5.peg.2145
			Tryptophan synthase beta chain (EC 4.2.1.20)	fig|439375.7.peg.855	fig|204722.5.peg.2147
			(R)-citramalate synthase (EC 2.3.1.182)	fig|439375.7.peg.2750	fig|204722.5.peg.691
			2-isopropylmalate synthase (EC 2.3.3.13)	fig|439375.7.peg.1686	fig|204722.5.peg.1593
			3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)	fig|439375.7.peg.992	fig|204722.5.peg.1940
			3-isopropylmalate dehydratase small subunit (EC 4.2.1.33)	fig|439375.7.peg.3452	fig|204722.5.peg.3101
			3-isopropylmalate dehydrogenase (EC 1.1.1.85)	fig|439375.7.peg.3441	fig|204722.5.peg.3109

Amino Acids and Derivatives		Branched-Chain Amino Acid Biosynthesis	Acetolactate synthase large subunit (EC 2.2.1.6)	fig|439375.7.peg.1905	fig|204722.5.peg.1414
			Acetolactate synthase small subunit (EC 2.2.1.6)	fig|439375.7.peg.1906	fig|204722.5.peg.1413
			Branched-chain amino acid aminotransferase (EC 2.6.1.42)	fig|439375.7.peg.1734, fig|439375.7.peg.3936	fig|204722.5.peg.2880, fig|204722.5.peg.2881
			Dihydroxy-acid dehydratase (EC 4.2.1.9)	fig|439375.7.peg.119	fig|204722.5.peg.101
			Ketol-acid reductoisomerase (EC 1.1.1.86)	fig|439375.7.peg.1914	fig|204722.5.peg.1405
			Leucine-responsive regulatory protein, regulator for leucine (or lrp) regulon and high-affinity branched-chain amino acid transport system	fig|439375.7.peg.1681, fig|439375.7.peg.1752, fig|439375.7.peg.3629	fig|204722.5.peg.1527, fig|204722.5.peg.1598
			Threonine dehydratase (EC 4.3.1.19)	fig|439375.7.peg.2245	fig|204722.5.peg.1065
			Threonine dehydratase, catabolic (EC 4.3.1.19)	fig|439375.7.peg.1908, fig|439375.7.peg.3628	
		HMG CoA Synthesis	Acetoacetyl-CoA synthetase (EC 6.2.1.16)	fig|439375.7.peg.37	fig|204722.5.peg.24
			Hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4)	fig|439375.7.peg.41	fig|204722.5.peg.18, fig|204722.5.peg.19
			Isovaleryl-CoA dehydrogenase (EC 1.3.99.10)	fig|439375.7.peg.38	fig|204722.5.peg.22
			Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4)	fig|439375.7.peg.40	fig|204722.5.peg.20
			Methylcrotonyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.4)	fig|439375.7.peg.39	fig|204722.5.peg.21
			Methylglutaconyl-CoA hydratase (EC 4.2.1.18)	fig|439375.7.peg.42	fig|204722.5.peg.17
			Predicted transcriptional regulator LiuR of leucine degradation pathway, MerR family	fig|439375.7.peg.2115, fig|439375.7.peg.4211	fig|204722.5.peg.1198, fig|204722.5.peg.3039
		Isoleucine degradation	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	fig|439375.7.peg.3071, fig|439375.7.peg.4195, fig|439375.7.peg.4206, fig|439375.7.peg.4885	fig|204722.5.peg.2440, fig|204722.5.peg.3008, fig|204722.5.peg.3311
			3-ketoacyl-CoA thiolase (EC 2.3.1.16)	fig|439375.7.peg.4207	fig|204722.5.peg.3009
			Branched-chain acyl-CoA dehydrogenase (EC 1.3.99.12)	fig|439375.7.peg.1971	fig|204722.5.peg.1335
			Branched-chain alpha-keto acid dehydrogenase, E1 component, alpha subunit (EC 1.2.4.4)	fig|439375.7.peg.3709	fig|204722.5.peg.2254, fig|204722.5.peg.2739, fig|204722.5.peg.3309, fig|204722.5.peg.3310
			Branched-chain alpha-keto acid dehydrogenase, E1 component, beta subunit (EC 1.2.4.4)	fig|439375.7.peg.3711	fig|204722.5.peg.2254, fig|204722.5.peg.2740, fig|204722.5.peg.3309, fig|204722.5.peg.3310
			Branched-chain amino acid aminotransferase (EC 2.6.1.42)	fig|439375.7.peg.1734, fig|439375.7.peg.3936	fig|204722.5.peg.2880, fig|204722.5.peg.2881
			Butyryl-CoA dehydrogenase (EC 1.3.99.2)	fig|439375.7.peg.3256, fig|439375.7.peg.4180	fig|204722.5.peg.2437, fig|204722.5.peg.2665, fig|204722.5.peg.3313
			Dihydrolipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.1.168)	fig|439375.7.peg.3712	fig|204722.5.peg.2255, fig|204722.5.peg.2741, fig|204722.5.peg.3307
			Dihydrolipoamide dehydrogenase of branched-chain alpha-keto acid dehydrogenase (EC 1.8.1.4)	fig|439375.7.peg.3713	fig|204722.5.peg.2742

	Branched-chain amino acids		Enoyl-CoA hydratase (EC 4.2.1.17)	fig|439375.7.peg.564, fig|439375.7.peg.4192, fig|439375.7.peg.4195	fig|204722.5.peg.427
			Enoyl-CoA hydratase [isoleucine degradation] (EC 4.2.1.17)	fig|439375.7.peg.4206	fig|204722.5.peg.3008
		Leucine Biosynthesis	2-isopropylmalate synthase (EC 2.3.3.13)	fig|439375.7.peg.1686	fig|204722.5.peg.1593
			3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)	fig|439375.7.peg.992	fig|204722.5.peg.1940
			3-isopropylmalate dehydratase small subunit (EC 4.2.1.33)	fig|439375.7.peg.3452	fig|204722.5.peg.3101
			3-isopropylmalate dehydrogenase (EC 1.1.1.85)	fig|439375.7.peg.3441	fig|204722.5.peg.3109
			Branched-chain amino acid aminotransferase (EC 2.6.1.42)	fig|439375.7.peg.1734, fig|439375.7.peg.3936	fig|204722.5.peg.2880, fig|204722.5.peg.2881
		Leucine Degradation and HMG-CoA Metabolism	Acetoacetyl-CoA synthetase (EC 6.2.1.16)	fig|439375.7.peg.37	fig|204722.5.peg.24
			Branched-chain acyl-CoA dehydrogenase (EC 1.3.99.12)	fig|439375.7.peg.1971	fig|204722.5.peg.1335
			Branched-chain alpha-keto acid dehydrogenase, E1 component, alpha subunit (EC 1.2.4.4)	fig|439375.7.peg.3709	fig|204722.5.peg.2254, fig|204722.5.peg.2739, fig|204722.5.peg.3309, fig|204722.5.peg.3310
			Branched-chain alpha-keto acid dehydrogenase, E1 component, beta subunit (EC 1.2.4.4)	fig|439375.7.peg.3711	fig|204722.5.peg.2254, fig|204722.5.peg.2740, fig|204722.5.peg.3309, fig|204722.5.peg.3310
			Branched-chain amino acid aminotransferase (EC 2.6.1.42)	fig|439375.7.peg.1734, fig|439375.7.peg.3936	fig|204722.5.peg.2880, fig|204722.5.peg.2881
			Dihydrolipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.1.168)	fig|439375.7.peg.3712	fig|204722.5.peg.2255, fig|204722.5.peg.2741, fig|204722.5.peg.3307
			Dihydrolipoamide dehydrogenase of branched-chain alpha-keto acid dehydrogenase (EC 1.8.1.4)	fig|439375.7.peg.3713	fig|204722.5.peg.2742
			Hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4)	fig|439375.7.peg.41	fig|204722.5.peg.18, fig|204722.5.peg.19
			Isovaleryl-CoA dehydrogenase (EC 1.3.99.10)	fig|439375.7.peg.38	fig|204722.5.peg.22
			Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4)	fig|439375.7.peg.40	fig|204722.5.peg.20
			Methylcrotonyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.4)	fig|439375.7.peg.39	fig|204722.5.peg.21
			Methylglutaconyl-CoA hydratase (EC 4.2.1.18)	fig|439375.7.peg.42	fig|204722.5.peg.17
			3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	fig|439375.7.peg.3071, fig|439375.7.peg.4195, fig|439375.7.peg.4206, fig|439375.7.peg.4885	fig|204722.5.peg.2440, fig|204722.5.peg.3008, fig|204722.5.peg.3311
			3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31)	fig|439375.7.peg.1970	fig|204722.5.peg.964, fig|204722.5.peg.1336
			Branched-chain acyl-CoA dehydrogenase (EC 1.3.99.12)	fig|439375.7.peg.1971	fig|204722.5.peg.1335
			Branched-chain alpha-keto acid dehydrogenase, E1 component, alpha subunit (EC 1.2.4.4)	fig|439375.7.peg.3709	fig|204722.5.peg.2254, fig|204722.5.peg.2739, fig|204722.5.peg.3309, fig|204722.5.peg.3310

	Valine degradation	Branched-chain alpha-keto acid dehydrogenase, E1 component, beta subunit (EC 1.2.4.4)	fig|439375.7.peg.3711	fig|204722.5.peg.2254, fig|204722.5.peg.2740, fig|204722.5.peg.3309, fig|204722.5.peg.3310
		Branched-chain amino acid aminotransferase (EC 2.6.1.42)	fig|439375.7.peg.1734, fig|439375.7.peg.3936	fig|204722.5.peg.2880, fig|204722.5.peg.2881
		Butyryl-CoA dehydrogenase (EC 1.3.99.2)	fig|439375.7.peg.3256, fig|439375.7.peg.4180	fig|204722.5.peg.2437, fig|204722.5.peg.2665, fig|204722.5.peg.3313
		Dihydrolipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.1.168)	fig|439375.7.peg.3712	fig|204722.5.peg.2255, fig|204722.5.peg.2741, fig|204722.5.peg.3307
		Dihydrolipoamide dehydrogenase of branched-chain alpha-keto acid dehydrogenase (EC 1.8.1.4)	fig|439375.7.peg.3713	fig|204722.5.peg.2742
		Enoyl-CoA hydratase (EC 4.2.1.17)	fig|439375.7.peg.564, fig|439375.7.peg.4192, fig|439375.7.peg.4195	fig|204722.5.peg.427
		Enoyl-CoA hydratase [valine degradation] (EC 4.2.1.17)	fig|439375.7.peg.2669	fig|204722.5.peg.771
		Methylmalonate-semialdehyde dehydrogenase (EC 1.2.1.27)	fig|439375.7.peg.1117	fig|204722.5.peg.1862
Glutamine, glutamate, aspartate, asparagine; ammonia assimilation	Glutamate dehydrogenases	NADP-specific glutamate dehydrogenase (EC 1.4.1.4)	fig|439375.7.peg.322, fig|439375.7.peg.4768	fig|204722.5.peg.234
		NAD-specific glutamate dehydrogenase (EC 1.4.1.2)	fig|439375.7.peg.4768	
		NAD-specific glutamate dehydrogenase (EC 1.4.1.2), large form	fig|439375.7.peg.1133	fig|204722.5.peg.1849
	Glutamine synthetases	Glutamine synthetase type I (EC 6.3.1.2)	fig|439375.7.peg.2193	fig|204722.5.peg.1015
		Glutamine synthetase type II, eukaryotic (EC 6.3.1.2)	fig|439375.7.peg.4328	
	Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis	Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4)	fig|439375.7.peg.3112	
		Aspartate aminotransferase (EC 2.6.1.1)	fig|439375.7.peg.437, fig|439375.7.peg.816, fig|439375.7.peg.1014, fig|439375.7.peg.1763, fig|439375.7.peg.2016, fig|439375.7.peg.2519, fig|439375.7.peg.3650, fig|439375.7.peg.4201	fig|204722.5.peg.1297, fig|204722.5.peg.1403, fig|204722.5.peg.1522, fig|204722.5.peg.1928
		Aspartate ammonia-lyase (EC 4.3.1.1)	Aspartate ammonia-lyase (EC 4.3.1.1)	fig|204722.5.peg.1993
		Aspartate racemase (EC 5.1.1.13)	fig|439375.7.peg.587	
		Glutamate racemase (EC 5.1.1.3)	fig|439375.7.peg.868, fig|439375.7.peg.2098	fig|204722.5.peg.1214
		Glutamate synthase [NADPH] large chain (EC 1.4.1.13)	fig|439375.7.peg.4450	fig|204722.5.peg.2274
		Glutamate synthase [NADPH] small chain (EC 1.4.1.13)	fig|439375.7.peg.4449	fig|204722.5.peg.2275
		Glutaminase (EC 3.5.1.2)	Glutaminase (EC 3.5.1.2)	fig|204722.5.peg.2556
		glutamine synthetase family protein	fig|439375.7.peg.4050, fig|439375.7.peg.4108	fig|204722.5.peg.2947, fig|204722.5.peg.2980
		Glutamine synthetase type I (EC 6.3.1.2)	fig|439375.7.peg.2193	fig|204722.5.peg.1015
		Glutamine synthetase type II, eukaryotic (EC 6.3.1.2)	fig|439375.7.peg.4328	

			L-asparaginase (EC 3.5.1.1)	fig|439375.7.peg.3556	fig|204722.5.peg.1995, fig|204722.5.peg.1997
			Leucine-responsive regulatory protein, regulator for leucine (or lrp) regulon and high-affinity branched-chain amino acid transport system	fig|439375.7.peg.1681, fig|439375.7.peg.1752, fig|439375.7.peg.3629	fig|204722.5.peg.1527, fig|204722.5.peg.1598
			NADP-specific glutamate dehydrogenase (EC 1.4.1.4)	fig|439375.7.peg.322, fig|439375.7.peg.4768	fig|204722.5.peg.234
			NAD-specific glutamate dehydrogenase (EC 1.4.1.2)	fig|439375.7.peg.4768	■
			NAD-specific glutamate dehydrogenase (EC 1.4.1.2), large form	fig|439375.7.peg.1133	fig|204722.5.peg.1849
	Histidine Metabolism	Histidine Biosynthesis	ATP phosphoribosyltransferase catalytic subunit (EC 2.4.2.17)	fig|439375.7.peg.3171	fig|204722.5.peg.2405
			ATP phosphoribosyltransferase regulatory subunit (EC 2.4.2.17)	fig|439375.7.peg.3170	fig|204722.5.peg.2404
			Histidinol dehydrogenase (EC 1.1.1.23)	fig|439375.7.peg.348, fig|439375.7.peg.3741	fig|204722.5.peg.261
			Histidinol-phosphate aminotransferase (EC 2.6.1.9)	fig|439375.7.peg.2792	fig|204722.5.peg.651
			Imidazole glycerol phosphate synthase amidotransferase subunit (EC 2.4.2.-)	fig|439375.7.peg.881	fig|204722.5.peg.2120
			Imidazole glycerol phosphate synthase cyclase subunit (EC 4.1.3.-)	fig|439375.7.peg.879	fig|204722.5.peg.2122
			Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19)	fig|439375.7.peg.883	fig|204722.5.peg.2118
			Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19)	fig|439375.7.peg.2267	fig|204722.5.peg.1090
			Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31)	fig|439375.7.peg.878	fig|204722.5.peg.2123
			Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase (EC 5.3.1.16)	fig|439375.7.peg.880	fig|204722.5.peg.2121
		Histidine Degradation	Conserved hypothetical protein (perhaps related to histidine degradation)	fig|439375.7.peg.1500	fig|204722.5.peg.3151
			Formiminoglutamic iminohydrolase (EC 3.5.3.13)	fig|439375.7.peg.1506	fig|204722.5.peg.3145
			Histidine ammonia-lyase (EC 4.3.1.3)	fig|439375.7.peg.1504	fig|204722.5.peg.3148
			Histidine utilization repressor	fig|439375.7.peg.1507, fig|439375.7.peg.3743, fig|439375.7.peg.4961, fig|439375.7.peg.4965	fig|204722.5.peg.3144
			Imidazolonepropionase (EC 3.5.2.7)	fig|439375.7.peg.1505	fig|204722.5.peg.3147
			N-formylglutamate deformylase (EC 3.5.1.68)	fig|439375.7.peg.1503	fig|204722.5.peg.3149
			Urocanate hydratase (EC 4.2.1.49)	fig|439375.7.peg.1502	fig|204722.5.peg.3150
		Cysteine Biosynthesis	Adenylylsulfate kinase (EC 2.7.1.25)	fig|439375.7.peg.213	fig|204722.5.peg.202
			Cystathionine gamma-lyase (EC 4.4.1.1)	fig|439375.7.peg.4548	■
			Cysteine synthase (EC 2.5.1.47)	fig|439375.7.peg.692, fig|439375.7.peg.1064	fig|204722.5.peg.2003, fig|204722.5.peg.2004
			Cysteine synthase B (EC 2.5.1.47)	fig|439375.7.peg.2248	fig|204722.5.peg.1067
			Phosphoadenylyl-sulfate reductase [thioredoxin] (EC 1.8.4.8)	fig|439375.7.peg.202	fig|204722.5.peg.191
			Serine acetyltransferase (EC 2.3.1.30)	fig|439375.7.peg.2027	fig|204722.5.peg.1281
			Sulfate adenylyltransferase subunit 1 (EC 2.7.7.4)	fig|439375.7.peg.213	fig|204722.5.peg.202
			Sulfate adenylyltransferase subunit 2 (EC 2.7.7.4)	fig|439375.7.peg.212	fig|204722.5.peg.201
			Sulfate and thiosulfate binding protein CysP	fig|439375.7.peg.127, fig|439375.7.peg.1954	fig|204722.5.peg.111, fig|204722.5.peg.1355

Lysine, threonine, methionine, and cysteine		Sulfate and thiosulfate import ATP-binding protein CysA (EC 3.6.3.25)	fig|439375.7.peg.130	fig|204722.5.peg.114
		Sulfate transport system permease protein CysT	fig|439375.7.peg.128, fig|439375.7.peg.1955	fig|204722.5.peg.112, fig|204722.5.peg.1353
		Sulfate transport system permease protein CysW	fig|439375.7.peg.129, fig|439375.7.peg.1956	fig|204722.5.peg.113, fig|204722.5.peg.1352
		Sulfite reductase [NADPH] flavoprotein alpha-component (EC 1.8.1.2)	■	fig|204722.5.peg.2451
		Sulfite reductase [NADPH] hemoprotein beta-component (EC 1.8.1.2)	fig|439375.7.peg.201	fig|204722.5.peg.190
	Lysine Biosynthesis DAP Pathway	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase (EC 2.3.1.117)	fig|439375.7.peg.1420	fig|204722.5.peg.3253
		Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)	fig|439375.7.peg.3445	fig|204722.5.peg.3105
		Aspartokinase (EC 2.7.2.4)	fig|439375.7.peg.1084	fig|204722.5.peg.1906
		Diaminopimelate decarboxylase (EC 4.1.1.20)	fig|439375.7.peg.1045	fig|204722.5.peg.2020
		Diaminopimelate epimerase (EC 5.1.1.7)	fig|439375.7.peg.972	fig|204722.5.peg.1966
		Dihydrodipicolinate reductase (EC 1.3.1.26)	fig|439375.7.peg.1393	fig|204722.5.peg.3276
		Dihydrodipicolinate synthase (EC 4.2.1.52)	fig|439375.7.peg.382, fig|439375.7.peg.2312, fig|439375.7.peg.2783, fig|439375.7.peg.3449, fig|439375.7.peg.3491, fig|439375.7.peg.4579	fig|204722.5.peg.660, fig|204722.5.peg.2619
		N-acetyl-L,L-diaminopimelate deacetylase (EC 3.5.1.47)	fig|439375.7.peg.2588, fig|439375.7.peg.3469	■
		N-succinyl-L,L-diaminopimelate desuccinylase (EC 3.5.1.18)	fig|439375.7.peg.1415	fig|204722.5.peg.3256
	Methionine Biosynthesis	5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20)	fig|439375.7.peg.1821	fig|204722.5.peg.1478
		5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13)	fig|439375.7.peg.208	fig|204722.5.peg.197
		Adenosylhomocysteinase (EC 3.3.1.1)	fig|439375.7.peg.867	fig|204722.5.peg.2135
		Cystathionine beta-lyase (EC 4.4.1.8)	fig|439375.7.peg.2696	fig|204722.5.peg.753
		Cystathionine gamma-lyase (EC 4.4.1.1)	fig|439375.7.peg.4548	■
		Cystathionine gamma-synthase (EC 2.5.1.48)	fig|439375.7.peg.378, fig|439375.7.peg.1066	fig|204722.5.peg.2001
		Cysteine synthase (EC 2.5.1.47)	fig|439375.7.peg.692, fig|439375.7.peg.1064	fig|204722.5.peg.2003, fig|204722.5.peg.2004
		Homoserine dehydrogenase (EC 1.1.1.3)	fig|439375.7.peg.2017	fig|204722.5.peg.1296
		Homoserine kinase (EC 2.7.1.39)	fig|439375.7.peg.630	fig|204722.5.peg.491, fig|204722.5.peg.3395
		Homoserine O-succinyltransferase (EC 2.3.1.46)	fig|439375.7.peg.3648	fig|204722.5.peg.2705
		Methionine ABC transporter ATP-binding protein	fig|439375.7.peg.1463, fig|439375.7.peg.2213, fig|439375.7.peg.3956	fig|204722.5.peg.1032, fig|204722.5.peg.3183
		Methionine ABC transporter permease protein	fig|439375.7.peg.1462, fig|439375.7.peg.3955	fig|204722.5.peg.3184
		Methionine ABC transporter substrate-binding protein	fig|439375.7.peg.778, fig|439375.7.peg.1464, fig|439375.7.peg.3957	fig|204722.5.peg.2212, fig|204722.5.peg.3181

			O-acetylhomoserine sulfhydrylase (EC 2.5.1.49)	fig|439375.7.peg.424, fig|439375.7.peg.2625	fig|204722.5.peg.318, fig|204722.5.peg.804
			O-succinylhomoserine sulfhydrylase (EC 2.5.1.48)	fig|439375.7.peg.424, fig|439375.7.peg.2625	fig|204722.5.peg.318, fig|204722.5.peg.804
			S-adenosylhomocysteine nucleosidase (EC 3.2.2.9)	fig|439375.7.peg.3208	fig|204722.5.peg.2574
			S-adenosylmethionine synthetase (EC 2.5.1.6)	fig|439375.7.peg.794	fig|204722.5.peg.2197
			Serine acetyltransferase (EC 2.3.1.30)	fig|439375.7.peg.2027	fig|204722.5.peg.1281
		Methionine Degradation	2-Oxobutyrate oxidase, putative	fig|439375.7.peg.3954	
			Adenosylhomocysteinase (EC 3.3.1.1)	fig|439375.7.peg.867	fig|204722.5.peg.2135
			Cystathionine gamma-lyase (EC 4.4.1.1)	fig|439375.7.peg.4548	
			Methionine ABC transporter ATP-binding protein	fig|439375.7.peg.1463, fig|439375.7.peg.2213, fig|439375.7.peg.3956	fig|204722.5.peg.1032, fig|204722.5.peg.3183
			Methionine ABC transporter permease protein	fig|439375.7.peg.1462, fig|439375.7.peg.3955	fig|204722.5.peg.3184
			Methionine ABC transporter substrate-binding protein	fig|439375.7.peg.778, fig|439375.7.peg.1464, fig|439375.7.peg.3957	fig|204722.5.peg.2212, fig|204722.5.peg.3181
			Pyruvate dehydrogenase E1 component (EC 1.2.4.1)	fig|439375.7.peg.699	
			S-adenosylhomocysteine nucleosidase (EC 3.2.2.9)	fig|439375.7.peg.3208	fig|204722.5.peg.2574
			S-adenosylmethionine synthetase (EC 2.5.1.6)	fig|439375.7.peg.794	fig|204722.5.peg.2197
		Threonine and Homoserine Biosynthesis	Aspartate aminotransferase (EC 2.6.1.1)	fig|439375.7.peg.437, fig|439375.7.peg.816, fig|439375.7.peg.1014, fig|439375.7.peg.1763, fig|439375.7.peg.2016, fig|439375.7.peg.2519, fig|439375.7.peg.3650, fig|439375.7.peg.4201	fig|204722.5.peg.1297, fig|204722.5.peg.1403, fig|204722.5.peg.1522, fig|204722.5.peg.1928
			Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)	fig|439375.7.peg.3445	fig|204722.5.peg.3105
			Aspartokinase (EC 2.7.2.4)	fig|439375.7.peg.1084	fig|204722.5.peg.1906
			Homoserine dehydrogenase (EC 1.1.1.3)	fig|439375.7.peg.2017	fig|204722.5.peg.1296
			Homoserine kinase (EC 2.7.1.39)	fig|439375.7.peg.630	fig|204722.5.peg.491, fig|204722.5.peg.3395
			Threonine synthase (EC 4.2.3.1)	fig|439375.7.peg.639, fig|439375.7.peg.704	fig|204722.5.peg.499
		Threonine degradation	FIG003492: Threonine dehydrogenase and related Zn-dependent dehydrogenases	fig|439375.7.peg.1693	fig|204722.5.peg.1587
			Low-specificity L-threonine aldolase (EC 4.1.2.5)	fig|439375.7.peg.4452	fig|204722.5.peg.2273
			Threonine dehydratase (EC 4.3.1.19)	fig|439375.7.peg.2245	fig|204722.5.peg.1065
			Threonine dehydratase, catabolic (EC 4.3.1.19)	fig|439375.7.peg.1908, fig|439375.7.peg.3628	
			Threonine dehydrogenase and related Zn-dependent dehydrogenases	fig|439375.7.peg.3612	
			Transcriptional regulator GabR of GABA utilization (GntR family with aminotransferase-like domain)	fig|439375.7.peg.3620	
		A Hypothetical Protein Related to Proline Metabolism	Hypothetical protein YggS, proline synthase co-transcribed bacterial homolog PROSC	fig|439375.7.peg.1144, fig|439375.7.peg.4307	fig|204722.5.peg.1836
			Pyrroline-5-carboxylate reductase (EC 1.5.1.2)	fig|439375.7.peg.4136	fig|204722.5.peg.2996

	Proline and 4-hydroxyproline	Proline Synthesis	Gamma-glutamyl phosphate reductase (EC 1.2.1.41)	fig|439375.7.peg.1104	fig|204722.5.peg.1875
			Glutamate 5-kinase (EC 2.7.2.11)	fig|439375.7.peg.1103	fig|204722.5.peg.1876
			NADP-specific glutamate dehydrogenase (EC 1.4.1.4)	fig|439375.7.peg.322, fig|439375.7.peg.4768	fig|204722.5.peg.234
			Pyrroline-5-carboxylate reductase (EC 1.5.1.2)	fig|439375.7.peg.4136	fig|204722.5.peg.2996
		Proline, 4-hydroxyproline uptake and utilization	1-pyrroline-4-hydroxy-2-carboxylate deaminase (EC 3.5.4.22)	fig|439375.7.peg.3044	fig|204722.5.peg.2456
			4-hydroxyproline epimerase (EC 5.1.1.8)	fig|439375.7.peg.1161	fig|204722.5.peg.1819
			Delta-1-pyrroline-5-carboxylate dehydrogenase (EC 1.5.1.12)	fig|439375.7.peg.4014	fig|204722.5.peg.2937
			L-Proline/Glycine betaine transporter ProP	fig|439375.7.peg.1328	fig|204722.5.peg.1707
			Not a Proline racemase, nor 4-hydroxyproline epimerase [missing catalytic residues]	fig|439375.7.peg.468	fig|204722.5.peg.351
			Predicted regulator PutR for proline utilization, GntR family	fig|439375.7.peg.1159, fig|439375.7.peg.1347	fig|204722.5.peg.1823, fig|204722.5.peg.3240, fig|204722.5.peg.3298, fig|204722.5.peg.3320
			Proline dehydrogenase (EC 1.5.99.8) (Proline oxidase)	fig|439375.7.peg.4014	fig|204722.5.peg.2937
			Proline iminopeptidase (EC 3.4.11.5)	fig|439375.7.peg.433, fig|439375.7.peg.3235	fig|204722.5.peg.327
			PutR, transcriptional activator of PutA and PutP	fig|439375.7.peg.4015	fig|204722.5.peg.2938
			Ureidoglycolate/malate/sulfolactate dehydrogenase family (EC 1.1.1.-)	fig|439375.7.peg.3045	fig|204722.5.peg.2457
	Aminosugars	Chitin and N-acetylglucosamine utilization	Glucosamine-6-phosphate deaminase [isomerizing], alternative (EC 3.5.99.6)	fig|439375.7.peg.1524	fig|204722.5.peg.3130
			hypothetical oxidoreductase related to N-acetylglucosamine utilization	fig|439375.7.peg.3706	fig|204722.5.peg.2736
			N-Acetyl-D-glucosamine ABC transport system ATP-binding protein	fig|439375.7.peg.3707, fig|439375.7.peg.4062	fig|204722.5.peg.2737, fig|204722.5.peg.2957
			N-Acetyl-D-glucosamine ABC transport system, permease protein 1	fig|439375.7.peg.2615, fig|439375.7.peg.3704	fig|204722.5.peg.2734
			N-Acetyl-D-glucosamine ABC transport system, permease protein 2	fig|439375.7.peg.2614, fig|439375.7.peg.3705	fig|204722.5.peg.2735
			N-Acetyl-D-glucosamine ABC transport system, sugar-binding protein	fig|439375.7.peg.3703	fig|204722.5.peg.2732
			N-acetylglucosamine kinase of eukaryotic type (EC 2.7.1.59)	fig|439375.7.peg.3274, fig|439375.7.peg.3702, fig|439375.7.peg.4343	fig|204722.5.peg.2731, fig|204722.5.peg.3347
			N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)	fig|439375.7.peg.1525	fig|204722.5.peg.3129
			Predicted transcriptional regulator of N-Acetylglucosamine utilization, GntR family	fig|439375.7.peg.1523, fig|439375.7.peg.3701	fig|204722.5.peg.2730, fig|204722.5.peg.3131
			2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2)	fig|439375.7.peg.978	fig|204722.5.peg.1958
			Acetoin dehydrogenase E1 component alpha-subunit (EC 1.2.4.-)	fig|439375.7.peg.4290	
			Acetoin dehydrogenase E1 component beta-subunit (EC 1.2.4.-)	fig|439375.7.peg.4289	

		Dehydrogenase complexes	Branched-chain alpha-keto acid dehydrogenase, E1 component, alpha subunit (EC 1.2.4.4)	fig|439375.7.peg.3709	fig|204722.5.peg.2254, fig|204722.5.peg.2739, fig|204722.5.peg.3309, fig|204722.5.peg.3310
			Branched-chain alpha-keto acid dehydrogenase, E1 component, beta subunit (EC 1.2.4.4)	fig|439375.7.peg.3711	fig|204722.5.peg.2254, fig|204722.5.peg.2740, fig|204722.5.peg.3309, fig|204722.5.peg.3310
			Cytosol aminopeptidase PepA (EC 3.4.11.1)	fig|439375.7.peg.2741	fig|204722.5.peg.701
			Dihydrolipoamide acetyltransferase component (E2) of acetoin dehydrogenase complex (EC 2.3.1.-)	fig|439375.7.peg.4288	
			Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)	fig|439375.7.peg.2167	fig|204722.5.peg.1147
			Dihydrolipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.1.168)	fig|439375.7.peg.3712	fig|204722.5.peg.2255, fig|204722.5.peg.2741, fig|204722.5.peg.3307
			Dihydrolipoamide dehydrogenase of 2-oxoglutarate dehydrogenase (EC 1.8.1.4)	fig|439375.7.peg.983	fig|204722.5.peg.1953
			Dihydrolipoamide dehydrogenase of branched-chain alpha-keto acid dehydrogenase (EC 1.8.1.4)	fig|439375.7.peg.3713	fig|204722.5.peg.2742
			Dihydrolipoamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase complex (EC 2.3.1.61)	fig|439375.7.peg.979	fig|204722.5.peg.1957
			Enoyl-CoA hydratase [branched-chain amino acid degradation] (EC 4.2.1.17)	fig|439375.7.peg.753	fig|204722.5.peg.2221, fig|204722.5.peg.2439, fig|204722.5.peg.3312
			Leucine-, isoleucine-, valine-, threonine-, and alanine-binding protein	fig|439375.7.peg.3894	fig|204722.5.peg.2246, fig|204722.5.peg.2861
			Pyruvate dehydrogenase E1 component (EC 1.2.4.1)	fig|439375.7.peg.699	
			Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1)	fig|439375.7.peg.2165	fig|204722.5.peg.1149
			Pyruvate dehydrogenase E1 component beta subunit (EC 1.2.4.1)	fig|439375.7.peg.2166	fig|204722.5.peg.1148
		Dihydroxyacetone kinases	Dihydroxyacetone kinase, ATP-dependent (EC 2.7.1.29)	fig|439375.7.peg.3252	
			Putative dihydroxyacetone kinase (EC 2.7.1.29), ADP-binding subunit	fig|439375.7.peg.4244, fig|439375.7.peg.4246, fig|439375.7.peg.4541	fig|204722.5.peg.1654, fig|204722.5.peg.1656
			Putative dihydroxyacetone kinase (EC 2.7.1.29), dihydroxyacetone binding subunit	fig|439375.7.peg.4243, fig|439375.7.peg.4245, fig|439375.7.peg.4542	fig|204722.5.peg.1655, fig|204722.5.peg.1657
			2-dehydro-3-deoxygluconate kinase (EC 2.7.1.45)	fig|439375.7.peg.2498	fig|204722.5.peg.869
			2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14)	fig|439375.7.peg.4430	fig|204722.5.peg.2304
			6-phosphogluconolactonase (EC 3.1.1.31), eukaryotic type	fig|439375.7.peg.4130	fig|204722.5.peg.2992
			D-glycerate 2-kinase (EC 2.7.1.-)	fig|439375.7.peg.491, fig|439375.7.peg.4763	fig|204722.5.peg.371
			Enolase (EC 4.2.1.11)	fig|439375.7.peg.2162, fig|439375.7.peg.4764	fig|204722.5.peg.1152
			Glucokinase (EC 2.7.1.2)	fig|439375.7.peg.1396	fig|204722.5.peg.3274
			Gluconate dehydratase (EC 4.2.1.39)	fig|439375.7.peg.3496, fig|439375.7.peg.3925	

Central carbohydrate metabolism	Entner-Doudoroff Pathway	Gluconokinase (EC 2.7.1.12)	fig|439375.7.peg.3919	■
		Gluconolactonase (EC 3.1.1.17)	fig|439375.7.peg.4082	■
		Glucose dehydrogenase, PQQ-dependent (EC 1.1.5.2)	fig|439375.7.peg.316	■
		Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)	fig|439375.7.peg.4129	fig|204722.5.peg.2991
		NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	fig|439375.7.peg.1242	fig|204722.5.peg.1755
		Phosphogluconate dehydratase (EC 4.2.1.12)	fig|439375.7.peg.4131	fig|204722.5.peg.2993, fig|204722.5.peg.2994
		Phosphoglycerate kinase (EC 2.7.2.3)	fig|439375.7.peg.1240	fig|204722.5.peg.1756
		Phosphoglycerate mutase (EC 5.4.2.1)	fig|439375.7.peg.1391	fig|204722.5.peg.3277
		Pyruvate kinase (EC 2.7.1.40)	fig|439375.7.peg.1215	fig|204722.5.peg.1776
	Glycolate, glyoxylate interconversions	D-Lactate dehydrogenase, cytochrome c-dependent (EC 1.1.2.4)	fig|439375.7.peg.1869	fig|204722.5.peg.1436
		Glycolate dehydrogenase (EC 1.1.99.14), FAD-binding subunit GlcE	fig|439375.7.peg.3162	fig|204722.5.peg.2396
		Glycolate dehydrogenase (EC 1.1.99.14), iron-sulfur subunit GlcF	fig|439375.7.peg.3163	fig|204722.5.peg.2397
		Glycolate dehydrogenase (EC 1.1.99.14), subunit GlcD	fig|439375.7.peg.3161	fig|204722.5.peg.2395
		Glycolate utilization operon transcriptional activator GlcC	fig|439375.7.peg.3158	fig|204722.5.peg.2392
		Glyoxylate reductase (EC 1.1.1.26)	fig|439375.7.peg.774	fig|204722.5.peg.2214
		Glyoxylate reductase (EC 1.1.1.79)	fig|439375.7.peg.774	fig|204722.5.peg.2214
		Hydroxypyruvate reductase (EC 1.1.1.81)	fig|439375.7.peg.774	fig|204722.5.peg.2214
		Phosphoglycolate phosphatase (EC 3.1.3.18)	fig|439375.7.peg.2197	fig|204722.5.peg.1019
		Transcriptional regulator, LysR family, in glycolate utilization operon	fig|439375.7.peg.3160	fig|204722.5.peg.2393
	Glycolysis and Gluconeogenesis	Enolase (EC 4.2.1.11)	fig|439375.7.peg.2162, fig|439375.7.peg.4764	fig|204722.5.peg.1152
		Fructose-1,6-bisphosphatase, GlpX type (EC 3.1.3.11)	fig|439375.7.peg.2020	fig|204722.5.peg.1293
		Fructose-1,6-bisphosphatase, type I (EC 3.1.3.11)	fig|439375.7.peg.3050	fig|204722.5.peg.3090
		Fructose-bisphosphate aldolase class I (EC 4.1.2.13)	fig|439375.7.peg.1238	■
		Fructose-bisphosphate aldolase class II (EC 4.1.2.13)	fig|439375.7.peg.3051	fig|204722.5.peg.3089
		Glucokinase (EC 2.7.1.2)	fig|439375.7.peg.1396	fig|204722.5.peg.3274
		Glucose-6-phosphate isomerase (EC 5.3.1.9)	fig|439375.7.peg.392	fig|204722.5.peg.298
		NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	fig|439375.7.peg.1242	fig|204722.5.peg.1755
		NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.13)	fig|439375.7.peg.1242	fig|204722.5.peg.1755
		Phosphoglycerate kinase (EC 2.7.2.3)	fig|439375.7.peg.1240	fig|204722.5.peg.1756
		Phosphoglycerate mutase (EC 5.4.2.1)	fig|439375.7.peg.1391	fig|204722.5.peg.3277
		Pyruvate kinase (EC 2.7.1.40)	fig|439375.7.peg.1215	fig|204722.5.peg.1776
		Pyruvate,phosphate dikinase (EC 2.7.9.1)	fig|439375.7.peg.722	fig|204722.5.peg.515
		Triosephosphate isomerase (EC 5.3.1.1)	fig|439375.7.peg.2156, fig|439375.7.peg.3053	fig|204722.5.peg.1158, fig|204722.5.peg.3087
	Glyoxylate bypass	Aconitate hydratase (EC 4.2.1.3)	fig|439375.7.peg.111	fig|204722.5.peg.94
		Citrate synthase (si) (EC 2.3.3.1)	fig|439375.7.peg.2147, fig|439375.7.peg.2207, fig|439375.7.peg.2208	fig|204722.5.peg.1168
		Isocitrate lyase (EC 4.1.3.1)	fig|439375.7.peg.4102	fig|204722.5.peg.1641
		Malate dehydrogenase (EC 1.1.1.37)	fig|439375.7.peg.975	fig|204722.5.peg.1962

			Malate synthase G (EC 2.3.3.9)	fig|439375.7.peg.1330	fig|204722.5.peg.1675
		Methylglyoxal Metabolism	Aldehyde dehydrogenase (EC 1.2.1.3)	fig|439375.7.peg.291, fig|439375.7.peg.1348, fig|439375.7.peg.1385, fig|439375.7.peg.2980, fig|439375.7.peg.4960	fig|204722.5.peg.209, fig|204722.5.peg.1879, fig|204722.5.peg.3239, fig|204722.5.peg.3282, fig|204722.5.peg.3385, fig|204722.5.peg.3402
			Aldehyde dehydrogenase A (EC 1.2.1.22)	fig|439375.7.peg.3946	fig|204722.5.peg.2886
			Aldehyde dehydrogenase B (EC 1.2.1.22)	fig|439375.7.peg.297, fig|439375.7.peg.1529	fig|204722.5.peg.216, fig|204722.5.peg.3126
			Hydroxyacylglutathione hydrolase (EC 3.1.2.6)	fig|439375.7.peg.968, fig|439375.7.peg.3688	fig|204722.5.peg.1970, fig|204722.5.peg.2716
			Lactoylglutathione lyase (EC 4.4.1.5)	fig|439375.7.peg.64, fig|439375.7.peg.2023	fig|204722.5.peg.60, fig|204722.5.peg.1287, fig|204722.5.peg.2251, fig|204722.5.peg.3096
			Methylglyoxal synthase (EC 4.2.3.3)	fig|439375.7.peg.1397	fig|204722.5.peg.3273
		Pentose phosphate pathway	6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	fig|439375.7.peg.4403	fig|204722.5.peg.2329
			6-phosphogluconolactonase (EC 3.1.1.31), eukaryotic type	fig|439375.7.peg.4130	fig|204722.5.peg.2992
			Fructose-6-phosphate phosphoketolase (EC 4.1.2.22)	fig|439375.7.peg.4920	fig|204722.5.peg.2597
			Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)	fig|439375.7.peg.4129	fig|204722.5.peg.2991
			Ribose 5-phosphate isomerase A (EC 5.3.1.6)	fig|439375.7.peg.2198	fig|204722.5.peg.1021
			Ribose 5-phosphate isomerase B (EC 5.3.1.6)	fig|439375.7.peg.3052	fig|204722.5.peg.3088
			Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)	fig|439375.7.peg.1722	fig|204722.5.peg.1557
			Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	fig|439375.7.peg.2506	fig|204722.5.peg.860
			Transaldolase (EC 2.2.1.2)	fig|439375.7.peg.1149	fig|204722.5.peg.1833
			Transketolase (EC 2.2.1.1)	fig|439375.7.peg.1243, fig|439375.7.peg.3049	fig|204722.5.peg.1754
			Transketolase, C-terminal section (EC 2.2.1.1)	fig|439375.7.peg.4997	■
			Transketolase, N-terminal section (EC 2.2.1.1)	fig|439375.7.peg.4996	■
			Xylulose-5-phosphate phosphoketolase (EC 4.1.2.9)	fig|439375.7.peg.4920	fig|204722.5.peg.2597
		Pyruvate Alanine Serine Interconversions	Alanine dehydrogenase (EC 1.4.1.1)	fig|439375.7.peg.4331	■
			Alanine racemase (EC 5.1.1.1)	fig|439375.7.peg.1514	fig|204722.5.peg.3140
			Branched-chain amino acid aminotransferase (EC 2.6.1.42)	fig|439375.7.peg.1734, fig|439375.7.peg.3936	fig|204722.5.peg.2880, fig|204722.5.peg.2881
			D-alanine aminotransferase (EC 2.6.1.21)	fig|439375.7.peg.1496, fig|439375.7.peg.3721, fig|439375.7.peg.4781	fig|204722.5.peg.3152
			D-amino acid dehydrogenase small subunit (EC 1.4.99.1)	fig|439375.7.peg.1160, fig|439375.7.peg.1513, fig|439375.7.peg.3873, fig|439375.7.peg.4248	fig|204722.5.peg.1820, fig|204722.5.peg.1821, fig|204722.5.peg.2843, fig|204722.5.peg.3141
			D-serine/D-alanine/glycine transporter	fig|439375.7.peg.4448	fig|204722.5.peg.2276
			L-serine dehydratase (EC 4.3.1.17)	fig|439375.7.peg.2120	fig|204722.5.peg.1194
			Omega-amino acid--pyruvate aminotransferase (EC 2.6.1.18)	fig|439375.7.peg.210, fig|439375.7.peg.1511	fig|204722.5.peg.199, fig|204722.5.peg.3143, fig|204722.5.peg.3396, fig|204722.5.peg.3397

		Pyruvate metabolism I: anaplerotic reactions, PEP	NAD-dependent malic enzyme (EC 1.1.1.38)	fig|439375.7.peg.2205	fig|204722.5.peg.1028
			NADP-dependent malic enzyme (EC 1.1.1.40)	fig|439375.7.peg.168	fig|204722.5.peg.151, fig|204722.5.peg.152
			Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49)	fig|439375.7.peg.874	fig|204722.5.peg.2126
			Pyruvate carboxyl transferase (EC 6.4.1.1)	fig|439375.7.peg.1169, fig|439375.7.peg.4770	fig|204722.5.peg.1809
			Pyruvate kinase (EC 2.7.1.40)	fig|439375.7.peg.1215	fig|204722.5.peg.1776
			Pyruvate,phosphate dikinase (EC 2.7.9.1)	fig|439375.7.peg.722	fig|204722.5.peg.515
		Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	Acetate kinase (EC 2.7.2.1)	fig|439375.7.peg.4919	fig|204722.5.peg.2598
			Acetyl-coenzyme A synthetase (EC 6.2.1.1)	fig|439375.7.peg.1142, fig|439375.7.peg.1236	fig|204722.5.peg.1758, fig|204722.5.peg.1839
			Aldehyde dehydrogenase (EC 1.2.1.3)	fig|439375.7.peg.291, fig|439375.7.peg.1348, fig|439375.7.peg.1385, fig|439375.7.peg.2980, fig|439375.7.peg.4960	fig|204722.5.peg.209, fig|204722.5.peg.1879, fig|204722.5.peg.3239, fig|204722.5.peg.3282, fig|204722.5.peg.3385, fig|204722.5.peg.3402
			Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)	fig|439375.7.peg.2167	fig|204722.5.peg.1147
			Dihydrolipoamide dehydrogenase of pyruvate dehydrogenase complex (EC 1.8.1.4)	fig|439375.7.peg.2169	fig|204722.5.peg.1146
			Phosphate acetyltransferase (EC 2.3.1.8)	fig|439375.7.peg.3658	[redacted]
			Pyruvate dehydrogenase E1 component (EC 1.2.4.1)	fig|439375.7.peg.699	[redacted]
			Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1)	fig|439375.7.peg.2165	fig|204722.5.peg.1149
			Pyruvate dehydrogenase E1 component beta subunit (EC 1.2.4.1)	fig|439375.7.peg.2166	fig|204722.5.peg.1148
		TCA Cycle	2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2)	fig|439375.7.peg.978	fig|204722.5.peg.1958
			Aconitate hydratase (EC 4.2.1.3)	fig|439375.7.peg.111	fig|204722.5.peg.94
			Citrate synthase (si) (EC 2.3.3.1)	fig|439375.7.peg.2147, fig|439375.7.peg.2207, fig|439375.7.peg.2208	fig|204722.5.peg.1168
			Dihydrolipoamide dehydrogenase of 2-oxoglutarate dehydrogenase (EC 1.8.1.4)	fig|439375.7.peg.983	fig|204722.5.peg.1953
			Dihydrolipoamide dehydrogenase of pyruvate dehydrogenase complex (EC 1.8.1.4)	fig|439375.7.peg.2169	fig|204722.5.peg.1146
			Dihydrolipoamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase complex (EC 2.3.1.61)	fig|439375.7.peg.979	fig|204722.5.peg.1957
			Fumarate hydratase class I, aerobic (EC 4.2.1.2)	fig|439375.7.peg.2340	fig|204722.5.peg.974
			Fumarate hydratase class II (EC 4.2.1.2)	fig|439375.7.peg.3173	fig|204722.5.peg.2409
			hypothetical protein that often co-occurs with aconitase	fig|439375.7.peg.109	fig|204722.5.peg.92
			Isocitrate dehydrogenase [NADP] (EC 1.1.1.42)	fig|439375.7.peg.2094	fig|204722.5.peg.1218
			Malate dehydrogenase (EC 1.1.1.37)	fig|439375.7.peg.975	fig|204722.5.peg.1962
			Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)	fig|439375.7.peg.998	fig|204722.5.peg.1936
			Succinate dehydrogenase iron-sulfur protein (EC 1.3.99.1)	fig|439375.7.peg.999	fig|204722.5.peg.1935
			Succinyl-CoA ligase [ADP-forming] alpha chain (EC 6.2.1.5)	fig|439375.7.peg.977	fig|204722.5.peg.1960
			Succinyl-CoA ligase [ADP-forming] beta chain (EC 6.2.1.5)	fig|439375.7.peg.976	fig|204722.5.peg.1961
			Fructose-1,6-bisphosphatase, GlpX type (EC 3.1.3.11)	fig|439375.7.peg.2020	fig|204722.5.peg.1293
			Fructose-1,6-bisphosphatase, type I (EC 3.1.3.11)	fig|439375.7.peg.3050	fig|204722.5.peg.3090

	CO2 fixation	Calvin-Benson cycle	Fructose-bisphosphate aldolase class I (EC 4.1.2.13)	fig|439375.7.peg.1238	■
			Fructose-bisphosphate aldolase class II (EC 4.1.2.13)	fig|439375.7.peg.3051	fig|204722.5.peg.3089
			NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	fig|439375.7.peg.1242	fig|204722.5.peg.1755
			NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.13)	fig|439375.7.peg.1242	fig|204722.5.peg.1755
			Phosphoglycerate kinase (EC 2.7.2.3)	fig|439375.7.peg.1240	fig|204722.5.peg.1756
			Phosphoribulokinase (EC 2.7.1.19)	fig|439375.7.peg.2893	■
			Ribose 5-phosphate isomerase A (EC 5.3.1.6)	fig|439375.7.peg.2198	fig|204722.5.peg.1021
			Ribose 5-phosphate isomerase B (EC 5.3.1.6)	fig|439375.7.peg.3052	fig|204722.5.peg.3088
			Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	fig|439375.7.peg.2506	fig|204722.5.peg.860
			Transketolase (EC 2.2.1.1)	fig|439375.7.peg.1243, fig|439375.7.peg.3049	fig|204722.5.peg.1754
			Transketolase, C-terminal section (EC 2.2.1.1)	fig|439375.7.peg.4997	■
			Transketolase, N-terminal section (EC 2.2.1.1)	fig|439375.7.peg.4996	■
			Triosephosphate isomerase (EC 5.3.1.1)	fig|439375.7.peg.2156, fig|439375.7.peg.3053	fig|204722.5.peg.1158, fig|204722.5.peg.3087
	Di- and oligosaccharides	Maltose and Maltodextrin Utilization	Aldose 1-epimerase (EC 5.1.3.3)	fig|439375.7.peg.2499	fig|204722.5.peg.868
			Maltose operon transcriptional repressor MalR, LacI family	fig|439375.7.peg.3087	fig|204722.5.peg.2519
			Maltose/maltodextrin ABC transporter, permease protein MalF	fig|439375.7.peg.332, fig|439375.7.peg.3089	fig|204722.5.peg.242, fig|204722.5.peg.2521
			Maltose/maltodextrin ABC transporter, permease protein MalG	fig|439375.7.peg.333, fig|439375.7.peg.375, fig|439375.7.peg.386, fig|439375.7.peg.3090	fig|204722.5.peg.243, fig|204722.5.peg.2522
			Maltose/maltodextrin ABC transporter, substrate binding periplasmic protein MalE	fig|439375.7.peg.331, fig|439375.7.peg.3088	fig|204722.5.peg.241, fig|204722.5.peg.2520
			Maltose/maltodextrin transport ATP-binding protein MalK (EC 3.6.3.19)	fig|439375.7.peg.334, fig|439375.7.peg.374, fig|439375.7.peg.387, fig|439375.7.peg.3091	fig|204722.5.peg.244, fig|204722.5.peg.2523
			Transcriptional activator of maltose regulon, MalT	fig|439375.7.peg.696	■
		Trehalose Biosynthesis	Alpha,alpha-trehalose-phosphate synthase [UDP-forming] (EC 2.4.1.15)	fig|439375.7.peg.2862	■
			Trehalose-6-phosphate phosphatase (EC 3.1.3.12)	fig|439375.7.peg.2863	■
		Acetoin, butanediol metabolism	Acetoin dehydrogenase E1 component alpha-subunit (EC 1.2.4.-)	fig|439375.7.peg.4290	■
			Acetoin dehydrogenase E1 component beta-subunit (EC 1.2.4.-)	fig|439375.7.peg.4289	■
			Acetolactate synthase large subunit (EC 2.2.1.6)	fig|439375.7.peg.1905	fig|204722.5.peg.1414
			Acetolactate synthase small subunit (EC 2.2.1.6)	fig|439375.7.peg.1906	fig|204722.5.peg.1413
			Dihydrolipoamide acetyltransferase component (E2) of acetoin dehydrogenase complex (EC 2.3.1.-)	fig|439375.7.peg.4288	■
			3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	fig|439375.7.peg.3071, fig|439375.7.peg.4195, fig|439375.7.peg.4206, fig|439375.7.peg.4885	fig|204722.5.peg.2440, fig|204722.5.peg.3008, fig|204722.5.peg.3311
			3-hydroxybutyryl-CoA dehydratase (EC 4.2.1.55)	fig|439375.7.peg.919	fig|204722.5.peg.2080

Carbohydrates	**Fermentation**	Acetyl-CoA fermentation to Butyrate	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157)	fig|439375.7.peg.1062, fig|439375.7.peg.4885	fig|204722.5.peg.2006, fig|204722.5.peg.2440, fig|204722.5.peg.3311
			3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)	fig|439375.7.peg.4195, fig|439375.7.peg.4206	fig|204722.5.peg.3008
			Acetyl-CoA acetyltransferase (EC 2.3.1.9)	fig|439375.7.peg.1181, fig|439375.7.peg.3257, fig|439375.7.peg.3882, fig|439375.7.peg.4196, fig|439375.7.peg.4207	fig|204722.5.peg.1799, fig|204722.5.peg.2849, fig|204722.5.peg.3009
			Butyryl-CoA dehydrogenase (EC 1.3.99.2)	fig|439375.7.peg.3256, fig|439375.7.peg.4180	fig|204722.5.peg.2437, fig|204722.5.peg.2665, fig|204722.5.peg.3313
			Electron transfer flavoprotein, alpha subunit	fig|439375.7.peg.1061	fig|204722.5.peg.2007
			Electron transfer flavoprotein, beta subunit	fig|439375.7.peg.1060	fig|204722.5.peg.2008
			Electron transfer flavoprotein-ubiquinone oxidoreductase (EC 1.5.5.1)	fig|439375.7.peg.2803	fig|204722.5.peg.639
			Enoyl-CoA hydratase (EC 4.2.1.17)	fig|439375.7.peg.564, fig|439375.7.peg.4192, fig|439375.7.peg.4195	fig|204722.5.peg.427
		Butanol Biosynthesis	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157)	fig|439375.7.peg.1062, fig|439375.7.peg.4885	fig|204722.5.peg.2006, fig|204722.5.peg.2440, fig|204722.5.peg.3311
			Acetyl-CoA acetyltransferase (EC 2.3.1.9)	fig|439375.7.peg.1181, fig|439375.7.peg.3257, fig|439375.7.peg.3882, fig|439375.7.peg.4196, fig|439375.7.peg.4207	fig|204722.5.peg.1799, fig|204722.5.peg.2849, fig|204722.5.peg.3009
			Butyryl-CoA dehydrogenase (EC 1.3.99.2)	fig|439375.7.peg.3256, fig|439375.7.peg.4180	fig|204722.5.peg.2437, fig|204722.5.peg.2665, fig|204722.5.peg.3313
			Enoyl-CoA hydratase (EC 4.2.1.17)	fig|439375.7.peg.564, fig|439375.7.peg.4192, fig|439375.7.peg.4195	fig|204722.5.peg.427
		Fermentations: Lactate	Acetate kinase (EC 2.7.2.1)	fig|439375.7.peg.4919	fig|204722.5.peg.2598
			Fructose-6-phosphate phosphoketolase (EC 4.1.2.22)	fig|439375.7.peg.4920	fig|204722.5.peg.2597
			Phosphate acetyltransferase (EC 2.3.1.8)	fig|439375.7.peg.3658	■
			Xylulose-5-phosphate phosphoketolase (EC 4.1.2.9)	fig|439375.7.peg.4920	fig|204722.5.peg.2597
		Deoxyribose and Deoxynucleoside Catabolism	Deoxyribose operon repressor, DeoR family	fig|439375.7.peg.2988	■
			Deoxyribose-phosphate aldolase (EC 4.1.2.4)	fig|439375.7.peg.2981	■
			Putative deoxyribose-specific ABC transporter, permease protein	fig|439375.7.peg.3791	■
			Ribokinase (EC 2.7.1.15)	fig|439375.7.peg.381, fig|439375.7.peg.2609, fig|439375.7.peg.2982, fig|439375.7.peg.4234, fig|439375.7.peg.4624	fig|204722.5.peg.2227
			2-dehydro-3-deoxygalactonokinase (EC 2.7.1.58)	fig|439375.7.peg.1491	fig|204722.5.peg.3158

		D-galactonate catabolism	2-dehydro-3-deoxyphosphogalactonate aldolase (EC 4.1.2.21)	fig|439375.7.peg.1492	fig|204722.5.peg.3157
			D-galactonate transporter		fig|204722.5.peg.1998
			Galactonate dehydratase (EC 4.2.1.6)	fig|439375.7.peg.1490	fig|204722.5.peg.3159
		D-Galacturonate and D-Glucuronate Utilization	2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14)	fig|439375.7.peg.4430	fig|204722.5.peg.2304
			6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	fig|439375.7.peg.4403	fig|204722.5.peg.2329
			Altronate hydrolase (EC 4.2.1.7)		fig|204722.5.peg.3022
			D-mannonate oxidoreductase (EC 1.1.1.57)		fig|204722.5.peg.3028, fig|204722.5.peg.3029
			Mannonate dehydratase (EC 4.2.1.8)		fig|204722.5.peg.3032
			Uronate isomerase (EC 5.3.1.12)		fig|204722.5.peg.3030
		D-gluconate and ketogluconates metabolism	2-dehydro-3-deoxygluconate kinase (EC 2.7.1.45)	fig|439375.7.peg.2498	fig|204722.5.peg.869
			5-keto-D-gluconate 5-reductase (EC 1.1.1.69)	fig|439375.7.peg.3920	
			Gluconate 2-dehydrogenase (EC 1.1.99.3), membrane-bound, cytochrome c	fig|439375.7.peg.3768	
			Gluconate 2-dehydrogenase (EC 1.1.99.3), membrane-bound, flavoprotein	fig|439375.7.peg.3769	
			Gluconate 2-dehydrogenase (EC 1.1.99.3), membrane-bound, gamma subunit	fig|439375.7.peg.3770	
			Gluconokinase (EC 2.7.1.12)	fig|439375.7.peg.3919	
			Glucose dehydrogenase, PQQ-dependent (EC 1.1.5.2)	fig|439375.7.peg.316	
			Low-affinity gluconate/H+ symporter GntU	fig|439375.7.peg.4444	
			2-dehydro-3-deoxygluconate kinase (EC 2.7.1.45)	fig|439375.7.peg.2498	fig|204722.5.peg.869
		D-ribose utilization	Ribokinase (EC 2.7.1.15)	fig|439375.7.peg.381, fig|439375.7.peg.2609, fig|439375.7.peg.2982, fig|439375.7.peg.4234, fig|439375.7.peg.4624	fig|204722.5.peg.2227
			Ribose 5-phosphate isomerase A (EC 5.3.1.6)	fig|439375.7.peg.2198	fig|204722.5.peg.1021
			Ribose 5-phosphate isomerase B (EC 5.3.1.6)	fig|439375.7.peg.3052	fig|204722.5.peg.3088
			Ribose ABC transport system, ATP-binding protein RbsA (TC 3.A.1.2.1)	fig|439375.7.peg.2950, fig|439375.7.peg.2986, fig|439375.7.peg.3213, fig|439375.7.peg.3224, fig|439375.7.peg.4079, fig|439375.7.peg.4236, fig|439375.7.peg.4239, fig|439375.7.peg.4544, fig|439375.7.peg.4619	fig|204722.5.peg.1661, fig|204722.5.peg.2231, fig|204722.5.peg.3219
			Ribose ABC transport system, high affinity permease RbsD (TC 3.A.1.2.1)	fig|439375.7.peg.1944	fig|204722.5.peg.1361
			Ribose ABC transport system, periplasmic ribose-binding protein RbsB (TC 3.A.1.2.1)	fig|439375.7.peg.2949, fig|439375.7.peg.2987, fig|439375.7.peg.3215, fig|439375.7.peg.4237	

	Monosaccharides		Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1)	fig|439375.7.peg.311, fig|439375.7.peg.2951, fig|439375.7.peg.2984, fig|439375.7.peg.2985, fig|439375.7.peg.3212, fig|439375.7.peg.3225, fig|439375.7.peg.3501, fig|439375.7.peg.4080, fig|439375.7.peg.4081, fig|439375.7.peg.4235, fig|439375.7.peg.4238, fig|439375.7.peg.4240, fig|439375.7.peg.4543, fig|439375.7.peg.4546, fig|439375.7.peg.4620, fig|439375.7.peg.4621, fig|439375.7.peg.4992	fig|204722.5.peg.1660, fig|204722.5.peg.2229, fig|204722.5.peg.2230, fig|204722.5.peg.3217, fig|204722.5.peg.3218
			Ribose operon repressor	fig|439375.7.peg.315, fig|439375.7.peg.4023	
		Fructose utilization	Fructokinase (EC 2.7.1.4)	fig|439375.7.peg.137, fig|439375.7.peg.189, fig|439375.7.peg.310	
			Fructokinase FrcK (EC 2.7.1.4)	fig|439375.7.peg.74	
			Fructose ABC transporter, ATP-binding component FrcA	fig|439375.7.peg.73	
			Fructose ABC transporter, permease component FrcC	fig|439375.7.peg.72	
			Fructose ABC transporter, substrate-binding component FrcB	fig|439375.7.peg.71	
			Transcriptional regulator FrcR for fructose utilization, ROK family	fig|439375.7.peg.70	
		L-rhamnose utilization	Aldehyde dehydrogenase A (EC 1.2.1.22)	fig|439375.7.peg.3946	fig|204722.5.peg.2886
			L-lactate dehydrogenase (EC 1.1.2.3)	fig|439375.7.peg.1517	fig|204722.5.peg.3137
			L-rhamnose mutarotase	fig|439375.7.peg.336, fig|439375.7.peg.3726	
			Predicted lactaldehyde dehydrogenase (EC 1.2.1.22)	fig|439375.7.peg.3732	
			Predicted L-rhamnose ABC transporter, ATP-binding component	fig|439375.7.peg.3729	
			Predicted L-rhamnose ABC transporter, substrate-binding component	fig|439375.7.peg.3730	
			Predicted L-rhamnose ABC transporter, transmembrane component 1	fig|439375.7.peg.3727	
			Predicted L-rhamnose ABC transporter, transmembrane component 2	fig|439375.7.peg.3728	
			Predicted L-rhamnose isomerase RhaI (EC 5.3.1.14)	fig|439375.7.peg.3733	
			Predicted rhamnulose-1-phosphate aldolase (EC 4.1.2.19)	fig|439375.7.peg.3732	
			Rhamnulokinase RhaK in alpha-proteobacteria (EC 2.7.1.5)	fig|439375.7.peg.3725	
			Transcriptional regulator of rhamnose utilization, DeoR family	fig|439375.7.peg.3731	
			Beta-mannosidase (EC 3.2.1.25)	fig|439375.7.peg.1544	

	Mannose Metabolism	Mannose-1-phosphate guanylyltransferase (GDP) (EC 2.7.7.22)	fig|439375.7.peg.2864	fig|204722.5.peg.557, fig|204722.5.peg.2562
		Mannose-6-phosphate isomerase (EC 5.3.1.8)	fig|439375.7.peg.2864	fig|204722.5.peg.558, fig|204722.5.peg.2562
		Phosphomannomutase (EC 5.4.2.8)	fig|439375.7.peg.2865	fig|204722.5.peg.556, fig|204722.5.peg.2563
	Xylose utilization	2-ketoglutaric semialdehyde dehydrogenase (EC 1.2.1.26)		fig|204722.5.peg.2612, fig|204722.5.peg.3300
		D-xylose transport ATP-binding protein XylG	fig|439375.7.peg.3564, fig|439375.7.peg.3573	fig|204722.5.peg.560, fig|204722.5.peg.3382
		Novel Xylose regulator from LacI family	fig|439375.7.peg.3571	fig|204722.5.peg.567
		Xylose ABC transporter, periplasmic xylose-binding protein XylF	fig|439375.7.peg.3572	fig|204722.5.peg.3381
		Xylose ABC transporter, permease protein XylH	fig|439375.7.peg.3565, fig|439375.7.peg.3574	fig|204722.5.peg.561, fig|204722.5.peg.3383
		Xylose isomerase (EC 5.3.1.5)	fig|439375.7.peg.3569	fig|204722.5.peg.565
		Xylulose kinase (EC 2.7.1.17)	fig|439375.7.peg.3570	fig|204722.5.peg.566
One-carbon Metabolism	One-carbon metabolism by tetrahydropterines	5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20)	fig|439375.7.peg.1821	fig|204722.5.peg.1478
		5-FCL-like protein	fig|439375.7.peg.3127, fig|439375.7.peg.3131	
		5-formyltetrahydrofolate cyclo-ligase (EC 6.3.3.2)	fig|439375.7.peg.1247	fig|204722.5.peg.1750
		Formyltetrahydrofolate deformylase (EC 3.5.1.10)	fig|439375.7.peg.1528	fig|204722.5.peg.3127
		Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9)	fig|439375.7.peg.4132	fig|204722.5.peg.2995
		Methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5)	fig|439375.7.peg.4132	fig|204722.5.peg.2995
	Serine-glyoxylate cycle	3-ketoacyl-CoA thiolase (EC 2.3.1.16)	fig|439375.7.peg.4207	fig|204722.5.peg.3009
		5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20)	fig|439375.7.peg.1821	fig|204722.5.peg.1478
		5-FCL-like protein	fig|439375.7.peg.3127, fig|439375.7.peg.3131	
		5-formyltetrahydrofolate cyclo-ligase (EC 6.3.3.2)	fig|439375.7.peg.1247	fig|204722.5.peg.1750
		Acetyl-CoA acetyltransferase (EC 2.3.1.9)	fig|439375.7.peg.1181, fig|439375.7.peg.3257, fig|439375.7.peg.3882, fig|439375.7.peg.4196, fig|439375.7.peg.4207	fig|204722.5.peg.1799, fig|204722.5.peg.2849, fig|204722.5.peg.3009
		Aconitate hydratase (EC 4.2.1.3)	fig|439375.7.peg.111	fig|204722.5.peg.94
		Citrate synthase (si) (EC 2.3.3.1)	fig|439375.7.peg.2147, fig|439375.7.peg.2207, fig|439375.7.peg.2208	fig|204722.5.peg.1168
		Enolase (EC 4.2.1.11)	fig|439375.7.peg.2162, fig|439375.7.peg.4764	fig|204722.5.peg.1152
		Fumarate hydratase class I, aerobic (EC 4.2.1.2)	fig|439375.7.peg.2340	fig|204722.5.peg.974
		Isocitrate lyase (EC 4.1.3.1)	fig|439375.7.peg.4102	fig|204722.5.peg.1641
		Malate dehydrogenase (EC 1.1.1.37)	fig|439375.7.peg.975	fig|204722.5.peg.1962
		Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9)	fig|439375.7.peg.4132	fig|204722.5.peg.2995
		Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4)	fig|439375.7.peg.40	fig|204722.5.peg.20
		Methylcrotonyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.4)	fig|439375.7.peg.39	fig|204722.5.peg.21

			Methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5)	fig|439375.7.peg.4132	fig|204722.5.peg.2995
			Methylmalonyl-CoA mutase (EC 5.4.99.2)	fig|439375.7.peg.2104	fig|204722.5.peg.1209
			Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49)	fig|439375.7.peg.874	fig|204722.5.peg.2126
			Propionyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.3)	fig|439375.7.peg.2106	fig|204722.5.peg.1207
			Serine hydroxymethyltransferase (EC 2.1.2.1)	fig|439375.7.peg.2664	fig|204722.5.peg.776
			Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)	fig|439375.7.peg.998	fig|204722.5.peg.1936
			Succinate dehydrogenase iron-sulfur protein (EC 1.3.99.1)	fig|439375.7.peg.999	fig|204722.5.peg.1935
			Succinyl-CoA ligase [ADP-forming] alpha chain (EC 6.2.1.5)	fig|439375.7.peg.977	fig|204722.5.peg.1960
			Succinyl-CoA ligase [ADP-forming] beta chain (EC 6.2.1.5)	fig|439375.7.peg.976	fig|204722.5.peg.1961
	Organic acids	Glycerate metabolism	2-dehydro-3-deoxyglucarate aldolase (EC 4.1.2.20)	fig|439375.7.peg.2510	fig|204722.5.peg.856
			2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60)	fig|439375.7.peg.490, fig|439375.7.peg.2354, fig|439375.7.peg.3924	fig|204722.5.peg.2366
			D-glycerate 2-kinase (EC 2.7.1.-)	fig|439375.7.peg.491, fig|439375.7.peg.4763	fig|204722.5.peg.371
			Glyoxylate carboligase (EC 4.1.1.47)	fig|439375.7.peg.487	■
			Hydroxypyruvate isomerase (EC 5.3.1.22)	fig|439375.7.peg.489	fig|204722.5.peg.2364
			Hydroxypyruvate reductase (EC 1.1.1.81)	fig|439375.7.peg.774	fig|204722.5.peg.2214
			Pyruvate kinase (EC 2.7.1.40)	fig|439375.7.peg.1215	fig|204722.5.peg.1776
		Lactate utilization	L-lactate dehydrogenase (EC 1.1.2.3)	fig|439375.7.peg.1517	fig|204722.5.peg.3137
			L-lactate permease	fig|439375.7.peg.1125	fig|204722.5.peg.732
		Propionyl-CoA to Succinyl-CoA Module	Methylmalonyl-CoA epimerase (EC 5.1.99.1)	fig|439375.7.peg.2539	fig|204722.5.peg.828
			Methylmalonyl-CoA mutase (EC 5.4.99.2)	fig|439375.7.peg.2104	fig|204722.5.peg.1209
			Propionyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.3)	fig|439375.7.peg.2105	fig|204722.5.peg.1208
			Propionyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.3)	fig|439375.7.peg.2106	fig|204722.5.peg.1207
		Erythritol utilization	Erythritol kinase EryA (EC 2.7.1.27)	fig|439375.7.peg.3058, fig|439375.7.peg.3065, fig|439375.7.peg.3230	fig|204722.5.peg.3081
			Erythritol phosphate dehydrogenase EryB	fig|439375.7.peg.3057	fig|204722.5.peg.3082
			Erythritol transcriptional regulator EryD	fig|439375.7.peg.3055	fig|204722.5.peg.3084
			Possible D-erythrulose 4-phosphate dehydrogenase EryC (EC 1.1.1.-)	fig|439375.7.peg.3056	fig|204722.5.peg.3083
			Predicted erythritol ABC transporter 2, ATP-binding component	fig|439375.7.peg.3060	fig|204722.5.peg.3077
			Predicted erythritol ABC transporter 2, hypothetical lipoprotein	fig|439375.7.peg.3059	fig|204722.5.peg.3078
			Predicted erythritol ABC transporter 2, permease component	fig|439375.7.peg.3061	fig|204722.5.peg.3076
			Predicted erythritol ABC transporter 2, substrate-binding component	fig|439375.7.peg.3062	fig|204722.5.peg.3074
			Aerobic glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)	fig|439375.7.peg.289	fig|204722.5.peg.207
			Glycerol kinase (EC 2.7.1.30)	fig|439375.7.peg.1135, fig|439375.7.peg.2592	fig|204722.5.peg.2660
			Glycerol uptake operon antiterminator regulatory protein	fig|439375.7.peg.2595	■

	Sugar alcohols	Glycerol and Glycerol-3-phosphate Uptake and Utilization	Glycerol-3-phosphate ABC transporter, periplasmic glycerol-3-phosphate-binding protein (TC 3.A.1.1.3)	fig|439375.7.peg.1756, fig|439375.7.peg.3914	fig|204722.5.peg.2868, fig|204722.5.peg.2905, fig|204722.5.peg.3411
			Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)	fig|439375.7.peg.2593, fig|439375.7.peg.3066, fig|439375.7.peg.3228	
			Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94)	fig|439375.7.peg.1019	fig|204722.5.peg.1923
			Glycerol-3-phosphate regulon repressor, DeoR family	fig|439375.7.peg.288	fig|204722.5.peg.206
			Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)	fig|439375.7.peg.2130	fig|204722.5.peg.1185
			SN-glycerol-3-phosphate transport ATP-binding protein UgpC (TC 3.A.1.1.3)	fig|439375.7.peg.679, fig|439375.7.peg.1759, fig|439375.7.peg.2610, fig|439375.7.peg.2612, fig|439375.7.peg.3866, fig|439375.7.peg.3917, fig|439375.7.peg.4151, fig|439375.7.peg.4152	fig|204722.5.peg.2871, fig|204722.5.peg.3414
			SN-glycerol-3-phosphate transport system permease protein UgpA (TC 3.A.1.1.3)	fig|439375.7.peg.1758, fig|439375.7.peg.3915, fig|439375.7.peg.4153, fig|439375.7.peg.4156	fig|204722.5.peg.2869, fig|204722.5.peg.3413
			SN-glycerol-3-phosphate transport system permease protein UgpE (TC 3.A.1.1.3)	fig|439375.7.peg.677, fig|439375.7.peg.3916, fig|439375.7.peg.4154	fig|204722.5.peg.2870
		Inositol catabolism	5-deoxy-glucuronate isomerase (EC 5.3.1.-)	fig|439375.7.peg.4007	fig|204722.5.peg.2932
			5-keto-2-deoxygluconokinase (EC 2.7.1.92)	fig|439375.7.peg.4004	fig|204722.5.peg.2928, fig|204722.5.peg.2929
			Epi-inositol hydrolase (EC 3.7.1.-)	fig|439375.7.peg.4005	fig|204722.5.peg.2930
			Inositol transport system ATP-binding protein	fig|439375.7.peg.1934	fig|204722.5.peg.1363
			Inositol transport system permease protein	fig|439375.7.peg.1933	fig|204722.5.peg.1364
			Inosose dehydratase (EC 4.2.1.44)	fig|439375.7.peg.4006	fig|204722.5.peg.2931
			Inosose isomerase (EC 5.3.99.-)	fig|439375.7.peg.3567	fig|204722.5.peg.563
			Myo-inositol 2-dehydrogenase (EC 1.1.1.18)	fig|439375.7.peg.1931, fig|439375.7.peg.4002	fig|204722.5.peg.2926
			Myo-inositol 2-dehydrogenase 2 (EC 1.1.1.18)		fig|204722.5.peg.1367
			Predicted transcriptional regulator of the myo-inositol catabolic operon	fig|439375.7.peg.4003	fig|204722.5.peg.2927
			uncharacterized domain	fig|439375.7.peg.4004	fig|204722.5.peg.2928, fig|204722.5.peg.2929
			Cell division protein BolA	fig|439375.7.peg.954	fig|204722.5.peg.2061
			Cell division protein FtsA	fig|439375.7.peg.1850	fig|204722.5.peg.1452
			Cell division protein FtsH (EC 3.4.24.-)	fig|439375.7.peg.1278, fig|439375.7.peg.1623, fig|439375.7.peg.4642	fig|204722.5.peg.1718
			Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129)	fig|439375.7.peg.1839	fig|204722.5.peg.1463
			Cell division protein FtsJ	fig|439375.7.peg.3977	fig|204722.5.peg.2897

Cell Division and Cell Cycle	**Cell cycle in Prokaryota**	Bacterial Cell Division	Cell division protein FtsK	fig|439375.7.peg.1006, fig|439375.7.peg.3716	fig|204722.5.peg.1929, fig|204722.5.peg.2745
			Cell division protein FtsQ	fig|439375.7.peg.1849	fig|204722.5.peg.1453
			Cell division protein FtsW	fig|439375.7.peg.1844	fig|204722.5.peg.1458
			Cell division protein FtsX	fig|439375.7.peg.1032	fig|204722.5.peg.2034
			Cell division protein FtsZ (EC 3.4.24.-)	fig|439375.7.peg.1851	fig|204722.5.peg.1451
			Cell division topological specificity factor MinE	fig|439375.7.peg.3122	fig|204722.5.peg.2539
			Cell division transporter, ATP-binding protein FtsE (TC 3.A.5.1.1)	fig|439375.7.peg.1031	fig|204722.5.peg.2035
			Cell division trigger factor (EC 5.2.1.8)	fig|439375.7.peg.2400	fig|204722.5.peg.912
			Cytoplasmic axial filament protein CafA and Ribonuclease G (EC 3.1.4.-)	fig|439375.7.peg.2387	fig|204722.5.peg.927
			GTP-binding protein Era	fig|439375.7.peg.2768	fig|204722.5.peg.675
			rRNA small subunit methyltransferase H	fig|439375.7.peg.1837	fig|204722.5.peg.1465
			Septum formation protein Maf	fig|439375.7.peg.344, fig|439375.7.peg.897	fig|204722.5.peg.257, fig|204722.5.peg.2103
			Septum site-determining protein MinC	fig|439375.7.peg.3120	fig|204722.5.peg.2537
			Septum site-determining protein MinD	fig|439375.7.peg.3121	fig|204722.5.peg.2538
			Signal recognition particle receptor protein FtsY (=alpha subunit) (TC 3.A.5.1.1)	fig|439375.7.peg.970	fig|204722.5.peg.1968
		Bacterial Cytoskeleton	Cell division protein FtsA	fig|439375.7.peg.1850	fig|204722.5.peg.1452
			Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129)	fig|439375.7.peg.1839	fig|204722.5.peg.1463
			Cell division protein FtsK	fig|439375.7.peg.1006, fig|439375.7.peg.3716	fig|204722.5.peg.1929, fig|204722.5.peg.2745
			Cell division protein FtsQ	fig|439375.7.peg.1849	fig|204722.5.peg.1453
			Cell division protein FtsW	fig|439375.7.peg.1844	fig|204722.5.peg.1458
			Cell division protein FtsZ (EC 3.4.24.-)	fig|439375.7.peg.1851	fig|204722.5.peg.1451
			Cell division topological specificity factor MinE	fig|439375.7.peg.3122	fig|204722.5.peg.2539
			Chromosome (plasmid) partitioning protein ParA	fig|439375.7.peg.906, fig|439375.7.peg.3337	fig|204722.5.peg.2093
			Chromosome (plasmid) partitioning protein ParB	fig|439375.7.peg.907	fig|204722.5.peg.2092
			Septum formation protein Maf	fig|439375.7.peg.344, fig|439375.7.peg.897	fig|204722.5.peg.257, fig|204722.5.peg.2103
			Septum site-determining protein MinC	fig|439375.7.peg.3120	fig|204722.5.peg.2537
			Septum site-determining protein MinD	fig|439375.7.peg.3121	fig|204722.5.peg.2538
			Sporulation initiation inhibitor protein Soj	fig|439375.7.peg.906	fig|204722.5.peg.2093
			Stage 0 sporulation protein J	fig|439375.7.peg.907	fig|204722.5.peg.2092
		Two cell division clusters relating to chromosome partitioning	Chromosome (plasmid) partitioning protein ParA	fig|439375.7.peg.906, fig|439375.7.peg.3337	fig|204722.5.peg.2093
			Chromosome (plasmid) partitioning protein ParB	fig|439375.7.peg.907	fig|204722.5.peg.2092
			Chromosome partition protein smc	fig|439375.7.peg.652	fig|204722.5.peg.512
			Ribonuclease III (EC 3.1.26.3)	fig|439375.7.peg.2769	fig|204722.5.peg.674
			Segregation and condensation protein A	fig|439375.7.peg.2477	fig|204722.5.peg.891
			Segregation and condensation protein B	fig|439375.7.peg.2476, fig|439375.7.peg.4897	fig|204722.5.peg.892
			Signal recognition particle receptor protein FtsY (=alpha subunit) (TC 3.A.5.1.1)	fig|439375.7.peg.970	fig|204722.5.peg.1968
			Signal recognition particle, subunit Ffh SRP54 (TC 3.A.5.1.1)	fig|439375.7.peg.1126	fig|204722.5.peg.1856

	Capsular and extracellular polysacchrides	dTDP-rhamnose synthesis	dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)	fig|439375.7.peg.2869, fig|439375.7.peg.3546	fig|204722.5.peg.2654
			dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133)	fig|439375.7.peg.2867	
			dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	fig|439375.7.peg.649, fig|439375.7.peg.2868, fig|439375.7.peg.4594	
			Glucose-1-phosphate cytidylyltransferase (EC 2.7.7.33)	fig|439375.7.peg.3548	
			Glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	fig|439375.7.peg.2870	
		Rhamnose containing glycans	Alpha-D-GlcNAc alpha-1,2-L-rhamnosyltransferase (EC 2.4.1.-)	fig|439375.7.peg.417	
			dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)	fig|439375.7.peg.2869, fig|439375.7.peg.3546	fig|204722.5.peg.2654
			dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133)	fig|439375.7.peg.2867	
			dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	fig|439375.7.peg.649, fig|439375.7.peg.2868, fig|439375.7.peg.4594	
			Glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	fig|439375.7.peg.2870	
			UDP-glucose 4-epimerase (EC 5.1.3.2)	fig|439375.7.peg.2257, fig|439375.7.peg.2710, fig|439375.7.peg.3117, fig|439375.7.peg.3544, fig|439375.7.peg.3563, fig|439375.7.peg.4593	fig|204722.5.peg.727, fig|204722.5.peg.1079, fig|204722.5.peg.2652, fig|204722.5.peg.2758, fig|204722.5.peg.3068
		Sialic Acid Metabolism	Glucosamine-1-phosphate N-acetyltransferase (EC 2.3.1.157)	fig|439375.7.peg.3805	fig|204722.5.peg.2799
			Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16)	fig|439375.7.peg.3804	fig|204722.5.peg.2798
			N-acetylglucosamine-1-phosphate uridyltransferase (EC 2.7.7.23)	fig|439375.7.peg.3805	fig|204722.5.peg.2799
			N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)	fig|439375.7.peg.1525	fig|204722.5.peg.3129
			N-acetylmannosamine kinase (EC 2.7.1.60)	fig|439375.7.peg.3646	fig|204722.5.peg.2624
			N-acetylmannosamine-6-phosphate 2-epimerase (EC 5.1.3.9)		fig|204722.5.peg.2624
			Phosphoglucosamine mutase (EC 5.4.2.10)	fig|439375.7.peg.1280	fig|204722.5.peg.1717
			Sialic acid utilization regulator, RpiR family	fig|439375.7.peg.3272	
			Sialic acid-induced transmembrane protein YjhT(NanM), possible mutarotase		fig|204722.5.peg.2625, fig|204722.5.peg.2626
			TRAP-type transport system, small permease component, predicted N-acetylneuraminate transporter	fig|439375.7.peg.3927, fig|439375.7.peg.4608	
			Beta N-acetyl-glucosaminidase (EC 3.2.1.52)	fig|439375.7.peg.2478	fig|204722.5.peg.890
			D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)	fig|439375.7.peg.944, fig|439375.7.peg.1481, fig|439375.7.peg.2123, fig|439375.7.peg.2182, fig|439375.7.peg.2263, fig|439375.7.peg.3900	fig|204722.5.peg.1003, fig|204722.5.peg.1086, fig|204722.5.peg.1191, fig|204722.5.peg.2071, fig|204722.5.peg.3168
			Membrane-bound lytic murein transglycosylase A precursor (EC 3.2.1.-)	fig|439375.7.peg.890	fig|204722.5.peg.2111

Cell Wall and Capsule	**Cell Wall and Capsule**	Murein Hydrolases	Membrane-bound lytic murein transglycosylase B precursor (EC 3.2.1.-)	fig|439375.7.peg.25, fig|439375.7.peg.1124, fig|439375.7.peg.1823, fig|439375.7.peg.4446	fig|204722.5.peg.35, fig|204722.5.peg.1474, fig|204722.5.peg.1475, fig|204722.5.peg.1858, fig|204722.5.peg.2289
			Membrane-bound lytic murein transglycosylase D precursor (EC 3.2.1.-)	fig|439375.7.peg.4732, fig|439375.7.peg.4736	
			N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)	fig|439375.7.peg.1830, fig|439375.7.peg.2385	fig|204722.5.peg.928, fig|204722.5.peg.1470
			Soluble lytic murein transglycosylase precursor (EC 3.2.1.-)	fig|439375.7.peg.2784	fig|204722.5.peg.658
		Peptidoglycan Biosynthesis	Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129)	fig|439375.7.peg.1839	fig|204722.5.peg.1463
			D-alanine--D-alanine ligase (EC 6.3.2.4)	fig|439375.7.peg.1848	fig|204722.5.peg.1291, fig|204722.5.peg.1454
			D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)	fig|439375.7.peg.944, fig|439375.7.peg.1481, fig|439375.7.peg.2123, fig|439375.7.peg.2182, fig|439375.7.peg.2263, fig|439375.7.peg.3900	fig|204722.5.peg.1003, fig|204722.5.peg.1086, fig|204722.5.peg.1191, fig|204722.5.peg.2071, fig|204722.5.peg.3168
			Glucosamine-1-phosphate N-acetyltransferase (EC 2.3.1.157)	fig|439375.7.peg.3805	fig|204722.5.peg.2799
			Glutamate racemase (EC 5.1.1.3)	fig|439375.7.peg.868, fig|439375.7.peg.2098	fig|204722.5.peg.1214
			Glutamine synthetase type I (EC 6.3.1.2)	fig|439375.7.peg.2193	fig|204722.5.peg.1015
			Glutamine synthetase type II, eukaryotic (EC 6.3.1.2)	fig|439375.7.peg.4328	
			Membrane-bound lytic murein transglycosylase B precursor (EC 3.2.1.-)	fig|439375.7.peg.25, fig|439375.7.peg.1124, fig|439375.7.peg.1823, fig|439375.7.peg.4446	fig|204722.5.peg.35, fig|204722.5.peg.1474, fig|204722.5.peg.1475, fig|204722.5.peg.1858, fig|204722.5.peg.2289
			Monofunctional biosynthetic peptidoglycan transglycosylase (EC 2.4.2.-)	fig|439375.7.peg.1177	fig|204722.5.peg.1803
			Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-)	fig|439375.7.peg.139, fig|439375.7.peg.2384, fig|439375.7.peg.2822, fig|439375.7.peg.3605	fig|204722.5.peg.121, fig|204722.5.peg.599, fig|204722.5.peg.930
			N-acetylglucosamine-1-phosphate uridyltransferase (EC 2.7.7.23)	fig|439375.7.peg.3805	fig|204722.5.peg.2799
			Phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13)	fig|439375.7.peg.1842	fig|204722.5.peg.1460
			Rare lipoprotein A precursor	fig|439375.7.peg.2181	fig|204722.5.peg.1002
			UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.1.1.158)	fig|439375.7.peg.1847	fig|204722.5.peg.1455
			UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	fig|439375.7.peg.350, fig|439375.7.peg.3273	fig|204722.5.peg.263
			UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (EC 2.4.1.227)	fig|439375.7.peg.1845	fig|204722.5.peg.1457

			UDP-N-acetylmuramate--alanine ligase (EC 6.3.2.8)	fig|439375.7.peg.1846	fig|204722.5.peg.1456
			UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9)	fig|439375.7.peg.1843	fig|204722.5.peg.1459
			UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase (EC 6.3.2.13)	fig|439375.7.peg.1840	fig|204722.5.peg.1462
			UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanine ligase (EC 6.3.2.10)	fig|439375.7.peg.1841	fig|204722.5.peg.1461
		Recycling of Peptidoglycan Amino Acids	AmpG permease	fig|439375.7.peg.3417	
			N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)	fig|439375.7.peg.1830, fig|439375.7.peg.2385	fig|204722.5.peg.928, fig|204722.5.peg.1470
		Recycling of Peptidoglycan Amino Sugars	Anhydro-N-acetylmuramic acid kinase (EC 2.7.1.-)	fig|439375.7.peg.3281	fig|204722.5.peg.942
			Beta N-acetyl-glucosaminidase (EC 3.2.1.52)	fig|439375.7.peg.2478	fig|204722.5.peg.890
			N-acetylmuramic acid 6-phosphate etherase (EC 4.2.-.-)	fig|439375.7.peg.3275	
		UDP-N-acetylmuramate from Fructose	Glucosamine-1-phosphate N-acetyltransferase (EC 2.3.1.157)	fig|439375.7.peg.3805	fig|204722.5.peg.2799
			Glucosamine-6-phosphate deaminase [isomerizing], alternative (EC 3.5.99.6)	fig|439375.7.peg.1524	fig|204722.5.peg.3130
			Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16)	fig|439375.7.peg.3804	fig|204722.5.peg.2798
			N-acetylglucosamine-1-phosphate uridyltransferase (EC 2.7.7.23)	fig|439375.7.peg.3805	fig|204722.5.peg.2799
			N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)	fig|439375.7.peg.1525	fig|204722.5.peg.3129
			N-acetylmuramic acid 6-phosphate etherase (EC 4.2.-.-)	fig|439375.7.peg.3275	
			Phosphoglucosamine mutase (EC 5.4.2.10)	fig|439375.7.peg.1280	fig|204722.5.peg.1717
			UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.1.1.158)	fig|439375.7.peg.1847	fig|204722.5.peg.1455
			UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	fig|439375.7.peg.350, fig|439375.7.peg.3273	fig|204722.5.peg.263
	Gram-Negative cell wall components	KDO2-Lipid A biosynthesis	2-Keto-3-deoxy-D-manno-octulosonate-8-phosphate synthase (EC 2.5.1.55)	fig|439375.7.peg.2161	fig|204722.5.peg.1153
			3-deoxy-D-manno-octulosonic-acid transferase (EC 2.-.-.-)	fig|439375.7.peg.3197	fig|204722.5.peg.2432
			3-deoxy-manno-octulosonate cytidylyltransferase (EC 2.7.7.38)	fig|439375.7.peg.17	fig|204722.5.peg.42
			Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase (EC 2.3.1.129)	fig|439375.7.peg.2144	fig|204722.5.peg.1171
			Lipid A biosynthesis lauroyl acyltransferase (EC 2.3.1.-)	fig|439375.7.peg.2505	fig|204722.5.peg.861
			Lipid A export ATP-binding/permease protein MsbA (EC 3.6.3.25)	fig|439375.7.peg.1394	fig|204722.5.peg.3275
			Lipid-A-disaccharide synthase (EC 2.4.1.182)	fig|439375.7.peg.2146	fig|204722.5.peg.1169
			Lipopolysaccharide ABC transporter, ATP-binding protein LptB	fig|439375.7.peg.180	fig|204722.5.peg.163
			Protein of unknown function DUF1009 clustered with KDO2-Lipid A biosynthesis genes	fig|439375.7.peg.2145	fig|204722.5.peg.1170
			Tetraacyldisaccharide 4'-kinase (EC 2.7.1.130)	fig|439375.7.peg.3198	fig|204722.5.peg.2433
			UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase (EC 2.3.1.-)	fig|439375.7.peg.2142	fig|204722.5.peg.1173
			UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase (EC 3.5.1.-)	fig|439375.7.peg.1852	fig|204722.5.peg.1449

		Lipid A-Ara4N pathway (Polymyxin resistance)	Polymyxin resistance protein ArnC, glycosyl transferase (EC 2.4.-.-)		fig|204722.5.peg.2355
			Polymyxin resistance protein ArnT, undecaprenyl phosphate-alpha-L-Ara4N transferase		fig|204722.5.peg.2357
			UDP-glucose dehydrogenase (EC 1.1.1.22)	fig|439375.7.peg.1810, fig|439375.7.peg.4591	fig|204722.5.peg.2760
		Lipopolysaccharide-related cluster in Alphaproteobacteria	3-deoxy-D-manno-octulosonic-acid transferase (EC 2.-.-.-)	fig|439375.7.peg.3197	fig|204722.5.peg.2432
			FIG043197: Inositol monophosphatase family protein	fig|439375.7.peg.3194	fig|204722.5.peg.2429
			Lipid A export ATP-binding/permease protein MsbA (EC 3.6.3.25)	fig|439375.7.peg.1394	fig|204722.5.peg.3275
			Murein endopeptidase	fig|439375.7.peg.1398	fig|204722.5.peg.3272
			Protein of unknown function DUF374	fig|439375.7.peg.3196	fig|204722.5.peg.441, fig|204722.5.peg.2431
			Tetraacyldisaccharide 4'-kinase (EC 2.7.1.130)	fig|439375.7.peg.3198	fig|204722.5.peg.2433
			TldE/PmbA protein, part of proposed TldE/TldD proteolytic complex (PMID 12029038)	fig|439375.7.peg.3193	fig|204722.5.peg.2428
			Uncharacterized protein, Bsl7517 homolog	fig|439375.7.peg.3195	fig|204722.5.peg.2430
	Biotin	Biotin biosynthesis	3-ketoacyl-CoA thiolase (EC 2.3.1.16)	fig|439375.7.peg.4207	fig|204722.5.peg.3009
			8-amino-7-oxononanoate synthase (EC 2.3.1.47)	fig|439375.7.peg.2964	fig|204722.5.peg.2711
			Adenosylmethionine-8-amino-7-oxononanoate aminotransferase (EC 2.6.1.62)	fig|439375.7.peg.2962, fig|439375.7.peg.2997	fig|204722.5.peg.2709
			Biotin synthase (EC 2.8.1.6)	fig|439375.7.peg.2965	fig|204722.5.peg.2712
			Biotin synthesis protein bioZ	fig|439375.7.peg.2961	fig|204722.5.peg.2708
			Biotin-protein ligase (EC 6.3.4.15)	fig|439375.7.peg.2541	fig|204722.5.peg.826
			Dethiobiotin synthetase (EC 6.3.3.3)	fig|439375.7.peg.2963	fig|204722.5.peg.2710
			Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	fig|439375.7.peg.396, fig|439375.7.peg.2839	fig|204722.5.peg.302
			predicted biotin regulatory protein BioR (GntR family)	fig|439375.7.peg.1252	fig|204722.5.peg.1745
			Substrate-specific component BioY of biotin ECF transporter	fig|439375.7.peg.729, fig|439375.7.peg.1251	fig|204722.5.peg.522, fig|204722.5.peg.1746
	Coenzyme A	Coenzyme A Biosynthesis	3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)	fig|439375.7.peg.454	fig|204722.5.peg.343
			Dephospho-CoA kinase (EC 2.7.1.24)	fig|439375.7.peg.895	fig|204722.5.peg.2105
			Ketol-acid reductoisomerase (EC 1.1.1.86)	fig|439375.7.peg.1914	fig|204722.5.peg.1405
			Pantoate--beta-alanine ligase (EC 6.3.2.1)	fig|439375.7.peg.453	fig|204722.5.peg.342
			Pantothenate kinase (EC 2.7.1.33)	fig|439375.7.peg.877	fig|204722.5.peg.2124
			Phosphopantetheine adenylyltransferase (EC 2.7.7.3)	fig|439375.7.peg.2290	fig|204722.5.peg.1116
			Phosphopantothenoylcysteine decarboxylase (EC 4.1.1.36)	fig|439375.7.peg.1379	fig|204722.5.peg.3288
			Phosphopantothenoylcysteine synthetase (EC 6.3.2.5)	fig|439375.7.peg.1379	fig|204722.5.peg.3288
			5-FCL-like protein	fig|439375.7.peg.3127, fig|439375.7.peg.3131	
			Glycine oxidase ThiO (EC 1.4.3.19)	fig|439375.7.peg.304	fig|204722.5.peg.223
			Hydroxymethylpyrimidine ABC transporter, ATPase component	fig|439375.7.peg.4749	
			Hydroxymethylpyrimidine ABC transporter, substrate-binding component	fig|439375.7.peg.300, fig|439375.7.peg.3130, fig|439375.7.peg.3749, fig|439375.7.peg.4042, fig|439375.7.peg.4748	fig|204722.5.peg.219, fig|204722.5.peg.2501

Cofactors, Vitamins, Prosthetic Groups, Pigments	Thiamin biosynthesis	Hydroxymethylpyrimidine ABC transporter, transmembrane component	fig|439375.7.peg.298, fig|439375.7.peg.3750, fig|439375.7.peg.4039, fig|439375.7.peg.4750	fig|204722.5.peg.217, fig|204722.5.peg.2502
		Phosphomethylpyrimidine kinase (EC 2.7.4.7)	fig|439375.7.peg.305	fig|204722.5.peg.224
		Sulfur carrier protein ThiS	fig|439375.7.peg.303	fig|204722.5.peg.222
		Thiamin ABC transporter, ATPase component	fig|439375.7.peg.1193	fig|204722.5.peg.1786
		Thiamin ABC transporter, substrate-binding component	fig|439375.7.peg.1195	fig|204722.5.peg.1784
		Thiamin ABC transporter, transmembrane component	fig|439375.7.peg.1194, fig|439375.7.peg.4401	fig|204722.5.peg.1785, fig|204722.5.peg.2331
		Thiamin pyrophosphokinase (EC 2.7.6.2)	fig|439375.7.peg.1196	fig|204722.5.peg.1783
		Thiaminase II (EC 3.5.99.2)	fig|439375.7.peg.299, fig|439375.7.peg.528	fig|204722.5.peg.218
		Thiamin-phosphate pyrophosphorylase (EC 2.5.1.3)	fig|439375.7.peg.301, fig|439375.7.peg.1262	fig|204722.5.peg.220, fig|204722.5.peg.1734
		Thiazole biosynthesis protein ThiG	fig|439375.7.peg.302	fig|204722.5.peg.221
Folate and pterines	Folate Biosynthesis	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase (EC 2.7.6.3)	fig|439375.7.peg.2223	fig|204722.5.peg.1043
		5-formyltetrahydrofolate cyclo-ligase (EC 6.3.3.2)	fig|439375.7.peg.1247	fig|204722.5.peg.1750
		Aminodeoxychorismate lyase (EC 4.1.3.38)	fig|439375.7.peg.4435	fig|204722.5.peg.2299
		Dihydrofolate reductase (EC 1.5.1.3)	fig|439375.7.peg.1387, fig|439375.7.peg.1894	fig|204722.5.peg.1423
		Dihydrofolate synthase (EC 6.3.2.12)	fig|439375.7.peg.859	fig|204722.5.peg.2143
		Dihydroneopterin aldolase (EC 4.1.2.25)	fig|439375.7.peg.2222	fig|204722.5.peg.1042
		Dihydropteroate synthase (EC 2.5.1.15)	fig|439375.7.peg.2221	fig|204722.5.peg.1041
		FolM Alternative dihydrofolate reductase 1	fig|439375.7.peg.2727	fig|204722.5.peg.712
		Folylpolyglutamate synthase (EC 6.3.2.17)	fig|439375.7.peg.859	fig|204722.5.peg.2143
		GTP cyclohydrolase I (EC 3.5.4.16) type 1	fig|439375.7.peg.2266	fig|204722.5.peg.1089
		Methionyl-tRNA formyltransferase (EC 2.1.2.9)	fig|439375.7.peg.1410	fig|204722.5.peg.3259
		Methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5)	fig|439375.7.peg.4132	fig|204722.5.peg.2995
		Para-aminobenzoate synthase, amidotransferase component (EC 2.6.1.85)	fig|439375.7.peg.1682	fig|204722.5.peg.1596
		Para-aminobenzoate synthase, aminase component (EC 2.6.1.85)	fig|439375.7.peg.4434	fig|204722.5.peg.2300
		Serine hydroxymethyltransferase (EC 2.1.2.1)	fig|439375.7.peg.2664	fig|204722.5.peg.776
		Thymidylate synthase (EC 2.1.1.45)	fig|439375.7.peg.1893	fig|204722.5.peg.1424
	Molybdenum cofactor biosynthesis	GTP cyclohydrolase I (EC 3.5.4.16) type 1	fig|439375.7.peg.2266	fig|204722.5.peg.1089
		GTP cyclohydrolase II (EC 3.5.4.25)	fig|439375.7.peg.577	fig|204722.5.peg.444
		Molybdate-binding domain of ModE	fig|439375.7.peg.3521	
		Molybdenum ABC transporter, periplasmic molybdenum-binding protein ModA (TC 3.A.1.8.1)	fig|439375.7.peg.4427	fig|204722.5.peg.2309
		Molybdenum cofactor biosynthesis protein MoaA	fig|439375.7.peg.2346	fig|204722.5.peg.971
		Molybdenum cofactor biosynthesis protein MoaC	fig|439375.7.peg.2152	fig|204722.5.peg.1162
		Molybdenum cofactor biosynthesis protein MoaD		fig|204722.5.peg.709
		Molybdenum cofactor biosynthesis protein MoaE	fig|439375.7.peg.2731	fig|204722.5.peg.708
		Molybdenum transport ATP-binding protein ModC (TC 3.A.1.8.1)	fig|439375.7.peg.4425	fig|204722.5.peg.2311

itamins, Prosthetic Groups, Pigments		Molybdenum cofactor biosynthesis	Molybdenum transport system permease protein ModB (TC 3.A.1.8.1)	fig|439375.7.peg.4426	fig|204722.5.peg.2310
			Molybdopterin biosynthesis enzyme	fig|439375.7.peg.48	fig|204722.5.peg.44
			Molybdopterin biosynthesis Mog protein, molybdochelatase	fig|439375.7.peg.3681	fig|204722.5.peg.2714
			Molybdopterin biosynthesis protein MoeA	fig|439375.7.peg.2151	fig|204722.5.peg.1163
			Molybdopterin biosynthesis protein MoeB	fig|439375.7.peg.6	fig|204722.5.peg.5
			Molybdopterin-guanine dinucleotide biosynthesis protein MobA	fig|439375.7.peg.2348	fig|204722.5.peg.970
			Molybdopterin-guanine dinucleotide biosynthesis protein MobB	fig|439375.7.peg.2349	fig|204722.5.peg.969
		Pterin carbinolamine dehydratase	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)	fig|439375.7.peg.4605	
			Fumarylacetoacetate hydrolase family protein	fig|439375.7.peg.75, fig|439375.7.peg.3926	fig|204722.5.peg.66
			Pterin-4-alpha-carbinolamine dehydratase (EC 4.2.1.96)	fig|439375.7.peg.97	fig|204722.5.peg.84
	Lipoic acid	Lipoic acid metabolism	Biotin-protein ligase (EC 6.3.4.15)	fig|439375.7.peg.2541	fig|204722.5.peg.826
			Lipoate synthase	fig|439375.7.peg.2171	fig|204722.5.peg.1144
			Lipoate-protein ligase A	fig|439375.7.peg.2329	
			Octanoate-[acyl-carrier-protein]-protein-N-octanoyltransferase	fig|439375.7.peg.3817	fig|204722.5.peg.2805
	NAD and NADP	NAD and NADP cofactor biosynthesis global	3-hydroxyanthranilate 3,4-dioxygenase (EC 1.13.11.6)	fig|439375.7.peg.4578	
			ADP-ribose pyrophosphatase (EC 3.6.1.13)	fig|439375.7.peg.4315	
			Amidases related to nicotinamidase	fig|439375.7.peg.4489, fig|439375.7.peg.4664	
			Glutamine amidotransferase chain of NAD synthetase	fig|439375.7.peg.2203	fig|204722.5.peg.1026
			Iojap protein	fig|439375.7.peg.1107	fig|204722.5.peg.1873
			Isochorismatase (EC 3.3.2.1) of siderophore biosynthesis		fig|204722.5.peg.2236
			L-aspartate oxidase (EC 1.4.3.16)	fig|439375.7.peg.457	
			NAD kinase (EC 2.7.1.23)	fig|439375.7.peg.2367	fig|204722.5.peg.952
			NAD synthetase (EC 6.3.1.5)	fig|439375.7.peg.2203	fig|204722.5.peg.1026
			Niacin transporter NiaP	fig|439375.7.peg.3724	fig|204722.5.peg.2747
			Nicotinamidase (EC 3.5.1.19)	fig|439375.7.peg.1804	fig|204722.5.peg.1491
			Nicotinamidase family protein YcaC	fig|439375.7.peg.4157, fig|439375.7.peg.4161	
			Nicotinate phosphoribosyltransferase (EC 2.4.2.11)	fig|439375.7.peg.133	fig|204722.5.peg.116
			Nicotinate-nucleotide adenylyltransferase (EC 2.7.7.18)	fig|439375.7.peg.1105	fig|204722.5.peg.1874
			NMN 5'-nucleotidase, extracellular (EC 3.1.3.5)	fig|439375.7.peg.2630	
			Quinolinate phosphoribosyltransferase [decarboxylating] (EC 2.4.2.19)	fig|439375.7.peg.458	
			Quinolinate synthetase (EC 4.1.99.-)	fig|439375.7.peg.456	
	Pyridoxine	Pyridoxin (Vitamin B6) Biosynthesis	1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7)	fig|439375.7.peg.584	fig|204722.5.peg.451
			4-hydroxythreonine-4-phosphate dehydrogenase (EC 1.1.1.262)	fig|439375.7.peg.2746, fig|439375.7.peg.3247	fig|204722.5.peg.695
			D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	fig|439375.7.peg.10, fig|439375.7.peg.1286, fig|439375.7.peg.1445, fig|439375.7.peg.3254, fig|439375.7.peg.3908, fig|439375.7.peg.4999	fig|204722.5.peg.6, fig|204722.5.peg.1712, fig|204722.5.peg.2671, fig|204722.5.peg.3205

Cofactors, Vi	Pyridoxine	Pyridoxin (Vitamin B6) Biosynthesis	NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	fig|439375.7.peg.1242	fig|204722.5.peg.1755
			Phosphoserine aminotransferase (EC 2.6.1.52)	fig|439375.7.peg.1285	fig|204722.5.peg.1714
			Predicted transcriptional regulator of pyridoxine metabolism	fig|439375.7.peg.4308	■
			Pyridoxal kinase (EC 2.7.1.35)	fig|439375.7.peg.1121, fig|439375.7.peg.4310	fig|204722.5.peg.1860
			Pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5)	fig|439375.7.peg.568	fig|204722.5.peg.432
			Pyridoxine 5'-phosphate synthase (EC 2.6.99.2)	fig|439375.7.peg.1911	fig|204722.5.peg.1409
	Quinone cofactors	Ubiquinone Biosynthesis	2-octaprenyl-6-methoxyphenol hydroxylase (EC 1.14.13.-)	fig|439375.7.peg.1002, fig|439375.7.peg.3796	fig|204722.5.peg.1933, fig|204722.5.peg.2789
			3-demethylubiquinone-9 3-methyltransferase (EC 2.1.1.64)	fig|439375.7.peg.1083	fig|204722.5.peg.1907
			3-polyprenyl-4-hydroxybenzoate carboxy-lyase (EC 4.1.1.-)	fig|439375.7.peg.3268, fig|439375.7.peg.4962	fig|204722.5.peg.2509
			3-polyprenyl-4-hydroxybenzoate carboxy-lyase UbiX (EC 4.1.1.-)	fig|439375.7.peg.3269, fig|439375.7.peg.4963	fig|204722.5.peg.2510
			4-hydroxybenzoate polyprenyltransferase (EC 2.5.1.-)	fig|439375.7.peg.567	fig|204722.5.peg.431
			Ubiquinone biosynthesis monooxygenase UbiB	fig|439375.7.peg.1378	fig|204722.5.peg.3289
			Ubiquinone/menaquinone biosynthesis methyltransferase UbiE (EC 2.1.1.-)	fig|439375.7.peg.1377	fig|204722.5.peg.3290
	Riboflavin, FMN, FAD	riboflavin to FAD	3,4-dihydroxy-2-butanone 4-phosphate synthase	fig|439375.7.peg.577	fig|204722.5.peg.444
			FMN adenylyltransferase (EC 2.7.7.2)	fig|439375.7.peg.3181	fig|204722.5.peg.2415
			Riboflavin kinase (EC 2.7.1.26)	fig|439375.7.peg.3181	fig|204722.5.peg.2415
			Riboflavin synthase alpha chain (EC 2.5.1.9)	fig|439375.7.peg.2661	fig|204722.5.peg.779
		Riboflavin, FMN and FAD metabolism	3,4-dihydroxy-2-butanone 4-phosphate synthase	fig|439375.7.peg.577	fig|204722.5.peg.444
			5-amino-6-(5-phosphoribosylamino)uracil reductase (EC 1.1.1.193)	fig|439375.7.peg.2662	fig|204722.5.peg.778
			6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9)	fig|439375.7.peg.2660, fig|439375.7.peg.3985	fig|204722.5.peg.780, fig|204722.5.peg.2906
			Diaminohydroxyphosphoribosylaminopyrimidine deaminase (EC 3.5.4.26)	fig|439375.7.peg.2662	fig|204722.5.peg.778
			FMN adenylyltransferase (EC 2.7.7.2)	fig|439375.7.peg.3181	fig|204722.5.peg.2415
			GTP cyclohydrolase II (EC 3.5.4.25)	fig|439375.7.peg.577	fig|204722.5.peg.444
			Riboflavin kinase (EC 2.7.1.26)	fig|439375.7.peg.3181	fig|204722.5.peg.2415
			Riboflavin synthase alpha chain (EC 2.5.1.9)	fig|439375.7.peg.2661	fig|204722.5.peg.779
		Cobalamin synthesis	Adenosylcobinamide-phosphate guanylyltransferase (EC 2.7.7.62)	fig|439375.7.peg.1975	fig|204722.5.peg.1330
			Adenosylcobinamide-phosphate synthase	fig|439375.7.peg.1991	fig|204722.5.peg.1316
			Cob(I)alamin adenosyltransferase (EC 2.5.1.17)	fig|439375.7.peg.1978	fig|204722.5.peg.1327
			Cobalamin biosynthesis protein BluB	fig|439375.7.peg.1388	fig|204722.5.peg.3279
			Cobalamin biosynthesis protein CbiG	fig|439375.7.peg.1996	fig|204722.5.peg.1311, fig|204722.5.peg.1323
			Cobalamin synthase	fig|439375.7.peg.2491	fig|204722.5.peg.877
			Cobalt-precorrin-2 C20-methyltransferase (EC 2.1.1.130)	fig|439375.7.peg.1997	fig|204722.5.peg.1310
			Cobalt-precorrin-3b C17-methyltransferase	fig|439375.7.peg.1996	fig|204722.5.peg.1311
			Cobalt-precorrin-4 C11-methyltransferase (EC 2.1.1.133)	fig|439375.7.peg.1985	fig|204722.5.peg.1322
			Cobalt-precorrin-6 synthase, anaerobic	fig|439375.7.peg.1987	fig|204722.5.peg.1320
			Cobalt-precorrin-6x reductase (EC 1.3.1.54)	fig|439375.7.peg.1986	fig|204722.5.peg.1321
			Cobalt-precorrin-8x methylmutase (EC 5.4.1.2)	fig|439375.7.peg.1998	fig|204722.5.peg.1309

	Tetrapyrroles		Cobyric acid synthase	fig|439375.7.peg.1972	fig|204722.5.peg.1333
			Cobyrinic acid A,C-diamide synthase	fig|439375.7.peg.1989	fig|204722.5.peg.1318
			L-threonine 3-O-phosphate decarboxylase (EC 4.1.1.81)	fig|439375.7.peg.1990	fig|204722.5.peg.1317
			Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase (EC 2.4.2.21)	fig|439375.7.peg.2490	fig|204722.5.peg.878
			Threonine kinase in B12 biosynthesis	fig|439375.7.peg.691	■
		Coenzyme B12 biosynthesis	5,6-dimethylbenzimidazole synthase, flavin destructase family	fig|439375.7.peg.1388	fig|204722.5.peg.3279
			Adenosylcobinamide amidohydrolase (EC 3.5.1.90)	fig|439375.7.peg.4628	■
			Adenosylcobinamide-phosphate guanylyltransferase (EC 2.7.7.62)	fig|439375.7.peg.1975	fig|204722.5.peg.1330
			Adenosylcobinamide-phosphate synthase	fig|439375.7.peg.1991	fig|204722.5.peg.1316
			Aerobic cobaltochelatase CobS subunit (EC 6.6.1.2)	fig|439375.7.peg.958	fig|204722.5.peg.2057
			Aerobic cobaltochelatase CobT subunit (EC 6.6.1.2)	fig|439375.7.peg.959	fig|204722.5.peg.2056
			CblX, a non-orthologous displasment for Alpha-ribazole-5'-phosphate phosphatase	fig|439375.7.peg.2492	fig|204722.5.peg.876
			CblY, a non-orthologous displasment for Alpha-ribazole-5'-phosphate phosphatase	fig|439375.7.peg.2493	fig|204722.5.peg.875
			Cob(I)alamin adenosyltransferase (EC 2.5.1.17)	fig|439375.7.peg.1978	fig|204722.5.peg.1327
			Cob(I)alamin adenosyltransferase PduO (EC 2.5.1.17)	fig|439375.7.peg.1056	fig|204722.5.peg.2012
			Cobalamin biosynthesis protein CbiG	fig|439375.7.peg.1996	fig|204722.5.peg.1311, fig|204722.5.peg.1323
			Cobalamin biosynthesis protein CobG	fig|439375.7.peg.1999	fig|204722.5.peg.1308
			Cobalamin synthase	fig|439375.7.peg.2491	fig|204722.5.peg.877
			Cobalt-precorrin-2 C20-methyltransferase (EC 2.1.1.130)	fig|439375.7.peg.1997	fig|204722.5.peg.1310
			Cobalt-precorrin-3b C17-methyltransferase	fig|439375.7.peg.1996	fig|204722.5.peg.1311
			Cobalt-precorrin-4 C11-methyltransferase (EC 2.1.1.133)	fig|439375.7.peg.1985	fig|204722.5.peg.1322
			Cobalt-precorrin-6 synthase, anaerobic	fig|439375.7.peg.1987	fig|204722.5.peg.1320
			Cobalt-precorrin-6x reductase (EC 1.3.1.54)	fig|439375.7.peg.1986	fig|204722.5.peg.1321
			Cobalt-precorrin-6y C15-methyltransferase [decarboxylating] (EC 2.1.1.-)	fig|439375.7.peg.2000	fig|204722.5.peg.1307
			Cobalt-precorrin-6y C5-methyltransferase (EC 2.1.1.-)	fig|439375.7.peg.2000	fig|204722.5.peg.1307
			Cobalt-precorrin-8x methylmutase (EC 5.4.1.2)	fig|439375.7.peg.1998	fig|204722.5.peg.1309
			CobN component of cobalt chelatase involved in B12 biosynthesis	fig|439375.7.peg.1977	fig|204722.5.peg.1328
			CobW GTPase involved in cobalt insertion for B12 biosynthesis	fig|439375.7.peg.1976	fig|204722.5.peg.1329
			Cobyric acid synthase	fig|439375.7.peg.1972	fig|204722.5.peg.1333
			Cobyrinic acid A,C-diamide synthase	fig|439375.7.peg.1989	fig|204722.5.peg.1318
			L-threonine 3-O-phosphate decarboxylase (EC 4.1.1.81)	fig|439375.7.peg.1990	fig|204722.5.peg.1317
			Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase (EC 2.4.2.21)	fig|439375.7.peg.2490	fig|204722.5.peg.878
			Outer membrane vitamin B12 receptor BtuB	fig|439375.7.peg.1927	fig|204722.5.peg.1371
			Predicted cobalt transporter CbtA	fig|439375.7.peg.1974	fig|204722.5.peg.1331
			Threonine kinase in B12 biosynthesis	fig|439375.7.peg.691	■
			Uroporphyrinogen-III methyltransferase (EC 2.1.1.107)	fig|439375.7.peg.199, fig|439375.7.peg.1988	fig|204722.5.peg.188, fig|204722.5.peg.1319
			Vitamin B12 ABC transporter, ATPase component BtuD	fig|439375.7.peg.1930, fig|439375.7.peg.2966	fig|204722.5.peg.1368

			Vitamin B12 ABC transporter, B12-binding component BtuF	fig|439375.7.peg.1928	fig|204722.5.peg.1370
			Vitamin B12 ABC transporter, permease component BtuC	fig|439375.7.peg.1929	fig|204722.5.peg.1369
		Heme and Siroheme Biosynthesis	5-aminolevulinate synthase (EC 2.3.1.37)	fig|439375.7.peg.438	fig|204722.5.peg.332
			Coproporphyrinogen III oxidase, aerobic (EC 1.3.3.3)	fig|439375.7.peg.1703	fig|204722.5.peg.1577
			Coproporphyrinogen III oxidase, oxygen-independent (EC 1.3.99.22)	fig|439375.7.peg.2775	fig|204722.5.peg.668, fig|204722.5.peg.3430
			Ferrochelatase, protoheme ferro-lyase (EC 4.99.1.1)	fig|439375.7.peg.4439	fig|204722.5.peg.2296
			Glutamate-1-semialdehyde aminotransferase (EC 5.4.3.8)		fig|204722.5.peg.2650, fig|204722.5.peg.3335
			Glutamyl-tRNA synthetase (EC 6.1.1.17)	fig|439375.7.peg.2148	fig|204722.5.peg.1167
			Porphobilinogen deaminase (EC 2.5.1.61)	fig|439375.7.peg.1021	fig|204722.5.peg.1920
			Porphobilinogen synthase (EC 4.2.1.24)	fig|439375.7.peg.2670	fig|204722.5.peg.770
			Precorrin-2 oxidase (EC 1.3.1.76)	fig|439375.7.peg.199	fig|204722.5.peg.188
			Radical SAM family enzyme, similar to coproporphyrinogen III oxidase, oxygen-independent, clustered with nucleoside-triphosphatase RdgB	fig|439375.7.peg.196	fig|204722.5.peg.184
			Sirohydrochlorin ferrochelatase (EC 4.99.1.4)	fig|439375.7.peg.199	fig|204722.5.peg.188
			Uroporphyrinogen III decarboxylase (EC 4.1.1.37)	fig|439375.7.peg.899	fig|204722.5.peg.2100
			Uroporphyrinogen-III methyltransferase (EC 2.1.1.107)	fig|439375.7.peg.199, fig|439375.7.peg.1988	fig|204722.5.peg.188, fig|204722.5.peg.1319
			Uroporphyrinogen-III synthase (EC 4.2.1.75)	fig|439375.7.peg.1022	fig|204722.5.peg.1919
	DNA Metabolism	DNA structural proteins, bacterial	DNA-binding protein HU	fig|439375.7.peg.4842	
			DNA-binding protein HU-beta	fig|439375.7.peg.2315	fig|204722.5.peg.1126
			Integration host factor alpha subunit	fig|439375.7.peg.2651	fig|204722.5.peg.788
			Integration host factor beta subunit	fig|439375.7.peg.175	fig|204722.5.peg.159
		Restriction-Modification System	Putative predicted metal-dependent hydrolase		fig|204722.5.peg.3059
			Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72)		fig|204722.5.peg.3056
			Type I restriction-modification system, restriction subunit R (EC 3.1.21.3)		fig|204722.5.peg.3058
			Type I restriction-modification system, specificity subunit S (EC 3.1.21.3)		fig|204722.5.peg.3057
		Type I Restriction-Modification	Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72)		fig|204722.5.peg.3056
			Type I restriction-modification system, restriction subunit R (EC 3.1.21.3)		fig|204722.5.peg.3058
			Type I restriction-modification system, specificity subunit S (EC 3.1.21.3)		fig|204722.5.peg.3057
		2-phosphoglycolate salvage	Phosphoglycolate phosphatase (EC 3.1.3.18)	fig|439375.7.peg.2197	fig|204722.5.peg.1019
			Putative phosphatase YfbT	fig|439375.7.peg.2495	fig|204722.5.peg.872
			Similar to phosphoglycolate phosphatase, clustered with ribosomal large subunit pseudouridine synthase C	fig|439375.7.peg.2191	fig|204722.5.peg.1013
		DNA Repair Base Excision	ATP-dependent DNA ligase (EC 6.5.1.1) clustered with Ku protein, LigD	fig|439375.7.peg.4495	
			ATP-dependent DNA ligase (EC 6.5.1.1) LigC	fig|439375.7.peg.4219	
			DNA ligase (EC 6.5.1.2)	fig|439375.7.peg.1855	fig|204722.5.peg.1446
			DNA polymerase I (EC 2.7.7.7)	fig|439375.7.peg.146	fig|204722.5.peg.127
			DNA-3-methyladenine glycosylase (EC 3.2.2.20)	fig|439375.7.peg.3167	fig|204722.5.peg.2401
			Endonuclease III (EC 4.2.99.18)	fig|439375.7.peg.187	fig|204722.5.peg.173

DNA Metabolism	DNA repair		Formamidopyrimidine-DNA glycosylase (EC 3.2.2.23)	fig|439375.7.peg.754	fig|204722.5.peg.2220
			Ku domain protein	fig|439375.7.peg.4494, fig|439375.7.peg.4496	
			Single-stranded-DNA-specific exonuclease RecJ (EC 3.1.-.-)	fig|439375.7.peg.2021	fig|204722.5.peg.1289
		DNA repair, bacterial	A/G-specific adenine glycosylase (EC 3.2.2.-)	fig|439375.7.peg.647	fig|204722.5.peg.508
			ADA regulatory protein	fig|439375.7.peg.508, fig|439375.7.peg.3442	fig|204722.5.peg.385, fig|204722.5.peg.3108
			Alkylated DNA repair protein AlkB	fig|439375.7.peg.3734	fig|204722.5.peg.2748
			DNA polymerase IV (EC 2.7.7.7)	fig|439375.7.peg.2404, fig|439375.7.peg.3845	fig|204722.5.peg.2831
			DNA polymerase-like protein PA0670	fig|439375.7.peg.82, fig|439375.7.peg.3296	fig|204722.5.peg.73
			DNA recombination protein RmuC	fig|439375.7.peg.1408	fig|204722.5.peg.3261
			DNA repair protein RadA	fig|439375.7.peg.601	fig|204722.5.peg.464
			DNA repair protein RadC	fig|439375.7.peg.2009	fig|204722.5.peg.1305
			DNA repair protein RecN	fig|439375.7.peg.1854	fig|204722.5.peg.1447
			DNA-cytosine methyltransferase (EC 2.1.1.37)	fig|439375.7.peg.1583	
			DNA-damage-inducible protein J		fig|204722.5.peg.2592
			Exodeoxyribonuclease III (EC 3.1.11.2)	fig|439375.7.peg.1008, fig|439375.7.peg.2485	fig|204722.5.peg.884, fig|204722.5.peg.2040
			Exodeoxyribonuclease VII large subunit (EC 3.1.11.6)	fig|439375.7.peg.3147	fig|204722.5.peg.2976
			Exodeoxyribonuclease VII small subunit (EC 3.1.11.6)	fig|439375.7.peg.579	fig|204722.5.peg.446
			Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63)	fig|439375.7.peg.205, fig|439375.7.peg.508, fig|439375.7.peg.3442	fig|204722.5.peg.194, fig|204722.5.peg.385, fig|204722.5.peg.3108
			RecA protein	fig|439375.7.peg.2088	fig|204722.5.peg.1223
			Single-stranded DNA-binding protein	fig|439375.7.peg.1612, fig|439375.7.peg.2309	fig|204722.5.peg.1123
			SOS-response repressor and protease LexA (EC 3.4.21.88)	fig|439375.7.peg.2150	fig|204722.5.peg.1164
		DNA repair, bacterial MutL-MutS system	DNA mismatch repair protein MutL	fig|439375.7.peg.3200	fig|204722.5.peg.2435
			DNA mismatch repair protein MutS	fig|439375.7.peg.169	fig|204722.5.peg.153
		DNA repair, bacterial photolyase	Deoxyribodipyrimidine photolyase (EC 4.1.99.3)	fig|439375.7.peg.361	
		DNA repair, bacterial RecFOR pathway	DNA recombination and repair protein RecF	fig|439375.7.peg.5	fig|204722.5.peg.4
			DNA recombination and repair protein RecO	fig|439375.7.peg.2767	fig|204722.5.peg.676
			RecA protein	fig|439375.7.peg.2088	fig|204722.5.peg.1223
			Recombination protein RecR	fig|439375.7.peg.24	fig|204722.5.peg.36
			Single-stranded DNA-binding protein	fig|439375.7.peg.1612, fig|439375.7.peg.2309	fig|204722.5.peg.1123
			Single-stranded-DNA-specific exonuclease RecJ (EC 3.1.-.-)	fig|439375.7.peg.2021	fig|204722.5.peg.1289
		DNA repair, UvrABC system	Excinuclease ABC subunit A	fig|439375.7.peg.2311	fig|204722.5.peg.1125
			Excinuclease ABC subunit B	fig|439375.7.peg.1741	fig|204722.5.peg.1537
			Excinuclease ABC subunit C	fig|439375.7.peg.2728	fig|204722.5.peg.711
		Nonhomologous End-Joining in Bacteria	ATP-dependent DNA ligase (EC 6.5.1.1) clustered with Ku protein, LigD	fig|439375.7.peg.4495	
			ATP-dependent DNA ligase (EC 6.5.1.1) LigC	fig|439375.7.peg.4219	
			Ku domain protein	fig|439375.7.peg.4494, fig|439375.7.peg.4496	
		Uracil-DNA glycosylase	Uracil-DNA glycosylase, family 4	fig|439375.7.peg.2804	fig|204722.5.peg.638
			Uracil-DNA glycosylase, family 5	fig|439375.7.peg.2781	fig|204722.5.peg.662

DNA replication	DNA topoisomerases, Type II, ATP-dependent	DNA gyrase subunit A (EC 5.99.1.3)	fig|439375.7.peg.2292	fig|204722.5.peg.1118
		DNA gyrase subunit B (EC 5.99.1.3)	fig|439375.7.peg.148	fig|204722.5.peg.129
		Topoisomerase IV subunit A (EC 5.99.1.-)	fig|439375.7.peg.2673	fig|204722.5.peg.767
		Topoisomerase IV subunit B (EC 5.99.1.-)	fig|439375.7.peg.3819	fig|204722.5.peg.2807
	DNA-replication	ATP-dependent DNA helicase RecG (EC 3.6.1.-)	fig|439375.7.peg.3803	fig|204722.5.peg.2797
		Chromosomal replication initiator protein DnaA	fig|439375.7.peg.3, fig|439375.7.peg.2711, fig|439375.7.peg.2834	fig|204722.5.peg.2, fig|204722.5.peg.588, fig|204722.5.peg.726
		Crossover junction endodeoxyribonuclease RuvC (EC 3.1.22.4)	fig|439375.7.peg.1266	fig|204722.5.peg.1731
		DNA polymerase I (EC 2.7.7.7)	fig|439375.7.peg.146	fig|204722.5.peg.127
		DNA polymerase III alpha subunit (EC 2.7.7.7)	fig|439375.7.peg.81, fig|439375.7.peg.2532, fig|439375.7.peg.3297	fig|204722.5.peg.72, fig|204722.5.peg.836
		DNA polymerase III beta subunit (EC 2.7.7.7)	fig|439375.7.peg.4	fig|204722.5.peg.3
		DNA polymerase III chi subunit (EC 2.7.7.7)	fig|439375.7.peg.2740	fig|204722.5.peg.702
		DNA polymerase III delta prime subunit (EC 2.7.7.7)	fig|439375.7.peg.2184	fig|204722.5.peg.1005
		DNA polymerase III delta subunit (EC 2.7.7.7)	fig|439375.7.peg.908	fig|204722.5.peg.2091
		DNA polymerase III epsilon subunit (EC 2.7.7.7)	fig|439375.7.peg.894	fig|204722.5.peg.2106
		DNA polymerase III subunits gamma and tau (EC 2.7.7.7)	fig|439375.7.peg.22	fig|204722.5.peg.38
		DNA primase (EC 2.7.7.-)	fig|439375.7.peg.1778	fig|204722.5.peg.1507
		DNA repair protein RecN	fig|439375.7.peg.1854	fig|204722.5.peg.1447
		Helicase PriA essential for oriC/DnaA-independent DNA replication	fig|439375.7.peg.1150	fig|204722.5.peg.1832
		Holliday junction DNA helicase RuvA	fig|439375.7.peg.1267	fig|204722.5.peg.1730
		Holliday junction DNA helicase RuvB	fig|439375.7.peg.1268	fig|204722.5.peg.1729
		RecA protein	fig|439375.7.peg.2088	fig|204722.5.peg.1223
		Recombination protein RecR	fig|439375.7.peg.24	fig|204722.5.peg.36
		Replicative DNA helicase (EC 3.6.1.-)	fig|439375.7.peg.247, fig|439375.7.peg.602, fig|439375.7.peg.824	fig|204722.5.peg.465
		Single-stranded-DNA-specific exonuclease RecJ (EC 3.1.-.-)	fig|439375.7.peg.2021	fig|204722.5.peg.1289
		Transcription-repair coupling factor	fig|439375.7.peg.3801	fig|204722.5.peg.2795
	Plasmid replication	Chromosome (plasmid) partitioning protein ParA	fig|439375.7.peg.906, fig|439375.7.peg.3337	fig|204722.5.peg.2093
		Chromosome (plasmid) partitioning protein ParB	fig|439375.7.peg.907	fig|204722.5.peg.2092
		Plasmid replication protein RepA	fig|439375.7.peg.4633, fig|439375.7.peg.4704, fig|439375.7.peg.4901, fig|439375.7.peg.4934, fig|439375.7.peg.4972	fig|204722.5.peg.3433
		Plasmid replication protein RepB	fig|439375.7.peg.4632, fig|439375.7.peg.4705, fig|439375.7.peg.4902, fig|439375.7.peg.4935, fig|439375.7.peg.4971	fig|204722.5.peg.3434

			Plasmid replication protein RepC	fig|439375.7.peg.4631, fig|439375.7.peg.4706, fig|439375.7.peg.4809, fig|439375.7.peg.4936, fig|439375.7.peg.4970	fig|204722.5.peg.2223
	Fatty acids	Acyl-CoA thioesterase II	Acyl-CoA thioesterase II (EC 3.1.2.-)	fig|439375.7.peg.1003	fig|204722.5.peg.1931
		Fatty Acid Biosynthesis FASII	(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase (EC 4.2.1.-)	fig|439375.7.peg.2143	fig|204722.5.peg.1172
			3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.60)	fig|439375.7.peg.780	fig|204722.5.peg.2210
			3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)	fig|439375.7.peg.610, fig|439375.7.peg.922, fig|439375.7.peg.925, fig|439375.7.peg.1189, fig|439375.7.peg.1235, fig|439375.7.peg.2206, fig|439375.7.peg.2341, fig|439375.7.peg.2646, fig|439375.7.peg.3083, fig|439375.7.peg.3513, fig|439375.7.peg.4128, fig|439375.7.peg.4758	fig|204722.5.peg.473, fig|204722.5.peg.729, fig|204722.5.peg.2073, fig|204722.5.peg.2077, fig|204722.5.peg.2252, fig|204722.5.peg.2990
			3-oxoacyl-[acyl-carrier-protein] synthase, KASI (EC 2.3.1.41)	fig|439375.7.peg.781	fig|204722.5.peg.2209
			3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.41)	fig|439375.7.peg.612, fig|439375.7.peg.2503	fig|204722.5.peg.476, fig|204722.5.peg.863
			3-oxoacyl-[acyl-carrier-protein] synthase, KASIII (EC 2.3.1.41)	fig|439375.7.peg.2652	fig|204722.5.peg.787
			Acetyl-coenzyme A carboxyl transferase alpha chain (EC 6.4.1.2)	fig|439375.7.peg.948	fig|204722.5.peg.2067
			Acetyl-coenzyme A carboxyl transferase beta chain (EC 6.4.1.2)	fig|439375.7.peg.858	fig|204722.5.peg.2144
			Acyl carrier protein	fig|439375.7.peg.242, fig|439375.7.peg.611, fig|439375.7.peg.1548, fig|439375.7.peg.2501	fig|204722.5.peg.474, fig|204722.5.peg.865
			Biotin carboxyl carrier protein of acetyl-CoA carboxylase	fig|439375.7.peg.2393	fig|204722.5.peg.921
			Biotin carboxylase of acetyl-CoA carboxylase (EC 6.3.4.14)	fig|439375.7.peg.2394	fig|204722.5.peg.919
			Enoyl-[acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9)	fig|439375.7.peg.572, fig|439375.7.peg.782	fig|204722.5.peg.435, fig|204722.5.peg.2208
			Enoyl-[acyl-carrier-protein] reductase [NADPH] (EC 1.3.1.10)	fig|439375.7.peg.3607	
			Holo-[acyl-carrier protein] synthase (EC 2.7.8.7)	fig|439375.7.peg.2771	fig|204722.5.peg.672
			Holo-[acyl-carrier protein] synthase, alternative (EC 2.7.8.7)		fig|204722.5.peg.2234
			Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)	fig|439375.7.peg.609	fig|204722.5.peg.472
			3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	fig|439375.7.peg.3071, fig|439375.7.peg.4195, fig|439375.7.peg.4206, fig|439375.7.peg.4885	fig|204722.5.peg.2440, fig|204722.5.peg.3008, fig|204722.5.peg.3311
			3-hydroxybutyryl-CoA dehydratase (EC 4.2.1.55)	fig|439375.7.peg.919	fig|204722.5.peg.2080

Fatty Acids, Lipids, and Isoprenoids	**Fatty Acids, Lipids, and Isoprenoids**	Polyhydroxybutyrate metabolism	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157)	fig|439375.7.peg.1062, fig|439375.7.peg.4885	fig|204722.5.peg.2006, fig|204722.5.peg.2440, fig|204722.5.peg.3311
			3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)	fig|439375.7.peg.4195, fig|439375.7.peg.4206	fig|204722.5.peg.3008
			3-ketoacyl-CoA thiolase (EC 2.3.1.16)	fig|439375.7.peg.4207	fig|204722.5.peg.3009
			Acetoacetyl-CoA synthetase (EC 6.2.1.16)	fig|439375.7.peg.37	fig|204722.5.peg.24
			Acetyl-CoA acetyltransferase (EC 2.3.1.9)	fig|439375.7.peg.1181, fig|439375.7.peg.3257, fig|439375.7.peg.3882, fig|439375.7.peg.4196, fig|439375.7.peg.4207	fig|204722.5.peg.1799, fig|204722.5.peg.2849, fig|204722.5.peg.3009
			D-beta-hydroxybutyrate dehydrogenase (EC 1.1.1.30)	fig|439375.7.peg.1172, fig|439375.7.peg.4191	fig|204722.5.peg.1806
			D-beta-hydroxybutyrate permease	fig|439375.7.peg.2572	■
			Enoyl-CoA hydratase (EC 4.2.1.17)	fig|439375.7.peg.564, fig|439375.7.peg.4192, fig|439375.7.peg.4195	fig|204722.5.peg.427
	Isoprenoids	Isoprenoid Biosynthesis	1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7)	fig|439375.7.peg.584	fig|204722.5.peg.451
			1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase (EC 1.17.7.1)	fig|439375.7.peg.1173	fig|204722.5.peg.1805
			2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (EC 4.6.1.12)	fig|439375.7.peg.2175	fig|204722.5.peg.1140
			2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase (EC 2.7.7.60)	fig|439375.7.peg.2175	fig|204722.5.peg.1140
			4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.148)	fig|439375.7.peg.547	fig|204722.5.peg.409
			4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2)	fig|439375.7.peg.629	fig|204722.5.peg.490
			Acetyl-CoA acetyltransferase (EC 2.3.1.9)	fig|439375.7.peg.1181, fig|439375.7.peg.3257, fig|439375.7.peg.3882, fig|439375.7.peg.4196, fig|439375.7.peg.4207	fig|204722.5.peg.1799, fig|204722.5.peg.2849, fig|204722.5.peg.3009
			Dimethylallyltransferase (EC 2.5.1.1)	fig|439375.7.peg.554, fig|439375.7.peg.1176	fig|204722.5.peg.416, fig|204722.5.peg.1804
			Geranyltranstransferase (farnesyldiphosphate synthase) (EC 2.5.1.10)	fig|439375.7.peg.554, fig|439375.7.peg.1176	fig|204722.5.peg.416, fig|204722.5.peg.1804
			Undecaprenyl pyrophosphate synthetase (EC 2.5.1.31)	fig|439375.7.peg.2138	fig|204722.5.peg.1177
		Polyprenyl Diphosphate Biosynthesis	Geranylgeranyl pyrophosphate synthetase (EC 2.5.1.29)	fig|439375.7.peg.554, fig|439375.7.peg.1176	fig|204722.5.peg.416, fig|204722.5.peg.1804
			Geranyltranstransferase (farnesyldiphosphate synthase) (EC 2.5.1.10)	fig|439375.7.peg.554, fig|439375.7.peg.1176	fig|204722.5.peg.416, fig|204722.5.peg.1804
			Octaprenyl-diphosphate synthase (EC 2.5.1.-)	fig|439375.7.peg.1176	fig|204722.5.peg.416, fig|204722.5.peg.1804
			Undecaprenyl pyrophosphate synthetase (EC 2.5.1.31)	fig|439375.7.peg.2138	fig|204722.5.peg.1177
			1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)	fig|439375.7.peg.802, fig|439375.7.peg.1035, fig|439375.7.peg.3032	fig|204722.5.peg.2032, fig|204722.5.peg.2189

	Phospholipids	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	Acyl carrier protein	fig|439375.7.peg.242, fig|439375.7.peg.611, fig|439375.7.peg.1548, fig|439375.7.peg.2501	fig|204722.5.peg.474, fig|204722.5.peg.865
			Acyl-phosphate:glycerol-3-phosphate O-acyltransferase PlsY	fig|439375.7.peg.3831	fig|204722.5.peg.2818
			Aerobic glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)	fig|439375.7.peg.289	fig|204722.5.peg.207
			Alcohol dehydrogenase (EC 1.1.1.1)	fig|439375.7.peg.292, fig|439375.7.peg.2504, fig|439375.7.peg.3765, fig|439375.7.peg.4052, fig|439375.7.peg.4825	fig|204722.5.peg.210, fig|204722.5.peg.862, fig|204722.5.peg.1075, fig|204722.5.peg.2614, fig|204722.5.peg.2948
			Aldehyde dehydrogenase (EC 1.2.1.3)	fig|439375.7.peg.291, fig|439375.7.peg.1348, fig|439375.7.peg.1385, fig|439375.7.peg.2980, fig|439375.7.peg.4960	fig|204722.5.peg.209, fig|204722.5.peg.1879, fig|204722.5.peg.3239, fig|204722.5.peg.3282, fig|204722.5.peg.3385, fig|204722.5.peg.3402
			Aldehyde dehydrogenase B (EC 1.2.1.22)	fig|439375.7.peg.297, fig|439375.7.peg.1529	fig|204722.5.peg.216, fig|204722.5.peg.3126
			Cardiolipin synthetase (EC 2.7.8.-)	fig|439375.7.peg.1383	fig|204722.5.peg.3284
			CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5)	fig|439375.7.peg.2729, fig|439375.7.peg.3028	fig|204722.5.peg.710
			CDP-diacylglycerol--serine O-phosphatidyltransferase (EC 2.7.8.8)	fig|439375.7.peg.595	fig|204722.5.peg.460
			Diacylglycerol kinase (EC 2.7.1.107)	fig|439375.7.peg.2202	fig|204722.5.peg.1025
			Glycerol kinase (EC 2.7.1.30)	fig|439375.7.peg.1135, fig|439375.7.peg.2592	fig|204722.5.peg.2660
			Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)	fig|439375.7.peg.2593, fig|439375.7.peg.3066, fig|439375.7.peg.3228	
			Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94)	fig|439375.7.peg.1019	fig|204722.5.peg.1923
			Phosphate:acyl-ACP acyltransferase PlsX	fig|439375.7.peg.2653	fig|204722.5.peg.786
			Phosphatidate cytidylyltransferase (EC 2.7.7.41)	fig|439375.7.peg.2139, fig|439375.7.peg.3033	fig|204722.5.peg.1176
			Phosphatidylglycerophosphatase B (EC 3.1.3.27)	fig|439375.7.peg.2695	fig|204722.5.peg.754, fig|204722.5.peg.2352
			Phosphatidylserine decarboxylase (EC 4.1.1.65)	fig|439375.7.peg.594	fig|204722.5.peg.459
	Triacylglycerols	Triacylglycerol metabolism	Lysophospholipase (EC 3.1.1.5)	fig|439375.7.peg.1814	fig|204722.5.peg.1485
			Lysophospholipase L2 (EC 3.1.1.5)	fig|439375.7.peg.4456	fig|204722.5.peg.2268
			Monoglyceride lipase (EC 3.1.1.23)	fig|439375.7.peg.1814	fig|204722.5.peg.1485
			Putative lipase in cluster with Phosphatidate cytidylyltransferase	fig|439375.7.peg.3029	
		ABC transporter alkylphosphonate	Phosphonate ABC transporter ATP-binding protein (TC 3.A.1.9.1)	fig|439375.7.peg.2297	
			Phosphonate ABC transporter permease protein phnE1 (TC 3.A.1.9.1)	fig|439375.7.peg.2294	

		(TC 3.A.1.9.1)	Phosphonate ABC transporter permease protein phnE2 (TC 3.A.1.9.1)	fig|439375.7.peg.2295	■
			Phosphonate ABC transporter phosphate-binding periplasmic component (TC 3.A.1.9.1)	fig|439375.7.peg.2296	■
		ABC transporter branched-chain amino acid (TC 3.A.1.4.1)	Branched-chain amino acid ABC transporter, amino acid-binding protein (TC 3.A.1.4.1)	fig|439375.7.peg.1992, fig|439375.7.peg.4571, fig|439375.7.peg.4661	fig|204722.5.peg.1315
			Branched-chain amino acid transport ATP-binding protein LivF (TC 3.A.1.4.1)	fig|439375.7.peg.1165, fig|439375.7.peg.1468, fig|439375.7.peg.3898, fig|439375.7.peg.4176, fig|439375.7.peg.4573, fig|439375.7.peg.4597, fig|439375.7.peg.4660	fig|204722.5.peg.1814, fig|204722.5.peg.1815, fig|204722.5.peg.2250, fig|204722.5.peg.2608, fig|204722.5.peg.2865, fig|204722.5.peg.3176, fig|204722.5.peg.3407, fig|204722.5.peg.3428
			Branched-chain amino acid transport ATP-binding protein LivG (TC 3.A.1.4.1)	fig|439375.7.peg.1164, fig|439375.7.peg.1469, fig|439375.7.peg.3897, fig|439375.7.peg.4598, fig|439375.7.peg.4662	fig|204722.5.peg.1816, fig|204722.5.peg.2249, fig|204722.5.peg.2606, fig|204722.5.peg.2607, fig|204722.5.peg.2864, fig|204722.5.peg.3175, fig|204722.5.peg.3427
			Branched-chain amino acid transport system permease protein LivM (TC 3.A.1.4.1)	fig|439375.7.peg.1163, fig|439375.7.peg.1466, fig|439375.7.peg.3896, fig|439375.7.peg.4174, fig|439375.7.peg.4575, fig|439375.7.peg.4599	fig|204722.5.peg.1817, fig|204722.5.peg.2248, fig|204722.5.peg.2863, fig|204722.5.peg.3178, fig|204722.5.peg.3425, fig|204722.5.peg.3426
			High-affinity branched-chain amino acid transport system permease protein LivH (TC 3.A.1.4.1)	fig|439375.7.peg.1162, fig|439375.7.peg.1467, fig|439375.7.peg.3895, fig|439375.7.peg.4173, fig|439375.7.peg.4576, fig|439375.7.peg.4600, fig|439375.7.peg.4659	fig|204722.5.peg.1818, fig|204722.5.peg.2247, fig|204722.5.peg.2605, fig|204722.5.peg.2862, fig|204722.5.peg.3177, fig|204722.5.peg.3405, fig|204722.5.peg.3424
			High-affinity leucine-specific transport system, periplasmic binding protein LivK (TC 3.A.1.4.1)	fig|439375.7.peg.1167, fig|439375.7.peg.1168, fig|439375.7.peg.4601	fig|204722.5.peg.1810, fig|204722.5.peg.1812, fig|204722.5.peg.2604, fig|204722.5.peg.2613, fig|204722.5.peg.3423
			Dipeptide transport ATP-binding protein DppD (TC 3.A.1.5.2)	fig|439375.7.peg.665, fig|439375.7.peg.1353, fig|439375.7.peg.1669, fig|439375.7.peg.2003, fig|439375.7.peg.3241, fig|439375.7.peg.3902, fig|439375.7.peg.3970	fig|204722.5.peg.1608, fig|204722.5.peg.3234

Membrane Transport	**ABC transporters**	ABC transporter dipeptide (TC 3.A.1.5.2)	Dipeptide transport ATP-binding protein DppF (TC 3.A.1.5.2)	fig|439375.7.peg.1354, fig|439375.7.peg.1670, fig|439375.7.peg.2002, fig|439375.7.peg.3110	fig|204722.5.peg.1607, fig|204722.5.peg.3233, fig|204722.5.peg.3319
			Dipeptide transport system permease protein DppB (TC 3.A.1.5.2)	fig|439375.7.peg.667, fig|439375.7.peg.1351, fig|439375.7.peg.1667, fig|439375.7.peg.2005, fig|439375.7.peg.2603, fig|439375.7.peg.3108, fig|439375.7.peg.3239, fig|439375.7.peg.3277, fig|439375.7.peg.3904, fig|439375.7.peg.3968, fig|439375.7.peg.4876	fig|204722.5.peg.1610, fig|204722.5.peg.3236, fig|204722.5.peg.3316
			Dipeptide transport system permease protein DppC (TC 3.A.1.5.2)	fig|439375.7.peg.668, fig|439375.7.peg.1352, fig|439375.7.peg.1668, fig|439375.7.peg.2004, fig|439375.7.peg.2604, fig|439375.7.peg.2923, fig|439375.7.peg.3137, fig|439375.7.peg.3240, fig|439375.7.peg.3278, fig|439375.7.peg.3473, fig|439375.7.peg.3903, fig|439375.7.peg.3967, fig|439375.7.peg.4300, fig|439375.7.peg.4785, fig|439375.7.peg.4877	fig|204722.5.peg.1609, fig|204722.5.peg.3235, fig|204722.5.peg.3304, fig|204722.5.peg.3317
			Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)	fig|439375.7.peg.666, fig|439375.7.peg.1350, fig|439375.7.peg.1666, fig|439375.7.peg.2006, fig|439375.7.peg.3107, fig|439375.7.peg.3135, fig|439375.7.peg.3238, fig|439375.7.peg.3276, fig|439375.7.peg.3686, fig|439375.7.peg.3905, fig|439375.7.peg.3969, fig|439375.7.peg.4581	fig|204722.5.peg.1611, fig|204722.5.peg.1612, fig|204722.5.peg.1613, fig|204722.5.peg.3237, fig|204722.5.peg.3308
			Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OppA (TC 3.A.1.5.1)	fig|439375.7.peg.2607, fig|439375.7.peg.2908, fig|439375.7.peg.3756, fig|439375.7.peg.3758, fig|439375.7.peg.3759, fig|439375.7.peg.4787	fig|204722.5.peg.2752, fig|204722.5.peg.2753

		ABC transporter oligopeptide (TC 3.A.1.5.1)	Oligopeptide transport ATP-binding protein OppD (TC 3.A.1.5.1)	fig|439375.7.peg.3279, fig|439375.7.peg.3948, fig|439375.7.peg.4301, fig|439375.7.peg.4784	fig|204722.5.peg.2618, fig|204722.5.peg.3318
			Oligopeptide transport ATP-binding protein OppF (TC 3.A.1.5.1)	fig|439375.7.peg.2605, fig|439375.7.peg.3242, fig|439375.7.peg.3901, fig|439375.7.peg.4137, fig|439375.7.peg.4878	fig|204722.5.peg.2617, fig|204722.5.peg.2997, fig|204722.5.peg.3302, fig|204722.5.peg.3326
			Oligopeptide transport system permease protein OppB (TC 3.A.1.5.1)	fig|439375.7.peg.11, fig|439375.7.peg.13, fig|439375.7.peg.3474, fig|439375.7.peg.3760, fig|439375.7.peg.3762	fig|204722.5.peg.7, fig|204722.5.peg.9, fig|204722.5.peg.2749, fig|204722.5.peg.2751, fig|204722.5.peg.3305, fig|204722.5.peg.3322
			Oligopeptide transport system permease protein OppC (TC 3.A.1.5.1)	fig|439375.7.peg.12, fig|439375.7.peg.3761, fig|439375.7.peg.4139	fig|204722.5.peg.8, fig|204722.5.peg.2750, fig|204722.5.peg.2999
	Lipoprotein sorting	Lipoprotein sorting system	Lipoprotein releasing system ATP-binding protein LolD	fig|439375.7.peg.2535	fig|204722.5.peg.835
			Lipoprotein releasing system transmembrane protein LolC	fig|439375.7.peg.2536	fig|204722.5.peg.834
	Membrane Transport	Choline Transport	Choline ABC transporter ATP-binding protein		fig|204722.5.peg.3418
			Choline ABC transporter permease protein		fig|204722.5.peg.3419
			Choline-binding lipoprotein		fig|204722.5.peg.3417
			Choline-sulfatase (EC 3.1.6.6)	fig|439375.7.peg.3478	fig|204722.5.peg.3416
		ECF class transporters	ATPase component NikO of energizing module of nickel ECF transporter		fig|204722.5.peg.1390
			Substrate-specific component BioY of biotin ECF transporter	fig|439375.7.peg.729, fig|439375.7.peg.1251	fig|204722.5.peg.522, fig|204722.5.peg.1746
			Substrate-specific component NikM of nickel ECF transporter		fig|204722.5.peg.1387
			Transmembrane component NikQ of energizing module of nickel ECF transporter		fig|204722.5.peg.1389
		Ferrous iron transporter EfeUOB, low-pH-induced	Ferrous iron transport periplasmic protein EfeO, contains peptidase-M75 domain and (frequently) cupredoxin-like domain	fig|439375.7.peg.4024, fig|439375.7.peg.4026	
			Ferrous iron transport permease EfeU	fig|439375.7.peg.4027	
			Ferrous iron transport peroxidase EfeB	fig|439375.7.peg.4025	
		Potassium homeostasis	Binding-protein-dependent transport systems inner membrane component:ATP/GTP-binding site motif A (P-loop) :TrkA-N:Potassium e	fig|439375.7.peg.1959	fig|204722.5.peg.1349
			Kup system potassium uptake protein	fig|439375.7.peg.1912	fig|204722.5.peg.1407
			Large-conductance mechanosensitive channel	fig|439375.7.peg.436	fig|204722.5.peg.331
			Osmosensitive K+ channel histidine kinase KdpD (EC 2.7.3.-)	fig|439375.7.peg.3943	
			Potassium efflux system KefA protein	fig|439375.7.peg.1962	fig|204722.5.peg.1345, fig|204722.5.peg.1346
			Potassium uptake protein TrkH	fig|439375.7.peg.1753	fig|204722.5.peg.1526
			Potassium-transporting ATPase A chain (EC 3.6.3.12) (TC 3.A.3.7.1)	fig|439375.7.peg.3939	

	Membrane Transport		Potassium-transporting ATPase B chain (EC 3.6.3.12) (TC 3.A.3.7.1)	fig|439375.7.peg.3941	
			Potassium-transporting ATPase C chain (EC 3.6.3.12) (TC 3.A.3.7.1)	fig|439375.7.peg.3942	
			putative Glutathione-regulated potassium-efflux system protein KefB	fig|439375.7.peg.3192	fig|204722.5.peg.2427
			Trk system potassium uptake protein TrkA	fig|439375.7.peg.2322	fig|204722.5.peg.1134
		Transport of Nickel and Cobalt	Additional component NikL of nickel ECF transporter		fig|204722.5.peg.1388
			Additional periplasmic component NikK of nickel ECF transporter	fig|439375.7.peg.4346	fig|204722.5.peg.1386
			ATPase component NikO of energizing module of nickel ECF transporter		fig|204722.5.peg.1390
			Nickel ABC transporter, periplasmic nickel-binding protein NikA (TC 3.A.1.5.3)		fig|204722.5.peg.3020
			Nickel responsive regulator NikR		fig|204722.5.peg.3021
			Nickel transport ATP-binding protein NikD (TC 3.A.1.5.3)		fig|204722.5.peg.3017
			Nickel transport ATP-binding protein NikE (TC 3.A.1.5.3)		fig|204722.5.peg.3016
			Nickel transport system permease protein NikB (TC 3.A.1.5.3)		fig|204722.5.peg.3019
			Nickel transport system permease protein NikC (TC 3.A.1.5.3)		fig|204722.5.peg.3018
			HupE-UreJ family metal transporter	fig|439375.7.peg.355, fig|439375.7.peg.2573	
			Predicted cobalt transporter CbtA	fig|439375.7.peg.1974	fig|204722.5.peg.1331
			Substrate-specific component NikM of nickel ECF transporter		fig|204722.5.peg.1387
			Transmembrane component NikQ of energizing module of nickel ECF transporter		fig|204722.5.peg.1389
	Uni- Sym- and Antiporters	Na(+) H(+) antiporter	Na+/H+ antiporter NhaA type	fig|439375.7.peg.549, fig|439375.7.peg.550, fig|439375.7.peg.2565	fig|204722.5.peg.412, fig|204722.5.peg.413
		Sodium Hydrogen Antiporter	Na(+) H(+) antiporter subunit A	fig|439375.7.peg.3689	fig|204722.5.peg.2717
			Na(+) H(+) antiporter subunit B	fig|439375.7.peg.3689	fig|204722.5.peg.2717
			Na(+) H(+) antiporter subunit C	fig|439375.7.peg.3690	fig|204722.5.peg.2718
			Na(+) H(+) antiporter subunit D	fig|439375.7.peg.3691	fig|204722.5.peg.2719
			Na(+) H(+) antiporter subunit E	fig|439375.7.peg.3692	fig|204722.5.peg.2720
			Na(+) H(+) antiporter subunit F	fig|439375.7.peg.3693	fig|204722.5.peg.2721
			Na(+) H(+) antiporter subunit G	fig|439375.7.peg.3694	fig|204722.5.peg.2722
	Metabolism of Aromatic Compounds	Aromatic Amin Catabolism	4-hydroxyphenylacetate 3-monooxygenase, reductase component (EC 1.6.8.-)	fig|439375.7.peg.1993, fig|439375.7.peg.4531	fig|204722.5.peg.1314
			Nitrilotriacetate monooxygenase component B (EC 1.14.13.-)	fig|439375.7.peg.2259	fig|204722.5.peg.1082
		Gentisare degradation	Fumarylacetoacetate hydrolase family protein	fig|439375.7.peg.75, fig|439375.7.peg.3926	fig|204722.5.peg.66
		Salicylate and gentisate catabolism	Fumarylacetoacetate hydrolase family protein	fig|439375.7.peg.75, fig|439375.7.peg.3926	fig|204722.5.peg.66
			Salicylate hydroxylase (EC 1.14.13.1)	fig|439375.7.peg.2681, fig|439375.7.peg.4569	fig|204722.5.peg.760, fig|204722.5.peg.973
			2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase (EC 4.1.2.-)		fig|204722.5.peg.3387

Metabolism of Aromatic Compounds	**Metabolism of central aromatic intermediates**	4-Hydroxyphenylacetic acid catabolic pathway	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (EC 5.3.3.-)		fig|204722.5.peg.3389
			2-oxo-hepta-3-ene-1,7-dioic acid hydratase (EC 4.2.-.-)		fig|204722.5.peg.3388
			4-hydroxyphenylacetate 3-monooxygenase, reductase component (EC 1.6.8.-)		fig|204722.5.peg.1314
			5-carboxymethyl-2-hydroxymuconate delta-isomerase (EC 5.3.3.10)		fig|204722.5.peg.3393
			5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase (EC 1.2.1.60)		fig|204722.5.peg.3392
			5-carboxymethyl-2-oxo-hex-3- ene-1,7-dioate decarboxylase (EC 4.1.1.68)		fig|204722.5.peg.3389
			Homoprotocatechuate degradative operon repressor		fig|204722.5.peg.3394
		Catechol branch of beta-ketoadipate pathway	3-oxoadipate CoA-transferase subunit A (EC 2.8.3.6)	fig|439375.7.peg.3884	fig|204722.5.peg.2851
			3-oxoadipate CoA-transferase subunit B (EC 2.8.3.6)	fig|439375.7.peg.3883	fig|204722.5.peg.2850
			Beta-ketoadipate enol-lactone hydrolase (EC 3.1.1.24)	fig|439375.7.peg.3889	fig|204722.5.peg.2856
			mandelate racemase/muconate lactonizing enzyme family protein	fig|439375.7.peg.335	fig|204722.5.peg.245
			Muconate cycloisomerase (EC 5.5.1.1)	fig|439375.7.peg.2211	fig|204722.5.peg.1030
		Central meta-cleavage pathway of aromatic compound degradation	2-oxo-hepta-3-ene-1,7-dioic acid hydratase (EC 4.2.-.-)		fig|204722.5.peg.3388
			5-carboxymethyl-2-hydroxymuconate delta-isomerase (EC 5.3.3.10)		fig|204722.5.peg.3393
			5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase (EC 1.2.1.60)		fig|204722.5.peg.3392
		Protocatechuate branch of beta-ketoadipate pathway	3-carboxy-cis,cis-muconate cycloisomerase (EC 5.5.1.2)	fig|439375.7.peg.3893	fig|204722.5.peg.2860
			3-oxoadipate CoA-transferase subunit A (EC 2.8.3.6)	fig|439375.7.peg.3884	fig|204722.5.peg.2851
			3-oxoadipate CoA-transferase subunit B (EC 2.8.3.6)	fig|439375.7.peg.3883	fig|204722.5.peg.2850
			4-carboxymuconolactone decarboxylase (EC 4.1.1.44)	fig|439375.7.peg.3890	fig|204722.5.peg.2857
			Beta-ketoadipate enol-lactone hydrolase (EC 3.1.1.24)	fig|439375.7.peg.3889	fig|204722.5.peg.2856
			Beta-ketoadipyl CoA thiolase (EC 2.3.1.-)	fig|439375.7.peg.3882, fig|439375.7.peg.4196	fig|204722.5.peg.2849
			Pca regulon regulatory protein PcaR	fig|439375.7.peg.3885	fig|204722.5.peg.2852
			Protocatechuate 3,4-dioxygenase alpha chain (EC 1.13.11.3)	fig|439375.7.peg.3892	fig|204722.5.peg.2859
			Protocatechuate 3,4-dioxygenase beta chain (EC 1.13.11.3)	fig|439375.7.peg.3891	fig|204722.5.peg.2858
	Peripheral pathways for catabolism of aromatic compounds	Benzoate catabolism	Acetyl-CoA C-acyltransferase (EC 2.3.1.16)	fig|439375.7.peg.3257	fig|204722.5.peg.2666
			Muconate cycloisomerase (EC 5.5.1.1)	fig|439375.7.peg.2211	fig|204722.5.peg.1030
		Benzoate degradation	benzoate MFS transporter BenK	fig|439375.7.peg.4186	
			Benzoate transport protein	fig|439375.7.peg.850, fig|439375.7.peg.4309	fig|204722.5.peg.2152
		Chloroaromatic degradation pathway	3-oxoadipate CoA-transferase subunit A (EC 2.8.3.6)	fig|439375.7.peg.3884	fig|204722.5.peg.2851
			3-oxoadipate CoA-transferase subunit B (EC 2.8.3.6)	fig|439375.7.peg.3883	fig|204722.5.peg.2850
			Beta-ketoadipate enol-lactone hydrolase (EC 3.1.1.24)	fig|439375.7.peg.3889	fig|204722.5.peg.2856
			Beta-ketoadipyl CoA thiolase (EC 2.3.1.-)	fig|439375.7.peg.3882, fig|439375.7.peg.4196	fig|204722.5.peg.2849
			Flagellar basal-body rod modification protein FlgD	fig|439375.7.peg.4359	fig|204722.5.peg.3362
			Flagellar biosynthesis protein FlhA	fig|439375.7.peg.4357	fig|204722.5.peg.3360
			Flagellar biosynthesis protein FlhB	fig|439375.7.peg.4393	fig|204722.5.peg.2341
			Flagellar biosynthesis protein FliR	fig|439375.7.peg.4356	fig|204722.5.peg.3359
			Flagellar L-ring protein FlgH	fig|439375.7.peg.4376	fig|204722.5.peg.2375
			Flagellar motor rotation protein MotA	fig|439375.7.peg.4388	fig|204722.5.peg.2347

Motility and Chemotaxis	**Flagellar motility in Prokaryota**	Flagellar motility	Flagellar motor rotation protein MotB	fig|439375.7.peg.1256, fig|439375.7.peg.4369	fig|204722.5.peg.1740, fig|204722.5.peg.3373
			Flagellar motor switch protein FliM	fig|439375.7.peg.4389	fig|204722.5.peg.2346
			Flagellar motor switch protein FliN	fig|439375.7.peg.4391	fig|204722.5.peg.2344
			Flagellum-specific ATP synthase FliI	fig|439375.7.peg.4385	fig|204722.5.peg.2350
			RNA polymerase sigma-54 factor RpoN	fig|439375.7.peg.181, fig|439375.7.peg.1307, fig|439375.7.peg.3554	fig|204722.5.peg.164
			Rrf2 family transcriptional regulator	fig|439375.7.peg.4344, fig|439375.7.peg.4530	fig|204722.5.peg.3348
		Flagellum	Flagellar basal-body P-ring formation protein FlgA	fig|439375.7.peg.4379	fig|204722.5.peg.2372
			Flagellar basal-body rod modification protein FlgD	fig|439375.7.peg.4359	fig|204722.5.peg.3362
			Flagellar basal-body rod protein FlgB	fig|439375.7.peg.4383	fig|204722.5.peg.2368
			Flagellar basal-body rod protein FlgC	fig|439375.7.peg.4382	fig|204722.5.peg.2369
			Flagellar basal-body rod protein FlgF	fig|439375.7.peg.4386, fig|439375.7.peg.4387	fig|204722.5.peg.2348, fig|204722.5.peg.2349
			Flagellar basal-body rod protein FlgG	fig|439375.7.peg.4380	fig|204722.5.peg.2371
			Flagellar biosynthesis protein FlhA	fig|439375.7.peg.4357	fig|204722.5.peg.3360
			Flagellar biosynthesis protein FlhB	fig|439375.7.peg.4393	fig|204722.5.peg.2341
			Flagellar biosynthesis protein FliL	fig|439375.7.peg.4375	fig|204722.5.peg.2376
			Flagellar biosynthesis protein FliP	fig|439375.7.peg.4374	fig|204722.5.peg.2377
			Flagellar biosynthesis protein FliQ	fig|439375.7.peg.4358	fig|204722.5.peg.3361
			Flagellar biosynthesis protein FliR	fig|439375.7.peg.4356	fig|204722.5.peg.3359
			Flagellar hook protein FlgE	fig|439375.7.peg.4364	fig|204722.5.peg.3367
			Flagellar hook-associated protein FlgK	fig|439375.7.peg.4363	fig|204722.5.peg.3366
			Flagellar hook-associated protein FlgL	fig|439375.7.peg.4362	fig|204722.5.peg.3365
			Flagellar hook-basal body complex protein FliE	fig|439375.7.peg.4381	fig|204722.5.peg.2370
			Flagellar hook-length control protein FliK	fig|439375.7.peg.4367	fig|204722.5.peg.3370
			Flagellar L-ring protein FlgH	fig|439375.7.peg.4376	fig|204722.5.peg.2375
			Flagellar motor rotation protein MotA	fig|439375.7.peg.4388	fig|204722.5.peg.2347
			Flagellar motor rotation protein MotB	fig|439375.7.peg.1256, fig|439375.7.peg.4369	fig|204722.5.peg.1740, fig|204722.5.peg.3373
			Flagellar motor switch protein FliG	fig|439375.7.peg.4392	fig|204722.5.peg.2342, fig|204722.5.peg.2343
			Flagellar motor switch protein FliM	fig|439375.7.peg.4389	fig|204722.5.peg.2346
			Flagellar motor switch protein FliN	fig|439375.7.peg.4391	fig|204722.5.peg.2344
			Flagellar M-ring protein FliF	fig|439375.7.peg.4371	fig|204722.5.peg.3375
			Flagellar P-ring protein FlgI	fig|439375.7.peg.4378	fig|204722.5.peg.2373
			Flagellar protein FlgJ [peptidoglycan hydrolase] (EC 3.2.1.-)	fig|439375.7.peg.4354	fig|204722.5.peg.3357
			Flagellar protein FliJ	fig|439375.7.peg.1652	fig|204722.5.peg.1627
			Flagellin protein FlaA	fig|439375.7.peg.4372	fig|204722.5.peg.3377
			Flagellum-specific ATP synthase FliI	fig|439375.7.peg.4385	fig|204722.5.peg.2350
			RNA polymerase sigma factor RpoD	fig|439375.7.peg.1780	fig|204722.5.peg.1506
			RNA polymerase sigma-54 factor RpoN	fig|439375.7.peg.181, fig|439375.7.peg.1307, fig|439375.7.peg.3554	fig|204722.5.peg.164
			Chemotaxis protein methyltransferase CheR (EC 2.1.1.80)	fig|439375.7.peg.1302, fig|439375.7.peg.4865	fig|204722.5.peg.1681

	Motility and Chemotaxis	Bacterial Chemotaxis	Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)	fig|439375.7.peg.666, fig|439375.7.peg.1350, fig|439375.7.peg.1666, fig|439375.7.peg.2006, fig|439375.7.peg.3107, fig|439375.7.peg.3135, fig|439375.7.peg.3238, fig|439375.7.peg.3276, fig|439375.7.peg.3686, fig|439375.7.peg.3905, fig|439375.7.peg.3969, fig|439375.7.peg.4581	fig|204722.5.peg.1611, fig|204722.5.peg.1612, fig|204722.5.peg.1613, fig|204722.5.peg.3237, fig|204722.5.peg.3308
			Flagellar motor switch protein FliG	fig|439375.7.peg.4392	fig|204722.5.peg.2342, fig|204722.5.peg.2343
			Flagellar motor switch protein FliM	fig|439375.7.peg.4389	fig|204722.5.peg.2346
			Flagellar motor switch protein FliN	fig|439375.7.peg.4391	fig|204722.5.peg.2344
			Maltose/maltodextrin ABC transporter, substrate binding periplasmic protein MalE	fig|439375.7.peg.331, fig|439375.7.peg.3088	fig|204722.5.peg.241, fig|204722.5.peg.2520
			Ribose ABC transporter, periplasmic ribose-binding protein RbsB (TC 3.A.1.2.1)	fig|439375.7.peg.3500, fig|439375.7.peg.3566, fig|439375.7.peg.4241, fig|439375.7.peg.4991	fig|204722.5.peg.562, fig|204722.5.peg.1659, fig|204722.5.peg.3220
Nitrogen Metabolism	**Nitrogen Metabolism**	Ammonia assimilation	[Protein-PII] uridylyltransferase (EC 2.7.7.59)	fig|439375.7.peg.167	fig|204722.5.peg.150
			Ammonium transporter	fig|439375.7.peg.1005	fig|204722.5.peg.1930
			Glutamate synthase [NADPH] large chain (EC 1.4.1.13)	fig|439375.7.peg.4450	fig|204722.5.peg.2274
			Glutamate synthase [NADPH] small chain (EC 1.4.1.13)	fig|439375.7.peg.4449	fig|204722.5.peg.2275
			Glutamate-ammonia-ligase adenylyltransferase (EC 2.7.7.42)	fig|439375.7.peg.2809	fig|204722.5.peg.631
			Glutamine synthetase type I (EC 6.3.1.2)	fig|439375.7.peg.2193	fig|204722.5.peg.1015
			Glutamine synthetase type II, eukaryotic (EC 6.3.1.2)	fig|439375.7.peg.4328	■
			Nitrogen regulation protein NR(II) (EC 2.7.3.-)	fig|439375.7.peg.2177	fig|204722.5.peg.1138
			Nitrogen regulatory protein P-II	fig|439375.7.peg.2194	fig|204722.5.peg.1016
		Denitrification	Copper-containing nitrite reductase (EC 1.7.2.1)	fig|439375.7.peg.1158, fig|439375.7.peg.4554	fig|204722.5.peg.2475
			Nitric oxide reductase activation protein NorD	fig|439375.7.peg.4565	fig|204722.5.peg.2467
			Nitric oxide reductase activation protein NorE	fig|439375.7.peg.4560	fig|204722.5.peg.2462
			Nitric oxide reductase activation protein NorQ	fig|439375.7.peg.4564	fig|204722.5.peg.2466
			Nitric oxide -responding transcriptional regulator NnrR (Crp/Fnr family)	fig|439375.7.peg.3264, fig|439375.7.peg.4556	fig|204722.5.peg.2477, fig|204722.5.peg.2498
			Nitric-oxide reductase subunit B (EC 1.7.99.7)	fig|439375.7.peg.4563	fig|204722.5.peg.2465
			Nitric-oxide reductase subunit C (EC 1.7.99.7)	fig|439375.7.peg.4562	fig|204722.5.peg.2464
			Nitrite reductase accessory protein NirV	fig|439375.7.peg.4555	fig|204722.5.peg.2476
			Nitrous oxide reductase maturation periplasmic protein NosX	fig|439375.7.peg.4515	fig|204722.5.peg.2497
			Nitrous oxide reductase maturation protein NosD	fig|439375.7.peg.4519	fig|204722.5.peg.2493
			Nitrous oxide reductase maturation protein NosF (ATPase)	fig|439375.7.peg.4518	fig|204722.5.peg.2494
			Nitrous oxide reductase maturation protein NosR	fig|439375.7.peg.4521	fig|204722.5.peg.2491
			Nitrous oxide reductase maturation protein, outer-membrane lipoprotein NosL	fig|439375.7.peg.4516	fig|204722.5.peg.2496

			Nitrous oxide reductase maturation transmembrane protein NosY	fig|439375.7.peg.4517	fig|204722.5.peg.2495
			Nitrous-oxide reductase (EC 1.7.99.6)	fig|439375.7.peg.4520	fig|204722.5.peg.2492
			NnrS protein involved in response to NO	fig|439375.7.peg.3048	fig|204722.5.peg.2500
		Nitrate and nitrite ammonification	Nitrate/nitrite transporter	fig|439375.7.peg.3036, fig|439375.7.peg.3522	fig|204722.5.peg.2517
			Respiratory nitrate reductase alpha chain (EC 1.7.99.4)	fig|439375.7.peg.3037	fig|204722.5.peg.2516
			Respiratory nitrate reductase beta chain (EC 1.7.99.4)	fig|439375.7.peg.3038	fig|204722.5.peg.2515
			Respiratory nitrate reductase delta chain (EC 1.7.99.4)	fig|439375.7.peg.3039	fig|204722.5.peg.2514
			Respiratory nitrate reductase gamma chain (EC 1.7.99.4)	fig|439375.7.peg.3040	fig|204722.5.peg.2513
		Nitrosative stress	NnrS protein involved in response to NO	fig|439375.7.peg.3048	fig|204722.5.peg.2500
	Detoxification	Housecleaning nucleoside triphosphate pyrophosphatases	5-nucleotidase SurE (EC 3.1.3.5)	fig|439375.7.peg.2471	fig|204722.5.peg.897
			Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)	fig|439375.7.peg.1323	fig|204722.5.peg.1702
			Nucleoside 5-triphosphatase RdgB (dHAPTP, dITP, XTP-specific) (EC 3.6.1.15)	fig|439375.7.peg.195	fig|204722.5.peg.183
		Nucleoside triphosphate pyrophospho	Nucleoside triphosphate pyrophosphohydrolase MazG	fig|439375.7.peg.2258	fig|204722.5.peg.1081
		Nudix proteins (nucleoside triphosphate hydrolases)	5-methyl-dCTP pyrophosphohydrolase (EC 3.6.1.-)	fig|439375.7.peg.1075	fig|204722.5.peg.1973
			ADP-ribose pyrophosphatase (EC 3.6.1.13)	fig|439375.7.peg.4315	
			Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)	fig|439375.7.peg.1323	fig|204722.5.peg.1702
			Hypothetical nudix hydrolase YeaB	fig|439375.7.peg.1698	fig|204722.5.peg.1582
			NADH pyrophosphatase (EC 3.6.1.22)	fig|439375.7.peg.19	fig|204722.5.peg.40
			Nudix hydrolase family protein PA3470	fig|439375.7.peg.373	fig|204722.5.peg.294
	Nucleosides and Nucleotides	De Novo Pyrimidine Synthesis	Aspartate carbamoyltransferase (EC 2.1.3.2)	fig|439375.7.peg.3829	fig|204722.5.peg.2816
			Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)	fig|439375.7.peg.1770	fig|204722.5.peg.1515
			Carbamoyl-phosphate synthase small chain (EC 6.3.5.5)	fig|439375.7.peg.1775	fig|204722.5.peg.1510
			Dihydroorotase (EC 3.5.2.3)	fig|439375.7.peg.2763, fig|439375.7.peg.3830	fig|204722.5.peg.680, fig|204722.5.peg.2817
			Dihydroorotate dehydrogenase (EC 1.3.3.1)	fig|439375.7.peg.430	fig|204722.5.peg.324
			Orotate phosphoribosyltransferase (EC 2.4.2.10)	fig|439375.7.peg.2777	fig|204722.5.peg.666
			Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23)	fig|439375.7.peg.829	fig|204722.5.peg.2166
			Uracil permease	fig|439375.7.peg.3004	fig|204722.5.peg.2659
			Uracil phosphoribosyltransferase (EC 2.4.2.9)	fig|439375.7.peg.1376	fig|204722.5.peg.3291
		Hydantoin metabolism	Beta-ureidopropionase (EC 3.5.1.6)	fig|439375.7.peg.371	fig|204722.5.peg.292
			Deacetylases, including yeast histone deacetylase and acetoin utilization protein	fig|439375.7.peg.578	fig|204722.5.peg.445
			Dihydropyrimidinase (EC 3.5.2.2)	fig|439375.7.peg.370	fig|204722.5.peg.291
			Hydantoin racemase (EC 5.1.99.-)	fig|439375.7.peg.1478, fig|439375.7.peg.4596	
			N-methylhydantoinase A (EC 3.5.2.14)	fig|439375.7.peg.4751	
			N-methylhydantoinase B (EC 3.5.2.14)	fig|439375.7.peg.4752	
		Purine Utilization	Guanine deaminase (EC 3.5.4.3)	fig|439375.7.peg.485	fig|204722.5.peg.370
			Xanthine dehydrogenase, iron-sulfur cluster and FAD-binding subunit A (1.17.1.4)	fig|439375.7.peg.480	fig|204722.5.peg.365
			Xanthine dehydrogenase, molybdenum binding subunit (EC 1.17.1.4)	fig|439375.7.peg.481	fig|204722.5.peg.366
			Xanthine permease	fig|439375.7.peg.1013	

Nucleosides and Nucleotides			Xanthine/uracil/thiamine/ascorbate permease family protein	fig|439375.7.peg.3932	fig|204722.5.peg.2874
			XdhC protein (assists in molybdopterin insertion into xanthine dehydrogenase)	fig|439375.7.peg.482	fig|204722.5.peg.367
		Ribonucleotide reduction	Glutaredoxin-like protein NrdH, required for reduction of Ribonucleotide reductase class Ib	fig|439375.7.peg.3102	fig|204722.5.peg.2530
			Ribonucleotide reductase of class Ib (aerobic), alpha subunit (EC 1.17.4.1)	fig|439375.7.peg.3104	fig|204722.5.peg.2532
			Ribonucleotide reductase of class Ib (aerobic), beta subunit (EC 1.17.4.1)	fig|439375.7.peg.3105	fig|204722.5.peg.2533
			Ribonucleotide reductase of class II (coenzyme B12-dependent) (EC 1.17.4.1)	fig|439375.7.peg.2238	fig|204722.5.peg.1055
			Ribonucleotide reductase transcriptional regulator NrdR	fig|439375.7.peg.2663	fig|204722.5.peg.777
			Ribonucleotide reduction protein NrdI	fig|439375.7.peg.3103	fig|204722.5.peg.2531
	Purines	De Novo Purine Biosynthesis	Adenylosuccinate lyase (EC 4.3.2.2)	fig|439375.7.peg.2507	fig|204722.5.peg.859
			Amidophosphoribosyltransferase (EC 2.4.2.14)	fig|439375.7.peg.598	fig|204722.5.peg.462
			IMP cyclohydrolase (EC 3.5.4.10)	fig|439375.7.peg.1136	fig|204722.5.peg.1847
			Phosphoribosylamine--glycine ligase (EC 6.3.4.13)	fig|439375.7.peg.566	fig|204722.5.peg.430
			Phosphoribosylaminoimidazole carboxylase ATPase subunit (EC 4.1.1.21)	fig|439375.7.peg.1218	fig|204722.5.peg.1773
			Phosphoribosylaminoimidazole carboxylase catalytic subunit (EC 4.1.1.21)	fig|439375.7.peg.1219	fig|204722.5.peg.1772
			Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)	fig|439375.7.peg.1136	fig|204722.5.peg.1847
			Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6)	fig|439375.7.peg.2513	fig|204722.5.peg.853
			Phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1)	fig|439375.7.peg.2714	fig|204722.5.peg.723
			Phosphoribosylformylglycinamidine synthase, glutamine amidotransferase subunit (EC 6.3.5.3)	fig|439375.7.peg.2515	fig|204722.5.peg.851
			Phosphoribosylformylglycinamidine synthase, PurS subunit (EC 6.3.5.3)	fig|439375.7.peg.2514	fig|204722.5.peg.852
			Phosphoribosylformylglycinamidine synthase, synthetase subunit (EC 6.3.5.3)	fig|439375.7.peg.2520	fig|204722.5.peg.848
			Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2)	fig|439375.7.peg.2715	fig|204722.5.peg.722
			Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)	fig|439375.7.peg.1722	fig|204722.5.peg.1557
		Purine conversions	Adenine deaminase (EC 3.5.4.2)	fig|439375.7.peg.3899	fig|204722.5.peg.2866
			Adenine phosphoribosyltransferase (EC 2.4.2.7)	fig|439375.7.peg.1714	fig|204722.5.peg.1564
			Adenylate kinase (EC 2.7.4.3)	fig|439375.7.peg.2079	fig|204722.5.peg.1234
			Adenylosuccinate lyase (EC 4.3.2.2)	fig|439375.7.peg.2507	fig|204722.5.peg.859
			Adenylosuccinate synthetase (EC 6.3.4.4)	fig|439375.7.peg.1288	fig|204722.5.peg.1710
			AMP nucleosidase (EC 3.2.2.4)	fig|439375.7.peg.2801	fig|204722.5.peg.641
			Deoxyguanosinetriphosphate triphosphohydrolase (EC 3.1.5.1)	fig|439375.7.peg.2482	fig|204722.5.peg.887
			GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2)	fig|439375.7.peg.3209	fig|204722.5.peg.2575
			Guanine deaminase (EC 3.5.4.3)	fig|439375.7.peg.485	fig|204722.5.peg.370
			Guanylate kinase (EC 2.7.4.8)	fig|439375.7.peg.615, fig|439375.7.peg.2298	fig|204722.5.peg.479, fig|204722.5.peg.1120
			Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)	fig|439375.7.peg.1043	fig|204722.5.peg.2022

			Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	fig|439375.7.peg.2040, fig|439375.7.peg.3203	fig|204722.5.peg.1275, fig|204722.5.peg.2566
			Inosine-uridine preferring nucleoside hydrolase (EC 3.2.2.1)	fig|439375.7.peg.2900, fig|439375.7.peg.4623	fig|204722.5.peg.2228
			Nucleoside diphosphate kinase (EC 2.7.4.6)	fig|439375.7.peg.2734	fig|204722.5.peg.706
			Polyphosphate kinase (EC 2.7.4.1)	fig|439375.7.peg.2679	fig|204722.5.peg.762
			Xanthine-guanine phosphoribosyltransferase (EC 2.4.2.22)	fig|439375.7.peg.2240	fig|204722.5.peg.1059
	Pyrimidines	pyrimidine conversions	Bis(5'-nucleosyl)-tetraphosphatase (asymmetrical) (EC 3.6.1.17)	fig|439375.7.peg.2128	fig|204722.5.peg.1187
			CTP synthase (EC 6.3.4.2)	fig|439375.7.peg.2160	fig|204722.5.peg.1154
			Cytidylate kinase (EC 2.7.4.14)	fig|439375.7.peg.31	fig|204722.5.peg.29
			Cytosine deaminase (EC 3.5.4.1)	fig|439375.7.peg.3466, fig|439375.7.peg.4040	
			Deoxycytidine triphosphate deaminase (EC 3.5.4.13)	fig|439375.7.peg.425	fig|204722.5.peg.319
			Nucleoside diphosphate kinase (EC 2.7.4.6)	fig|439375.7.peg.2734	fig|204722.5.peg.706
			Thioredoxin reductase (EC 1.8.1.9)	fig|439375.7.peg.1754, fig|439375.7.peg.2219, fig|439375.7.peg.3745	fig|204722.5.peg.1039, fig|204722.5.peg.1525
			Thymidylate kinase (EC 2.7.4.9)	fig|439375.7.peg.902, fig|439375.7.peg.2183	fig|204722.5.peg.1004, fig|204722.5.peg.2097
			Thymidylate synthase (EC 2.1.1.45)	fig|439375.7.peg.1893	fig|204722.5.peg.1424
			Uracil phosphoribosyltransferase (EC 2.4.2.9)	fig|439375.7.peg.1376	fig|204722.5.peg.3291
		Pyrimidine utilization	Beta-ureidopropionase (EC 3.5.1.6)	fig|439375.7.peg.371	fig|204722.5.peg.292
			Dihydropyrimidinase (EC 3.5.2.2)	fig|439375.7.peg.370	fig|204722.5.peg.291
			Dihydropyrimidine dehydrogenase [NADP+] (EC 1.3.1.2)	fig|439375.7.peg.388	fig|204722.5.peg.295
			Pyridine nucleotide-disulphide oxidoreductase associated with reductive pyrimidine catabolism	fig|439375.7.peg.389	fig|204722.5.peg.296
			Pyrimidine ABC transporter, ATP-binding protein	fig|439375.7.peg.369, fig|439375.7.peg.3129	
			Pyrimidine ABC transporter, substrate-binding component	fig|439375.7.peg.366	
			Pyrimidine ABC transporter, transmembrane component 1	fig|439375.7.peg.368	
			Pyrimidine ABC transporter, transmembrane component 2	fig|439375.7.peg.367	
			Transcriptional regulator RutR of pyrimidine catabolism (TetR family)	fig|439375.7.peg.372	fig|204722.5.peg.293
			Uracil permease	fig|439375.7.peg.3004	fig|204722.5.peg.2659
Phages, Prophages, Transposable elements	**Bacteriophage structural proteins**	Phage capsid proteins	Phage capsid and scaffold	fig|439375.7.peg.256	
		Phage capsid proteins	Phage major capsid protein		fig|204722.5.peg.605
		Phage tail fiber proteins	Phage tail fibers		fig|204722.5.peg.2388
	Phages, Prophages, Transposable elements	Phage packaging machinery	Phage portal protein	fig|439375.7.peg.260, fig|439375.7.peg.1577, fig|439375.7.peg.2433	fig|204722.5.peg.602
			Phage terminase large subunit	fig|439375.7.peg.254	
			Phage terminase, large subunit	fig|439375.7.peg.1881, fig|439375.7.peg.2435	
			Alkylphosphonate utilization operon protein PhnA	fig|439375.7.peg.1805	fig|204722.5.peg.1490
			ATP-binding protein PhnN	fig|439375.7.peg.2298	fig|204722.5.peg.1120
			Metal-dependent hydrolase involved in phosphonate metabolism	fig|439375.7.peg.2299, fig|439375.7.peg.2496	fig|204722.5.peg.871

Phosphorus Metabolism	**Phosphorus Metabolism**	Alkylphosphonate utilization	PhnB protein	fig|439375.7.peg.1649	
			PhnG protein	fig|439375.7.peg.2306	
			PhnH protein	fig|439375.7.peg.2305	
			PhnI protein	fig|439375.7.peg.2304	
			PhnJ protein	fig|439375.7.peg.2303	
			Phosphonates transport ATP-binding protein PhnK	fig|439375.7.peg.2302	
			Phosphonates transport ATP-binding protein PhnL	fig|439375.7.peg.2301	
			Protein RcsF	fig|439375.7.peg.2497	fig|204722.5.peg.870
			Transcriptional regulator PhnF	fig|439375.7.peg.2307	fig|204722.5.peg.1121
		High affinity phosphate transporter and control of PHO regulon	Phosphate ABC transporter, periplasmic phosphate-binding protein PstS (TC 3.A.1.7.1)	fig|439375.7.peg.815	fig|204722.5.peg.2175
			Phosphate regulon sensor protein PhoR (SphS) (EC 2.7.13.3)	fig|439375.7.peg.405	fig|204722.5.peg.312
			Phosphate regulon transcriptional regulatory protein PhoB (SphR)	fig|439375.7.peg.810	fig|204722.5.peg.2180
			Phosphate transport ATP-binding protein PstB (TC 3.A.1.7.1)	fig|439375.7.peg.812	fig|204722.5.peg.2178
			Phosphate transport system permease protein PstA (TC 3.A.1.7.1)	fig|439375.7.peg.813	fig|204722.5.peg.2177
			Phosphate transport system permease protein PstC (TC 3.A.1.7.1)	fig|439375.7.peg.814	fig|204722.5.peg.2176
			Phosphate transport system regulatory protein PhoU	fig|439375.7.peg.811	fig|204722.5.peg.2179
			Polyphosphate kinase (EC 2.7.4.1)	fig|439375.7.peg.2679	fig|204722.5.peg.762
		Phosphate metabolism	1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)	fig|439375.7.peg.802, fig|439375.7.peg.1035, fig|439375.7.peg.3032	fig|204722.5.peg.2032, fig|204722.5.peg.2189
			Alkaline phosphatase (EC 3.1.3.1)	fig|439375.7.peg.2926	fig|204722.5.peg.1221, fig|204722.5.peg.2832
			Alkaline phosphatase like protein		fig|204722.5.peg.447
			Apolipoprotein N-acyltransferase (EC 2.3.1.-)	fig|439375.7.peg.796	fig|204722.5.peg.2195
			Exopolyphosphatase (EC 3.6.1.11)	fig|439375.7.peg.2678, fig|439375.7.peg.3976	fig|204722.5.peg.763, fig|204722.5.peg.2896
			FIG000233: metal-dependent hydrolase	fig|439375.7.peg.798	fig|204722.5.peg.2193
			Inorganic pyrophosphatase (EC 3.6.1.1)	fig|439375.7.peg.1036, fig|439375.7.peg.1290	fig|204722.5.peg.2030
			Integral membrane protein YggT, involved in response to extracytoplasmic stress (osmotic shock)	fig|439375.7.peg.1037	fig|204722.5.peg.2029
			Magnesium and cobalt efflux protein CorC	fig|439375.7.peg.797	fig|204722.5.peg.2194
			NAD(P) transhydrogenase alpha subunit (EC 1.6.1.2)	fig|439375.7.peg.1452, fig|439375.7.peg.1453	fig|204722.5.peg.3194, fig|204722.5.peg.3195
			NAD(P) transhydrogenase subunit beta (EC 1.6.1.2)	fig|439375.7.peg.1454	fig|204722.5.peg.3193
			Phosphate ABC transporter, periplasmic phosphate-binding protein PstS (TC 3.A.1.7.1)	fig|439375.7.peg.815	fig|204722.5.peg.2175
			Phosphate regulon sensor protein PhoR (SphS) (EC 2.7.13.3)	fig|439375.7.peg.405	fig|204722.5.peg.312
			Phosphate regulon transcriptional regulatory protein PhoB (SphR)	fig|439375.7.peg.810	fig|204722.5.peg.2180
			Phosphate starvation-inducible ATPase PhoH with RNA binding motif	fig|439375.7.peg.799	fig|204722.5.peg.2192

			Phosphate transport ATP-binding protein PstB (TC 3.A.1.7.1)	fig|439375.7.peg.812	fig|204722.5.peg.2178
			Phosphate transport system permease protein PstA (TC 3.A.1.7.1)	fig|439375.7.peg.813	fig|204722.5.peg.2177
			Phosphate transport system permease protein PstC (TC 3.A.1.7.1)	fig|439375.7.peg.814	fig|204722.5.peg.2176
			Phosphate transport system regulatory protein PhoU	fig|439375.7.peg.811	fig|204722.5.peg.2179
			Polyphosphate kinase (EC 2.7.4.1)	fig|439375.7.peg.2679	fig|204722.5.peg.762
			Pyrophosphate-energized proton pump (EC 3.6.1.1)	fig|439375.7.peg.2657	fig|204722.5.peg.782
			Sodium-dependent phosphate transporter	fig|439375.7.peg.1777	fig|204722.5.peg.1508
	Potassium metabolism	Glutathione-regulated potassium-efflux system and associated functions	Glutathione-regulated potassium-efflux system protein KefB	fig|439375.7.peg.4335, fig|439375.7.peg.4657	■
			Trk system potassium uptake protein TrkA	fig|439375.7.peg.2322	fig|204722.5.peg.1134
		Ribosome biogenesis bacterial	16S rRNA processing protein RimM	fig|439375.7.peg.987	fig|204722.5.peg.1950
			Dimethyladenosine transferase (EC 2.1.1.-)	fig|439375.7.peg.2747	fig|204722.5.peg.694
			Inactive homolog of metal-dependent proteases, putative molecular chaperone	fig|439375.7.peg.804	fig|204722.5.peg.2187
			LSU m3Psi1915 methyltransferase RlmH	fig|439375.7.peg.1108	fig|204722.5.peg.1872
			Ribosomal large subunit pseudouridine synthase A (EC 4.2.1.70)	fig|439375.7.peg.1095	■
			Ribosomal large subunit pseudouridine synthase C (EC 4.2.1.70)	fig|439375.7.peg.2189	fig|204722.5.peg.1011
			Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)	fig|439375.7.peg.1294	fig|204722.5.peg.1678
			Ribosomal protein L11 methyltransferase (EC 2.1.1.-)	fig|439375.7.peg.1860	fig|204722.5.peg.1443
			Ribosomal protein S6 glutaminyl transferase	fig|439375.7.peg.819	■
			Ribosomal-protein-S18p-alanine acetyltransferase (EC 2.3.1.-)	fig|439375.7.peg.803	fig|204722.5.peg.2188
			Ribosomal-protein-S5p-alanine acetyltransferase	fig|439375.7.peg.637	fig|204722.5.peg.497
			tRNA (Guanine37-N1) -methyltransferase (EC 2.1.1.31)	fig|439375.7.peg.988	fig|204722.5.peg.1949
		Ribosome LSU bacterial	LSU ribosomal protein L10p (P0)	fig|439375.7.peg.2048	fig|204722.5.peg.1267
			LSU ribosomal protein L11p (L12e)	fig|439375.7.peg.2046	fig|204722.5.peg.1269
			LSU ribosomal protein L13p (L13Ae)	fig|439375.7.peg.2628	fig|204722.5.peg.802
			LSU ribosomal protein L14p (L23e)	fig|439375.7.peg.2068	fig|204722.5.peg.1245
			LSU ribosomal protein L15p (L27Ae)	fig|439375.7.peg.2077	fig|204722.5.peg.1236
			LSU ribosomal protein L16p (L10e)	fig|439375.7.peg.2065	fig|204722.5.peg.1248
			LSU ribosomal protein L17p	fig|439375.7.peg.2083	fig|204722.5.peg.1229
			LSU ribosomal protein L18p (L5e)	fig|439375.7.peg.2074	fig|204722.5.peg.1239
			LSU ribosomal protein L19p	fig|439375.7.peg.990	fig|204722.5.peg.1942
			LSU ribosomal protein L1p (L10Ae)	fig|439375.7.peg.2047	fig|204722.5.peg.1268
			LSU ribosomal protein L20p	fig|439375.7.peg.844	fig|204722.5.peg.2158
			LSU ribosomal protein L21p	fig|439375.7.peg.1098	fig|204722.5.peg.1883
			LSU ribosomal protein L22p (L17e)	fig|439375.7.peg.2063	fig|204722.5.peg.1250
			LSU ribosomal protein L23p (L23Ae)	fig|439375.7.peg.2060	fig|204722.5.peg.1253
			LSU ribosomal protein L24p (L26e)	fig|439375.7.peg.2069	fig|204722.5.peg.1244
			LSU ribosomal protein L25p	fig|439375.7.peg.1719	fig|204722.5.peg.1559
			LSU ribosomal protein L27p	fig|439375.7.peg.1099	fig|204722.5.peg.1882
			LSU ribosomal protein L28p	fig|439375.7.peg.962	fig|204722.5.peg.2050
			LSU ribosomal protein L29p (L35e)	fig|439375.7.peg.2066	fig|204722.5.peg.1247

	Protein biosynthesis		LSU ribosomal protein L2p (L8e)	fig|439375.7.peg.2061	fig|204722.5.peg.1252
			LSU ribosomal protein L30p (L7e)	fig|439375.7.peg.2076	fig|204722.5.peg.1237
			LSU ribosomal protein L31p	fig|439375.7.peg.1254	fig|204722.5.peg.1742
			LSU ribosomal protein L32p	fig|439375.7.peg.1178	fig|204722.5.peg.1802
			LSU ribosomal protein L33p	fig|439375.7.peg.3840	fig|204722.5.peg.2826
			LSU ribosomal protein L34p	fig|439375.7.peg.1429	fig|204722.5.peg.3246
			LSU ribosomal protein L35p	fig|439375.7.peg.845	fig|204722.5.peg.2157
			LSU ribosomal protein L36p	fig|439375.7.peg.1217	fig|204722.5.peg.1774
			LSU ribosomal protein L3p (L3e)	fig|439375.7.peg.2058	fig|204722.5.peg.1255
			LSU ribosomal protein L4p (L1e)	fig|439375.7.peg.2059	fig|204722.5.peg.1254
			LSU ribosomal protein L5p (L11e)	fig|439375.7.peg.2070	fig|204722.5.peg.1243
			LSU ribosomal protein L6p (L9e)	fig|439375.7.peg.2073	fig|204722.5.peg.1240
			LSU ribosomal protein L7/L12 (P1/P2)	fig|439375.7.peg.2049	fig|204722.5.peg.1266
			LSU ribosomal protein L9p	fig|439375.7.peg.605	fig|204722.5.peg.467
		Ribosome SSU bacterial	SSU ribosomal protein S10p (S20e)	fig|439375.7.peg.2057	fig|204722.5.peg.1256
			SSU ribosomal protein S11p (S14e)	fig|439375.7.peg.2081	fig|204722.5.peg.1232
			SSU ribosomal protein S12p (S23e)	fig|439375.7.peg.2053	fig|204722.5.peg.1260
			SSU ribosomal protein S13p (S18e)	fig|439375.7.peg.2080	fig|204722.5.peg.1233
			SSU ribosomal protein S14p (S29e)	fig|439375.7.peg.2071	fig|204722.5.peg.1242
			SSU ribosomal protein S15p (S13e)	fig|439375.7.peg.786	fig|204722.5.peg.2205
			SSU ribosomal protein S16p	fig|439375.7.peg.1128	fig|204722.5.peg.1854
			SSU ribosomal protein S17p (S11e)	fig|439375.7.peg.2067	fig|204722.5.peg.1246
			SSU ribosomal protein S18p	fig|439375.7.peg.607	fig|204722.5.peg.469
			SSU ribosomal protein S19p (S15e)	fig|439375.7.peg.2062	fig|204722.5.peg.1251
			SSU ribosomal protein S1p	fig|439375.7.peg.30	fig|204722.5.peg.31
			SSU ribosomal protein S20p	fig|439375.7.peg.2	fig|204722.5.peg.2222
			SSU ribosomal protein S21p	fig|439375.7.peg.1459	fig|204722.5.peg.3188
			SSU ribosomal protein S2p (SAe)	fig|439375.7.peg.2133	fig|204722.5.peg.1181
			SSU ribosomal protein S3p (S3e)	fig|439375.7.peg.2064	fig|204722.5.peg.1249
			SSU ribosomal protein S4p (S9e)	fig|439375.7.peg.2526	fig|204722.5.peg.842
			SSU ribosomal protein S5p (S2e)	fig|439375.7.peg.2075	fig|204722.5.peg.1238
			SSU ribosomal protein S6p	fig|439375.7.peg.608	fig|204722.5.peg.470
			SSU ribosomal protein S7p (S5e)	fig|439375.7.peg.2054	fig|204722.5.peg.1259
			SSU ribosomal protein S8p (S15Ae)	fig|439375.7.peg.2072	fig|204722.5.peg.1241
			SSU ribosomal protein S9p (S16e)	fig|439375.7.peg.2629	fig|204722.5.peg.801
		Translation elongation factors bacterial	Translation elongation factor G	fig|439375.7.peg.2055	fig|204722.5.peg.1258
			Translation elongation factor LepA	fig|439375.7.peg.1406	fig|204722.5.peg.3264
			Translation elongation factor P	fig|439375.7.peg.1260	fig|204722.5.peg.1736
			Translation elongation factor Ts	fig|439375.7.peg.2134	fig|204722.5.peg.1180
			Translation elongation factor Tu	fig|439375.7.peg.2043, fig|439375.7.peg.2056	fig|204722.5.peg.1257, fig|204722.5.peg.1272
		Translation initiation factors bacterial	Methionyl-tRNA formyltransferase (EC 2.1.2.9)	fig|439375.7.peg.1410	fig|204722.5.peg.3259
			Ribosome-binding factor A	fig|439375.7.peg.788	fig|204722.5.peg.2203
			Translation initiation factor 1	fig|439375.7.peg.345	fig|204722.5.peg.258
			Translation initiation factor 2	fig|439375.7.peg.789	fig|204722.5.peg.2202
			Translation initiation factor 3	fig|439375.7.peg.847	fig|204722.5.peg.2155
			Hypothetical protein YaeJ with similarity to translation release factor	fig|439375.7.peg.875	fig|204722.5.peg.2125

Protein Metabolism	Translation termination factors bacterial	Methionine aminopeptidase (EC 3.4.11.18)	fig|439375.7.peg.87, fig|439375.7.peg.2010	fig|204722.5.peg.1304
		Peptide chain release factor 1	fig|439375.7.peg.1086	fig|204722.5.peg.1904
		Peptide chain release factor 2	fig|439375.7.peg.2383	fig|204722.5.peg.932
		Peptide chain release factor 3	fig|439375.7.peg.1381	fig|204722.5.peg.3287
		Peptide deformylase (EC 3.5.1.88)	fig|439375.7.peg.1409, fig|439375.7.peg.3255	fig|204722.5.peg.2672, fig|204722.5.peg.3260
		Peptidyl-tRNA hydrolase (EC 3.1.1.29)	fig|439375.7.peg.1718	fig|204722.5.peg.1560
		Ribosome recycling factor	fig|439375.7.peg.2137	fig|204722.5.peg.1178
		tmRNA-binding protein SmpB	fig|439375.7.peg.2782	fig|204722.5.peg.661
	tRNA aminoacylation, Ala	Alanyl-tRNA synthetase (EC 6.1.1.7)	fig|439375.7.peg.2089	fig|204722.5.peg.1222
	tRNA aminoacylation, Ala	Alanyl-tRNA synthetase domain protein	fig|439375.7.peg.2249	fig|204722.5.peg.1068
	tRNA aminoacylation, Arg	Arginyl-tRNA synthetase (EC 6.1.1.19)	fig|439375.7.peg.2481	fig|204722.5.peg.888
	tRNA aminoacylation, Asp and Asn	Aspartyl-tRNA synthetase (EC 6.1.1.12)	fig|439375.7.peg.2675	fig|204722.5.peg.765
	tRNA aminoacylation, Asp and Asn	Aspartyl-tRNA(Asn) amidotransferase subunit A (EC 6.3.5.6)	fig|439375.7.peg.3822	fig|204722.5.peg.2810
	tRNA aminoacylation, Asp and Asn	Aspartyl-tRNA(Asn) amidotransferase subunit B (EC 6.3.5.6)	fig|439375.7.peg.2399	fig|204722.5.peg.913
	tRNA aminoacylation, Asp and Asn	Aspartyl-tRNA(Asn) amidotransferase subunit C (EC 6.3.5.6)	fig|439375.7.peg.3824	fig|204722.5.peg.2811
	tRNA aminoacylation, Asp and Asn	Aspartyl-tRNA(Asn) synthetase (EC 6.1.1.23)	fig|439375.7.peg.2675	fig|204722.5.peg.765
	tRNA aminoacylation, Cys	Cysteinyl-tRNA synthetase (EC 6.1.1.16)	fig|439375.7.peg.2753	fig|204722.5.peg.689
	tRNA aminoacylation, Glu and Gln	Glutamyl-tRNA synthetase (EC 6.1.1.17)	fig|439375.7.peg.2148	fig|204722.5.peg.1167
	tRNA aminoacylation, Glu and Gln	Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.7)	fig|439375.7.peg.3822	fig|204722.5.peg.2810
	tRNA aminoacylation, Glu and Gln	Glutamyl-tRNA(Gln) amidotransferase subunit B (EC 6.3.5.7)	fig|439375.7.peg.2399	fig|204722.5.peg.913
	tRNA aminoacylation, Glu and Gln	Glutamyl-tRNA(Gln) amidotransferase subunit C (EC 6.3.5.7)	fig|439375.7.peg.3824	fig|204722.5.peg.2811
	tRNA aminoacylation, Glu and Gln	Glutamyl-tRNA(Gln) synthetase (EC 6.1.1.24)	fig|439375.7.peg.2204	fig|204722.5.peg.1027
	tRNA aminoacylation, Gly	Glycyl-tRNA synthetase alpha chain (EC 6.1.1.14)	fig|439375.7.peg.557	fig|204722.5.peg.418
	tRNA aminoacylation, Gly	Glycyl-tRNA synthetase beta chain (EC 6.1.1.14)	fig|439375.7.peg.558	fig|204722.5.peg.420
	tRNA aminoacylation, His	Histidyl-tRNA synthetase (EC 6.1.1.21)	fig|439375.7.peg.3169	fig|204722.5.peg.2403
	tRNA aminoacylation, Ile	Isoleucyl-tRNA synthetase (EC 6.1.1.5)	fig|439375.7.peg.3183	fig|204722.5.peg.2416
	tRNA aminoacylation, Leu	Leucyl-tRNA synthetase (EC 6.1.1.4)	fig|439375.7.peg.1145	fig|204722.5.peg.1835
	tRNA aminoacylation, Lys	Lysyl-tRNA synthetase (class I) (EC 6.1.1.6)	fig|439375.7.peg.4144	fig|204722.5.peg.3005
	tRNA aminoacylation, Met	Methionyl-tRNA synthetase (EC 6.1.1.10)	fig|439375.7.peg.2185	fig|204722.5.peg.1007
	tRNA aminoacylation, Phe	Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20)	fig|439375.7.peg.842	fig|204722.5.peg.2160
	tRNA aminoacylation, Phe	Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20)	fig|439375.7.peg.841	fig|204722.5.peg.2161
	tRNA aminoacylation, Pro	Prolyl-tRNA synthetase (EC 6.1.1.15)	fig|439375.7.peg.2537	fig|204722.5.peg.833
	tRNA aminoacylation, Ser	Archaeal seryl-tRNA synthetase-related sequence	fig|439375.7.peg.1546	
	tRNA aminoacylation, Ser	Seryl-tRNA synthetase (EC 6.1.1.11)	fig|439375.7.peg.2472	fig|204722.5.peg.896
	tRNA aminoacylation, Thr	Threonyl-tRNA synthetase (EC 6.1.1.3)	fig|439375.7.peg.2262	fig|204722.5.peg.1085
	tRNA aminoacylation, Trp	Tryptophanyl-tRNA synthetase (EC 6.1.1.2)	fig|439375.7.peg.164	fig|204722.5.peg.148
	tRNA aminoacylation, Tyr	Tyrosyl-tRNA synthetase (EC 6.1.1.1)	fig|439375.7.peg.2378	fig|204722.5.peg.941
	tRNA aminoacylation, Val	Valyl-tRNA synthetase (EC 6.1.1.9)	fig|439375.7.peg.2357	fig|204722.5.peg.961
		tRNA-Ala-CGC		fig|204722.5.rna.48
		tRNA-Ala-GGC	fig|439375.7.rna.1	fig|204722.5.rna.1
		tRNA-Arg-ACG	fig|439375.7.rna.5	fig|204722.5.rna.5
		tRNA-Arg-CCG	fig|439375.7.rna.37	fig|204722.5.rna.16
		tRNA-Cys-GCA	fig|439375.7.rna.60	fig|204722.5.rna.54
		tRNA-Gly-CCC	fig|439375.7.rna.34	fig|204722.5.rna.17

		tRNAs	tRNA-Gly-GCC	fig|439375.7.rna.23, fig|439375.7.rna.57	fig|204722.5.rna.57, fig|204722.5.rna.58
			tRNA-Leu-CAA	fig|439375.7.rna.8	fig|204722.5.rna.47
			tRNA-Leu-CAG	fig|439375.7.rna.25	fig|204722.5.rna.59
			tRNA-Leu-GAG	fig|439375.7.rna.36	fig|204722.5.rna.19, fig|204722.5.rna.20
			tRNA-Phe-GAA	fig|439375.7.rna.3	fig|204722.5.rna.3
			tRNA-Pro-CGG	fig|439375.7.rna.2	fig|204722.5.rna.2
			tRNA-Pro-GGG	fig|439375.7.rna.45	fig|204722.5.rna.10
			tRNA-Ser-CGA	fig|439375.7.rna.15	fig|204722.5.rna.39
			tRNA-Ser-GGA	fig|439375.7.rna.24	fig|204722.5.rna.60
			tRNA-Trp-CCA	fig|439375.7.rna.33	fig|204722.5.rna.21
			tRNA-Val-CAC	fig|439375.7.rna.38	fig|204722.5.rna.15
			tRNA-Val-GAC	fig|439375.7.rna.70	fig|204722.5.rna.50
		Universal GTPases	COG0536: GTP-binding protein Obg	fig|439375.7.peg.1102	fig|204722.5.peg.1877
			GTPase and tRNA-U34 5-formylation enzyme TrmE	fig|439375.7.peg.903	fig|204722.5.peg.2096
			GTP-binding and nucleic acid-binding protein YchF	fig|439375.7.peg.1717	fig|204722.5.peg.1561
			GTP-binding protein EngA	fig|439375.7.peg.521	fig|204722.5.peg.393
			GTP-binding protein EngB	fig|439375.7.peg.1426	fig|204722.5.peg.3249
			GTP-binding protein Era	fig|439375.7.peg.2768	fig|204722.5.peg.675
			GTP-binding protein HflX	fig|439375.7.peg.2320	fig|204722.5.peg.1130
			GTP-binding protein TypA/BipA	fig|439375.7.peg.3460	fig|204722.5.peg.3093
			Signal recognition particle receptor protein FtsY (=alpha subunit) (TC 3.A.5.1.1)	fig|439375.7.peg.970	fig|204722.5.peg.1968
			Signal recognition particle, subunit Ffh SRP54 (TC 3.A.5.1.1)	fig|439375.7.peg.1126	fig|204722.5.peg.1856
			Translation elongation factor G	fig|439375.7.peg.2055	fig|204722.5.peg.1258
			Translation elongation factor LepA	fig|439375.7.peg.1406	fig|204722.5.peg.3264
			Translation elongation factor Tu	fig|439375.7.peg.2043, fig|439375.7.peg.2056	fig|204722.5.peg.1257, fig|204722.5.peg.1272
			Translation initiation factor 2	fig|439375.7.peg.789	fig|204722.5.peg.2202
		Aminopeptidases (EC 3.4.11.-)	Aminopeptidase S (Leu, Val, Phe, Tyr preference) (EC 3.4.11.24)	fig|439375.7.peg.806	fig|204722.5.peg.2183
			Cytosol aminopeptidase PepA (EC 3.4.11.1)	fig|439375.7.peg.2741	fig|204722.5.peg.701
			Membrane alanine aminopeptidase N (EC 3.4.11.2)	fig|439375.7.peg.2807	fig|204722.5.peg.635
			Peptidase B (EC 3.4.11.23)	fig|439375.7.peg.770	fig|204722.5.peg.2218
			Xaa-Pro aminopeptidase (EC 3.4.11.9)	fig|439375.7.peg.1859	fig|204722.5.peg.1444
		Proteasome bacterial	ATP-dependent Clp protease ATP-binding subunit ClpX	fig|439375.7.peg.2317	fig|204722.5.peg.1128
			ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92)	fig|439375.7.peg.512, fig|439375.7.peg.1576, fig|439375.7.peg.1886, fig|439375.7.peg.2319	fig|204722.5.peg.1129
			ATP-dependent hsl protease ATP-binding subunit HslU	fig|439375.7.peg.886	fig|204722.5.peg.2115
			ATP-dependent protease HslV (EC 3.4.25.-)	fig|439375.7.peg.884	fig|204722.5.peg.2116
			ATP-dependent protease La (EC 3.4.21.53) Type I	fig|439375.7.peg.2316	fig|204722.5.peg.1127
			Uncharacterized protein, similar to the N-terminal domain of Lon protease	fig|439375.7.peg.3439	fig|204722.5.peg.3112
			Arginine-tRNA-protein transferase (EC 2.3.2.8)	fig|439375.7.peg.2672	fig|204722.5.peg.768

Protein degradation	Protein degradation	Asp-X dipeptidase	fig|439375.7.peg.670, fig|439375.7.peg.3234, fig|439375.7.peg.4299	
		Deblocking aminopeptidase (EC 3.4.11.-)	fig|439375.7.peg.3106	
		Dipeptidyl carboxypeptidase Dcp (EC 3.4.15.5)	fig|439375.7.peg.3458	fig|204722.5.peg.3095
		Leucyl/phenylalanyl-tRNA--protein transferase (EC 2.3.2.6)	fig|439375.7.peg.2395	fig|204722.5.peg.918
	Proteolysis in bacteria, ATP-dependent	ATP-dependent Clp protease adaptor protein ClpS	fig|439375.7.peg.2124	fig|204722.5.peg.1189
		ATP-dependent Clp protease ATP-binding subunit ClpA	fig|439375.7.peg.2125, fig|439375.7.peg.4643	fig|204722.5.peg.1188
		ATP-dependent Clp protease ATP-binding subunit ClpX	fig|439375.7.peg.2317	fig|204722.5.peg.1128
		ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92)	fig|439375.7.peg.512, fig|439375.7.peg.1576, fig|439375.7.peg.1886, fig|439375.7.peg.2319	fig|204722.5.peg.1129
		ATP-dependent hsl protease ATP-binding subunit HslU	fig|439375.7.peg.886	fig|204722.5.peg.2115
		ATP-dependent protease HslV (EC 3.4.25.-)	fig|439375.7.peg.884	fig|204722.5.peg.2116
		ATP-dependent protease La (EC 3.4.21.53) Type I	fig|439375.7.peg.2316	fig|204722.5.peg.1127
		ClpB protein	fig|439375.7.peg.1089	fig|204722.5.peg.1899
		DNA repair protein RadA	fig|439375.7.peg.601	fig|204722.5.peg.464
Protein folding	GroEL GroES	Heat shock protein 60 family chaperone GroEL	fig|439375.7.peg.3177	fig|204722.5.peg.2412
		Heat shock protein 60 family co-chaperone GroES	fig|439375.7.peg.3178	fig|204722.5.peg.2413
	Peptidyl-prolyl cis-trans isomerase	Foldase protein PrsA precursor (EC 5.2.1.8)	fig|439375.7.peg.1072	fig|204722.5.peg.1976
		Peptidyl-prolyl cis-trans isomerase ppiD (EC 5.2.1.8)	fig|439375.7.peg.2155, fig|439375.7.peg.3041	fig|204722.5.peg.1159, fig|204722.5.peg.2512
		Survival protein SurA precursor (Peptidyl-prolyl cis-trans isomerase SurA) (EC 5.2.1.8)	fig|439375.7.peg.2745	fig|204722.5.peg.696
	Periplasmic disulfide interchange	Cytochrome c-type biogenesis protein CcdA (DsbD analog)	fig|439375.7.peg.3359, fig|439375.7.peg.3807	fig|204722.5.peg.2800
		Cytochrome c-type biogenesis protein CcmG/DsbE, thiol:disulfide oxidoreductase	fig|439375.7.peg.118	fig|204722.5.peg.100
		Cytochrome c-type biogenesis protein DsbD, protein-disulfide reductase (EC 1.8.1.8)	fig|439375.7.peg.503, fig|439375.7.peg.3406	
		Periplasmic thiol:disulfide interchange protein DsbA	fig|439375.7.peg.651	fig|204722.5.peg.511
		Periplasmic thiol:disulfide oxidoreductase DsbB, required for DsbA reoxidation	fig|439375.7.peg.1334	fig|204722.5.peg.1671
	Protein chaperones	Chaperone protein DnaJ	fig|439375.7.peg.832	fig|204722.5.peg.2164
		Chaperone protein DnaK	fig|439375.7.peg.834	fig|204722.5.peg.2163
		ClpB protein	fig|439375.7.peg.1089	fig|204722.5.peg.1899
		DnaJ-class molecular chaperone CbpA	fig|439375.7.peg.571	fig|204722.5.peg.434
		Heat shock protein GrpE	fig|439375.7.peg.191	fig|204722.5.peg.178
	Lipoprotein Biosynthesis	Apolipoprotein N-acyltransferase (EC 2.3.1.-)	fig|439375.7.peg.796	fig|204722.5.peg.2195
		Lipoprotein signal peptidase (EC 3.4.23.36)	fig|439375.7.peg.171, fig|439375.7.peg.3358	fig|204722.5.peg.155
		Prolipoprotein diacylglyceryl transferase (EC 2.4.99.-)	fig|439375.7.peg.1727	fig|204722.5.peg.1552
	Peptide methionine sulfoxide reductase	Peptide methionine sulfoxide reductase MsrA (EC 1.8.4.11)	fig|439375.7.peg.1372	fig|204722.5.peg.3293
		Peptide methionine sulfoxide reductase MsrB (EC 1.8.4.12)	fig|439375.7.peg.3520	fig|204722.5.peg.2664
		MiaB family protein, possibly involved in tRNA or rRNA modification	fig|439375.7.peg.971	fig|204722.5.peg.1967

	Protein processing and modification	Ribosomal protein S12p Asp methylthiotransferase	Ribosomal protein S12p Asp88 (E. coli) methylthiotransferase	fig|439375.7.peg.3788	fig|204722.5.peg.2782
			SSU ribosomal protein S12p (S23e)	fig|439375.7.peg.2053	fig|204722.5.peg.1260
			tRNA-i(6)A37 methylthiotransferase	fig|439375.7.peg.801	fig|204722.5.peg.2190
		Ribosomal protein S5p acylation	Ribosomal-protein-S5p-alanine acetyltransferase	fig|439375.7.peg.637	fig|204722.5.peg.497
			SSU ribosomal protein S5p (S2e)	fig|439375.7.peg.2075	fig|204722.5.peg.1238
		Signal peptidase	Lipoprotein signal peptidase (EC 3.4.23.36)	fig|439375.7.peg.171, fig|439375.7.peg.3358	fig|204722.5.peg.155
			Signal peptidase I (EC 3.4.21.89)	fig|439375.7.peg.526, fig|439375.7.peg.2770	fig|204722.5.peg.673
	Secretion	Twin-arginine translocation system	Twin-arginine translocation protein TatA	fig|439375.7.peg.2475	fig|204722.5.peg.893
			Twin-arginine translocation protein TatB	fig|439375.7.peg.2474	fig|204722.5.peg.894
			Twin-arginine translocation protein TatC	fig|439375.7.peg.2473	fig|204722.5.peg.895
	Selenoproteins	Selenocysteine metabolism	L-seryl-tRNA(Sec) selenium transferase (EC 2.9.1.1)	fig|439375.7.peg.3012	■
			Selenide,water dikinase (EC 2.7.9.3)	fig|439375.7.peg.3005	■
			selenocysteine-containing	fig|439375.7.peg.3008	■
			Selenocysteine-specific translation elongation factor	fig|439375.7.peg.3014	■
and Cell signaling	**Programmed Cell Death and Toxin-antitoxin Systems**	Murein hydrolase regulation and cell death	Antiholin-like protein LrgA	fig|439375.7.peg.4168	■
			CidA-associated membrane protein CidB	fig|439375.7.peg.448	fig|204722.5.peg.339
			Holin-like protein CidA	fig|439375.7.peg.447	fig|204722.5.peg.338
			LrgA-associated membrane protein LrgB	fig|439375.7.peg.4167	■
			LysR family regulatory protein CidR	fig|439375.7.peg.446, fig|439375.7.peg.3378	fig|204722.5.peg.337
			Preprotein translocase subunit SecG (TC 3.A.5.1.1)	fig|439375.7.peg.2157	fig|204722.5.peg.1157
		Phd-Doc, YdcE-YdcD toxin-antitoxin (programmed cell death) systems	Death on curing protein, Doc toxin	fig|439375.7.peg.2854	fig|204722.5.peg.574
			Prevent host death protein, Phd antitoxin	fig|439375.7.peg.2853	fig|204722.5.peg.575
		Toxin-antitoxin systems (other than RelBE and MazEF)	HigA protein (antitoxin to HigB)	fig|439375.7.peg.673, fig|439375.7.peg.4941	■
			HigB toxin protein	fig|439375.7.peg.4940	■
		cAMP signaling in bacteria	Adenine phosphoribosyltransferase (EC 2.4.2.7)	fig|439375.7.peg.1714	fig|204722.5.peg.1564
			ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92)	fig|439375.7.peg.512, fig|439375.7.peg.1576, fig|439375.7.peg.1886, fig|439375.7.peg.2319	fig|204722.5.peg.1129
			cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	fig|439375.7.peg.285, fig|439375.7.peg.1010, fig|439375.7.peg.3523, fig|439375.7.peg.4487	fig|204722.5.peg.204, fig|204722.5.peg.2041, fig|204722.5.peg.2628
			ElaA protein	fig|439375.7.peg.152	fig|204722.5.peg.133
			Putative Heme-regulated two-component response regulator	fig|439375.7.peg.1358, fig|439375.7.peg.3816	fig|204722.5.peg.3228
			Putative hemin-binding lipoprotein	fig|439375.7.peg.3135	fig|204722.5.peg.3321
		DNA-binding regulatory proteins, strays	Hydrogen peroxide-inducible genes activator	fig|439375.7.peg.3204, fig|439375.7.peg.4000	fig|204722.5.peg.2568, fig|204722.5.peg.2924
			LysR family transcriptional regulator STM2281	fig|439375.7.peg.1677	■
			LysR family transcriptional regulator STM3121	fig|439375.7.peg.3562	fig|204722.5.peg.2663
		Global Two-component Regulator PrrBA in Proteobacteria	Dna binding response regulator PrrA (RegA)	fig|439375.7.peg.159	fig|204722.5.peg.143
			Sensor histidine kinase PrrB (RegB) (EC 2.7.3.-)	fig|439375.7.peg.157	fig|204722.5.peg.139

Regulation	**Regulation and Cell signaling**	Orphan regulatory proteins	Glycine cleavage system transcriptional activator GcvA	fig|439375.7.peg.2705, fig|439375.7.peg.4123, fig|439375.7.peg.4254	
			Sensor protein basS/pmrB (EC 2.7.3.-)	fig|439375.7.peg.3409	
			Sensory histidine kinase QseC	fig|439375.7.peg.501	
			Two-component sensor histidine kinase PleC	fig|439375.7.peg.2808	
			Two-component system response regulator QseB	fig|439375.7.peg.502, fig|439375.7.peg.2819, fig|439375.7.peg.3410	
		The Chv regulatory system of Alphaproteobacteria	DNA-binding response regulator ChvI	fig|439375.7.peg.873	fig|204722.5.peg.2127
			Phosphocarrier protein, nitrogen regulation associated	fig|439375.7.peg.869	fig|204722.5.peg.2132
			PTS system permease (IIAMan), nitrogen regulatory IIA protein	fig|439375.7.peg.870	fig|204722.5.peg.2131
			Sensor histidine kinase ChvG (EC 2.7.3.-)	fig|439375.7.peg.872	fig|204722.5.peg.2128
		Zinc regulated enzymes	C4-type zinc finger protein, DksA/TraR family	fig|439375.7.peg.2228	fig|204722.5.peg.1048
			Carbonic anhydrase (EC 4.2.1.1)	fig|439375.7.peg.1123, fig|439375.7.peg.3003	fig|204722.5.peg.1859, fig|204722.5.peg.3003
			Cysteinyl-tRNA synthetase (EC 6.1.1.16)	fig|439375.7.peg.2753	fig|204722.5.peg.689
			Dihydroorotase (EC 3.5.2.3)	fig|439375.7.peg.2763, fig|439375.7.peg.3830	fig|204722.5.peg.680, fig|204722.5.peg.2817
			GTP cyclohydrolase I (EC 3.5.4.16) type 1	fig|439375.7.peg.2266	fig|204722.5.peg.1089
			N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)	fig|439375.7.peg.1830, fig|439375.7.peg.2385	fig|204722.5.peg.928, fig|204722.5.peg.1470
			Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19)	fig|439375.7.peg.2267	fig|204722.5.peg.1090
			Porphobilinogen synthase (EC 4.2.1.24)	fig|439375.7.peg.2670	fig|204722.5.peg.770
			Putative metal chaperone, involved in Zn homeostasis, GTPase of COG0523 family	fig|439375.7.peg.1441, fig|439375.7.peg.4345	fig|204722.5.peg.3211, fig|204722.5.peg.3349
			Queuosine biosynthesis QueD, PTPS-I	fig|439375.7.peg.1058	fig|204722.5.peg.2010
			Zinc uptake regulation protein ZUR	fig|439375.7.peg.4350	fig|204722.5.peg.3353
	ATP synthases	F0F1-type ATP synthase	ATP synthase A chain (EC 3.6.3.14)	fig|439375.7.peg.534, fig|439375.7.peg.2648	fig|204722.5.peg.398
			ATP synthase alpha chain (EC 3.6.3.14)	fig|439375.7.peg.1153	fig|204722.5.peg.1829
			ATP synthase B chain (EC 3.6.3.14)	fig|439375.7.peg.537	fig|204722.5.peg.401
			ATP synthase B' chain (EC 3.6.3.14)	fig|439375.7.peg.536	fig|204722.5.peg.400
			ATP synthase beta chain (EC 3.6.3.14)	fig|439375.7.peg.1155	fig|204722.5.peg.1827
			ATP synthase C chain (EC 3.6.3.14)	fig|439375.7.peg.535	fig|204722.5.peg.399
			ATP synthase delta chain (EC 3.6.3.14)	fig|439375.7.peg.1152, fig|439375.7.peg.1809	fig|204722.5.peg.1487, fig|204722.5.peg.1830
			ATP synthase epsilon chain (EC 3.6.3.14)	fig|439375.7.peg.1156	fig|204722.5.peg.1826
			ATP synthase gamma chain (EC 3.6.3.14)	fig|439375.7.peg.1154	fig|204722.5.peg.1828
			ATP synthase protein I	fig|439375.7.peg.533	fig|204722.5.peg.397
			Anaerobic dehydrogenases, typically selenocysteine-containing	fig|439375.7.peg.2717	fig|204722.5.peg.720
			Arsenate reductase (EC 1.20.4.1)	fig|439375.7.peg.346, fig|439375.7.peg.2308, fig|439375.7.peg.3354, fig|439375.7.peg.3355, fig|439375.7.peg.4857, fig|439375.7.peg.4931	fig|204722.5.peg.259, fig|204722.5.peg.1001

	Electron accepting reactions	Anaerobic respiratory reductases	Butyryl-CoA dehydrogenase (EC 1.3.99.2)	fig|439375.7.peg.3256, fig|439375.7.peg.4180	fig|204722.5.peg.2437, fig|204722.5.peg.2665, fig|204722.5.peg.3313
			Electron transfer flavoprotein-ubiquinone oxidoreductase (EC 1.5.5.1)	fig|439375.7.peg.2803	fig|204722.5.peg.639
			Ferredoxin reductase	fig|439375.7.peg.3395, fig|439375.7.peg.4036, fig|439375.7.peg.4225	fig|204722.5.peg.2944
			Ferric reductase (1.6.99.14)	fig|439375.7.peg.4305	■
		Terminal cytochrome C oxidases	Cytochrome c oxidase polypeptide I (EC 1.9.3.1)	fig|439375.7.peg.622	fig|204722.5.peg.483
			Cytochrome c oxidase polypeptide II (EC 1.9.3.1)	fig|439375.7.peg.621	fig|204722.5.peg.482
			Cytochrome c oxidase polypeptide III (EC 1.9.3.1)	fig|439375.7.peg.626	fig|204722.5.peg.487
			Cytochrome c oxidase subunit CcoN (EC 1.9.3.1)	fig|439375.7.peg.500	fig|204722.5.peg.379
			Cytochrome c oxidase subunit CcoO (EC 1.9.3.1)	fig|439375.7.peg.499	fig|204722.5.peg.378
			Cytochrome c oxidase subunit CcoP (EC 1.9.3.1)	fig|439375.7.peg.496	fig|204722.5.peg.376
			Cytochrome c oxidase subunit CcoQ (EC 1.9.3.1)	fig|439375.7.peg.497	fig|204722.5.peg.377
			Cytochrome c oxidase, subunit IV (EC 1.9.3.1)	fig|439375.7.peg.1451	fig|204722.5.peg.3196
			membrane c-type cytochrome cy	fig|439375.7.peg.16	fig|204722.5.peg.43
			Type cbb3 cytochrome oxidase biogenesis protein CcoG, involved in Cu oxidation	fig|439375.7.peg.495	fig|204722.5.peg.375
			Type cbb3 cytochrome oxidase biogenesis protein CcoS, involved in heme b insertion	fig|439375.7.peg.492	fig|204722.5.peg.372
		Terminal cytochrome d ubiquinol oxid	Cytochrome d ubiquinol oxidase subunit I (EC 1.10.3.-)	fig|439375.7.peg.3698	fig|204722.5.peg.2727
			Cytochrome d ubiquinol oxidase subunit II (EC 1.10.3.-)	fig|439375.7.peg.3699	fig|204722.5.peg.2728
			Transport ATP-binding protein CydC	fig|439375.7.peg.3697	fig|204722.5.peg.2726
			Transport ATP-binding protein CydD	fig|439375.7.peg.3696	fig|204722.5.peg.2725
			Cytochrome O ubiquinol oxidase subunit I (EC 1.10.3.-)	fig|439375.7.peg.50	fig|204722.5.peg.47
			Cytochrome O ubiquinol oxidase subunit II (EC 1.10.3.-)	fig|439375.7.peg.49	fig|204722.5.peg.46
			Cytochrome O ubiquinol oxidase subunit III (EC 1.10.3.-)	fig|439375.7.peg.51	fig|204722.5.peg.48
			Cytochrome O ubiquinol oxidase subunit IV (EC 1.10.3.-)	fig|439375.7.peg.52	fig|204722.5.peg.49
		Terminal cytochrome oxidases	Cytochrome d ubiquinol oxidase subunit I (EC 1.10.3.-)	fig|439375.7.peg.3698	fig|204722.5.peg.2727
			Cytochrome d ubiquinol oxidase subunit II (EC 1.10.3.-)	fig|439375.7.peg.3699	fig|204722.5.peg.2728
			Cytochrome O ubiquinol oxidase subunit I (EC 1.10.3.-)	fig|439375.7.peg.50	fig|204722.5.peg.47
			Cytochrome O ubiquinol oxidase subunit II (EC 1.10.3.-)	fig|439375.7.peg.49	fig|204722.5.peg.46
			Cytochrome O ubiquinol oxidase subunit III (EC 1.10.3.-)	fig|439375.7.peg.51	fig|204722.5.peg.48
			Cytochrome O ubiquinol oxidase subunit IV (EC 1.10.3.-)	fig|439375.7.peg.52	fig|204722.5.peg.49
			Transport ATP-binding protein CydC	fig|439375.7.peg.3697	fig|204722.5.peg.2726
			Transport ATP-binding protein CydD	fig|439375.7.peg.3696	fig|204722.5.peg.2725
		Ubiquinone Menaquinone-cytochrome c reductase complexes	ubiquinol cytochrome C oxidoreductase, cytochrome C1 subunit	fig|439375.7.peg.1713	fig|204722.5.peg.1566
			Ubiquinol-cytochrome C reductase iron-sulfur subunit (EC 1.10.2.2)	fig|439375.7.peg.1711	fig|204722.5.peg.1568
			Ubiquinol--cytochrome c reductase, cytochrome B subunit (EC 1.10.2.2)	fig|439375.7.peg.1712	fig|204722.5.peg.1567
		Formate dehydrogenase	Formate dehydrogenase O alpha subunit (EC 1.2.1.2)	fig|439375.7.peg.3008	■
			Formate dehydrogenase O beta subunit (EC 1.2.1.2)	fig|439375.7.peg.3009	■
			Formate dehydrogenase O gamma subunit (EC 1.2.1.2)	fig|439375.7.peg.3010	■
			NADH ubiquinone oxidoreductase chain A (EC 1.6.5.3)	fig|439375.7.peg.2556	fig|204722.5.peg.812
			NADH:ubiquinone oxidoreductase 17.2 kD subunit	fig|439375.7.peg.2397	fig|204722.5.peg.915

Respiration	**Electron donating reactions**	Respiratory Complex I	NADH-ubiquinone oxidoreductase chain B (EC 1.6.5.3)	fig|439375.7.peg.2555	fig|204722.5.peg.813
			NADH-ubiquinone oxidoreductase chain C (EC 1.6.5.3)	fig|439375.7.peg.2554	fig|204722.5.peg.814
			NADH-ubiquinone oxidoreductase chain D (EC 1.6.5.3)	fig|439375.7.peg.2552	fig|204722.5.peg.815
			NADH-ubiquinone oxidoreductase chain E (EC 1.6.5.3)	fig|439375.7.peg.2551	fig|204722.5.peg.816
			NADH-ubiquinone oxidoreductase chain F (EC 1.6.5.3)	fig|439375.7.peg.2550	fig|204722.5.peg.817
			NADH-ubiquinone oxidoreductase chain G (EC 1.6.5.3)	fig|439375.7.peg.2549	fig|204722.5.peg.818
			NADH-ubiquinone oxidoreductase chain H (EC 1.6.5.3)	fig|439375.7.peg.2548	fig|204722.5.peg.819
			NADH-ubiquinone oxidoreductase chain I (EC 1.6.5.3)	fig|439375.7.peg.2547	fig|204722.5.peg.820
			NADH-ubiquinone oxidoreductase chain J (EC 1.6.5.3)	fig|439375.7.peg.2546	fig|204722.5.peg.821
			NADH-ubiquinone oxidoreductase chain K (EC 1.6.5.3)	fig|439375.7.peg.2545	fig|204722.5.peg.822
			NADH-ubiquinone oxidoreductase chain L (EC 1.6.5.3)	fig|439375.7.peg.2544	fig|204722.5.peg.823
			NADH-ubiquinone oxidoreductase chain M (EC 1.6.5.3)	fig|439375.7.peg.2543	fig|204722.5.peg.824
			NADH-ubiquinone oxidoreductase chain N (EC 1.6.5.3)	fig|439375.7.peg.2542	fig|204722.5.peg.825
		Respiratory dehydrogenases 1	Aerobic glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)	fig|439375.7.peg.289	fig|204722.5.peg.207
			D-amino acid dehydrogenase small subunit (EC 1.4.99.1)	fig|439375.7.peg.1160, fig|439375.7.peg.1513, fig|439375.7.peg.3873, fig|439375.7.peg.4248	fig|204722.5.peg.1820, fig|204722.5.peg.1821, fig|204722.5.peg.2843, fig|204722.5.peg.3141
			Glucose dehydrogenase, PQQ-dependent (EC 1.1.5.2)	fig|439375.7.peg.316	■
			Glucose-methanol-choline (GMC) oxidoreductase:NAD binding site	fig|439375.7.peg.62, fig|439375.7.peg.921	fig|204722.5.peg.2078
			Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)	fig|439375.7.peg.2593, fig|439375.7.peg.3066, fig|439375.7.peg.3228	■
			L-lactate dehydrogenase (EC 1.1.2.3)	fig|439375.7.peg.1517	fig|204722.5.peg.3137
			NADH dehydrogenase (EC 1.6.99.3)	fig|439375.7.peg.3640	fig|204722.5.peg.2699
			Proline dehydrogenase (EC 1.5.99.8) (Proline oxidase)	fig|439375.7.peg.4014	fig|204722.5.peg.2937
		Succinate dehydrogenase	Succinate dehydrogenase cytochrome b-556 subunit	fig|439375.7.peg.996	fig|204722.5.peg.1938
			Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)	fig|439375.7.peg.998	fig|204722.5.peg.1936
			Succinate dehydrogenase hydrophobic membrane anchor protein	fig|439375.7.peg.997	fig|204722.5.peg.1937
			Succinate dehydrogenase iron-sulfur protein (EC 1.3.99.1)	fig|439375.7.peg.999	fig|204722.5.peg.1935
		Biogenesis of cbb3-type cytochrome c oxidases	Type cbb3 cytochrome oxidase biogenesis protein CcoG, involved in Cu oxidation	fig|439375.7.peg.495	fig|204722.5.peg.375
			Type cbb3 cytochrome oxidase biogenesis protein CcoH	fig|439375.7.peg.494	fig|204722.5.peg.374
			Type cbb3 cytochrome oxidase biogenesis protein CcoI	fig|439375.7.peg.493	fig|204722.5.peg.373
			Type cbb3 cytochrome oxidase biogenesis protein CcoS, involved in heme b insertion	fig|439375.7.peg.492	fig|204722.5.peg.372
			ABC transporter involved in cytochrome c biogenesis, ATPase component CcmA	fig|439375.7.peg.113	fig|204722.5.peg.96
			ABC transporter involved in cytochrome c biogenesis, CcmB subunit	fig|439375.7.peg.114	fig|204722.5.peg.97
			Cytochrome c heme lyase subunit CcmF	fig|439375.7.peg.2814	fig|204722.5.peg.626
			Cytochrome c heme lyase subunit CcmH	fig|439375.7.peg.2816	fig|204722.5.peg.624
			Cytochrome c heme lyase subunit CcmL	fig|439375.7.peg.2813	fig|204722.5.peg.627
			Cytochrome c-type biogenesis protein CcdA (DsbD analog)	fig|439375.7.peg.3359, fig|439375.7.peg.3807	fig|204722.5.peg.2800
			Cytochrome c-type biogenesis protein CcmC, putative heme lyase for CcmE	fig|439375.7.peg.116	fig|204722.5.peg.98

	Respiration	Biogenesis of c-type cytochromes	Cytochrome c-type biogenesis protein CcmD, interacts with CcmCE	fig|439375.7.peg.117	fig|204722.5.peg.99
			Cytochrome c-type biogenesis protein CcmE, heme chaperone	fig|439375.7.peg.2815	fig|204722.5.peg.625
			Cytochrome c-type biogenesis protein CcmG/DsbE, thiol:disulfide oxidoreductase	fig|439375.7.peg.118	fig|204722.5.peg.100
			Cytochrome c-type biogenesis protein DsbD, protein-disulfide reductase (EC 1.8.1.8)	fig|439375.7.peg.503, fig|439375.7.peg.3406	
			Periplasmic thiol:disulfide interchange protein DsbA	fig|439375.7.peg.651	fig|204722.5.peg.511
			Periplasmic thiol:disulfide oxidoreductase DsbB, required for DsbA reoxidation	fig|439375.7.peg.1334	fig|204722.5.peg.1671
			Thiol:disulfide oxidoreductase TlpA	fig|439375.7.peg.1048	fig|204722.5.peg.2017
		Biogenesis of cytochrome c oxidases	Cytochrome oxidase biogenesis protein Cox11-CtaG, copper delivery to Cox1	fig|439375.7.peg.624, fig|439375.7.peg.625	fig|204722.5.peg.485, fig|204722.5.peg.486
			Cytochrome oxidase biogenesis protein Sco1/SenC/PrrC, putative copper metallochaperone	fig|439375.7.peg.1861, fig|439375.7.peg.3360	fig|204722.5.peg.1442
			Cytochrome oxidase biogenesis protein Surf1, facilitates heme A insertion	fig|439375.7.peg.628, fig|439375.7.peg.3714	fig|204722.5.peg.489, fig|204722.5.peg.2743
			Ferredoxin--NADP(+) reductase (EC 1.18.1.2)	fig|439375.7.peg.462	fig|204722.5.peg.344
			Heme A synthase, cytochrome oxidase biogenesis protein Cox15-CtaA	fig|439375.7.peg.2635	fig|204722.5.peg.797
			Heme O synthase, protoheme IX farnesyltransferase (EC 2.5.1.-) COX10-CtaB	fig|439375.7.peg.623	fig|204722.5.peg.484
		Formate hydrogenase	Formate dehydrogenase chain D (EC 1.2.1.2)	fig|439375.7.peg.3986	fig|204722.5.peg.2907, fig|204722.5.peg.2908
			formate dehydrogenase formation protein FdhE	fig|439375.7.peg.3011	
			Formate dehydrogenase O alpha subunit (EC 1.2.1.2)	fig|439375.7.peg.3008	
			Formate dehydrogenase O beta subunit (EC 1.2.1.2)	fig|439375.7.peg.3009	
			Formate dehydrogenase O gamma subunit (EC 1.2.1.2)	fig|439375.7.peg.3010	
			Putative formate dehydrogenase oxidoreductase protein	fig|439375.7.peg.1518	fig|204722.5.peg.3136
		Soluble cytochromes and functionally related electron carriers	Cytochrome c2	fig|439375.7.peg.3096	fig|204722.5.peg.2389
			Ferredoxin		fig|204722.5.peg.2596
			Ferredoxin, 2Fe-2S	fig|439375.7.peg.2218	fig|204722.5.peg.1038
			Putative diheme cytochrome c-553	fig|439375.7.peg.725, fig|439375.7.peg.2842	
		ATP-dependent RNA helicases, bacterial	ATP-dependent RNA helicase Atu1833	fig|439375.7.peg.2366	fig|204722.5.peg.953
			ATP-dependent RNA helicase RhlE	fig|439375.7.peg.2246	fig|204722.5.peg.1066
		Methylthiotransferases	MiaB family protein, possibly involved in tRNA or rRNA modification	fig|439375.7.peg.971	fig|204722.5.peg.1967
			Ribosomal protein S12p Asp88 (E. coli) methylthiotransferase	fig|439375.7.peg.3788	fig|204722.5.peg.2782
			tRNA-i(6)A37 methylthiotransferase	fig|439375.7.peg.801	fig|204722.5.peg.2190
			glutamyl-Q-tRNA synthetase	fig|439375.7.peg.1331	fig|204722.5.peg.1674
			GTP cyclohydrolase I (EC 3.5.4.16) type 1	fig|439375.7.peg.2266	fig|204722.5.peg.1089
			Inosine-uridine preferring nucleoside hydrolase (EC 3.2.2.1)	fig|439375.7.peg.2900, fig|439375.7.peg.4623	fig|204722.5.peg.2228
			NADPH dependent preQ0 reductase	fig|439375.7.peg.2110	fig|204722.5.peg.1203
			Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	fig|439375.7.peg.2288, fig|439375.7.peg.2289	fig|204722.5.peg.1114, fig|204722.5.peg.1115

RNA Metabolism	RNA processing and modification	Queuosine-Archaeosine Biosynthesis	Permease of the drug/metabolite transporter (DMT) superfamily	fig|439375.7.peg.390, fig|439375.7.peg.1015, fig|439375.7.peg.1052, fig|439375.7.peg.1661, fig|439375.7.peg.1747, fig|439375.7.peg.2703, fig|439375.7.peg.3116, fig|439375.7.peg.3515	fig|204722.5.peg.1532, fig|204722.5.peg.1908, fig|204722.5.peg.1927, fig|204722.5.peg.3069
			Putative preQ0 transporter	fig|439375.7.peg.961	fig|204722.5.peg.2049
			Queuosine Biosynthesis QueC ATPase	fig|439375.7.peg.1059	fig|204722.5.peg.2009
			Queuosine biosynthesis QueD, PTPS-I	fig|439375.7.peg.1058	fig|204722.5.peg.2010
			Queuosine Biosynthesis QueE Radical SAM	fig|439375.7.peg.1057	fig|204722.5.peg.2011
			Radical SAM family enzyme, similar to coproporphyrinogen III oxidase, oxygen-independent, clustered with nucleoside-triphosphatase RdgB	fig|439375.7.peg.196	fig|204722.5.peg.184
			S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 5.-.-.-)	fig|439375.7.peg.2287	fig|204722.5.peg.1113
			tRNA-guanine transglycosylase (EC 2.4.2.29)	fig|439375.7.peg.2286	fig|204722.5.peg.989, fig|204722.5.peg.1112
		RNA processing and degradation, bacterial	3'-to-5' exoribonuclease RNase R	fig|439375.7.peg.3835	fig|204722.5.peg.2822
			Cytoplasmic axial filament protein CafA and Ribonuclease G (EC 3.1.4.-)	fig|439375.7.peg.2387	fig|204722.5.peg.927
			Ribonuclease III (EC 3.1.26.3)	fig|439375.7.peg.2769	fig|204722.5.peg.674
		tRNA processing	Ribonuclease BN (EC 3.1.-.-)	fig|439375.7.peg.1053	fig|204722.5.peg.2015
			Ribonuclease D (EC 3.1.26.3)	fig|439375.7.peg.2677	fig|204722.5.peg.764
			Ribonuclease P protein component (EC 3.1.26.5)	fig|439375.7.peg.1428	fig|204722.5.peg.3247
			Ribonuclease PH (EC 2.7.7.56)	fig|439375.7.peg.193	fig|204722.5.peg.181
			tRNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8)	fig|439375.7.peg.1902	fig|204722.5.peg.1416
			tRNA pseudouridine synthase A (EC 4.2.1.70)	fig|439375.7.peg.1411	fig|204722.5.peg.2420, fig|204722.5.peg.3258
			tRNA pseudouridine synthase B (EC 4.2.1.70)	fig|439375.7.peg.787	fig|204722.5.peg.2204
			tRNA(Ile)-lysidine synthetase	fig|439375.7.peg.1277	fig|204722.5.peg.1719
			tRNA-i(6)A37 methylthiotransferase	fig|439375.7.peg.801	fig|204722.5.peg.2190
			tRNA-specific adenosine-34 deaminase (EC 3.5.4.-)	fig|439375.7.peg.3186	fig|204722.5.peg.2419
	Transcription	RNA polymerase bacterial	DNA-directed RNA polymerase alpha subunit (EC 2.7.7.6)	fig|439375.7.peg.2082	fig|204722.5.peg.1231
			DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)	fig|439375.7.peg.2050	fig|204722.5.peg.1265
			DNA-directed RNA polymerase beta' subunit (EC 2.7.7.6)	fig|439375.7.peg.2051	fig|204722.5.peg.1264
			DNA-directed RNA polymerase omega subunit (EC 2.7.7.6)	fig|439375.7.peg.2779	fig|204722.5.peg.664
		Rrf2 family transcriptional regulators	Iron-responsive repressor RirA	fig|439375.7.peg.3778	fig|204722.5.peg.2778
			Rrf2 family transcriptional regulator	fig|439375.7.peg.4344, fig|439375.7.peg.4530	fig|204722.5.peg.3348
			Rrf2 family transcriptional regulator, group III	fig|439375.7.peg.3744	
			COG2740: Predicted nucleic-acid-binding protein implicated in transcription termination	fig|439375.7.peg.790	fig|204722.5.peg.2201
			Regulator of nucleoside diphosphate kinase	fig|439375.7.peg.3844	fig|204722.5.peg.2830
			ribosomal protein L7Ae family protein	fig|439375.7.peg.790	fig|204722.5.peg.2201
			Transcription antitermination protein NusG	fig|439375.7.peg.2045	fig|204722.5.peg.1270

	Transcription	Transcription factors bacterial	Transcription elongation factor GreA	fig|439375.7.peg.1750	fig|204722.5.peg.1529
			Transcription elongation factor GreB	fig|439375.7.peg.2855	fig|204722.5.peg.573
			Transcription termination factor Rho	fig|439375.7.peg.901	fig|204722.5.peg.2098
			Transcription termination protein NusA	fig|439375.7.peg.791	fig|204722.5.peg.2200
			Transcription termination protein NusB	fig|439375.7.peg.2659	fig|204722.5.peg.781
			Transcription-repair coupling factor	fig|439375.7.peg.3801	fig|204722.5.peg.2795
		Transcription initiation, bacterial sigma factors	RNA polymerase sigma factor RpoD	fig|439375.7.peg.1780	fig|204722.5.peg.1506
			RNA polymerase sigma factor RpoH	fig|439375.7.peg.1293	fig|204722.5.peg.1677
			RNA polymerase sigma factor RpoH-related protein	fig|439375.7.peg.1190	fig|204722.5.peg.1790
			RNA polymerase sigma-54 factor RpoN	fig|439375.7.peg.181, fig|439375.7.peg.1307, fig|439375.7.peg.3554	fig|204722.5.peg.164
			RNA polymerase sigma-70 factor	fig|439375.7.peg.1510, fig|439375.7.peg.1788	fig|204722.5.peg.1685
	Cold shock	Cold shock, CspA family of proteins	Cold shock protein CspA	fig|439375.7.peg.1767	fig|204722.5.peg.438, fig|204722.5.peg.1520
			Cold shock protein CspB	fig|439375.7.peg.2024	fig|204722.5.peg.1285
			Cold shock protein CspG	fig|439375.7.peg.1738	fig|204722.5.peg.1539
	Detoxification	Glutathione-dependent pathway of formaldehyde detoxification	S-(hydroxymethyl)glutathione dehydrogenase (EC 1.1.1.284)	fig|439375.7.peg.153	fig|204722.5.peg.134, fig|204722.5.peg.135
			S-formylglutathione hydrolase (EC 3.1.2.12)	fig|439375.7.peg.150	fig|204722.5.peg.131
		Resistance to chromium compounds	Chromate transport protein ChrA	fig|439375.7.peg.1721, fig|439375.7.peg.4854, fig|439375.7.peg.4928	■
		Uptake of selenate and selenite	Sulfate and thiosulfate import ATP-binding protein CysA (EC 3.6.3.25)	fig|439375.7.peg.130	fig|204722.5.peg.114
			Various polyols ABC transporter, ATP-binding component	fig|439375.7.peg.4019	fig|204722.5.peg.2481
			Various polyols ABC transporter, periplasmic substrate-binding protein	fig|439375.7.peg.4022	■
			Various polyols ABC transporter, permease component 1	fig|439375.7.peg.4021	■
			Various polyols ABC transporter, permease component 2	fig|439375.7.peg.4020	■
	Osmotic stress	Choline and Betaine Uptake and Betaine Biosynthesis	Betaine aldehyde dehydrogenase (EC 1.2.1.8)	fig|439375.7.peg.2858	fig|204722.5.peg.569
			Choline dehydrogenase (EC 1.1.99.1)	fig|439375.7.peg.923, fig|439375.7.peg.2857	fig|204722.5.peg.570, fig|204722.5.peg.2076, fig|204722.5.peg.2611, fig|204722.5.peg.3179
			Choline-sulfatase (EC 3.1.6.6)	fig|439375.7.peg.3478	fig|204722.5.peg.3416
			HTH-type transcriptional regulator BetI	fig|439375.7.peg.2856	fig|204722.5.peg.571
			L-proline glycine betaine ABC transport system permease protein ProV (TC 3.A.1.12.1)	fig|439375.7.peg.319, fig|439375.7.peg.1671, fig|439375.7.peg.4058	fig|204722.5.peg.230, fig|204722.5.peg.1606, fig|204722.5.peg.2953
			L-proline glycine betaine ABC transport system permease protein ProW (TC 3.A.1.12.1)	fig|439375.7.peg.318, fig|439375.7.peg.320, fig|439375.7.peg.1672, fig|439375.7.peg.4057	fig|204722.5.peg.229, fig|204722.5.peg.231, fig|204722.5.peg.1605, fig|204722.5.peg.2952
			L-proline glycine betaine binding ABC transporter protein ProX (TC 3.A.1.12.1)	fig|439375.7.peg.1673, fig|439375.7.peg.3068, fig|439375.7.peg.3479	fig|204722.5.peg.1604, fig|204722.5.peg.2951

Stress Response	Osmotic stress		Sarcosine oxidase alpha subunit (EC 1.5.3.1)	fig|439375.7.peg.325, fig|439375.7.peg.1964	fig|204722.5.peg.237, fig|204722.5.peg.1342, fig|204722.5.peg.1343
			Sarcosine oxidase beta subunit (EC 1.5.3.1)	fig|439375.7.peg.323, fig|439375.7.peg.4611	fig|204722.5.peg.235
			Sarcosine oxidase delta subunit (EC 1.5.3.1)	fig|439375.7.peg.324	fig|204722.5.peg.236
			Sarcosine oxidase gamma subunit (EC 1.5.3.1)	fig|439375.7.peg.326	fig|204722.5.peg.238
		Ectoine biosynthesis and regulation	L-ectoine synthase (EC 4.2.1.-)	fig|439375.7.peg.2938	■
		Osmoregulation	Aquaporin Z	fig|439375.7.peg.1028	fig|204722.5.peg.2038
			Outer membrane protein A precursor	fig|439375.7.peg.523	■
		Synthesis of osmoregulated periplasmic glucans	2)glucan export ATP-binding/permease protein NdvA (EC 3.6.3.42)&subsystem_name=Synthesis_of_osmoregulated_periplasmic_glucans'>Beta-(1-->2)glucan export ATP-binding/permease protein NdvA (EC 3.6.3.42)	fig|439375.7.peg.2188	fig|204722.5.peg.1010
			Cyclic beta-1,2-glucan modification transmembrane protein	fig|439375.7.peg.295	■
			Cyclic beta-1,2-glucan synthase (EC 2.4.1.-)	fig|439375.7.peg.132	fig|204722.5.peg.115
			OpgC protein	fig|439375.7.peg.1263	fig|204722.5.peg.1733
		Glutaredoxins	Competence protein F homolog, phosphoribosyltransferase domain	fig|439375.7.peg.1078	fig|204722.5.peg.1912
			Glutaredoxin 3 (Grx2)	fig|439375.7.peg.1079	fig|204722.5.peg.1911
			Glutaredoxin-like protein NrdH, required for reduction of Ribonucleotide reductase class Ib	fig|439375.7.peg.3102	fig|204722.5.peg.2530
			Uncharacterized monothiol glutaredoxin ycf64-like	fig|439375.7.peg.2522	fig|204722.5.peg.846
		Glutathione: Biosynthesis and gamma-glutamyl cycle	Gamma-glutamyltranspeptidase (EC 2.3.2.2)	fig|439375.7.peg.4583	■
			Glutamate--cysteine ligase (EC 6.3.2.2)	fig|439375.7.peg.3149	fig|204722.5.peg.2975
			Glutathione synthetase (EC 6.3.2.3)	fig|439375.7.peg.826	fig|204722.5.peg.2169
			Similar to 5-oxoprolinase (EC 3.5.2.9) and Methylhydantoinases A, B (EC 3.5.2.14)	fig|439375.7.peg.3972	fig|204722.5.peg.2892
		Glutathione: Non-redox reactions	Glutathione S-transferase (EC 2.5.1.18)	fig|439375.7.peg.34, fig|439375.7.peg.1360, fig|439375.7.peg.2093, fig|439375.7.peg.2799	fig|204722.5.peg.644, fig|204722.5.peg.3226
			Glutathione S-transferase family protein	fig|439375.7.peg.1403, fig|439375.7.peg.2516, fig|439375.7.peg.2723	fig|204722.5.peg.714, fig|204722.5.peg.850, fig|204722.5.peg.3269
			Glutathione S-transferase, omega (EC 2.5.1.18)	fig|439375.7.peg.1691	fig|204722.5.peg.1589
			Glutathione S-transferase, unnamed subgroup 2 (EC 2.5.1.18)	fig|439375.7.peg.395	■
			Glutathione S-transferase, unnamed subgroup (EC 2.5.1.18)	■	fig|204722.5.peg.1521
			Hydroxyacylglutathione hydrolase (EC 3.1.2.6)	fig|439375.7.peg.968, fig|439375.7.peg.3688	fig|204722.5.peg.1970, fig|204722.5.peg.2716
			Lactoylglutathione lyase (EC 4.4.1.5)	fig|439375.7.peg.64, fig|439375.7.peg.2023	fig|204722.5.peg.60, fig|204722.5.peg.1287, fig|204722.5.peg.2251, fig|204722.5.peg.3096
			SAM-dependent methyltransferase 2, in cluster with Hydroxyacylglutathione hydrolase (EC 3.1.2.6)	fig|439375.7.peg.1042	fig|204722.5.peg.2023
			Uncharacterized glutathione S-transferase-like protein	fig|439375.7.peg.2353	fig|204722.5.peg.965
			Glutaredoxin 3 (Grx2)	fig|439375.7.peg.1079	fig|204722.5.peg.1911

Oxidative stress	Glutathione: Redox cycle	Glutaredoxin-like protein NrdH, required for reduction of Ribonucleotide reductase class Ib	fig|439375.7.peg.3102	fig|204722.5.peg.2530
		Glutathione reductase (EC 1.8.1.7)	fig|439375.7.peg.2200	fig|204722.5.peg.1023
		Uncharacterized monothiol glutaredoxin ycf64-like	fig|439375.7.peg.2522	fig|204722.5.peg.846
	Oxidative stress	Catalase (EC 1.11.1.6)	fig|439375.7.peg.3205, fig|439375.7.peg.4871, fig|439375.7.peg.4882	fig|204722.5.peg.2569
		Ferroxidase (EC 1.16.3.1)	fig|439375.7.peg.805	fig|204722.5.peg.2185
		Hydrogen peroxide-inducible genes activator	fig|439375.7.peg.3204, fig|439375.7.peg.4000	fig|204722.5.peg.2568, fig|204722.5.peg.2924
		Iron-binding ferritin-like antioxidant protein	fig|439375.7.peg.805	fig|204722.5.peg.2185
		Iron-responsive regulator Irr	fig|439375.7.peg.779	fig|204722.5.peg.380, fig|204722.5.peg.2211
		Manganese superoxide dismutase (EC 1.15.1.1)		fig|204722.5.peg.583
		NnrS protein involved in response to NO	fig|439375.7.peg.3048	fig|204722.5.peg.2500
		Non-specific DNA-binding protein Dps	fig|439375.7.peg.805	fig|204722.5.peg.2185
		Organic hydroperoxide resistance protein	fig|439375.7.peg.3447	fig|204722.5.peg.3103
		Organic hydroperoxide resistance transcriptional regulator	fig|439375.7.peg.3446	fig|204722.5.peg.3104
		Peroxidase (EC 1.11.1.7)	fig|439375.7.peg.4884	
		Phytochrome, two-component sensor histidine kinase (EC 2.7.3.-)	fig|439375.7.peg.4635	
		Redox-sensitive transcriptional activator SoxR	fig|439375.7.peg.3098	
		Superoxide dismutase [Cu-Zn] precursor (EC 1.15.1.1)	fig|439375.7.peg.3995	fig|204722.5.peg.2918
		Superoxide dismutase [Fe] (EC 1.15.1.1)	fig|439375.7.peg.463, fig|439375.7.peg.2849	
		transcriptional regulator, Crp/Fnr family	fig|439375.7.peg.2776, fig|439375.7.peg.3035, fig|439375.7.peg.4910	fig|204722.5.peg.667, fig|204722.5.peg.2518
		Zinc uptake regulation protein ZUR	fig|439375.7.peg.4350	fig|204722.5.peg.3353
	Protection from Reactive Oxygen Species	Catalase (EC 1.11.1.6)	fig|439375.7.peg.3205, fig|439375.7.peg.4871, fig|439375.7.peg.4882	fig|204722.5.peg.2569
		Peroxidase (EC 1.11.1.7)	fig|439375.7.peg.4884	
		Manganese superoxide dismutase (EC 1.15.1.1)		fig|204722.5.peg.583
		Superoxide dismutase [Cu-Zn] precursor (EC 1.15.1.1)	fig|439375.7.peg.3995	fig|204722.5.peg.2918
		Superoxide dismutase [Fe] (EC 1.15.1.1)	fig|439375.7.peg.463, fig|439375.7.peg.2849	
Periplasmic Stress	Periplasmic Stress Response	HtrA protease/chaperone protein	fig|439375.7.peg.1898, fig|439375.7.peg.2812	fig|204722.5.peg.628, fig|204722.5.peg.1419
		Survival protein SurA precursor (Peptidyl-prolyl cis-trans isomerase SurA) (EC 5.2.1.8)	fig|439375.7.peg.2745	fig|204722.5.peg.696
	Flavohaemoglobin	ABC-type Fe3+-siderophore transport system, permease 2 component	fig|439375.7.peg.2967	
		Chaperone protein DnaJ	fig|439375.7.peg.832	fig|204722.5.peg.2164
		Chaperone protein DnaK	fig|439375.7.peg.834	fig|204722.5.peg.2163
		Glutathione synthetase (EC 6.3.2.3)	fig|439375.7.peg.826	fig|204722.5.peg.2169
		Heat shock protein GrpE	fig|439375.7.peg.191	fig|204722.5.peg.178
		Heat-inducible transcription repressor HrcA	fig|439375.7.peg.192	fig|204722.5.peg.179

	Stress Response	Heat shock dnaK gene cluster extended	MiaB family protein, possibly involved in tRNA or rRNA modification	fig|439375.7.peg.971	fig|204722.5.peg.1967
			Nucleoside 5-triphosphatase RdgB (dHAPTP, dITP, XTP-specific) (EC 3.6.1.15)	fig|439375.7.peg.195	fig|204722.5.peg.183
			Radical SAM family enzyme, similar to coproporphyrinogen III oxidase, oxygen-independent, clustered with nucleoside-triphosphatase RdgB	fig|439375.7.peg.196	fig|204722.5.peg.184
			Ribonuclease PH (EC 2.7.7.56)	fig|439375.7.peg.193	fig|204722.5.peg.181
			Ribosomal protein L11 methyltransferase (EC 2.1.1.-)	fig|439375.7.peg.1860	fig|204722.5.peg.1443
			Ribosomal RNA small subunit methyltransferase E (EC 2.1.1.-)	fig|439375.7.peg.3150	fig|204722.5.peg.2974
			Ribosome-associated heat shock protein implicated in the recycling of the 50S subunit (S4 paralog)	fig|439375.7.peg.1185	fig|204722.5.peg.1795
			RNA polymerase sigma factor RpoH	fig|439375.7.peg.1293	fig|204722.5.peg.1677
			rRNA small subunit methyltransferase I	fig|439375.7.peg.197	fig|204722.5.peg.185
			tmRNA-binding protein SmpB	fig|439375.7.peg.2782	fig|204722.5.peg.661
			Translation elongation factor LepA	fig|439375.7.peg.1406	fig|204722.5.peg.3264
		Hfl operon	GTP-binding protein HflX	fig|439375.7.peg.2320	fig|204722.5.peg.1130
			HflC protein	fig|439375.7.peg.1896	fig|204722.5.peg.1421
			HflK protein	fig|439375.7.peg.1895	fig|204722.5.peg.1422
			Putative inner membrane protein YjeT (clustered with HflC)	fig|439375.7.peg.1897	fig|204722.5.peg.1420
			RNA-binding protein Hfq	fig|439375.7.peg.2321	fig|204722.5.peg.1131
Sulfur Metabolism	**Inorganic sulfur assimilation**	Inorganic Sulfur Assimilation	3'(2'),5'-bisphosphate nucleotidase (EC 3.1.3.7)	fig|439375.7.peg.214	fig|204722.5.peg.203
			4Fe-4S ferredoxin, iron-sulfur binding	fig|439375.7.peg.1186	fig|204722.5.peg.1793
			Adenylylsulfate kinase (EC 2.7.1.25)	fig|439375.7.peg.213	fig|204722.5.peg.202
			Adenylyl-sulfate reductase [thioredoxin] (EC 1.8.4.10)	fig|439375.7.peg.202	fig|204722.5.peg.191
			Conserved hypothetical protein probably involved in sulfate reduction	fig|439375.7.peg.200	fig|204722.5.peg.189
			Ferredoxin		fig|204722.5.peg.2596
			Ferredoxin--NADP(+) reductase (EC 1.18.1.2)	fig|439375.7.peg.462	fig|204722.5.peg.344
			Oxidoreductase probably involved in sulfite reduction	fig|439375.7.peg.203	fig|204722.5.peg.192
			Phosphoadenylyl-sulfate reductase [thioredoxin] (EC 1.8.4.8)	fig|439375.7.peg.202	fig|204722.5.peg.191
			Sulfate adenylyltransferase subunit 1 (EC 2.7.7.4)	fig|439375.7.peg.213	fig|204722.5.peg.202
			Sulfate adenylyltransferase subunit 2 (EC 2.7.7.4)	fig|439375.7.peg.212	fig|204722.5.peg.201
			Sulfate and thiosulfate binding protein CysP	fig|439375.7.peg.127, fig|439375.7.peg.1954	fig|204722.5.peg.111, fig|204722.5.peg.1355
			Sulfate and thiosulfate import ATP-binding protein CysA (EC 3.6.3.25)	fig|439375.7.peg.130	fig|204722.5.peg.114
			Sulfate transport system permease protein CysT	fig|439375.7.peg.128, fig|439375.7.peg.1955	fig|204722.5.peg.112, fig|204722.5.peg.1353
			Sulfate transport system permease protein CysW	fig|439375.7.peg.129, fig|439375.7.peg.1956	fig|204722.5.peg.113, fig|204722.5.peg.1352
			Sulfite reductase [NADPH] flavoprotein alpha-component (EC 1.8.1.2)		fig|204722.5.peg.2451
			Sulfite reductase [NADPH] hemoprotein beta-component (EC 1.8.1.2)	fig|439375.7.peg.201	fig|204722.5.peg.190

S	**Organic sulfur assimilation**	Alkanesulfonate assimilation	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	fig|439375.7.peg.3670, fig|439375.7.peg.3751, fig|439375.7.peg.4038	
			ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	fig|439375.7.peg.3671	
			ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	fig|439375.7.peg.3669	
			FMN reductase (EC 1.5.1.29)	fig|439375.7.peg.4181	
		Taurine Utilization	Taurine transport ATP-binding protein TauB	fig|439375.7.peg.3663	
			Taurine transport system permease protein TauC	fig|439375.7.peg.3662	
			Taurine-binding periplasmic protein TauA	fig|439375.7.peg.3664	
	Sulfur Metabolism	Thioredoxin-disulfide reductase	Alkyl hydroperoxide reductase protein C (EC 1.6.4.-)	fig|439375.7.peg.3999	fig|204722.5.peg.2923
			Alkylhydroperoxidase protein D	fig|439375.7.peg.3998	fig|204722.5.peg.2922
			Hydrogen peroxide-inducible genes activator	fig|439375.7.peg.3204, fig|439375.7.peg.4000	fig|204722.5.peg.2568, fig|204722.5.peg.2924
			Thiol peroxidase, Bcp-type (EC 1.11.1.15)	fig|439375.7.peg.2380	fig|204722.5.peg.939
			Thioredoxin reductase (EC 1.8.1.9)	fig|439375.7.peg.1754, fig|439375.7.peg.2219, fig|439375.7.peg.3745	fig|204722.5.peg.1039, fig|204722.5.peg.1525
	Adhesion	Widespread colonization island	Flp pilus assembly protein CpaD	fig|439375.7.peg.764	
			Flp pilus assembly protein RcpC/CpaB	fig|439375.7.peg.761	
			Flp pilus assembly protein TadB	fig|439375.7.peg.767	
			Flp pilus assembly protein TadD, contains TPR repeat	fig|439375.7.peg.769	
			Flp pilus assembly protein, pilin Flp	fig|439375.7.peg.2622	
			Similar to secretin RcpA/CpaC, associated with Flp pilus assembly	fig|439375.7.peg.757	
			Similar to TadZ/CpaE, associated with Flp pilus assembly	fig|439375.7.peg.756	
			Type II/IV secretion system ATP hydrolase TadA/VirB11/CpaF, TadA subfamily	fig|439375.7.peg.766	
			Type II/IV secretion system ATPase TadZ/CpaE, associated with Flp pilus assembly	fig|439375.7.peg.765	
			Type II/IV secretion system protein TadC, associated with Flp pilus assembly	fig|439375.7.peg.768	
			Type II/IV secretion system secretin RcpA/CpaC, associated with Flp pilus assembly	fig|439375.7.peg.763	
			Type IV prepilin peptidase TadV/CpaA	fig|439375.7.peg.760	
		Heme, hemin uptake and utilization systems in GramPositives	Hemin transport protein HmuS	fig|439375.7.peg.3782	
			Hypothetical, distant similarity with heme-degrading oxygenase IsdG	fig|439375.7.peg.3785	fig|204722.5.peg.2779
			Iron compound ABC uptake transporter substrate-binding protein	fig|439375.7.peg.3962	fig|204722.5.peg.2887
			Similar to hypothetical protein DUF454	fig|439375.7.peg.817	fig|204722.5.peg.2174
		Hemin transport system	ABC-type hemin transport system, ATPase component	fig|439375.7.peg.3779	
			Hemin ABC transporter, permease protein	fig|439375.7.peg.3780	
			Hemin transport protein HmuS	fig|439375.7.peg.3782	
			Outer membrane receptor proteins, mostly Fe transport	fig|439375.7.peg.4261	
			Periplasmic hemin-binding protein	fig|439375.7.peg.3781	
			TonB-dependent hemin , ferrichrome receptor	fig|439375.7.peg.3784	

	Iron Scavenging Mechanisms	Siderophore Aerobactin	Citrate:6-N-acetyl-6-N-hydroxy-L-lysine ligase, alpha subunit (EC 6.3.2.27), aerobactin biosynthesis protein IucA	fig|439375.7.peg.3412, fig|439375.7.peg.3414	■
			Ferric hydroxamate ABC transporter (TC 3.A.1.14.3), ATP-binding protein FhuC	fig|439375.7.peg.3635	■
			Ferric hydroxamate ABC transporter (TC 3.A.1.14.3), permease component FhuB	fig|439375.7.peg.2917	■
			Ferric hydroxamate outer membrane receptor FhuA	fig|439375.7.peg.4304	■
			L-lysine 6-monooxygenase [NADPH] (EC 1.14.13.59), aerobactin biosynthesis protein IucD	fig|439375.7.peg.3411	■
			N6-hydroxylysine O-acetyltransferase (EC 2.3.1.102), aerobactin biosynthesis protein IucB	fig|439375.7.peg.3413	■
		Siderophore assembly kit	ABC-type Fe3+-siderophore transport system, permease 2 component	fig|439375.7.peg.2967	■
			ABC-type Fe3+-siderophore transport system, permease component	fig|439375.7.peg.2968	■
			ABC-type hemin transport system, ATPase component	fig|439375.7.peg.3779	■
			Ferric hydroxamate ABC transporter (TC 3.A.1.14.3), ATP-binding protein FhuC	fig|439375.7.peg.3635	■
			Ferric hydroxamate ABC transporter (TC 3.A.1.14.3), permease component FhuB	fig|439375.7.peg.2917	■
			Ferric hydroxamate outer membrane receptor FhuA	fig|439375.7.peg.4304	■
			Ferric reductase (1.6.99.14)	fig|439375.7.peg.4305	■
			Hemin ABC transporter, permease protein	fig|439375.7.peg.3780	■
			Hemin transport protein HmuS	fig|439375.7.peg.3782	■
			Periplasmic hemin-binding protein	fig|439375.7.peg.3781	■
			Siderophore biosynthesis protein, monooxygenase	fig|439375.7.peg.3411	■
			Siderophore synthetase component, ligase	fig|439375.7.peg.3412	■
			Siderophore synthetase large component, acetyltransferase	fig|439375.7.peg.3414	■
			Siderophore synthetase small component, acetyltransferase	fig|439375.7.peg.3413	■
			TonB-dependent hemin , ferrichrome receptor	fig|439375.7.peg.3784	■
		Arsenic resistance	Arsenate reductase (EC 1.20.4.1)	fig|439375.7.peg.346, fig|439375.7.peg.2308, fig|439375.7.peg.3354, fig|439375.7.peg.3355, fig|439375.7.peg.4857, fig|439375.7.peg.4931	fig|204722.5.peg.259, fig|204722.5.peg.1001
			Arsenic resistance protein ArsH	fig|439375.7.peg.3352	■
			Arsenical-resistance protein ACR3	fig|439375.7.peg.3353	■
		Beta-lactamase	Beta-lactamase (EC 3.5.2.6)	fig|439375.7.peg.2724	■
			Beta-lactamase class C and other penicillin binding proteins	fig|439375.7.peg.3243, fig|439375.7.peg.3280	■
			Metal-dependent hydrolases of the beta-lactamase superfamily I	fig|439375.7.peg.2187	fig|204722.5.peg.1009
			Cobalt-zinc-cadmium resistance protein	fig|439375.7.peg.1684, fig|439375.7.peg.3086	fig|204722.5.peg.1594

Virulence	Resistance to antibiotics and toxic compounds	Cobalt-zinc-cadmium resistance	Cobalt-zinc-cadmium resistance protein CzcD	fig|439375.7.peg.3362, fig|439375.7.peg.3380, fig|439375.7.peg.3389, fig|439375.7.peg.4113	fig|204722.5.peg.513
			DNA-binding heavy metal response regulator	fig|439375.7.peg.2811	fig|204722.5.peg.629
			Heavy metal resistance transcriptional regulator HmrR	fig|439375.7.peg.3307	
			Probable Co/Zn/Cd efflux system membrane fusion protein	fig|439375.7.peg.364, fig|439375.7.peg.4228	fig|204722.5.peg.289
			Transcriptional regulator, MerR family	fig|439375.7.peg.317, fig|439375.7.peg.965, fig|439375.7.peg.2650, fig|439375.7.peg.3364	fig|204722.5.peg.228, fig|204722.5.peg.789, fig|204722.5.peg.2052
		Copper homeostasis	Blue copper oxidase CueO precursor	fig|439375.7.peg.3996	fig|204722.5.peg.2919
			CopG protein	fig|439375.7.peg.2667, fig|439375.7.peg.3386	
			Copper chaperone	fig|439375.7.peg.2362, fig|439375.7.peg.3383, fig|439375.7.peg.3398, fig|439375.7.peg.4224	fig|204722.5.peg.956
			Copper-translocating P-type ATPase (EC 3.6.3.4)	fig|439375.7.peg.307, fig|439375.7.peg.493, fig|439375.7.peg.966, fig|439375.7.peg.3363, fig|439375.7.peg.3388, fig|439375.7.peg.3397, fig|439375.7.peg.4792, fig|439375.7.peg.4922	fig|204722.5.peg.227, fig|204722.5.peg.373, fig|204722.5.peg.2053
			Cu(I)-responsive transcriptional regulator	fig|439375.7.peg.3394	
			Cytochrome c heme lyase subunit CcmF	fig|439375.7.peg.2814	fig|204722.5.peg.626
			Cytochrome c heme lyase subunit CcmH	fig|439375.7.peg.2816	fig|204722.5.peg.624
			Multicopper oxidase	fig|439375.7.peg.3390	
		Fosfomycin resistance	Fosfomycin resistance protein FosX		fig|204722.5.peg.2794
		Mercury resistance operon	Mercuric ion reductase (EC 1.16.1.1)	fig|439375.7.peg.3312	
			Periplasmic mercury(+2) binding protein	fig|439375.7.peg.3309	
		Multidrug Resistance Efflux Pumps	Acriflavin resistance protein	fig|439375.7.peg.365, fig|439375.7.peg.2283, fig|439375.7.peg.3023, fig|439375.7.peg.4229	fig|204722.5.peg.290, fig|204722.5.peg.1109
			Macrolide export ATP-binding/permease protein MacB (EC 3.6.3.-)	fig|439375.7.peg.1318, fig|439375.7.peg.3717	fig|204722.5.peg.1697, fig|204722.5.peg.1698
			Macrolide-specific efflux protein MacA	fig|439375.7.peg.1319, fig|439375.7.peg.3718	fig|204722.5.peg.1699
			Membrane fusion protein of RND family multidrug efflux pump	fig|439375.7.peg.399	
			Multidrug-efflux transporter, major facilitator superfamily (MFS) (TC 2.A.1)		fig|204722.5.peg.2989
			RND efflux system, inner membrane transporter CmeB	fig|439375.7.peg.400, fig|439375.7.peg.2568	fig|204722.5.peg.305, fig|204722.5.peg.2549

			RND efflux system, membrane fusion protein CmeA	fig|439375.7.peg.2569, fig|439375.7.peg.3024	fig|204722.5.peg.304, fig|204722.5.peg.2550
			Transcription repressor of multidrug efflux pump acrAB operon, TetR (AcrR) family	fig|439375.7.peg.398	fig|204722.5.peg.303
			Type I secretion outer membrane protein, TolC precursor	fig|439375.7.peg.2359	fig|204722.5.peg.959
		Resistance to fluoroquinolones	DNA gyrase subunit A (EC 5.99.1.3)	fig|439375.7.peg.2292	fig|204722.5.peg.1118
			DNA gyrase subunit B (EC 5.99.1.3)	fig|439375.7.peg.148	fig|204722.5.peg.129
			Topoisomerase IV subunit A (EC 5.99.1.-)	fig|439375.7.peg.2673	fig|204722.5.peg.767
			Topoisomerase IV subunit B (EC 5.99.1.-)	fig|439375.7.peg.3819	fig|204722.5.peg.2807
	Type III, Type IV, Type VI, ESAT secretion systems	Type 4 secretion and conjugative transfer	Conjugative transfer protein TrbB	fig|439375.7.peg.3367	■
			Conjugative transfer protein TrbC	fig|439375.7.peg.3368	■
			Conjugative transfer protein TrbD	fig|439375.7.peg.3369	■
			Conjugative transfer protein TrbE	fig|439375.7.peg.3370	■
			Conjugative transfer protein TrbF	fig|439375.7.peg.3374	■
			Conjugative transfer protein TrbG	fig|439375.7.peg.3375	■
			Conjugative transfer protein TrbI	fig|439375.7.peg.3376	■
			Conjugative transfer protein TrbJ	fig|439375.7.peg.3371	■
			Conjugative transfer protein TrbL	fig|439375.7.peg.3373	■
			IncQ plasmid conjugative transfer protein TraG	fig|439375.7.peg.715	■
			Outer membrane and periplasm component of type IV secretion of T-DNA complex, has secretin-like domain, VirB9	fig|439375.7.peg.719	■
			Ync	fig|439375.7.peg.4852	■
			Ynd	fig|439375.7.peg.4853	■
	Virulence	Siderophore Enterobactin	Ferric enterobactin transport ATP-binding protein FepC (TC 3.A.1.14.2)	fig|439375.7.peg.4259	■
			Ferric enterobactin transport system permease protein FepG (TC 3.A.1.14.2)	fig|439375.7.peg.4256	■
			Ferric enterobactin-binding periplasmic protein FepB (TC 3.A.1.14.2)	fig|439375.7.peg.4258	■
		Ton and Tol transport systems	4-hydroxybenzoyl-CoA thioesterase family active site	fig|439375.7.peg.1269	fig|204722.5.peg.1728
			Biopolymer transport protein ExbD/TolR	fig|439375.7.peg.1271, fig|439375.7.peg.1315	fig|204722.5.peg.1694, fig|204722.5.peg.1726
			iron-chelator utilization protein	fig|439375.7.peg.2001	■
			MotA/TolQ/ExbB proton channel family protein	fig|439375.7.peg.1270, fig|439375.7.peg.1314	fig|204722.5.peg.1693, fig|204722.5.peg.1727
			Outer membrane lipoprotein omp16 precursor	fig|439375.7.peg.1275	fig|204722.5.peg.1722
			Protein-L-isoaspartate O-methyltransferase (EC 2.1.1.77)	fig|439375.7.peg.2360, fig|439375.7.peg.2470, fig|439375.7.peg.4461	fig|204722.5.peg.898, fig|204722.5.peg.958
			TolA protein	fig|439375.7.peg.1272	fig|204722.5.peg.1725
			tolB protein precursor, periplasmic protein involved in the tonb-independent uptake of group A colicins	fig|439375.7.peg.1273	fig|204722.5.peg.1724
			TonB-dependent hemin , ferrichrome receptor	fig|439375.7.peg.3784	■
			TonB-dependent receptor	fig|439375.7.peg.1316, fig|439375.7.peg.3418, fig|439375.7.peg.3960	fig|204722.5.peg.1695
			TPR repeat containing exported protein	fig|439375.7.peg.1276	fig|204722.5.peg.1720
			Type I secretion outer membrane protein, TolC precursor	fig|439375.7.peg.2359	fig|204722.5.peg.959

Table S4. Genes in genomic regions that are unique to the genus *Brucella*.

Region	Other identifier	Accession Number	PATRIC Locus Tag	RefSeq Locus Tag	Start	End	Length	Strand	AA Length	Gene Symbol	Product	Size (nt)
1	GIBs2	NC_004310	VBIBruSui107850_0600	BR0584	578022	578534	513	-	170		hypothetical protein	11674
			VBIBruSui107850_0601	BR0585	578497	579732	1236	-	411		Phage DNA Packaging Protein	
			VBIBruSui107850_0602	BR0586	579764	580957	1194	-	397		Phage portal protein	
			VBIBruSui107850_0603	BR0587	580954	581331	378	-	125		hypothetical protein	
			VBIBruSui107850_0604	BR0588	581318	581986	669	-	222		Phage prohead protease, HK97 family	
			VBIBruSui107850_0605	BR0589	582008	583282	1275	-	424		Phage major capsid protein	
			VBIBruSui107850_0606	BR0590	583453	584013	561	-	186		homologue of Rhodobacter capsulatus gene transfer agent (GTA) orfg6	
			VBIBruSui107850_0607	BR0591	584010	584348	339	-	112		hypothetical protein	
			VBIBruSui107850_0608	BR0592	584345	584512	168	-	55		hypothetical protein	
			VBIBruSui107850_0609	BR0593	584472	584879	408	-	135		Gene Transfer Agent (GTA) ORFG08	
			VBIBruSui107850_0610	BR0594	584920	585333	414	-	137		Gene Transfer Agent (GTA) ORFG09	
			VBIBruSui107850_0611	BR0595	585330	585671	342	-	113		Gene Transfer Agent (GTA) ORFG10	
			VBIBruSui107850_0612		585715	585885	171	-	56		hypothetical protein	
			VBIBruSui107850_0613	BR0597	585890	586435	546	-	181		Gene Transfer Agent (GTA) ORFG11	
			VBIBruSui107850_0614	BR0585	586438	587070	633	-	210		Gene Transfer Agent (GTA) ORFG12	
			VBIBruSui107850_0615	BR0599	587067	587942	876	-	291		FAD/FMN-containing dehydrogenases	
			VBIBruSui107850_0616	BR0600	587939	588373	435	-	144		NLP/P60 family protein	
			VBIBruSui107850_0617		588377	589696	1320	-	439		hypothetical protein	
2		NC_004310	VBIBruSui107850_1073	BR1059	1029023	1030564	1542	+	513		Multidrug resistance protein B	4018
			VBIBruSui107850_1074	BR1060	1030564	1031664	1101	+	366		Multidrug resistance protein A	
			VBIBruSui107850_1075	BR1061	1032058	1033041	984	-	327		Alcohol dehydrogenase	
3		NC_004310	VBIBruSui107850_1377		1316762	1316911	150	-	49		hypothetical protein	13038
			VBIBruSui107850_1378	BR1356	1317048	1317308	261	-	86	*ureA*	Urease gamma subunit	
			VBIBruSui107850_1379	BR1357	1317357	1317836	480	-	159	*ureB*	Urease beta subunit	
			VBIBruSui107850_1380	BR1358	1317876	1319597	1722	-	573	*ureC*	Urease alpha subunit	
			VBIBruSui107850_1381	BR1359	1319645	1320250	606	-	201	*ureE*	Urease accessory protein UreE	
			VBIBruSui107850_1382	BR1360	1320222	1320953	732	-	243	*ureF*	Urease accessory protein UreF	
			VBIBruSui107850_1383	BR1361	1320969	1321607	639	-	212	*ureG*	Urease accessory protein UreG	
			VBIBruSui107850_1384	BR1362	1321607	1322515	909	-	302	*ureD*	Urease accessory protein UreD	
			VBIBruSui107850_1385	BR1363	1322525	1323577	1053	-	350		Eukaryotic-type low-affinity urea transporter	
			VBIBruSui107850_1386	BR1364	1323604	1324362	759	-	252	*nikK*	Additional periplasmic component NikK of nickel ECF transporter	
			VBIBruSui107850_1387	BR1365	1324382	1325017	636	-	211	*nikM*	Substrate-specific component NikM of nickel ECF transporter	
			VBIBruSui107850_1388	BR1366	1325014	1325640	627	-	208	*nikL*	Additional component NikL of nickel ECF transporter	
			VBIBruSui107850_1389	BR1367	1325637	1326401	765	-	254	*nikQ*	Transmembrane component NikQ of energizing module of nickel ECF transporter	
			VBIBruSui107850_1390	BR1368	1326398	1327117	720	-	239	*nikO*	ATPase component NikO of energizing module of nickel ECF transporter	
			VBIBruSui107850_1391		1327138	1327950	813	+	270		Putative membrane protein precursor	
			VBIBruSui107850_1392		1327963	1328334	372	+	123		INTEGRAL MEMBRANE PROTEIN	
			VBIBruSui107850_1393	BR1371	1328843	1329646	804	-	267		hypothetical protein	
			VBIBruSui107850_1394		1329657	1329800	144	-	47		hypothetical protein	
4	SAR 1-14		VBIBruSui107850_1648	BR1620	1566008	1567765	1758	-	585		hypothetical protein	

		NC_004310	VBIBruSui107850_1649	BR1621	1567793	1568395	603	-	200	*marC*	Multiple antibiotic resistance protein marC	5972
			VBIBruSui107850_1650	BR1622	1568698	1569459	762	-	253	*omp31*	Outer membrane protein	
			VBIBruSui107850_1651	BR1623	1569596	1570939	1344	+	447		Patatin-like phospholipase domain precursor	
			VBIBruSui107850_1652	BR1625	1571447	1571548	102	+	33		hypothetical protein	
			VBIBruSui107850_1653	BR1626	1571699	1571980	282	-	93		hypothetical protein	
5		NC_004311	VBIBruSui107850_2234	BRA0012	9684	10409	726	+	241		4'-phosphopantetheinyl transferase entD; Holo-[acyl-carrier protein] synthase,	6797
			VBIBruSui107850_2235	BRA0013	10399	11175	777	+	258	*entA*	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase	
			VBIBruSui107850_2236	BRA0014	11175	12047	873	+	290	*entB*	Isochorismatase of siderophore biosynthesis	
			VBIBruSui107850_2237	BRA0015	12099	13718	1620	+	539	*entE*	2,3-dihydroxybenzoate-AMP ligase	
			VBIBruSui107850_2238	BRA0016	13825	14892	1068	+	355	*entC*	Isochorismate synthase of siderophore biosynthesis	
			VBIBruSui107850_2239	BRA0017	15141	16481	1341	-	446		Amide synthase component of siderophore synthetase	
6	mgtc	NC_004311	VBIBruSui107850_2257	BRA0035	32593	32886	294	-	97		hypothetical protein	6630
			VBIBruSui107850_2258	BRA0036	32840	33121	282	+	93		hypothetical protein	
			VBIBruSui107850_2259	BRA0037	33239	35956	2718	-	905	*mgtA*	Mg(2+) transport ATPase, P-type	
			VBIBruSui107850_2260	BRA0038	36218	36391	174	-	57		hypothetical protein	
			VBIBruSui107850_2261	BRA0039	36522	36725	204	-	67		hypothetical protein	
			VBIBruSui107850_2262	BRA0040	36727	37443	717	-	238		Mg(2+) transport ATPase protein C	
			VBIBruSui107850_2263	BRA0041	37575	38588	1014	-	337		Sensor histidine kinase	
			VBIBruSui107850_2264	BRA0042	38585	39223	639	-	212		DNA-binding response regulator, LuxR family	
7		NC_004311	VBIBruSui107850_2352	BRA0131	128083	129018	936	+	311		Phosphatidylglycerophosphatase B	3626
			VBIBruSui107850_2353	BRA0132	129048	129203	156	-	51		hypothetical protein	
			VBIBruSui107850_2354	BRA0134	129604	129999	396	-	131		hypothetical protein	
			VBIBruSui107850_2355	BRA0135	129996	130976	981	-	326		Polymyxin resistance protein ArnC, glycosyl transferase	
			VBIBruSui107850_2356	BRA0136	130960	131709	750	-	249		cellobiose phosphotransferase system celC	
8		NC_004311	VBIBruSui107850_2437	BRA0220	207135	208289	1155	+	384		Butyryl-CoA dehydrogenase	17519
			VBIBruSui107850_2438	BRA0221	208346	208975	630	+	209		Transcriptional regulator, IclR family	
			VBIBruSui107850_2439	BRA0222	209460	210221	762	-	253		Enoyl-CoA hydratase [branched-chain amino acid degradation]	
			VBIBruSui107850_2440	BRA0223	210226	211755	1530	-	509		3-hydroxybutyryl-CoA dehydrogenase; 3-hydroxyacyl-CoA dehydrogenase	
			VBIBruSui107850_2441	BRA0224	211978	213219	1242	-	413		L-carnitine dehydratase/bile acid-inducible protein F	
			VBIBruSui107850_2442		213203	213709	507	+	168		2,4-dienoyl-CoA reductase [NADPH]	
			VBIBruSui107850_2443		213700	214371	672	+	223		2,4-dienoyl-CoA reductase [NADPH]	
			VBIBruSui107850_2444	BRA0226	214457	214921	465	-	154		Mercuric resistance operon regulatory protein	
			VBIBruSui107850_2445	BRA0227	214967	215674	708	+	235		ThiJ/PfpI family protein	
			VBIBruSui107850_2446	BRA0228	215905	217248	1344	+	447		Sensor histidine kinase	
			VBIBruSui107850_2447		217245	217454	210	+	69		TWO COMPONENT RESPONSE REGULATOR	
			VBIBruSui107850_2448		217458	217913	456	+	151		TWO COMPONENT RESPONSE REGULATOR	
			VBIBruSui107850_2449	BRA0231	218177	218449	273	-	90		hypothetical protein	
			VBIBruSui107850_2450	BRA0232	218617	219087	471	-	156		hypothetical protein	
			VBIBruSui107850_2451	BRA0233	219098	221302	2205	-	734		Sulfite reductase [NADPH] flavoprotein alpha-component	
			VBIBruSui107850_2452	BRA0234	221283	222260	978	-	325		Thiamin biosynthesis lipoprotein ApbE	
			VBIBruSui107850_2453	BRA0235	222303	223478	1176	+	391		C-DI-GMP PHOSPHODIESTERASE A	
			VBIBruSui107850_2454	BRA0236	223761	224654	894	+	297		INTEGRAL MEMBRANE PROTEIN	
9			VBIBruSui107850_2552		318095	319054	960	-	319		Glutamate decarboxylase	
			VBIBruSui107850_2553		319079	319489	411	-	136		Glutamate decarboxylase	
			VBIBruSui107850_2554		319489	319635	147	-	48		hypothetical protein	

		NC_004311	VBIBruSui107850_2555		319816	321096	1281	-	426		Probable glutamate/gamma-aminobutyrate antiporter	8592
			VBIBruSui107850_2556	BRA0340	321132	322085	954	-	317		Glutaminase	
			VBIBruSui107850_2557	BRA0341	322233	322577	345	-	114	*hdeA*	hdeA protein	
			VBIBruSui107850_2558	BRA0344	323177	323341	165	-	54		hypothetical protein	
			VBIBruSui107850_2559	BRA0344	323418	325010	1593	+	530		RTN PROTEIN	
			VBIBruSui107850_2560	BRA0345	325305	325571	267	+	88		hypothetical protein	
			VBIBruSui107850_2561	BRA0346	325911	326687	777	-	258		transcriptional regulator, LysR family	
10		NC_004311	VBIBruSui107850_2614	BRA0401	383533	384660	1128	-	375		Alcohol dehydrogenase	13461
			VBIBruSui107850_2615	BRA0402	384907	385860	954	-	317		oxidoreductase, putative	
			VBIBruSui107850_2616	BRA0403	386451	386645	195	+	64		hypothetical protein	
			VBIBruSui107850_2617	BRA0404	386912	387841	930	+	309	*oppF*	Oligopeptide transport ATP-binding protein OppF (TC 3.A.1.5.1)	
			VBIBruSui107850_2618	BRA0405	387862	388878	1017	+	338	*oppD*	Oligopeptide transport ATP-binding protein OppD (TC 3.A.1.5.1)	
			VBIBruSui107850_2619	BRA0406	388889	389806	918	+	305		Dihydrodipicolinate synthase	
			VBIBruSui107850_2620	BRA0407	389826	390698	873	+	290		Peptide ABC transporter, permease protein	
			VBIBruSui107850_2621	BRA0408	390700	391659	960	+	319		OLIGOPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN APPB	
			VBIBruSui107850_2622	BRA0409	391759	393336	1578	+	525		Peptide ABC transporter, periplasmic peptide-binding protein	
			VBIBruSui107850_2623	BRA0410	393339	394067	729	+	242		Transcriptional regulator, GntR family	
			VBIBruSui107850_2624	BRA0411	394266	395804	1539	-	512		N-acetylmannosamine-6-phosphate 2-epimerase / N-acetylmannosamine kinase	
			VBIBruSui107850_2625		395828	396010	183	-	60		Sialic acid-induced transmembrane protein YjhT(NanM), possible mutarotase	
			VBIBruSui107850_2626	BRA0413	396089	396994	906	-	301		Sialic acid-induced transmembrane protein YjhT(NanM), possible mutarotase	
11	SAR 2-7	NC_004311	VBIBruSui107850_2832	BRA0616	602010	604199	2190	-	729		Alkaline phosphatase	6606
			VBIBruSui107850_2833	BRA0617	604179	604301	123	+	40		hypothetical protein	
			VBIBruSui107850_2834	BRA0618	604728	605450	723	+	240		Phytochrome-like protein; Cph2	
			VBIBruSui107850_2835	BRA0621	606348	606725	378	+	125		Endonuclease V	
			VBIBruSui107850_2836	BRA0622	606866	607171	306	-	101		hypothetical protein	
			VBIBruSui107850_2837	BRA0623	607316	607504	189	-	62		hypothetical protein	
			VBIBruSui107850_2838	BRA0625	607555	607848	294	-	97		hypothetical protein	
			VBIBruSui107850_2839	BRA0626	607942	608616	675	-	224		DNA polymerase III, epsilon subunit:DNA polymerase 3, epsilon subunit	
12	SAR 2-8	NC_004311	VBIBruSui107850_3011	BRA0796	780107	780301	195	+	64		hypothetical protein	8913
			VBIBruSui107850_3012	BRA0797	780298	780576	279	+	92		hypothetical protein	
			VBIBruSui107850_3013	BRA0799	780885	781079	195	+	64		hypothetical protein	
			VBIBruSui107850_3014		781598	781762	165	-	54		TRANSCRIPTIONAL REGULATORY PROTEIN, LYSR FAMILY	
			VBIBruSui107850_3015	BRA0800	782085	783245	1161	-	386		acyl-CoA dehydrogenase family protein	
			VBIBruSui107850_3016		783378	784178	801	+	266	*nikE*	Nickel transport ATP-binding protein NikE (TC 3.A.1.5.3)	
			VBIBruSui107850_3017	BRA0801	784175	784963	789	+	262	*nikD*	Nickel transport ATP-binding protein NikD (TC 3.A.1.5.3)	
			VBIBruSui107850_3018	BRA0802	784960	785832	873	+	290	*nikC*	Nickel transport system permease protein NikC (TC 3.A.1.5.3)	
			VBIBruSui107850_3019	BRA0803	785829	786773	945	+	314	*nikB*	Nickel transport system permease protein NikB (TC 3.A.1.5.3)	
			VBIBruSui107850_3020	BRA0804	786775	788355	1581	+	526	*nikA*	Nickel ABC transporter, periplasmic nickel-binding protein NikA (TC 3.A.1.5.3)	
			VBIBruSui107850_3021	BRA0805	788622	789020	399	-	132	*nikR*	Nickel responsive regulator NikR	
13			VBIBruSui107850_3422	BRA1192	1194686	1195585	900	-	299		Transcriptional regulator, AraC family	
			VBIBruSui107850_3423	BRA1193	1195801	1196955	1155	-	384	*livK*	High-affinity leucine-specific transport system, periplasmic binding protein LivK (TC 3.A.1.4.1)	
			VBIBruSui107850_3424	BRA1194	1197157	1198020	864	-	287	*livH*	High-affinity branched-chain amino acid transport system permease protein LivH (TC 3.A.1.4.1)	
			VBIBruSui107850_3425		1198017	1198658	642	-	213	*livM*	Branched-chain amino acid transport system permease protein LivM (TC 3.A.1.4.1)	

		NC_004311	VBIBruSui107850_3426		1198701	1198964	264	-	87	*livM*	Branched-chain amino acid transport system permease protein LivM (TC 3.A.1.4.1)	9897
			VBIBruSui107850_3427	BRA1196	1198961	1199695	735	-	244	*livG*	Branched-chain amino acid transport ATP-binding protein LivG (TC 3.A.1.4.1)	
			VBIBruSui107850_3428	BRA1197	1199692	1200420	729	-	242	*livF*	Branched-chain amino acid transport ATP-binding protein LivF (TC 3.A.1.4.1)	
			VBIBruSui107850_3429	BRA1198	1200449	1202152	1704	+	567	*cadA*	cadmium-translocating P-type ATPase	
			VBIBruSui107850_3430	BRA1199	1202669	1204021	1353	+	450	*hemN*	Coproporphyrinogen III oxidase, oxygen-independent	
			VBIBruSui107850_3431	BRA1200	1204063	1204245	183	-	60		hypothetical protein	
			VBIBruSui107850_3432	BRA1201	1204305	1204583	279	+	92		hypothetical protein	
14		NC_004311	VBIBruSui107850_3384		1154316	1155155	840	-	279		regulatory protein for 2-phenylethylamine catabolism	24985
			VBIBruSui107850_3385	BRA1155	1155255	1156661	1407	-	468		Aldehyde dehydrogenase	
			VBIBruSui107850_3386		1156661	1156798	138	-	45		hypothetical protein	
			VBIBruSui107850_3387	BRA1156	1156818	1157627	810	+	269	*hpaI*	2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase	
			VBIBruSui107850_3388	BRA1158	1157845	1158648	804	+	267	*hpaH*	2-oxo-hepta-3-ene-1,7-dioic acid hydratase	
			VBIBruSui107850_3389	BRA1159	1158652	1159518	867	+	288		2-hydroxyhepta-2,4-diene-1,7-dioate isomerase / 5-carboxymethyl-2-oxo-hex-3- ene-	
			VBIBruSui107850_3390		1159587	1160261	675	+	224		homoprotocatechuate 2,3-dioxygenase	
			VBIBruSui107850_3391		1160262	1160525	264	+	87		homoprotocatechuate 2,3-dioxygenase	
			VBIBruSui107850_3392	BRA1161	1160622	1162136	1515	+	504	*hpaE*	5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase	
			VBIBruSui107850_3393	BRA1162	1162206	1162652	447	+	148	*hpcD*	5-carboxymethyl-2-hydroxymuconate delta-isomerase	
			VBIBruSui107850_3394	BRA1163	1162764	1163255	492	-	163	*hpaR*	Homoprotocatechuate degradative operon repressor	
			VBIBruSui107850_3395	BRA1164	1163245	1164237	993	+	330		Homoserine kinase	
			VBIBruSui107850_3396	BRA1165	1164242	1165525	1284	+	427		Omega-amino acid--pyruvate aminotransferase	
			VBIBruSui107850_3397	BRA1166	1165527	1166885	1359	+	452		Omega-amino acid--pyruvate aminotransferase	
			VBIBruSui107850_3398	BRA1167	1166898	1167542	645	+	214		HYDROLASE FAMILY PROTEIN	
			VBIBruSui107850_3399	BRA1168	1167539	1168795	1257	+	418		Transcriptional regulator	
			VBIBruSui107850_3400		1168795	1169577	783	+	260		Transcriptional regulator, IclR family	
			VBIBruSui107850_3401	BRA1170	1169869	1171320	1452	-	483		AMINO ACID PERMEASE	
			VBIBruSui107850_3402	BRA1171	1171392	1172870	1479	-	492		Aldehyde dehydrogenase	
			VBIBruSui107850_3403	BRA1172	1173053	1174711	1659	-	552		Exoenzymes regulatory protein aepA precursor	
			VBIBruSui107850_3404	BRA1173	1174778	1175959	1182	-	393		branched-chain amino acid ABC transporter, periplasmic amino acid-binding protein, putative	
			VBIBruSui107850_3405	BRA1174	1176032	1176901	870	-	289		High-affinity branched-chain amino acid transport system permease protein LivH (TC 3.A.1.4.1)	
			VBIBruSui107850_3406	BRA1175	1176888	1178600	1713	-	570		HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT SYSTEM PERMEASE	
			VBIBruSui107850_3407	BRA1176	1178597	1179301	705	-	234		Branched-chain amino acid transport ATP-binding protein LivF (TC 3.A.1.4.1)	
15	virB	NC_004311	VBIBruSui107850_2278	BRA0058	56135	56653	518	-	172	*virB12*	IncQ plasmid conjugative transfer protein TraP	11049
			VBIBruSui107850_2279	BRA0059	56802	57860	1059	-	352	*virB11*	ATPase provides energy for both assembly of type IV secretion complex and secretion of T-DNA complex (VirB11)	
			VBIBruSui107850_2280	BRA0060	57868	59043	1176	-	391	*virB10*	Inner membrane protein forms channel for type IV secretion of T-DNA complex (VirB10)	
			VBIBruSui107850_2281	BRA0061	59040	59909	870	-	289	*virB9*	Forms the bulk of type IV secretion complex that spans outer membrane and periplasm (VirB9)	
			VBIBruSui107850_2282	BRA0062	59906	60625	720	-	239	*virB8*	Inner membrane protein forms channel for type IV secretion of T-DNA complex (VirB8)	
				BRA0063	60628	60801	173	-	57	*virB7*	type IV secretion protein VirB7	
			VBIBruSui107850_2283	BRA0064	60965	62008	1044	-	347	*virB6*	Integral inner membrane protein of type IV secretion complex (VirB6)	
			VBIBruSui107850_2284	BRA0065	62192	62908	717	-	238	*virB5*	Minor pilin of type IV secretion complex (VirB5)	

			VBIBruSui107850_2285	BRA0066	62913	65411	2499	-	832	*virB4*	ATPase provides energy for both assembly of type IV secretion complex and secretion of T-DNA complex (VirB4)	
			VBIBruSui107850_2286	BRA0067	65408	65674	267	-	88	*virB3*	Inner membrane protein forms channel for type IV secretion of T-DNA complex (VirB3)	
			VBIBruSui107850_2287	BRA0068	65772	65933	162	-	53	*virB2*	Major pilus subunit of type IV secretion complex (VirB2)	
			VBIBruSui107850_2288	BRA0069	66525	67184	660	-	219	*virB1*	Bores hole in peptidoglycan layer allowing type IV secretion complex assembly to occur (VirB1)	
16	Wbk	NC_004310	VBIBruSui107850_0535	BR0517	516587	517366	780	+	259	*wbkC*	formyltransferase, putative	18298
			VBIBruSui107850_0536	BR0518	517393	518247	855	+	284	*wbkB*	WbkB protein	
			VBIBruSui107850_0537	BR0519	518244	519110	867	+	288	*wzt*	O-antigen export system, ATP-binding protein	
			VBIBruSui107850_0538	BR0520	518999	519796	798	+	265	*wzm*	O-antigen export system permease protein RfbD	
			VBIBruSui107850_0539	BR0521	519796	520899	1104	+	367	*per*	Perosamine synthase	
			VBIBruSui107850_0540	BR0522	520907	521995	1089	+	362	*gmd*	GDP-mannose 4,6 dehydratase	
			VBIBruSui107850_0541	BR0523	522616	522942	327	-	108		ISBm1, transposase orfA	
			VBIBruSui107850_0542		523271	524059	789	-	262		TRANSPOSASE	
			VBIBruSui107850_0543		524252	524497	246	-	81		Transposase	
			VBIBruSui107850_0544	BR0527	524494	524886	393	-	130		IS711, transposase orfB	
			VBIBruSui107850_0545	BR0528	525001	525126	126	-	41		TRANSPOSASE	
			VBIBruSui107850_0546	BR0529	525257	526375	1119	-	372	*wbkA*	MANNOSYLTRANSFERASE	
			VBIBruSui107850_0547		526400	526801	402	-	133		IS5 family element, transposase orfA	
			VBIBruSui107850_0548	BR0531	526798	527238	441	-	146		TRANSPOSASE	
			VBIBruSui107850_0549		527133	527258	126	+	41		hypothetical protein	
			VBIBruSui107850_0550		527328	527702	375	+	124		TRANSPOSASE	
			VBIBruSui107850_0551		527702	527839	138	+	45		hypothetical protein	
			VBIBruSui107850_0552	BR0533	528014	528475	462	-	153		ISBm1, transposase orfA	
			VBIBruSui107850_0554	BR0534	528394	528810	417	-	138		TRANSPOSASE	
			VBIBruSui107850_0555		529194	529469	276	-	91		TRANSPOSASE	
			VBIBruSui107850_0556	BR0537	529702	531039	1338	-	445	*manB*	Phosphomannomutase	
			VBIBruSui107850_0557	BR0538	531079	532488	1410	-	469	*manC*	Mannose-1-phosphate guanylyltransferase (GDP)	
			VBIBruSui107850_0558	BR0539	532521	533693	1173	-	390	*manA*	Mannose-6-phosphate isomerase	
			VBIBruSui107850_0559	BR0540	533776	534885	1110	-	369	*wbkE*	Glycosyltransferase	

Table S5. Genes in genomic regions that are unique to the core *Brucella* clade.

Refernce genome	Region	Other identifier	Accession Number	PATRIC Locus Tag	RefSeq Locus Tag	Start	End	Strand	AA Length	Gene Symbol	Product	Size
Brucella suis 1330	core 1	SAR1-2	NC_004310	VBIBruSui107850_0266	BR0256	265358	267196	-	612		site-specific recombinase, phage integrase family	6917
				VBIBruSui107850_0267	BR0257	267186	267299	+	37		hypothetical protein	
				VBIBruSui107850_0268	BR0258	267516	267713	-	65		BRO family protein	
				VBIBruSui107850_0269	BR0259	267726	267920	-	64		hypothetical protein	
				VBIBruSui107850_0270		268203	268799	+	198		hypothetical protein	
				VBIBruSui107850_0271	BR0260	268821	269129	-	102		Site-specific recombinase, resolvase family	
				VBIBruSui107850_0272		269080	269310	-	76		RECOMBINASE	
				VBIBruSui107850_0273	BR0261	269666	271051	-	461		hypothetical protein	
				VBIBruSui107850_0274		271515	271634	+	39		hypothetical protein	
				VBIBruSui107850_0275	BR0262	271624	271818	-	64		hypothetical protein	
				VBIBruSui107850_0276		272171	272275	-	34		hypothetical protein	
Brucella suis 1330	core 2	SAR1-5	NC_004310	VBIBruSui107850_0734	BR0722	706067	706828	-	253		hypothetical protein	15953
				VBIBruSui107850_0735	BR0723	707049	707495	+	148		exonuclease, putative	
				VBIBruSui107850_0736	BR0724	707985	708434	+	149		Adenylate kinase, archaeal type	
				VBIBruSui107850_0737	BR0725	708527	710095	+	522		Acetyltransferase, GNAT family	
				VBIBruSui107850_0738	BR0726	710037	710831	+	264		TRANSCRIPTIONAL REGULATOR	
				VBIBruSui107850_0739	BR0727	710856	711275	+	139		hypothetical protein	
				VBIBruSui107850_0740		711754	711870	+	38		hypothetical protein	
				VBIBruSui107850_0741		711934	712062	+	42		hypothetical protein	
				VBIBruSui107850_0742	BR0729	712551	714665	-	704		TRANSPOSASE	
				VBIBruSui107850_0743	BR0730	714631	715608	-	325		transposition protein, putative	
				VBIBruSui107850_0744	BR0731	715605	717182	-	525		hypothetical protein	
				VBIBruSui107850_0745		717237	717443	-	68		hypothetical protein	
				VBIBruSui107850_0746	BR0733	717481	717672	+	63		hypothetical protein	
				VBIBruSui107850_0747	BR0734	717919	719226	-	435		hypothetical protein	
				VBIBruSui107850_0748		719680	721053	-	457		exclusion of bacteriophage Ap1	
				VBIBruSui107850_0749	BR0735	721142	722020	-	292		hypothetical protein	
Brucella suis 1330	core 3	SAR 1-6	NC_004310	VBIBruSui107850_0805		775163	775288	-	41		hypothetical protein	2643
				VBIBruSui107850_0806	BR0796	776058	776567	-	169		hypothetical protein	
				VBIBruSui107850_0807	BR0797	776564	776959	-	131		hypothetical protein	
				VBIBruSui107850_0808	BR0798	777214	777348	-	44		hypothetical protein	
				VBIBruSui107850_0809	BR0799	777405	777806	+	133		hypothetical protein	
Brucella suis 1330	core 4	GI2		VBIBruSui107850_0977	BR0966	937800	938825	+	341		site-specific recombinase, phage integrase family	
				VBIBruSui107850_0978		938812	938937	+	41		hypothetical protein	
				VBIBruSui107850_0979	BR0967	939000	940202	-	400		hypothetical protein	
				VBIBruSui107850_0980	BR0968	940199	940429	-	76		hypothetical protein	
				VBIBruSui107850_0981	BR0969	940426	940701	-	91		hypothetical protein	
				VBIBruSui107850_0982		940810	940971	+	53		hypothetical protein	
				VBIBruSui107850_0983	BR0970	940928	941311	-	127		hypothetical protein	
				VBIBruSui107850_0984	BR0971	941546	942256	-	236		25 KDA OUTER-MEMBRANE IMMUNOGENIC PROTEIN PRECURSOR	

			NC_004310	VBIBruSui107850_0985		942456	942587	+	43		hypothetical protein	10035
				VBIBruSui107850_0986	BR0972	942604	942789	+	61		hypothetical protein	
				VBIBruSui107850_0987	BR0974	943122	943373	+	83		hypothetical protein	
				VBIBruSui107850_0988	BR0975	943436	943681	+	81		hypothetical protein	
				VBIBruSui107850_0989		943844	944452	-	202		tRNA-guanine transglycosylase	
				VBIBruSui107850_0990		944645	944890	-	81		Transposase	
				VBIBruSui107850_0991		944887	945165	-	92		IS711, transposase orfB	
				VBIBruSui107850_0992		945062	945280	-	72		IS711, transposase orfB	
				VBIBruSui107850_0993	BR0979	945359	946054	-	231		hypothetical protein	
				VBIBruSui107850_0994	BR0980	946189	947835	-	548		hypothetical protein	
Brucella suis 1330	core 5	GI1	NC_004310	VBIBruSui107850_1092		1047968	1048147	-	59		hypothetical protein	7183
				VBIBruSui107850_1094	BR1079	1049816	1050142	-	108		hypothetical protein	
				VBIBruSui107850_1095		1050484	1050585	+	33		hypothetical protein	
				VBIBruSui107850_1096		1050602	1050706	+	34		hypothetical protein	
				VBIBruSui107850_1097	BR1080	1051059	1051253	+	64		hypothetical protein	
				VBIBruSui107850_1098		1051243	1051362	-	39		hypothetical protein	
				VBIBruSui107850_1099	BR1081	1051826	1053211	+	461		hypothetical protein	
				VBIBruSui107850_1100		1053567	1053797	+	76		RECOMBINASE	
				VBIBruSui107850_1101	BR1082	1053748	1054056	+	102		Site-specific recombinase, resolvase family	
				VBIBruSui107850_1102		1054078	1054674	-	198		hypothetical protein	
				VBIBruSui107850_1103		1054957	1055151	+	64		hypothetical protein	
Brucella suis 1330	core 6	SAR 1-12	NC_004310	VBIBruSui107850_1496		1426437	1426556	+	39		hypothetical protein	2800
				VBIBruSui107850_1497	BR1470	1426897	1427013	-	38		hypothetical protein	
				VBIBruSui107850_1498	BR1471	1427067	1427294	+	75		hypothetical protein	
				VBIBruSui107850_1499	BR1472	1427421	1427774	-	117		hypothetical protein	
				VBIBruSui107850_1500	BR1473	1427935	1428378	+	147		hypothetical protein	
				VBIBruSui107850_1501	BR1474	1429118	1429237	-	39		Site-specific recombinase, phage integrase family	
Brucella suis 1330	core 7	SAR 1-16	NC_004310	VBIBruSui107850_1886	BR1852	1782720	1784648	-	642		Transcriptional regulator, Cro/CI family	3125
				VBIBruSui107850_1887	BR1853	1784645	1785319	-	224		AzlC family protein	
				VBIBruSui107850_1888	BR1854	1785732	1785845	-	37		hypothetical protein	
Brucella suis 1330	core 8	SAR1-17	NC_004310	VBIBruSui107850_2044	BR2008	1929792	1930091	-	99		hypothetical protein	5286
				VBIBruSui107850_2045	BR2009	1930120	1931640	+	506		intimin/invasin family protein	
				VBIBruSui107850_2046	BR2010	1931640	1932719	+	359		hypothetical protein	
				VBIBruSui107850_2047	BR2012	1933522	1935078	+	518		hypothetical protein	
Brucella suis 1330	core 9	IncP	NC_004311	VBIBruSui107850_2576	BRA0362	343647	344903	-	418		Integrase	17696
				VBIBruSui107850_2577	BRA0364	345499	346557	-	352		Plasmid replication initiator protein	
				VBIBruSui107850_2578	BRA0365	347606	347932	+	108		hypothetical protein	
				VBIBruSui107850_2579	BRA0366	347935	349578	+	547	*trbL*	Conjugative transfer protein TrbL	
				VBIBruSui107850_2580	BRA0367	349581	349763	+	60		hypothetical protein	
				VBIBruSui107850_2581	BRA0368	349766	350482	+	238	*trbJ*	Conjugative transfer protein TrbJ	
				VBIBruSui107850_2582	BRA0369	350655	350807	-	50		hypothetical protein	
				VBIBruSui107850_2583	BRA0370	350825	350953	+	42		hypothetical protein	
				VBIBruSui107850_2584		351862	351978	+	38		hypothetical protein	
				VBIBruSui107850_2585	BRA0372	352183	352320	-	45		traJ protein	
				VBIBruSui107850_2586	BRA0373	352317	354269	-	650		TraI protein	
				VBIBruSui107850_2587	BRA0374	354676	356235	+	519		hypothetical protein	
				VBIBruSui107850_2588	BRA0375	356254	357279	+	341		hypothetical protein	
				VBIBruSui107850_2589	BRA0376	357313	357972	+	219		hypothetical protein	

				VBIBruSui107850_2590	BRA0377	358217	359938	+	573		hypothetical protein	
				VBIBruSui107850_2591	BRA0378	360180	361100	+	306		hypothetical protein	
				VBIBruSui107850_2592	BRA0379	361149	361343	+	64		DNA-damage-inducible protein J	
Brucella suis 1330	core 10	SAR2-10	NC_004311	VBIBruSui107850_3049	BRA0833	818865	819587	-	240		hypothetical protein	13113
				VBIBruSui107850_3050	BRA0834	819594	819923	+	109		hypothetical protein	
				VBIBruSui107850_3051	BRA0835	820233	820349	-	38		hypothetical protein	
				VBIBruSui107850_3052	BRA0836	820645	820842	+	65		hypothetical protein	
				VBIBruSui107850_3053	BRA0837	820911	821066	-	51		hypothetical protein	
				VBIBruSui107850_3054	BRA0838	821860	822000	+	46		hypothetical protein	
				VBIBruSui107850_3055	BRA0839	822161	822793	-	210		hypothetical protein	
				VBIBruSui107850_3056	BRA0840	822801	824327	-	508	*hsdM*	Type I restriction-modification system, DNA-methyltransferase subunit M	
				VBIBruSui107850_3057	BRA0841	824317	825540	-	407	*hsdS*	Type I restriction-modification system, specificity subunit S	
				VBIBruSui107850_3058	BRA0842	825537	828506	-	989	*hsdR*	Type I restriction-modification system, restriction subunit R	
				VBIBruSui107850_3059	BRA0843	828503	829243	-	246		Putative predicted metal-dependent hydrolase	
				VBIBruSui107850_3060	BRA0844	829212	830180	-	322		TRANSPORTER	
				VBIBruSui107850_3061		830398	830544	-	48		hypothetical protein	
				VBIBruSui107850_3062		830560	831978	-	472		hypothetical protein	
Brucella suis 1330	core 11	GI5		VBIBruSui107850_3297	BRA1073	1056214	1056495	+	93		TRANSPOSASE	
				VBIBruSui107850_3298	BRA1074	1056737	1057468	-	243		Predicted regulator PutR for proline utilization, GntR family	
				VBIBruSui107850_3299	BRA1075	1057465	1057593	-	42		hypothetical protein	
				VBIBruSui107850_3300	BRA1076	1057664	1059106	+	480		2-ketoglutaric semialdehyde dehydrogenase	
				VBIBruSui107850_3301	BRA1077	1059118	1060380	+	420		CAIB/BAIF family protein	
				VBIBruSui107850_3302	BRA1078	1060436	1061440	+	334	*oppF*	Oligopeptide transport ATP-binding protein OppF (TC 3.A.1.5.1)	
				VBIBruSui107850_3303	BRA1079	1061433	1062398	+	321	*oppD*	Oligopeptide transport ATP-binding protein oppD (TC 3.A.1.5.1)	
				VBIBruSui107850_3304	BRA1080	1062483	1063328	+	281	*oppC*	Dipeptide transport system permease protein DppC (TC 3.A.1.5.2)	
				VBIBruSui107850_3305	BRA1081	1063340	1064353	+	337	*oppB*	Oligopeptide transport system permease protein OppB (TC 3.A.1.5.1)	
				VBIBruSui107850_3306	BRA1082	1064529	1065335	-	268		Transcriptional regulator, IclR family	
				VBIBruSui107850_3307		1065395	1066681	-	428		Dihydrolipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex	
				VBIBruSui107850_3308	BRA1084	1066765	1068324	+	519		Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)	
				VBIBruSui107850_3309		1068414	1069154	+	246		Branched-chain alpha-keto acid dehydrogenase, E1 component, alpha subunit / Branched-chain alpha-keto acid dehydrogenase, E1 component, beta subunit	
				VBIBruSui107850_3310		1069144	1070586	+	480		Branched-chain alpha-keto acid dehydrogenase, E1 component, alpha subunit / Branched-chain alpha-keto acid dehydrogenase, E1 component, beta subunit	
				VBIBruSui107850_3311	BRA1086	1070601	1072121	+	506		3-hydroxybutyryl-CoA dehydrogenase, 3-hydroxyacyl-CoA dehydrogenase	
				VBIBruSui107850_3312	BRA1087	1072123	1072905	+	260		Enoyl-CoA hydratase [branched-chain amino acid degradation]	
				VBIBruSui107850_3313	BRA1088	1073088	1074230	-	380		Butyryl-CoA dehydrogenase	

			NC_004311	VBIBruSui107850_3314	BRA1089	1074673	1076841	-	722		Penicillin acylase	47632
				VBIBruSui107850_3315	BRA1090	1076864	1078408	-	514		Peptide ABC transporter, periplasmic peptide-binding protein	
				VBIBruSui107850_3316	BRA1092	1078610	1079509	-	299	*oppB*	Dipeptide transport system permease protein DppB (TC 3.A.1.5.2)	
				VBIBruSui107850_3317	BRA1093	1079502	1080392	-	296	*oppC*	Dipeptide transport system permease protein DppC (TC 3.A.1.5.2)	
				VBIBruSui107850_3318	BRA1094	1080395	1081393	-	332	*oppD*	Oligopeptide transport ATP-binding protein OppD (TC 3.A.1.5.1)	
				VBIBruSui107850_3319		1081381	1082358	-	325	*DppF*	Dipeptide transport ATP-binding protein DppF (TC 3.A.1.5.2)	
				VBIBruSui107850_3320	BRA1096	1082617	1083330	-	237		Predicted regulator PutR for proline utilization, GntR family	
				VBIBruSui107850_3321	BRA1097	1083456	1084952	-	498		Putative hemin-binding lipoprotein	
				VBIBruSui107850_3322	BRA1098	1084988	1085998	-	336	*oppB*	Oligopeptide transport system permease protein OppB (TC 3.A.1.5.1)	
				VBIBruSui107850_3323	BRA1099	1085995	1086828	-	277	*oppC*	Oligopeptide transport system permease protein oppC (TC 3.A.1.5.1)	
				VBIBruSui107850_3324		1086828	1086965	-	45	*oppD*	Oligopeptide transport ATP-binding protein oppD (TC 3.A.1.5.1)	
				VBIBruSui107850_3325		1087412	1087528	+	38		hypothetical protein	
				VBIBruSui107850_3326	BRA1101	1087816	1088793	-	325	*oppF*	Oligopeptide transport ATP-binding protein OppF (TC 3.A.1.5.1)	
				VBIBruSui107850_3327	BRA1102	1088856	1089665	-	269		antibiotic-induced protein Drp35	
				VBIBruSui107850_3328	BRA1103	1089680	1091098	-	472		Amidase family protein	
				VBIBruSui107850_3329		1091144	1091779	+	211	*potD*	ABC transporter, periplasmic spermidine putrescine-binding protein PotD (TC 3.A.1.11.1)	
				VBIBruSui107850_3330		1091731	1092171	+	146	*potD*	ABC transporter, periplasmic spermidine putrescine-binding protein PotD (TC 3.A.1.11.1)	
				VBIBruSui107850_3331	BRA1105	1092218	1093021	+	267	*potC*	Spermidine Putrescine ABC transporter permease component potC (TC 3.A.1.11.1)	
				VBIBruSui107850_3332	BRA1106	1093018	1093884	+	288	*potB*	Spermidine Putrescine ABC transporter permease component PotB (TC 3.A.1.11.1)	
				VBIBruSui107850_3333		1093889	1094143	+	84	*potA*	Putrescine transport ATP-binding protein PotA (TC 3.A.1.11.1)	
				VBIBruSui107850_3334		1094195	1094932	+	245	*potA*	Putrescine transport ATP-binding protein PotA (TC 3.A.1.11.1)	
				VBIBruSui107850_3335	BRA1108	1095264	1096499	-	411		Glutamate-1-semialdehyde aminotransferase	
				VBIBruSui107850_3336	BRA1109	1096649	1098328	-	559		Blr3550 protein	
				VBIBruSui107850_3337	BRA1110	1098524	1099183	-	219		Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases	
				VBIBruSui107850_3338	BRA1111	1099278	1100537	-	419		Predicted pyridoxine biosynthesis protein (probably from glycolaldehyde)	
				VBIBruSui107850_3339	BRA1112	1100515	1101027	-	170		hypothetical protein	
				VBIBruSui107850_3340	BRA1113	1101036	1101320	+	94		PEMK-LIKE PROTEIN 1	
				VBIBruSui107850_3341		1101751	1102269	+	172		D-LACTATE DEHYDROGENASE	
				VBIBruSui107850_3342	BRA1115	1102687	1102968	-	93		TRANSPOSASE	
				VBIBruSui107850_3343	BRA1116	1103223	1103846	-	207		TRANSPOSASE	
Brucella abortus 2308	core 12	GI3		VBIBruMel86222_0263		256325	256654	+	109		hypothetical protein	
				VBIBruMel86222_0264	BAB1_0250	256868	258022	-	384		Integrase	
				VBIBruMel86222_0265	BAB1_0252	258533	258751	-	72		hypothetical protein	

				VBIBruMel86222_0266	BAB1_0253	258752	258961	-	69		hypothetical protein	
				VBIBruMel86222_0267	BAB1_0254	258928	259272	-	114		hypothetical protein	
				VBIBruMel86222_0268	BAB1_0255	259269	260150	-	293		virulence-associated protein E	
				VBIBruMel86222_0269		260264	261310	-	348		Hyphotheical protein	
				VBIBruMel86222_0270		261358	261675	-	105		Hyphotheical protein	
				VBIBruMel86222_0271		262124	262261	-	45		hypothetical protein	
				VBIBruMel86222_0272		262266	262418	-	50		hypothetical protein	
				VBIBruMel86222_0273	BAB1_0258	262547	263431	-	294		hypothetical protein	
				VBIBruMel86222_0274	BAB1_0259	263566	263742	-	58		hypothetical protein	
				VBIBruMel86222_0275	BAB1_0260	263940	265859	-	639	*flgJ*	Flagellar protein FlgJ [peptidoglycan hydrolase]	
				VBIBruMel86222_0276		266369	266782	-	137		Hypothetical Membrane Spanning Protein	
			NC_007618	VBIBruMel86222_0277		266886	267890	-	334		Hypothetical Membrane Spanning Protein	20296
				VBIBruMel86222_0278		267873	268055	+	60		hypothetical protein	
				VBIBruMel86222_0279	BAB1_0263	268232	268396	-	54		hypothetical protein	
				VBIBruMel86222_0280	BAB1_0265	269352	269498	-	48		hypothetical protein	
				VBIBruMel86222_0281	BAB1_0266	269495	269701	-	68		hypothetical protein	
				VBIBruMel86222_0282		269695	269862	+	55		hypothetical protein	
				VBIBruMel86222_0283	BAB1_0268	270202	270435	+	77		hypothetical protein	
				VBIBruMel86222_0284	BAB1_0270	270965	271513	-	182		Zinc-dependent metallopeptidase	
				VBIBruMel86222_0285	BAB1_0273	272920	273165	+	81		hypothetical protein	
				VBIBruMel86222_0286	BAB1_0274	273261	273488	-	75		hypothetical protein	
				VBIBruMel86222_0287	BAB1_0275	273554	273844	-	96		hypothetical protein	
				VBIBruMel86222_0288	BAB1_0276	273841	274380	-	179		hypothetical protein	
				VBIBruMel86222_0289		274517	274654	-	45		hypothetical protein	
				VBIBruMel86222_0290	BAB1_0277	274651	275259	-	202		hypothetical protein	
				VBIBruMel86222_0291	BAB1_0279	275959	276621	+	220	*btp1*	hypothetical protein	
Brucella ceti Cudo	core 13	26.5kb		VBIBruCet28239_2944	BCETI_6000865	836910	837365	-	151		TRm24 transposase	
				VBIBruCet28239_2945		837548	837682	-	44		hypothetical protein	
				VBIBruCet28239_2946	BCETI_6000867	838012	838788	+	258		Modification methylase HindV	
				VBIBruCet28239_2947	BCETI_6000869	839825	840214	+	129		hypothetical protein	
				VBIBruCet28239_2948		840410	840646	+	78		Transposase and inactivated derivatives-like protein	
				VBIBruCet28239_2949	BCETI_6000870	840844	841806	+	320		transcriptional regulator, AraC family	
				VBIBruCet28239_2950	BCETI_6000871	842058	843821	-	587		N-methylhydantoinase B	
				VBIBruCet28239_2951	BCETI_6000872	843935	846016	-	693		N-methylhydantoinase A	
				VBIBruCet28239_2952		846074	847429	-	451		Cytosine permease	
				VBIBruCet28239_2953	BCETI_6000873	847465	848841	-	458		Adenosylmethionine-8-amino-7-oxononanoate aminotransferase	
				VBIBruCet28239_2954		848997	849110	+	37		hypothetical protein	
				VBIBruCet28239_2955		849279	849740	+	153		DNA for TA region of Ti plasmid	
				VBIBruCet28239_2956		849691	851568	-	625		Transposase	
				VBIBruCet28239_2957	BCETI_6000875	851621	852211	+	196		hypothetical protein	
				VBIBruCet28239_2958	BCETI_6000876	852582	853763	+	393		3-ketoacyl-CoA thiolase @ Acetyl-CoA acetyltransferase	
				VBIBruCet28239_2959	BCETI_6000877	853775	854704	+	309		Electron transfer flavoprotein, alpha subunit	
				VBIBruCet28239_2960	BCETI_6000878	854857	855603	+	248		Electron transfer flavoprotein, beta subunit	
				VBIBruCet28239_2961	BCETI_6000879	855732	856844	+	370		Enoyl-CoA hydratase [isoleucine degradation] / 3-hydroxyacyl-CoA dehydrogenase	
				VBIBruCet28239_2962	BCETI_6000880	856932	858506	+	524		COG0028: Thiamine pyrophosphate-requiring enzymes	

		NZ_ACJD01000006	VBIBruCet28239_2963	BCETI_6000881	858574	860721	+	715		Acetyl-CoA synthetase (ADP-forming) alpha and beta chains, putative	65330
			VBIBruCet28239_2964	BCETI_6000882	860765	861460	+	231		hypothetical protein	
			VBIBruCet28239_2965	BCETI_6000883	861502	862659	+	385		probable acyl-CoA dehydrogenase	
			VBIBruCet28239_2966	BCETI_6000884	862672	863451	+	259		Enoyl-CoA hydratase	
			VBIBruCet28239_2967		863514	864260	+	248		Enoyl-CoA hydratase	
			VBIBruCet28239_2968		864337	865146	+	269		spermidine/putrescine ABC transporter, permease protein	
			VBIBruCet28239_2969	BCETI_6000887	865152	865841	+	229	*potB*	Spermidine Putrescine ABC transporter permease component PotB (TC 3.A.1.11.1)	
			VBIBruCet28239_2970		865919	866080	+	53	*potB*	Spermidine Putrescine ABC transporter permease component PotB (TC 3.A.1.11.1)	
			VBIBruCet28239_2971	BCETI_6000889	866080	867177	+	365	*potA*	Putrescine transport ATP-binding protein PotA (TC 3.A.1.11.1)	
			VBIBruCet28239_2972	BCETI_6000890	867299	868330	+	343	*potD*	ABC transporter, periplasmic spermidine putrescine-binding protein PotD (TC 3.A.1.11.1)	
			VBIBruCet28239_2973	BCETI_6000891	868481	869410	+	309		Enoyl-[acyl-carrier-protein] reductase [FMN]	
			VBIBruCet28239_2974	BCETI_6000892	870129	870440	-	103		putative membrane protein	
			VBIBruCet28239_2975		870505	870774	-	89		hypothetical protein	
			VBIBruCet28239_2976	BCETI_6000894	870743	871528	-	261		Enoyl-CoA hydratase	
			VBIBruCet28239_2977		871608	872627	-	339		aldehyde dehydrogenase family protein	
			VBIBruCet28239_2978		872761	873063	-	100		aldehyde dehydrogenase family protein	
			VBIBruCet28239_2979		873216	873335	+	39		hypothetical protein	
			VBIBruCet28239_2980	BCETI_6000896	873509	875161	-	550		hypothetical protein	
			VBIBruCet28239_2981	BCETI_6000898	876113	876241	+	42		hypothetical protein	
			VBIBruCet28239_2982	BCETI_6000899	876719	877198	-	159		ISBm1, transposase orfA	
			VBIBruCet28239_2984	BCETI_6000900	877117	877533	-	138		TRANSPOSASE	
			VBIBruCet28239_2985		878003	878119	-	38		hypothetical protein	
			VBIBruCet28239_2986	BCETI_6000901	878102	879400	+	432		hypothetical protein	
			VBIBruCet28239_2987	BCETI_6000902	879629	880939	+	436		putative cytoplasmic protein	
			VBIBruCet28239_2988	BCETI_6000903	881186	881773	-	195		TRANSPOSASE	
			VBIBruCet28239_2989	BCETI_6000904	881830	882129	-	99		TRANSPOSASE	
			VBIBruCet28239_2990	BCETI_6000905	882152	882274	-	40		hypothetical protein	
			VBIBruCet28239_2991	BCETI_6000906	882390	882926	-	178		hypothetical protein	
			VBIBruCet28239_2992	BCETI_6000908	883364	884227	+	287		transposase	
			VBIBruCet28239_2993	BCETI_6000909	884351	885364	-	337		Transposase	
			VBIBruCet28239_2994	BCETI_6000911	885986	886369	+	127		hypothetical protein	
			VBIBruCet28239_2995	BCETI_6000912	886419	886688	+	89		hypothetical protein	
			VBIBruCet28239_2996		886756	887907	-	383		Possible integrase-like protein	
			VBIBruCet28239_2997	BCETI_6000915	887924	888223	+	99		IS3 family element, transposase orfB	
			VBIBruCet28239_2998	BCETI_6000916	888250	888369	+	39		hypothetical protein	
			VBIBruCet28239_2999		888528	888734	-	68		hypothetical protein	
			VBIBruCet28239_3000		888694	888807	-	37		hypothetical protein	
			VBIBruCet28239_3001	BCETI_6000918	889031	890017	+	328		putative ABC transporter ATP-binding protein	
			VBIBruCet28239_3002	BCETI_6000919	890010	890990	+	326		Oligopeptide transport ATP-binding protein OppD (TC 3.A.1.5.1)	

			VBIBruCet28239_3003	BCETI_6000920	890987	891808	+	273	Cell processes; Transport of small molecules; amino acids, amines, peptides	
			VBIBruCet28239_3004	BCETI_6000921	891813	892748	+	311	Cell processes; Transport of small molecules; amino acids, amines, peptides	
			VBIBruCet28239_3005	BCETI_6000922	892842	894452	+	536	Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)	
			VBIBruCet28239_3006	BCETI_6000923	894580	895776	+	398	amidohydrolase family	
			VBIBruCet28239_3007	BCETI_6000924	896646	896774	-	42	hypothetical protein	
			VBIBruCet28239_3008		897019	897159	+	46	hypothetical protein	
			VBIBruCet28239_3009		897134	897469	-	111	transposase, Tn3 familiy	
			VBIBruCet28239_3010	BCETI_6000930	899517	900380	-	287	transposase	
			VBIBruCet28239_3011	BCETI_6000931	900582	902240	+	552	filamentous haemagglutinin family outer membrane protein	