Table S4: combined results of the reciprocal blast comparisons against 38 Roseobacter genomes. Orthologous genes with an e-value of the corresponding blast hit <1e-20 and and min. global alignment of 30%are coloured.

| locus tag | Annotation | COG category | primary hits? | Ruegeria sp. TM1040 | R. pomeroyi DSS-3 | R. sp. TM1040 | Ruegeria sp. TM1040 | Ruegeria sp. KLH11 | Ruegeria sp. TM1040 | Ruegeria sp. TM1040 | Ruegeria sp. TM1040 | Ruegeria sp. TM1040 | Ruegeria sp. TM1040 | Ruegeria sp. TM1040 | Roseobacter litoralis Otw-7 | Roseobacter denitrificans OCh114 | Roseobacter litoralis Oslo | Roseobacter denitrificans ATCC33942 | Octadecabacter arcticus 238 | Octadecabacter antarcticus 307 | Octadecabacter sp. CCS3 | Octadecabacter sp. GG7 | Octadecabacter sp. R2-8 | Octadecabacter sp. R2-8 | Octadecabacter sp. R2-8 | Roseobacter sp. SK209-2-6 | Roseobacter sp. SK209-2-6 | Roseobacter sp. SK209-2-6 | Roseobacter sp. SK209-2-6 | Roseobacter sp. SK209-2-6 | Roseobacter sp. TM1040 | Roseobacter sp. TM1040 | Roseobacter sp. TM1040 | Roseobacter sp. TM1040 | Roseobacter sp. 27 | Roseobacter sp. 27 | Roseobacter sp. 27 | Roseobacter sp. 27 | Citreicella sp. 357 | Citreicella sp. 357 | Citreicella sp. 357

RCA23_c01930	HrpB:ATP-dependent RNA helicase HrpB (3.6.4.13)	COG1643	L
RCA23_c01940	LAO/AO transport system ATPase	COG1703	E
RCA23_c01950	RpmB:50S ribosomal protein L28	COG0227	J
RCA23_c01960	hypothetical protein		
RCA23_c01970	LepA:GTP-binding protein LepA	COG0481	M
RCA23_c01980	hypothetical protein, alpha/beta hydrolase-like	COG0596	R
RCA23_c01990	putative ring-cleaving dioxygenase	COG0346	E
RCA23_c02000	GlyA:serine hydroxymethyltransferase GlyA (2.1.2.1)	COG0112	E
RCA23_c02010	putative inorganic polyphosphate/ATP-NAD kinase PpnK (2.7.1.23)	COG0061	H
RCA23_c02020	PrpE:propionate--CoA ligase PrpE (6.2.1.17)	COG0365	I
RCA23_c02030	hypothetical protein	COG1917	S
RCA23_c02040	Cdd:cytidine deaminase Cdd (3.5.4.5)	COG0295	F
RCA23_c02050	DeoA:thymidine phosphorylase DeoA (2.4.2.4)	COG0213	F
RCA23_c02060	DeoB:phosphopentomutase DeoB (5.4.2.7)	COG1015	G
RCA23_c02070	Add:adenosine deaminase Add (3.5.4.4)	COG1816	F
RCA23_c02080	Upp:uracil phosphoribosyltransferase Upp (2.4.2.9)	COG0035	F
RCA23_c02090	hypothetical protein		
RCA23_c02100	WaaA:3-deoxy-D-manno-octulosonic-acid transferase WaaA (2.4.--.-)	COG1519	M
RCA23_c02110	L-sorbose 1-dehydrogenase (1.1.99.32)	COG2303	E
RCA23_c02120	putative N-acylneuraminate cytidylyltransferase	COG1083	M
RCA23_c02130	ArnB1:UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase ArnB	COG0399	M
RCA23_c02140	hypothetical protein	COG3119	P
RCA23_c02150	hypothetical protein, nucleoside triphosphate hydrolases-like	COG1122	P
RCA23_c02160	S-adenosyl-L-methionine-dependentmethyltransferas e	COG2226	H
RCA23_c02170	hypothetical protein		
RCA23_c02180	AbkC:medium-chain-fatty-acid--CoA ligase AbkC (6.2.1.--)	COG0318	I
RCA23_c02190	hypothetical protein DUF6 transmembrane	COG0697	G
RCA23_c02200	FadD1:fatty acid oxidation complex alpha subunit FadJ (4.2.1.17;5.1.2.3)	COG1250	I
RCA23_c02210	hypothetical protein		
RCA23_c02220	short chain dehydrogenase (1.1.1.--)	COG0183	I
RCA23_c02230	putative glutathione S-transferase	COG0625	O
RCA23_c02240	MmgC:acyl-CoA dehydrogenase MmgC (1.3.99.--)	COG1960	I
RCA23_c02250	putative HTH-type transcriptional regulator, MerR family	COG0789	K
RCA23_c02260	putative HTH-type transcriptional regulator, MerR family	COG0789	K
RCA23_c02270	hypothetical protein, transmembrane protein DUF2899		
RCA23_c02280	hypothetical protein, thioesterase	COG2050	Q
RCA23_c02290	hypothetical protein, thioesterase	COG2050	Q
RCA23_c02300	DinF:DNA-damage-inducible protein F	COG0534	V
RCA23_c02310	PyrD:dihydroorotate dehydrogenase PyrD (1.3.5.2)	COG0167	F
RCA23_c02320	hypothetical protein DUF952	COG3502	S
RCA23_c02330	SurE:5'-nucleotidase SurE (3.1.3.5)	COG0737	F
RCA23_c02340	hypothetical protein	COG3409	M
RCA23_c02350	GlyQ:glycyl-tRNA synthase alpha subunit GlyQ (6.1.1.14)	COG0752	J
RCA23_c02360	hypothetical protein		
RCA23_c02370	GlyS:glycyl-tRNA synthase beta subunit GlyS (6.1.1.14)	COG0751	J
RCA23_c02380	PpdK:pyruvate, phosphate dikinase PpdK (2.7.9.1)	COG0574	G
RCA23_c02390	putative cell wall hydrolase	COG3773	M
RCA23_c02400	hypothetical protein, dihydroneopterin aldolase	COG1539	H
RCA23_c02410	FolP:dihydropteroate synthase FolP (2.5.1.15)	COG0294	H
RCA23_c02420	putative integral membrane protein DUF6	COG0697	G
RCA23_c02430	IlvC:ketol-acid reductoisomerase IlvC (1.1.1.86)	COG0059	E
RCA23_c02440	putative transcriptional regulator, asnC family	COG1522	K
RCA23_c02450	putative transcriptional regulator, asnC family	COG1522	K
RCA23_c02460	hypothetical protein	COG0075	E
RCA23_c02470	UbiH:2-octaprenyl-6-methoxyphenol hydroxylase UbiH (1.14.13.-)	COG0654	H
RCA23_c02480	putative pyrimidine 5-nucleotidase	COG1011	R
RCA23_c02490	putative HTH-type transcriptional regulator, GntR family	COG1802	K
RCA23_c02500	YdaM:uncharacterized glycosyltransferase YdaM (2.4.--.-)	COG1215	M
RCA23_c02510	CarA:carbamoyl-phosphate synthase small chain CarA (6.3.5.5)	COG0505	E
RCA23_c02520	GatB/Yqe/Y family protein	COG1610	S
RCA23_c02530	hypothetical protein	COG5488	S
RCA23_c02540	CbaD:cytochrome c oxidase subunit 1 (1.9.3.1)	COG0843	C
RCA23_c02550	LipB:octanoyltransferase LipB (2.3.1.181)	COG0321	H
RCA23_c02560	hypothetical protein, LytTr transcriptional regulator	COG3279	K
RCA23_c02570	membrane protein-like	COG3395	S
RCA23_c02590	arylsulfatase (3.1.6.1)	COG3119	P
RCA23_c02600	NADPH dehydrogenas (1.6.99.1)	COG1902	C
RCA23_c02610	IdnD:L-idonate 5-dehydrogenase IdnD (1.1.1.264)	COG1063	E
RCA23_c02620	Gnx1:gluconate 5-dehydrogenase Gnx (1.1.1.69)	COG1028	I
RCA23_c02630	YgbJ:uncharacterized oxidoreductase YgbJ (1.1.--.-)	COG2084	I
RCA23_c02640	hypothetical protein, xylose isomerase-like	COG1082	G
RCA23_c02650	GyaR1:glyoxylate reductase GyaR (1.1.1.26)	COG1052	C
RCA23_c02660	hypothetical protein		
RCA23_c02670	hypothetical protein, AdC-like	COG1296	E
RCA23_c02680	pbbTfkB: transketolase (2.2.1.1)	COG0021	G
RCA23_c02690	hypothetical protein	COG4091	E
RCA23_c02700	transketolase, alpha subunit (2.2.1.1)	COG3959	G
RCA23_c02710	transketolase, beta-subunit (2.2.1.1)	COG3958	G
RCA23_c02720	putative 3-hydroxyisobutyrate dehydrogenase (1.1.1.31)	COG2084	I
RCA23_c02730	putative 3-hydroxyisobutyrate dehydrogenase (1.1.1.31)	COG2084	I
RCA23_c02740	FabG1:3-oxoacyl-(acyl-carrier-protein) reductase FabG (1.1.1.100)	COG1028	I
RCA23_c02750	HTH-type transcriptional regulator, LysR family	COG0583	K
RCA23_c02760	putative HTH-type transcriptional regulator, GntR family	COG1802	K
RCA23_c02770	DctP1:TRAP dicarboxylate transporter, subunit DctP	COG4663	Q
RCA23_c02780	DctQ:TRAP dicarboxylate transporter, subunit DctQ	COG4665	Q
RCA23_c02790	TRAP dicarboxylate transporter, DctM subunit DctM	COG4664	Q
RCA23_c02800	hypothetical protein	COG0240	C
RCA23_c02810	hypothetical protein DUF1537	COG1395	S
RCA23_c02820	putative ribulose bisphosphate carboxylase large chain	COG1850	G
RCA23_c02830	hypothetical protein, NAD dependent epimerase / dehydratase family	COG0451	M
RCA23_c02840	GarR1:2-hydroxy-3-oxopropionate reductase GarR (1.1.1.60)	COG2084	I
RCA23_c02850	hypothetical protein		
RCA23_c02860	UxaA:altronate hydrolase UxaA (4.2.1.7)	COG2721	G
RCA23_c02870	putative oxidoreductase	COG0673	R
RCA23_c02880	GarR2:2-hydroxy-3-oxopropionate reductase GarR (1.1.1.60)	COG2084	I
RCA23_c02890	SamS:adenosylmethionine uptake transporter Sam	COG0697	G
RCA23_c02900	KdgK:2-dehydro-3-deoxygluconokinase KdgK (2.7.1.45)	COG0524	G
RCA23_c02910	UxuB:D-mannonate oxidoreductase UxuB (1.1.1.57)	COG0246	G
RCA23_c02920	UxaC:uronate isomerase UxaC (5.3.1.12)	COG1904	G
RCA23_c02930	putative oxidoreductase	COG0673	R
RCA23_c02940	putative oxidoreductase	COG0673	R
RCA23_c02950	putative oxidoreductase	COG0673	R
RCA23_c02960	UxuA:mannonate dehydratase UxuA (4.2.1.8)	COG1312	G
RCA23_c02970	long-chain-fatty-acid--CoA ligase (6.2.1.3)	COG0318	I
RCA23_c02980	BdhA:D-beta-hydroxybutyrate dehydrogenase BdhA (1.1.1.30)	COG1028	I
RCA23_c02990	ActP:copper-transporting P-type ATPase ActP (3.6.3.4)	COG2217	P
RCA23_c03000	HmrR:HTH-type transcriptional regulator (copper efflux regulator)	COG0789	K
RCA23_c03010	hypothetical protein	COG3937	S
RCA23_c03020	hypothetical protein		
RCA23_c03030	Icd:isocitrate dehydrogenase Icd (1.1.1.42)	COG2838	C
RCA23_c03040	integral membrane protein DUF6	COG0697	G
RCA23_c03050	SoxE:flavocytochrome c cytochrome subunit SoxE	COG3474	C
RCA23_c03060	SoxF1:sulfide dehydrogenase [flavocytochrome c] flavoprotein chain SoxF (1.8.	COG0446	R
RCA23_c03070	hypothetical protein, CsnC-like	COG1764	O
RCA23_c03080	putative dimethyl sulfoniopropionate demethylase DmdA	COG0404	E
RCA23_c03090	transcriptional regulator, AsnC family	COG1522	K
RCA23_c03100	glutathione S-transferase (2.5.1.18)	COG0625	O
RCA23_c03120	hypothetical protein, ribonuclease, ErG family	COG1530	J
RCA23_c03130	Maf-like protein	COG0424	D
RCA23_c03140	InfA:translation initiation factor IF-1	COG0361	J
RCA23_c03150	hypothetical protein, low molecular weight phosphotyrosine protein phosphatase	COG0394	T
RCA23_c03160	hypothetical protein UPF0262	COG5328	S
RCA23_c03170	HisD1:histidinol dehydrogenase HisD (1.1.1.23)	COG0141	E
RCA23_c03180	hypothetical protein		
RCA23_c03190	MurA:UDP-N-acetylglucosamine 1- carboxyvinyltransferase MurA (2.5.1.7)	COG0766	M
RCA23_c03210	PASPAC sensor hybrid histidine kinase	COG0642	T
RCA23_c03220	3OG-Fe(II) oxygenase	COG3491	R
RCA23_c03230	putative lysine exporter protein	COG1280	E
RCA23_c03240	putative carbon monoxide dehydrogenase subunit G	COG3427	S
RCA23_c03250	hypothetical protein, XdhC and CoxI family	COG1975	O
RCA23_c03260	putative MFS-type transporter	COG2814	G
RCA23_c03270	AFG1-like ATPase	COG1485	R
RCA23_c03280	FolC:bifunctional protein FolC (6.3.2.17;6.3.2.12)	COG0285	H
RCA23_c03290	AccD:acetyl-coenzyme A carboxylase carboxyl transferase beta subunit AccD (6	COG0777	I
RCA23_c03300	hypothetical protein, CAAX amino terminal protease-like	COG1266	R
RCA23_c03310	IlvD1:dihydroxy-acid dehydratase IlvD (4.2.1.9)	COG0129	E
RCA23_c03320	hypothetical protein		
RCA23_c03330	hypothetical protein		
RCA23_c03340	hypothetical protein		
RCA23_c03350	hypothetical protein, OmpA family	COG2885	M
RCA23_c03360	hypothetical protein, peroxidase-like protein	COG2128	S
RCA23_c03370	hypothetical protein, acetyltransferase-like	COG0456	R
RCA23_c03380	hypothetical protein, probably molybdopterin binding	COG1058	R
RCA23_c03390	SfsA:sugar fermentation stimulation protein SfsA	COG1489	R
RCA23_c03400	Map:methionine aminopeptidase Map (3.4.11.18)	COG0024	J
RCA23_c03410	RhlE1:ATP-dependent RNA helicase RhlE (3.6.4.13)	COG0513	L
RCA23_c03420	putative ribosomal RNA small subunit methyltransferase D	COG0742	L
RCA23_c03430	ThcD:rhodocoxin reductase ThcD (1.18.1.-)	COG0446	R
RCA23_c03440	peroxiredoxin (1.11.1.15)	COG0678	O
RCA23_c03450	dterin-4-alpha-carbinolamine dehydratase (4.2.1.96)	COG2154	H
RCA23_c03460	hypothetical protein DUF482	COG3146	S
RCA23_c03470	putative glycerophosphoryl diester phosphodiesterase	COG5584	C
RCA23_c03480	putative endoribonuclease L-PSP	COG0251	J
RCA23_c03490	type I secretion system protein, HlyD family	COG1566	V
RCA23_c03500	type I secretion system ATP-binding component	COG4618	R
RCA23_c03510	putative type I secretion system protein, transmembrane domain	COG4618	R
RCA23_c03520	VacJ like lipoprotein	COG2853	M
RCA23_c03530	putative toluene tolerance protein	COG2854	Q
RCA23_c03540	MrcB:penicillin-binding protein 1B (2.4.1.129;3.4.--.-)	COG0744	M
RCA23_c03550	TyrB:aromatic-amino-acid aminotransferase TyrB (2.6.1.57)	COG1448	E
RCA23_c03560	SseA:3-mercaptopyruvate sulfurtransferase SseA (2.8.1.2)	COG0607	P
RCA23_c03570	SmpB:SsrA-binding protein SmpB	COG0691	O
RCA23_c03580	DapA1:dihydrodipicolinate synthase DapA (4.2.1.52)	COG0329	E
RCA23_c03590	Slt:soluble lytic murein transglycosylase Slt (4.2.2.-)	COG0741	M
RCA23_c03600	hypothetical protein DUF6 transmembrane	COG0697	G
RCA23_c03610	hypothetical protein DUF752	COG4121	S
RCA23_c03620	putative FAD-dependent oxidoreductase	COG0665	E
RCA23_c03630	hypothetical protein, glycosaldoxidoxygenase superfamily	COG0346	E
RCA23_c03640	hypothetical protein		
RCA23_c03650	hypothetical protein		
RCA23_c03660	CobO:cob(I)yrinic acid a,c-diamide adenosyltransferase CobO (2.5.1.17)	COG2109	H
RCA23_c03670	hypothetical protein		
RCA23_c03680	oligopeptide/dipeptide ABC transporter, ATP- binding protein	COG0444	E
RCA23_c03690	oligopeptide/dipeptide ABC transporter, ATP- binding protein	COG0444	E
RCA23_c03700	oligopeptide/dipeptide ABC transporter, permease protein	COG1173	E
RCA23_c03710	oligopeptide/dipeptide ABC transporter, permease protein	COG0601	E
RCA23_c03720	oligopeptide/dipeptide ABC transporter, periplasmic substrate-binding protein	COG0747	E
RCA23_c03730	HTH-type transcriptional regulator, LysR family	COG0583	K
RCA23_c03740	putative amidohydrolase 3	COG1574	R
RCA23_c03750	cobalamin biosynthesis CobW-like	COG0523	R
RCA23_c03760	hypothetical protein, restriction endonuclease type IV-like	COG4127	S
RCA23_c03770	OpuAA:glycine betaine transport ATP-binding protein OpuAA (3.6.3.32)	COG4175	E
RCA23_c03780	OpuAB:glycine betaine transport system permease protein OpuAB	COG4176	E
RCA23_c03790	OpuAC:glycine betaine transporter substrate-binding protein OpuAC	COG4113	E
RCA23_c03800	fatty acid desaturase	COG3239	I
RCA23_c03810	OdbD1:CoA-transferase family III protein involved in DMSP degradation	COG1804	C
RCA23_c03820	GapI:glyceraldehyde-3-phosphate dehydrogenase Gap (1.2.1.12)	COG0057	G
RCA23_c03830	ClpP:ATP-dependent Clp protease proteolytic subunit ClpP (3.4.21.92)	COG0740	O
RCA23_c03840	ClpX:ATP-dependent Clp protease ATP-binding subunit ClpX	COG1219	O
RCA23_c03850	putative NADH ubiquinone oxidoreductase subunit NDUFA12	COG3761	C
RCA23_c03860	hypothetical protein	COG1463	Q
RCA23_c03870	hypothetical protein	COG4765	S
RCA23_c03880	Aat:leucyl/phenylalanyl-tRNA--protein transferase Aat (2.3.2.6)	COG2360	O
RCA23_c03890	AccC1:biotin carboxylase AccC (6.3.4.14)	COG4770	I
RCA23_c03900	AcsA1:acetyl-coenzyme A synthase AcsA (6.2.1.1)	COG0365	I
RCA23_c03910	LivF:high-affinity branched-chain amino acid transport ATP-binding protein LivF	COG0410	E
RCA23_c03920	BraF:high-affinity branched-chain amino acid transport ATP-binding protein BraF	COG0411	E
RCA23_c03930	putative branched-chain amino acid transport system permease protein	COG4177	E
RCA23_c03940	putative branched-chain amino acid transport system permease protein	COG0559	E
RCA23_c03950	hypothetical protein	COG0683	E
RCA23_c03960	hypothetical protein, DNA binding helix-turn helix proteins	COG1396	K
RCA23_c03970	putative response regulator receiver protein, CheY like	COG0745	T

RCA23_c03980	hypothetical protein		
RCA23_c03990	WalK sensor protein kinase WalK (2.7.13.3)	COG0591	E
RCA23_c04000	hypothetical protein DUF442	COG3453	S
RCA23_c04010	hypothetical protein		
RCA23_c04020	hypothetical protein	COG3750	S
RCA23_c04030	hypothetical protein		
RCA23_c04040	putative Fe(3+)-transport system protein SfuB	COG1178	P
RCA23_c04060	integrase	COG0582	L
RCA23_c04070	hypothetical protein	COG3945	S
RCA23_c04080	hypothetical protein		
RCA23_c04090	UDP-N-acetylglucosamine--peptide N- acetylglucosaminyltransferase subunit (2	COG0457	R
RCA23_c04100	esterase, SGNH hydrolase-type	COG2755	E
RCA23_c04110	hypothetical protein		
RCA23_c04120	hypothetical protein, tetratricopeptide repeat	COG0790	R
RCA23_c04130	hypothetical protein		
RCA23_c04140	hypothetical protein		
RCA23_c04150	hypothetical protein		
RCA23_c04160	hypothetical protein, RmlC-like cupin family	COG3450	R
RCA23_c04170	hypothetical protein		
RCA23_c04180	hypothetical protein, DUF3127		
RCA23_c04190	putative nucleoside triphosphate hydrolase, ATPase domain	COG1066	O
RCA23_c04200	zinc-dependent metalloprotease (3.4.24.-)	COG2931	Q
RCA23_c04210	HTH-type transcriptional regulator, AsnC family	COG1522	K
RCA23_c04220	integrase	COG2801	L
RCA23_c04230	putative ion channel		
RCA23_c04240	integrase	COG4974	L
RCA23_c04250	GcnS-like N-acetyltransferase	COG1670	J
RCA23_c04260	integrase	COG0582	L
RCA23_c04280	hypothetical protein, NAD dependent epimerase / dehydratase family	COG0702	M
RCA23_c04290	UppP:undecaprenyl-diphosphatase UppP (3.6.1.27)	COG1968	V
RCA23_c04300	GltD:glutamate synthase [NADPH] small chain GltD (1.4.1.13)	COG0493	E
RCA23_c04310	GltB:glutamate synthase [NADPH] large chain GltB (1.4.1.13)	COG0069	E
RCA23_c04320	MtgA:monofunctional biosynthetic peptidoglycan transglycosylase MtgA (2.4.2.-	COG0744	M
RCA23_c04330	putative glutathione S-transferase	COG0625	O
RCA23_c04340	putative electron transport protein yjiS	COG1600	C
RCA23_c04360	hypothetical protein	COG5266	P
RCA23_c04350	hypothetical protein		
RCA23_c04370	IlvE:branched-chain-amino-acid aminotransferase IlvE (2.6.1.42)	COG0115	E
RCA23_c04380	PetP:HTH-type transcriptional regulator PetP	COG1846	K
RCA23_c04390	PetR:protein PetR	COG0745	T
RCA23_c04400	putative deacetylase, histone deacetylase superfamily protein-like	COG0123	B
RCA23_c04410	XseB:exodeoxyribonuclease 7 small subunit XseB (3.1.11.6)	COG1722	L
RCA23_c04420	hpA:geranyltransfransferase hpA (2.5.1.10)	COG0142	H
RCA23_c04430	Dxs1:1-deoxy-D-xylulose-5-phosphate synthase Dxs (2.2.1.7)	COG1154	H
RCA23_c04440	hypothetical protein, NAD dependent epimerase/dehydratase	COG0451	M
RCA23_c04450	hypothetical protein		
RCA23_c04460	hypothetical protein		
RCA23_c04470	CaiD:carnitinyl-CoA dehydratase CaiD (4.2.1.-)	COG1024	I
RCA23_c04480	hypothetical protein, CoA-binding	COG1042	C
RCA23_c04490	putative acyl-CoA dehydrogenase YngJ (1.3.99.-)	COG1960	I
RCA23_c04500	transcriptional regulator, AraC family	COG4977	K
RCA23_c04510	class II aldolase	COG0235	G
RCA23_c04520	ArsC:arsenate reductase ArsC (1.2.4.1)	COG1393	P
RCA23_c04530	Ade:adenine deaminase Ade (3.5.4.2)	COG1001	F
RCA23_c04540	Amn:AMP nucleosidase Amn (3.2.2.4)	COG0775	F
RCA23_c04550	HupDNA-binding protein HU	COG0776	L
RCA23_c04560	inner membrane protein DUF6	COG0697	G
RCA23_c04570	hypothetical protein, cytochrome C biogenesis protein	COG0785	O
RCA23_c04580	hypothetical protein, thioredoxin	COG0526	O
RCA23_c04590	hypothetical protein	COG3222	S
RCA23_c04600	DapE:succinyl-diaminopimelate desuccinylase DapE (3.5.1.18)	COG0624	E
RCA23_c04610	hypothetical protein		
RCA23_c04620	DapD:2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N- succinyltransferase DapD	COG2171	E
RCA23_c04630	L-threonine ammonia-lyase (4.3.1.19)	COG1171	E
RCA23_c04640	RlmH:ribosomal RNA large subunit methyltransferase N (2.1.1.-)	COG0820	R
RCA23_c04650	hypothetical protein		
RCA23_c04660	L-asparaginase II (3.5.1.1)	COG4448	E
RCA23_c04670	SerB:phosphoserine phosphatase SerB (3.1.3.3)	COG0560	E
RCA23_c04680	hypothetical protein		
RCA23_c04690	SerC:phosphoserine aminotransferase SerC (2.6.1.52)	COG1932	H
RCA23_c04700	SerA:D-3-phosphoglycerate dehydrogenase SerA (1.1.1.95)	COG0111	H
RCA23_c04710	metallophosphoesterase		
RCA23_c04720	RppH:RNA pyrophosphohydrolase RppH (3.6.1.-)	COG0494	L
RCA23_c04730	ClpA:carboxy-terminal-processing protease ClpA (3.4.21.102)	COG0793	M
RCA23_c04740	GpmI:2,3-bisphosphoglycerate-independent phosphoglycerate mutase GpmI (5.4	COG0696	G
RCA23_c04750	putative protein ImuB		
RCA23_c04760	hypothetical protein		
RCA23_c04770	hypothetical protein, NlpC/P60	COG0791	M
RCA23_c04780	putative cytosol aminopeptidase PepA (3.4.11.1)	COG0260	E
RCA23_c04790	hypothetical protein		
RCA23_c04800	CynT:carbonic anhydrase CynT (4.2.1.1)	COG0288	P
RCA23_c04810	AscI:aspartate-semialdehyde dehydrogenase AscI (1.2.1.11)	COG0136	E
RCA23_c04820	MFS-type transporter	COG2223	P
RCA23_c04830	short chain dehydrogenase	COG4221	R
RCA23_c04840	FAD dependent oxidoreductase	COG0665	E
RCA23_c04850	MttB2:trimethylamine methyltransferase MttB (2.1.1.-)	COG5598	H
RCA23_c04860	aldehyde dehydrogenase (1.2.1.3)	COG1012	C
RCA23_c04870	DapA2:dihydrodipicolinate synthase DapA (4.2.1.52)	COG0329	E
RCA23_c04880	transcriptional regulator, GntR family	COG1802	K
RCA23_c04890	hypothetical protein		
RCA23_c04900	LeuB:isopropylmalate dehydrogenase LeuB (1.1.1.85)	COG0473	C
RCA23_c04910	hypothetical protein		
RCA23_c04920	LeuD1:3-isopropylmalate dehydratase small subunit LeuD (4.2.1.33)	COG0066	E
RCA23_c04930	LeuC1:3-isopropylmalate dehydratase large subunit LeuC (4.2.1.33)	COG0065	E
RCA23_c04940	hypothetical protein, DUF2075		
RCA23_c04950	hypothetical protein DUF143	COG0799	S
RCA23_c04960	RlmH:ribosomal RNA large subunit methyltransferase H (2.1.1.-)	COG1576	S
RCA23_c04970	AdhI:alcohol dehydrogenase class-3 AdhI (1.1.1.1,1.1.1.284)	COG1062	C
RCA23_c04980	putative membrane transport protein	COG0679	R
RCA23_c04990	YesG:S-formylglutathione hydrolase YesG (3.1.2.12)	COG0627	R
RCA23_c05000	soluble pyridine nucleotide transhydrogenase (1.6.1.1)	COG1249	C
RCA23_c05010	hypothetical protein DUF188	COG1671	S
RCA23_c05020	putative integral membrane protein	COG0697	G
RCA23_c05030	putative HAD-superfamily hydrolase	COG1011	R
RCA23_c05040	putative ornithine cyclodeaminase	COG2423	E
RCA23_c05050	CobN:aerobic cobaltochelatase subunit CobN (6.6.1.2)	COG1429	H
RCA23_c05060	hypothetical protein, acetyltransferase-like	COG0456	R
RCA23_c05070	CobW protein CobW	COG0523	R
RCA23_c05080	hypothetical protein DUF1636	COG5469	S
RCA23_c05090	CbtA:possible cobalt transporter, subunit CbtA	COG5446	S
RCA23_c05100	hypothetical protein, Di-haem cytochrome c peroxidase	COG1858	P
RCA23_c05110	hypothetical protein	COG4188	R
RCA23_c05120	hypothetical protein		
RCA23_c05130	XylR:xylose repressor XylR	COG1940	K
RCA23_c05140	XylF:D-xylose-binding periplasmic protein XylF	COG4213	G
RCA23_c05150	XylH:xylose transport system permease protein XylH	COG4214	G
RCA23_c05160	XylG:xylose ABC transporter, ATP-binding protein XylG (3.6.3.17)	COG1129	G
RCA23_c05170	XylB1:xylulose kinase XylB (2.7.1.17)	COG1070	G
RCA23_c05180	XylA:xylose isomerase XylA (5.3.1.5)	COG2115	G
RCA23_c05190	LcfB:long-chain-fatty-acid--CoA ligase LcfB	COG0318	I
RCA23_c05200	malonyl-CoA decarboxylase (4.1.1.9)		
RCA23_c05210	acyl-CoA dehydrogenase (1.3.99.-)	COG1960	I
RCA23_c05220	hypothetical protein DUF81		
RCA23_c05230	PckA:phosphoenolpyruvate carboxykinase PckA (4.1.1.49)	COG1866	C
RCA23_c05240	ChvI:two component signal transduction response regulator receiver protein Ch	COG0745	T
RCA23_c05250	ChvG1:two component signal transduction histidine kinase ChvG	COG0642	T
RCA23_c05260	hypothetical protein, HPr serine kinase	COG1493	T
RCA23_c05270	putative P-loop containing ATPase	COG1660	R
RCA23_c05280	hypothetical protein, PTS system mannose- specific EIIA component	COG2893	G
RCA23_c05290	PhoD:phosphocarrier protein NPr (2.7.11.-)	COG1925	G
RCA23_c05300	EtfA:electron transfer flavoprotein alpha subunit EtfA	COG2025	C
RCA23_c05310	EtfB:electron transfer flavoprotein beta subunit EtfB	COG2086	C
RCA23_c05320	CobO2:cob(I)yrinic acid a,c-diamide adenosyltransferase CobO (2.5.1.17)	COG2096	S
RCA23_c05330	putative short chain dehydrogenase	COG4221	R
RCA23_c05340	ParC:DNA topoisomerase 4 subunit A (5.99.1.-)	COG0188	L
RCA23_c05350	hypothetical protein DUF898	COG4269	S
RCA23_c05360	peptidase M48 Ste24p (3.4.24.-)	COG4783	R
RCA23_c05370	hypothetical protein		
RCA23_c05380	TufB:elongation factor Tu (EF-Tu)	COG0050	J
RCA23_c05400	hypothetical protein, DUF560		
RCA23_c05410	HipO1:hippurate hydrolase HipO (3.5.1.32)	COG1473	R
RCA23_c05420	GsiA1:glutathione import ATP-binding protein GsiA (3.6.3.-)	COG1123	R
RCA23_c05430	AppA:oligopeptide-binding protein AppA	COG0747	E
RCA23_c05440	AppB:oligopeptide transport system permease protein AppB	COG0601	E
RCA23_c05450	AppC:oligopeptide transport system permease protein AppC	COG1173	E
RCA23_c05460	ABC transporter ATP-binding protein	COG1131	V
RCA23_c05470	inner membrane transport permease	COG0842	V
RCA23_c05480	hypothetical protein, peptidase family S49	COG0616	O
RCA23_c05490	putative sodium/calcium exchanger protein	COG5330	P
RCA23_c05500	putative short cpnotein	COG1028	I
RCA23_c05510	LvrC:LvrABC system protein C	COG0322	L
RCA23_c05520	CDP-diacylglycerol--glycerol-3-phosphate 3- phosphatidyltransferase (2.7.8.5)	COG0558	I
RCA23_c05530	MoaD1:molybdopterin-converting factor subunit MoaD	COG1977	H
RCA23_c05540	MoaE1:molybdopterin synthase catalytic subunit MoaE	COG0314	H
RCA23_c05550	hypothetical protein		
RCA23_c05560	hypothetical protein, CmpA	COG2885	M
RCA23_c05570	UbiA prenyltransferase (2.5.1.-)	COG0382	H
RCA23_c05580	RNA methyltransferase	COG1385	S
RCA23_c05590	hypothetical protein		
RCA23_c05600	glutamate--cysteine ligase (6.3.2.2)	COG3572	H
RCA23_c05610	PlsY:glycerol-3-phosphate acyltransferase PlsY (2.3.1.-)	COG3344	S
RCA23_c05620	PyrC1:dihydroorotase PyrC (3.5.2.3)	COG0044	F
RCA23_c05630	PyrB:aspartate carbamoyltransferase PyrB (2.1.3.2)	COG0540	F
RCA23_c05640	uracil DNA glycosylase family protein	COG1573	L
RCA23_c05650	MoaB:molybdenum cofactor biosynthesis protein MoaB	COG0521	H
RCA23_c05660	putative efflux transporter, RND family, membrane fusion protein	COG1566	V
RCA23_c05670	transporter, AcrB/AcrD/AcrF family	COG0841	V
RCA23_c05680	hypothetical protein	COG4233	O
RCA23_c05690	hypothetical protein DUF179	COG1678	K
RCA23_c05700	acyl-CoA dehydrogenase (1.3.99.-)	COG1960	I
RCA23_c05710	putative metallo-beta-lactamase family protein	COG0491	R
RCA23_c05720	hypothetical protein		
RCA23_c05730	putative branched-chain amino acid transport protein	COG4392	S
RCA23_c05740	AdtC:protein AdtC	COG1296	E
RCA23_c05750	FdhD1:formate dehydrogenase accessory protein FdhD	COG1526	C
RCA23_c05760	MobA:molybdopterin-guanine dinucleotide biosynthesis protein MobA	COG0746	H
RCA23_c05770	MobB1:molybdopterin-guanine dinucleotide biosynthesis protein MobB	COG1763	H
RCA23_c05780	MoaA1:molybdopterin biosynthesis protein MoaA	COG0303	H
RCA23_c05790	GreA:transcription elongation factor GreA	COG0782	K
RCA23_c05800	electron transfer flavoprotein-ubiquinone oxidoreductase (1.5.5.1)	COG0644	C
RCA23_c05810	tetratricopeptide repeat-containing protein	COG0457	R
RCA23_c05820	IspE:4-diphosphocytidyl-2C-methyl-D-erythritol 2- phosphate synthase IspE (2.7	COG1947	I
RCA23_c05830	IspB:octaprenyl-diphosphate synthase IspB (2.5.1.-)	COG0142	H
RCA23_c05840	hypothetical protein, methyltransferase	COG4123	R
RCA23_c05850	PhaB:acetoacetyl-CoA reductase PhaB (1.1.1.36)	COG1028	I
RCA23_c05860	PhaA2:acetyl-CoA acetyltransferase PhaA (2.3.1.9)	COG0183	I
RCA23_c05870	signaling protein	COG2200	T
RCA23_c05880	TagDNA-3-methyladenine glycosylase 1 (3.2.2.20)	COG2818	L
RCA23_c05890	TlpA:thiol:disulfide interchange protein TlpA	COG0526	O
RCA23_c05900	ArgH:argininosuccinate lyase ArgH (4.3.2.1)	COG0165	E
RCA23_c05910	hypothetical protein		
RCA23_c05920	LysA:diaminopimelate decarboxylase LysA (4.1.1.20)	COG0019	E
RCA23_c05930	hypothetical protein	COG3196	D
RCA23_c05940	putative acyltransferase	COG0204	I
RCA23_c05950	glyoxalase/fikomycin resistance protein	COG2764	S
RCA23_c05960	hypothetical protein, pyridoxamine 5'-phosphate oxidase	COG3576	R
RCA23_c05970	AccA:acetyl-coenzyme A carboxylase carboxyl transferase alpha subunit AccA (4	COG0825	I
RCA23_c05980	CitE1:citrate lyase beta subunit CitE (4.1.3.6,4.1.3.34)	COG2301	G
RCA23_c05990	hypothetical protein DUF1611	COG3367	S
RCA23_c06000	YcjE:L-Ala-D/L-Glu epimerase YcjE (5.1.1.-)	COG4948	M
RCA23_c06010	DatD:D-alanine aminotransferase Dat (2.6.1.21)	COG0115	E
RCA23_c06020	hypothetical, OmpA-like		

RCA23_c06030	hypothetical protein	COG3743	S
RCA23_c06040	hypothetical protein DUF1244	COG3492	S
RCA23_c06050	N-formylglutamate amidohydrolase	COG3931	E
RCA23_c06060	PykF:pyruvate kinase PykF (2.7.1.40)	COG0469	G
RCA23_c06070	hypothetical protein		
RCA23_c06080	RpmI:50S ribosomal protein L35	COG0291	J
RCA23_c06090	RplT:50S ribosomal protein L20	COG0292	J
RCA23_c06100	putative sulfatase family protein	COG1404	O
RCA23_c06110	hypothetical protein		
RCA23_c06120	hypothetical protein, lipid A biosynthesis acyltransferase	COG1560	M
RCA23_c06130	PheS:phenylalanyl-tRNA synthase alpha chain PheS (6.1.1.20)	COG0016	J
RCA23_c06140	glutamine amidotransferase class-I (6.3.5.2)	COG0518	F
RCA23_c06150	PheT:phenylalanyl-tRNA synthase beta chain PheT (6.1.1.20)	COG0072	J
RCA23_c06160	putative HTH-type transcriptional regulator	COG1522	K
RCA23_c06170	RpsU:ribosomal protein S21	COG0828	J
RCA23_c06180	putative ubiquinone biosynthesis protein COQ9	COG5590	S
RCA23_c06190	putative quinone oxidoreductase	COG0604	C
RCA23_c06200	hypothetical protein DUF1013	COG3820	S
RCA23_c06210	RecR:recombination protein RecR	COG0353	L
RCA23_c06220	hypothetical protein	COG0718	S
RCA23_c06230	DnaX:DNA polymerase III subunit tau (2.7.7.7)	COG2812	L
RCA23_c06240	NudC:NADH pyrophosphatase NudC (3.6.1.22)	COG2816	L
RCA23_c06250	hypothetical protein	COG3832	S
RCA23_c06260	PheA:prephenate dehydratase PheA (4.2.1.51)	COG0077	E
RCA23_c06270	CycM:cytochrome c-552	COG3474	C
RCA23_c06280	ABC transporter extracellular solute-binding protein	COG4166	E
RCA23_c06290	ABC transporter permease protein	COG4174	R
RCA23_c06300	ABC transporter permease protein	COG4239	R
RCA23_c06310	putative oligopeptide ABC transporter ATP- binding protein	COG4172	R
RCA23_c06320	fumarylacetoacetate hydrolase family protein	COG0179	Q
RCA23_c06330	DacF:D-alanyl-D-alanine carboxypeptidase DacF (3.4.16.4)	COG1686	M
RCA23_c06340	haloacid dehalogenase domain protein hydrolase (3.-.-.-)	COG1011	R
RCA23_c06350	ClpS:ATP-dependent Clp protease adaptor protein ClpS	COG2127	S
RCA23_c06360	putative methyltransferase	COG2813	J
RCA23_c06370	putative short chain dehydrogenase	COG1028	I
RCA23_c06380	HemF:coproporphyrinogen 3 oxidase, aerobic (1.3.3.3)	COG4408	H
RCA23_c06390	oxidoreductase, FAD-binding protein	COG4097	P
RCA23_c06400	D-lactate dehydrogenase	COG0277	C
RCA23_c06420	integrase		GI 3
RCA23_c06430	mandelate racemase (5.1.2.2)	COG4948	M
RCA23_c06440	fumarylacetoacetate hydrolase family protein	COG0179	Q
RCA23_c06450	short-chain dehydrogenase/reductase	COG1028	I
RCA23_c06460	amidohydrolase	COG3618	R
RCA23_c06470	aldo/keto reductase	COG0667	C
RCA23_c06480	ABC transporter, permease protein	COG0600	P
RCA23_c06490	ABC transporter, permease protein	COG0600	P
RCA23_c06500	hypothetical protein		
RCA23_c06510	sulfonate/nitrate ABC transporter, ATPase	COG1116	P
RCA23_c06520	ABC transporter, periplasmic substrate-binding protein	COG0715	P
RCA23_c06530	arylsulfatase	COG3119	P
RCA23_c06540	transcriptional regulator, GntR family	COG1802	K
RCA23_c06550	hypothetical protein	COG4974	L
RCA23_c06560	hypothetical protein	COG1618	F
RCA23_c06570	hypothetical protein		
RCA23_c06580	hypothetical protein		
RCA23_c06590	hypothetical protein		
RCA23_c06600	hypothetical protein		
RCA23_c06610	hypothetical protein		
RCA23_c06620	hypothetical protein		
RCA23_c06630	hypothetical protein	COG3000	I
RCA23_c06640	transcriptional regulator, AsnC family	COG1522	K
RCA23_c06650	AspC1:aspartate aminotransferase AspC (2.6.1.1)	COG0436	E
RCA23_c06660	BdhI:3-hydroxybutyrate dehydrogenase BdhI (1.1.1.-,1.1.1.30)	COG1028	I
RCA23_c06670	putative fumarylacetoacetate hydrolase	COG0179	Q
RCA23_c06680	oxidoreductase, short chain dehydrogenase/reductase family protein	COG1028	I
RCA23_c06690	dimethylmenaquinone methyltransferase	COG0684	H
RCA23_c06700	hypothetical protein	COG3970	R
RCA23_c06710	AldH:NADP-dependent fatty aldehyde dehydrogenase AldH (1.2.1.4)	COG1012	C
RCA23_c06720	putative dihydrodipicolinate synthase	COG0329	E
RCA23_c06730	transcriptional regulator protein, LacI family	COG1609	K
RCA23_c06740	DctP2:TRAP dicarboxylate transporter, subunit DctP	COG1638	G
RCA23_c06750	DctQ2:TRAP dicarboxylate transporter, subunit DctQ	COG3090	G
RCA23_c06760	DctM2:TRAP dicarboxylate transporter, subunit DctM	COG1593	G
RCA23_c06770	DadA1:D-amino acid dehydrogenase small subunit DadA (1.4.99.1)	COG0665	E
RCA23_c06780	mandelate racemase/muconate lactonizing protein	COG4948	M
RCA23_c06790	DapA3:dihydrodipicolinate synthase DapA (4.2.1.52)	COG0329	E
RCA23_c06800	uncharacterized oxidoreductase, YjmC	COG2055	C
RCA23_c06810	SoxB1:sarcosine oxidase beta subunit SoxB (1.5.3.1)	COG0665	E
RCA23_c06820	SoxD1:sarcosine oxidase delta subunit SoxD (1.5.3.1)	COG4311	E
RCA23_c06830	SoxA1:sarcosine oxidase alpha subunit SoxA (1.5.3.1)	COG0404	E
RCA23_c06840	SoxG1:sarcosine oxidase gamma subunit SoxG (1.5.3.1)	COG4583	E
RCA23_c06850	hypothetical protein, DUF6 transmembrane protein	COG0697	G
RCA23_c06860	putative phage integrase		GI 3
RCA23_c06870	putative amidase	COG0154	J
RCA23_c06880	integrase	COG4974	L
RCA23_c06890	putative helicase		GI 3
RCA23_c06900	transposase	COG3316	L
RCA23_c06910	HTH-type transcriptional regulator, LuxR family	COG2197	T
RCA23_c06920	putative oxidoreductase, molybdopterin binding	COG3915	S
RCA23_c06930	signal transduction histidine kinase	COG0642	T
RCA23_c06940	RtbA:glucose-1-phosphate thymidylyltransferase RtbA (2.7.7.24)	COG1209	M
RCA23_c06950	hypothetical protein, chain length determinant protein	COG0489	D
RCA23_c06960	polysaccharide export protein	COG1596	M
RCA23_c06970	hypothetical protein, Vam2-like	COG5652	S
RCA23_c06980	type I secretion system membrane fusion protein, HlyD family	COG1566	V
RCA23_c06990	type I secretion system ATP-binding component, HlyB family	COG2274	V
RCA23_c07000	type I secretion outer membrane protein, TolC family	COG1538	M
RCA23_c07010	putative serralysin-like metalloprotease	COG2931	Q
RCA23_c07020	RtbD:dTDP-4-dehydrorhamnose reductase RtbD (1.1.1.133)	COG1091	M
RCA23_c07030	RtbB:dTDP-glucose 4,6-dehydratase RtbB (4.2.1.46)	COG1088	M
RCA23_c07040	RtbC:dTDP-4-dehydrorhamnose 3,5-epimerase RtbC (5.1.3.13)	COG1898	M
RCA23_c07050	hypothetical protein		
RCA23_c07060	glycosyltransferase	COG0438	M
RCA23_c07070	putative glycosyltransferase	COG0438	M
RCA23_c07080	hypothetical protein, UDP- glycosyltransferase/glycogen phosphorylase-like	COG0438	M
RCA23_c07090	polysaccharide biosynthesis protein		GI 3
RCA23_c07100	AmB2:UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase AmB	COG0399	M
RCA23_c07110	hypothetical, WxcM-like	COG0110	R
RCA23_c07120	hypothetical protein, WxcM-like		
RCA23_c07130	hypothetical protein, acyltransferase-like	COG1670	J
RCA23_c07140	UDP-glucose/GDP-mannose dehydrogenase family protein	COG0677	M
RCA23_c07150	S-adenosyl-L-methionine-dependentmethyltransferas e		
RCA23_c07160	LspL1:UDP-glucuronate 5'-epimerase LspL (5.1.3.12)	COG0451	M
RCA23_c07170	transcriptional regulator, MarR family	COG1846	K
RCA23_c07180	NusG2:transcription antitermination protein NusG	COG0250	K
RCA23_c07190	hypothetical protein	COG1434	S
RCA23_c07200	LpcC:lipopolysaccharide core biosynthesis mannosyltransferase LpcC (2.4.-.-)	COG0438	M
RCA23_c07210	hypothetical protein		
RCA23_c07220	undecaprenyl-phosphate alpha-N- acetylglucosaminyl 1-phosphate transferase (	COG0472	M
RCA23_c07230	hypothetical protein, transmembrane		
RCA23_c07240	hypothetical protein, transmembrane		
RCA23_c07250	transposase, IS4 family protein		
RCA23_c07260	putative transposase	COG3039	L
RCA23_c07270	hypothetical protein, transmembrane		
RCA23_c07280	hypothetical protein, transmembrane		
RCA23_c07290	transposase	COG3316	L
RCA23_c07300	GlgA:glycogen synthase GlgA (2.4.1.21)	COG0297	G
RCA23_c07310	GlgX:glycogen debranching enzyme GlgX (3.2.1.-)	COG1523	G
RCA23_c07320	PgmcphosphoglucomutasePgm (5.4.2.2)	COG0033	G
RCA23_c07330	putative alpha-glucosidase AgdA (3.2.1.20)	COG0366	G
RCA23_c07340	transposase	COG3316	L
RCA23_c07350	YtnL:uncharacterized hydrolase YtnL	COG1473	R
RCA23_c07360	GsiB:glutathione-binding protein GsiB	COG0747	E
RCA23_c07370	GsiC:glutathione transport system permease protein GsiC	COG0601	E
RCA23_c07380	dipeptide transport system permease protein	COG1173	E
RCA23_c07390	GsiA2:glutathione import ATP-binding protein GsiA (3.6.3.-)	COG4172	R
RCA23_c07400	peptidase family S58	COG3191	E
RCA23_c07410	AldA:aldehyde dehydrogenase AldA (1.2.1.3)	COG1012	C
RCA23_c07420	FabG2:3-oxoacyl-(acyl-carrier-protein) reductase FabG (1.1.1.100)	COG1028	I
RCA23_c07430	amidase (3.5.1.4)	COG0154	J
RCA23_c07440	MFS-type transporter	COG2807	P
RCA23_c07450	peptidase M20D amidohydrolase	COG1473	R
RCA23_c07460	transposase	COG3316	L
RCA23_c07470	integrase	COG2801	L
RCA23_c07480	transposase		
RCA23_c07490	hypothetical protein, DUF3764		
RCA23_c07500	hypothetical protein		
RCA23_c07510	hypothetical protein, beta-lactam-insensitive peptidoglycan transpeptidase YkuD	COG1376	S
RCA23_c07520	hypothetical protein		
RCA23_c07530	ABC transporter, ATP-binding protein, SbmA/BacA- like family	COG1133	I
RCA23_c07540	hypothetical protein		
RCA23_c07550	hypothetical protein		
RCA23_c07560	integrase	COG2801	L
RCA23_c07570	hypothetical protein		
RCA23_c07580	hypothetical protein		
RCA23_c07590	FlcC:flagellin FlcC	COG1344	N
RCA23_c07600	RpoN:RNA polymerase sigma-54	COG1508	K
RCA23_c07610	hypothetical protein, cyclic nucleotide-binding- like		
RCA23_c07620	hypothetical protein	COG0664	T
RCA23_c07630	hypothetical protein		
RCA23_c07640	hypothetical protein		
RCA23_c07650	hypothetical protein		
RCA23_c07660	FlhB:flagellar biosynthesis protein FlhB	COG1377	N
RCA23_c07670	FlrR:flagellar biosynthetic protein FlrR	COG1684	N
RCA23_c07680	FlcQ:flagellar biosynthetic protein FlcQ	COG1987	N
RCA23_c07690	FlcP:flagellar biosynthetic protein FlcP	COG1338	N
RCA23_c07700	FlbN:flagellar motor switch protein FlbN	COG1886	N
RCA23_c07710	FlbM:flagellar motor switch proteins FlbM	COG1868	N
RCA23_c07720	FlbL1:protein FlbL	COG1580	N
RCA23_c07730	putative flagellar hook-length control protein FlbK	COG3144	N
RCA23_c07740	putative flagellar export protein FlbJ		
RCA23_c07750	FlbI:flagellar protein export ATPase FlbI (3.6.3.14)	COG1157	N
RCA23_c07760	putative flagellar assembly protein FlbH		
RCA23_c07770	FlbG:flagellar motor switch protein G	COG1536	N
RCA23_c07780	FlbF:flagellar M-ring protein FlbF	COG1766	N
RCA23_c07790	FlbE:flagellar hook-basal body complex subunit FlbE	COG1677	N
RCA23_c07800	FlbD:transcriptional regulatory protein FlbD	COG2204	T
RCA23_c07810	FlbL2:protein FlbL	COG1580	N
RCA23_c07820	hypothetical protein		
RCA23_c07830	FlbS:flagellar protein FlbS	COG1516	N
RCA23_c07840	hypothetical protein		
RCA23_c07850	hypothetical protein		
RCA23_c07860	FlgG1:flagellar basal-body rod protein FlgG	COG4786	N
RCA23_c07870	Ca- channel, voltage-gated family protein (3.6.1.-)	COG0038	P
RCA23_c07880	hypothetical protein, lysozym-like	COG0741	M
RCA23_c07890	FlgL:flagellar hook-associated protein FlgL	COG1344	N
RCA23_c07900	FlgK:flagellar hook-associated protein FlgK	COG1256	N
RCA23_c07910	FlgJ:flagellar rod assembly protein/muramidase FlgJ	COG3951	M
RCA23_c07920	FlgI:flagellar P-ring protein FlgI	COG1706	N
RCA23_c07930	FlgH:flagellar L-ring protein FlgH	COG2063	N
RCA23_c07940	FlgG2:flagellar basal-body rod protein FlgG	COG4786	N
RCA23_c07950	putative flagellar basal body rod protein FlgF	COG4786	N
RCA23_c07960	FlgE:flagellar hook protein FlgE	COG1749	N
RCA23_c07970	FlgD:flagellar basal body rod modification protein FlgD	COG1843	N
RCA23_c07980	FlgC:flagellar basal-body rod protein FlgC	COG1558	N
RCA23_c07990	FlgB:flagellar basal-body rod protein FlgB	COG1815	N
RCA23_c08000	hypothetical protein		
RCA23_c08010	hypothetical protein		
RCA23_c08020	FlaR:RNA polymerase, sigma factor for flagellar operon FlaA	COG1191	K
RCA23_c08030	putative flagellar biosynthesis protein FlbG	COG0455	D
RCA23_c08040	FlhF:flagellar biosynthesis protein FlhF	COG1419	N
RCA23_c08050	FlhA:flagellar biosynthesis protein FlhA	COG1298	N

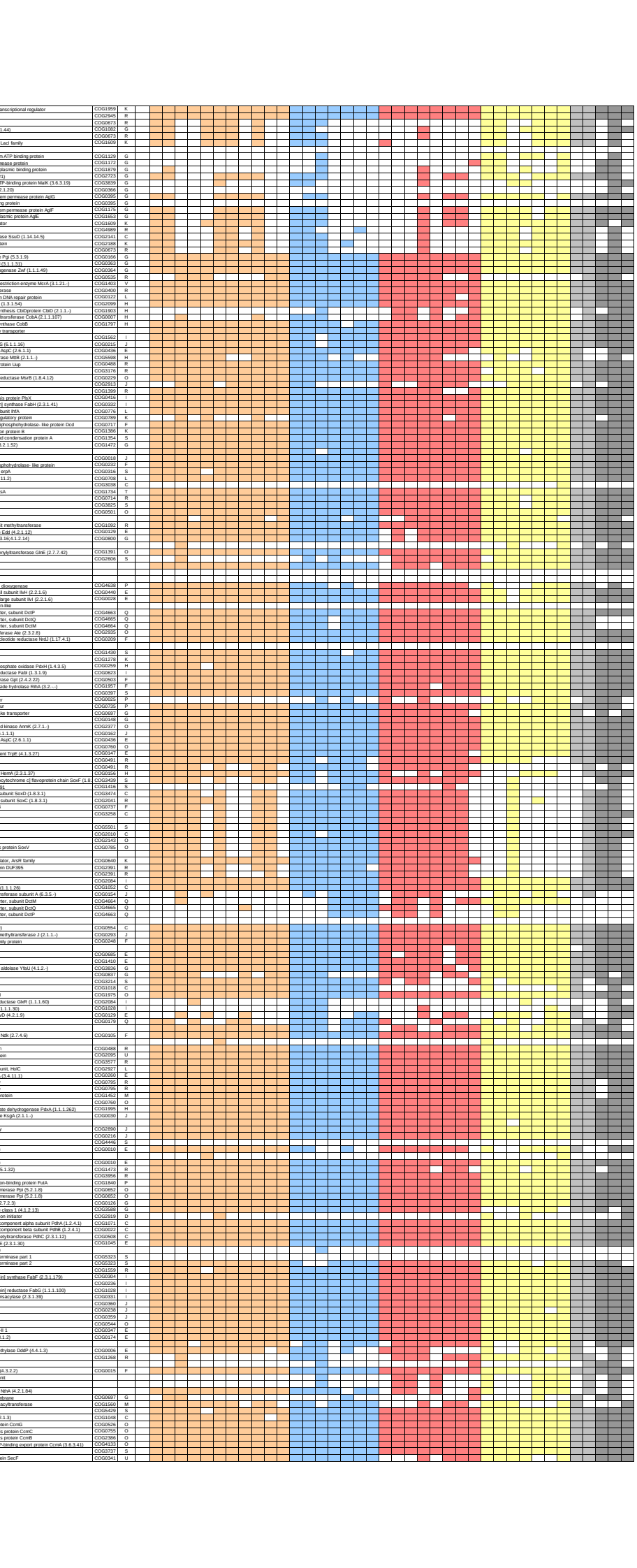
RCA23_c08060	hypothetical membrane lipoprotein, DUF400		GI 3
RCA23_c08070	hypothetical protein		GI 3
RCA23_c08080	FlgA:flagellar basal body P-ring biosynthesis protein FlgA	COG1261	N
RCA23_c08090	putative negative regulator of flagellin synthesis FlgM		GI 3
RCA23_c08100	hypothetical protein		GI 3
RCA23_c08110	hypothetical protein, HCP-like	COG0790	R
RCA23_c08120	hypothetical protein		GI 3
RCA23_c08130	sigma54 specific transcriptional regulator, Fis family	COG2204	T
RCA23_c08140	FlbD:flagellar hook-associated protein FlbD	COG1345	N
RCA23_c08150	MotB:chemotaxis protein MotB	COG1360	N
RCA23_c08160	MotA:chemotaxis protein MotA	COG1291	N
RCA23_c08170	hypothetical protein, DUF1566		GI 3
RCA23_c08180	putative transmembrane protein, DUF6		GI 3
RCA23_c08190	putative polyketide hydroxylase SchC (1.14.13.-)	COG0654	H
RCA23_c08200	aldehyde dehydrogenase (1.2.1.3)	COG1012	C
RCA23_c08210	AcmsD:2-amino-3-carboxymuconate-6-semialdehyde decarboxylase (4.1.1.45)	COG2159	R
RCA23_c08220	transcriptional regulator, IclR family	COG1414	K
RCA23_c08230	TRAP transporter, 4TM/12TM fusion protein	COG4666	R
RCA23_c08240	TRAP transporter solute receptor, TAXI family	COG2358	R
RCA23_c08250	thiamine pyrophosphate enzyme-like TPP-binding	COG0028	E
RCA23_c08260	hypothetical protein	COG2268	S
RCA23_c08270	short chain dehydrogenase (1.1.1.-)	COG1028	I
RCA23_c08280	putative aldehyde dehydrogenase yfmT (1.2.1.3)	COG1012	C
RCA23_c08290	branched-chain amino acid ABC transporter, ATP- binding protein	COG0410	E
RCA23_c08300	branched-chain amino acid ABC transporter, ATP- binding protein	COG0411	E
RCA23_c08310	putative transporter, permease protein	COG4177	E
RCA23_c08320	putative transporter, permease protein	COG0559	E
RCA23_c08330	putative transporter, periplasmic binding protein	COG0683	E
RCA23_c08340	hypothetical protein, PspF protein-like	COG2828	S
RCA23_c08350	4-carboxy-4-hydroxy-2-oxoadipate aldolase/oxaloacetate decarboxylase (4.1.1.-	COG0684	H
RCA23_c08360	putative N-acetylglucosaminyl- phosphatidylinositol de-N-acetylase (3.5.1.89)	COG2120	S
RCA23_c08370	hypothetical protein		
RCA23_c08380	transcriptional regulator	COG1802	K
RCA23_c08390	GcvT1:aminomethyltransferase GcvT (2.1.2.10)	COG0404	E
RCA23_c08400	DctP3:TRAP dicarboxylate transporter, subunit DctP	COG1638	G
RCA23_c08410	putative TRAP transporter, DctQ component	COG3090	G
RCA23_c08420	DctM3:TRAP dicarboxylate transporter, subunit DctM	COG1593	G
RCA23_c08430	XylE:metapyrocatechase XylE (1.13.11.2)	COG2514	R
RCA23_c08440	MFS-type transporter	COG2814	G
RCA23_c08450	hypothetical protein, cytochrome c		
RCA23_c08460	hypothetical protein, copper resistance protein C	COG2372	R
RCA23_c08470	hypothetical protein, copper resistance protein D	COG1276	P
RCA23_c08480	hypothetical protein	COG3613	F
RCA23_c08490	hypothetical protein		
RCA23_c08500	hypothetical protein		
RCA23_c08510	fumarate reductase flavoprotein subunit (1.3.99.1)	COG1053	C
RCA23_c08520	PrpB:methylisocitrate lyase PrpB (4.1.3.30)	COG2513	G
RCA23_c08530	putative isochorismatase family protein	COG1335	Q
RCA23_c08540	HyuA1:hydantoin utilization protein A (3.5.2.-)	COG0145	E
RCA23_c08550	HyuB1:hydantoin utilization protein B (3.5.2.14)	COG0146	E
RCA23_c08560	hypothetical protein	COG1942	R
RCA23_c08570	HTH-type transcriptional regulator, GntR family	COG2188	K
RCA23_c08580	LeuC2:3-isopropylmalate dehydratase large subunit LeuC (4.2.1.33)	COG0065	E
RCA23_c08590	LeuD2:3-isopropylmalate dehydratase small subunit LeuD (4.2.1.33)	COG0066	E
RCA23_c08600	DctP4:TRAP dicarboxylate transporter, subunit DctP	COG1638	G
RCA23_c08610	putative TRAP transporter, DctQ component	COG3090	G
RCA23_c08620	DctM4:TRAP dicarboxylate transporter, subunit DctM	COG1593	G
RCA23_c08630	putative glutamate synthase [NADPH] small chain	COG0493	E
RCA23_c08640	hypothetical protein, dihydroorotate dehydrogenase	COG0167	F
RCA23_c08650	putative HTH-type transcriptional regulator	COG1309	K
RCA23_c08660	AmaB:N-carbamoyl-L-amino acid hydrolase AmaB (3.5.1.87)	COG0624	E
RCA23_c08670	DhtD:hydantoinase/dihydropyrimidinase Dht (3.5.2.2)	COG0044	F
RCA23_c08680	ABC transporter ATP-binding protein	COG1116	P
RCA23_c08690	putative ABC transporter permease protein	COG0600	P
RCA23_c08700	putative ABC transporter permease protein	COG0600	P
RCA23_c08710	putative thiamine biosynthesis protein	COG0715	P
RCA23_c08720	putative integral membrane protein DUF6	COG0697	G
RCA23_c08730	hypothetical protein DUF6	COG0697	G
RCA23_c08740	PhoR:alkaline phosphatase synthesis sensor protein PhoR (2.7.13.3)	COG5002	T
RCA23_c08750	putative phosphate binding protein PstS	COG0226	P
RCA23_c08760	putative phosphate transport system permease protein PstC	COG0573	P
RCA23_c08770	putative phosphate transport system permease protein PstA	COG0581	P
RCA23_c08780	PstB:phosphate import ATP-binding protein PstB (3.6.3.27)	COG1117	P
RCA23_c08790	PhoU:phosphate transport system regulatory protein PhoU	COG0704	P
RCA23_c08800	PhoB:phosphate regulon transcriptional protein PhoB	COG0745	T
RCA23_c08810	putative hippurate hydrolase protein (3.5.1.32)	COG1473	R
RCA23_c08820	UreD:urease accessory protein UreD	COG0829	O
RCA23_c08830	UreA:urease gamma subunit UreA (3.5.1.5)	COG0831	E
RCA23_c08840	UreB:urease beta subunit UreB (3.5.1.5)	COG0832	E
RCA23_c08850	UreC:urease alpha subunit UreC (3.5.1.5)	COG0804	E
RCA23_c08860	UreE:urease accessory protein UreE	COG2371	O
RCA23_c08870	UreF:urease accessory protein UreF	COG0830	O
RCA23_c08880	UreG:urease accessory protein UreG	COG0378	O
RCA23_c08890	integrase	COG2801	L
RCA23_c08900	hypothetical protein	COG4585	T
RCA23_c08910	AlkJ1:glucose-methanol-choline oxidoreductase AlkJ (1.1.99.-)	COG2303	E
RCA23_c08920	hypothetical protein, YaeQ family protein	COG4681	S
RCA23_c08930	hypothetical protein, DUF6 transmembrane protein	COG0697	G
RCA23_c08940	UgdDUDP-glucose 6-dehydrogenase Ugd (1.1.1.22)	COG1004	M
RCA23_c08950	WaaA2:3-deoxy-D-manno-octulosonic-acid transferase WaaA (2.4.--)	COG1519	M
RCA23_c08960	WecB:UDP-N-acetylglucosamine 2-epimerase WecB (5.1.3.14)	COG0381	M
RCA23_c08970	putative N-acetylneuramic acid synthase	COG2089	M
RCA23_c08980	hypothetical protein		
RCA23_c08990	hypothetical protein	COG1651	O
RCA23_c09000	BetC:choline-sulfatase BetC (3.1.6.6)	COG3119	P
RCA23_c09010	permease	COG2233	F
RCA23_c09020	hypothetical protein		
RCA23_c09030	membrane dipeptidase (3.4.13.19)	COG2355	E
RCA23_c09040	hypothetical protein		
RCA23_c09050	hypothetical protein		
RCA23_c09060	TruA:tRNA pseudouridine synthase A (5.4.99.12)	COG0101	J
RCA23_c09070	YcjX-like protein	COG3106	R
RCA23_c09080	hypothetical protein, acetyltransferase-like	COG0456	R
RCA23_c09090	hypothetical protein	COG3768	S
RCA23_c09100	IleS:isoleucyl-tRNA synthase IleS (6.1.1.5)	COG0060	J
RCA23_c09110	putative integral membrane protein DUF6		
RCA23_c09120	Pcs:phosphatidylcholine synthase Pcs (2.7.8.24)	COG1183	I
RCA23_c09130	putative tyrosine recombinase xerC	COG4974	L
RCA23_c09140	hypothetical protein	COG3159	S
RCA23_c09150	transaldolase (2.2.1.2)	COG0176	G
RCA23_c09160	PriA:primosomal protein N' (3.6.1.-)	COG1198	L
RCA23_c09170	McmA1:methylmalonyl-CoA mutase McmA (5.4.99.2)	COG1884	I
RCA23_c09180	PlsB:glycerol-3-phosphate acyltransferase PlsB (2.3.1.15)	COG2937	I
RCA23_c09190	Ccr:crotonyl-CoA reductase Ccr	COG0604	C
RCA23_c09200	putative ATPase	COG0507	L
RCA23_c09210	MtbB3:trimethylamine methyltransferase MtbB (2.1.1.-)	COG5598	H
RCA23_c09220	hypothetical protein DUF1052	COG5321	S
RCA23_c09240	hypothetical protein, DUF411	COG3019	R
RCA23_c09250	hypothetical protein		
RCA23_c09260	hypothetical protein		
RCA23_c09270	hypothetical protein	COG4642	S
RCA23_c09280	hypothetical protein	COG3904	S
RCA23_c09290	putative DNA-binding protein, transposase-like	COG3415	L
RCA23_c09300	HTH-type transcriptional regulator, LysR family	COG0583	K
RCA23_c09310	hypothetical protein		
RCA23_c09320	hypothetical protein, hydrolase-like	COG0627	R
RCA23_c09330	putative integrase	COG2801	L
RCA23_c09340	putative transposase		
RCA23_c09350	hypothetical protein, ornithine cyclodeaminase- like	COG2423	E
RCA23_c09360	LugB-like protein	COG1346	M
RCA23_c09370	hypothetical protein	COG1380	R
RCA23_c09380	putative branched-chain-amino-acid aminotransferase IlvE (2.6.1.42)	COG0115	E
RCA23_c09390	GarR:2-hydroxy-3-oxopropionate reductase GarR (1.1.1.60)	COG2084	I
RCA23_c09400	Bcr:bicyclomycin resistance protein Bcr	COG2814	G
RCA23_c09410	hypothetical protein		
RCA23_c09420	hypothetical protein, photolyase	COG3046	R
RCA23_c09430	DNA photolyase, FAD-binding/cryptochrome	COG0415	L
RCA23_c09440	CoxS1:carbon monoxide dehydrogenase small chain CoxS (1.2.99.2)	COG2080	C
RCA23_c09450	CoxL1:carbon monoxide dehydrogenase large chain CoxL (1.2.99.2)	COG1529	C
RCA23_c09460	CoxM1:carbon monoxide dehydrogenase medium chain CoxM (1.2.99.2)	COG1319	C
RCA23_c09470	putative chaperone coxO, AAA ATPase	COG0714	R
RCA23_c09480	CoxE-like protein	COG3552	R
RCA23_c09490	IolB1:5-deoxy-glucuronate isomerase IolB (5.3.1.-)	COG3718	G
RCA23_c09500	branched-chain amino acid transport protein, AitD-like	COG4392	S
RCA23_c09510	branched-chain amino acid transport protein, AitC-like	COG1296	E
RCA23_c09520	alpha-IPM synthase/homocitrate synthase	COG0119	E
RCA23_c09530	cytochrome P450	COG2124	Q
RCA23_c09540	DctP5:TRAP dicarboxylate transporter, subunit DctP	COG1638	G
RCA23_c09550	DctQ3:TRAP dicarboxylate transporter, subunit DctQ	COG3090	G
RCA23_c09560	DctM5:TRAP dicarboxylate transporter, subunit DctM	COG1593	G
RCA23_c09570	putative citrate transporter	COG4471	P
RCA23_c09580	TpiA:triosephosphate isomerase TpiA (5.3.1.1)	COG0149	G
RCA23_c09590	putative regulator protein of competence- specific genes TloX	COG3070	K
RCA23_c09600	SufA: iron-sulfur cluster assembly protein	COG0316	S
RCA23_c09610	hypothetical protein DUF59	COG0151	R
RCA23_c09620	Tgt:queuine tRNA-ribosyltransferase Tgt (2.4.2.29)	COG0343	J
RCA23_c09630	hypothetical protein		
RCA23_c09640	LonA:ATP-dependent protease La (3.4.21.53)	COG0466	O
RCA23_c09650	putative phosphoglycerate mutase family protein	COG0406	G
RCA23_c09670	PcmL:protein-L-isoaspartate O-methyltransferase PcmL (2.1.1.77)	COG2518	O
RCA23_c09680	outer membrane efflux protein	COG1538	M
RCA23_c09690	hypothetical protein		
RCA23_c09700	CobQ:cobyric acid synthase CobQ	COG1492	H
RCA23_c09710	hypothetical protein		
RCA23_c09720	EfpTranslation elongation factor P	COG0231	J
RCA23_c09730	YgfZ:hypothetical protein tRNA modifying protein YgfZ	COG0354	R
RCA23_c09740	putative glycosyltransferase, family 2	COG0463	M
RCA23_c09750	MsbA:lipid A export ATP-binding/permease protein MsbA (3.6.3.-)	COG1132	V
RCA23_c09760	SgaA1:serine--glycolylate aminotransferase SgaA (2.6.1.45)	COG0075	E
RCA23_c09770	HisC1:histidinol-phosphate aminotransferase HisC (2.6.1.9)	COG0079	E
RCA23_c09780	ValS:valyl-tRNA synthase ValS (6.1.1.9)	COG0525	J
RCA23_c09790	hypothetical protein, metal-dependent phosphohydrolase	COG4341	R
RCA23_c09800	putative phytanoyl-CoA dioxygenase family protein	COG5285	Q
RCA23_c09810	Hydvdenum-containing hydroxylase	COG1529	C
RCA23_c09820	hypothetical protein DUF2235	COG3673	S
RCA23_c09830	MetF:5,10-methylenetetrahydrofolate reductase MetF (1.5.1.20)	COG0685	E
RCA23_c09840	MetR:HTH-type transcriptional regulator MetR	COG0583	K
RCA23_c09850	SuhB:inositol-1-monophosphatase SuhB (3.1.3.25)	COG0483	G
RCA23_c09860	hypothetical protein	COG3063	N
RCA23_c09880	transcriptional regulator, HdfR family	COG1733	K
RCA23_c09890	hypothetical protein, DUF3764		
RCA23_c09900	hypothetical protein		
RCA23_c09910	hypothetical protein, DsrE/IF-like	COG1553	P
RCA23_c09920	Gpo:glutathione peroxidase Gpo (1.11.1.9)	COG0386	O
RCA23_c09930	putative ion channel		
RCA23_c09950	hypothetical protein		
RCA23_c09940	RluD:ribosomal large subunit pseudouridine synthase D (5.4.99.-)	COG0564	J
RCA23_c09960	RpoH1:RNA polymerase sigma-32 factor RpoH	COG0568	K
RCA23_c09970	putative oxidoreductase	COG0673	R
RCA23_c09980	YibG:oligoendopeptidase F (3.4.24.-)	COG1164	E
RCA23_c09990	RhmA:2-keto-3-deoxy-L-rhamnonate aldolase RhmA (4.1.2.-)	COG3836	G
RCA23_c10000	hypothetical protein, lysophospholipase L2	COG2267	I
RCA23_c10010	putative sterol-binding protein	COG3255	I
RCA23_c10020	hypothetical protein		
RCA23_c10030	RhlB:ATP-dependent RNA helicase RhlB	COG4581	L
RCA23_c10040	putative heat shock protein	COG1188	J
RCA23_c10050	FdxA:ferredoxin FdxA	COG1146	C
RCA23_c10060	putative transcriptional regulator, CarD family	COG1329	K
RCA23_c10070	CobS1:cobalamin-5-phosphate synthase CobS (2.-.-.-)	COG0368	H
RCA23_c10080	CobT1:nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	COG0236	H
RCA23_c10090	hypothetical protein		
RCA23_c10100	glyoxalase/bleomycin resistance protein	COG3565	R

RCA23_c10110	hypothetical protein		
RCA23_c10120	BetA1:choline dehydrogenase BetA (1.1.99.1)	COG2303	E
RCA23_c10140	RlmB:23S rRNA (guanosine-2'-O-)-methyltransferase RlmB (2.1.1.-)	COG0566	J
RCA23_c10150	HisE:phosphoribosyl-ATP pyrophosphatase HisE (3.6.1.31)	COG0140	E
RCA23_c10160	HisF:imidazole glycerol phosphate synthase subunit HisF (4.1.3.-)	COG0107	E
RCA23_c10170	HisA:1-(5-phosphoribosyl)-5-[(5- phosphoribosylamino)methylideneamino] imidaz	COG0106	E
RCA23_c10180	HisH:imidazole glycerol phosphate synthase, glutamine amidotransferase subunit	COG0118	E
RCA23_c10190	HisB:imidazoleglycerol-phosphate dehydratase HisB (4.2.1.19)	COG0131	E
RCA23_c10210	hypothetical protein, calcineurin-like phosphoesterase-like	COG1409	R
RCA23_c10220	Pyc:pyruvate carboxylase Pyc (6.4.1.1)	COG1038	C
RCA23_c10230	LldD11:L-lactate dehydrogenase lldD (1.1.2.3)	COG1304	C
RCA23_c10240	putative DNA helicase II (3.6.4.12)	COG0210	L
RCA23_c10250	PuuB1:gamma-glutamylputrescine oxidoreductase PuuB (1.4.3.-)	COG0665	E
RCA23_c10260	putative cysteine/O-acetylserine efflux protein	COG1280	E
RCA23_c10270	hypothetical protein		
RCA23_c10280	putative protein Mrp	COG0489	D
RCA23_c10290	hypothetical protein		
RCA23_c10300	hypothetical protein, MraZ	COG2001	S
RCA23_c10310	MraW:S-adenosyl-L-methionine-dependent methyltransferase MraW (2.1.1.-)	COG0275	M
RCA23_c10320	hypothetical protein	COG5462	S
RCA23_c10330	peptidoglycan synthase FtsI (2.4.1.129)	COG0768	M
RCA23_c10340	MurE:UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2, 6- diaminopimelate ligase	COG0769	M
RCA23_c10350	putative UDP-N-acetylmuramoyl-tripeptide--D- alanyl-D-alanine ligase MurF (6.3	COG0770	M
RCA23_c10360	MraY:phospho-N-acetylmuramoyl-pentapeptide- transferase MraY (2.7.8.13)	COG0472	M
RCA23_c10370	MurD:UDP-N-acetylmuramoylalanine--D-glutamate ligase MurD (6.3.2.9)	COG0771	M
RCA23_c10380	putative glycosyltransferase, sugar binding region	COG2774	M
RCA23_c10390	putative galactoside 2-alpha-L- fucosyltransferase 1		
RCA23_c10400	hypothetical protein		
RCA23_c10410	hypothetical protein	COG3306	M
RCA23_c10420	hypothetical protein HI0933	COG2081	R
RCA23_c10430	FtsW:cell division protein FtsW	COG0772	D
RCA23_c10440	MurG:UDP-N-acetylglucosamine--N-acetylmuramyl- (pentapeptide) pyrophospho	COG0707	M
RCA23_c10450	MurC:UDP-N-acetylmuramate--L-alanine ligase MurC (6.3.2.8)	COG0773	M
RCA23_c10460	permease of the drug/metabolite transporter superfamily	COG0697	G
RCA23_c10470	MurB:UDP-N-acetylenolpyruvylglucosamine reductase MurB (1.1.1.158)	COG0812	M
RCA23_c10480	DdlD:alanine--D-alanine ligase Ddl (6.3.2.4)	COG1181	M
RCA23_c10490	putative cell division protein FtsQ		
RCA23_c10500	FtsA:cell division protein FtsA	COG0849	D
RCA23_c10510	FtsZ:cell division protein FtsZ	COG0206	D
RCA23_c10520	LpxC:UDP-3-O-(3-hydroxymyristoyl) N-acetylglucosamine deacetylase LpxC (3.5	COG0774	M
RCA23_c10530	outer membrane assembly lipoprotein	COG4105	R
RCA23_c10540	RecN:DNA repair protein RecN	COG0497	L
RCA23_c10550	hypothetical protein DUF427	COG2343	S
RCA23_c10560	putative Xaa-Pro aminopeptidase	COG2006	E
RCA23_c10570	CobT2:aerobic cobaltochelatase subunit CobT (6.6.1.2)	COG4547	H
RCA23_c10580	CobS2:aerobic cobaltochelatase subunit CobS (6.6.1.2)	COG0714	R
RCA23_c10590	hypothetical protein, DnaJ	COG0484	O
RCA23_c10600	putative stress-induced morphogenes, BolA type	COG0271	T
RCA23_c10610	GatB:aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit GatB (6.3.5.-)	COG0064	J
RCA23_c10620	PepN:aminopeptidase N (3.4.11.2)	COG0308	E
RCA23_c10630	GlcB:malate synthase GlcB (2.3.3.9)	COG2225	C
RCA23_c10640	hypothetical protein DUF336	COG3193	R
RCA23_c10650	hypothetical protein		
RCA23_c10660	PuuD:gamma-glutamyl-gamma-aminobutyrate hydrolase PuuD (3.5.1.94)	COG2071	R
RCA23_c10670	putative D-beta-hydroxybutyrate dehydrogenase	COG1028	I
RCA23_c10680	PntA:NAD(P) transhydrogenase alpha subunit PntA (1.6.1.2)	COG1288	C
RCA23_c10690	PntB:NAD(P) transhydrogenase beta subunit PntB (1.6.1.2)	COG1282	C
RCA23_c10700	hypothetical protein	COG4949	S
RCA23_c10710	putative acetylornithine deacetylase ArgE	COG0624	E
RCA23_c10720	MoaA1:molybdenum cofactor biosynthesis protein MoaA	COG2896	H
RCA23_c10730	AcsA2:acetyl-coenzyme A synthase AcsA (6.2.1.1)	COG0365	I
RCA23_c10740	hypothetical protein	COG4321	R
RCA23_c10750	hypothetical protein		
RCA23_c10760	FumC:fumarate hydratase class II (4.2.1.2)	COG0114	C
RCA23_c10770	hypothetical protein	COG3814	S
RCA23_c10780	putative chromate transport protein	COG2059	P
RCA23_c10790	hydantoinase / oxoprolinase family protein	COG0145	E
RCA23_c10800	hypothetical protein		
RCA23_c10810	putative quinone oxidoreductase yhdH (1.6.5.-)	COG0604	C
RCA23_c10820	SufS1:cysteine desulfurase SufS (2.8.1.7;4.4.1.16)	COG0520	E
RCA23_c10830	PnrB1:deoxyribodipyrimidine photo-lyase PnrB (4.1.99.3)	COG0415	L
RCA23_c10840	CfaJ:cyclopropane-fatty-acyl-phospholipid synthase CfaJ (2.1.1.79)	COG2230	M
RCA23_c10850	NudF:ADP-ribose pyrophosphatase NudF (3.6.1.13)	COG0494	L
RCA23_c10860	CysK1:cysteine synthase CysK (2.5.1.47)	COG0031	E
RCA23_c10870	MscS:mechanosensitive ion channel protein MscS	COG3264	M
RCA23_c10890	putative phage integrase	COG4974	L
RCA23_c10900	hypothetical protein		
RCA23_c10910	hypothetical protein, tetratricopeptide domain TPR-1	COG0457	R
RCA23_c10920	hypothetical protein, resolvase-like	COG1961	L
RCA23_c10930	hypothetical protein, DUF2924		
RCA23_c10940	putative TRAP transporter solute receptor	COG2358	R
RCA23_c10950	TRAP transporter, 4TM/12TM fusion protein	COG4666	R
RCA23_c10960	putative sulfatase YidJ (3.6.1.-)	COG3119	P
RCA23_c10970	arylsulfatase (3.1.6.1)	COG1234	R
RCA23_c10980	siderophore interactin protein, vibriobactin utilization protein-like	COG2375	P
RCA23_c10990	hypothetical protein, metallo-beta-lactamase	COG2015	Q
RCA23_c11000	DctP6:TRAP dicarboxylate transporter, subunit DctP	COG1638	G
RCA23_c11010	glutathione S-transferase (2.5.1.18)	COG0625	O
RCA23_c11020	DctQ4:TRAP dicarboxylate transporter, subunit DctQ	COG3090	G
RCA23_c11030	DctM6:TRAP dicarboxylate transporter, subunit DctM	COG1593	G
RCA23_c11040	hypothetical protein, DUF6 transmembrane protein	COG0697	G
RCA23_c11050	ferric reductase like transmembrane component family		
RCA23_c11060	hypothetical protein		
RCA23_c11070	hypothetical protein		
RCA23_c11080	sulfatase family protein	COG3119	P
RCA23_c11090	short-chain dehydrogenase/reductase SDR	COG1028	I
RCA23_c11100	MaiA:maleylacetoacetate isomerase MaiA (5.2.1.2)	COG0625	O
RCA23_c11110	salicylaldehyde dehydrogenase (1.2.1.65)	COG1012	C
RCA23_c11120	transcriptional regulator, GntR family	COG1802	K
RCA23_c11130	transposase	COG3316	L
RCA23_c11140	putative phage integrase	COG4974	L
RCA23_c11150	hypothetical protein, alginate lyase-lyase		
RCA23_c11160	HTH-type transcriptional regulator, GntR family	COG1802	K
RCA23_c11170	branched-chain amino acid ABC transporter, periplasmic substrate-binding prote	COG0683	E
RCA23_c11180	branched-chain amino acid ABC transporter, permease protein	COG0559	E
RCA23_c11190	branched-chain amino acid ABC transporter, permease protein	COG4177	E
RCA23_c11200	branched-chain amino acid ABC transporter, ATP- binding protein	COG0411	E
RCA23_c11210	branched-chain amino acid ABC transporter, ATP- binding protein	COG0410	E
RCA23_c11220	HyuE:hydantoin racemase HyuE (5.1.99.5)	COG4126	E
RCA23_c11230	transposase	COG3316	L
RCA23_c11240	GlnQ:glutamine transport ATP-binding protein GlnQ	COG1126	E
RCA23_c11250	putative inner membrane amino-acid ABC transporter permease protein	COG0765	E
RCA23_c11260	transposase	COG3316	L
RCA23_c11270	CoxC:transcriptional regulator CoxC	COG1300	T
RCA23_c11280	CoxM2:carbon monoxide dehydrogenase medium chain CoxM (1.2.99.2)	COG1319	C
RCA23_c11290	CoxS2:carbon monoxide dehydrogenase small chain CoxS (1.2.99.2)	COG2080	C
RCA23_c11300	CoxL2:carbon monoxide dehydrogenase large chain CoxL (1.2.99.2)	COG1529	C
RCA23_c11310	CoxD:AAA+ ATPase chaperone CoxD	COG0714	R
RCA23_c11320	CoxE:carbon monoxide dehydrogenase accessory protein CoxE	COG3552	R
RCA23_c11330	CoxF:carbon monoxide dehydrogenase accessory protein CoxF	COG1975	O
RCA23_c11340	hypothetical protein	COG2068	R
RCA23_c11350	CoxG:carbon monoxide dehydrogenase protein CoxG	COG3427	S
RCA23_c11360	CoxI:carbon monoxide dehydrogenase accessory protein CoxI	COG1975	O
RCA23_c11370	transposase	COG3316	L
RCA23_c11380	dienelactone hydrolase (3.1.1.45)	COG0412	Q
RCA23_c11390	aldo/keto reductase	COG0667	C
RCA23_c11400	MdlA:mandelate racemase MdlA (5.1.2.2)	COG4948	M
RCA23_c11410	hypothetical protein DUF1498	COG3822	R
RCA23_c11420	two-component system, sensor histidine kinase protein	COG0642	T
RCA23_c11430	two-component system, response regulator protein	COG0745	T
RCA23_c11440	hypothetical protein	COG3181	S
RCA23_c11450	putative tripartite tricarboxylate transporter (TTT) protein TctA	COG3333	S
RCA23_c11460	hypothetical protein	COG3328	S
RCA23_c11470	D-isomer specific 2-hydroxyacid dehydrogenase (1.1.1.95)	COG0111	H
RCA23_c11480	putative ammonia monooxygenase	COG3180	R
RCA23_c11490	transcriptional regulator	COG1802	K
RCA23_c11500	fumarate reductase flavoprotein subunit FccA (1.3.99.1)	COG1053	C
RCA23_c11510	AspC2:aspartate aminotransferase AspC (2.6.1.1)	COG0436	E
RCA23_c11520	hypothetical protein		
RCA23_c11530	GlpD1:aerobic glycerol-3-phosphate dehydrogenase GlpD (1.1.99.5)	COG0578	C
RCA23_c11540	GlpD2:aerobic glycerol-3-phosphate dehydrogenase GlpD (1.1.99.5)	COG0578	C
RCA23_c11550	hypothetical protein	COG1192	D
RCA23_c11560	CheW:chemotaxis protein CheW	COG0835	N
RCA23_c11570	Tar:methyl-accepting chemotaxis protein II	COG0840	N
RCA23_c11580	ChpA:chemotaxis histidine kinase CheA (2.7.13.3)	COG0643	N
RCA23_c11590	response regulator	COG2114	T
RCA23_c11600	CheR:chemotaxis protein methyltransferase CheR (2.1.1.80)	COG1352	N
RCA23_c11610	CheB:chemotaxis response regulator protein-glutamate methylesterase CheB (3	COG2201	N
RCA23_c11620	metal-dependent hydrolase	COG1235	R
RCA23_c11630	integrase	COG2801	L
RCA23_c11640	methyltransferase, PldM family		
RCA23_c11650	hypothetical protein, sugar transferase-like		
RCA23_c11660	aldo/keto reductase	COG0667	C
RCA23_c11670	hypothetical protein		
RCA23_c11680	hypothetical protein	COG0790	R
RCA23_c11690	hypothetical protein	COG4430	S
RCA23_c11700	hypothetical protein	COG2755	E
RCA23_c11710	phytanoyl-CoA dioxygenase family protein	COG2265	Q
RCA23_c11720	putative bacterial extracellular solute binding protein, family 3	COG1791	S
RCA23_c11730	hypothetical protein		
RCA23_c11740	SOUL heme-binding protein		
RCA23_c11750	AslA:arylsulfatase precursor (3.1.6.1)	COG3119	P
RCA23_c11760	hypothetical protein DUF583		
RCA23_c11770	integrase	COG2801	L
RCA23_c11780	hypothetical protein	COG3616	E
RCA23_c11790	GlnA1:glutamine synthase GlnA (6.3.1.2)	COG0174	E
RCA23_c11800	putative HTH-type transcriptional regulator, RpiR family	COG1737	K
RCA23_c11810	N-formylglutamate amidohydrolase	COG3931	E
RCA23_c11820	putative isochorismatase family protein	COG1335	Q
RCA23_c11830	branched-chain amino acid ABC transporter, ATP- binding protein	COG0411	E
RCA23_c11840	branched-chain amino acid ABC transporter, periplasmic binding protein	COG0683	E
RCA23_c11850	branched-chain amino acid ABC transporter, ATP- binding protein	COG0410	E
RCA23_c11860	branched-chain amino acid ABC transporter, permease protein	COG0559	E
RCA23_c11870	branched-chain amino acid ABC transporter, permease protein	COG4177	E
RCA23_c11880	acetamidase/formamidase family protein	COG2421	C
RCA23_c11890	hypothetical protein	COG1028	I
RCA23_c11910	putative prophage integrase	COG0582	L
RCA23_c11920	hypothetical protein		
RCA23_c11930	hypothetical protein		
RCA23_c11940	putative AAA ATPase (2.7.7.-)	COG3598	L
RCA23_c11950	hypothetical protein		
RCA23_c11960	hypothetical protein		
RCA23_c11970	hypothetical protein		
RCA23_c11980	hypothetical protein		
RCA23_c11990	branched-chain amino acid ABC transporter, ATP- binding protein	COG0410	E
RCA23_c12000	branched-chain amino acid ABC transporter, ATP- binding protein	COG0411	E
RCA23_c12010	branched-chain amino acid ABC transporter, permease protein	COG4177	E
RCA23_c12020	branched-chain amino acid ABC transporter, permease protein	COG0559	E
RCA23_c12030	branched-chain amino acid ABC transporter, periplasmic binding protein	COG0683	E
RCA23_c12040	enoyl-CoA hydratase/carnithine racemase (4.2.1.-)	COG1024	I
RCA23_c12050	acetyl-CoA synthase-like protein	COG0318	I
RCA23_c12060	dehydrogenase iron-sulfur-binding subunit	COG2080	C
RCA23_c12070	dehydrogenase FAD-binding subunit	COG1319	C
RCA23_c12080	dehydrogenase molybdenum-binding subunit	COG1529	C
RCA23_c12090	putative HTH-type transcriptional regulator, AraC family	COG2207	K
RCA23_c12100	periplasmic binding protein-like	COG1879	G
RCA23_c12110	ROK family transcriptional repressor	COG1940	K
RCA23_c12120	xylose isomerase	COG1082	G
RCA23_c12130	sugar ABC transporter, periplasmic binding protein	COG1879	G
RCA23_c12140	putative oxidoreductase	COG0673	R
RCA23_c12150	sugar ABC transporter, ATP-binding protein	COG1129	G
RCA23_c12160	sugar ABC transporter, permease protein	COG1172	G

RCA23_c12170	hypothetical protein, monooxygenase-like	COG1359	S	GI 5
RCA23_c12180	hypothetical protein	COG1082	G	GI 5
RCA23_c12190	putative oxidoreductase	COG0673	R	GI 5
RCA23_c12200	peptidase M20D, amidohydrolase (3.5.1.32)	COG1473	R	GI 5
RCA23_c12210	X-Pro dipeptidase (3.4.13.9)	COG0006	E	GI 5
RCA23_c12220	hypothetical protein			GI 5
RCA23_c12230	hypothetical protein, transmembrane			GI 5
RCA23_c12240	hypothetical protein, DNA breaking rejoining enzymes family protein-like			GI 5
RCA23_c12250	hypothetical protein			GI 5
RCA23_c12260	hypothetical protein			GI 5
RCA23_c12270	hypothetical protein			GI 5
RCA23_c12280	type I restriction-modification system, M subunit (2.1.1.72)	COG0286	V	GI 5
RCA23_c12290	type I restriction-modification system, S subunit (3.1.21.3)	COG0732	V	GI 5
RCA23_c12300	type I restriction-modification system, R subunit (3.1.21.3)	COG0610	V	GI 5
RCA23_c12310	hypothetical protein	COG3012	S	GI 5
RCA23_c12320	hypothetical protein	COG2865	K	GI 5
RCA23_c12330	hypothetical protein			GI 5
RCA23_c12340	hypothetical protein, DNA helicase-like protein			GI 5
RCA23_c12350	hypothetical protein			GI 5
RCA23_c12360	integrase	COG0582	L	GI 5
RCA23_c12370	hypothetical protein			GI 5
RCA23_c12380	hypothetical protein			GI 5
RCA23_c12390	hypothetical protein			GI 5
RCA23_c12400	hypothetical protein			GI 5
RCA23_c12410	hypothetical protein, DUF1994			GI 5
RCA23_c12420	exonuclease I	COG2925	L	GI 5
RCA23_c12430	transpeptidase, penicillin binding protein	COG4953	M	GI 5
RCA23_c12440	hypothetical protein	COG2373	R	GI 5
RCA23_c12450	hypothetical protein			GI 5
RCA23_c12460	hypothetical protein			GI 5
RCA23_c12470	type III restriction enzyme, res subunit	COG1061	K	GI 5
RCA23_c12480	putative type III restriction system protein, mod subunit			GI 5
RCA23_c12490	putative serine/threonine protein kinase	COG0515	R	GI 5
RCA23_c12500	serine/threonine protein phosphatase PrpC (3.1.3.16)	COG0631	T	GI 5
RCA23_c12510	DNA helicase, UvrD/REP type	COG0210	L	GI 5
RCA23_c12520	hypothetical protein	COG1463	Q	GI 5
RCA23_c12530	hypothetical protein, OmpA/MotB-like	COG1360	N	GI 5
RCA23_c12540	hypothetical protein			GI 5
RCA23_c12550	ATP-dependent helicase	COG0553	K	GI 5
RCA23_c12560	hypothetical protein			GI 5
RCA23_c12570	hypothetical protein			GI 5
RCA23_c12580	hypothetical protein			GI 5
RCA23_c12590	hypothetical protein			GI 5
RCA23_c12600	hypothetical protein			GI 5
RCA23_c12610	hypothetical protein			GI 5
RCA23_c12620	hypothetical protein			GI 5
RCA23_c12630	integrase	COG2801	L	GI 5
RCA23_c12640	hypothetical protein			GI 5
RCA23_c12650	hypothetical protein			GI 5
RCA23_c12660	DNA integration/recombination/inversion protein			GI 5
RCA23_c12690	putative beta-lactamase-like protein	COG0491	R	
RCA23_c12680	EnvZ:osmolarity sensor protein EnvZ (2.7.13.3)	COG0642	T	
RCA23_c12700	hypothetical protein			
RCA23_c12710	RplU:50S ribosomal protein L21	COG0261	J	
RCA23_c12720	50S ribosomal protein L27	COG0211	J	
RCA23_c12730	hypothetical protein, LysE type translocator	COG1280	E	
RCA23_c12740	putative acetyltransferase	COG1670	J	
RCA23_c12750	GCN5-like N-acetyltransferase	COG1670	J	
RCA23_c12760	Obg:GTP-binding protein Obg	COG0536	R	
RCA23_c12770	ProB:glutamate 5-kinase ProB (2.7.2.11)	COG0263	E	
RCA23_c12780	ProA:gamma-glutamyl phosphate reductase ProA (1.2.1.41)	COG0014	E	
RCA23_c12800	hypothetical protein	COG5385	S	
RCA23_c12790	hypothetical protein			
RCA23_c12810	hypothetical protein	COG3176	R	
RCA23_c12820	putative phosphate acyltransferase	COG0204	I	
RCA23_c12830	ThiE:thiamine-phosphate pyrophosphorylase ThiE (2.5.1.3)	COG0352	H	
RCA23_c12840	TrmJ:tRNA (cytidine/uridine-2'-O-)-methyltransferase TrmJ (2.1.1.-)	COG0565	J	
RCA23_c12850	CtaA:heme A synthase CtaA (1.3.-.-)	COG1612	O	
RCA23_c12860	thermostable carboxypeptidase 1 (3.4.17.19)	COG2317	E	
RCA23_c12870	GyrA:DNA gyrase subunit A (5.99.1.3)	COG0188	L	
RCA23_c12880	hypothetical protein	COG1495	O	
RCA23_c12890	DesR family protein	COG1238	S	
RCA23_c12900	hypothetical protein			GI 6
RCA23_c12910	putative sncaL-like poly/ketide cyclase	COG3631	R	GI 6
RCA23_c12920	hypothetical protein, DUF1330	COG5470	S	GI 6
RCA23_c12930	hypothetical protein, DUF3303			GI 6
RCA23_c12940	hypothetical protein, transmembrane			GI 6
RCA23_c12950	hypothetical protein, transmembrane			GI 6
RCA23_c12960	integrase	COG2801	L	GI 6
RCA23_c12970	hypothetical protein			GI 6
RCA23_c12980	site-specific recombinase, resolvase family protein	COG1961	L	GI 6
RCA23_c12990	hypothetical protein	COG4731	S	GI 6
RCA23_c13000	hypothetical protein			GI 6
RCA23_c13010	transposase	COG3415	L	GI 6
RCA23_c13020	RpsS2:ribosomal protein S21	COG0828	J	GI 6
RCA23_c13030	hypothetical protein			GI 6
RCA23_c13040	integrase	COG2801	L	GI 6
RCA23_c13050	hypothetical protein			GI 6
RCA23_c13060	putative phage integrase	COG0582	L	GI 6
RCA23_c13080	putative phage integrase	COG0582	L	GI 6
RCA23_c13090	hypothetical protein, GYD domain	COG4274	S	GI 6
RCA23_c13100	hypothetical protein			GI 6
RCA23_c13110	hypothetical protein			GI 6
RCA23_c13120	hypothetical protein			GI 6
RCA23_c13130	integrase	COG2801	L	GI 6
RCA23_c13140	hypothetical protein	COG5586	S	GI 6
RCA23_c13150	hypothetical protein			GI 6
RCA23_c13160	hypothetical protein			GI 6
RCA23_c13170	hypothetical protein	COG4274	S	GI 6
RCA23_c13180	hypothetical protein			GI 6
RCA23_c13190	hypothetical protein			GI 6
RCA23_c13210	PurM:phosphoribosylformylglycinamidine cyclo-ligase PurM (6.3.3.1)	COG0150	F	
RCA23_c13220	PurN:phosphoribosylglycinamide formyltransferase PurN (2.1.2.2)	COG0299	F	
RCA23_c13230	RnmJ:ribonuclease D (3.1.13.5)	COG0349	J	
RCA23_c13240	SufE: cystein desulfuration protein	COG2166	R	
RCA23_c13250	hypothetical protein			
RCA23_c13260	putative methionine synthase (B12 dependent) subunit 2	COG5012	R	
RCA23_c13270	putative methionine synthase (B12 dependent) subunit 1	COG0646	E	
RCA23_c13280	PurC:phosphoribosylaminoimidazole-succinocarboxamide synthase PurC (6.3.2	COG0152	F	
RCA23_c13290	PurS:phosphoribosylformylglycinamidine (FGAM) synthase PurS	COG1828	F	
RCA23_c13300	PurQ:phosphoribosylformylglycinamidine synthase PurQ (6.3.5.3)	COG0047	F	
RCA23_c13310	DctB:C4-dicarboxylate transport sensor protein DctB (2.7.13.3)	COG4191	T	
RCA23_c13320	DctD:C4-dicarboxylate transport transcriptional regulatory protein DctD	COG2204	T	
RCA23_c13330	Rne:ribonuclease E (3.1.26.12)	COG1530	J	
RCA23_c13340	putative sulfurtransferase tusA	COG0425	O	
RCA23_c13350	cytochrome C biogenesis protein transmembrane region	COG0785	O	
RCA23_c13360	hypothetical protein			
RCA23_c13370	putative cytochrome P450	COG2124	Q	
RCA23_c13380	DNA alkylation repair enzyme	COG4912	L	
RCA23_c13390	hypothetical protein	COG3153	R	
RCA23_c13400	GlmS:glucosamine--fructose-6-phosphate aminotransferase GlmS (2.6.1.16)	COG0449	M	
RCA23_c13410	GlmU:bifunctional protein GlmU (2.7.7.23,2.3.1.157)	COG1207	M	
RCA23_c13420	putative HAD-superfamily hydrolase	COG0546	R	
RCA23_c13440	MmgE/PrpD family protein (4.2.1.79)	COG2079	R	
RCA23_c13430	putative pyridoxal-phosphate-dependent aminotransferase	COG0399	M	
RCA23_c13450	isovaleryl-CoA dehydrogenase (1.3.99.10)	COG1960	I	
RCA23_c13460	hypothetical protein			
RCA23_c13470	MccB:methylcrotonoyl-CoA carboxylase beta subunit MccB (6.4.1.4)	COG4799	I	
RCA23_c13480	hypothetical protein			
RCA23_c13490	MccA:methylcrotonoyl-CoA carboxylase alpha subunit MccA (6.4.1.4)	COG4770	I	
RCA23_c13500	MvaB:hydroxymethylglutaryl-CoA lyase MvaB (4.1.3.4)	COG0119	E	
RCA23_c13510	putative methylglutaconyl-CoA hydratase	COG1024	I	
RCA23_c13520	NuoA:NADH-quinone oxidoreductase subunit A (1.6.99.5)	COG0838	C	
RCA23_c13530	NuoB:ADH-quinone oxidoreductase subunit NuoB (1.6.99.5)	COG0377	C	
RCA23_c13540	hypothetical protein DUF2158	COG5475	S	
RCA23_c13550	NuoC:NADH-quinone oxidoreductase subunit C (1.6.99.5)	COG0852	C	
RCA23_c13560	hypothetical protein			
RCA23_c13570	NuoD:NADH-quinone oxidoreductase subunit D (1.6.99.5)	COG0649	C	
RCA23_c13580	NuoE:NADH-quinone oxidoreductase subunit E (1.6.99.5)	COG1905	C	
RCA23_c13590	hypothetical protein			
RCA23_c13600	NuoF:NADH-quinone oxidoreductase subunit F (1.6.99.5)	COG1894	C	
RCA23_c13610	hypothetical protein			
RCA23_c13620	NuoG:NADH-quinone oxidoreductase subunit G (1.6.99.5)	COG1034	C	
RCA23_c13630	hypothetical protein			
RCA23_c13640	NuoH:NADH-quinone oxidoreductase subunit H (1.6.99.5)	COG1005	C	
RCA23_c13650	NuoI:NADH-quinone oxidoreductase subunit I (1.6.99.5)	COG1143	C	
RCA23_c13660	NuoJ:NADH-quinone oxidoreductase subunit J (1.6.99.5)	COG0839	C	
RCA23_c13670	NuoK:NADH-quinone oxidoreductase subunit K (1.6.99.5)	COG0713	C	
RCA23_c13680	NuoL:NADH-quinone oxidoreductase subunit L (1.6.99.5)	COG1009	C	
RCA23_c13690	NuoM:NADH-quinone oxidoreductase subunit M (1.6.99.5)	COG1008	C	
RCA23_c13700	NuoN:NADH-quinone oxidoreductase subunit N (1.6.99.5)	COG1007	C	
RCA23_c13710	biotin (acetyl-CoA-carboxylase) ligase (6.3.4.15)	COG0340	H	
RCA23_c13720	CoaX:type III pantothenate kinase CoaX (2.7.1.33)	COG1521	K	
RCA23_c13730	putative ribonuclease	COG0595	R	
RCA23_c13740	RhlE2:ATP-dependent RNA helicase RhlE (3.6.4.13)	COG0513	L	
RCA23_c13750	PrfC:peptide chain release factor 3	COG4108	J	
RCA23_c13760	hypothetical protein			
RCA23_c13770	putative short chain dehydrogenase	COG1028	I	
RCA23_c13780	arsenite methyltransferase (2.1.1.137)	COG2226	H	
RCA23_c13790	FbpC:Fe(3+) ions import ATP-binding protein FbpC (3.6.3.30)	COG3842	E	
RCA23_c13800	putative helix-turn-helix protein	COG2378	K	
RCA23_c13810	putative sec-independent protein translocase protein TatA	COG1826	U	
RCA23_c13820	putative sec-independent protein translocase protein TatB	COG1826	U	
RCA23_c13830	putative sec-independent protein translocase protein TatC	COG0805	U	
RCA23_c13840	hypothetical protein DUF815	COG2607	R	
RCA23_c13850	putative peptidoglycan-binding peptidase	COG0739	M	
RCA23_c13860	PcmZ:protein-L-isoaspartate O-methyltransferase Pcm (2.1.1.77)	COG2518	O	
RCA23_c13870	SurE2:5'-nucleotidase SurE (3.1.3.5)	COG0496	R	
RCA23_c13880	putative short chain dehydrogenase	COG1028	I	
RCA23_c13890	PurF:amidophosphoribosyltransferase PurF (2.4.2.14)	COG0034	F	
RCA23_c13900	putative colicin V production protein			
RCA23_c13910	RadA:DNA repair protein RadA	COG1066	O	
RCA23_c13920	ABC transporter ATP-binding protein	COG1127	Q	
RCA23_c13930	hypothetical protein DUF140	COG0767	Q	
RCA23_c13940	Alr:alanine racemase, biosynthetic (5.1.1.1)	COG0787	M	
RCA23_c13950	DnaB:replicative DNA helicase DnaB (3.6.4.12)	COG0305	L	
RCA23_c13960	PyrE:orotate phosphoribosyltransferase PyrE (2.4.2.10)	COG0461	F	
RCA23_c13970	PyrC2:dihydroorotase PyrC (3.5.2.3)	COG0418	F	
RCA23_c13980	hypothetical protein			
RCA23_c13990	hypothetical protein			
RCA23_c14000	hypothetical protein			
RCA23_c14010	Mdh:malate dehydrogenase Mdh (1.1.1.37)	COG0039	C	
RCA23_c14020	CitE2:citrate lyase beta subunit CitE (4.1.3.6,4.1.3.34)	COG2301	G	
RCA23_c14030	putative mesaconyl-CoA hydratase	COG2030	I	
RCA23_c14040	SdhC:succinate dehydrogenase cytochrome b556 subunit SdhC	COG2009	C	
RCA23_c14050	SdhD:succinate dehydrogenase hydrophobic membrane anchor subunit SdhD	COG2142	C	
RCA23_c14060	SdhA:succinate dehydrogenase flavoprotein subunit SdhA (1.3.99.1)	COG1053	C	
RCA23_c14070	hypothetical protein			
RCA23_c14080	SdhB:succinate dehydrogenase iron-sulfur subunit SdhB (1.3.99.1)	COG0479	C	
RCA23_c14090	purine nucleoside phosphorylase deoD-type (2.4.2.1)	COG0813	F	
RCA23_c14100	acetyltransferase (2.3.1.-)	COG1246	E	
RCA23_c14110	TrpA:tryptophan synthase alpha chain TrpA (4.2.1.20)	COG0159	E	
RCA23_c14120	EngD:GTP-dependent nucleic acid-binding protein EngD	COG0012	J	
RCA23_c14130	Non-specific ribonucleoside hydrolase rihC (3.2.-.-)	COG1957	F	
RCA23_c14150	hypothetical protein DUF583	COG1664	M	GI 7
RCA23_c14160	HtpX:protease HtpX (3.4.24.-)	COG5501	O	GI 7
RCA23_c14170	Histone deacetylase	COG0123	B	GI 7
RCA23_c14180	TspO1:peripheral-type benzodiazepine receptor/signal transduction protein TspO	COG3476	T	GI 7
RCA23_c14190	Hin:DNA-invertase Hin	COG1961	L	GI 7
RCA23_c14200	hypothetical protein			GI 7
RCA23_c14210	hypothetical protein			GI 7
RCA23_c14220	hypothetical protein, RmlC-like cupin family	COG3450	R	GI 7

RCA23_c14230	Integrase	COG4974	L
RCA23_c14240	hypothetical membrane protein		
RCA23_c14260	hypothetical protein	COG4530	S
RCA23_c14270	hypothetical protein DUF45	COG1451	R
RCA23_c14280	HTH-type transcriptional regulator, GntR family	COG1802	K
RCA23_c14290	Lpd1: dihydrolipoyl dehydrogenase Lpd (1.8.1.4)	COG1249	C
RCA23_c14300	SucB: dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate	COG0508	C
RCA23_c14310	SucA:2-oxoglutarate dehydrogenase E1 component SucA (1.2.4.2)	COG0567	C
RCA23_c14320	SucD1:succinyl-CoA ligase [ADP-forming] alpha subunit SucD (6.2.1.5)	COG0074	C
RCA23_c14330	SucC:succinyl-CoA ligase [ADP-forming] beta subunit SucC (6.2.1.5)	COG0045	C
RCA23_c14340	butyryl-CoA dehydrogenase (1.2.99.2)	COG1960	I
RCA23_c14350	InfC:translation initiation factor IF-3	COG0290	J
RCA23_c14360	Fpr:ferredoxin--NADP reductase Fpr (1.18.1.2)	COG1018	C
RCA23_c14370	hypothetical protein	COG3749	S
RCA23_c14380	hypothetical protein	COG0175	E
RCA23_c14390	Cyst:cys/isr: sulfite reductase (ferredoxin) (1.8.7.1)	COG0155	P
RCA23_c14400	hypothetical protein		
RCA23_c14410	CysG:siroheme synthase CysG (2.1.1.107,4.99.1.4)	COG0007	H
RCA23_c14420	HTH-type transcriptional regulator, AsnC family	COG1522	K
RCA23_c14450	peptidase	COG0624	E
RCA23_c14460	hypothetical protein	COG1426	S
RCA23_c14470	IspG:4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase IspG (1.17.7.1)	COG0821	I
RCA23_c14480	TPR-repeat containing protein	COG4783	R
RCA23_c14490	aspartate aminotransferase (2.6.1.1)	COG0436	E
RCA23_c14500	MrcA:penicillin-binding protein 1A (2.4.2.-,3.4.-.-)	COG5009	M
RCA23_c14510	PrfB:peptide chain release factor 2	COG1186	J
RCA23_c14520	hypothetical protein DUF583	COG1664	M
RCA23_c14530	putative peptidase, M23 family	COG0739	M
RCA23_c14540	hypothetical protein DUF455	COG2833	S
RCA23_c14550	Bcp:peroxiredoxin Bcp (1.11.1.15)	COG1225	O
RCA23_c14560	hypothetical protein		
RCA23_c14570	QueA:S-adenosylmethionine:tRNA ribosyltransferase- isomerase QueA (5.-.-.-)	COG0809	J
RCA23_c14580	MFS-type transporter		
RCA23_c14590	hypothetical protein DUF924	COG3803	S
RCA23_c14600	Lpd2: dihydrolipoyl dehydrogenase Lpd (1.8.1.4)	COG1249	C
RCA23_c14610	LivFA:livr/ABC system protein A	COG0178	L
RCA23_c14620	MmgE:PrpD family protein	COG2079	R
RCA23_c14630	MmsB1:3-hydroxyisobutyrate dehydrogenase MmsB (1.1.1.31)	COG2084	
RCA23_c14640	3-hydroxyisobutyryl-CoA hydrolase (3.1.2.4)	COG1024	I
RCA23_c14650	isobutyryl-CoA dehydrogenase (1.3.99.-)	COG1960	I
RCA23_c14660	MmsA:methylmalonate-semialdehyde dehydrogenase MmsA (1.2.1.27;1.2.1.18)	COG1012	C
RCA23_c14670	putative HTH-type transcriptional regulator, LysR family	COG0583	K
RCA23_c14680	CoaD:phosphopantetheine adenylyltransferase CoaD (2.7.7.3)	COG0669	H
RCA23_c14690	Gap2:glyceraldehyde-3-phosphate dehydrogenase Gap (1.2.1.12)	COG0057	G
RCA23_c14700	Gap3:glyceraldehyde-3-phosphate dehydrogenase Gap (1.2.1.12)	COG0057	G
RCA23_c14710	TktA:transketolase TktA (2.2.1.1)	COG0021	G
RCA23_c14720	hypothetical protein		
RCA23_c14730	ZapA:cell division protein ZapA	COG3027	S
RCA23_c14740	putative glutaredoxin	COG0278	O
RCA23_c14750	hypothetical protein		
RCA23_c14760	hypothetical protein, BolA-like	COG0271	T
RCA23_c14770	PurL:phosphoribosylformylglycinamidine synthase PurL (6.3.5.3)	COG0046	F
RCA23_c14780	HTH-type transcriptional regulator, LysR family	COG0583	K
RCA23_c14790	hypothetical protein, pyruvate ferredoxin/flavodoxin oxidoreductase	COG4231	C
RCA23_c14800	MurI:glutamate racemase MurI (5.1.1.3)	COG0796	M
RCA23_c14810	ArgC:N-acetyl-gamma-glutamyl-phosphate reductase ArgC (1.2.1.38)	COG0002	E
RCA23_c14820	CcmE:cytochrome c-type biogenesis protein CcmE	COG2332	O
RCA23_c14830	CcmF:cytochrome c-type biogenesis protein CcmF	COG1138	O
RCA23_c14840	CcmH:cytochrome c-type biogenesis protein CcmH	COG3088	O
RCA23_c14850	putative enoyl-CoA hydratase FadB (4.2.1.17)	COG1024	I
RCA23_c14860	hypothetical protein		
RCA23_c14870	GltA:citrate synthase GltA (2.3.3.1)	COG0372	C
RCA23_c14880	GlxX:glutamyl-tRNA synthase 2 (6.1.1.17)	COG0008	J
RCA23_c14890	hypothetical protein competence protein E	COG0658	R
RCA23_c14900	LexA:LexA repressor (3.4.21.88)	COG1974	K
RCA23_c14910	MoaA2:molybdopterin biosynthesis protein MoaA	COG0303	H
RCA23_c14920	MoaC:molybdenum cofactor biosynthesis protein MoaC	COG0315	H
RCA23_c14930	TrpC:indole-3-glycerol phosphate synthase TrpC (4.1.1.48)	COG0134	E
RCA23_c14940	TrpD:anthranilate phosphoribosyltransferase TrpD (2.4.2.18)	COG0547	E
RCA23_c14950	TrpG:anthranilate synthase component TrpG (4.1.3.27)	COG0512	E
RCA23_c14960	hypothetical protein, divergent polysaccharide deacetylase		
RCA23_c14970	hypothetical protein		
RCA23_c14990	hypothetical protein	COG3108	S
RCA23_c15000	putative L,D-transpeptidase YcbB (2.-.-.-)	COG2989	S
RCA23_c15010	LpxD:UDP-3-O-(3-hydroxymyristoyl) glucosamine N- acyltransferase LpxD (2.3.1	COG1044	M
RCA23_c15020	acyl carrier protein	COG0236	I
RCA23_c15030	FabF1:3-oxoacyl-(acyl-carrier-protein] synthase FabF (2.3.1.179)	COG0304	I
RCA23_c15040	hypothetical protein, invasion protein B	COG5342	R
RCA23_c15050	inner membrane protein	COG4536	P
RCA23_c15060	XerD:tyrosine recombinase XerD	COG4974	L
RCA23_c15070	hypothetical protein		
RCA23_c15080	hypothetical protein		
RCA23_c15090	AroK1:shikimate kinase AroK (2.7.1.71)	COG0703	E
RCA23_c15100	AroB:3-dehydroquinate synthase AroB (4.2.3.4)	COG0337	E
RCA23_c15110	single-stranded DNA-binding protein	COG0629	L
RCA23_c15120	GslA3:glutathione import ATP-binding protein GslA (3.6.3.-)	COG0444	E
RCA23_c15130	putative ABC transporter inner membrane component	COG1173	E
RCA23_c15140	putative ABC transporter permease protein	COG0601	E
RCA23_c15150	ABC transporter extracellular solute-binding protein	COG0747	E
RCA23_c15160	MiaA:tRNA delta(2)-isopentenylpyrophosphate transferase MiaA (2.5.1.8)	COG0324	J
RCA23_c15170	PyrH:uridylate kinase PyrH (2.7.4.22)	COG0528	F
RCA23_c15180	Frr:ribosome recycling factor Frr	COG0233	J
RCA23_c15190	UppS:undecaprenyl pyrophosphate synthase UppS (2.5.1.31)	COG0020	I
RCA23_c15200	putative cytidyltransferase	COG0575	I
RCA23_c15210	Dxr:1-deoxy-D-xylulose 5-phosphate reductoisomerase Dxr (1.1.1.267)	COG0743	I
RCA23_c15220	RseP:RIP metalloprotease RseP	COG0750	M
RCA23_c15230	putative outer membrane assembly factor	COG4775	M
RCA23_c15240	putative outer lein		
RCA23_c15250	FabZ:(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase FabZ (4.2.1.-)	COG0764	I
RCA23_c15260	LpxA:acyl-[acyl-carrier-protein]--UDP-N- acetylglucosamine O-acyltransferase L	COG1043	M
RCA23_c15270	hypothetical protein DUF1009	COG3494	S
RCA23_c15280	LpxB:lipid-A-disaccharide synthase LpxB (2.4.1.182)	COG0763	M
RCA23_c15290	TrmU:tRNA (5-methylaminomethyl-2-thiouridylate)- methyltransferase TrmU (2.1.	COG0482	J
RCA23_c15300	hypothetical protein		
RCA23_c15310	CtrA:cell cycle transcriptional regulator	COG0745	T
RCA23_c15320	LigA:DNA ligase LigA (6.5.1.2)	COG0272	L
RCA23_c15330	RecG:ATP-dependent DNA helicase RecG (3.6.4.12)	COG1200	L
RCA23_c15340	hypothetical protein		
RCA23_c15350	hypothetical protein	COG0822	C
RCA23_c15360	Hist:phosphoribosyl-AMP cyclohydrolase Hist (3.5.4.19)	COG0139	E
RCA23_c15370	GluQ:glutamyl-Q tRNA(Asp) synthase GluQ (6.1.1.-)	COG0008	J
RCA23_c15380	hypothetical protein, methyltransferase	COG4976	R
RCA23_c15390	Gid:tRNA uridine 5-carboxymethylaminomethyl modification enzyme Gid	COG1206	J
RCA23_c15400	putative crotonase	COG1024	I
RCA23_c15410	putative thioesterase	COG2050	Q
RCA23_c15420	RplM:50S ribosomal protein L13	COG0102	J
RCA23_c15430	RpsI:30S ribosomal protein S9	COG0103	J
RCA23_c15440	Integrase		
RCA23_c15460	BetA2:choline dehydrogenase BetA (1.1.99.1)	COG2303	E
RCA23_c15470	ABC transporter, permease protein	COG4662	H
RCA23_c15480	ABC transporter, ATP-binding protein	COG1131	V
RCA23_c15490	ABC transporter, periplasmic substrate-binding protein	COG2998	H
RCA23_c15500	hypothetical membrane protein	COG1238	S
RCA23_c15510	hypothetical protein DUF6 family, transmembrane	COG2962	R
RCA23_c15520	hypothetical protein	COG2068	R
RCA23_c15530	dimethylglycine dehydrogenase (1.5.99.2)	COG0404	E
RCA23_c15540	dimethylglycine dehydrogenase (1.5.99.2)	COG0404	E
RCA23_c15550	short-chain dehydrogenase/reductase SDR	COG1028	I
RCA23_c15560	hypothetical transmembrane protein	COG3788	R
RCA23_c15570	hypothetical protein, tetR regulator	COG1309	K
RCA23_c15580	MetA:homoserine O-succinyltransferase MetA (2.3.1.46)	COG1897	E
RCA23_c15590	hypothetical protein		
RCA23_c15600	putative integral membrane protein	COG2510	S
RCA23_c15610	GcnS-like N-acetyltransferase	COG1670	J
RCA23_c15620	GuaA:GMP synthase GuaA (6.3.5.2)	COG0519	F
RCA23_c15630	MtlB4:trimethylamine methyltransferase MtlB (2.1.1.-)	COG5598	H
RCA23_c15640	hypothetical protein		
RCA23_c15650	LipA:lipoyl synthase LipA (2.8.1.8)	COG0320	H
RCA23_c15660	hypothetical protein		
RCA23_c15670	Hpt:hypoxanthine phosphoribosyltransferase Hpt (2.4.2.8)	COG0634	F
RCA23_c15680	hypothetical protein	COG2867	I
RCA23_c15690	AmtB:ammonium transporter AmtB	COG0004	P
RCA23_c15700	putative competence-damaged protein	COG1546	R
RCA23_c15710	PgpA:phosphatidylglycerophosphatase A (3.1.3.27)	COG1267	I
RCA23_c15720	IspF:2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase IspF (4.6.1.12)	COG0245	I
RCA23_c15730	DusB:tRNA-dihydrouridine synthase B (1.-.-.-)	COG0042	J
RCA23_c15740	NtrB:histidine kinase, nitrogen regulation protein NtrB (2.7.13.3)	COG3852	T
RCA23_c15750	NtrC:nitrogen regulation protein NtrC	COG2204	T
RCA23_c15760	NtrY:histidine kinase, nitrogen regulation protein NtrY (2.7.13.3)	COG5000	T
RCA23_c15770	NtrX:nitrogen assimilation regulatory protein NtrX	COG2204	T
RCA23_c15780	TrkA:Trk system potassium uptake protein TrkA	COG0569	P
RCA23_c15790	putative Trk system potassium uptake protein trkH	COG0168	P
RCA23_c15800	Hfq:RNA-binding protein Hfq	COG1923	R
RCA23_c15810	HflX:GTP-binding protein HflX	COG2262	R
RCA23_c15820	QuiP:acyl-homoserine lactone acylase QuiP (3.5.1.97)	COG2366	R
RCA23_c15830	hypothetical protein	COG2930	S
RCA23_c15840	HemB:delta-aminolevulinic acid dehydratase HemB (4.2.1.24)	COG0113	H
RCA23_c15850	hypothetical protein		
RCA23_c15860	Mfd:transcription-repair-coupling factor Mfd (3.6.1.-)	COG1197	L
RCA23_c15870	putative DSBA-like thioredoxin family protein	COG2761	O
RCA23_c15880	long-chain-fatty-acid-CoA ligase (6.2.1.3)	COG0318	I
RCA23_c15890	HTH-type transcriptional regulator	COG1396	K
RCA23_c15900	AqpZ:aquaporin AqpZ	COG0580	G
RCA23_c15910	putative extracellular solute-binding protein	COG4166	E
RCA23_c15920	LysE:lysine exporter protein LysE	COG1279	R
RCA23_c15930	hypothetical protein DUF502	COG2928	S
RCA23_c15940	PsuG:pseudouridine-5'-phosphate glycosidase PsuG (3.2.-.-)	COG2313	Q
RCA23_c15950	hypothetical protein, pfkB family carbohydrate kinase	COG0524	G
RCA23_c15960	CspA1:cold shock protein CspA	COG1278	K
RCA23_c15970	RpsB:30S ribosomal protein S2	COG0052	J
RCA23_c15980	Tsf:elongation factor Ts	COG0264	J
RCA23_c15990	hypothetical protein		
RCA23_c16000	hypothetical protein, acetyltransferase-like	COG1670	J
RCA23_c16010	hypothetical protein, transcription factor NusA like		
RCA23_c16020	putative phenylacetic acid degradation protein	COG0663	R
RCA23_c16030	Gmk:guanylate kinase Gmk (2.7.4.8)	COG0194	F
RCA23_c16040	hypothetical protein, YycC-like	COG1561	S
RCA23_c16050	hypothetical protein, DUF1457	COG5388	S
RCA23_c16060	phospho-2-dehydro-3-deoxyheptonate aldolase (2.5.1.54)	COG3200	E
RCA23_c16070	putative HTH-type transcriptional regulator, AraC family	COG4977	K
RCA23_c16080	putative amino-acid binding protein	COG0683	E
RCA23_c16090	putative branched-chain amino acid transport ATP- binding protein	COG0411	E
RCA23_c16100	putative branched-chain amino acid transport ATP- binding protein	COG0410	E
RCA23_c16110	putative branched-chain amino acid transport system permease protein	COG0559	E
RCA23_c16120	putative branched-chain amino acid transport system permease protein	COG4177	E
RCA23_c16130	TypA:GTP-binding protein TypA	COG1217	T
RCA23_c16140	hypothetical protein DUF1330	COG2470	S
RCA23_c16150	AlaS:alanyl-tRNA synthase AlaS (6.1.1.7)	COG0013	J
RCA23_c16160	RecA:protein RecA	COG0468	L
RCA23_c16170	hypothetical protein		
RCA23_c16180	sensor transduction histidine kianse	COG0642	T
RCA23_c16190	hypothetical protein		
RCA23_c16200	hypothetical protein, NOL1/NOP2/Sun family	COG0144	J
RCA23_c16210	GuaB:inosine-5'-monophosphate dehydrogenase GuaB (1.1.1.205)	COG0516	F
RCA23_c16220	hypothetical protein	COG3894	R
RCA23_c16240	SufS2:cysteine desulfurase SufS (2.8.1.7;4.4.1.16)	COG0520	E
RCA23_c16250	hypothetical protein		
RCA23_c16260	hypothetical protein		
RCA23_c16270	SufD:FeS assembly protein SufD	COG0719	O
RCA23_c16280	SufC:FeS assembly ATPase SufC	COG0396	O
RCA23_c16290	SufB:FeS assembly protein SufB	COG0719	O
RCA23_c16300	putative aminotransferase	COG1104	E

RCA23_c16310	IscR: iron-sulfur cluster assembly transcriptional regulator	COG1959	K
RCA23_c16320	hypothetical protein	COG2945	R
RCA23_c16330	putative oxidoreductase	COG0673	R
RCA23_c16340	IolE:inosose dehydratase IolE (4.2.1.44)	COG1082	G
RCA23_c16350	putative oxidoreductase	COG0673	R
RCA23_c16360	HTH-type transcriptional repressor, LacI family	COG1609	K
RCA23_c16370	hypothetical protein		
RCA23_c16380	sugar (ribose) ABC transport system ATP binding protein	COG1129	G
RCA23_c16390	sugar (ribose) ABC transporter permease protein	COG1172	G
RCA23_c16400	sugar (ribose) ABC transporter periplasmic binding protein	COG1879	G
RCA23_c16410	BglA:beta-glucosidase BglA (3.2.1.21)	COG2723	G
RCA23_c16420	MalK:maltose/maltodextrin import ATP-binding protein MalK (3.6.3.19)	COG1839	G
RCA23_c16430	putative alpha-glucosidase AglA (3.2.1.20)	COG0366	G
RCA23_c16440	AglG:alpha-glucoside transport system permease protein AglG	COG0395	G
RCA23_c16450	ABC transporter, membrane spanning protein	COG0395	G
RCA23_c16460	AglF:alpha-glucoside transport system permease protein AglF	COG1175	G
RCA23_c16470	AglE:alpha-glucosides-binding periplasmic protein AglE	COG1653	G
RCA23_c16480	AglR:HTH-type transcriptional regulator	COG1609	K
RCA23_c16490	oxidoreductase	COG4989	R
RCA23_c16500	SsuD:alkanesulfonate monooxygenase SsuD (1.14.14.5)	COG2141	C
RCA23_c16510	putative regulatory DNA binding protein	COG2188	K
RCA23_c16520	putative oxidoreductase	COG0673	R
RCA23_c16530	Pgi:glucose-6-phosphate isomerase Pgi (5.3.1.9)	COG0166	G
RCA23_c16540	PgdS:phosphogluconolactonase Pgl (3.1.1.31)	COG0363	G
RCA23_c16550	Zwf:glucose-6-phosphate 1-dehydrogenase Zwf (1.1.1.49)	COG0364	G
RCA23_c16560	hypothetical protein, radical SAM	COG0535	R
RCA23_c16570	putative 5-methylcytosine-specific restriction enzyme McrA (3.1.21.-)	COG1403	V
RCA23_c16580	putative phospholipase/carboxylesterase	COG0400	R
RCA23_c16590	HHH:GPD superfamily base excision DNA repair protein	COG0122	L
RCA23_c16600	CobK:precorrin-6A reductase CobK (1.3.1.54)	COG2099	H
RCA23_c16610	CbiD:cobalamin (vitamin B12) biosynthesis CbiD|protein CbiD (2.1.1.-)	COG1903	H
RCA23_c16620	CobA:uroporphyrinogen-III C-methyltransferase CobA (2.1.1.107)	COG0007	H
RCA23_c16630	CobB:cobyrinic acid A,C-diamide synthase CobB	COG1797	H
RCA23_c16640	putative major facilitator superfamily transporter		
RCA23_c16650	hypothetical protein	COG1562	I
RCA23_c16660	CysS:cysteinyl-tRNA synthase CysS (6.1.1.16)	COG0215	J
RCA23_c16670	AspC3:aspartate aminotransferase AspC (2.6.1.1)	COG0436	E
RCA23_c16680	MtrB5:trimethylamine methyltransferase MtrB (2.1.1.-)	COG5598	H
RCA23_c16690	Uup:ABC transporter ATP-binding protein Uup	COG0488	R
RCA23_c16700	hypothetical protein	COG3176	R
RCA23_c16710	MsrB:peptide methionine sulfoxide reductase MsrB (1.8.4.12)	COG0229	O
RCA23_c16720	hypothetical protein, lipoprotein	COG2913	J
RCA23_c16730	hypothetical protein	COG1399	R
RCA23_c16740	PlsX:fatty acid/phospholipid synthesis protein PlsX	COG0416	I
RCA23_c16750	FabH:3-oxoacyl-[acyl-carrier-protein] synthase FabH (2.3.1.41)	COG0332	I
RCA23_c16760	IHA:integration host factor alpha subunit IHA	COG0776	L
RCA23_c16770	hypothetical protein, MerR family regulatory protein	COG0789	K
RCA23_c16790	Dcd:deoxyguanosinetriphosphate triphosphohydrolase- like protein Dcd	COG0717	F
RCA23_c16800	putative segregation and condensation protein B	COG1386	K
RCA23_c16810	hypothetical protein, segregation and condensation protein A	COG1354	S
RCA23_c16820	NagZ:beta-hexosaminidase NagZ (3.2.1.52)	COG1472	G
RCA23_c16830	hypothetical protein		
RCA23_c16840	arginyl-tRNA synthase (6.1.1.19)	COG0018	J
RCA23_c16850	deoxyguanosinetriphosphate triphosphohydrolase- like protein	COG0232	F
RCA23_c16860	putative iron-sulfur insertion protein erpA	COG0316	S
RCA23_c16870	HthA:exodeoxyribonuclease III (3.1.11.2)	COG0708	L
RCA23_c16880	putative cytochrome B561	COG3038	C
RCA23_c16890	putative dnak suppressor protein dksA	COG1734	T
RCA23_c16900	hypothetical protein	COG0714	R
RCA23_c16910	hypothetical protein	COG3825	S
RCA23_c16920	putative peptidase, M48 family	COG0501	O
RCA23_c16930	hypothetical protein		
RCA23_c16940	putative ribosomal RNA large subunit methyltransferase	COG1092	R
RCA23_c16950	Edd:phosphogluconate dehydratase Edd (4.2.1.12)	COG0129	E
RCA23_c16960	Eda:KHG/KDPG aldolase Eda (4.1.3.16,4.1.2.14)	COG0800	G
RCA23_c16970	hypothetical protein		
RCA23_c16980	GlnE:glutamate--ammonia-ligase adenylyltransferase GlnE (2.7.7.42)	COG1391	O
RCA23_c16990	hypothetical protein	COG2606	S
RCA23_c17000	hypothetical protein		
RCA23_c17010	hypothetical protein		
RCA23_c17020	hypothetical protein		
RCA23_c17030	putative aromatic-ring-hydroxylating dioxygenase	COG4638	P
RCA23_c17040	putative acetolactate synthase small subunit IlvH (2.2.1.6)	COG0440	E
RCA23_c17050	IlvI:acetolactate synthase isozyme large subunit IlvI (2.2.1.6)	COG0028	E
RCA23_c17060	hypothetical membrane protein, porin-like		
RCA23_c17070	DctP7:TRAP dicarboxylate transporter, subunit DctP	COG4663	Q
RCA23_c17080	DctQ5:TRAP dicarboxylate transporter, subunit DctQ	COG4665	Q
RCA23_c17090	DctM7:TRAP dicarboxylate transporter, subunit DctM	COG4664	Q
RCA23_c17100	putative arginyl-tRNA--protein transferase Ate (2.3.2.8)	COG0935	O
RCA23_c17110	NrdJ:vitamin B12-dependent ribonucleotide reductase NrdJ (1.17.4.1)	COG0209	F
RCA23_c17120	hypothetical protein		
RCA23_c17140	hypothetical protein DUF192	COG1430	S
RCA23_c17150	cold shock protein	COG1278	K
RCA23_c17160	PdxH:pyridoxine/pyridoxamine 5'-phosphate oxidase PdxH (1.4.3.5)	COG0259	H
RCA23_c17170	FabI:enoyl-[acyl-carrier-protein] reductase FabI (1.3.1.9)	COG0623	I
RCA23_c17180	Gpt:xanthine phosphoribosyltransferase Gpt (2.4.2.22)	COG0503	F
RCA23_c17190	RihA:pyrimidine-specific ribonucleoside hydrolase RihA (3.2.-.-)	COG1957	F
RCA23_c17200	hypothetical protein LPF0061	COG0397	S
RCA23_c17210	putative sodium/hydrogen exchanger	COG0025	P
RCA23_c17220	Fur:ferric uptake regulator protein Fur	COG0735	P
RCA23_c17230	putative S-adenosylmethionine uptake transporter	COG0697	G
RCA23_c17240	Eno:enolase Eno (4.2.1.11)	COG0148	G
RCA23_c17250	AmnK:anhydro-N-acetylmuramic acid kinase AmnK (2.7.1.-)	COG2377	O
RCA23_c17260	TyrS:tyrosyl-tRNA synthase TyrS (6.1.1.1)	COG0162	J
RCA23_c17270	AspC4:aspartate aminotransferase AspC (2.6.1.1)	COG0436	E
RCA23_c17280	hypothetical protein	COG0760	O
RCA23_c17290	TrpE:anthranilate synthase component TrpE (4.1.3.27)	COG0147	E
RCA23_c17300	putative protein soxG	COG0491	R
RCA23_c17310	putative protein soxH	COG0491	R
RCA23_c17320	HemA2:5-aminolevulinate synthase HemA (2.3.1.37)	COG0156	H
RCA23_c17330	SoxF2:sulfite dehydrogenase [flavocytochrome c] flavoprotein chain SoxF (1.8.	COG1439	S
RCA23_c17340	domain of unknown function DUF1791	COG1416	S
RCA23_c17350	SoxD2:sulfite oxidase cytochrome subunit SoxD (1.8.3.1)	COG3474	C
RCA23_c17360	SoxC:sulfite oxidase molybdopterin subunit SoxC (1.8.3.1)	COG2041	R
RCA23_c17370	SoxB2:sulfur oxidation protein SoxB	COG0737	F
RCA23_c17380	SoxA2:diheme cytochrome c	COG3258	C
RCA23_c17390	SoxZ:protein SoxZ		
RCA23_c17400	SoxY:protein SoxY	COG5501	S
RCA23_c17410	SoxX:cytochrome c	COG2010	C
RCA23_c17420	SoxW:thioredoxin SoxW	COG2143	O
RCA23_c17430	SoxV:cytochrome c-type biogenesis protein SoxV	COG0785	O
RCA23_c17440	SoxS:protein SoxS		
RCA23_c17450	SoxR:HTH-type transcriptional regulator, ArsR family	COG0640	K
RCA23_c17460	putative SoxT, transmembrane protein DUF395	COG2391	R
RCA23_c17470	hypothetical protein DUF395	COG2391	R
RCA23_c17480	NAD-binding protein	COG2084	I
RCA23_c17490	GyaR2:glioxylate reductase GyaR (1.1.1.26)	COG1052	C
RCA23_c17500	GatA2:glutamyl-tRNA(Gln) amidotransferase subunit A (6.3.5.-)	COG0154	J
RCA23_c17510	DctMB:TRAP dicarboxylate transporter, subunit DctM	COG4664	Q
RCA23_c17520	DctQB:TRAP dicarboxylate transporter, subunit DctQ	COG4665	Q
RCA23_c17530	DctPB:TRAP dicarboxylate transporter, subunit DctP	COG4663	Q
RCA23_c17540	hypothetical protein		
RCA23_c17550	GlpK:glycerol kinase GlpK (2.7.1.30)	COG0554	C
RCA23_c17560	RrmJ:ribosomal RNA large subunit methyltransferase J (2.1.1.-)	COG0293	J
RCA23_c17570	putative PpaX|PpgA phosphatase family protein	COG0248	F
RCA23_c17580	hypothetical protein		
RCA23_c17590	hypothetical protein	COG0685	E
RCA23_c17600	pterin domain containing enzyme	COG1410	E
RCA23_c17610	YfaU:2-keto-3-deoxy-L-rhamnonate aldolase YfaU (4.1.2.-)	COG3836	G
RCA23_c17620	Glk:glucokinase Glk (2.7.1.2)	COG0837	G
RCA23_c17630	hypothetical protein DUF1006	COG3214	S
RCA23_c17640	inductive dehalogenase	COG1018	C
RCA23_c17650	hypothetical protein, XdhC and CoxI	COG1975	O
RCA23_c17660	GlxR:2-hydroxy-3-oxopropionate reductase GlxR (1.1.1.60)	COG2084	I
RCA23_c17670	3-hydroxybutyrate dehydrogenase (1.1.1.30)	COG1028	I
RCA23_c17680	IlvD2:dihydroxy-acid dehydratase IlvD (4.2.1.9)	COG0129	E
RCA23_c17690	fumarylacetoacetate hydrolase	COG0179	Q
RCA23_c17700	hypothetical protein		
RCA23_c17710	Ndk:nucleoside diphosphate kinase Ndk (2.7.4.6)	COG0105	F
RCA23_c17720	hypothetical protein		
RCA23_c17730	ABC transporter ATP-binding protein	COG0488	R
RCA23_c17740	IstsC family integral membrane protein	COG3095	U
RCA23_c17750	hypothetical protein	COG3577	R
RCA23_c17760	putative DNA polymerase III chi subunit, HolC	COG2927	L
RCA23_c17770	PepA:cytosol aminopeptidase PepA (3.4.11.1)	COG0260	E
RCA23_c17780	putative permease, YjgP/YjgQ family	COG0795	R
RCA23_c17790	putative permease, YjgP/YjgQ family	COG0795	R
RCA23_c17800	putative organic solvent tolerance protein	COG1452	M
RCA23_c17810	hypothetical protein, SurA	COG0760	O
RCA23_c17820	PdxA:4-hydroxythreonine-4-phosphate dehydrogenase PdxA (1.1.1.262)	COG1995	H
RCA23_c17830	KsgA:dimethyladenosine transferase KsgA (2.1.1.-)	COG0030	J
RCA23_c17840	hypothetical protein		
RCA23_c17850	modification methylase, HemK family	COG2890	J
RCA23_c17860	PrfA:peptide chain release factor 1	COG0216	J
RCA23_c17870	hypothetical protein	COG4446	S
RCA23_c17880	SpeB1:agmatinase SpeB (3.5.3.11)	COG0010	E
RCA23_c17890	alpha/beta hydrolase		
RCA23_c17900	SpeB2:agmatinase SpeB (3.5.3.11)	COG0010	E
RCA23_c17910	HpO2:hippurate hydrolase HpO (3.5.1.32)	COG1473	R
RCA23_c17920	MauG:protein MauG	COG3956	R
RCA23_c17930	FutA:ABC transporter periplasmic iron-binding protein FutA	COG1840	P
RCA23_c17940	putative peptidyl-prolyl cis-trans isomerase Ppi (5.2.1.8)	COG0652	O
RCA23_c17950	putative peptidyl-prolyl cis-trans isomerase Ppi (5.2.1.8)	COG0652	O
RCA23_c17960	PgkC:phosphoglycerate kinase PgkC (2.7.2.3)	COG0126	G
RCA23_c17970	FdaA:fructose-bisphosphate aldolase class 1 (4.1.2.13)	COG5588	G
RCA23_c17980	hypothetical protein, septum formation initiator	COG2919	D
RCA23_c17990	PdhA:pyruvate dehydrogenase E1 component alpha subunit PdhA (1.2.4.1)	COG1071	C
RCA23_c18000	PdhB:pyruvate dehydrogenase E1 component beta subunit PdhB (1.2.4.1)	COG0022	C
RCA23_c18010	PdhC:dihydrolipoyllysine-residue acetyltransferase PdhC (2.3.1.12)	COG0508	C
RCA23_c18020	CysE:serine acetyltransferase CysE (2.3.1.30)	COG1045	E
RCA23_c18030	putative gene transfer agent protein		
RCA23_c18040	putative gene transfer agent large terminase part 1	COG5323	S
RCA23_c18050	putative gene transfer agent large terminase part 2	COG5323	S
RCA23_c18060	aminodeoxychorismate lyase	COG1559	R
RCA23_c18070	FabF2:3-oxoacyl-[acyl-carrier-protein] synthase FabF (2.3.1.179)	COG0304	I
RCA23_c18080	AcpP:acyl carrier protein AcpP	COG0236	I
RCA23_c18090	FabG3:3-oxoacyl-[acyl-carrier-protein] reductase FabG (1.1.1.100)	COG1028	I
RCA23_c18100	malonyl CoA-acyl carrier protein transacylase (2.3.1.39)	COG0331	I
RCA23_c18110	RpsF:30S ribosomal protein S6	COG0360	J
RCA23_c18120	RpsR:30S ribosomal protein S18	COG0238	J
RCA23_c18130	RplE:50S ribosomal protein L9	COG0359	J
RCA23_c18140	Tig:trigger factor (TF)	COG0544	O
RCA23_c18160	GlnB1:nitrogen regulatory protein P-II 1	COG0347	E
RCA23_c18170	GlnA2:glutamine synthase GlnA (6.3.1.2)	COG0174	E
RCA23_c18190	hypothetical protein		
RCA23_c18180	DddP:dimethylpropiothetin dethiomethylase DddP (4.4.1.3)	COG0006	E
RCA23_c18200	hypothetical protein, BioY-like	COG1268	R
RCA23_c18210	hypothetical protein		
RCA23_c18220	PurB:adenylosuccinate lyase PurB (4.3.2.2)	COG0015	F
RCA23_c18230	putative nitrile hydratase, beta subunit		
RCA23_c18240	hypothetical protein		
RCA23_c18250	NthA:nitrile hydratase alpha subunit NthA (4.2.1.84)		
RCA23_c18260	hypothetical protein DUF6 transmembrane	COG0697	G
RCA23_c18270	putative lipid A biosynthesis lauroyl acyltransferase	COG1560	M
RCA23_c18280	hypothetical protein	COG5429	S
RCA23_c18290	AcnA:aconitate hydratase AcnA (4.2.1.3)	COG1049	C
RCA23_c18300	CcmG:cytochrome c biogenesis protein CcmG	COG0526	O
RCA23_c18310	CcmC:cytochrome c-type biogenesis protein CcmC	COG0755	O
RCA23_c18320	CcmB:cytochrome c-type biogenesis protein CcmB	COG2386	O
RCA23_c18330	CcmA:cytochrome c biogenesis ATP-binding export protein CcmA (3.6.3.41)	COG4133	O
RCA23_c18340	hypothetical protein	COG3737	S
RCA23_c18350	SecF:protein export membrane protein SecF	COG0341	U



RCA23_c18360	SecD protein export membrane protein SecD	COG0342	U
RCA23_c18370	putative immunogenic membrane protein YajC	COG1862	U
RCA23_c18380	SerS:seryl-tRNA synthase SerS (6.1.1.11)	COG0172	J
RCA23_c18390	hypothetical protein, alpha/beta hydrolase-like	COG2267	I
RCA23_c18400	EngA:GTP-binding protein EngA	COG1160	R
RCA23_c18410	putative quinoprotein	COG1520	S
RCA23_c18420	hypothetical protein DUF2133	COG4649	S
RCA23_c18430	RND efflux transporter, MFP subunit	COG0845	M
RCA23_c18440	RND efflux transporter, permease protein	COG0841	V
RCA23_c18450	ABC transporter ATP-binding protein	COG5265	O
RCA23_c18460	hypothetical protein, peptidoglycan-binding protein domain LysM	COG1652	S
RCA23_c18470	RarD:protein RarD	COG2962	R
RCA23_c18480	SodB:superoxide dismutase SodB (1.15.1.1)	COG0605	P
RCA23_c18490	SoxG2:sarcosine oxidase subunit SoxG (1.5.3.1)	COG4583	E
RCA23_c18500	SoxA3:sarcosine oxidase alpha subunit SoxA (1.5.3.1)	COG0404	E
RCA23_c18510	SoxD3:sarcosine oxidase subunit SoxD (1.5.3.1)	COG4311	E
RCA23_c18520	SoxB3:sarcosine oxidase beta subunit SoxB (1.5.3.1)	COG0665	E
RCA23_c18530	CycH:cytochrome c-type biogenesis protein CycH	COG4235	O
RCA23_c18540	hypothetical protein	COG0816	L
RCA23_c18550	hypothetical protein DUF1289	COG3313	R
RCA23_c18560	hypothetical protein		
RCA23_c18570	hypothetical protein DUF81	COG0730	R
RCA23_c18580	Dus:tRNA-dihydrouridine synthase Dus (1.-.-.-)	COG0042	J
RCA23_c18590	putative peroxiredoxin (thioredoxin reductase)	COG0678	O
RCA23_c18600	benzaldehyde dehydrogenase	COG1012	C
RCA23_c18610	hypothetical protein		
RCA23_c18620	hypothetical protein	COG2130	R
RCA23_c18630	MFS-type transporter	COG2814	G
RCA23_c18640	sorbitol dehydrogenase (1.1.1.14)	COG1028	I
RCA23_c18650	6-hydroxynicotinate 3-monooxygenase (1.14.13.-)	COG0654	H
RCA23_c18660	hypothetical protein		
RCA23_c18670	glycerate kinase	COG2379	G
RCA23_c18680	putative carboxymuconolactone decarboxylase	COG5599	S
RCA23_c18690	FadH:2,4-dienoyl-CoA reductase [NADPH] (1.3.1.34)	COG1902	C
RCA23_c18700	thiamine pyrophosphate protein	COG0028	E
RCA23_c18710	RGrhtB: dTDP-glucose 4,6-dehydratase (4.2.1.46)	COG1088	M
RCA23_c18720	hypothetical protein		
RCA23_c18730	BetA3:choline dehydrogenase BetA (1.1.99.1)	COG2303	E
RCA23_c18740	ScoB:succinyl-CoA:3-ketoacid-coenzyme A transferase subunit ScoB (2.8.3.5)	COG2057	I
RCA23_c18750	ScoA:succinyl-CoA:3-ketoacid-coenzyme A transferase subunit ScoA (2.8.3.5)	COG1788	I
RCA23_c18760	hypothetical membrane protein		
RCA23_c18770	putative dimethyl sulfoniopropionate demethylase DmdA	COG4004	E
RCA23_c18780	HyuA2:hydantoin utilization protein A (3.5.2..)	COG0145	E
RCA23_c18790	HyuB2:hydantoin utilization protein B (3.5.2.14)	COG0146	E
RCA23_c18800	FAD dependent oxidoreductase	COG0665	E
RCA23_c18810	hypothetical protein, 3-beta hydroxysteroid dehydrogenase	COG0451	M
RCA23_c18820	hypothetical protein, serine/threonine-protein kinase	COG1262	S
RCA23_c18830	hypothetical protein	COG0457	R
RCA23_c18840	hypothetical protein DUF1989	COG3665	S
RCA23_c18850	putative diaminopropionate ammonia-lyase	COG1171	E
RCA23_c18860	hypothetical protein, metallopeptidase M24	COG0006	E
RCA23_c18870	hypothetical protein, Asp/Glu/hydantoin racemase	COG3473	Q
RCA23_c18880	putative 3-oxoadipate enol-lactonase 2, alpha/beta hydrolase family	COG0596	R
RCA23_c18890	hypothetical protein DUF1185		
RCA23_c18900	LimB:limonene 1,2-monooxygenase LimB (1.14.--.-)	COG2141	C
RCA23_c18910	aldehyde dehydrogenase, cytosolic (1.2.1.3)	COG1012	C
RCA23_c18920	PotC:ABC transporter, spermidine/putrescine import, permease protein PotC	COG1177	E
RCA23_c18930	PotB1:ABC transporter, spermidine/putrescine import, permease protein PotB	COG1176	E
RCA23_c18940	PotD:ABC transporter, spermidine/putrescine import, substrate binding protein P	COG0687	E
RCA23_c18950	PhaA1:ABC transporter, spermidine/putrescine import, ATP-binding protein PotA	COG3842	E
RCA23_c18960	putative nitrilotriacetate monooxygenase component B	COG1853	R
RCA23_c18970	hypothetical protein, DUF268		
RCA23_c18980	hypothetical protein DUF28	COG0217	S
RCA23_c18990	sodium/sulphate symporter	COG0471	P
RCA23_c19000	hypothetical protein	COG0697	G
RCA23_c19010	hypothetical protein	COG1692	S
RCA23_c19020	osmotically inducible OsmC-like protein	COG1764	O
RCA23_c19030	3-hydroxyacyl-CoA dehydrogenase, NAD-binding	COG1250	I
RCA23_c19040	AroK2:shikimate kinase AroK (2.7.1.71)	COG0703	E
RCA23_c19050	thioesterase-like protein	COG0824	R
RCA23_c19060	BoxA:benzoyl-CoA oxygenase component A (1.14.12.21)	COG0369	P
RCA23_c19070	BoxB:benzoyl-CoA oxygenase component B (1.14.12.21)	COG3396	S
RCA23_c19080	BoxC:benzoyl-CoA-dihydrodiol lyase BoxC (4.1.2.44)	COG1024	
RCA23_c19090	hypothetical protein DUF309		
RCA23_c19100	alpha/beta hydrolase	COG0596	R
RCA23_c19110	benzoate-coenzyme A ligase (6.2.1.25)	COG0318	I
RCA23_c19120	putative 5-formyltetrahydrofolate cyclo-ligase family protein	COG0212	H
RCA23_c19130	MgtE:magnesium transporter MgtE	COG2239	P
RCA23_c19140	GuaD:guanine deaminase GuaD (3.5.4.3)	COG0402	F
RCA23_c19150	putative hydroxydechloroatrazine ethylaminohydrolase	COG0402	F
RCA23_c19160	putative inositol monophosphatase family protein	COG0483	G
RCA23_c19170	putative helix-turn-helix protein	COG1396	K
RCA23_c19180	putative alcohol dehydrogenase	COG0604	C
RCA23_c19190	putative inner membrane protein	COG0670	R
RCA23_c19200	hypothetical protein		
RCA23_c19210	putative N-acetylmuramoyl-L-alanine amidase amiD	COG3023	V
RCA23_c19220	hypothetical protein		
RCA23_c19230	GatA3:glutamyl-tRNA(Gln) amidotransferase subunit A (6.3.5.-)	COG0154	J
RCA23_c19240	GatC:aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit GatC (6.3.5.-)	COG0721	J
RCA23_c19250	putative deaminase	COG0590	F
RCA23_c19260	putative ribosomal large subunit pseudouridine synthase B	COG1187	J
RCA23_c19270	ModC:molybdate ABC transporter, ATP-binding protein ModC (3.6.3.29)	COG4148	P
RCA23_c19280	ModB:molybdate ABC transporter, permease protein ModB	COG4149	P
RCA23_c19290	ModA:molybdate ABC transporter, substrate binding protein ModA	COG0725	P
RCA23_c19300	hypothetical protein, NUDIX hydrolase	COG0494	L
RCA23_c19310	hypothetical protein DUF1178	COG5319	S
RCA23_c19320	LysC:aspartokinase LysC (2.7.2.4)	COG0527	E
RCA23_c19330	PstI:phosphoenolpyruvate-protein phosphotransferase PstI (2.7.3.9)	COG3605	T
RCA23_c19340	hypothetical protein, acetyltransferase-like	COG3153	R
RCA23_c19350	hypothetical protein	COG1853	R
RCA23_c19360	putative sulfate transporter	COG0659	P
RCA23_c19370	MtrP:methylthioadenosine phosphorylase MtrP (2.4.2.28)	COG0005	F
RCA23_c19380	Apt:adenine phosphoribosyltransferase Apt (2.4.2.7)	COG0503	F
RCA23_c19390	RimJ:ribosomal-protein-alanine acetyltransferase RimJ (2.3.1.128)	COG1670	J
RCA23_c19400	YmxG:uncharacterized zinc protease YmxG (3.4.24.-)	COG0612	R
RCA23_c19410	ThrC:threonine synthase ThrC (4.2.3.1)	COG0498	E
RCA23_c19420	hypothetical protein, SURF1	COG1346	S
RCA23_c19430	CtaE:cytochrome c oxidase subunit 3 (1.9.3.1)	COG1845	C
RCA23_c19440	CtaG:cytochrome c oxidase assembly protein CtaG	COG3175	O
RCA23_c19450	CtaB:protoheme IX farnesyltransferase CtaB (2.5.1..)	COG0109	O
RCA23_c19460	CtaC:cytochrome c oxidase subunit 2 precursor (1.9.3.1)	COG1622	C
RCA23_c19470	TtdD:protein TtdD	COG0312	R
RCA23_c19480	SMF family protein	COG0758	L
RCA23_c19490	TopA:DNA topoisomerase TopA (5.99.1.2)	COG0550	L
RCA23_c19500	Fba:fructose-bisphosphate aldolase Fba (4.1.2.13)	COG0191	G
RCA23_c19510	IolB2:5-deoxy-glucuronate isomerase IolB (5.3.1..)	COG3718	G
RCA23_c19520	IolC:5-dehydro-2-deoxygluconokinase IolC (2.7.1.92)	COG0524	G
RCA23_c19530	IolD:3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase IolD (3.7.1..)	COG3962	E
RCA23_c19540	hypothetical protein DUF989	COG3748	S
RCA23_c19550	UrarH:5-hydroxyisourate hydrolase UrarH (3.5.2.17)	COG2351	R
RCA23_c19560	uric acid degradation bifunctional protein PucL (1.7.3.3/4.1.1..)	COG3195	S
RCA23_c19570	putative allantoin catabolism protein YibA	COG3257	R
RCA23_c19580	SoxB4:sarcosine oxidase beta subunit SoxB (1.5.3.1)	COG0665	E
RCA23_c19590	SoxD4:sarcosine oxidase subunit SoxD (1.5.3.1)	COG4311	E
RCA23_c19600	SoxA4:sarcosine oxidase alpha subunit SoxA (1.5.3.1)	COG0404	E
RCA23_c19610	SoxG3:sarcosine oxidase subunit SoxG (1.5.3.1)	COG4583	E
RCA23_c19620	putative HTH-type transcriptional regulator, AraC family	COG4977	K
RCA23_c19630	putative DNA-binding protein	COG1396	K
RCA23_c19640	putative membrane protein		
RCA23_c19650	hypothetical protein		
RCA23_c19660	hypothetical protein, thioesterase	COG2050	Q
RCA23_c19670	hypothetical protein, calcineurin-like phosphoesterase-like	COG1407	R
RCA23_c19680	putative DEAD/DEAH box helicase	COG1201	R
RCA23_c19690	FolD:bifunctional enzyme FolD (1.5.1.5;3.5.4.9)	COG0190	H
RCA23_c19700	Fhs:formate--tetrahydrofolate ligase Fhs (6.3.4.3)	COG2759	F
RCA23_c19710	hypothetical protein		
RCA23_c19720	FtsH:cell division protease FtsH (3.4.24.-)	COG0465	O
RCA23_c19730	TilS:tRNA(Ile)-lysidine synthase TilS (6.3.4.-)	COG0037	D
RCA23_c19740	hypothetical protein	COG1729	S
RCA23_c19750	Pal:peptidoglycan-associated lipoprotein Pal	COG2885	M
RCA23_c19760	TolB:Tol-Pal system beta propeller repeat protein TolB	COG0823	U
RCA23_c19770	hypothetical protein, TolA-like		
RCA23_c19780	TolR:biopolymer transport protein TolR	COG0848	U
RCA23_c19790	biopolymer transport protein TolQ	COG0811	U
RCA23_c19800	acyl-CoA thioester hydrolase (3.1.2..)	COG0824	R
RCA23_c19810	hypothetical protein		
RCA23_c19820	RuvB:holliday junction ATP-dependent DNA helicase RuvB (3.6.4.12)	COG2255	L
RCA23_c19830	RuvA:holliday junction ATP-dependent DNA helicase RuvA (3.6.4.12)	COG0632	L
RCA23_c19840	RuvC:crossover junction endodeoxyribonuclease RuvC (3.1.22.4)	COG0817	L
RCA23_c19850	putative ribosomal protein L11 methyltransferase	COG2264	J
RCA23_c19860	MsrA:peptide methionine sulfoxide reductase MsrA (1.8.4.11)	COG0225	O
RCA23_c19870	hypothetical protein, major facilitator superfamily transporter		
RCA23_c19880	LldD2:L-lactate dehydrogenase lldD (1.1.2.3)	COG1304	C
RCA23_c19890	DalT:BCCT family transporter involved in DMSP uptake	COG1292	M
RCA23_c19900	putative MFS-type transporter		
RCA23_c19910	RplY:50S ribosomal protein L25	COG1825	J
RCA23_c19920	Pth:peptidyl-tRNA hydrolase Pth (3.1.1.29)	COG0193	J
RCA23_c19930	hypothetical protein	COG4427	S
RCA23_c19940	hypothetical protein	COG3651	S
RCA23_c19950	TrpB:tryptophan synthase beta chain TrpB (4.2.1.20)	COG0133	E
RCA23_c19960	TrpF:N-(5'-phosphoribosyl)anthranilate isomerase TrpF (5.3.1.24)	COG0135	E
RCA23_c19970	hypothetical protein		
RCA23_c19980	IHfB:integration host factor beta subunit IHfB	COG0776	L
RCA23_c19990	RpsA:30S ribosomal protein S1	COG0539	J
RCA23_c20000	hypothetical protein		
RCA23_c20010	hypothetical protein, lacI family HTH-type regulatory protein	COG1609	K
RCA23_c20020	putative phytanoyl-CoA dioxygenase	COG5285	Q
RCA23_c20030	aldo/keto reductase	COG0667	C
RCA23_c20040	Cmk:cytidylate kinase Cmk (2.7.4.14)	COG0283	F
RCA23_c20050	AroA:3-phosphoshikimate 1-carboxyvinyltransferase AroA (2.5.1.19)	COG0128	E
RCA23_c20060	TrmB:tRNA (guanine-N(7)-)-methyltransferase TrmB (2.1.1.33)	COG0220	R
RCA23_c20070	MetK:S-adenosylmethionine synthase MetK (2.5.1.6)	COG0192	H
RCA23_c20080	Lnt:apolipoprotein N-acyltransferase Lnt (2.3.1.-)	COG0815	M
RCA23_c20090	putative magnesium and cobalt efflux protein	COG1253	R
RCA23_c20100	hypothetical protein UPF0054	COG0319	R
RCA23_c20110	PrcH-like protein	COG1702	T
RCA23_c20120	RNA modification enzyme, MiaB family	COG0621	J
RCA23_c20130	hypothetical protein		
RCA23_c20140	putative ferric uptake regulator family protein	COG0735	P
RCA23_c20150	FabA:3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase FabA (4.2.1.60)	COG0764	I
RCA23_c20160	FabB:3-oxoacyl-[acyl-carrier-protein] synthase FabB (2.3.1.41)	COG0304	I
RCA23_c20170	FabI2:enoyl-[acyl-carrier-protein] reductase FabI (1.3.1.9)	COG0623	I
RCA23_c20180	SRY:threo-3-hydroxyaspartate ammonia-lyase SRY (4.3.1.16)	COG1171	E
RCA23_c20190	2-haloalkanoic acid dehalogenase (3.8.1.2)	COG1011	R
RCA23_c20200	CatD:3-oxoadipate enol-lactonase CatD (3.1.1.24)	COG0596	R
RCA23_c20210	putative tetracycline resistance protein, class C	COG2814	G
RCA23_c20220	NAD/mycothiol-dependent formaldehyde dehydrogenase (1.2.1.66)	COG1062	C
RCA23_c20230	DgoD:D-galactonate dehydratase DgoD (4.2.1.6)	COG4948	M
RCA23_c20240	dimethylglycine dehydrogenase	COG0404	E
RCA23_c20250	MtbB6:trimethylamine methyltransferase MtbB (2.1.1..)	COG5598	H
RCA23_c20260	hypothetical protein	COG0607	P
RCA23_c20270	uncharacterized aminotransferase (2.6.1..)	COG0161	H
RCA23_c20280	GcvT2:aminomethyltransferase, mitochondrial (2.1.2.10)	COG0404	E
RCA23_c20290	GcvH:glycine cleavage system protein GcvH	COG0509	E
RCA23_c20300	GcvP:glycine dehydrogenase GcvP (1.4.4.2)	COG1003	E
RCA23_c20310	DsdA2:D-amino acid dehydrogenase small subunit DsdA (1.4.99.1)	COG0665	E
RCA23_c20320	PotF:putrescine ABC transport system putrescine- binding periplasmic protein P	COG0687	E
RCA23_c20330	PotG:putrescine ABC transport system ATP-binding protein PotG	COG3842	E
RCA23_c20340	PotI:putrescine ABC transport system permease protein PotI	COG1177	E
RCA23_c20350	PotB2:putrescine ABC transport system permease protein PotB	COG1176	E
RCA23_c20360	Ileske 2Fe-2S domain protein	COG4638	P
RCA23_c20370	DctM6:TRAP dicarboxylate transporter, subunit DctM	COG1593	G

RCA23_c20380	hypothetical protein	COG3090	G
RCA23_c20390	putative TRAP transporter DctP subunit	COG1638	G
RCA23_c20400	putative phytanoyl-CoA dioxygenase	COG5285	Q
RCA23_c20410	putative phenylacetic acid degradation NADH oxidoreductase paaE (1.-.-.-)	COG1018	C
RCA23_c20420	PaaD:phenylacetate-CoA oxygenase, subunit PaaD	COG2151	R
RCA23_c20430	PaaC:phenylacetate-CoA oxygenase, subunit PaaC	COG3396	S
RCA23_c20440	PaaB:phenylacetate-CoA oxygenase, subunit PaaB	COG3460	Q
RCA23_c20450	PaaA:phenylacetate-CoA oxygenase, subunit PaaA	COG3396	S
RCA23_c20460	PaaX:phenylacetic acid degradation operon negative regulatory protein PaaX	COG3327	K
RCA23_c20470	PaaZ:phenylacetic acid degradation protein PaaZ	COG1012	C
RCA23_c20480	putative enoyl-CoA hydratase PaaG (4.2.1.17)	COG1024	I
RCA23_c20490	PaaI:acyl-coenzyme A thioesterase PaaI (3.1.2.-)	COG0824	Q
RCA23_c20500	PaaJ:beta-ketoadipyl CoA thiolase PaaJ (2.3.1.9)	COG0183	I
RCA23_c20510	PaaK:phenylacetate-CoA ligase PaaK (6.2.1.30)	COG1541	H
RCA23_c20520	putative HTH-type transcriptional regulator, TetR family	COG1309	K
RCA23_c20530	AroQ:3-dehydroquinate dehydratase AroQ (4.2.1.10)	COG0757	E
RCA23_c20540	tyrosine decarboxylase (4.1.1.25)	COG0076	E
RCA23_c20550	putative short chain dehydrogenase	COG0300	R
RCA23_c20560	hypothetical protein, acetyltransferase-like	COG1247	M
RCA23_c20570	CsaA:protein CsaA	COG0073	R
RCA23_c20580	ProC:pyrroline-5-carboxylate reductase ProC (1.5.1.2)	COG0345	E
RCA23_c20590	hypothetical protein DUF1790	COG5465	S
RCA23_c20600	hypothetical protein DUF526	COG2960	S
RCA23_c20610	Lgt:prolipoprotein diacylglycerol transferase Lgt (2.4.99.-)	COG0682	M
RCA23_c20620	hypothetical protein DUF185	COG1565	S
RCA23_c20630	multi-copper polyphenol oxidoreductase laccase	COG1496	S
RCA23_c20640	hypothetical protein		
RCA23_c20650	Lrp:leucine-responsive regulatory protein Lrp	COG1522	K
RCA23_c20660	TrxB:thioredoxin reductase TrxB (1.8.1.9)	COG0492	O
RCA23_c20670	CysC:bifunctional sulfate adenylyltransferase / adenylyl-sulfate kinase CysC (2.	COG2046	P
RCA23_c20680	hypothetical protein DUF1150		
RCA23_c20690	IbpA2:small heat shock protein IbpA	COG0071	O
RCA23_c20700	hypothetical protein DUF465	COG5481	S
RCA23_c20710	PurE:N5-carboxyaminoimidazole ribonucleotide mutase PurE (5.4.99.18)	COG0041	F
RCA23_c20720	PurK:N5-carboxyaminoimidazole ribonucleotide synthase PurK (6.3.4.18)	COG0026	F
RCA23_c20730	hypothetical protein	COG1075	R
RCA23_c20740	GroEL:chaperonin GroEL	COG0459	O
RCA23_c20750	GroS:chaperonin GroS	COG0234	O
RCA23_c20760	hypothetical protein		
RCA23_c20770	hypothetical protein		
RCA23_c20780	hypothetical protein		
RCA23_c20790	creatinase	COG0006	E
RCA23_c20800	putative membrane lipoprotein		
RCA23_c20810	hypothetical protein DUF261	COG5482	S
RCA23_c20820	putative manganese-dependent inorganic pyrophosphatase PpaC (3.6.1.1)	COG1227	C
RCA23_c20830	hypothetical protein, HAD family hydrolase	COG0647	G
RCA23_c20840	putative MatC-like dehydratase	COG2030	I
RCA23_c20850	RibF:riboflavin biosynthesis protein RibF (2.7.1.26;2.7.7.2)	COG0196	H
RCA23_c20860	hypothetical protein UPF0260	COG2983	S
RCA23_c20870	LiaE:low specificity L-threonine aldolase liaE (4.1.2.5)	COG2008	E
RCA23_c20880	hypothetical protein, 2-hydroxychromene- 2- carboxylate isomerase-like	COG3917	Q
RCA23_c20890	Prs:ribose-phosphate pyrophosphokinase Prs (2.7.6.1)	COG0462	F
RCA23_c20900	hypothetical protein		
RCA23_c20910	AtpC:ATP synthase epsilon chain AtpC (3.6.3.14)	COG0355	C
RCA23_c20920	AtpD:ATP synthase beta subunit AtpD (3.6.3.14)	COG0055	C
RCA23_c20930	AtpG:ATP synthase gamma chain AtpG (3.6.3.14)	COG0224	C
RCA23_c20940	AtpA:ATP synthase alpha subunit AtpA (3.6.3.14)	COG0056	C
RCA23_c20950	AtpH:ATP synthase delta chain AtpH (3.6.3.14)	COG0712	C
RCA23_c20960	hypothetical protein		
RCA23_c20970	GloB:hydroxyacylglutathione hydrolase GloB (3.1.2.6)	COG0491	R
RCA23_c20980	ClpA:ATP-dependent Clp protease ATP-binding subunit ClpA	COG0542	O
RCA23_c20990	hypothetical protein, OmpA	COG1360	N
RCA23_c21000	hypothetical protein		
RCA23_c21010	putative cation transport protein ChaC	COG3703	P
RCA23_c21020	hypothetical protein	COG1357	S
RCA23_c21030	TyrC:protein TyrC (1.3.1.43;1.3.1.12)	COG0287	E
RCA23_c21040	HisC2:histidinol-phosphate aminotransferase HisC (2.6.1.9)	COG0079	E
RCA23_c21050	RpsD:30S ribosomal protein S4	COG0522	J
RCA23_c21060	cold-shock DEAD box protein A (3.6.4.13)	COG0513	L
RCA23_c21070	hypothetical protein DUF393	COG3011	S
RCA23_c21080	vitamin B12-dependent ribonucleoside-diphosphate reductase (1.17.4.1)	COG0209	F
RCA23_c21090	hypothetical protein	COG5458	S
RCA23_c21100	HisG:ATP-phosphoribosyltransferase HisG (2.4.2.17)	COG0040	E
RCA23_c21110	HisZ:ATP phosphoribosyltransferase regulatory subunit HisZ	COG3705	E
RCA23_c21120	HisS:histidyl-tRNA synthase HisS (6.1.1.21)	COG0124	J
RCA23_c21130	hypothetical protein	COG2900	S
RCA23_c21140	DnaE2:DNA polymerase III 1 alpha subunit DnaE (2.7.7.7)	COG0587	L
RCA23_c21150	XdhA:xanthine dehydrogenase XdhA (1.17.1.4)	COG4630	F
RCA23_c21160	XdhB:xanthine dehydrogenase XdhB (1.17.1.4)	COG4631	F
RCA23_c21170	XdhC:xanthine dehydrogenase accessory protein XdhC	COG1975	O
RCA23_c21180	sugar ABC transporter, ATP-binding protein	COG3845	R
RCA23_c21190	sugar ABC transporter, permease protein	COG4603	R
RCA23_c21200	ABC transporter permease protein	COG1079	R
RCA23_c21210	putative basic membrane protein	COG1744	R
RCA23_c21220	putative FAD dependent oxidoreductase	COG0665	E
RCA23_c21230	dimethylglycine dehydrogenase (1.5.99.2)	COG0404	E
RCA23_c21240	PanC:pantothenate synthase PanC (6.3.2.1)	COG0414	H
RCA23_c21250	PanB:1:3-methyl-2-oxobutanoate hydroxymethyltransferase PanB (2.1.2.11)	COG0413	H
RCA23_c21260	hypothetical protein	COG3807	S
RCA23_c21270	Dcp:peptidyl-dipeptidase Dcp (3.4.15.5)	COG0339	E
RCA23_c21280	MoeB:molybdopterin biosynthesis protein MoeB	COG0476	H
RCA23_c21290	Dut:deoxyuridine 5'-triphosphate nucleotidohydrolase Dut (3.6.1.23)	COG0756	F
RCA23_c21300	CoaBC:coenzyme A biosynthesis bifunctional protein CoaBC (4.1.1.36;6.3.2.5)	COG0452	H
RCA23_c21310	RpoH2:RNA polymerase sigma-32 factor RpoH	COG0568	K
RCA23_c21320	CobP:bifunctional adenosylcobalamin biosynthesis protein CobP (2.7.1.156;2.7	COG0087	H
RCA23_c21330	putative phosphoglycerate mutase family protein	COG0406	G
RCA23_c21340	hypothetical protein, glutathione S-transferase	COG0625	O
RCA23_c21350	glutathione S-transferase family protein		
RCA23_c21360	magnesium chelatase-like protein	COG0606	O
RCA23_c21370	magnesium chelatase	COG0606	O
RCA23_c21380	putative transmembrane protein		
RCA23_c21390	putative sulfite exporter TauE/SafE	COG0730	R
RCA23_c21400	branched-chain amino acid transporter, permease component	COG1079	R
RCA23_c21410	branched-chain amino acid transporter, permease component	COG4603	R
RCA23_c21420	ABC transporter ATP-binding protein	COG3845	R
RCA23_c21430	putative ABC transporter, periplasmic substrate- binding protein	COG1744	R
RCA23_c21440	hypothetical protein, acetyltransferase-like	COG0456	R
RCA23_c21450	NfU-like protein	COG0694	O
RCA23_c21460	putative universal stress protein	COG0589	T
RCA23_c21470	TrpS:tryptophanyl-tRNA synthase TrpS (6.1.1.2)	COG0180	J
RCA23_c21480	hypothetical protein, rhomboid protease	COG0705	R
RCA23_c21490	MviN:virulence factor MviN homolg	COG0728	R
RCA23_c21500	GlnD:uridylyltransferase GlnD (2.7.7.59)	COG2844	O
RCA23_c21510	hypothetical protein	COG0683	E
RCA23_c21520	putative tetrapyrrole methylase	COG0313	R
RCA23_c21530	hypothetical protein UPF0102	COG0792	L
RCA23_c21540	GshB:glutathione synthase GshB (6.3.2.3)	COG0189	H
RCA23_c21550	putative esterase/lipase	COG0657	I
RCA23_c21560	NusB:NusB-like protein NusB	COG0781	K
RCA23_c21570	RibH:6,7-dimethyl-8-ribityllumazine synthase RibH (2.5.1.9)	COG0054	H
RCA23_c21580	RibB:riboflavin biosynthesis protein RibB (4.1.99.12)	COG0108	H
RCA23_c21590	RibE:riboflavin synthase alpha chain RibE (2.5.1.9)	COG0307	H
RCA23_c21600	putative capsule polysaccharide export protein	COG3563	M
RCA23_c21610	putative polysaccharide export protein	COG1596	M
RCA23_c21620	putative capsule polysaccharide export protein	COG3563	M
RCA23_c21630	RibD:riboflavin biosynthesis protein RibD (3.5.4.26;1.1.1.193)	COG0117	H
RCA23_c21640	NrdR:transcriptional repressor NrdR	COG1327	K
RCA23_c21650	RpoD:RNA polymerase sigma factor RpoD	COG0568	K
RCA23_c21660	DnaG:DNA primase DnaG (2.7.7.-)	COG0358	L
RCA23_c21670	SoxG4:sarcosine oxidase subunit SoxG (1.5.3.1)	COG4583	E
RCA23_c21680	SoxA5:sarcosine oxidase alpha subunit SoxA (1.5.3.1)	COG0404	E
RCA23_c21690	SoxD5:sarcosine oxidase subunit SoxD (1.5.3.1)	COG4311	E
RCA23_c21700	SoxB5:sarcosine oxidase beta subunit SoxB (1.5.3.1)	COG0665	E
RCA23_c21710	Psd:phosphatidylserine decarboxylase proenzyme Psd (4.1.1.65)	COG0688	I
RCA23_c21720	dacylglycerol kinase (2.7.1.107)	COG0818	M
RCA23_c21730	putative sulfatase	COG2194	R
RCA23_c21740	hypothetical protein, CDP-alcohol phosphatidyltransferase-like	COG1183	I
RCA23_c21750	hypothetical protein	COG0671	I
RCA23_c21760	hypothetical protein	COG2194	R
RCA23_c21770	hypothetical protein, DUF1705	COG2194	R
RCA23_c21780	GluD:glutamate dehydrogenase GluD (1.4.1.3)	COG0334	E
RCA23_c21790	hypothetical protein		
RCA23_c21800	GarR4:2-hydroxy-3-oxopropionate reductase GarR (1.1.1.60)	COG2084	I
RCA23_c21810	reductive dehalogenase	COG1600	C
RCA23_c21820	ktrn	COG1741	R
RCA23_c21830	transcriptional regulator	COG1309	K
RCA23_c21840	hypothetical protein		
RCA23_c21850	Hom:homoserine dehydrogenase Hom (1.1.1.3)	COG0460	E
RCA23_c21860	GlpX:fructose-1,6-bisphosphatase class II (3.1.3.11)	COG1494	G
RCA23_c21870	putative single-stranded-DNA:specific exonuclease	COG0608	L
RCA23_c21890	ComE:sulfopyruvate decarboxylase beta subunit ComE (4.1.1.79)	COG0028	E
RCA23_c21900	ComD:sulfopyruvate decarboxylase alpha subunit ComD (4.1.1.79)	COG4032	R
RCA23_c21910	zinc-type alcohol dehydrogenase	COG1063	E
RCA23_c21920	Gno2:gluconate 5-dehydrogenase Gno (1.1.1.69)	COG1028	I
RCA23_c21930	HisD2:histidinol dehydrogenase HisD (1.1.1.23)	COG0141	E
RCA23_c21940	HTH-type transcriptional regulator, LacI family	COG1609	K
RCA23_c21950	HTH-type transcriptional regulator, IclR family	COG1414	K
RCA23_c21960	AdhJ2:alcohol dehydrogenase AdhJ (1.1.99.-)	COG2303	E
RCA23_c21970	TerC:integral membrane protein TerC	COG0861	P
RCA23_c21980	putative TRAP transporter, DctP subunit	COG4663	Q
RCA23_c21990	DctM:DctQ TRAP transporter, DctM/DcxD subunit	COG4664	Q
RCA23_c22000	dimethylamine methyltransferase (2.1.1.-)	COG5598	H
RCA23_c22010	putative HAD-family hydrolase	COG0546	R
RCA23_c22020	hypothetical protein		
RCA23_c22030	hypothetical protein		
RCA23_c22040	hypothetical protein		
RCA23_c22050	hypothetical protein	COG5349	S
RCA23_c22060	hypothetical protein, NUDIX hydrolase	COG2494	L
RCA23_c22070	hypothetical protein		
RCA23_c22080	putative fatty acid desaturase	COG3239	I
RCA23_c22090	putative helix-turn-helix protein	COG1396	K
RCA23_c22100	short chain dehydrogenase (1.1.1.-)	COG1028	I
RCA23_c22110	putative 3-hydroxyacyl-CoA dehydrogenase	COG1250	I
RCA23_c22130	hypothetical protein, DUF849	COG3246	S
RCA23_c22120	transcriptional regulator, AraC family	COG4977	K
RCA23_c22140	Tas:protein Tas	COG0667	C
RCA23_c22150	hypothetical protein	COG4544	S
RCA23_c22160	putative MFS-type transporter	COG2211	G
RCA23_c22170	MetG:methionyl-tRNA synthase MetG (6.1.1.10)	COG0143	J
RCA23_c22190	integrase		GI B
RCA23_c22200	integrase	COG4974	L GI B
RCA23_c22210	putative nucleotidyl transferase	COG1210	M GI B
RCA23_c22220	hypothetical protein		GI B
RCA23_c22230	hypothetical protein		GI B
RCA23_c22240	putative replication factor C, small subunit	COG2256	L GI B
RCA23_c22250	hypothetical protein		GI B
RCA23_c22260	hypothetical protein		GI B
RCA23_c22270	ParB-like nuclease	COG1475	K GI B
RCA23_c22280	CadA:cadmium-transporting ATPase CadA (3.6.3.3)	COG2217	P GI B
RCA23_c22290	hypothetical protein	COG3034	S GI B
RCA23_c22300	putative lipoprotein signal peptidase	COG0597	M GI B
RCA23_c22310	putative ZIP zinc transporter	COG0428	P GI B
RCA23_c22320	hypothetical protein DUF411	COG3019	R GI B
RCA23_c22330	SCO-like protein	COG1999	R GI B
RCA23_c22340	hypothetical protein	COG2847	S GI B
RCA23_c22350	hypothetical protein	COG1651	O GI B
RCA23_c22360	hypothetical protein, disulfide bond formation protein	COG1495	O GI B
RCA23_c22370	SCO-like protein	COG1999	R GI B
RCA23_c22380	putative HTH-type transcriptional regulator	COG0789	K GI B
RCA23_c22390	hypothetical protein UPF0060	COG1742	S GI B
RCA23_c22400	hypothetical protein		GI B
RCA23_c22410	hypothetical protein		GI B

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RCA23_c26510	hypothetical protein		GI 10
RCA23_c26520	hypothetical protein	COG1709	K
RCA23_c26530	hypothetical protein		GI 10
RCA23_c26540	putative RTX toxin and hemolysin-type calcium binding protein		GI 10
RCA23_c26550	putative RTX toxin and hemolysin-type calcium binding protein		GI 10
RCA23_c26560	type I secretion outer membrane protein, TolC family	COG1538	M
RCA23_c26570	type I secretion system ATP-binding component	COG2274	V
RCA23_c26580	type I RTX secretion system membrane fusion protein, HlyD family	COG1566	V
RCA23_c26590	hypothetical protein		GI 10
RCA23_c26600	hypothetical protein		GI 10
RCA23_c26610	hypothetical protein		GI 10
RCA23_c26620	hypothetical protein		GI 10
RCA23_c26630	hypothetical protein DUF2125		GI 10
RCA23_c26640	Asp/Glu racemase (5.1.1.-)	COG3473	Q
RCA23_c26650	cystathionine beta-lyase (4.4.1.8)	COG0626	E
RCA23_c26660	PhrB2:deoxyribodipyrimidine photo-lyase PhrB (4.1.99.3)	COG0415	L
RCA23_c26670	hypothetical protein	COG3380	R
RCA23_c26680	Gcp:O-sialylglycoprotein endopeptidase Gcp (3.4.24.57)	COG0533	O
RCA23_c26690	SusS/YcjO/YndC/YwfC family protein	COG0009	J
RCA23_c26700	putative glycoprotease family protein	COG1214	O
RCA23_c26710	hypothetical protein LPF0079	COG0802	R
RCA23_c26720	xylose isomerase family protein	COG3622	G
RCA23_c26730	putative phage integrase	COG0582	L
RCA23_c26740	hypothetical protein		GI 10
RCA23_c26750	putative prophage regulatory protein	COG3311	K
RCA23_c26760	hypothetical protein		GI 10
RCA23_c26770	DNA polymerase	COG0749	L
RCA23_c26780	hypothetical protein		GI 10
RCA23_c26790	hypothetical protein, snoal_like polyketide cyclase	COG5485	R
RCA23_c26800	hypothetical protein		GI 10
RCA23_c26810	glyoxalase/bleomycin resistance protein/dioxygenase superfamily protein		GI 10
RCA23_c26820	hypothetical protein		GI 10
RCA23_c26830	putative ABC transporter permease protein	COG0395	G
RCA23_c26840	putative ABC transporter permease protein	COG1175	G
RCA23_c26850	putative ABC transporter extracellular solute binding protein	COG1653	G
RCA23_c26860	ABC transporter ATP-binding protein	COG3839	G
RCA23_c26870	HisD3:histidinol dehydrogenase HisD (1.1.1.23)	COG0141	E
RCA23_c26880	hypothetical protein, snoal_like polyketide cyclase	COG5485	R
RCA23_c26890	short chain dehydrogenase	COG1028	I
RCA23_c26900	putative HTH-type transcriptional regulator LacI family	COG1609	K
RCA23_c26910	hypothetical protein, snoal_like polyketide cyclase		GI 10
RCA23_c26920	hypothetical protein		GI 10
RCA23_c26930	hypothetical protein, 2-hydroxypropyl-CoM lyase- like	COG0620	E
RCA23_c26940	hypothetical protein, alpha/beta hydrolase-like	COG0596	R
RCA23_c26950	hypothetical protein	COG0684	H
RCA23_c26960	MmsB2:3-hydroxyisobutyrate dehydrogenase MmsB (1.1.1.31)	COG2084	I
RCA23_c26970	HsD3:dihydroxy-acid dehydratase IlvD (4.2.1.9)	COG0129	E
RCA23_c26980	hypothetical protein	COG4091	E
RCA23_c26990	putative choline (or alcohol) dehydrogenase (1.1.99.1)	COG2303	E
RCA23_c27000	aldehyde dehydrogenase (1.2.1.3)	COG1012	C
RCA23_c27010	transporter, LysE family	COG1280	E
RCA23_c27020	DctM11:TRAP dicarboxylate transporter, subunit DctM	COG4664	Q
RCA23_c27030	DctQ8:TRAP dicarboxylate transporter, subunit DctQ	COG4665	Q
RCA23_c27040	DctP10:TRAP dicarboxylate transporter, subunit DctP	COG4663	Q
RCA23_c27050	transcriptional regulator, LysR family	COG0583	K
RCA23_c27060	mandelate racemase/muconate lactonizing enzyme	COG4948	M
RCA23_c27070	Zn-dependant oxidoreductase	COG0604	C
RCA23_c27090	HTH-type transcriptional regulator, LysR family	COG0583	K
RCA23_c27100	class II aldolase	COG0235	G
RCA23_c27110	fatty acid desaturase	COG3239	I
RCA23_c27120	PanB2:3-methyl-2-oxobutanoate hydroxymethyltransferase PanB (2.1.2.11)	COG0413	H
RCA23_c27130	putative nesfe (2Fe-2S) protein	COG2146	P
RCA23_c27150	hypothetical protein	COG1441	K
RCA23_c27160	arginase family protein	COG0010	E
RCA23_c27170	hypothetical protein	COG1082	G
RCA23_c27180	putative HTH-type transcriptional regulator, AraC family	COG2169	F
RCA23_c27190	hypothetical protein, fatty acid desaturase	COG3239	I
RCA23_c27200	AMP-dependent synthase / ligase	COG0318	I
RCA23_c27210	ABC transporter ATP-binding protein	COG1132	V
RCA23_c27220	spore coat family protein		
RCA23_c27230	PapD-like chaperone involved in fimbrial biogenesis	COG3121	N
RCA23_c27240	fimbrial biogenesis outer membrane usher protein	COG3188	N
RCA23_c27250	fimbrial biogenesis outer membrane usher protein	COG3188	N
RCA23_c27260	hypothetical protein		
RCA23_c27280	hypothetical protein	COG0697	G
RCA23_c27290	RpoC:DNA-directed RNA polymerase beta subunit RpoC (2.7.7.6)	COG0086	K
RCA23_c27300	RpoB:DNA-directed RNA polymerase beta subunit RpoB (2.7.7.6)	COG0085	K
RCA23_c27310	RplL:50S ribosomal protein L7/L12	COG0222	J
RCA23_c27320	RplJ:50S ribosomal protein L10	COG0244	J
RCA23_c27330	RplA:50S ribosomal protein L1	COG0081	J
RCA23_c27340	RplK:50S ribosomal protein L11	COG0080	J
RCA23_c27350	NusG:transcription antitermination protein NusG	COG0250	K
RCA23_c27360	SecE:preprotein translocase, subunit SecE	COG0690	U
RCA23_c27370	hypothetical protein		
RCA23_c27430	hypothetical protein		
RCA23_c27440	hypothetical protein, transmembrane		
RCA23_c27450	hypothetical protein		
RCA23_c27460	putative acetolactate synthase isozyme 1 large subunit	COG0028	E
RCA23_c27470	putative cation transporter	COG0168	P
RCA23_c27480	FolE:GTP cyclohydrolase FolE (3.5.4.16)	COG1469	S
RCA23_c27490	MetZ:O-succinylhomoserine sulfhydrylase MetZ (2.5.1.-)	COG0626	E
RCA23_c27500	hypothetical protein	COG0625	O
RCA23_c27510	putative intracellular septation protein	COG2917	D
RCA23_c27520	hypothetical protein	COG0697	G
RCA23_c27530	putative cell division protein	COG0552	U
RCA23_c27540	NuoEF:NADH-quinone oxidoreductase subunits E/F (fused) (1.6.99.5)	COG1894	C
RCA23_c27550	XseA:exodeoxyribonuclease 7 large subunit XseA (3.1.11.6)	COG1570	L
RCA23_c27560	PurD:phosphoribosylamine--glycine ligase PurD (6.3.4.13)	COG0151	F
RCA23_c27570	hypothetical protein, ferredoxin	COG0633	C
RCA23_c27580	hypothetical protein	COG0587	L
RCA23_c27590	periplasmic serine protease DO-like (3.4.21..)	COG0265	O
RCA23_c27600	putative protein MfC	COG0330	O
RCA23_c27610	HlkC:protein HlkC	COG0330	O
RCA23_c27620	Gor:glutathione reductase Gor (1.8.1.7)	COG1249	C
RCA23_c27630	RpiA:ribose-5-phosphate isomerase A (5.3.1.6)	COG0120	G
RCA23_c27640	hypothetical protein		
RCA23_c27650	SdaB:L-serine dehydratase SdaB (4.3.1.17)	COG1760	E
RCA23_c27660	putative integral membrane protein	COG0697	G
RCA23_c27670	hypothetical protein, thiamine pyrophosphokinase	COG1564	H
RCA23_c27680	hypothetical protein		
RCA23_c27690	hypothetical protein		
RCA23_c27700	hypothetical protein		
RCA23_c27710	PurA:adenylosuccinate synthase PurA (6.3.4.4)	COG0104	F
RCA23_c27720	SecG:preprotein translocase, SecG subunit SecG		
RCA23_c27730	CTP synthase (6.3.4.2)	COG0504	F
RCA23_c27740	hypothetical protein, DUF1330	COG5470	S
RCA23_c27750	hypothetical protein DUF1332	COG4103	S
RCA23_c27760	hypothetical protein	COG3221	P
RCA23_c27770	amino acid transport ATP-binding protein	COG4598	E
RCA23_c27780	putative amino acid transport extracellular solute binding protein	COG0834	E
RCA23_c27790	putative ABC transporter inner membrane component	COG4215	E
RCA23_c27800	putative amino acid transport permease protein	COG4160	E
RCA23_c27810	PuuA2:gamma-glutamylputrescine synthase PuuA (6.3.1.11)	COG0174	E
RCA23_c27820	hypothetical protein, glutamine amidotransferase class I	COG0518	F
RCA23_c27830	PuuA3:gamma-glutamylputrescine synthase PuuA (6.3.1.11)	COG0174	E
RCA23_c27840	PuuB2:gamma-glutamylputrescine oxidoreductase PuuB (1.4.3..)	COG0665	E
RCA23_c27850	aminotransferase class III (2.6.1..)	COG0161	H
RCA23_c27860	putative PHB synthesis repressor protein	COG5394	S
RCA23_c27870	hypothetical protein		
RCA23_c27880	PhaC:poly(R)-hydroxyalkanoic acid synthase PhaC (2.3.1..)	COG3243	I
RCA23_c27890	PhaZ:polyhydroxyalkanoate depolymerase PhaZ	COG4553	I
RCA23_c27900	putative ribosome biogenesis GTPase RsgA (3.6.1..)	COG1162	R
RCA23_c27910	hypothetical protein, alpha/beta hydrolase-like	COG0596	R
RCA23_c27920	hypothetical protein		
RCA23_c27930	hypothetical protein, alpha/beta hydrolase-like	COG0596	R
RCA23_c27940	ThrS:threonyl-tRNA synthase ThrS (6.1.1.3)	COG0441	J
RCA23_c27950	hypothetical protein, ArsC	COG1393	P
RCA23_c27960	thymidylate synthase (2.1.1.148)	COG1351	F
RCA23_c27970	putative glyoxalase/bleomycin resistance protein/dioxygenase superfamily protei	COG3346	E
RCA23_c27980	hypothetical protein		
RCA23_c27990	putative transcriptional regulatorm marR family	COG1846	K
RCA23_c28000	hypothetical protein DUF339	COG2938	S
RCA23_c28010	hypothetical protein, DNA binding	COG1813	K
RCA23_c28020	AatA:aspartate aminotransferase AatA (2.6.1.1)	COG0436	E
RCA23_c28030	hypothetical protein		
RCA23_c28040	NorM:multidrug resistance protein NorM	COG0534	V
RCA23_c28050	ParE:DNA topoisomerase 4 subunit B (5.99.1..)	COG0187	L
RCA23_c28060	hypothetical protein	COG3238	S
RCA23_c28070	putative malate/L-lactate dehydrogenase	COG2055	C
RCA23_c28080	LolD:lipoprotein-releasing system ATP-binding protein LolD (3.6.3..)	COG1136	V
RCA23_c28090	lipoprotein-releasing system transmembrane protein, lolC/E family	COG4591	M
RCA23_c28100	ProS:prolyl-tRNA synthase ProS (6.1.1.15)	COG0442	J
RCA23_c28110	hypothetical protein DUF20	COG0628	R
RCA23_c28120	hypothetical protein	COG0593	L
RCA23_c28130	Ppk:polyphosphate kinase Ppk (2.7.4.1)	COG0855	P
RCA23_c28140	putative phosphatase	COG0248	F
RCA23_c28150	hypothetical protein, DnaJ	COG1076	O
RCA23_c28160	hypothetical protein		
RCA23_c28170	McmA2:methylmalonyl-CoA mutase McmA (5.4.99.2)	COG1884	I
RCA23_c28180	hypothetical protein		
RCA23_c28190	AccC2:biotin carboxylase AccC (6.3.4.14)	COG4770	I
RCA23_c28200	hypothetical protein		
RCA23_c28210	propionyl-CoA carboxylase beta chain, mitochondrial precursor (6.4.1.3)	COG4799	I
RCA23_c28220	putative major facilitator superfamily transporter	COG2814	G
RCA23_c28230	hypothetical protein	COG3800	R
RCA23_c28240	BetB:betaine aldehyde dehydrogenase BetB (1.2.1.8)	COG1012	C
RCA23_c28250	hypothetical protein	COG0697	G
RCA23_c28260	DctM12:TRAP dicarboxylate transporter, DctM subunit DctM	COG1593	G
RCA23_c28270	putative TRAP transporter, DctQ component	COG4665	Q
RCA23_c28280	putative TRAP transporter extracellular solute binding protein, family 7	COG1638	G
RCA23_c28290	transcriptional regulator, LacI family	COG1609	K
RCA23_c28300	hypothetical protein, DUF81 family	COG0730	R
RCA23_c28310	SgaA2:serine--glycine aminotransferase SgaA (2.6.1.45)	COG0075	E
RCA23_c28320	DltD:lactate dehydrogenase Dlt (1.1.2.4)	COG0277	C
RCA23_c28330	hypothetical protein		
RCA23_c28340	AMP-binding enzyme	COG0318	I
RCA23_c28350	SucD2:succinate-semialdehyde dehydrogenase SucD (1.2.1.76)	COG1012	C
RCA23_c28360	hypothetical protein	COG3333	S
RCA23_c28370	hypothetical protein		
RCA23_c28380	putative tripartite tricarboxylate transporter family receptor	COG3181	S
RCA23_c28390	putative ETC complex I subunit		
RCA23_c28450	YedZ:sulfoxide reductase heme-binding subunit YedZ	COG2717	S
RCA23_c28460	YedY:sulfoxide reductase catalytic subunit YedY (1.8.--)	COG2041	R
RCA23_c28470	FabG5:3-oxoacyl-[acyl-carrier-protein] reductase FabG (1.1.1.100)	COG1028	I
RCA23_c28480	putative haloacid dehalogenase-like hydrolase	COG0637	R
RCA23_c28490	ClpB:chaperone protein ClpB	COG0542	O
RCA23_c28500	PyrF:orotidine 5'-phosphate decarboxylase PyrF (4.1.1.23)	COG0284	F
RCA23_c28510	hypothetical protein		
RCA23_c28520	SPFH domain/Band 7 family protein	COG0330	O
RCA23_c28530	DinB:DNA polymerase IV (2.7.7.7)	COG0389	L
RCA23_c28540	putative N-formylglutamate amidohydrolase	COG3741	E
RCA23_c28560	hypothetical protein, phenylacetate-coenzyme A ligase	COG1541	H
RCA23_c28570	high-affinity branched-chain amino acid transporter ATP-binding protein	COG0410	E
RCA23_c28580	hypothetical protein	COG0683	E
RCA23_c28590	high-affinity branched-chain amino acid transporter permease protein	COG4177	E
RCA23_c28600	high-affinity branched-chain amino acid transporter permease protein	COG0559	E
RCA23_c28610	high-affinity branched-chain amino acid transporter ATP-binding protein	COG0411	E
RCA23_c28620	putative long-chain-fatty-acid-CoA ligase (6.2.1..)	COG1022	I
RCA23_c28630	TruB:tRNA pseudouridine synthase B (5.4.99..)	COG0130	J
RCA23_c28650	RbfA:ribosome-binding factor A	COG0858	J
RCA23_c28640	DapA4:dihydrodipicolinate synthase DapA (4.2.1.52)	COG0289	E
RCA23_c28660	hypothetical protein DUF1674	COG5508	S

RCA23_c28670	putative ribosomal RNA small subunit methyltransferase B	COG0144	J
RCA23_c28680	hypothetical protein, heparinase III/III	COG5360	S
RCA23_c28690	PurH bifunctional purine biosynthesis protein PurH (2.1.2.3;3.5.4.10)	COG0138	F
RCA23_c28700	signal peptidase II (3.4.23.36)	COG0597	M
RCA23_c28710	uncharacterized zinc protease y4wA (3.4.24..)	COG0612	R
RCA23_c28720	uncharacterized zinc protease y4wB (3.4.24..)	COG0612	R
RCA23_c28730	MutL DNA mismatch repair protein MutL	COG0323	L
RCA23_c28740	putative RmuC family protein	COG1322	S
RCA23_c28750	ChrR transcriptional activator ChrR	COG3806	T
RCA23_c28760	SigK RNA polymerase sigma factor SigK	COG1595	K
RCA23_c28770	hypothetical protein	COG2907	R
RCA23_c28780	hypothetical protein DUF1365	COG3496	S
RCA23_c28790	hypothetical protein	COG2211	G
RCA23_c28800	hypothetical protein		
RCA23_c28810	putative short chain dehydrogenase	COG4221	R
RCA23_c28820	saccharopine dehydrogenase (NAD+-L-lysine- forming) (1.5.1.7)	COG3288	C
RCA23_c28830	putative glutathione S-transferase	COG0625	O
RCA23_c28840	putative phosphoglycerate mutase family protein	COG0406	G
RCA23_c28850	Fdh formate dehydrogenase Fdh (1.2.1.2)	COG3383	R
RCA23_c28860	hypothetical protein	COG1357	S
RCA23_c28870	hypothetical protein DUF1643	COG4333	S
RCA23_c28880	DehH haloacetate dehalogenase DehH (3.8.1.3)	COG0596	R
RCA23_c28890	RpsO 30S ribosomal protein S15	COG0184	J
RCA23_c28900	hypothetical protein, DUF6 transmembrane protein	COG0697	G
RCA23_c28910	Pnp polyribonucleotide nucleotidyltransferase Pnp (2.7.7.8)	COG1185	J
RCA23_c28920	aldehyde dehydrogenase (1.2.1.3)	COG1012	C
RCA23_c28930	RluA ribosomal large subunit pseudouridine synthase A (5.4.99..)	COG0564	J
RCA23_c28940	OmG protein OmG		
RCA23_c28950	hypothetical protein, DUF940 putative lipoprotein		
RCA23_c28960	hypothetical protein		
RCA23_c28970	GalE UDP-glucose 4-epimerase GalE (5.1.3.2)	COG1087	M
RCA23_c28980	putative FAD linked oxidase	COG0277	C
RCA23_c28990	Ffh signal recognition particle protein Ffh	COG0541	U
RCA23_c29000	putative chorismate mutase type II	COG1605	E
RCA23_c29010	RpsP 30S ribosomal protein S16	COG0228	J
RCA23_c29020	RimM ribosome maturation factor RimM	COG0806	J
RCA23_c29030	TrmD tRNA (guanine-N(1)-)-methyltransferase TrmD (2.1.1.31)	COG0336	J
RCA23_c29040	RplS 50S ribosomal protein L19	COG0335	J
RCA23_c29050	RpmE 50S ribosomal protein L31	COG0254	J
RCA23_c29060	MipZ ATPase MipZ	COG1192	D
RCA23_c29070	fructokinase (2.7.1.4)	COG0524	G
RCA23_c29080	PobA 2-hydroxybenzoate hydroxylase PobA (1.14.13.2)	COG0654	H
RCA23_c29090	KynU kynureninase KynU (3.7.1.3)	COG3844	E
RCA23_c29100	HTH-type transcriptional regulator, GntR family	COG1802	K
RCA23_c29110	hypothetical protein, glutathione S-transferase	COG0625	O
RCA23_c29120	L-threonine 3-dehydrogenase (1.1.1.103)	COG0451	M
RCA23_c29130	enoyl-CoA hydratase (4.2.1.17)	COG1024	I
RCA23_c29140	enoyl-CoA hydratase (4.2.1.17)	COG1250	I
RCA23_c29150	FadN2 3-hydroxyacyl-CoA dehydrogenase FadN (1.1.1.35)	COG1028	I
RCA23_c29160	hypothetical protein		
RCA23_c29170	integrase	COG4974	L
RCA23_c29180	hypothetical protein, porin-like		
RCA23_c29190	LeuS leucyl-tRNA synthase LeuS (6.1.1.4)	COG0495	J
RCA23_c29200	hypothetical protein DUF2159		
RCA23_c29210	hypothetical protein		
RCA23_c29220	hypothetical protein, glutathione S-transferase	COG0625	O
RCA23_c29230	hypothetical protein	COG2081	R
RCA23_c29240	hypothetical protein, porin		
RCA23_c29250	hypothetical protein, alanine racemase-like	COG0325	R
RCA23_c29260	hypothetical protein, YkuD	COG3786	S
RCA23_c29270	RibA GTP cyclohydrolase II RibA (3.5.4.25)	COG0807	H
RCA23_c29280	response regulator receiver protein	COG0745	T
RCA23_c29290	hydratase/decarboxylase (4.1.1..)	COG3971	Q
RCA23_c29300	5-carboxymethyl-2-hydroxymuconate delta- isomerase (5.3.3.10)	COG0179	Q
RCA23_c29310	5-carboxymethyl-2-hydroxymuconate delta isomerase (5.3.3.10)	COG3232	E
RCA23_c29320	hypothetical protein, HTH-type transcriptional regulator, MarR family	COG1846	K
RCA23_c29330	HpaH 4-hydroxyphenylacetate 3-monooxygenase oxygenase component HpaH	COG2368	Q
RCA23_c29340	ABC sugar transporter, ATPase subunit	COG3839	G
RCA23_c29350	MtlK mannitol 2-dehydrogenase MtlK (1.1.1.67)	COG0246	G
RCA23_c29360	transcriptional regulator, AraC family	COG2207	K
RCA23_c29370	ABC sugar transporter, permease protein	COG0395	G
RCA23_c29380	ABC sugar transporter, permease protein	COG1175	G
RCA23_c29390	ABC transporter, periplasmic substrate-binding protein	COG1653	G
RCA23_c29400	putative flavohemoglobin / bacterial hemoglobin	COG1017	C
RCA23_c29410	hypothetical protein		
RCA23_c29420	NhaA Na+/H+ antiporter NhaA	COG3004	P
RCA23_c29430	hypothetical protein		
RCA23_c29440	hypothetical protein DUF55	COG2947	S
RCA23_c29450	Ycd protein Ycd	COG2350	S
RCA23_c29460	GpsA glycerol-3-phosphate dehydrogenase GpsA (1.1.1.94)	COG0240	C
RCA23_c29470	HemD hypothetical protein, uroporphyrinogen-III synthase HemD	COG1587	H
RCA23_c29480	hypothetical protein	COG3264	M
RCA23_c29490	hypothetical protein, HemY	COG3898	S
RCA23_c29500	transcriptional regulatory protein, Ars family	COG0640	K
RCA23_c29510	BchO magnesium-chelatase subunit BchO (6.6.1.1)	COG0596	R
RCA23_c29520	BchD magnesium-chelatase subunit BchD (6.6.1.1)	COG1240	H
RCA23_c29530	BchI magnesium-chelatase subunit BchI (6.6.1.1)	COG1239	H
RCA23_c29540	CrtA spheroidene monooxygenase CrtA (1.-.-.-)		
RCA23_c29550	CrtI phytoene dehydrogenase CrtI (1.14.99..)	COG1233	Q
RCA23_c29560	CrtB phytoene synthase CrtB (2.5.1.32)	COG1562	I
RCA23_c29570	CrtC hydroxyneurosporene dehydrogenase CrtC (1.-.-.-)		
RCA23_c29580	CrtD methoxyneurosporene dehydrogenase CrtD (1.14.99..)	COG1233	Q
RCA23_c29590	CrtE geranylgeranyl pyrophosphate synthase CrtE (2.5.1.29)	COG0142	H
RCA23_c29600	CrtF hydroxyneurosporene methyltransferase CrtF (2.1.1..)		
RCA23_c29610	BchC 2-desacetyl-2-hydroxyethyl bacteriochlorophyllide A dehydrogenase BchC	COG1063	E
RCA23_c29620	BchX chlorophyllide reductase BchX (1.3.1..)	COG1348	P
RCA23_c29630	BchY chlorophyllide reductase BchY (1.18.1..)		
RCA23_c29640	BchZ chlorophyllide reductase subunit BchZ (1.18.-.-)	COG2710	C
RCA23_c29650	PufQ protein PufQ		
RCA23_c29660	PufB light-harvesting protein B-870 beta chain PufB		
RCA23_c29670	PufA light-harvesting protein B-870 alpha chain PufA		
RCA23_c29680	PufL reaction center protein L chain PufL		
RCA23_c29690	PufM reaction center protein M chain PufM		
RCA23_c29700	protein PufX		
RCA23_c29710	Dxs 2-1-deoxy-D-xylulose-5-phosphate synthase Dxs (2.2.1.7)	COG1154	H
RCA23_c29720	IdI2 isopentenyl-diphosphate delta-isomerase Idi (5.3.3.2)	COG1443	I
RCA23_c29730	BchP geranylgeranyl reductase BchP	COG0654	C
RCA23_c29740	bacteriochlorophyll synthase 44.5 kDa chain		
RCA23_c29750	BchG bacteriochlorophyll synthase BchG	COG0382	H
RCA23_c29760	cytochrome c-551	COG3474	C
RCA23_c29770	HemE uroporphyrinogen decarboxylase HemE (4.1.1.37)	COG0407	H
RCA23_c29780	HemC porphobilinogen deaminase HemC (2.5.1.61)	COG0181	H
RCA23_c29790	hypothetical protein, hmk-like	COG0702	M
RCA23_c29800	HemA 2,5-aminolevulinate synthase HemA (2.3.1.37)	COG0156	H
RCA23_c29810	hypothetical protein		
RCA23_c29820	AcsF aerobic Mg-protoporphyrin IX monomethyl ester oxidative cyclase AcsF (1.14.13.81)		
RCA23_c29830	hypothetical protein		
RCA23_c29840	hypothetical protein		
RCA23_c29850	hypothetical protein		
RCA23_c29860	PuhA reaction center protein PuhA		
RCA23_c29870	PucC protein PucC		
RCA23_c29880	BchM magnesium-protoporphyrin O-methyltransferase BchM (2.1.1.11)	COG2227	H
RCA23_c29890	BchL light-independent protochlorophyllide reductase iron-sulfur ATP-binding prot	COG1348	P
RCA23_c29900	BchH magnesium-chelatase subunit BchH (6.6.1.1)	COG1429	H
RCA23_c29910	BchB light-independent protochlorophyllide reductase subunit BchB (1.18.-.-)	COG2710	C
RCA23_c29920	BchN light-independent protochlorophyllide reductase subunit BchN	COG2710	C
RCA23_c29930	BchF 2-vinyl bacteriochlorophyllide hydratase BchF (4.2.1..)		
RCA23_c29940	putative transcriptional regulator PpaA		
RCA23_c29950	PpsR transcriptional regulator PpsR	COG3829	K
RCA23_c29960	hypothetical protein	COG5012	R
RCA23_c29970	FixJ transcriptional regulator protein FixJ	COG4566	T
RCA23_c29980	TspO2 peripheral-type benzodiazepine receptor/signal transduction protein TspO	COG3476	T
RCA23_c29990	hypothetical protein, integral membrane proteins YeeE/YedE	COG2391	R
RCA23_c30000	hypothetical protein, integral membrane proteins YeeE/YedE	COG2391	R
RCA23_c30010	putative beta-lactamase hydrolase-like protein	COG0491	R
RCA23_c30020	hypothetical protein	COG0453	S
RCA23_c30030	sulphate transporter	COG0659	P
RCA23_c30040	amidase (3.5.1.4)	COG0154	J
RCA23_c30050	hypothetical protein		
RCA23_c30060	Aph aminoglycoside phosphotransferase Aph (2.7.1.95)		
RCA23_c30070	hypothetical protein	COG2885	M
RCA23_c30080	DnaJ chaperone protein DnaJ	COG0484	O
RCA23_c30090	DnaK chaperone protein DnaK	COG0443	O
RCA23_c30100	putative alpha-ketoglutarate-dependent dioxygenase AlkB	COG3145	L
RCA23_c30110	putative ABC-2 type transporter	COG1682	G
RCA23_c30120	CysQ 3'(2'),5' bisphosphate nucleotidase CysQ (3.1.3.7)	COG1218	P
RCA23_c30130	GalU UTP-glucose-1-phosphate uridylyltransferase GalU (2.7.7.9)	COG1210	M
RCA23_c30140	hypothetical protein	COG0463	M
RCA23_c30150	hypothetical protein		
RCA23_c30160	hypothetical protein beta-1,6-N- acetylglucosaminyltransferases		
RCA23_c30170	hypothetical protein		
RCA23_c30180	PtsN nitrogen regulatory protein PtsN (2.7.1..)	COG1762	G
RCA23_c30190	putative sigma 54 modulation protein	COG1544	J
RCA23_c30200	LptB lipopolysaccharide export system ATP-binding protein LptB (3.6.3..)	COG1137	R
RCA23_c30210	putative lipopolysaccharide export system protein LptA	COG1934	S
RCA23_c30220	hypothetical protein		
RCA23_c30230	putative 3'-5'-exonuclease	COG0349	J
RCA23_c30240	glycine amidinotransferase (2.1.4.1)	COG1834	E
RCA23_c30250	hypothetical protein	COG4123	R
RCA23_c30260	hypothetical protein, metal-dependent phosphohydrolase	COG1896	R
RCA23_c30270	AhcY S-adenosyl-L-homocysteine hydrolase AhcY (3.3.1.1)	COG0469	H
RCA23_c30280	RegA photosynthetic apparatus regulatory protein RegA	COG4567	T
RCA23_c30290	SenC protein SenC	COG1999	R
RCA23_c30300	RegB sensor histidine kinase RegB (2.7.13.3)	COG0642	T
RCA23_c30310	hypothetical protein		
RCA23_c30320	hypothetical protein, aminoglycoside phosphotransferase	COG3178	R
RCA23_c30330	hypothetical protein, nucleotidyl transferase	COG1208	M
RCA23_c30340	AddB double-strand break repair protein AddB	COG3893	L
RCA23_c30350	AddA double-strand break repair helicase AddA	COG1074	L
RCA23_c30360	TrxA thioredoxin TrxA	COG3118	O
RCA23_c30370	HslV ATP-dependent protease HslV (3.4.25..)	COG5405	O
RCA23_c30380	HslU ATP-dependent hsl protease ATP-binding subunit HslU	COG1220	O
RCA23_c30390	MFS-type transporter	COG2814	G
RCA23_c30400	hypothetical protein, Smr protein/MutS2	COG2840	S
RCA23_c30410	putative lytic murein transglycosylase	COG2821	M
RCA23_c30420	hypothetical protein, TIM44	COG4395	S
RCA23_c30430	putative cytoplasmic membrane protein FxsA	COG3030	R
RCA23_c30440	SecB protein-export protein SecB	COG1952	U
RCA23_c30450	DnaQ DNA polymerase III subunit epsilon (2.7.7.7)	COG0847	L
RCA23_c30460	CoaE dephospho-CoA kinase CoaE (2.7.1.24)	COG0237	H
RCA23_c30470	AroE shikimate 5-dehydrogenase AroE (1.1.1.25)	COG0169	E
RCA23_c30480	Rho transcription termination factor Rho (3.6.1..)	COG1158	K
RCA23_c30490	MnmE tRNA modification GTPase MnmE (3.6.-.-)	COG0486	R
RCA23_c30500	MnmG tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG	COG0445	D
RCA23_c30510	RsmG ribosomal RNA small subunit methyltransferase G (2.1.1..)	COG0357	M
RCA23_c30520	ParA chromosome-partitioning protein ParA	COG1192	D
RCA23_c30530	ParB chromosome-partitioning protein ParB	COG1475	K
RCA23_c30540	HemN oxygen-independent coproporphyrinogen III oxidase HemN (1.3.99.22)	COG0635	H
RCA23_c30550	RdgB nucleoside-triphosphatase RdgB (3.6.1.15)	COG0127	F
RCA23_c30560	Rph ribonuclease PH (2.7.7.56)	COG0689	J
RCA23_c30570	HrcA heat-inducible transcription repressor HrcA	COG1420	K
RCA23_c30580	GrpE protein GrpE	COG0576	O
RCA23_c30590	MutS DNA mismatch repair protein MutS	COG0249	L
RCA23_c30600	MaeB NADP-dependent malic enzyme MaeB (1.1.1.40)	COG0281	C
RCA23_c30610	BfkB family carbohydrate kinase	COG0524	G
RCA23_c30620	putative aminotransferase class IV	COG0115	E
RCA23_c30630	hypothetical protein, branched-chain-amino-acid aminotransferase-like		
RCA23_c30640	ArgG argininosuccinate synthase ArgG (6.3.4.5)	COG0137	E
RCA23_c30650	threonine dehydratase, biosynthetic (4.3.1.19)	COG1171	E
RCA23_c30660	putative NUDIX hydrolase	COG0494	L
RCA23_c30670	HslO heat shock protein 33	COG1281	O
RCA23_c30680	putative NUDIX hydrolase	COG0494	L

RCA23_c30690	hypothetical protein, poly A polymerase	COG0617	J
RCA23_c30700	ABC transporter ATP-binding/permease protein	COG1132	V
RCA23_c30710	hypothetical protein	COG2265	J
RCA23_c30720	ion transport protein		
RCA23_c30730	hypothetical protein	COG3034	S
RCA23_c30740	hypothetical protein, SCP-like extracellular protein	COG2340	S
RCA23_c30750	hypothetical protein	COG1376	S
RCA23_c30760	HemH ferrochelatase HemH (4.99.1.1)	COG0276	H
RCA23_c30770	hypothetical protein		
RCA23_c30780	hypothetical protein, ComF/GntX family	COG1040	R
RCA23_c30790	GrxC glutaredoxin GrxC	COG0695	O
RCA23_c30800	putative carbon-nitrogen hydrolase	COG0388	R
RCA23_c30810	putative HTH-type transcriptional regulator, MarR family	COG1846	K
RCA23_c30820	UbiG 3-demethylubiquinone-9 3-O-methyltransferase UbiG (2.1.1.64)	COG2227	H
RCA23_c30830	Pip proline iminopeptidase Pip (3.4.11.5)	COG0596	R
RCA23_c30840	putative peptide transport system permease protein	COG0601	E
RCA23_c30850	putative peptide transport system permease protein	COG1173	E
RCA23_c30860	peptide transport system ATP-binding protein	COG1123	R
RCA23_c30870	putative periplasmic peptide-binding protein	COG0747	E
RCA23_c30880	hypothetical protein UPF0090	COG0779	S
RCA23_c30890	NusA transcription elongation protein NusA	COG0195	K
RCA23_c30900	hypothetical protein DUF448	COG2740	K
RCA23_c30910	InfB translation initiation factor IF-2	COG0532	J
RCA23_c30920	putative matator MutT protein	COG1051	F
RCA23_c30930	ArgJ arginine biosynthesis bifunctional protein ArgJ (2.3.1.35;2.3.1.1)	COG1364	E
RCA23_c30940	putative peptidyl/prolyl isomerase	COG0760	O
RCA23_c30950	SecA protein translocase subunit SecA	COG0653	U
RCA23_c30960	putative O-acetyltransferase OatA	COG1835	I
RCA23_c30970	hypothetical protein	COG4922	S
RCA23_c30980	hypothetical protein, transcriptional regulator- like	COG1733	K
RCA23_c30990	LspL 2,7,0P-gluconorate 5'-epimerase LspL (5.1.3.12)	COG0451	M
RCA23_c31000	hypothetical protein		
RCA23_c31010	GlmM phosphoglucosamine mutase GlmM (5.4.2.10)	COG1109	G
RCA23_c31020	putative ubiquinone biosynthesis protein UbiB	COG0661	R
RCA23_c31030	UbiE ubiquinone/menaquinone biosynthesis methyltransferase UbiE (2.1.1--)	COG2226	H
RCA23_c31040	MutM formamidopyrimidine-DNA glycosylase MutM (3.2.2.23;4.2.99.18)	COG0266	L
RCA23_c31050	enoyl-CoA hydratase/isomerase	COG1024	I
RCA23_c31060	RpsT 30S ribosomal protein S20	COG0268	J