Table S6: COG categories, genomic islands, normalized read counts (NPKM) of the transcripts at stations 9 (bloom,night) and 13 (bloom, day) and differences between night and day

locus_tag	start	stop	annotation	COG ID	COG category	genomic island	NPKM station 9 bloom-night	NPKM station 13 bloom-day	NPKM difference night-day
RCA23_c00010	101	1447	chromosomal replication initiatior protein DnaA	COG0593	L		617	502	115
RCA23_c00020	1550	2668	DNA polymerase III beta subunit DnaN	COG0592	L		605	575	30
RCA23_c00030	2778	3800	DNA replication and repair protein RecF	COG1195	L		358	419	-61
RCA23_c00040	3797	4417	hypothetical protein, LysE type translocator	COG1280	E		455	635	-180
RCA23_c00050	4567	6984	DNA gyrase subunit B	COG0187	L		599	596	3
RCA23_c00060	7002	8384	FAD dependent oxidoreductase	COG0665	E		339	421	-82
RCA23_c00070	9282	8392	hypothetical protein, rhodanese-like sulphurtransferase	COG1054	R		414	392	22
RCA23_c00080	9413	10003	pyrazinamidase/nicotinamidase PncA	COG1335	Q		456	502	-46
RCA23_c00090	10003	11295	nicotinate phosphoribosyltransferase PncB	COG1488	H		608	548	60
RCA23_c00100	12224	11292	aminoglycoside phosphotransferase	COG2334	R		392	456	-64
RCA23_c00110	13477	12221	putative aminotransferase class III	COG0160	E		255	339	-84
RCA23_c00120	13889	13467	putative peptide chain release factor	COG1186	J		432	659	-227
RCA23_c00130	14772	14128	hypothetical integral membrane protein	COG1738	S		378	472	-94
RCA23_c00140	15799	14879	penicillin-insensitive murein endopeptidase MepA	COG3770	M		424	459	-35
RCA23_c00150	17181	15796	putative MFS-type transporter	COG2270	R		588	535	53
RCA23_c00160	17672	17241	hypothetical protein	COG0824	R		354	357	-3
RCA23_c00170	17836	18201	hypothetical protein, YGGT family	COG0762	S		446	469	-23
RCA23_c00180	18217	20277	ATP-dependent DNA helicase RecQ	COG0514	L		362	427	-65
RCA23_c00190	20300	21073	hypothetical protein DUF328	COG3022	S		375	423	-48
RCA23_c00200	21576	21070	isopentenyl-diphosphate delta-isomerase Idi	COG1443	I		495	470	25
RCA23_c00210	21812	23056	5-aminolevulinate synthase HemA	COG0156	H		577	477	100
RCA23_c00220	23097	23540	cytochrome c2	COG3474	C		489	500	-11
RCA23_c00230	24777	23602	acetyl-CoA acetyltransferase PhaA	COG0183	I		276	293	-17
RCA23_c00240	24942	27992	DNA polymerase III 2 alpha subunit DnaE	COG0587	L		333	404	-71

RCA23_c00250	28122	28625	transcription antitermination protein NusG	COG0250	K	338	431	-93
RCA23_c00260	29748	28636	putative lytic murein transglycosylase	COG2951	M	373	308	65
RCA23_c00270	31991	29745	putative ribonuclease R	COG0557	K	415	447	-32
RCA23_c00280	32084	32503	hypothetical protein DUF461	COG2847	S	758	537	221
RCA23_c00290	33615	32512	chorismate synthase AroC	COG0082	E	389	392	-3
RCA23_c00300	34180	34422	hypothetical protein			461	357	104
RCA23_c00310	34649	35638	thiamine-binding periplasmic protein ThiB	COG4143	H	445	484	-39
RCA23_c00320	35638	37182	thiamine transport system permease protein ThiP	COG1178	P	287	490	-203
RCA23_c00330	37151	37867	thiamine import ATP-binding protein ThiQ	COG3840	H	337	496	-159
RCA23_c00340	38720	37920	cytochrome c1	COG2857	C	615	381	234
RCA23_c00350	40072	38735	cytochrome b	COG1290	C	894	546	348
RCA23_c00360	40644	40072	ubiquinol-cytochrome c reductase iron-sulfur subunit PetA	COG0723	C	566	383	183
RCA23_c00370	41451	40837	hypothetical protein, glutathione S-transferase	COG0625	O	244	366	-122
RCA23_c00380	42523	41495	inositol 2-dehydrogenase IdhA	COG0673	R	282	357	-75
RCA23_c00390	42704	44050	protein PmbA	COG0312	R	317	402	-85
RCA23_c00400	44043	44810	putative inositol monophosphatase	COG0483	G	442	524	-82
RCA23_c00410	44819	45955	putative 3-deoxy-D-manno-octulosonic-acid transferase	COG1519	M	381	447	-66
RCA23_c00420	45952	46938	tetraacyldisaccharide 4'-kinase LpxK	COG1663	M	299	391	-92
RCA23_c00430	47600	46941	hypothetical protein, thioredoxin	COG1651	O	615	604	11
RCA23_c00440	48123	47602	hypothetical protein DUF721	COG5389	S	395	653	-258
RCA23_c00450	48220	49254	A/G-specific adenine glycosylase YfhQ	COG1194	L	216	265	-49
RCA23_c00460	49425	50567	alkane 1-monooxygenase AlkB			705	622	83
RCA23_c00470	51766	50654	modification methylase CcrM	COG0863	L	547	559	-12
RCA23_c00480	52492	51857	ribonuclease HII	COG0164	L	826	659	167
RCA23_c00490	52617	53405	putative exodeoxyribonuclease III	COG0708	L	412	409	3
RCA23_c00500	53466	54383	hypothetical protein, thioredoxin	COG3118	O	360	421	-61
RCA23_c00510	54410	55051	putative ATP-dependent protease La (LON)	COG2802	R	461	381	80
RCA23_c00520	55048	55233	hypothetical protein, Trm112p-like	COG2835	S	557	439	118
RCA23_c00530	56447	55230	putative 2-octaprenyl-6-methoxyphenol hydroxylase	COG0654	H	336	427	-91
RCA23_c00540	56547	57857	glutamyl-tRNA(Gln) amidotransferase subunit A	COG0154	J	218	476	-258

RCA23_c00550	57922	59085	LL-diaminopimelate aminotransferase DapL	COG0436	E		518	488	30
RCA23_c00560	59099	61888	putative DNA transclocase FtsK	COG1674	D		506	510	-4
RCA23_c00570	61992	62549	putative outer membrane lipoprotein carrier protein LolA	COG2834	M		382	413	-31
RCA23_c00580	63223	62720	hypothetical protein	COG4764	S		478	353	125
RCA23_c00590	63513	63836	hemimethylated DNA-binding protein, YccV like	COG3785	S		588	541	47
RCA23_c00600	65410	63833	putative gamma-glutamyltransferase ywrD	COG0405	E		253	306	-53
RCA23_c00610	65571	66749	acetyl-CoA acetyltransferase ThlA	COG0183	I		289	358	-69
RCA23_c00620	66761	67216	hypothetical protein	COG1956	T		801	697	104
RCA23_c00630	67302	67871	putative HTH-type transcriptional regulator	COG1396	K		624	670	-46
RCA23_c00640	67871	68488	hypothetical protein, homoserine/homoserine lactone efflux	COG1280	E		417	485	-68
RCA23_c00650	68502	69128	LysE-type translocator	COG1280	E		274	391	-117
RCA23_c00660	69140	71587	dimethylglycine dehydrogenase	COG0404	E		513	451	62
RCA23_c00670	71603	72469	putative homocysteine S-methyltransferase	COG2040	E		334	377	-43
RCA23_c00680	72474	72929	pyridoxamine 5'-phosphate oxidase-like protein, FMN-bindir	COG3576	R		400	404	-4
RCA23_c00690	72966	75419	sarcosine dehydrogenase	COG0404	E		503	505	-2
RCA23_c00700	75596	76150	hypothetical protein	COG0790	R		229	273	-44
RCA23_c00710	77326	76202	putative agmatine deiminase AguA	COG2957	E		244	302	-58
RCA23_c00720	78340	77450	Cl- channel, voltage-gated family protein	COG0038	P		169	179	-10
RCA23_c00730	79210	78368	Cl- channel, voltage-gated family protein	COG0038	P		284	229	55
RCA23_c00750	79638	80468	diaminopimelate epimerase DapF	COG0253	E	GI 1	356	453	-97
RCA23_c00760	80465	81721	(dimethylallyl)adenosine tRNA methylthiotransferase MiaB	COG0621	J	GI 1	300	392	-92
RCA23_c00770	81775	82368	hypothetical protein, glutathione S-transferotein	COG0625	O	GI 1	340	473	-133
RCA23_c00780	83403	82369	HTH-type transcriptional regulator, LacI family	COG1609	K	GI 1	392	377	15
RCA23_c00790	84698	84859	hypothetical protein			GI 1	512	328	184
RCA23_c00800	85627	85304	hypothetical protein	COG4274	S	GI 1	503	298	205
RCA23_c00810	86298	86852	hypothetical protein, phosphoglycerate mutase-like	COG0406	G	GI 1	577	360	217
RCA23_c00820	86971	87357	hypothetical protein	COG0790	R	GI 1	602	405	197
RCA23_c00830	87971	87558	hypothetical protein, glyoxalase/bleomycin resistance protei	COG0346	E	GI 1	350	319	31
RCA23_c00840	88760	88251	putative phage integrase	COG4974	L	GI 1	284	247	37
RCA23_c00850	89246	89632	hypothetical protein			GI 1	12	10	2

RCA23_c00860	89849	90679	hypothetical protein			GI 1	44	43	1
RCA23_c00870	92517	91066	putative endonuclease			GI 1	1	0	1
RCA23_c00880	93431	93994	DNA integration/recombination/invertion protein	COG1961	L	GI 1	253	243	10
RCA23_c00890	94002	94223	hypothetical protein			GI 1	529	399	130
RCA23_c00900	94400	95290	hypothetical protein, peptidoglycan binding-like			GI 1	0	0	0
RCA23_c00910	95706	96575	hypothetical protein			GI 1	28	29	-1
RCA23_c00920	98235	96589	putative phage integrase	COG4974	L	GI 1	54	35	19
RCA23_c00940	98894	98478	putative HTH-type transcriptional repressor, ArsR family	COG0640	K		463	367	96
RCA23_c00950	99032	99355	ATP synthase protein I				599	344	255
RCA23_c00960	99360	100142	ATP synthase subunit AtpB	COG0356	C		361	248	113
RCA23_c00970	100189	100425	ATP synthase subunit c				766	349	417
RCA23_c01000	102506	101736	pyruvate dehydrogenase complex repressor	COG2186	K		376	382	-6
RCA23_c01010	103165	102623	inner membrane lipoprotein YiaD	COG2885	M		265	319	-54
RCA23_c01020	103461	104105	endonuclease III	COG0177	L		351	403	-52
RCA23_c01030	104102	105094	putative pfkB family carbohydrate kinase	COG0524	G		636	568	68
RCA23_c01040	105925	105104	hypothetical protein				439	403	36
RCA23_c01050	106040	106831	glycosyl transferase family 14				610	421	189
RCA23_c01060	106838	107617	hypothetical protein				588	434	154
RCA23_c01070	107628	108008	HIT-like protein	COG0537	F		461	501	-40
RCA23_c01080	108944	108024	ABC transporter ATP binding protein	COG1131	V		655	495	160
RCA23_c01090	109004	109222	hypothetical protein	COG4391	S		754	472	282
RCA23_c01100	109664	109233	hypothetical protein				564	410	154
RCA23_c01110	109753	112548	DNA polymerase I	COG0749	L		456	441	15
RCA23_c01120	112575	113720	cystathionine gamma-synthase MetB	COG0626	E		208	301	-93
RCA23_c01130	113714	114265	ribosomal large subunit pseudouridine synthase RluE	COG1187	J		276	499	-223
RCA23_c01140	114879	114286	hypothetical protein DUF1285	COG3816	S		371	533	-162
RCA23_c01150	114939	115946	ATPase, MoxR type	COG0714	R		192	243	-51
RCA23_c01160	115943	116806	hypothetical protein	COG1721	R		276	277	-1
RCA23_c01170	116803	119550	hypothetical protein				224	357	-133
RCA23_c01180	119595	121607	hypothetical protein DUF1355	COG5426	S		287	442	-155

RCA23_c01190	122292	123830	glycolate oxidase subunit GlcD	COG0277	C	492	613	-121
RCA23_c01200	123827	124996	glycolate oxidase subunit GlcE	COG0277	C	449	505	-56
RCA23_c01210	124996	126312	glycolate oxidase iron-sulfur subunit GlcF	COG0247	C	438	414	24
RCA23_c01220	126476	127198	hypothetical protein, trypsin	COG3591	E	379	640	-261
RCA23_c01230	128473	127643	putative chitinase	COG3325	G	43	18	25
RCA23_c01240	129159	129614	small heat shock protein IbpA	COG0071	O	1.541	759	782
RCA23_c01250	131155	129680	succinate-semialdehyde dehydrogenase GabD	COG1012	C	335	398	-63
RCA23_c01260	131221	132024	hypothetical protein	COG0657	I	241	333	-92
RCA23_c01270	132344	132021	hypothetical protein	COG5617	S	233	327	-94
RCA23_c01280	133081	132341	putative cyclopentanol dehydrogenase CpnA	COG1028	I	381	387	-6
RCA23_c01290	133264	133566	hypothetical protein			287	356	-69
RCA23_c01300	133661	134278	hypothetical protein DUF1523			469	370	99
RCA23_c01310	136598	134286	aldehyde dehydrogenase	COG1012	C	256	353	-97
RCA23_c01320	137589	136603	deoxyribose-phosphate aldolase DeoC	COG0274	F	287	273	14
RCA23_c01330	137692	138366	ribulose-phosphate 3-epimerase, chromosomal	COG0036	G	290	386	-96
RCA23_c01340	140190	138385	hemolysin-type calcium-binding region			322	456	-134
RCA23_c01350	140316	143915	5-oxoprolinase (ATP-hydrolyzing)	COG0145	E	257	381	-124
RCA23_c01360	145374	144022	aminotransferase class-III	COG0161	H	314	322	-8
RCA23_c01370	145865	145371	ureidoglycolate hydrolase AllA	COG3194	F	551	501	50
RCA23_c01380	146898	145891	aldose 1-epimerase GalM	COG2017	G	273	397	-124
RCA23_c01390	148778	146898	beta-galactosidase BgaB	COG1874	G	225	271	-46
RCA23_c01400	149622	148786	putative gluconolactonase	COG3386	G	260	321	-61
RCA23_c01410	150218	149616	2-dehydro-3-deoxy-6-phosphogalactonate aldolase DgoA	COG0800	G	205	303	-98
RCA23_c01420	151120	150215	2-dehydro-3-deoxygalactonokinase DgoK	COG3734	G	202	287	-85
RCA23_c01430	151884	151117	short chain dehydrogenase	COG1028	I	245	234	11
RCA23_c01440	154013	151929	alpha-galactosidase RafA	COG3345	G	239	275	-36
RCA23_c01450	154942	154043	putative ABC transporter inner membrane component	COG0395	G	388	341	47
RCA23_c01460	155930	154920	putative ABC transporter inner membrane component	COG1175	G	389	289	100
RCA23_c01470	157438	156014	putative extracellular solute-binding protein	COG1653	G	365	261	104
RCA23_c01480	157460	158245	HTH-type transcriptional regulator, IclR family	COG1414	K	141	131	10

RCA23_c01490	158266	159324	sugar ABC transporter ATP-binding protein	COG3839	G	231	267	-36
RCA23_c01500	160108	159344	Sulfite exporter TauE/SafE			177	299	-122
RCA23_c01510	161562	160108	putative transcriptional regulator, gntR family	COG1167	K	244	244	0
RCA23_c01520	163233	161716	taurine--pyruvate aminotransferase Tpa	COG0161	H	341	283	58
RCA23_c01530	163567	164568	taurine ABC transporter, periplasmic binding protein TauA	COG4521	P	501	386	115
RCA23_c01540	164690	165496	taurine ABC transport system ATP-binding protein TauB	COG1116	P	614	476	138
RCA23_c01550	165493	166803	taurine ABC transport system permease protein TauC	COG0600	P	618	484	134
RCA23_c01560	169252	166847	dimethylglycine dehydrogenase	COG0404	E	324	431	-107
RCA23_c01570	169351	170925	trimethylamine methyltransferase MttB	COG5598	H	239	366	-127
RCA23_c01580	173231	170928	3-hydroxyacyl-CoA dehydrogenase FadN	COG1250	I	294	374	-80
RCA23_c01590	174034	173246	hypothetical protein	COG0596	R	346	339	7
RCA23_c01600	175440	174031	O-acetylhomoserine (thiol)-lyase CysD	COG2873	E	375	470	-95
RCA23_c01610	175521	177014	putative signaling protein	COG2200	T	515	534	-19
RCA23_c01620	177159	178928	sulfoacetaldehyde acetyltransferase Xsc	COG0028	E	486	430	56
RCA23_c01630	178940	179944	phosphate acetyltransferase Pta	COG0280	C	250	314	-64
RCA23_c01640	179971	182781	DMSO reductase chain A	COG0243	C	273	340	-67
RCA23_c01650	182778	183659	alpha/beta hydrolase	COG0596	R	217	299	-82
RCA23_c01660	183656	184402	DMSO reductase chain B	COG0437	C	282	401	-119
RCA23_c01670	184402	185274	DMSO reductase chain C	COG3302	R	342	514	-172
RCA23_c01680	186741	185380	sodium:alanine symporter	COG1115	E	347	371	-24
RCA23_c01690	187519	186917	thymidine kinase Tdk	COG1435	F	259	365	-106
RCA23_c01700	187650	188366	NADPH-dependent FMN reductase	COG0431	R	400	533	-133
RCA23_c01710	191838	188422	carbamoyl-phosphate synthase large chain CarB	COG0458	E	371	400	-29
RCA23_c01720	192331	191858	HTH-type transcriptional regulator, AsnC family	COG1522	K	562	484	78
RCA23_c01730	192395	192673	hypothetical protein			876	934	-58
RCA23_c01740	192769	194544	aspartyl-tRNA synthase AspS	COG0173	J	459	475	-16
RCA23_c01750	194967	194602	hypothetical protein			335	405	-70
RCA23_c01760	195297	195013	putative signal transduction response regulator receiver pro	COG2197	T	358	337	21
RCA23_c01770	195361	195822	methylmalonyl-CoA epimerase	COG0346	E	605	483	122
RCA23_c01780	195850	196143	hypothetical protein DUF1467	COG5454	S	593	437	156

RCA23_c01790	196798	196100	hypothetical protein DUF540	COG2981	E	452	400	52
RCA23_c01800	197310	196795	putative nitroreductase	COG0778	C	264	302	-38
RCA23_c01810	198509	197412	histone deacetylase-like amidohydrolase HdaH	COG0123	B	254	420	-166
RCA23_c01820	198760	198527	hypothetical protein			331	417	-86
RCA23_c01830	198898	199593	hypothetical protein, peptidase family M48	COG0501	O	218	295	-77
RCA23_c01840	199628	199873	hypothetical protein			216	359	-143
RCA23_c01850	201592	200219	ribosomal protein S12 methylthiotransferase RimO	COG0621	J	203	311	-108
RCA23_c01860	203057	201645	hypothetical protein, transmembrane			183	253	-70
RCA23_c01870	203697	203125	GcrA cell cycle regulator	COG5352	S	261	323	-62
RCA23_c01880	203799	204602	ABC-2 type transport system membrane protein	COG0842	V	589	598	-9
RCA23_c01890	204812	205990	acetylornithine aminotransferase ArgD	COG4992	E	327	501	-174
RCA23_c01900	206062	206985	ornithine carbamoyltransferase ArgF	COG0078	E	299	408	-109
RCA23_c01910	207091	207885	hypothetical protein			277	502	-225
RCA23_c01920	207908	209323	6-phosphogluconate dehydrogenase GntZ	COG0362	G	254	365	-111
RCA23_c01930	211949	209328	ATP-dependent RNA helicase HrpB	COG1643	L	228	291	-63
RCA23_c01940	211993	212991	LAO/AO transport system ATPase	COG1703	E	204	314	-110
RCA23_c01950	213208	213495	50S ribosomal protein L28	COG0227	J	729	469	260
RCA23_c01960	213684	214121	hypothetical protein			684	509	175
RCA23_c01970	214253	216049	GTP-binding protein LepA	COG0481	M	566	504	62
RCA23_c01980	216818	216063	hypothetical protein, alpha/beta hydrolase-like	COG0596	R	269	374	-105
RCA23_c01990	216901	217473	putative ring-cleaving dioxygenase	COG0346	E	435	594	-159
RCA23_c02000	218824	217544	serine hydroxymethyltransferase GlyA	COG0112	E	425	364	61
RCA23_c02010	218982	219755	putative inorganic polyphosphate/ATP-NAD kinase PpnK	COG0061	G	432	438	-6
RCA23_c02020	222034	220145	propionate--CoA ligase PrpE	COG0365	I	297	361	-64
RCA23_c02030	222198	223292	hypothetical protein	COG1917	S	290	425	-135
RCA23_c02040	223384	223809	cytidine deaminase Cdd	COG0295	F	257	367	-110
RCA23_c02050	223809	225131	thymidine phosphorylase DeoA	COG0213	F	209	351	-142
RCA23_c02060	225142	226296	phosphopentomutase DeoB	COG1015	G	241	350	-109
RCA23_c02070	226293	227261	adenosine deaminase Add	COG1816	F	392	461	-69
RCA23_c02080	227588	228214	uracil phosphoribosyltransferase Upp	COG0035	F	717	465	252

RCA23_c02090	228449	228868	hypothetical protein			647	366	281
RCA23_c02100	230234	228900	3-deoxy-D-manno-octulosonic-acid transferase WaaA	COG1519	M	739	512	227
RCA23_c02110	231721	230234	L-sorbose 1-dehydrogenase	COG2303	E	814	536	278
RCA23_c02120	232388	231708	putative N-acylneuraminate cytidylyltransferase	COG1083	M	721	442	279
RCA23_c02130	233528	232392	UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotrar	COG0399	M	732	488	244
RCA23_c02140	236514	234343	hypothetical protein	COG3119	P	188	160	28
RCA23_c02150	237421	236696	hypothetical protein, nucleoside triphosphate hydrolases-lik	COG1122	P	241	189	52
RCA23_c02160	238069	237422	S-adenosyl-L-methionine-dependent methyltransferase	COG2226	H	312	194	118
RCA23_c02170	239306	238389	hypothetical protein			275	268	7
RCA23_c02180	241023	239398	medium-chain-fatty-acid--CoA ligase AlkK	COG0318	I	311	345	-34
RCA23_c02190	241093	241995	hypothetical protein DUF6 transmembrane	COG0697	G	423	493	-70
RCA23_c02200	244207	242024	fatty acid oxidation complex alpha subunit FadJ	COG1250	I	352	406	-54
RCA23_c02210	244632	244219	hypothetical protein			532	651	-119
RCA23_c02220	245865	244654	short chain dehydrogenase	COG0183	I	230	341	-111
RCA23_c02230	246509	245877	putative glutathione S-transferase	COG0625	O	519	394	125
RCA23_c02240	248334	246553	acyl-CoA dehydrogenase MmgC	COG1960	I	389	367	22
RCA23_c02250	248746	248357	putative HTH-type transcriptional regulator, MerR family	COG0789	K	557	407	150
RCA23_c02260	249251	248883	putative HTH-type transcriptional regulator, MerR family	COG0789	K	553	505	48
RCA23_c02270	250441	249299	hypothetical protein, transmembrane protein DUF2899			442	566	-124
RCA23_c02280	250528	250956	hypothetical protein, thioesterase	COG2050	Q	148	209	-61
RCA23_c02290	250953	251453	hypothetical protein, thioesterase	COG2050	Q	252	263	-11
RCA23_c02300	251446	252768	DNA-damage-inducible protein F	COG0534	V	309	520	-211
RCA23_c02310	253850	252789	dihydroorotate dehydrogenase PyrD	COG0167	F	240	322	-82
RCA23_c02320	254185	253847	hypothetical protein DUF952	COG3502	S	527	496	31
RCA23_c02330	254360	255892	5'-nucleotidase SurE	COG0737	F	403	477	-74
RCA23_c02340	257694	255964	hypothetical protein	COG3409	M	265	336	-71
RCA23_c02350	257885	258799	glycyl-tRNA synthase alpha subunit GlyQ	COG0752	J	609	605	4
RCA23_c02360	258799	259317	hypothetical protein			393	433	-40
RCA23_c02370	259317	261374	glycyl-tRNA synthase beta subunit GlyS	COG0751	J	339	366	-27
RCA23_c02380	261437	263977	pyruvate, phosphate dikinase PpdK	COG0574	G	240	338	-98

RCA23_c02390	264078	264761	putative cell wall hydrolase	COG3773	M	429	521	-92
RCA23_c02400	264811	265737	hypothetical protein, dihydroneopterin aldolase	COG1539	H	326	427	-101
RCA23_c02410	265734	266720	dihydropteroate synthase FolP	COG0294	H	218	368	-150
RCA23_c02420	267675	266692	putative integral membrane protein DUF6	COG0697	G	277	365	-88
RCA23_c02430	268729	267707	ketol-acid reductoisomerase IlvC	COG0059	E	455	347	108
RCA23_c02440	268864	269319	putative transcriptional regulator, asnC family	COG1522	K	260	420	-160
RCA23_c02450	269316	269771	putative transcriptional regulator, asnC family	COG1522	K	255	394	-139
RCA23_c02460	269846	270979	hypothetical protein	COG0075	E	378	383	-5
RCA23_c02470	272183	270987	2-octaprenyl-6-methoxyphenol hydroxylase UbiH	COG0654	H	210	332	-122
RCA23_c02480	272931	272161	putative pyrimidine 5-nucleotidase	COG1011	R	348	434	-86
RCA23_c02490	273012	273620	putative HTH-type transcriptional regulator, GntR family	COG1802	K	242	345	-103
RCA23_c02500	275505	273580	uncharacterized glycosyltransferase YdaM	COG1215	M	317	431	-114
RCA23_c02510	276701	275577	carbamoyl-phosphate synthase small chain CarA	COG0505	E	362	363	-1
RCA23_c02520	276880	277338	GatB/YqeY family protein	COG1610	S	554	518	36
RCA23_c02530	277906	277379	hypothetical protein	COG5488	S	343	384	-41
RCA23_c02540	279835	278162	cytochrome c oxidase subunit 1	COG0843	C	599	404	195
RCA23_c02550	280700	280038	octanoyltransferase LipB	COG0321	H	284	374	-90
RCA23_c02560	281476	280700	hypothetical protein, LytTr transcriptional regulator	COG3279	K	157	207	-50
RCA23_c02570	281566	282084	membrane protein-like	COG5395	S	319	344	-25
RCA23_c02590	284544	282886	arylsulfatase	COG3119	P	331	339	-8
RCA23_c02600	284793	285923	NADPH dehydrogenas	COG1902	C	211	275	-64
RCA23_c02610	287001	285961	L-idonate 5-dehydrogenase IdnD	COG1063	E	214	271	-57
RCA23_c02620	287045	287839	gluconate 5-dehydrogenase Gno	COG1028	I	244	357	-113
RCA23_c02630	288037	288939	uncharacterized oxidoreductase YgbJ	COG2084	I	282	358	-76
RCA23_c02640	288936	289799	hypothetical protein, xylose isomerase-like	COG1082	G	259	421	-162
RCA23_c02650	290765	289839	glyoxylate reductase GyaR	COG1052	C	275	373	-98
RCA23_c02660	290938	290762	hypothetical protein			401	386	15
RCA23_c02670	290989	291273	hypothetical protein, AzlC-like	COG1296	E	119	114	5
RCA23_c02680	293832	291886	cbbT/tktB: transketolase	COG0021	G	35	55	-20
RCA23_c02690	295174	293834	hypothetical protein	COG4091	E	45	80	-35

RCA23_c02700	295374	296207	transketolase, alpha subunit	COG3959	G	64	84	-20
RCA23_c02710	296204	297247	transketolase, beta-subunit	COG3958	G	33	56	-23
RCA23_c02720	297249	297809	putative 3-hydroxyisobutyrate dehydrogenase	COG2084	I	23	47	-24
RCA23_c02730	297809	298171	putative 3-hydroxyisobutyrate dehydrogenase	COG2084	I	41	116	-75
RCA23_c02740	298168	298920	3-oxoacyl-[acyl-carrier-protein] reductase FabG	COG1028	I	63	100	-37
RCA23_c02750	299907	298930	HTH-type transcriptional regulator, LysR family	COG0583	K	53	71	-18
RCA23_c02760	300726	300040	putative HTH-type transcriptional regulator, GntR family	COG1802	K	134	109	25
RCA23_c02770	300938	301951	TRAP dicarboxylate transporter, subunit DctP	COG4663	Q	153	99	54
RCA23_c02780	302000	302872	TRAP dicarboxylate transporter, subunit DctQ	COG4665	Q	180	134	46
RCA23_c02800	304513	305322	hypothetical protein	COG0240	C	83	98	-15
RCA23_c02810	305336	306664	hypothetical protein DUF1537	COG3395	S	99	119	-20
RCA23_c02820	306661	307920	putative ribulose bisphosphate carboxylase large chain	COG1850	G	55	88	-33
RCA23_c02830	308882	307917	hypothetical protein, NAD dependent epimerase / dehydrata	COG0451	M	98	93	5
RCA23_c02840	309016	309939	2-hydroxy-3-oxopropionate reductase GarR	COG2084	I	65	89	-24
RCA23_c02850	310592	310035	hypothetical protein			69	68	1
RCA23_c02860	310977	312479	altronate hydrolase UxaA	COG2721	G	287	313	-26
RCA23_c02870	312455	313480	putative oxidoreductase	COG0673	R	374	392	-18
RCA23_c02880	313516	314403	2-hydroxy-3-oxopropionate reductase GarR	COG2084	I	370	358	12
RCA23_c02890	314406	315287	S-adenosylmethionine uptake transporter Sam	COG0697	G	714	584	130
RCA23_c02900	315284	316147	2-dehydro-3-deoxygluconokinase KdgK	COG0524	G	444	419	25
RCA23_c02910	317333	316134	D-mannonate oxidoreductase UxuB	COG0246	G	274	353	-79
RCA23_c02920	318704	317334	uronate isomerase UxaC	COG1904	G	271	302	-31
RCA23_c02930	318798	319817	putative oxidoreductase	COG0673	R	175	238	-63
RCA23_c02940	319829	320809	putative oxidoreductase	COG0673	R	304	345	-41
RCA23_c02950	320806	321861	putative oxidoreductase	COG0673	R	242	272	-30
RCA23_c02960	321849	323057	mannonate dehydratase UxuA	COG1312	G	216	284	-68
RCA23_c02970	323103	324641	long-chain-fatty-acid--CoA ligase	COG0318	I	230	340	-110
RCA23_c02980	324634	325440	D-beta-hydroxybutyrate dehydrogenase BdhA	COG1028	I	247	448	-201
RCA23_c02990	325531	327783	copper-transporting P-type ATPase ActP	COG2217	P	292	457	-165
RCA23_c03000	327811	328200	HTH-type transcriptional regulator (copper efflux regulator)	COG0789	K	384	514	-130

RCA23_c03010	328492	328253	hypothetical protein	COG3937	S	328	304	24
RCA23_c03020	328847	329161	hypothetical protein			479	454	25
RCA23_c03030	331571	329382	isocitrate dehydrogenase Icd	COG2838	C	360	383	-23
RCA23_c03040	332596	331688	integral membrane protein DUF6	COG0697	G	370	367	3
RCA23_c03050	332863	333540	flavocytochrome c cytochrome subunit SoxE	COG3474	C	492	664	-172
RCA23_c03060	333621	334832	sulfide dehydrogenase [flavocytochrome c] flavoprotein cha	COG0446	R	319	404	-85
RCA23_c03070	335365	334916	hypothetical protein, OsmC-like	COG1764	O	444	380	64
RCA23_c03080	336582	335440	putative dimethyl sulfoniopropionate demethylase DmdA	COG0404	E	508	485	23
RCA23_c03090	337231	336746	transcriptional regulator, AsnC family	COG1522	K	732	486	246
RCA23_c03100	338152	338784	glutathione S-transferase	COG0625	O	93	79	14
RCA23_c03120	340630	339608	hypothetical protein, ribonuclease, E/G family	COG1530	J	306	281	25
RCA23_c03130	341160	340627	Maf-like protein	COG0424	D	156	192	-36
RCA23_c03140	341419	341201	translation initiation factor IF-1	COG0361	J	574	601	-27
RCA23_c03150	342020	341622	hypothetical protein, low molecular weight phosphotyrosine	COG0394	T	491	374	117
RCA23_c03160	342565	342086	hypothetical protein UPF0262	COG5328	S	455	421	34
RCA23_c03170	343866	342565	histidinol dehydrogenase HisD	COG0141	E	235	274	-39
RCA23_c03180	344390	343932	hypothetical protein			233	414	-181
RCA23_c03190	345655	344387	UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA	COG0766	M	277	290	-13
RCA23_c03210	346329	347666	PAS/PAC sensor hybrid histidine kinase	COG0642	T	293	203	90
RCA23_c03220	347759	348817	2OG-Fe(II) oxygenase	COG3491	R	359	267	92
RCA23_c03230	348821	349465	putative lysine exporter protein	COG1280	E	425	357	68
RCA23_c03240	349742	350194	putative carbon monoxide dehydrogenase subunit G	COG3427	S	365	468	-103
RCA23_c03250	350184	351113	hypothetical protein, XdhC and CoxI family	COG1975	O	275	339	-64
RCA23_c03260	352364	351108	putative MFS-type transporter	COG2814	G	383	409	-26
RCA23_c03270	352457	353512	AFG1-like ATPase	COG1485	R	237	332	-95
RCA23_c03280	354792	353509	bifunctional protein FolC	COG0285	H	200	338	-138
RCA23_c03290	355709	354789	acetyl-coenzyme A carboxylase carboxyl transferase beta s	COG0777	I	408	418	-10
RCA23_c03300	356729	355773	hypothetical protein, CAAX amino terminal protease-like	COG1266	R	413	454	-41
RCA23_c03310	356791	358524	dihydroxy-acid dehydratase IlvD	COG0129	E	332	368	-36
RCA23_c03320	358660	359103	hypothetical protein			227	276	-49

RCA23_c03330	359279	360058	hypothetical protein			249	344	-95
RCA23_c03340	360076	360423	hypothetical protein			380	445	-65
RCA23_c03350	361268	360426	hypothetical protein, OmpA family	COG2885	M	332	403	-71
RCA23_c03360	361905	361339	hypothetical protein, peroxidase-like protein	COG2128	S	428	461	-33
RCA23_c03370	362627	361902	hypothetical protein, acetyltransferase-like	COG0456	R	256	347	-91
RCA23_c03380	363346	362624	hypothetical protein, probably molybdopterin binding	COG1058	R	218	322	-104
RCA23_c03390	363392	364114	sugar fermentation stimulation protein SfsA	COG1489	R	302	425	-123
RCA23_c03400	364191	365000	methionine aminopeptidase Map	COG0024	J	369	393	-24
RCA23_c03410	366577	365054	ATP-dependent RNA helicase RhlE	COG0513	L	275	300	-25
RCA23_c03420	367398	366829	putative ribosomal RNA small subunit methyltransferase D	COG0742	L	236	306	-70
RCA23_c03430	368600	367395	rhodocoxin reductase ThcD	COG0446	R	286	329	-43
RCA23_c03440	368681	369172	peroxiredoxin	COG0678	O	574	527	47
RCA23_c03450	369613	369326	pterin-4-alpha-carbinolamine dehydratase	COG2154	H	559	495	64
RCA23_c03460	370797	369610	hypothetical protein DUF482	COG3146	S	291	351	-60
RCA23_c03470	371604	370849	putative glycerophosphoryl diester phosphodiesterase	COG0584	C	398	441	-43
RCA23_c03480	372065	371601	putative endoribonuclease L-PSP	COG0251	J	345	507	-162
RCA23_c03490	373364	372132	type I secretion system protein, HlyD family	COG1566	V	257	378	-121
RCA23_c03500	374871	373411	type I secretion system ATP-binding component	COG4618	R	195	310	-115
RCA23_c03510	375137	374874	putative type I secretion system protein, transmembrane do	COG4618	R	484	480	4
RCA23_c03520	375269	376000	VacJ like lipoprotein	COG2853	M	564	440	124
RCA23_c03530	375984	376589	putative toluene tolerance protein	COG2854	Q	423	353	70
RCA23_c03540	378789	376654	penicillin-binding protein 1B	COG0744	M	283	374	-91
RCA23_c03550	380155	378971	aromatic-amino-acid aminotransferase TyrB	COG1448	E	343	390	-47
RCA23_c03560	381012	380155	3-mercaptopyruvate sulfurtransferase SseA	COG2897	P	307	316	-9
RCA23_c03570	381576	381100	SsrA-binding protein SmpB	COG0691	O	752	622	130
RCA23_c03580	382567	381680	dihydrodipicolinate synthase DapA	COG0329	E	245	271	-26
RCA23_c03590	382609	384669	soluble lytic murein transglycosylase Slt	COG0741	M	231	304	-73
RCA23_c03600	385589	384717	hypothetical protein DUF6 transmembrane	COG0697	G	244	358	-114
RCA23_c03610	386248	385586	hypothetical protein DUF752	COG4121	S	268	375	-107
RCA23_c03620	386288	387352	putative FAD-dependent oxidoreductase	COG0665	E	279	439	-160

RCA23_c03630	387390	387752	hypothetical protein, glyoxalase/dioxygenase superfamily	COG0346	E	217	367	-150
RCA23_c03640	388138	387773	hypothetical protein			350	445	-95
RCA23_c03650	388488	388135	hypothetical protein			529	416	113
RCA23_c03660	389111	388503	cob(I)yrinic acid a,c-diamide adenosyltransferase CobO	COG2109	H	496	404	92
RCA23_c03670	389202	389606	hypothetical protein			210	318	-108
RCA23_c03680	390600	389629	oligopeptide/dipeptide ABC transporter, ATP-binding protei	COG0444	E	260	314	-54
RCA23_c03690	391589	390600	oligopeptide/dipeptide ABC transporter, ATP-binding protei	COG0444	E	238	350	-112
RCA23_c03700	392467	391586	oligopeptide/dipeptide ABC transporter, permease protein	COG1173	E	262	357	-95
RCA23_c03710	393441	392464	oligopeptide/dipeptide ABC transporter, permease protein	COG0601	E	439	395	44
RCA23_c03720	395073	393502	oligopeptide/dipeptide ABC transporter, periplasmic substra	COG0747	E	379	323	56
RCA23_c03730	396231	395302	HTH-type transcriptional regulator, LysR family	COG0583	K	497	494	3
RCA23_c03740	396411	397982	putative amidohydrolase 3	COG1574	R	232	346	-114
RCA23_c03750	397979	398881	cobalamin biosynthesis CobW-like	COG0523	R	249	331	-82
RCA23_c03760	398992	400035	hypothetical protein, restriction endonuclease type IV-like	COG4127	S	241	213	28
RCA23_c03770	401165	400095	glycine betaine transport ATP-binding protein OpuAA	COG4175	E	439	469	-30
RCA23_c03780	402193	401162	glycine betaine transport system permease protein OpuAB	COG4176	E	459	546	-87
RCA23_c03790	403226	402258	glycine betaine transporter substrate-binding protein OpuA	COG2113	E	364	379	-15
RCA23_c03800	403626	404708	fatty acid desaturase	COG3239	I	370	432	-62
RCA23_c03810	405832	404717	CoA-transferase family III protein involved in DMSP degrad	COG1804	C	286	378	-92
RCA23_c03820	405843	406949	glyceraldehyde-3-phosphate dehydrogenase Gap	COG0057	G	320	495	-175
RCA23_c03830	407067	407687	ATP-dependent Clp protease proteolytic subunit ClpP	COG0740	O	732	497	235
RCA23_c03840	407812	409077	ATP-dependent Clp protease ATP-binding subunit ClpX	COG1219	O	680	551	129
RCA23_c03850	409209	409592	putative NADH ubiquinone oxidoreductase subunit NDUFA	COG3761	C	786	483	303
RCA23_c03860	409597	410043	ABC-type transport system involved in resistance to organi	COG1463	Q	548	559	-11
RCA23_c03870	410043	410402	Uncharacterized protein conserved in bacteria (DUF2155)	COG4765	S	308	397	-89
RCA23_c03880	411007	410366	leucyl/phenylalanyl-tRNA--protein transferase Aat	COG2360	O	466	513	-47
RCA23_c03890	412356	411004	biotin carboxylase AccC	COG4770	I	318	325	-7
RCA23_c03900	414969	413026	acetyl-coenzyme A synthase AcsA	COG0365	I	265	296	-31
RCA23_c03910	415768	415037	high-affinity branched-chain amino acid transport ATP-bindi	COG0410	E	232	342	-110
RCA23_c03920	416529	415771	high-affinity branched-chain amino acid transport ATP-bindi	COG0411	E	513	381	132

RCA23_c03930	417743	416541	putative branched-chain amino acid transport system perme	COG4177	E		708	525	183
RCA23_c03940	418779	417748	putative branched-chain amino acid transport system perme	COG0559	E		636	469	167
RCA23_c03950	420231	418885	hypothetical protein	COG0683	E		472	393	79
RCA23_c03960	420457	421773	hypothetical protein, DNA binding helix-turn helix proteins	COG1396	K		304	375	-71
RCA23_c03970	421836	422207	putative response regulator receiver protein, CheY like	COG0745	T		506	409	97
RCA23_c03980	422204	422473	hypothetical protein				308	532	-224
RCA23_c03990	422474	425128	sensor protein kinase WalK	COG0591	E		309	414	-105
RCA23_c04000	425546	425109	hypothetical protein DUF442	COG3453	S		331	346	-15
RCA23_c04010	425805	425593	hypothetical protein				528	443	85
RCA23_c04020	425917	426168	hypothetical protein	COG3750	S		925	593	332
RCA23_c04030	427065	426184	hypothetical protein				688	461	227
RCA23_c04040	427159	428790	putative Fe(3+)-transport system protein SfuB	COG1178	P		329	410	-81
RCA23_c04060	428970	430124	integrase	COG0582	L	GI 2	37	28	9
RCA23_c04070	430197	430778	hypothetical protein	COG3945	S	GI 2	17	8	9
RCA23_c04080	434845	431570	hypothetical protein			GI 2	41	29	12
RCA23_c04090	434910	437174	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltra	COG0457	R	GI 2	20	13	7
RCA23_c04100	440084	439434	esterase, SGNH hydrolase-type	COG2755	E	GI 2	0	0	0
RCA23_c04110	440656	440258	hypothetical protein			GI 2	235	150	85
RCA23_c04120	441029	441403	hypothetical protein, tetratricopeptide repeat	COG0790	R	GI 2	76	63	13
RCA23_c04130	441971	441678	hypothetical protein			GI 2	270	161	109
RCA23_c04140	442447	442121	hypothetical protein			GI 2	223	168	55
RCA23_c04150	442788	442444	hypothetical protein			GI 2	224	151	73
RCA23_c04160	443599	443222	hypothetical protein, RmlC-like cupin family	COG3450	R	GI 2	4	15	-11
RCA23_c04170	444724	444101	hypothetical protein			GI 2	45	28	17
RCA23_c04180	445304	444918	hypothetical protein, DUF3127			GI 2	56	66	-10
RCA23_c04190	446438	445509	putative nucleoside triphosphate hydrolase, ATPase domai	COG1066	O	GI 2	14	20	-6
RCA23_c04200	447532	449187	zinc-dependent metalloprotease	COG2931	Q	GI 2	119	65	54
RCA23_c04210	449574	449230	HTH-type transcriptional regulator, AsnC family	COG1522	K	GI 2	160	127	33
RCA23_c04220	450860	449781	integrase	COG2801	L	GI 2	0	0	0
RCA23_c04230	453456	452530	putative ion channel			GI 2	549	372	177

RCA23_c04240	454720	453746	integrase	COG4974	L	GI 2	326	288	38
RCA23_c04250	455125	455838	Gcn5-like N-acetyltransferase	COG1670	J	GI 2	8	1	7
RCA23_c04260	457797	456643	integrase	COG0582	L	GI 2	166	139	27
RCA23_c04280	458139	459119	hypothetical protein, NAD dependent epimerase / dehydrata	COG0702	M		246	375	-129
RCA23_c04290	459936	459124	undecaprenyl-diphosphatase UppP	COG1968	V		192	274	-82
RCA23_c04300	460124	461578	glutamate synthase [NADPH] small chain GltD	COG0493	E		382	340	42
RCA23_c04310	461639	466186	glutamate synthase [NADPH] large chain GltB	COG0069	E		343	411	-68
RCA23_c04320	466290	467033	monofunctional biosynthetic peptidoglycan transglycosylase	COG0744	M		271	373	-102
RCA23_c04330	467132	467752	putative glutathione S-transferase	COG0625	O		483	589	-106
RCA23_c04340	467733	468776	putative electron transport protein yjeS	COG1600	C		231	349	-118
RCA23_c04360	469585	468773	hypothetical protein	COG5266	P		307	349	-42
RCA23_c04350	469584	470741	hypothetical protein				351	560	-209
RCA23_c04370	471709	470840	branched-chain-amino-acid aminotransferase IlvE	COG0115	E		279	331	-52
RCA23_c04380	471872	472384	HTH-type transcriptional regulator PetP	COG1846	K		317	270	47
RCA23_c04390	472381	473094	protein PetR	COG0745	T		277	371	-94
RCA23_c04400	473091	474020	putative deacytelase, histone deacetylase superfamily prote	COG0123	B		332	484	-152
RCA23_c04410	474013	474255	exodeoxyribonuclease 7 small subunit XseB	COG1722	L		304	484	-180
RCA23_c04420	474215	475159	geranyltranstransferase IspA	COG0142	H		225	362	-137
RCA23_c04430	475200	477101	1-deoxy-D-xylulose-5-phosphate synthase Dxs	COG1154	H		238	320	-82
RCA23_c04440	478007	477105	hypothetical protein, NAD dependent epimerase/dehydratas	COG0451	M		220	302	-82
RCA23_c04450	478232	478657	hypothetical protein				298	338	-40
RCA23_c04460	478753	479079	hypothetical protein				446	435	11
RCA23_c04470	479921	479142	carnitinyl-CoA dehydratase CaiD	COG1024	I		337	370	-33
RCA23_c04480	481945	479918	hypothetical protein, CoA-binding	COG1042	C		232	293	-61
RCA23_c04490	483157	481997	putative acyl-CoA dehydrogenase YngJ	COG1960	I		288	270	18
RCA23_c04500	483234	484166	transcriptional regulator, AraC family	COG4977	K		204	299	-95
RCA23_c04510	484951	484196	class II aldolase	COG0235	G		278	347	-69
RCA23_c04520	485442	485014	arsenate reductase ArsC	COG1393	P		218	288	-70
RCA23_c04530	485529	487343	adenine deaminase Ade	COG1001	F		223	310	-87
RCA23_c04540	487330	488805	AMP nucleosidase Amn	COG0775	F		382	319	63

RCA23_c04550	488882	489214	DNA-binding protein HU	COG0776	L	749	586	163
RCA23_c04560	489360	490229	inner membrane protein DUF6	COG0697	G	402	597	-195
RCA23_c04570	490303	491016	hypothetical protein, cytochrome C biogenesis protein	COG0785	O	316	423	-107
RCA23_c04580	491039	491449	hypothetical protein, thioredoxin	COG0526	O	398	399	-1
RCA23_c04590	492021	491446	hypothetical protein	COG3222	S	181	253	-72
RCA23_c04600	493168	492038	succinyl-diaminopimelate desuccinylase DapE	COG0624	E	242	273	-31
RCA23_c04610	493554	493168	hypothetical protein			369	407	-38
RCA23_c04620	494478	493591	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltrans	COG2171	E	248	351	-103
RCA23_c04630	495411	494482	L-threonine ammonia-lyase	COG1171	E	204	305	-101
RCA23_c04640	496617	495427	ribosomal RNA large subunit methyltransferase N	COG0820	R	322	367	-45
RCA23_c04650	497212	496688	hypothetical protein			320	378	-58
RCA23_c04660	497318	498349	L-asparaginase II	COG4448	E	194	300	-106
RCA23_c04670	499288	498410	phosphoserine phosphatase SerB	COG0560	E	220	310	-90
RCA23_c04680	499417	499902	hypothetical protein			382	415	-33
RCA23_c04690	500025	501251	phosphoserine aminotransferase SerC	COG1932	H	301	441	-140
RCA23_c04700	501306	502901	D-3-phosphoglycerate dehydrogenase SerA	COG0111	H	369	392	-23
RCA23_c04710	502898	503629	metallophosphoesterase			240	328	-88
RCA23_c04720	504126	503641	RNA pyrophosphohydrolase RppH	COG0494	L	234	236	-2
RCA23_c04730	505467	504130	carboxy-terminal-processing protease CtpA	COG0793	M	363	371	-8
RCA23_c04740	507182	505665	2,3-bisphosphoglycerate-independent phosphoglycerate mu	COG0696	G	294	331	-37
RCA23_c04750	507362	508978	putative protein ImuB			218	304	-86
RCA23_c04760	509201	509545	hypothetical protein			401	555	-154
RCA23_c04770	510291	509542	hypothetical protein, NlpC/P60	COG0791	M	244	388	-144
RCA23_c04780	511667	510288	putative cytosol aminopeptidase PepA	COG0260	E	203	280	-77
RCA23_c04790	512156	511782	hypothetical protein			280	370	-90
RCA23_c04800	512302	512970	carbonic anhydrase CynT	COG0288	P	701	454	247
RCA23_c04810	514074	513052	aspartate-semialdehyde dehydrogenase Asd	COG0136	E	777	529	248
RCA23_c04820	515330	514140	MFS-type transporter	COG2223	P	321	277	44
RCA23_c04830	515444	516199	short chain dehydrogenase	COG4221	R	260	362	-102
RCA23_c04840	517557	516226	FAD dependent oxidoreductase	COG0665	E	173	210	-37

RCA23_c04850	519110	517560	trimethylamine methyltransferase MttB	COG5598	H	269	395	-126
RCA23_c04860	520642	519152	aldehyde dehydrogenase	COG1012	C	229	319	-90
RCA23_c04870	521547	520639	dihydrodipicolinate synthase DapA	COG0329	E	277	336	-59
RCA23_c04880	522241	521537	transcriptional regulator, GntR family	COG1802	K	322	303	19
RCA23_c04890	523118	522333	hypothetical protein			258	358	-100
RCA23_c04900	524284	523202	isopropylmalate dehydrogenase LeuB	COG0473	C	304	357	-53
RCA23_c04910	525496	524363	hypothetical protein			267	377	-110
RCA23_c04920	526231	525626	3-isopropylmalate dehydratase small subunit LeuD	COG0066	E	458	387	71
RCA23_c04930	527634	526231	3-isopropylmalate dehydratase large subunit LeuC	COG0065	E	288	275	13
RCA23_c04940	528605	528072	hypothetical protein, DUF2975			207	247	-40
RCA23_c04950	528844	529257	hypothetical protein DUF143	COG0799	S	450	364	86
RCA23_c04960	529257	529727	ribosomal RNA large subunit methyltransferase H	COG1576	S	245	311	-66
RCA23_c04970	529799	530911	alcohol dehydrogenase class-3 AdhI	COG1062	C	294	435	-141
RCA23_c04980	531014	531961	putative membrane transport protein	COG0679	R	233	422	-189
RCA23_c04990	532000	532896	S-formylglutathione hydrolase YeiG	COG0627	R	250	354	-104
RCA23_c05000	532900	534324	soluble pyridine nucleotide transhydrogenase	COG1249	C	327	370	-43
RCA23_c05010	534321	534755	hypothetical protein DUF188	COG1671	S	235	386	-151
RCA23_c05020	534844	535797	putative integral membrane protein	COG0697	G	439	594	-155
RCA23_c05030	535823	536443	putative HAD-superfamily hydrolase	COG1011	R	270	379	-109
RCA23_c05040	536452	537399	putative ornithine cyclodeaminase	COG2423	E	225	304	-79
RCA23_c05050	541032	537361	aerobic cobaltochelatase subunit CobN	COG1429	H	208	291	-83
RCA23_c05060	541732	541283	hypothetical protein, acetyltransferase-like	COG0456	R	273	241	32
RCA23_c05070	542827	541736	protein CobW	COG0523	R	298	352	-54
RCA23_c05080	542896	543240	hypothetical protein DUF1636	COG5469	S	269	436	-167
RCA23_c05090	543928	543248	possible cobalt transporter, subunit CbtA	COG5446	S	213	300	-87
RCA23_c05100	544412	545827	Cytochrome c peroxidase	COG1858	P	296	759	-463
RCA23_c05110	546982	545975	hypothetical protein	COG4188	R	350	299	51
RCA23_c05120	549014	547548	hypothetical protein			258	381	-123
RCA23_c05130	550285	549011	xylose repressor XylR	COG1940	K	245	284	-39
RCA23_c05140	550504	551532	D-xylose-binding periplasmic protein XylF	COG4213	G	906	544	362

RCA23_c05150	551693	553006	xylose transport system permease protein XylH	COG4214	G	453	505	-52
RCA23_c05160	553018	553776	xylose ABC transporter, ATP-binding protein XylG	COG1129	G	597	619	-22
RCA23_c05170	553780	555234	xylulose kinase XylB	COG1070	G	231	268	-37
RCA23_c05180	555316	556617	xylose isomerase XylA	COG2115	G	393	363	30
RCA23_c05190	558142	556625	long-chain-fatty-acid--CoA ligase LcfB	COG0318	I	319	296	23
RCA23_c05200	559391	558144	malonyl-CoA decarboxylase			373	355	18
RCA23_c05210	561272	559614	acyl-CoA dehydrogenase	COG1960	I	256	352	-96
RCA23_c05220	561381	562196	hypothetical protein DUF81			360	365	-5
RCA23_c05230	563871	562240	phosphoenolpyruvate carboxykinase PckA	COG1866	C	523	455	68
RCA23_c05240	564119	564820	two component signal transduction response regulator rece	COG0745	T	486	575	-89
RCA23_c05250	564856	566508	two component signal transduction histidine kinase ChvG	COG0642	T	217	329	-112
RCA23_c05260	566513	566974	hypothetical protein, HPr serine kinase	COG1493	T	220	332	-112
RCA23_c05270	566967	567878	putative P-loop containing ATPase	COG1660	R	307	374	-67
RCA23_c05280	567875	568264	hypothetical protein, PTS system mannose-specific EIIA co	COG2893	G	251	493	-242
RCA23_c05290	568274	568540	phosphocarrier protein NPr	COG1925	G	259	480	-221
RCA23_c05300	569551	568622	electron transfer flavoprotein alpha subunit EtfA	COG2025	C	357	393	-36
RCA23_c05310	570309	569551	electron transfer flavoprotein beta subunit EtfB	COG2086	C	490	366	124
RCA23_c05320	571054	570482	cob(I)yrinic acid a,c-diamide adenosyltransferase CobO	COG2096	S	330	335	-5
RCA23_c05330	572154	571324	putative short chain dehydrogenase	COG4221	R	327	465	-138
RCA23_c05340	572337	574667	DNA topoisomerase 4 subunit A	COG0188	L	319	408	-89
RCA23_c05350	574828	576000	hypothetical protein DUF898	COG4269	S	147	227	-80
RCA23_c05360	576002	577117	peptidase M48 Ste24p	COG4783	R	216	344	-128
RCA23_c05370	577197	577787	hypothetical protein			310	426	-116
RCA23_c05380	577907	579082	elongation factor Tu (EF-Tu)	COG0050	J	14	5	9
RCA23_c05400	580699	579374	hypothetical protein, DUF560			336	441	-105
RCA23_c05410	582022	580856	hippurate hydrolase HipO	COG1473	R	256	365	-109
RCA23_c05420	583851	582037	glutathione import ATP-binding protein GsiA	COG1123	R	260	312	-52
RCA23_c05430	584120	585829	oligopeptide-binding protein AppA	COG0747	E	394	382	12
RCA23_c05440	585905	586912	oligopeptide transport system permease protein AppB	COG0601	E	420	433	-13
RCA23_c05450	586905	587870	oligopeptide transport system permease protein AppC	COG1173	E	428	438	-10

RCA23_c05460	587971	588900	ABC transporter ATP-binding protein	COG1131	V	711	476	235
RCA23_c05470	588897	589658	inner membrane transport permease	COG0842	V	729	644	85
RCA23_c05480	589709	590494	hypothetical protein, peptidase family S49	COG0616	O	594	456	138
RCA23_c05490	590678	591637	putative sodium/calcium exchanger protein	COG0530	P	399	489	-90
RCA23_c05500	591649	592425	putative short cprotein	COG1028	I	366	403	-37
RCA23_c05510	592554	594575	UvrABC system protein C	COG0322	L	372	374	-2
RCA23_c05520	594704	595360	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltra	COG0558	I	788	670	118
RCA23_c05530	595366	595617	molybdopterin-converting factor subunit MoaD	COG1977	H	349	415	-66
RCA23_c05540	595619	596086	molybdopterin synthase catalytic subunit MoaE	COG0314	H	385	464	-79
RCA23_c05550	596425	596096	hypothetical protein			362	278	84
RCA23_c05560	598304	596418	hypothetical protein, OmpA	COG2885	M	263	298	-35
RCA23_c05570	599317	598358	UbiA prenyltransferase	COG0382	H	237	327	-90
RCA23_c05580	599330	600049	RNA methyltransferase	COG1385	S	221	259	-38
RCA23_c05590	600046	600558	hypothetical protein			265	322	-57
RCA23_c05600	600631	602001	glutamate--cysteine ligase	COG3572	H	440	391	49
RCA23_c05610	602642	602034	glycerol-3-phosphate acyltransferase PlsY	COG0344	S	259	318	-59
RCA23_c05620	603898	602639	dihydroorotase PyrC	COG0044	F	245	261	-16
RCA23_c05630	604984	604040	aspartate carbamoyltransferase PyrB	COG0540	F	333	548	-215
RCA23_c05640	605144	605956	uracil DNA glycosylase family protein	COG1573	L	152	228	-76
RCA23_c05650	605953	606495	molybdenum cofactor biosynthesis protein MoaB	COG0521	H	237	295	-58
RCA23_c05660	606597	608030	putative efflux transporter, RND family, membrane fusion pr	COG1566	V	265	305	-40
RCA23_c05670	608034	611426	transporter, AcrB/AcrD/AcrF family	COG0841	V	347	446	-99
RCA23_c05680	612217	611423	hypothetical protein	COG4233	O	221	319	-98
RCA23_c05690	612351	612965	hypothetical protein DUF179	COG1678	K	253	362	-109
RCA23_c05700	613054	614754	acyl-CoA dehydrogenase	COG1960	I	300	339	-39
RCA23_c05710	614764	615792	putative metallo-beta-lactamase family protein	COG0491	R	238	425	-187
RCA23_c05720	616040	616657	hypothetical protein			369	420	-51
RCA23_c05730	616959	616630	putative branched-chain amino acid transport protein	COG4392	S	293	366	-73
RCA23_c05740	617657	616956	protein AzlC	COG1296	E	276	375	-99
RCA23_c05750	617712	618581	formate dehydrogenase accessory protein FdhD	COG1526	C	297	394	-97

RCA23_c05760	618578	619183	molybdopterin-guanine dinucleotide biosynthesis protein Mc	COG0746	H	193	329	-136
RCA23_c05770	619180	619677	molybdopterin-guanine dinucleotide biosynthesis protein Mc	COG1763	H	159	338	-179
RCA23_c05780	619674	620930	molybdopterin biosynthesis protein MoeA	COG0303	H	162	269	-107
RCA23_c05790	621450	620965	transcription elongation factor GreA	COG0782	K	496	392	104
RCA23_c05800	621745	623397	electron transfer flavoprotein-ubiquinone oxidoreductase	COG0644	C	384	446	-62
RCA23_c05810	623502	625211	tetratricopeptide repeat-containing protein	COG0457	R	227	360	-133
RCA23_c05820	625201	626028	4-diphosphocytidyl-2C-methyl-D-erythritol 2-phosphate synt	COG1947	I	217	334	-117
RCA23_c05830	627043	626045	octaprenyl-diphosphate synthase IspB	COG0142	H	264	336	-72
RCA23_c05840	627656	628066	hypothetical protein, methyltransferase	COG4123	R	203	250	-47
RCA23_c05850	629161	628439	acetoacetyl-CoA reductase PhaB	COG1028	I	301	347	-46
RCA23_c05860	630460	629267	acetyl-CoA acetyltransferase PhaA	COG0183	I	348	300	48
RCA23_c05870	631425	630640	signaling protein	COG2200	T	475	385	90
RCA23_c05880	631516	632085	DNA-3-methyladenine glycosylase 1	COG2818	L	457	429	28
RCA23_c05890	632617	632066	thiol:disulfide interchange protein TlpA	COG0526	O	277	392	-115
RCA23_c05900	632642	634030	argininosuccinate lyase ArgH	COG0165	E	259	303	-44
RCA23_c05910	634155	634472	hypothetical protein			386	409	-23
RCA23_c05920	634558	635823	diaminopimelate decarboxylase LysA	COG0019	E	332	435	-103
RCA23_c05930	635848	638316	hypothetical protein	COG1196	D	232	318	-86
RCA23_c05940	639228	639956	putative acyltransferase	COG0204	I	437	429	8
RCA23_c05950	640216	640605	glyoxalase/bleomycin resistance protein	COG2764	S	365	382	-17
RCA23_c05960	640646	641269	hypothetical protein, pyridoxamine 5'-phosphate oxidase	COG3576	R	273	303	-30
RCA23_c05970	642246	641284	acetyl-coenzyme A carboxylase carboxyl transferase alpha	COG0825	I	360	382	-22
RCA23_c05980	643307	642348	malyl-CoA ligase	COG2301	G	231	247	-16
RCA23_c05990	643594	644595	hypothetical protein DUF1611	COG3367	S	277	316	-39
RCA23_c06000	644712	645674	L-Ala-D/L-Glu epimerase YcjG	COG4948	M	259	446	-187
RCA23_c06010	645679	646539	D-alanine aminotransferase Dat	COG0115	E	337	480	-143
RCA23_c06020	646631	648778	hypothetical, OmpA-like			226	313	-87
RCA23_c06030	648803	649246	hypothetical protein	COG3743	S	411	402	9
RCA23_c06040	649545	649243	hypothetical protein DUF1244	COG3492	S	260	392	-132
RCA23_c06050	650297	649542	N-formylglutamate amidohydrolase	COG3931	E	349	368	-19

RCA23_c06060	650384	651832	pyruvate kinase PykF	COG0469	G	393	434	-41
RCA23_c06070	651832	652062	hypothetical protein			624	591	33
RCA23_c06080	652176	652376	50S ribosomal protein L35	COG0291	J	871	606	265
RCA23_c06090	652391	652753	50S ribosomal protein L20	COG0292	J	873	409	464
RCA23_c06100	652996	655311	putative subtilase family protein	COG1404	O	455	421	34
RCA23_c06110	655323	655715	hypothetical protein			809	570	239
RCA23_c06120	655813	656757	hypothetical protein, lipid A biosynthesis acyltransferase	COG1560	M	291	395	-104
RCA23_c06130	656869	657942	phenylalanyl-tRNA synthase alpha chain PheS	COG0016	J	304	451	-147
RCA23_c06140	657976	658701	glutamine amidotransferase class-I	COG0518	F	224	306	-82
RCA23_c06150	658701	661094	phenylalanyl-tRNA synthase beta chain PheT	COG0072	J	331	354	-23
RCA23_c06160	661282	661740	putative HTH-type transcriptional regulator	COG1522	K	798	641	157
RCA23_c06170	662019	661819	ribsomal protein S21	COG0828	J	1.005	915	90
RCA23_c06180	662122	662802	putative ubiquinone biosynthesis protein COQ9	COG5590	S	271	315	-44
RCA23_c06190	662830	663807	putative quinone oxidoreductase	COG0604	C	276	335	-59
RCA23_c06200	663977	664744	hypothetical protein DUF1013	COG3820	S	569	525	44
RCA23_c06210	665637	665044	recombination protein RecR	COG0353	L	391	437	-46
RCA23_c06220	665998	665654	hypothetical protein	COG0718	S	517	458	59
RCA23_c06230	667857	666067	DNA polymerase III subunit tau	COG2812	L	205	268	-63
RCA23_c06240	668143	669114	NADH pyrophosphatase Nudc	COG2816	L	277	428	-151
RCA23_c06250	669178	669648	hypothetical protein	COG3832	S	389	485	-96
RCA23_c06260	670475	669645	prephenate dehydratase PheA	COG0077	E	256	261	-5
RCA23_c06270	670580	671113	cytochrome c-552	COG3474	C	552	407	145
RCA23_c06280	671321	673186	ABC transporter extracellular solute-binding protein	COG4166	E	474	456	18
RCA23_c06290	673188	674267	ABC transporter permease protein	COG4174	R	595	473	122
RCA23_c06300	674264	675379	ABC transporter permease protein	COG4239	R	319	447	-128
RCA23_c06310	675376	676956	putative oligopeptide ABC transporter ATP-binding protein	COG4172	R	373	488	-115
RCA23_c06320	677633	676953	fumarylacetoacetate hydrolase family protein	COG0179	Q	215	253	-38
RCA23_c06330	679120	677702	D-alanyl-D-alanine carboxypeptidase DacF	COG1686	M	158	204	-46
RCA23_c06340	680015	679311	haloacid dehalogenase domain protein hydrolase	COG1011	R	406	341	65
RCA23_c06350	680085	680423	ATP-dependent Clp protease adapter protein ClpS	COG2127	S	541	439	102

RCA23_c06360	680427	681377	putative methyltransferase	COG2813	J		262	313	-51
RCA23_c06370	681417	682220	putative short chain dehydrogenase	COG1028	I		340	389	-49
RCA23_c06380	682229	683110	coproporphyrinogen 3 oxidase, aerobic	COG0408	H		253	334	-81
RCA23_c06390	683515	684843	oxidoreductase, FAD-binding protein	COG4097	P		282	382	-100
RCA23_c06400	686376	684955	D-lactate dehydrogenase	COG0277	C		399	414	-15
RCA23_c06420	686652	688244	integrase			GI 3	177	118	59
RCA23_c06430	690078	688801	mandelate racemase	COG4948	M	GI 3	36	16	20
RCA23_c06440	690933	690091	fumarylacetoacetate hydrolase family protein	COG0179	Q	GI 3	11	14	-3
RCA23_c06450	691708	690977	short-chain dehydrogenase/reductase	COG1028	I	GI 3	29	17	12
RCA23_c06460	692579	691701	amidohydrolase	COG3618	R	GI 3	20	19	1
RCA23_c06470	693475	692576	aldo/keto reductase	COG0667	C	GI 3	5	12	-7
RCA23_c06480	694269	693475	ABC transporter, permease protein	COG0600	P	GI 3	26	17	9
RCA23_c06490	695094	694273	ABC transporter, permease protein	COG0600	P	GI 3	32	16	16
RCA23_c06500	695378	695091	hypothetical protein			GI 3	18	11	7
RCA23_c06510	696208	695414	sulfonate/nitrate ABC transporter, ATPase	COG1116	P	GI 3	12	10	2
RCA23_c06520	697212	696214	ABC transporter, periplasmic substrate-binding protein	COG0715	P	GI 3	37	10	27
RCA23_c06530	698756	697293	arylsulfatase	COG3119	P	GI 3	18	10	8
RCA23_c06540	699421	698753	transcriptional regulator, GntR family	COG1802	K	GI 3	18	11	7
RCA23_c06550	700594	700028	hypothetical protein	COG4974	L	GI 3	18	32	-14
RCA23_c06560	701422	700781	hypothetical protein	COG1618	F	GI 3	59	54	5
RCA23_c06570	702310	701492	hypothetical protein			GI 3	393	273	120
RCA23_c06580	702492	703271	hypothetical protein			GI 3	142	92	50
RCA23_c06590	703826	703494	hypothetical protein			GI 3	885	731	154
RCA23_c06600	704277	703819	hypothetical protein			GI 3	675	432	243
RCA23_c06610	705323	704697	hypothetical protein			GI 3	515	372	143
RCA23_c06620	705475	705801	hypothetical protein			GI 3	472	348	124
RCA23_c06630	706774	707259	hypothetical protein	COG3000	I	GI 3	9	7	2
RCA23_c06640	707893	707468	transcriptional regulator, AsnC family	COG1522	K	GI 3	31	39	-8
RCA23_c06650	707989	709179	aspartate aminotransferase AspC	COG0436	E	GI 3	8	32	-24
RCA23_c06660	709204	709950	3-hydroxybutyrate dehydrogenase Bdh	COG1028	I	GI 3	5	26	-21

RCA23_c06670	709963	710817	putative fumarylacetoacetate hydrolase	COG0179	Q	GI 3	9	43	-34
RCA23_c06680	710820	711548	oxidoreductase, short chain dehydrogenase/reductase fami	COG1028	I	GI 3	11	45	-34
RCA23_c06690	711582	712247	dimethylmenaquinone methyltransferase	COG0684	H	GI 3	29	50	-21
RCA23_c06700	712286	713434	hypothetical protein	COG3970	R	GI 3	6	3	3
RCA23_c06710	713447	714952	NADP-dependent fatty aldehyde dehydrogenase AldH	COG1012	C	GI 3	3	2	1
RCA23_c06720	714981	715886	putative dihydrodipicolinate synthase	COG0329	E	GI 3	1	0	1
RCA23_c06730	716879	716205	transcriptional regulator protein, LacI family	COG1609	K	GI 3	33	53	-20
RCA23_c06740	717413	718414	TRAP dicarboxylate transporter, subunit DctP	COG1638	G	GI 3	9	9	0
RCA23_c06750	718496	719083	TRAP dicarboxylate transporter, subunit DctQ	COG3090	G	GI 3	10	14	-4
RCA23_c06760	719077	720369	TRAP dicarboxylate transporter, subunit DctM	COG1593	G	GI 3	9	11	-2
RCA23_c06770	720515	721783	D-amino acid dehydrogenase small subunit DadA	COG0665	E	GI 3	21	32	-11
RCA23_c06780	721815	722963	mandelate racemase/muconate lactonizing protein	COG4948	M	GI 3	30	54	-24
RCA23_c06790	722960	723874	dihydrodipicolinate synthase DapA	COG0329	E	GI 3	20	31	-11
RCA23_c06800	723995	725005	uncharacterized oxidoreductase, YjmC	COG2055	C	GI 3	22	34	-12
RCA23_c06810	725230	726555	sarcosine oxidase beta subunit SoxB	COG0665	E	GI 3	11	28	-17
RCA23_c06820	726567	726854	sarcosine oxidase delta subunit SoxD	COG4311	E	GI 3	13	24	-11
RCA23_c06830	726851	729808	sarcosine oxidase alpha subunit SoxA	COG0404	E	GI 3	11	27	-16
RCA23_c06840	729801	730364	sarcosine oxidase gamma subunit SoxG	COG4583	E	GI 3	61	59	2
RCA23_c06850	730372	731262	hypothetical protein, DUF6 transmembrane protein	COG0697	G	GI 3	44	63	-19
RCA23_c06860	732526	734097	putative phage integrase			GI 3	112	112	0
RCA23_c06870	734370	735797	putative amidase	COG0154	J	GI 3	49	26	23
RCA23_c06880	736558	735992	integrase	COG4974	L	GI 3	37	23	14
RCA23_c06890	737386	736745	putative helicase			GI 3	48	32	16
RCA23_c06900	737522	738220	transposase	COG3316	L	GI 3	491	601	-110
RCA23_c06910	739014	738397	HTH-type transcriptional regulator, LuxR family	COG2197	T	GI 3	34	36	-2
RCA23_c06920	739172	739651	putative oxidoreductase, molybdopterin binding	COG3915	S	GI 3	39	27	12
RCA23_c06930	739769	742216	signal transduction histidine kinase	COG0642	T	GI 3	52	35	17
RCA23_c06940	742420	743505	glucose-1-phosphate thymidylyltransferase RfbA	COG1209	M	GI 3	61	48	13
RCA23_c06950	743565	745631	hypothetical protein, chain length determinant protein	COG0489	D	GI 3	59	63	-4
RCA23_c06960	745621	747042	polysaccharide export protein	COG1596	M	GI 3	56	55	1

RCA23_c06970	747621	748013	hypothetical protein, VanZ-like	COG5652	S	GI 3	100	76	24
RCA23_c06980	749389	748190	type I secretion system membrane fusion protein, HlyD fam	COG1566	V	GI 3	76	75	1
RCA23_c06990	751598	749475	type I secretion system ATP-binding component, HlyB famil	COG2274	V	GI 3	96	91	5
RCA23_c07000	752950	751595	type I secretion outer membrane protein, TolC family	COG1538	M	GI 3	63	59	4
RCA23_c07010	754718	752955	putative serralysin-like metalloprotease	COG2931	Q	GI 3	104	122	-18
RCA23_c07020	755773	754919	dTDP-4-dehydrorhamnose reductase RfbD	COG1091	M	GI 3	20	33	-13
RCA23_c07030	756831	755770	dTDP-glucose 4,6-dehydratase RfbB	COG1088	M	GI 3	19	42	-23
RCA23_c07040	757401	756838	dTDP-4-dehydrorhamnose 3,5-epimerase RfbC	COG1898	M	GI 3	22	40	-18
RCA23_c07050	758505	757435	hypothetical protein			GI 3	148	223	-75
RCA23_c07060	759584	758505	glycosyltransferase	COG0438	M	GI 3	33	43	-10
RCA23_c07070	761170	759905	putative glycosyltransferase	COG0438	M	GI 3	38	25	13
RCA23_c07080	762479	761430	hypothetical protein, UDP-glycosyltransferase/glycogen phc	COG0438	M	GI 3	10	28	-18
RCA23_c07090	764009	762492	polysaccharide biosynthesis protein			GI 3	33	56	-23
RCA23_c07100	765109	764015	UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotrar	COG0399	M	GI 3	24	51	-27
RCA23_c07110	765867	765106	hypothetical, WxcM-like	COG0110	R	GI 3	13	35	-22
RCA23_c07120	766099	765860	hypothetical protein, WxcM-like			GI 3	46	77	-31
RCA23_c07130	766651	766103	hypothetical protein, acyltransferase-like	COG1670	J	GI 3	42	46	-4
RCA23_c07140	767913	766648	UDP-glucose/GDP-mannose dehydrogenase family protein	COG0677	M	GI 3	73	172	-99
RCA23_c07150	768637	767906	S-adenosyl-L-methionine-dependent methyltransferase			GI 3	28	48	-20
RCA23_c07160	769668	768634	UDP-glucoronate 5'-epimerase LspL	COG0451	M	GI 3	105	167	-62
RCA23_c07170	770090	769713	transcriptional regulator, MarR family	COG1846	K	GI 3	42	63	-21
RCA23_c07180	770490	771002	transcription antitermination protein NusG	COG0250	K	GI 3	53	62	-9
RCA23_c07190	771959	771234	hypothetical protein	COG1434	S	GI 3	9	28	-19
RCA23_c07200	773130	771961	lipopolysaccharide core biosynthesis mannosyltransferase l	COG0438	M	GI 3	10	34	-24
RCA23_c07210	773759	773974	hypothetical protein			GI 3	21	47	-26
RCA23_c07220	774136	775224	undecaprenyl-phosphate alpha-N-acetylglucosaminyl 1-pho	COG0472	M	GI 3	54	68	-14
RCA23_c07230	775393	775839	hypothetical protein, transmembrane			GI 3	8	10	-2
RCA23_c07240	775844	776335	hypothetical protein, transmembrane			GI 3	5	12	-7
RCA23_c07250	777374	776907	transposase, IS4 family protein			GI 3	31	65	-34
RCA23_c07260	777803	777396	putative transposase	COG3039	L	GI 3	20	43	-23

RCA23_c07270	778001	778423	hypothetical protein, transmembrane			GI 3	15	10	5
RCA23_c07280	778428	778958	hypothetical protein, transmembrane			GI 3	20	11	9
RCA23_c07290	779627	780334	transposase	COG3316	L	GI 3	2	0	2
RCA23_c07300	780406	780888	glycogen synthase GlgA	COG0297	G	GI 3	30	39	-9
RCA23_c07310	780903	782972	glycogen debranching enzyme GlgX	COG1523	G	GI 3	71	40	31
RCA23_c07320	783008	784639	phosphoglucomutase Pgm	COG0033	G	GI 3	102	70	32
RCA23_c07330	786248	784641	putative alpha-glucosidase AglA	COG0366	G	GI 3	83	58	25
RCA23_c07340	786430	787128	transposase	COG3316	L	GI 3	425	503	-78
RCA23_c07350	787553	788764	uncharacterized hydrolase YtnL	COG1473	R	GI 3	507	377	130
RCA23_c07360	789242	790729	glutathione-binding protein GsiB	COG0747	E	GI 3	315	289	26
RCA23_c07370	790792	791688	glutathione transport system permease protein GsiC	COG0601	E	GI 3	208	284	-76
RCA23_c07380	791735	792535	dipeptide transport system permease protein	COG1173	E	GI 3	267	375	-108
RCA23_c07390	792532	794106	glutathione import ATP-binding protein GsiA	COG4172	R	GI 3	231	291	-60
RCA23_c07400	794103	795125	peptidase family S58	COG3191	E	GI 3	192	322	-130
RCA23_c07410	795122	796576	aldehyde dehydrogenase AldA	COG1012	C	GI 3	211	236	-25
RCA23_c07420	796585	797325	3-oxoacyl-[acyl-carrier-protein] reductase FabG	COG1028	I	GI 3	252	304	-52
RCA23_c07430	797368	798825	amidase	COG0154	J	GI 3	305	284	21
RCA23_c07440	800908	799691	MFS-type transporter	COG2807	P	GI 3	377	182	195
RCA23_c07450	801403	802311	peptidase M20D amidohydrolase	COG1473	R	GI 3	8	4	4
RCA23_c07460	802343	802858	transposase	COG3316	L	GI 3	8	5	3
RCA23_c07470	802913	803992	integrase	COG2801	L	GI 3	0	0	0
RCA23_c07480	804013	804228	transposase			GI 3	0	3	-3
RCA23_c07490	804774	804520	hypothetical protein, DUF3764			GI 3	230	97	133
RCA23_c07500	805349	804861	hypothetical protein			GI 3	65	47	18
RCA23_c07510	805760	806716	hypothetical protein, beta-lactam-insensitive peptidoglycan	COG1376	S	GI 3	158	81	77
RCA23_c07520	807253	807663	hypothetical protein			GI 3	286	208	78
RCA23_c07530	809049	807802	ABC transporter, ATP-binding protein, SbmA/BacA-like fam	COG1133	I	GI 3	53	47	6
RCA23_c07540	809116	809526	hypothetical protein			GI 3	67	64	3
RCA23_c07550	809659	809790	hypothetical protein			GI 3	141	42	99
RCA23_c07560	810944	809865	integrase	COG2801	L	GI 3	0	0	0

RCA23_c07570	811605	811252	hypothetical protein			GI 3	8	5	3
RCA23_c07580	812189	812058	hypothetical protein			GI 3	26	6	20
RCA23_c07590	814705	812846	flagellin FliC	COG1344	N	GI 3	26	16	10
RCA23_c07600	815060	816535	RNA polymerase sigma-54	COG1508	K	GI 3	135	86	49
RCA23_c07610	816917	816549	hypothetical protein, cyclic nucleotide-binding-like			GI 3	141	82	59
RCA23_c07620	817270	816917	hypothetical protein	COG0664	T	GI 3	133	74	59
RCA23_c07630	818209	817400	hypothetical protein			GI 3	213	115	98
RCA23_c07640	819031	818219	hypothetical protein			GI 3	368	158	210
RCA23_c07650	819467	819249	hypothetical protein			GI 3	386	127	259
RCA23_c07660	820626	819469	flagellar biosynthesis protein FlhB	COG1377	N	GI 3	257	130	127
RCA23_c07670	821440	820619	flagellar biosynthetic protein FliR	COG1684	N	GI 3	329	132	197
RCA23_c07680	821706	821437	flagellar biosynthetic protein FliQ	COG1987	N	GI 3	317	104	213
RCA23_c07690	822534	821713	flagellar biosynthetic protein FliP	COG1338	N	GI 3	239	115	124
RCA23_c07700	823188	822874	flagellar motor switch protein FliN	COG1886	N	GI 3	289	124	165
RCA23_c07710	824193	823201	flagellar motor switch proteins FliM	COG1868	N	GI 3	246	108	138
RCA23_c07720	824801	824208	protein FliL	COG1580	N	GI 3	391	159	232
RCA23_c07730	826771	824819	putative flagellar hook-length control protein FliK	COG3144	N	GI 3	140	72	68
RCA23_c07740	827248	826829	putative flagellar export protein FliJ			GI 3	144	84	60
RCA23_c07750	828581	827250	flagellar protein export ATPase FliI	COG1157	N	GI 3	114	77	37
RCA23_c07760	829597	828578	putative flagellar assembly protein FliH			GI 3	127	93	34
RCA23_c07770	830634	829594	flagellar motor switch protein G	COG1536	N	GI 3	199	111	88
RCA23_c07780	832414	830663	flagellar M-ring protein FliF	COG1766	N	GI 3	232	111	121
RCA23_c07790	832771	832457	flagellar hook-basal body complex subunit FliE	COG1677	N	GI 3	213	77	136
RCA23_c07800	833940	832786	transcriptional regulatory protein FlbD	COG2204	T	GI 3	241	104	137
RCA23_c07810	834232	834771	protein FliL	COG1580	N	GI 3	61	56	5
RCA23_c07820	834836	835009	hypothetical protein			GI 3	115	56	59
RCA23_c07830	835109	835480	flagellar protein FliS	COG1516	N	GI 3	167	93	74
RCA23_c07840	835599	836012	hypothetical protein			GI 3	232	133	99
RCA23_c07850	836532	836771	hypothetical protein			GI 3	93	80	13
RCA23_c07860	837607	836804	flagellar basal-body rod protein FlgG	COG4786	N	GI 3	112	62	50

RCA23_c07870	837665	839437	Cl- channel, voltage-gated family protein	COG0038	P	GI 3	104	68	36
RCA23_c07880	840278	839442	hypothetical protein, lysozym-like	COG0741	M	GI 3	195	92	103
RCA23_c07890	841546	840275	flagellar hook-associated protein FlgL	COG1344	N	GI 3	211	119	92
RCA23_c07900	845822	841581	flagellar hook-associated protein FlgK	COG1256	N	GI 3	153	98	55
RCA23_c07910	846175	845825	flagellar rod assembly protein/muramidase FlgJ	COG3951	M	GI 3	135	104	31
RCA23_c07920	847324	846188	flagellar P-ring protein FlgI	COG1706	N	GI 3	94	71	23
RCA23_c07930	847901	847338	flagellar L-ring protein FlgH	COG2063	N	GI 3	244	102	142
RCA23_c07940	848820	848032	flagellar basal-body rod protein FlgG	COG4786	N	GI 3	249	113	136
RCA23_c07950	849559	848882	putative flagellar basal body rod protein FlgF	COG4786	N	GI 3	295	125	170
RCA23_c07960	853429	849668	flagellar hook protein FlgE	COG1749	N	GI 3	209	100	109
RCA23_c07970	854213	853497	flagellar basal body rod modification protein FlgD	COG1843	N	GI 3	181	100	81
RCA23_c07980	854630	854214	flagellar basal-body rod protein FlgC	COG1558	N	GI 3	213	123	90
RCA23_c07990	855018	854632	flagellar basal-body rod protein FlgB	COG1815	N	GI 3	313	132	181
RCA23_c08000	855113	855655	hypothetical protein			GI 3	220	107	113
RCA23_c08010	855658	856014	hypothetical protein			GI 3	197	80	117
RCA23_c08020	856748	856023	RNA polymerase, sigma factor for flagellar operon FliA	COG1191	K	GI 3	268	92	176
RCA23_c08030	857551	856745	putative flagellar biosynthesis protein FlhG	COG0455	D	GI 3	198	108	90
RCA23_c08040	858864	857548	flagellar biosynthesis protein FlhF	COG1419	N	GI 3	195	100	95
RCA23_c08050	861023	858861	flagellar biosynthesis protein FlhA	COG1298	N	GI 3	263	115	148
RCA23_c08060	861272	861865	hypothetical membrane lipoprotein, DUF400			GI 3	172	125	47
RCA23_c08070	861871	863016	hypothetical protein			GI 3	101	55	46
RCA23_c08080	863013	863753	flagellar basal body P-ring biosynthesis protein FlgA	COG1261	N	GI 3	126	70	56
RCA23_c08090	863767	864087	putative negative regulator of flagellin synthesis FlgM			GI 3	206	93	113
RCA23_c08100	864117	864407	hypothetical protein			GI 3	258	96	162
RCA23_c08110	865057	864425	hypothetical protein, HCP-like	COG0790	R	GI 3	235	100	135
RCA23_c08120	865443	865054	hypothetical protein			GI 3	143	71	72
RCA23_c08130	865619	866770	sigma54 specific transcriptional regulator, Fis family	COG2204	T	GI 3	203	110	93
RCA23_c08140	868379	866742	flagellar hook-associated protein FliD	COG1345	N	GI 3	223	93	130
RCA23_c08150	869677	868454	chemotaxis protein MotB	COG1360	N	GI 3	231	134	97
RCA23_c08160	870477	869716	chemotaxis protein MotA	COG1291	N	GI 3	299	109	190

RCA23_c08170	870634	871101	hypothetical protein, DUF1566			GI 3	266	154	112
RCA23_c08180	872040	871126	putative transmembrane protein, DUF6			GI 3	397	243	154
RCA23_c08190	874242	872701	putative polyketide hydroxylase SchC	COG0654	H	GI 3	97	68	29
RCA23_c08200	875672	874248	aldehyde dehydrogenase	COG1012	C		60	52	8
RCA23_c08210	876685	875669	2-amino-3-carboxymuconate-6-semialdehyde decarboxylas	COG2159	R		118	61	57
RCA23_c08220	877470	876682	transcriptional regulator, IclR family	COG1414	K		66	69	-3
RCA23_c08230	879401	877467	TRAP transporter, 4TM/12TM fusion protein	COG4666	R		129	84	45
RCA23_c08240	880430	879408	TRAP transporter solute receptor, TAXI family	COG2358	R		86	70	16
RCA23_c08250	880496	882190	thiamine pyrophosphate enzyme-like TPP-binding	COG0028	E		76	72	4
RCA23_c08260	883788	882265	hypothetical protein	COG2268	S		86	60	26
RCA23_c08270	884588	883800	short chain dehydrogenase	COG1028	I		72	42	30
RCA23_c08280	886066	884591	putative aldehyde dehydrogenase yfmT	COG1012	C		119	66	53
RCA23_c08290	887201	886068	branched-chain amino acid ABC transporter, ATP-binding p	COG0410	E		113	70	43
RCA23_c08300	887913	887194	branched-chain amino acid ABC transporter, ATP-binding p	COG0411	E		146	96	50
RCA23_c08310	888863	887931	putative transporter, permease protein	COG4177	E		173	81	92
RCA23_c08320	889732	888860	putative transporter, permease protein	COG0559	E		110	69	41
RCA23_c08330	890937	889783	putative transporter, periplasmic binding protein	COG0683	E		122	74	48
RCA23_c08340	892154	891102	hypothetical protein, PrpF protein-like	COG2828	S		55	59	-4
RCA23_c08350	892833	892168	4-carboxy-4-hydroxy-2-oxoadipate aldolase/oxaloacetate de	COG0684	H		56	60	-4
RCA23_c08360	893753	893019	putative N-acetylglucosaminyl-phosphatidylinositol de-N-ac	COG2120	S		107	67	40
RCA23_c08370	894248	894994	hypothetical protein				161	125	36
RCA23_c08380	895147	895896	transcriptional regulator	COG1802	K		93	88	5
RCA23_c08390	895914	897314	aminomethyltransferase GcvT	COG0404	E		185	101	84
RCA23_c08400	897391	898368	TRAP dicarboxylate transporter, subunit DctP	COG1638	G		97	61	36
RCA23_c08410	898371	898883	TRAP dicarboxylate transporter, subunit DctQ	COG3090	G		178	92	86
RCA23_c08420	898880	900184	TRAP dicarboxylate transporter, subunit DctM	COG1593	G		153	93	60
RCA23_c08430	900268	901209	metapyrocatechase XylE	COG2514	R		158	84	74
RCA23_c08440	901273	902451	MFS-type transporter	COG2814	G		111	95	16
RCA23_c08450	902749	903183	hypothetical protein, cytochrome c				143	79	64
RCA23_c08460	903218	903562	hypothetical protein, copper resistance protein C	COG2372	R		155	96	59

RCA23_c08470	903559	904410	hypothetical protein, copper resistance protein D	COG1276	P	165	111	54
RCA23_c08480	904753	905184	hypothetical protein	COG3613	F	132	101	31
RCA23_c08490	906165	905899	hypothetical protein			227	118	109
RCA23_c08500	906640	906996	hypothetical protein			170	169	1
RCA23_c08510	908415	907033	fumarate reductase flavoprotein subunit	COG1053	C	185	220	-35
RCA23_c08520	909253	908387	methylisocitrate lyase PrpB	COG2513	G	240	253	-13
RCA23_c08530	909870	909250	putative isochorismatase family protein	COG1335	Q	229	231	-2
RCA23_c08540	911929	909872	hydantoin utilization protein A	COG0145	E	178	191	-13
RCA23_c08550	913620	911926	hydantoin utilization protein B	COG0146	E	229	209	20
RCA23_c08560	914183	913617	hypothetical protein	COG1942	R	249	209	40
RCA23_c08570	914328	915128	HTH-type transcriptional regulator, GntR family	COG2188	K	138	206	-68
RCA23_c08580	915125	916531	3-isopropylmalate dehydratase large subunit LeuC	COG0065	E	226	214	12
RCA23_c08590	916558	917142	3-isopropylmalate dehydratase small subunit LeuD	COG0066	E	214	212	2
RCA23_c08600	917203	918216	TRAP dicarboxylate transporter, subunit DctP	COG1638	G	530	304	226
RCA23_c08610	918309	918773	TRAP transporter, subunit DctQ	COG3090	G	514	328	186
RCA23_c08620	918773	920080	TRAP dicarboxylate transporter, subunit DctM	COG1593	G	622	381	241
RCA23_c08630	920337	921674	putative glutamate synthase [NADPH] small chain	COG0493	E	375	303	72
RCA23_c08640	921674	922978	hypothetical protein, dihydrooronate dehydrogenase	COG0167	F	574	518	56
RCA23_c08650	923623	923021	putative HTH-type transcriptional regulator	COG1309	K	816	569	247
RCA23_c08660	923793	925058	N-carbamoyl-L-amino acid hydrolase AmaB	COG0624	E	600	475	125
RCA23_c08670	925095	926549	D-hydantoinase/dihydropyrimidinase Dht	COG0044	F	586	467	119
RCA23_c08680	926592	927374	ABC transporter ATP-binding protein	COG1116	P	627	416	211
RCA23_c08690	927402	928322	putative ABC transporter permease protein	COG0600	P	660	505	155
RCA23_c08700	928319	929161	putative ABC transporter permease protein	COG0600	P	913	619	294
RCA23_c08710	929210	930205	putative thiamine biosynthesis protein	COG0715	P	713	465	248
RCA23_c08720	931297	930413	putative integral membrane proein DUF6	COG0697	G	967	590	377
RCA23_c08730	932791	931913	hypothetical protein DUF6	COG0697	G	693	436	257
RCA23_c08740	933010	934104	alkaline phosphatase synthesis sensor protein PhoR	COG5002	T	428	407	21
RCA23_c08750	934233	935270	putative phosphate binding protein PstS	COG0226	P	488	443	45
RCA23_c08760	935370	936857	putative phosphate transport system permease protein Pst	COG0573	P	413	525	-112

RCA23_c08770	936857	938185	putative phosphate transport system permease protein Pst	COG0581	P	472	478	-6
RCA23_c08780	938190	938996	phosphate import ATP-binding protein PstB	COG1117	P	497	610	-113
RCA23_c08790	939007	939699	phosphate transport system regulatory protein PhoU	COG0704	P	608	544	64
RCA23_c08800	939724	940413	phosphate regulon transl protein PhoB	COG0745	T	1.061	623	438
RCA23_c08810	940589	941791	putative hippurate hydrolase protei	COG1473	R	206	127	79
RCA23_c08820	942193	942954	urease accessory protein UreD	COG0829	O	648	456	192
RCA23_c08830	942958	943260	urease gamma subunit UreA	COG0831	E	478	528	-50
RCA23_c08840	943270	943575	urease beta subunit UreB	COG0832	E	217	341	-124
RCA23_c08850	943575	945314	urease alpha subunit UreC	COG0804	E	415	369	46
RCA23_c08860	945314	945787	urease accessory protein UreE	COG2371	O	361	376	-15
RCA23_c08870	945957	946415	urease accessory protein UreF	COG0830	O	517	461	56
RCA23_c08880	946427	947074	urease accessory protein UreG	COG0378	O	698	524	174
RCA23_c08890	948686	947607	integrase	COG2801	L	0	0	0
RCA23_c08900	948917	949201	hypothetical protein	COG4585	T	780	501	279
RCA23_c08910	951070	949424	glucose-methanol-choline oxidoreductase AlkJ	COG2303	E	382	383	-1
RCA23_c08920	951279	951830	hypothetical protein, YaeQ family protein	COG4681	S	731	502	229
RCA23_c08930	953443	952526	hypothetical protein, DUF6 transmembrane protein	COG0697	G	592	558	34
RCA23_c08940	953803	954969	UDP-glucose 6-dehydrogenase Ugd	COG1004	M	456	389	67
RCA23_c08950	956602	955373	3-deoxy-D-manno-octulosonic-acid transferase WaaA	COG1519	M	251	308	-57
RCA23_c08960	957788	956628	UDP-N-acetylglucosamine 2-epimerase WecB	COG0381	M	421	408	13
RCA23_c08970	958846	957815	putative N-acetylneuramic acid synthase	COG2089	M	556	454	102
RCA23_c08980	959840	958926	hypothetical protein			595	416	179
RCA23_c08990	960088	960732	hypothetical protein	COG1651	O	387	414	-27
RCA23_c09000	960843	962327	choline-sulfatase BetC	COG3119	P	445	476	-31
RCA23_c09010	963713	962403	permease	COG2233	F	269	317	-48
RCA23_c09020	964049	964585	hypothetical protein			249	294	-45
RCA23_c09030	964737	965636	membrane dipeptidase	COG2355	E	283	328	-45
RCA23_c09040	965633	967285	hypothetical protein			232	375	-143
RCA23_c09050	967282	967791	hypothetical protein			138	237	-99
RCA23_c09060	968589	967816	tRNA pseudouridine synthase A	COG0101	J	255	224	31

RCA23_c09070	968867	970279	YcjX-like protein	COG3106	R		270	373	-103
RCA23_c09080	970276	970722	hypothetical protein, acetyltransferase-like	COG0456	R		298	384	-86
RCA23_c09090	970715	971731	hypothetical protein	COG3768	S		237	411	-174
RCA23_c09100	971937	974843	isoleucyl-tRNA synthase IleS	COG0060	J		370	394	-24
RCA23_c09110	974910	975746	putative integral membrane protein DUF6				282	479	-197
RCA23_c09120	976432	975743	phosphatidylcholine synthase Pcs	COG1183	I		316	382	-66
RCA23_c09130	977409	976468	putative tyrosine recombinase xerC	COG4974	L		184	268	-84
RCA23_c09140	978135	977416	hypothetical protein	COG3159	S		307	263	44
RCA23_c09150	978835	978182	transaldolase	COG0176	G		540	374	166
RCA23_c09160	978925	981114	primosomal protein N'	COG1198	L		227	311	-84
RCA23_c09170	983095	981122	methylmalonyl-CoA mutase McmA	COG1884	I		237	293	-56
RCA23_c09180	983235	984599	glycerol-3-phosphate acyltransferase PlsB	COG2937	I		324	355	-31
RCA23_c09190	984707	985993	crotonyl-CoA reductase Ccr	COG0604	C		367	438	-71
RCA23_c09200	986057	987634	putative ATPase	COG0507	L		241	328	-87
RCA23_c09210	989413	987845	trimethylamine methyltransferase MttB	COG5598	H		191	262	-71
RCA23_c09220	989431	989895	hypothetical protein DUF1052	COG5321	S		188	298	-110
RCA23_c09240	990785	991279	hypothetical protein, DUF411	COG3019	R	GI 4	13	25	-12
RCA23_c09250	991576	991869	hypothetical protein			GI 4	0	0	0
RCA23_c09260	992104	992391	hypothetical protein			GI 4	5	2	3
RCA23_c09270	993390	992584	MORN repeat	COG4642	S	GI 4	16	14	2
RCA23_c09280	993934	993512	hypothetical protein	COG3904	S	GI 4	0	7	-7
RCA23_c09290	994038	995099	putative DNA-binding protein, transposase-like	COG3415	L	GI 4	0	0	0
RCA23_c09300	996057	995158	HTH-type transcriptional regulator, LysR family	COG0583	K	GI 4	4	1	3
RCA23_c09310	996333	999947	protein of unknown function, DUF285/Bacterial Ig-like domain			GI 4	4	1	3
RCA23_c09320	1000260	1001186	Predicted esterase	COG0627	R	GI 4	0	0	0
RCA23_c09330	1002131	1001247	transposase	COG2801	L	GI 4	28	98	-70
RCA23_c09340	1002367	1002143	putative transposase			GI 4	35	50	-15
RCA23_c09350	1003498	1002938	hypothetical protein, ornithine cyclodeaminase-like	COG2423	E		0	1	-1
RCA23_c09360	1004444	1003728	LrgB-like protein	COG1346	M		289	250	39
RCA23_c09370	1004794	1004441	hypothetical protein	COG1380	R		347	346	1

RCA23_c09380	1005815	1004916	putative branched-chain-amino-acid aminotransferase IlvE	COG0115	E	518	431	87
RCA23_c09390	1006761	1005865	2-hydroxy-3-oxopropionate reductase GarR	COG2084	I	343	293	50
RCA23_c09400	1008113	1006908	bicyclomycin resistance protein Bcr	COG2814	G	355	357	-2
RCA23_c09410	1008660	1008187	hypothetical protein			338	365	-27
RCA23_c09420	1010198	1008657	hypothetical protein, photolyase	COG3046	R	441	449	-8
RCA23_c09430	1010370	1011587	DNA photolyase, FAD-binding/cryptochrome	COG0415	L	245	277	-32
RCA23_c09440	1011944	1012426	carbon monoxide dehydrogenase small chain CoxS	COG2080	C	366	386	-20
RCA23_c09450	1012438	1014798	carbon monoxide dehydrogenase large chain CoxL	COG1529	C	282	324	-42
RCA23_c09460	1014811	1015602	carbon monoxide dehydrogenase medium chain CoxM	COG1319	C	294	374	-80
RCA23_c09470	1015645	1016556	MoxR-like ATPase	COG0714	R	367	401	-34
RCA23_c09480	1016556	1017776	CoxE-like protein	COG3552	R	237	272	-35
RCA23_c09490	1017882	1018688	5-deoxy-glucuronate isomerase IolB	COG3718	G	236	430	-194
RCA23_c09500	1019039	1018707	branched-chain amino acid transport protein, AzlD-like	COG4392	S	236	313	-77
RCA23_c09510	1019743	1019036	branched-chain amino acid transport protein, AzlC-like	COG1296	E	322	361	-39
RCA23_c09520	1021462	1019804	alpha-IPM synthase/homocitrate synthase	COG0119	E	268	314	-46
RCA23_c09530	1022656	1021499	cytochrome P450	COG2124	Q	179	259	-80
RCA23_c09540	1022810	1023811	TRAP dicarboxylate transporter, subunit DctP	COG1638	G	437	429	8
RCA23_c09550	1023966	1024568	TRAP dicarboxylate transporter, subunit DctQ	COG3090	G	573	365	208
RCA23_c09560	1024573	1026420	TRAP dicarboxylate transporter, subunit DctM	COG1593	G	283	338	-55
RCA23_c09570	1026486	1028369	putative citrate transporter	COG0471	P	356	376	-20
RCA23_c09580	1029097	1028366	triosephosphate isomerase TpiA	COG0149	G	264	327	-63
RCA23_c09590	1029454	1029137	putative regulator protein of competence-specific genes Tfo	COG3070	K	392	409	-17
RCA23_c09600	1029816	1029451	hypothetical protein, iron-sulfur cluster assembly protein	COG0316	S	520	454	66
RCA23_c09610	1030445	1029936	hypothetical protein DUF59	COG2151	R	242	320	-78
RCA23_c09620	1030469	1031599	queuine tRNA-ribosyltransferase Tgt	COG0343	J	237	292	-55
RCA23_c09630	1032099	1031611	hypothetical protein			216	256	-40
RCA23_c09640	1032374	1034782	ATP-dependent protease La	COG0466	O	795	491	304
RCA23_c09650	1034823	1035461	putative phosphoglycerate mutase family protein	COG0406	G	245	244	1
RCA23_c09670	1035777	1036430	protein-L-isoaspartate O-methyltransferase Pcm	COG2518	O	703	588	115
RCA23_c09680	1036466	1037830	outer membrane efflux protein	COG1538	M	327	323	4

RCA23_c09690	1037905	1038228	hypothetical protein			190	242	-52
RCA23_c09700	1039719	1038262	cobyric acid synthase CobQ	COG1492	H	274	372	-98
RCA23_c09710	1040228	1039917	hypothetical protein			1.161	530	631
RCA23_c09720	1040445	1041008	translation elongation factor P	COG0231	J	447	318	129
RCA23_c09730	1041736	1041005	hypothetical protein tRNA modifying protein YgfZ	COG0354	R	362	405	-43
RCA23_c09740	1041797	1042474	putative glycosyltransferase, family 2	COG0463	M	225	395	-170
RCA23_c09750	1044299	1042530	lipid A export ATP-binding/permease protein MsbA	COG1132	V	290	354	-64
RCA23_c09760	1044403	1045608	serine--glyoxylate aminotransferase SgaA	COG0075	E	201	278	-77
RCA23_c09770	1046719	1045610	histidinol-phosphate aminotransferase HisC	COG0079	E	210	281	-71
RCA23_c09780	1049682	1046755	valyl-tRNA synthase ValS	COG0525	J	332	382	-50
RCA23_c09790	1050340	1049744	hypothetical protein, metal-dependent phosphohydrolase	COG4341	R	276	359	-83
RCA23_c09800	1051209	1050337	putative phytanoyl-CoA dioxygenase family protein	COG5285	Q	412	427	-15
RCA23_c09810	1051351	1053636	molybdenum-containing hydroxylase	COG1529	C	264	374	-110
RCA23_c09820	1053643	1054722	hypothetical protein DUF2235	COG3673	S	304	419	-115
RCA23_c09830	1056046	1055225	5,10-methylenetetrahydrofolate reductase MetF	COG0685	E	229	270	-41
RCA23_c09840	1056143	1057048	HTH-type transcriptional regulator MetR	COG0583	K	226	312	-86
RCA23_c09850	1057134	1057898	inositol-1-monophosphatase SuhB	COG0483	G	292	283	9
RCA23_c09860	1057986	1058552	hypothetical protein	COG3063	N	278	328	-50
RCA23_c09880	1059277	1058798	transcriptional regulator, HxlR family	COG1733	K	534	437	97
RCA23_c09890	1059447	1059785	hypothetical protein, DUF3764			523	370	153
RCA23_c09900	1059839	1060168	hypothetical protein			293	227	66
RCA23_c09910	1060204	1060566	hypothetical protein, DsrE/F-like	COG1553	P	359	278	81
RCA23_c09920	1061259	1060684	glutathione peroxidase Gpo	COG0386	O	225	261	-36
RCA23_c09930	1062249	1061521	putative ion channel			421	440	-19
RCA23_c09950	1063201	1062944	hypothetical protein			347	292	55
RCA23_c09940	1063248	1064246	ribosomal large subunit pseudouridine synthase D	COG0564	J	255	339	-84
RCA23_c09960	1064374	1065270	RNA polymerase sigma-32 factor RpoH	COG0568	K	1.034	612	422
RCA23_c09970	1065351	1066337	putative oxidoreductase	COG0673	R	384	351	33
RCA23_c09980	1068332	1066503	oligoendopeptidase F	COG1164	E	339	303	36
RCA23_c09990	1068520	1069284	2-keto-3-deoxy-L-rhamnonate aldolase RhmA	COG3836	G	273	331	-58

RCA23_c10000	1070216	1069269	hypothetical protein, lysophospholipase L2	COG2267	I	278	289	-11
RCA23_c10010	1070506	1070216	putative sterol-binding protein	COG3255	I	284	291	-7
RCA23_c10020	1070580	1071140	hypothetical protein			335	350	-15
RCA23_c10030	1071160	1073967	ATP-dependent RNA helicase RhlB	COG4581	L	260	318	-58
RCA23_c10040	1074051	1074341	putative heat shock protein	COG1188	J	158	222	-64
RCA23_c10050	1074410	1074748	ferredoxin FdxA	COG1146	C	427	421	6
RCA23_c10060	1074901	1075419	putative transcriptional regulator, CarD family	COG1329	K	344	315	29
RCA23_c10070	1076242	1075490	cobalamin-5-phosphate synthase CobS	COG0368	H	135	170	-35
RCA23_c10080	1076326	1077339	nicotinate-nucleotide--dimethylbenzimidazole phosphoribos	COG2038	H	180	268	-88
RCA23_c10090	1079387	1077345	hypothetical protein			166	262	-96
RCA23_c10100	1079592	1080008	glyoxalase/bleomycin resistance protein	COG3565	R	433	479	-46
RCA23_c10110	1080998	1080018	hypothetical protein			392	375	17
RCA23_c10120	1081235	1082887	choline dehydrogenase BetA	COG2303	E	290	336	-46
RCA23_c10140	1083425	1084330	23S rRNA (guanosine-2'-O-)-methyltransferase RlmB	COG0566	J	274	297	-23
RCA23_c10150	1084647	1084342	phosphoribosyl-ATP pyrophosphatase HisE	COG0140	E	293	375	-82
RCA23_c10160	1085378	1084644	imidazole glycerol phosphate synthase subunit HisF	COG0107	E	188	248	-60
RCA23_c10170	1086150	1085434	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylider	COG0106	E	179	178	1
RCA23_c10180	1086818	1086180	imidazole glycerol phosphate synthase, glutamine amidotra	COG0118	E	345	348	-3
RCA23_c10190	1087410	1086823	imidazoleglycerol-phosphate dehydratase HisB	COG0131	E	327	348	-21
RCA23_c10210	1088751	1087954	hypothetical protein, calcineurin-like phosphoesterase-like	COG1409	R	418	358	60
RCA23_c10220	1092218	1088778	pyruvate carboxylase Pyc	COG1038	C	237	292	-55
RCA23_c10230	1093522	1092374	L-lactate dehydrogenase IldD	COG1304	C	281	304	-23
RCA23_c10240	1093655	1096048	putative DNA helicase II	COG0210	L	226	333	-107
RCA23_c10250	1096133	1097425	gamma-glutamylputrescine oxidoreductase PuuB	COG0665	E	199	255	-56
RCA23_c10260	1098046	1097444	putative cysteine/O-acetylserine efflux protein	COG1280	E	283	451	-168
RCA23_c10270	1098056	1098466	hypothetical protein			1.083	672	411
RCA23_c10280	1098622	1099686	putative protein Mrp	COG0489	D	232	370	-138
RCA23_c10290	1099713	1099967	hypothetical protein			599	383	216
RCA23_c10300	1100315	1100818	hypothetical protein, MraZ	COG2001	S	449	455	-6
RCA23_c10310	1100821	1101810	S-adenosyl-L-methionine-dependent methyltransferase Mra	COG0275	M	231	309	-78

RCA23_c10320	1101807	1102151	hypothetical protein	COG5462	S	369	361	8
RCA23_c10330	1102148	1103929	peptidoglycan synthase FtsI	COG0768	M	297	335	-38
RCA23_c10340	1103952	1105430	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminop	COG0769	M	234	338	-104
RCA23_c10350	1105430	1106848	putative UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alan	COG0770	M	223	280	-57
RCA23_c10360	1106866	1107948	phospho-N-acetylmuramoyl-pentapeptide-transferase MraY	COG0472	M	295	395	-100
RCA23_c10370	1108005	1109384	UDP-N-acetylmuramoylalanine--D-glutamate ligase MurD	COG0771	M	241	377	-136
RCA23_c10380	1109471	1110160	putative glycosyltransferase, sugar binding region	COG3774	M	549	438	111
RCA23_c10390	1110834	1110157	putative galactoside 2-alpha-L-fucosyltransferase 1			675	419	256
RCA23_c10400	1110875	1111054	hypothetical protein			439	354	85
RCA23_c10410	1111162	1111935	hypothetical protein	COG3306	M	476	358	118
RCA23_c10420	1113153	1111963	hypothetical protein HI0933	COG2081	R	190	222	-32
RCA23_c10430	1113229	1114434	cell division protein FtsW	COG0772	D	301	420	-119
RCA23_c10440	1114424	1115530	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide	COG0707	M	176	275	-99
RCA23_c10450	1115530	1116921	UDP-N-acetylmuramate--L-alanine ligase MurC	COG0773	M	264	342	-78
RCA23_c10460	1117803	1116925	permease of the drug/metabolite transporter superfamily	COG0697	G	226	272	-46
RCA23_c10470	1117895	1118863	UDP-N-acetylenolpyruvoylglucosamine reductase MurB	COG0812	M	208	372	-164
RCA23_c10480	1118953	1119843	D-alanine--D-alanine ligase Ddl	COG1181	M	235	430	-195
RCA23_c10490	1119879	1120751	putative cell division protein FtsQ			316	447	-131
RCA23_c10500	1120748	1122082	cell division protein FtsA	COG0849	D	275	404	-129
RCA23_c10510	1122236	1123780	cell division protein FtsZ	COG0206	D	341	361	-20
RCA23_c10520	1123992	1124912	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacet	COG0774	M	325	407	-82
RCA23_c10530	1125020	1125835	outer membrane assembly lipoprotein	COG4105	R	458	485	-27
RCA23_c10540	1125852	1127504	DNA repair protein RecN	COG0497	L	240	362	-122
RCA23_c10550	1127863	1127501	hypothetical protein DUF427	COG2343	S	394	461	-67
RCA23_c10560	1129669	1127879	putative Xaa-Pro aminopeptidase	COG0006	E	249	396	-147
RCA23_c10570	1131630	1129756	aerobic cobaltochelatase subunit CobT	COG4547	H	258	346	-88
RCA23_c10580	1132654	1131668	aerobic cobaltochelatase subunit CobS	COG0714	R	585	452	133
RCA23_c10590	1133471	1132833	hypothetical protein, DnaJ	COG0484	O	694	495	199
RCA23_c10600	1133514	1133801	putative stress-induced morphoprotein, BolA type	COG0271	T	335	420	-85
RCA23_c10610	1135336	1133825	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit	COG0064	J	356	465	-109

RCA23_c10620	1137977	1135425	aminopeptidase N	COG0308	E		257	346	-89
RCA23_c10630	1138196	1140334	malate synthase GlcB	COG2225	C		371	390	-19
RCA23_c10640	1140396	1140824	hypothetical protein DUF336	COG3193	R		225	350	-125
RCA23_c10650	1140906	1141109	hypothetical protein				218	311	-93
RCA23_c10660	1141119	1141883	gamma-glutamyl-gamma-aminobutyrate hydrolase PuuD	COG2071	R		209	324	-115
RCA23_c10670	1142635	1141880	putative D-beta-hydroxybutyrate dehydrogenase	COG1028	I		198	280	-82
RCA23_c10680	1142794	1144365	NAD(P) transhydrogenase alpha subunit PntA	COG3288	C		325	332	-7
RCA23_c10690	1144379	1145812	NAD(P) transhydrogenase beta subunit PntB	COG1282	C		435	457	-22
RCA23_c10700	1145880	1147163	hypothetical protein	COG4949	S		357	421	-64
RCA23_c10710	1147211	1148374	putative acetylornithine deacetylase ArgE	COG0624	E		296	398	-102
RCA23_c10720	1149375	1148371	molybdenum cofactor biosynthesis protein MoaA	COG2896	H		223	295	-72
RCA23_c10730	1149576	1151222	acetyl-coenzyme A synthase AcsA	COG0365	I		196	332	-136
RCA23_c10740	1151397	1151173	hypothetical protein	COG4321	R		261	309	-48
RCA23_c10750	1151573	1151397	hypothetical protein				286	384	-98
RCA23_c10760	1152961	1151570	fumarate hydratase class II	COG0114	C		301	362	-61
RCA23_c10770	1153500	1153036	hypothetical protein	COG3814	S		562	428	134
RCA23_c10780	1154840	1153572	putative chromate transport protein	COG2059	P		332	384	-52
RCA23_c10790	1155189	1157231	hydantoinase / oxoprolinase family protein	COG0145	E		170	273	-103
RCA23_c10800	1157331	1157729	hypothetical protein				647	502	145
RCA23_c10810	1158217	1159203	putative quinone oxidoreductase yhdH	COG0604	C		214	264	-50
RCA23_c10820	1159306	1160529	cysteine desulfurase SufS	COG0520	E		246	312	-66
RCA23_c10830	1160550	1161962	deoxyribodipyrimidine photo-lyase PhrB	COG0415	L		227	252	-25
RCA23_c10840	1162037	1163245	cyclopropane-fatty-acyl-phospholipid synthase Cfa	COG2230	M		546	408	138
RCA23_c10850	1163253	1164371	ADP-ribose pyrophosphatase NudF	COG0494	L		289	351	-62
RCA23_c10860	1164417	1165454	cysteine synthase CysK	COG0031	E		402	390	12
RCA23_c10870	1165441	1167759	mechanosensitive ion channel protein MscS	COG3264	M		353	377	-24
RCA23_c10890	1168102	1169268	putative phage integrase	COG4974	L	GI 5	13	11	2
RCA23_c10900	1173155	1169922	hypothetical protein			GI 5	18	15	3
RCA23_c10910	1173220	1175214	hypothetical protein, tetratricopetide domain TPR-1	COG0457	R	GI 5	22	11	11
RCA23_c10920	1177861	1176257	hypothetical protein, resolvase-like	COG1961	L	GI 5	799	557	242

RCA23_c10930	1178310	1177858	hypothetical protein, DUF2924			GI 5	237	234	3
RCA23_c10940	1178871	1179848	putative TRAP transporter solute receptor	COG2358	R	GI 5	239	214	25
RCA23_c10950	1179941	1182292	TRAP transporter, 4TM/12TM fusion protein	COG4666	R	GI 5	386	349	37
RCA23_c10960	1182304	1183887	putative sulfatase YidJ	COG3119	P	GI 5	325	398	-73
RCA23_c10970	1183893	1184789	arylsulfatase	COG1234	R	GI 5	306	236	70
RCA23_c10980	1184804	1185622	siderophore interactin protein, vibriobactin utilization protein	COG2375	P	GI 5	477	318	159
RCA23_c10990	1186917	1185640	hypothetical protein, metallo-beta-lactamase	COG2015	Q	GI 5	550	453	97
RCA23_c11000	1187177	1188193	TRAP dicarboxylate transporter, subunit DctP	COG1638	G	GI 5	417	318	99
RCA23_c11010	1188369	1189034	glutathione S-transferase	COG0625	O	GI 5	357	294	63
RCA23_c11020	1189053	1189601	TRAP dicarboxylate transporter, subunit DctQ	COG3090	G	GI 5	459	306	153
RCA23_c11030	1189598	1190959	TRAP dicarboxylate transporter, subunit DctM	COG1593	G	GI 5	284	244	40
RCA23_c11040	1190995	1191909	hypothetical protein, DUF6 transmembrane protein	COG0697	G	GI 5	228	198	30
RCA23_c11050	1192027	1192302	ferric reductase like transmembrane component family			GI 5	221	170	51
RCA23_c11060	1192990	1192559	hypothetical protein			GI 5	458	332	126
RCA23_c11070	1194176	1192992	hypothetical protein			GI 5	378	282	96
RCA23_c11080	1195854	1194217	sulfatase family protein	COG3119	P	GI 5	477	324	153
RCA23_c11090	1196618	1195860	short-chain dehydrogenase/reductase SDR	COG1028	I	GI 5	479	340	139
RCA23_c11100	1197395	1196637	maleylacetoacetate isomerase MaiA	COG0625	O	GI 5	545	391	154
RCA23_c11110	1198888	1197452	salicylaldehyde dehydrogenase	COG1012	C	GI 5	411	357	54
RCA23_c11120	1199107	1199895	transcriptional regulator, GntR family	COG1802	K	GI 5	419	355	64
RCA23_c11130	1200361	1200789	transposase	COG3316	L	GI 5	2	12	-10
RCA23_c11140	1200946	1202112	putative phage integrase	COG4974	L	GI 5	1	1	0
RCA23_c11150	1202483	1204498	hypothetical protein, alginate lyase-lyase			GI 5	2	3	-1
RCA23_c11160	1205812	1205189	HTH-type transcriptional regulator, GntR family	COG1802	K	GI 5	339	300	39
RCA23_c11170	1206137	1207324	branched-chain amino acid ABC transporter, periplasmic su	COG0683	E	GI 5	438	334	104
RCA23_c11180	1207409	1208311	branched-chain amino acid ABC transporter, permease pro	COG0559	E	GI 5	327	313	14
RCA23_c11190	1208316	1209296	branched-chain amino acid ABC transporter, permease pro	COG4177	E	GI 5	497	346	151
RCA23_c11200	1209320	1210075	branched-chain amino acid ABC transporter, ATP-binding p	COG0411	E	GI 5	414	325	89
RCA23_c11210	1210079	1210801	branched-chain amino acid ABC transporter, ATP-binding p	COG0410	E	GI 5	408	292	116
RCA23_c11220	1210808	1211491	hydantoin racemase HyuE	COG4126	E	GI 5	395	264	131

RCA23_c11230	1211851	1212558	transposase	COG3316	L	GI 5	66	52	14
RCA23_c11240	1213785	1212979	glutamine transport ATP-binding protein GlnQ	COG1126	E	GI 5	32	11	21
RCA23_c11250	1214500	1213802	putative inner membrane amino-acid ABC transporter perm	COG0765	E	GI 5	46	11	35
RCA23_c11260	1214805	1215512	transposase	COG3316	L	GI 5	10	6	4
RCA23_c11270	1216048	1217244	transcriptional regulator CoxC	COG3300	T	GI 5	224	150	74
RCA23_c11280	1217360	1218214	carbon monoxide dehydrogenase medium chain CoxM	COG1319	C	GI 5	83	69	14
RCA23_c11290	1218225	1218719	carbon monoxide dehydrogenase small chain CoxS	COG2080	C	GI 5	77	78	-1
RCA23_c11300	1218716	1221142	carbon monoxide dehydrogenase large chain CoxL	COG1529	C	GI 5	130	117	13
RCA23_c11310	1221188	1222063	AAA+ ATPase chaperone CoxD	COG0714	R	GI 5	129	129	0
RCA23_c11320	1222060	1223241	carbon monoxide dehydrogenase accessory protein CoxE	COG3552	R	GI 5	68	81	-13
RCA23_c11330	1223238	1224017	carbon monoxide dehydrogenase accessory protein CoxF	COG1975	O	GI 5	63	69	-6
RCA23_c11340	1224010	1224600	hypothetical protein	COG2068	R	GI 5	75	70	5
RCA23_c11350	1224727	1225182	carbon monoxide dehydrogenase protein CoxG	COG3427	S	GI 5	111	80	31
RCA23_c11360	1225187	1226101	carbon monoxide dehydrogenase accessory protein CoxI	COG1975	O	GI 5	120	110	10
RCA23_c11370	1226311	1226796	transposase	COG3316	L	GI 5	34	32	2
RCA23_c11380	1227061	1227807	dienelactone hydrolase	COG0412	Q	GI 5	337	347	-10
RCA23_c11390	1228850	1227804	aldo/keto reductase	COG0667	C	GI 5	243	227	16
RCA23_c11400	1230223	1229126	mandelate racemase MdlA	COG4948	M	GI 5	299	385	-86
RCA23_c11410	1231189	1230335	hypothetical protein DUF1498	COG3822	R	GI 5	363	506	-143
RCA23_c11420	1232598	1231231	two-component system, sensor histidine kinase protein	COG0642	T	GI 5	218	328	-110
RCA23_c11430	1233299	1232595	two-component system, response regulator protein	COG0745	T	GI 5	255	357	-102
RCA23_c11440	1233404	1234510	hypothetical protein	COG3181	S	GI 5	441	342	99
RCA23_c11450	1234593	1236608	putative tripartite tricarboxylate transporter (TTT) protein Tc	COG3333	S	GI 5	543	448	95
RCA23_c11460	1236605	1237696	hypothetical protein	COG2828	S	GI 5	288	325	-37
RCA23_c11470	1237724	1238692	D-isomer specific 2-hydroxyacid dehydrogenase	COG0111	H	GI 5	297	421	-124
RCA23_c11480	1239793	1238756	putative ammonia monooxygenase	COG3180	R	GI 5	263	351	-88
RCA23_c11490	1240440	1239790	transcriptional regulator	COG1802	K	GI 5	194	307	-113
RCA23_c11500	1240489	1241970	fumarate reductase flavoprotein subunit FccA	COG1053	C	GI 5	282	318	-36
RCA23_c11510	1242188	1243363	aspartate aminotransferase AspC	COG0436	E	GI 5	321	400	-79
RCA23_c11520	1244165	1243431	hypothetical protein			GI 5	269	385	-116

RCA23_c11530	1244807	1244235	aerobic glycerol-3-phosphate dehydrogenase GlpD	COG0578	C	GI 5	198	314	-116
RCA23_c11540	1245824	1244865	aerobic glycerol-3-phosphate dehydrogenase GlpD	COG0578	C	GI 5	239	288	-49
RCA23_c11550	1247291	1247935	hypothetical protein	COG1192	D	GI 5	29	30	-1
RCA23_c11560	1247928	1249136	chemotaxis protein CheW	COG0835	N	GI 5	27	26	1
RCA23_c11570	1249188	1251065	methyl-accepting chemotaxis protein II	COG0840	N	GI 5	62	37	25
RCA23_c11580	1251091	1254051	chemotaxis histidine kinase CheA	COG0643	N	GI 5	40	20	20
RCA23_c11590	1254048	1256066	response regulator CheY	COG2114	T	GI 5	36	14	22
RCA23_c11600	1256078	1256908	chemotaxis protein methyltransferase CheR	COG1352	N	GI 5	0	6	-6
RCA23_c11610	1256889	1257911	chemotaxis response regulator protein-glutamate methylest	COG2201	N	GI 5	13	11	2
RCA23_c11620	1258541	1259149	metal-dependent hydrolase	COG1235	R	GI 5	125	59	66
RCA23_c11630	1260667	1259588	integrase	COG2801	L	GI 5	0	0	0
RCA23_c11640	1261553	1260729	methyltransferase, FkbM family			GI 5	13	25	-12
RCA23_c11650	1262611	1261847	hypothetical protein, sugar transferase-like			GI 5	33	35	-2
RCA23_c11660	1263686	1262811	aldo/keto reductase	COG0667	C	GI 5	35	36	-1
RCA23_c11670	1264642	1264917	hypothetical protein			GI 5	44	45	-1
RCA23_c11680	1265571	1265173	hypothetical protein	COG0790	R	GI 5	13	13	0
RCA23_c11690	1266818	1266246	hypothetical protein	COG4430	S	GI 5	255	166	89
RCA23_c11700	1267451	1268101	hypothetical protein	COG2755	E	GI 5	0	0	0
RCA23_c11710	1268699	1269586	phytanoyl-CoA dioxygenase family protein	COG5285	Q	GI 5	343	209	134
RCA23_c11720	1270243	1270815	putative bacterial extracellular solute binding protein, family	COG1791	S	GI 5	67	79	-12
RCA23_c11730	1271031	1271468	hypothetical protein			GI 5	73	29	44
RCA23_c11740	1272798	1272199	SOUL heme-binding protein			GI 5	321	247	74
RCA23_c11750	1273478	1274995	arylsulfatase precursor	COG3119	P	GI 5	113	132	-19
RCA23_c11760	1275232	1275627	hypothetical protein DUF583			GI 5	7	10	-3
RCA23_c11770	1275804	1276883	integrase	COG2801	L	GI 5	0	0	0
RCA23_c11780	1277985	1276918	hypothetical protein	COG3616	E	GI 5	368	281	87
RCA23_c11790	1279810	1278509	glutamine synthase GlnA type I	COG0174	E	GI 5	3	7	-4
RCA23_c11800	1280652	1279807	putative HTH-type transcriptional regulator, RpiR family	COG1737	K	GI 5	11	5	6
RCA23_c11810	1280733	1281500	N-formylglutamate amidohydrolase	COG3931	E	GI 5	9	7	2
RCA23_c11820	1281497	1282138	putative isochorismatase family protein	COG1335	Q	GI 5	5	11	-6

RCA23_c11830	1282131	1282853	branched-chain amino acid ABC transporter, ATP-binding p	COG0411	E	GI 5	7	1	6
RCA23_c11840	1282882	1284033	branched-chain amino acid ABC transporter, periplasmic bi	COG0683	E	GI 5	10	5	5
RCA23_c11850	1284085	1284783	branched-chain amino acid ABC transporter, ATP-binding p	COG0410	E	GI 5	4	1	3
RCA23_c11860	1284783	1285679	branched-chain amino acid ABC transporter, permease pro	COG0559	E	GI 5	7	4	3
RCA23_c11870	1285754	1286698	branched-chain amino acid ABC transporter, permease pro	COG4177	E	GI 5	15	7	8
RCA23_c11880	1286708	1287646	acetamidase/formamidase family protein	COG2421	C	GI 5	1	6	-5
RCA23_c11890	1288192	1288902	hypothetical protein	COG1028	I	GI 5	468	321	147
RCA23_c11910	1289550	1290728	putative prophage integrase	COG0582	L	GI 5	13	8	5
RCA23_c11920	1290725	1291072	hypothetical protein			GI 5	16	9	7
RCA23_c11930	1291427	1292068	hypothetical protein			GI 5	79	49	30
RCA23_c11940	1292185	1293384	putative AAA ATPase	COG3598	L	GI 5	82	62	20
RCA23_c11950	1294040	1293531	hypothetical protein			GI 5	4	3	1
RCA23_c11960	1294894	1294163	hypothetical protein			GI 5	16	4	12
RCA23_c11970	1295139	1295579	hypothetical protein			GI 5	76	54	22
RCA23_c11980	1295579	1295947	hypothetical protein			GI 5	33	14	19
RCA23_c11990	1296908	1296210	branched-chain amino acid ABC transporter, ATP-binding p	COG0410	E	GI 5	45	35	10
RCA23_c12000	1297654	1296914	branched-chain amino acid ABC transporter, ATP-binding p	COG0411	E	GI 5	45	36	9
RCA23_c12010	1298634	1297651	branched-chain amino acid ABC transporter, permease pro	COG4177	E	GI 5	76	71	5
RCA23_c12020	1299559	1298666	branched-chain amino acid ABC transporter, permease pro	COG0559	E	GI 5	66	89	-23
RCA23_c12030	1300733	1299567	branched-chain amino acid ABC transporter, periplasmic bi	COG0683	E	GI 5	53	48	5
RCA23_c12040	1301568	1300768	enoyl-CoA hydratase/carnithine racemase	COG1024	I	GI 5	36	56	-20
RCA23_c12050	1303130	1301586	acetyl-CoA synthase-like protein	COG0318	I	GI 5	55	58	-3
RCA23_c12060	1303632	1303123	dehydrogenase iron-sulfur-binding subunit	COG2080	C	GI 5	49	59	-10
RCA23_c12070	1304444	1303620	dehydrogenase FAD-binding subunit	COG1319	C	GI 5	26	41	-15
RCA23_c12080	1307380	1304441	dehydrogenase molybdenum-binding subunit	COG1529	C	GI 5	41	48	-7
RCA23_c12090	1308419	1307487	putative HTH-type transcriptional regulator, AraC family	COG2207	K	GI 5	71	67	4
RCA23_c12100	1310095	1309085	periplasmic binding protein-like	COG1879	G	GI 5	18	16	2
RCA23_c12110	1311473	1310106	ROK family transcriptional repressor	COG1940	K	GI 5	9	11	-2
RCA23_c12120	1311642	1312454	xylose isomerase	COG1082	G	GI 5	8	13	-5
RCA23_c12130	1312504	1313622	sugar ABC transporter, periplasmic binding protein	COG1879	G	GI 5	11	9	2

RCA23_c12140	1313694	1314857	putative oxidoreductase	COG0673	R	GI 5	11	16	-5
RCA23_c12150	1314857	1316431	sugar ABC transporter, ATP-binding protein	COG1129	G	GI 5	11	11	0
RCA23_c12160	1316418	1317386	sugar ABC transporter, permease protein	COG1172	G	GI 5	12	24	-12
RCA23_c12170	1317389	1317691	hypothetical protein, monoxygenase-like	COG1359	S	GI 5	18	23	-5
RCA23_c12180	1317805	1318863	hypothetical protein	COG1082	G	GI 5	30	18	12
RCA23_c12190	1318867	1320018	putative oxidoreductase	COG0673	R	GI 5	29	25	4
RCA23_c12200	1320689	1321837	peptidase M20D, amidohydrolase	COG1473	R	GI 5	229	226	3
RCA23_c12210	1321840	1322985	X-Pro dipeptidase	COG0006	E	GI 5	289	228	61
RCA23_c12220	1324296	1323853	hypothetical protein			GI 5	18	9	9
RCA23_c12230	1325069	1324293	hypothetical protein, transmembrane			GI 5	12	12	0
RCA23_c12240	1325832	1327037	hypothetical protein, DNA breaking rejoining enzymes family protein-like			GI 5	37	26	11
RCA23_c12250	1327137	1328645	hypothetical protein			GI 5	1	0	1
RCA23_c12260	1328729	1329205	hypothetical protein			GI 5	10	5	5
RCA23_c12270	1329553	1329744	hypothetical protein			GI 5	0	13	-13
RCA23_c12280	1330088	1331644	type I restriction-modification system, M subunit	COG0286	V	GI 5	10	4	6
RCA23_c12290	1331637	1332842	type I restriction-modification system, S subunit	COG0732	V	GI 5	8	2	6
RCA23_c12300	1332842	1335937	type I restriction-modification system, R subunit	COG0610	V	GI 5	0	4	-4
RCA23_c12310	1336026	1337000	hypothetical protein	COG3012	S	GI 5	0	0	0
RCA23_c12320	1337142	1338152	hypothetical protein	COG2865	K	GI 5	0	0	0
RCA23_c12330	1338762	1338241	hypothetical protein			GI 5	0	0	0
RCA23_c12340	1340773	1338905	hypothetical protein, DNA helicase-like protein			GI 5	2	0	2
RCA23_c12350	1340970	1341416	hypothetical protein			GI 5	0	0	0
RCA23_c12360	1341557	1342156	integrase	COG0582	L	GI 5	0	1	-1
RCA23_c12370	1342597	1342181	hypothetical protein			GI 5	0	0	0
RCA23_c12380	1343211	1342702	hypothetical protein			GI 5	0	0	0
RCA23_c12390	1343382	1344026	hypothetical protein			GI 5	9	2	7
RCA23_c12400	1344489	1344037	hypothetical protein			GI 5	2	1	1
RCA23_c12410	1346190	1345639	hypothetical protein, DUF1994			GI 5	386	183	203
RCA23_c12420	1347575	1346172	exonuclease I	COG2925	L	GI 5	154	111	43
RCA23_c12430	1349548	1347575	transpeptidase, penicillin binding protein	COG4953	M	GI 5	127	64	63

RCA23_c12440	1354560	1349545	hypothetical protein	COG2373	R	GI 5	122	64	58
RCA23_c12450	1355067	1354687	hypothetical protein			GI 5	63	63	0
RCA23_c12460	1355322	1355774	hypothetical protein			GI 5	12	9	3
RCA23_c12470	1357492	1355828	type III restriction enzyme, res subunit	COG1061	K	GI 5	36	25	11
RCA23_c12480	1358034	1357498	putative type III restriction system protein, mod subunit			GI 5	25	14	11
RCA23_c12490	1358097	1359374	putative serine/threonine protein kinase	COG0515	R	GI 5	10	16	-6
RCA23_c12500	1359362	1360081	serine/threonine protein phosphatase PrpC	COG0631	T	GI 5	12	14	-2
RCA23_c12510	1362272	1360134	DNA helicase, UvrD/REP type	COG0210	L	GI 5	6	6	0
RCA23_c12520	1362274	1364124	hypothetical protein	COG1463	Q	GI 5	4	4	0
RCA23_c12530	1364121	1365416	hypothetical protein, OmpA/MotB-like	COG1360	N	GI 5	1	2	-1
RCA23_c12540	1365416	1367443	hypothetical protein			GI 5	2	1	1
RCA23_c12550	1367457	1370579	ATP-dependent helicase	COG0553	K	GI 5	5	5	0
RCA23_c12560	1371410	1370973	hypothetical protein			GI 5	7	3	4
RCA23_c12570	1372098	1371616	hypothetical protein			GI 5	11	7	4
RCA23_c12580	1372594	1372277	hypothetical protein			GI 5	4	4	0
RCA23_c12590	1372881	1373252	hypothetical protein			GI 5	14	2	12
RCA23_c12600	1373306	1374205	hypothetical protein			GI 5	9	5	4
RCA23_c12610	1374516	1374866	hypothetical protein			GI 5	0	0	0
RCA23_c12620	1374971	1375435	hypothetical protein			GI 5	0	0	0
RCA23_c12630	1375674	1376117	integrase	COG2801	L	GI 5	376	216	160
RCA23_c12640	1377304	1376135	hypothetical protein			GI 5	2	0	2
RCA23_c12650	1377893	1377396	hypothetical protein			GI 5	0	0	0
RCA23_c12660	1378200	1377955	DNA integration/recombination/invertion protein			GI 5	0	21	-21
RCA23_c12690	1379769	1378858	putative beta-lactamase-like protein	COG0491	R		250	305	-55
RCA23_c12680	1379768	1381060	osmolarity sensor protein EnvZ	COG0642	T		253	396	-143
RCA23_c12700	1381130	1381954	hypothetical protein				591	515	76
RCA23_c12710	1382060	1382731	50S ribosomal protein L21	COG0261	J		514	314	200
RCA23_c12720	1382738	1383007	50S ribosomal protein L27	COG0211	J		403	469	-66
RCA23_c12730	1383092	1383730	hypothetical protein, LysE type translocator	COG1280	E		245	351	-106
RCA23_c12740	1383727	1384263	putative acetyltransferase	COG1670	J		321	372	-51

RCA23_c12750	1384267	1384815	GCN5-like N-acetyltransferase	COG1670	J		202	299	-97
RCA23_c12760	1384812	1385840	GTP-binding protein Obg	COG0536	R		389	466	-77
RCA23_c12770	1385828	1386934	glutamate 5-kinase ProB	COG0263	E		322	395	-73
RCA23_c12780	1386950	1388206	gamma-glutamyl phosphate reductase ProA	COG0014	E		246	337	-91
RCA23_c12800	1388851	1388243	hypothetical protein	COG5385	S		346	369	-23
RCA23_c12790	1388850	1389026	hypothetical protein				186	377	-191
RCA23_c12810	1389099	1389872	hypothetical protein	COG3176	R		184	338	-154
RCA23_c12820	1389890	1390708	putative phosphate acyltransferase	COG0204	I		235	353	-118
RCA23_c12830	1391398	1390754	thiamine-phosphate pyrophosphorylase ThiE	COG0352	H		312	391	-79
RCA23_c12840	1391480	1392226	tRNA (cytidine/uridine-2'-O-)-methyltransferase TrmJ	COG0565	J		302	372	-70
RCA23_c12850	1392274	1393416	heme A synthase CtaA	COG1612	O		363	447	-84
RCA23_c12860	1393413	1394894	thermostable carboxypeptidase 1	COG2317	E		450	426	24
RCA23_c12870	1398094	1395344	DNA gyrase subunit A	COG0188	L		289	359	-70
RCA23_c12880	1399028	1398543	hypothetical protein	COG1495	O		189	308	-119
RCA23_c12890	1399603	1399025	DedA family protein	COG1238	S		295	288	7
RCA23_c12900	1400438	1399839	hypothetical protein			GI 6	458	361	97
RCA23_c12910	1401810	1401337	putative snoaL-like polyketide cyclase	COG3631	R	GI 6	222	195	27
RCA23_c12920	1402164	1402454	hypothetical protein, DUF1330	COG5470	S	GI 6	264	216	48
RCA23_c12930	1402883	1403188	hypothetical protein, DUF3303			GI 6	110	73	37
RCA23_c12940	1403986	1403495	hypothetical protein, transmembrane			GI 6	27	27	0
RCA23_c12950	1404278	1403991	hypothetical protein, transmembrane			GI 6	11	14	-3
RCA23_c12960	1404422	1405501	integrase	COG2801	L	GI 6	0	0	0
RCA23_c12970	1406068	1406265	hypothetical protein			GI 6	0	0	0
RCA23_c12980	1406863	1406288	site-specific recombinase, resolvase family protein	COG1961	L	GI 6	149	119	30
RCA23_c12990	1407072	1407455	hypothetical protein	COG4731	S	GI 6	437	256	181
RCA23_c13000	1407781	1407981	hypothetical protein			GI 6	17	6	11
RCA23_c13010	1409183	1408122	transposase	COG3415	L	GI 6	0	0	0
RCA23_c13020	1410237	1410437	ribsomal protein S21	COG0828	J	GI 6	301	250	51
RCA23_c13030	1410572	1410739	hypothetical protein			GI 6	484	243	241
RCA23_c13040	1410794	1411873	integrase	COG2801	L	GI 6	0	0	0

RCA23_c13050	1413278	1411980	hypothetical protein			GI 6	524	297	227
RCA23_c13060	1414337	1413294	putative phage integrase	COG0582	L	GI 6	476	307	169
RCA23_c13080	1414822	1415982	putative phage integrase	COG0582	L	GI 6	243	165	78
RCA23_c13090	1417647	1417237	hypothetical protein, GYD domain	COG4274	S	GI 6	33	42	-9
RCA23_c13100	1417942	1418304	hypothetical protein			GI 6	4	0	4
RCA23_c13110	1418856	1418572	hypothetical protein			GI 6	224	134	90
RCA23_c13120	1419178	1420584	hypothetical protein			GI 6	92	69	23
RCA23_c13130	1420645	1421724	integrase	COG2801	L	GI 6	0	0	0
RCA23_c13140	1422270	1422037	hypothetical protein	COG5586	S	GI 6	138	77	61
RCA23_c13150	1422868	1422398	hypothetical protein			GI 6	83	93	-10
RCA23_c13160	1423763	1423269	hypothetical protein			GI 6	217	204	13
RCA23_c13170	1424625	1424954	hypothetical protein	COG4274	S	GI 6	458	401	57
RCA23_c13180	1425131	1425541	hypothetical protein			GI 6	484	312	172
RCA23_c13190	1425553	1425708	hypothetical protein			GI 6	314	205	109
RCA23_c13210	1425849	1426889	phosphoribosylformylglycinamidine cyclo-ligase PurM	COG0150	F		228	287	-59
RCA23_c13220	1426886	1427464	phosphoribosylglycinamide formyltransferase PurN	COG0299	F		356	390	-34
RCA23_c13230	1427543	1428700	ribonuclease D	COG0349	J		533	523	10
RCA23_c13240	1428736	1429146	SufE-like protein	COG2166	R		396	545	-149
RCA23_c13250	1429745	1429143	hypothetical protein				328	397	-69
RCA23_c13260	1430578	1429871	putative methionine synthase (B12 dependent) subunit 2	COG5012	R		318	404	-86
RCA23_c13270	1431745	1430717	putative methionine synthase (B12 dependent) subunit 1	COG0646	E		255	293	-38
RCA23_c13280	1431913	1432788	phosphoribosylaminoimidazole-succinocarboxamide syntha	COG0152	F		544	497	47
RCA23_c13290	1432805	1433035	phosphoribosylformylglycinamidine (FGAM) synthase PurS	COG1828	F		429	477	-48
RCA23_c13300	1433035	1433703	phosphoribosylformylglycinamidine synthase PurQ	COG0047	F		256	362	-106
RCA23_c13310	1433749	1435512	C4-dicarboxylate transport sensor protein DctB	COG4191	T		424	436	-12
RCA23_c13320	1435515	1436849	C4-dicarboxylate transport transcriptional regulatory protein	COG2204	T		309	329	-20
RCA23_c13330	1437325	1440108	ribonuclease E	COG1530	J		255	309	-54
RCA23_c13340	1440411	1440178	putative sulfurtransferase tusA	COG0425	O		247	389	-142
RCA23_c13350	1440615	1441367	cytochrome C biogenesis protein transmembrane region	COG0785	O		246	383	-137
RCA23_c13360	1441476	1442669	hypothetical protein				167	250	-83

RCA23_c13370	1442666	1444039	putative cytochrome P450	COG2124	Q	149	243	-94
RCA23_c13380	1444734	1444045	DNA alkylation repair enzyme	COG4912	L	200	224	-24
RCA23_c13390	1445375	1444875	hypothetical protein	COG3153	R	535	551	-16
RCA23_c13400	1447484	1445661	glucosamine--fructose-6-phosphate aminotransferase Glm	COG0449	M	266	262	4
RCA23_c13410	1448847	1447489	bifunctional protein GlmU	COG1207	M	241	239	2
RCA23_c13420	1448966	1449634	putative HAD-superfamily hydrolase	COG0546	R	158	222	-64
RCA23_c13440	1450935	1449619	MmgE/PrpD family protein	COG2079	R	213	307	-94
RCA23_c13430	1450926	1452245	putative pyridoxal-phosphate-dependent aminotransferase	COG0399	M	302	360	-58
RCA23_c13450	1452356	1453519	isovaleryl-CoA dehydrogenase	COG1960	I	393	399	-6
RCA23_c13460	1453516	1454001	hypothetical protein			340	392	-52
RCA23_c13470	1454014	1455594	methylcrotonoyl-CoA carboxylase beta subunit MccB	COG4799	I	176	239	-63
RCA23_c13480	1455563	1456069	hypothetical protein			283	455	-172
RCA23_c13490	1456066	1457997	methylcrotonoyl-CoA carboxylase alpha subunit MccA	COG4770	I	216	303	-87
RCA23_c13500	1457994	1458887	hydroxymethylglutaryl-CoA lyase MvaB	COG0119	E	169	249	-80
RCA23_c13510	1458877	1459662	putative methylglutaconyl-CoA hydratase	COG1024	I	202	268	-66
RCA23_c13520	1459788	1460153	NADH-quinone oxidoreductase subunit A	COG0838	C	661	586	75
RCA23_c13530	1460153	1460677	NADH-quinone oxidoreductase subunit NuoB	COG0377	C	486	555	-69
RCA23_c13540	1460682	1460888	hypothetical protein DUF2158	COG5475	S	652	610	42
RCA23_c13550	1460885	1461496	NADH-quinone oxidoreductase subunit C	COG0852	C	607	461	146
RCA23_c13560	1461557	1462396	hypothetical protein			533	476	57
RCA23_c13570	1462446	1463657	NADH-quinone oxidoreductase subunit D	COG0649	C	551	526	25
RCA23_c13580	1463723	1464529	NADH-quinone oxidoreductase subunit E	COG1905	C	409	436	-27
RCA23_c13590	1464577	1464804	hypothetical protein			413	373	40
RCA23_c13600	1464810	1466105	NADH-quinone oxidoreductase subunit F	COG1894	C	469	416	53
RCA23_c13610	1466139	1466543	hypothetical protein			322	392	-70
RCA23_c13620	1466546	1468564	NADH-quinone oxidoreductase subunit G	COG1034	C	305	351	-46
RCA23_c13630	1468569	1468826	hypothetical protein			466	384	82
RCA23_c13640	1468823	1469860	NADH-quinone oxidoreductase subunit H	COG1005	C	757	586	171
RCA23_c13650	1469865	1470359	NADH-quinone oxidoreductase subunit I	COG1143	C	602	413	189
RCA23_c13660	1470382	1470987	NADH-quinone oxidoreductase subunit J	COG0839	C	636	482	154

RCA23_c13670	1470984	1471289	NADH-quinone oxidoreductase subunit K	COG0713	C	821	637	184
RCA23_c13680	1471296	1473413	NADH-quinone oxidoreductase subunit L	COG1009	C	437	408	29
RCA23_c13690	1473413	1474963	NADH-quinone oxidoreductase subunit M	COG1008	C	532	545	-13
RCA23_c13700	1474980	1476422	NADH-quinone oxidoreductase subunit N	COG1007	C	401	459	-58
RCA23_c13710	1476424	1477155	biotin-[acetyl-CoA-carboxylase] ligase	COG0340	H	229	269	-40
RCA23_c13720	1477167	1477937	type III pantothenate kinase CoaX	COG1521	K	366	445	-79
RCA23_c13730	1477937	1479601	putative ribonuclease	COG0595	R	374	437	-63
RCA23_c13740	1481465	1479801	ATP-dependent RNA helicase RhlE	COG0513	L	354	399	-45
RCA23_c13750	1483232	1481634	peptide chain release factor 3	COG4108	J	313	275	38
RCA23_c13760	1484260	1483316	hypothetical protein			571	437	134
RCA23_c13770	1484470	1485249	putative short chain dehydrogenase	COG1028	I	262	331	-69
RCA23_c13780	1485369	1486409	arsenite methyltransferase	COG2226	H	400	459	-59
RCA23_c13790	1486465	1487541	Fe(3+) ions import ATP-binding protein FbpC	COG3842	E	250	357	-107
RCA23_c13800	1488367	1487555	putative helix-turn-helix protein	COG2378	K	292	291	1
RCA23_c13810	1488388	1488582	sec-independent protein translocase protein TatA	COG1826	U	505	457	48
RCA23_c13820	1488618	1489190	sec-independent protein translocase protein TatB	COG1826	U	330	343	-13
RCA23_c13830	1489187	1490077	sec-independent protein translocase protein TatC	COG0805	U	517	496	21
RCA23_c13840	1490074	1490913	hypothetical protein DUF815	COG2607	R	258	376	-118
RCA23_c13850	1492065	1490932	putative peptidoglycan-binding peptidase	COG0739	M	224	279	-55
RCA23_c13860	1492751	1492104	protein-L-isoaspartate O-methyltransferase Pcm	COG2518	O	271	340	-69
RCA23_c13870	1493504	1492755	5'-nucleotidase SurE	COG0496	R	249	361	-112
RCA23_c13880	1494293	1493628	putative short chain dehydrogenase	COG1028	I	171	181	-10
RCA23_c13890	1495797	1494328	amidophosphoribosyltransferase PurF	COG0034	F	308	326	-18
RCA23_c13900	1496469	1495963	putative colicin V production protein			695	461	234
RCA23_c13910	1497899	1496541	DNA repair protein RadA	COG1066	O	241	276	-35
RCA23_c13920	1498723	1497977	ABC transporter ATP-binding protein	COG1127	Q	240	329	-89
RCA23_c13930	1499508	1498720	hypothetical protein DUF140	COG0767	Q	233	367	-134
RCA23_c13940	1500548	1499505	alanine racemase, biosynthetic	COG0787	M	293	329	-36
RCA23_c13950	1502120	1500630	replicative DNA helicase DnaB	COG0305	L	362	394	-32
RCA23_c13960	1503031	1502354	orotate phosphoribosyltransferase PyrE	COG0461	F	442	359	83

RCA23_c13970	1504098	1503058	dihydroorotase PyrC	COG0418	F		202	251	-49
RCA23_c13980	1504207	1504548	hypothetical protein				487	337	150
RCA23_c13990	1504659	1504880	hypothetical protein				1.964	903	1.061
RCA23_c14000	1505732	1504914	hypothetical protein				387	351	36
RCA23_c14010	1507107	1506076	malate dehydrogenase Mdh	COG0039	C		211	210	1
RCA23_c14020	1507213	1508112	citrate lyase beta subunit CitE	COG2301	G		312	379	-67
RCA23_c14030	1508312	1509337	putative mesaconyl-CoA hydratase	COG2030	I		265	408	-143
RCA23_c14040	1509578	1509898	succinate dehydrogenase cytochrome b556 subunit SdhC	COG2009	C		557	392	165
RCA23_c14050	1509911	1510282	succinate dehydrogenase hydrophobic membrane anchor s	COG2142	C		433	353	80
RCA23_c14060	1510301	1512106	succinate dehydrogenase flavoprotein subunit SdhA	COG1053	C		278	316	-38
RCA23_c14070	1512106	1512408	hypothetical protein				327	285	42
RCA23_c14080	1512506	1513285	succinate dehydrogenase iron-sulfur subunit SdhB	COG0479	C		697	511	186
RCA23_c14090	1514072	1513368	purine nucleoside phosphorylase deoD-type	COG0813	F		306	402	-96
RCA23_c14100	1514517	1514077	acetyltransferase	COG1246	E		267	373	-106
RCA23_c14110	1515360	1514536	tryptophan synthase alpha chain TrpA	COG0159	E		426	401	25
RCA23_c14120	1515506	1516603	GTP-dependent nucleic acid-binding protein EngD	COG0012	J		325	304	21
RCA23_c14130	1516647	1517570	Non-specific ribonucleoside hydrolase rihC	COG1957	F		193	264	-71
RCA23_c14150	1518098	1518574	hypothetical protein DUF583	COG1664	M	GI 7	165	88	77
RCA23_c14160	1519456	1518554	protease HtpX	COG0501	O	GI 7	279	171	108
RCA23_c14170	1521395	1520490	histone deacetylase	COG0123	B	GI 7	75	50	25
RCA23_c14180	1521466	1521981	peripheral-type benzodiazepine receptor/signal transductior	COG3476	T	GI 7	102	83	19
RCA23_c14190	1522156	1522710	DNA-invertase Hin	COG1961	L	GI 7	122	64	58
RCA23_c14200	1523534	1524067	hypothetical protein			GI 7	24	29	-5
RCA23_c14210	1524259	1524588	hypothetical protein			GI 7	272	263	9
RCA23_c14220	1526125	1525748	hypothetical protein, RmlC-like cupin family	COG3450	R	GI 7	126	63	63
RCA23_c14230	1527629	1526337	integrase	COG4974	L	GI 7	158	126	32
RCA23_c14240	1528430	1529155	hypothetical membrane protein			GI 7	498	284	214
RCA23_c14260	1530033	1529710	hypothetical protein	COG4530	S		830	585	245
RCA23_c14270	1530131	1530841	hypothetical protein DUF45	COG1451	R		190	223	-33
RCA23_c14280	1530914	1531564	HTH-type transcriptional regulator, GntR family	COG1802	K		187	228	-41

RCA23_c14290	1533239	1531851	dihydrolipoyl dehydrogenase Lpd	COG1249	C	466	368	98
RCA23_c14300	1534890	1533394	dihydrolipoyllysine-residue succinyltransferase component	COG0508	C	303	288	15
RCA23_c14310	1537852	1534895	2-oxoglutarate dehydrogenase E1 component SucA	COG0567	C	473	404	69
RCA23_c14320	1538893	1538009	succinyl-CoA ligase [ADP-forming] alpha subunit SucD	COG0074	C	358	285	73
RCA23_c14330	1540169	1538973	succinyl-CoA ligase [ADP-forming] beta subunit SucC	COG0045	C	690	360	330
RCA23_c14340	1541555	1540356	butyryl-CoA dehydrogenase	COG1960	I	341	300	41
RCA23_c14350	1542165	1541704	translation initiation factor IF-3	COG0290	J	630	362	268
RCA23_c14360	1543174	1542341	ferredoxin--NADP reductase Fpr	COG1018	C	336	418	-82
RCA23_c14370	1543641	1543234	hypothetical protein	COG3749	S	253	220	33
RCA23_c14380	1543877	1543641	cysH'	COG0175	E	232	182	50
RCA23_c14390	1545545	1543881	cysI/sir: sulfite reductase (ferredoxin)	COG0155	P	294	400	-106
RCA23_c14400	1545843	1545547	hypothetical protein			228	310	-82
RCA23_c14410	1547228	1545834	siroheme synthase CysG	COG0007	H	185	248	-63
RCA23_c14420	1547360	1547827	HTH-type transcriptional regulator, AsnC family	COG1522	K	378	390	-12
RCA23_c14450	1549602	1548220	peptidase	COG0624	E	247	316	-69
RCA23_c14460	1549872	1551119	hypothetical protein	COG1426	S	263	283	-20
RCA23_c14470	1551156	1552289	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase Isp	COG0821	I	231	303	-72
RCA23_c14480	1553599	1552286	TPR-repeat containing protein	COG4783	R	216	239	-23
RCA23_c14490	1553648	1554796	aspartate aminotransferase	COG0436	E	243	353	-110
RCA23_c14500	1554989	1557526	penicillin-binding protein 1A	COG5009	M	262	302	-40
RCA23_c14510	1557611	1558735	peptide chain release factor 2	COG1186	J	431	474	-43
RCA23_c14520	1559286	1558798	hypothetical protein DUF583	COG1664	M	284	384	-100
RCA23_c14530	1560550	1559276	putative peptidase, M23 family	COG0739	M	336	341	-5
RCA23_c14540	1561570	1560740	hypothetical protein DUF455	COG2833	S	240	368	-128
RCA23_c14550	1562037	1561567	peroxiredoxin Bcp	COG1225	O	290	273	17
RCA23_c14560	1562118	1565399	hypothetical protein			277	331	-54
RCA23_c14570	1565470	1566519	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	COG0809	J	222	302	-80
RCA23_c14580	1566591	1567847	MFS-type transporter			516	456	60
RCA23_c14590	1567922	1568500	hypothetical protein DUF924	COG3803	S	230	272	-42
RCA23_c14600	1568608	1570005	dihydrolipoyl dehydrogenase Lpd	COG1249	C	446	363	83

RCA23_c14610	1570379	1573255	uvrABC system protein A	COG0178	L	350	381	-31
RCA23_c14620	1574577	1573252	MmgE/PrpD family protein	COG2079	R	259	359	-100
RCA23_c14630	1575459	1574587	3-hydroxyisobutyrate dehydrogenase MmsB	COG2084	I	182	158	24
RCA23_c14640	1576498	1575461	3-hydroxyisobutyryl-CoA hydrolase	COG1024	I	249	295	-46
RCA23_c14650	1577670	1576495	isobutyryl-CoA dehydrogenase	COG1960	I	231	285	-54
RCA23_c14660	1579264	1577765	methylmalonate-semialdehyde dehydrogenase MmsA	COG1012	C	289	334	-45
RCA23_c14670	1579359	1580273	putative HTH-type transcriptional regulator, LysR family	COG0583	K	195	319	-124
RCA23_c14680	1580359	1580856	phosphopantetheine adenylyltransferase CoaD	COG0669	H	397	393	4
RCA23_c14690	1581884	1580877	glyceraldehyde-3-phosphate dehydrogenase Gap	COG0057	G	443	402	41
RCA23_c14700	1583056	1582103	glyceraldehyde-3-phosphate dehydrogenase Gap	COG0057	G	317	344	-27
RCA23_c14710	1585311	1583296	transketolase TktA	COG0021	G	257	307	-50
RCA23_c14720	1585511	1585894	hypothetical protein			236	322	-86
RCA23_c14730	1585887	1586291	cell division protein ZapA	COG3027	S	366	260	106
RCA23_c14740	1586719	1586354	putative glutaredoxin	COG0278	O	643	378	265
RCA23_c14750	1586969	1586709	hypothetical protein			556	382	174
RCA23_c14760	1587213	1586971	hypothetical protein, BolA-like	COG0271	T	488	401	87
RCA23_c14770	1589513	1587267	phosphoribosylformylglycinamidine synthase PurL	COG0046	F	254	340	-86
RCA23_c14780	1590634	1589726	HTH-type transcriptional regulator, LysR family	COG0583	K	322	383	-61
RCA23_c14790	1590763	1594146	hypothetical protein, pyruvate ferredoxin/flavodoxin oxidore	COG4231	C	194	266	-72
RCA23_c14800	1594236	1595048	glutamate racemase MurI	COG0796	M	356	334	22
RCA23_c14810	1595120	1596148	N-acetyl-gamma-glutamyl-phosphate reductase ArgC	COG0002	E	564	441	123
RCA23_c14820	1596148	1596600	cytochrome c-type biogenesis protein CcmE	COG2332	O	291	279	12
RCA23_c14830	1596707	1598668	cytochrome c-type biogenesis protein CcmF	COG1138	O	404	410	-6
RCA23_c14840	1598722	1599117	cytochrome c-type biogenesis protein CcmH	COG3088	O	315	462	-147
RCA23_c14850	1599159	1599935	putative enoyl-CoA hydratase FadB	COG1024	I	285	353	-68
RCA23_c14860	1600258	1600728	hypothetical protein			544	317	227
RCA23_c14870	1602134	1600809	citrate synthase GltA	COG0372	C	642	370	272
RCA23_c14880	1603561	1602152	glutamyl-tRNA synthase 2	COG0008	J	390	320	70
RCA23_c14890	1603619	1605670	hypothetical protein competence protein E	COG0658	R	263	389	-126
RCA23_c14900	1606374	1605667	LexA repressor	COG1974	K	337	368	-31

RCA23_c14910	1607624	1606449	molybdopterin biosynthesis protein MoeA	COG0303	H	152	180	-28
RCA23_c14920	1608103	1607621	molybdenum cofactor biosynthesis protein MoaC	COG0315	H	261	210	51
RCA23_c14930	1608916	1608104	indole-3-glycerol phosphate synthase TrpC	COG0134	E	180	257	-77
RCA23_c14940	1609952	1608933	anthranilate phosphoribosyltransferase TrpD	COG0547	E	184	199	-15
RCA23_c14950	1610530	1609949	anthranilate synthase component TrpG	COG0512	E	229	330	-101
RCA23_c14960	1610679	1611788	hypothetical protein, divergent polysaccharide deacetylase			278	342	-64
RCA23_c14970	1612782	1611811	hypothetical protein			318	371	-53
RCA23_c14990	1613796	1613200	hypothetical protein	COG3108	S	294	342	-48
RCA23_c15000	1614095	1615693	putative L,D-transpeptidase YcbB	COG2989	S	337	409	-72
RCA23_c15010	1615723	1616820	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransfera	COG1044	M	307	313	-6
RCA23_c15020	1616840	1617097	acyl carrier protein	COG0236	I	752	635	117
RCA23_c15030	1617101	1618309	3-oxoacyl-[acyl-carrier-protein] synthase FabF	COG0304	I	360	368	-8
RCA23_c15040	1618913	1618323	hypothetical protein, invasion protein B	COG5342	R	470	365	105
RCA23_c15050	1620585	1619287	inner membrane protein	COG4536	P	535	395	140
RCA23_c15060	1621505	1620585	tyrosine recombinase XerD	COG4974	L	356	425	-69
RCA23_c15070	1622956	1621502	hypothetical protein			267	381	-114
RCA23_c15080	1623167	1622958	hypothetical protein			401	504	-103
RCA23_c15090	1623212	1623763	shikimate kinase AroK	COG0703	E	556	623	-67
RCA23_c15100	1623760	1624878	3-dehydroquinate synthase AroB	COG0337	E	227	392	-165
RCA23_c15110	1625462	1624944	single-stranded DNA-binding protein	COG0629	L	285	427	-142
RCA23_c15120	1627772	1625688	glutathione import ATP-binding protein GsiA	COG0444	E	341	366	-25
RCA23_c15130	1629378	1627777	putative ABC transporter inner membrane component	COG1173	E	271	317	-46
RCA23_c15140	1630432	1629392	putative ABC transporter permease protein	COG0601	E	407	407	0
RCA23_c15150	1632178	1630532	ABC transporter extracellular solute-binding protein	COG0747	E	250	204	46
RCA23_c15160	1633423	1632533	tRNA delta(2)-isopentenylpyrophosphate transferase MiaA	COG0324	J	194	325	-131
RCA23_c15170	1633522	1634253	uridylate kinase PyrH	COG0528	F	352	335	17
RCA23_c15180	1634275	1634841	ribosome recycling factor Frr	COG0233	J	393	363	30
RCA23_c15190	1634856	1635563	undecaprenyl pyrophosphate synthase UppS	COG0020	I	318	350	-32
RCA23_c15200	1635560	1636345	putative cytidylyltransferase	COG0575	I	183	309	-126
RCA23_c15210	1636345	1637505	1-deoxy-D-xylulose 5-phosphate reductoisomerase Dxr	COG0743	I	155	311	-156

RCA23_c15220	1637498	1638829	RIP metalloprotease RseP	COG0750	M	293	380	-87
RCA23_c15230	1638949	1641297	putative outer membrane assembly factor	COG4775	M	444	390	54
RCA23_c15240	1641399	1641863	putative outer tein			412	324	88
RCA23_c15250	1641972	1642433	(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase Fal	COG0764	I	326	374	-48
RCA23_c15260	1642430	1643227	acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acy	COG1043	M	283	369	-86
RCA23_c15270	1643232	1644035	hypothetical protein DUF1009	COG3494	S	199	315	-116
RCA23_c15280	1644032	1645186	lipid-A-disaccharide synthase LpxB	COG0763	M	225	289	-64
RCA23_c15290	1646325	1645189	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransfer	COG0482	J	270	301	-31
RCA23_c15300	1646437	1646721	hypothetical protein			191	235	-44
RCA23_c15310	1646802	1647515	cell cycle transcriptional regulator	COG0745	T	662	573	89
RCA23_c15320	1647766	1649886	DNA ligase LigA	COG0272	L	331	351	-20
RCA23_c15330	1649883	1651973	ATP-dependent DNA helicase RecG	COG1200	L	233	326	-93
RCA23_c15340	1653286	1652261	hypothetical protein			341	418	-77
RCA23_c15350	1653842	1653390	hypothetical protein	COG0822	C	206	275	-69
RCA23_c15360	1653910	1654266	phosphoribosyl-AMP cyclohydrolase HisI	COG0139	E	288	223	65
RCA23_c15370	1655153	1654284	glutamyl-Q tRNA(Asp) synthase GluQ	COG0008	J	175	221	-46
RCA23_c15380	1655731	1655150	hypothetical protein, methyltransferase	COG4976	R	245	288	-43
RCA23_c15390	1657149	1655812	tRNA uridine 5-carboxymethylaminomethyl modification enz	COG1206	J	217	276	-59
RCA23_c15400	1657978	1657190	putative crotonase	COG1024	I	321	314	7
RCA23_c15410	1658033	1658455	putative thioesterase	COG2050	Q	219	259	-40
RCA23_c15420	1658600	1659058	50S ribosomal protein L13	COG0102	J	681	369	312
RCA23_c15430	1659062	1659550	30S ribosomal protein S9	COG0103	J	324	197	127
RCA23_c15440	1659763	1661193	integrase			1	0	1
RCA23_c15460	1663623	1661959	choline dehydrogenase BetA	COG2303	E	197	307	-110
RCA23_c15470	1663885	1664619	ABC transporter, permease protein	COG4662	H	250	357	-107
RCA23_c15480	1664613	1665329	ABC transporter, ATP-binding protein	COG1131	V	208	301	-93
RCA23_c15490	1665326	1666123	ABC transporter, periplasmic substrate-binding protein	COG2998	H	273	269	4
RCA23_c15500	1666130	1666561	hypothetical membrane protein	COG1238	S	257	388	-131
RCA23_c15510	1666576	1667487	hypothetical protein DUF6 family, transmembrane	COG2962	R	263	325	-62
RCA23_c15520	1668078	1667497	hypothetical protein	COG2068	R	284	389	-105

RCA23_c15530	1670501	1668111	dimethylglycine dehydrogenase	COG0404	E	282	264	18
RCA23_c15540	1670705	1673146	dimethylglycine dehydrogenase	COG0404	E	272	341	-69
RCA23_c15550	1674027	1673149	short-chain dehydrogenase/reductase SDR	COG1028	I	334	424	-90
RCA23_c15560	1674074	1674460	hypothetical transmembrane protein	COG3788	R	458	440	18
RCA23_c15570	1675087	1674470	hypothetical protein, tetR regulator	COG1309	K	206	240	-34
RCA23_c15580	1676054	1675137	homoserine O-succinyltransferase MetA	COG1897	E	361	398	-37
RCA23_c15590	1676950	1676060	hypothetical protein			409	301	108
RCA23_c15600	1677863	1677015	putative integral membrane protein	COG2510	S	444	337	107
RCA23_c15610	1678994	1678410	Gcn5-like N-acetyltransferase	COG1670	J	276	171	105
RCA23_c15620	1681717	1680161	GMP synthase GuaA	COG0519	F	282	260	22
RCA23_c15630	1681941	1683413	trimethylamine methyltransferase MttB	COG5598	H	243	240	3
RCA23_c15640	1683982	1684989	hypothetical protein			313	290	23
RCA23_c15650	1685077	1686024	lipoyl synthase LipA	COG0320	H	597	400	197
RCA23_c15660	1686218	1686039	hypothetical protein			488	401	87
RCA23_c15670	1686751	1686215	hypoxanthine phosphoribosyltransferase Hpt	COG0634	F	754	569	185
RCA23_c15680	1686817	1687272	hypothetical protein	COG2867	I	446	375	71
RCA23_c15690	1688506	1687319	ammonium transporter AmtB	COG0004	P	357	340	17
RCA23_c15700	1689126	1688647	putative competence-damaged protein	COG1546	R	144	266	-122
RCA23_c15710	1689584	1689123	phosphatidylglycerophosphatase A	COG1267	I	217	316	-99
RCA23_c15720	1690723	1689581	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase IspF	COG0245	I	197	251	-54
RCA23_c15730	1690934	1691875	tRNA-dihydrouridine synthase B	COG0042	J	294	356	-62
RCA23_c15740	1691872	1692936	histidine kinase, nitrogen regulation protein NtrB	COG3852	T	361	518	-157
RCA23_c15750	1693055	1694299	nitrogen regulation protein NtrC	COG2204	T	515	426	89
RCA23_c15760	1694375	1696633	histidine kinase, nitrogen regulation protein NtrY	COG5000	T	356	352	4
RCA23_c15770	1696630	1698030	nitrogen assimilation regulatory protein NtrX	COG2204	T	504	383	121
RCA23_c15780	1698108	1699484	Trk system potassium uptake protein TrkA	COG0569	P	427	389	38
RCA23_c15790	1699487	1700971	putative Trk system potassium uptake protein trkH	COG0168	P	482	534	-52
RCA23_c15800	1701080	1701313	RNA-binding protein Hfq	COG1923	R	693	491	202
RCA23_c15810	1701319	1702623	GTP-binding protein HflX	COG2262	R	414	423	-9
RCA23_c15820	1705060	1702583	acyl-homoserine lactone acylase QuiP	COG2366	R	244	335	-91

RCA23_c15830	1705687	1705130	hypothetical protein	COG2930	S	247	295	-48
RCA23_c15840	1706785	1705775	delta-aminolevulinic acid dehydratase HemB	COG0113	H	238	353	-115
RCA23_c15850	1706883	1707368	hypothetical protein			400	448	-48
RCA23_c15860	1707395	1710835	transcription-repair-coupling factor Mfd	COG1197	L	287	350	-63
RCA23_c15870	1711473	1710832	putative DSBA-like thioredoxin family protein	COG2761	Q	297	350	-53
RCA23_c15880	1712966	1711470	long-chain-fatty-acid-CoA ligase	COG0318	I	183	288	-105
RCA23_c15890	1713007	1713654	HTH-type transcriptional regulator	COG1396	K	344	355	-11
RCA23_c15900	1714310	1713651	aquaporin AqpZ	COG0580	G	476	472	4
RCA23_c15910	1716201	1714342	putative extracellular solute-binding protein	COG4166	E	453	381	72
RCA23_c15920	1716981	1716376	lysine exporter protein LysE	COG1279	R	534	383	151
RCA23_c15930	1717676	1716978	hypothetical protein DUF502	COG2928	S	372	301	71
RCA23_c15940	1718674	1717751	pseudouridine-5'-phosphate glycosidase PsuG	COG2313	Q	184	280	-96
RCA23_c15950	1719592	1718678	hypothetical protein, pfkB family carbohydrate kinase	COG0524	G	194	242	-48
RCA23_c15960	1719832	1720038	cold shock protein CspA	COG1278	K	361	291	70
RCA23_c15970	1720408	1721112	30S ribosomal protein S2	COG0052	J	423	286	137
RCA23_c15980	1721186	1722061	elongation factor Ts	COG0264	J	443	397	46
RCA23_c15990	1723202	1722168	hypothetical protein			215	203	12
RCA23_c16000	1723712	1723203	hypothetical protein, acetyltransferase-like	COG1670	J	194	134	60
RCA23_c16010	1724127	1723705	hypothetical protein, transcription factor NusA like			194	156	38
RCA23_c16020	1724961	1724428	putative phenylacetic acid degradation protein	COG0663	R	265	270	-5
RCA23_c16030	1725592	1724951	guanylate kinase Gmk	COG0194	F	475	457	18
RCA23_c16040	1726466	1725597	hypothetical protein, YicC-like	COG1561	S	323	347	-24
RCA23_c16050	1726645	1727271	hypothetical protein, DUF1457	COG5388	S	144	183	-39
RCA23_c16060	1728661	1727291	phospho-2-dehydro-3-deoxyheptonate aldolase	COG3200	E	330	309	21
RCA23_c16070	1728824	1729837	putative HTH-type transcriptional regulator, AraC family	COG4977	K	326	340	-14
RCA23_c16080	1729969	1731150	putative amino-acid binding protein	COG0683	E	196	180	16
RCA23_c16090	1731226	1732005	putative branched-chain amino acid transport ATP-binding	COG0411	E	241	251	-10
RCA23_c16100	1732002	1732715	putative branched-chain amino acid transport ATP-binding	COG0410	E	163	218	-55
RCA23_c16110	1732719	1733732	putative branched-chain amino acid transport system perme	COG0559	E	255	366	-111
RCA23_c16120	1733729	1735063	putative branched-chain amino acid transport system perme	COG4177	E	234	308	-74

RCA23_c16130	1735123	1736940	GTP-binding protein TypA	COG1217	T	275	334	-59
RCA23_c16140	1737304	1737014	hypothetical protein DUF1330	COG5470	S	210	320	-110
RCA23_c16150	1740028	1737311	alanyl-tRNA synthase AlaS	COG0013	J	300	335	-35
RCA23_c16160	1741231	1740119	protein RecA	COG0468	L	701	482	219
RCA23_c16170	1741383	1741979	hypothetical protein			495	354	141
RCA23_c16180	1743391	1741988	sensor transduction histidine kianse	COG0642	T	488	383	105
RCA23_c16190	1744278	1743409	hypothetical protein			338	362	-24
RCA23_c16200	1745526	1744369	hypothetical protein, NOL1/NOP2/sun family	COG0144	J	284	351	-67
RCA23_c16210	1746815	1745526	inosine-5'-monophosphate dehydrogenase GuaB	COG0516	F	165	267	-102
RCA23_c16220	1747235	1749274	hypothetical protein	COG3894	R	252	383	-131
RCA23_c16240	1750674	1749451	cysteine desulfurase SufS	COG0520	E	271	289	-18
RCA23_c16250	1751249	1750671	hypothetical protein			453	462	-9
RCA23_c16260	1751722	1751246	hypothetical protein			225	326	-101
RCA23_c16270	1752993	1751728	FeS assembly protein SufD	COG0719	O	389	321	68
RCA23_c16280	1753748	1752993	FeS assembly ATPase SufC	COG0396	O	763	557	206
RCA23_c16290	1755321	1753810	FeS assembly protein SufB	COG0719	O	654	401	253
RCA23_c16300	1756376	1755327	putative cysteine desulfurase	COG1104	E	226	294	-68
RCA23_c16310	1756801	1756373	HTH-type transcriptional regulator Rrf2	COG1959	K	288	297	-9
RCA23_c16320	1757012	1757665	hypothetical protein	COG2945	R	375	324	51
RCA23_c16330	1757780	1758907	putative oxidoreductase	COG0673	R	247	281	-34
RCA23_c16340	1758960	1759811	inosose dehydratase IolE	COG1082	G	288	364	-76
RCA23_c16350	1759823	1760977	putative oxidoreductase	COG0673	R	306	350	-44
RCA23_c16360	1762000	1760999	HTH-type transcriptional repressor, LacI family	COG1609	K	336	279	57
RCA23_c16370	1762217	1762014	hypothetical protein			574	457	117
RCA23_c16380	1762996	1762214	sugar (ribose) ABC-transport system ATP binding protein	COG1129	G	573	414	159
RCA23_c16390	1764085	1763012	sugar (ribose) ABC transporter permease protein	COG1172	G	736	471	265
RCA23_c16400	1765194	1764175	sugar (ribose) ABC transporter periplasmic binding protein	COG1879	G	541	324	217
RCA23_c16410	1766724	1765405	beta-glucosidase BglA	COG2723	G	315	289	26
RCA23_c16420	1767779	1766721	maltose/maltodextrin import ATP-binding protein MalK	COG3839	G	335	415	-80
RCA23_c16430	1769330	1767780	putative alpha-glucosidase AglA	COG0366	G	330	387	-57

RCA23_c16440	1770025	1769333	alpha-glucoside transport system permease protein AglG	COG0395	G	485	419	66
RCA23_c16450	1770558	1770022	ABC transporter, membrane spanning protein	COG0395	G	344	327	17
RCA23_c16460	1771823	1770570	alpha-glucoside transport system permease protein AglF	COG1175	G	696	565	131
RCA23_c16470	1773262	1771922	alpha-glucosides-binding periplasmic protein AglE	COG1653	G	753	462	291
RCA23_c16480	1773635	1774675	HTH-type transcriptional regulator	COG1609	K	265	360	-95
RCA23_c16490	1775566	1774682	oxidoreductase	COG4989	R	197	228	-31
RCA23_c16500	1776723	1775566	alkanesulfonate monooxygenase SsuD	COG2141	C	310	287	23
RCA23_c16510	1776787	1777521	putative regulatory DNA binding protein	COG2188	K	311	294	17
RCA23_c16520	1777531	1778616	putative oxidoreductase	COG0673	R	256	312	-56
RCA23_c16530	1780202	1778613	glucose-6-phosphate isomerase Pgi	COG0166	G	219	289	-70
RCA23_c16540	1780889	1780212	6-phosphogluconolactonase Pgl	COG0363	G	228	320	-92
RCA23_c16550	1782340	1780889	glucose-6-phosphate 1-dehydrogenase Zwf	COG0364	G	280	364	-84
RCA23_c16560	1782518	1783450	hypothetical protein, radical SAM	COG0535	R	211	260	-49
RCA23_c16570	1784031	1783447	putative 5-methylcytosine-specific restriction enzyme McrA	COG1403	V	336	360	-24
RCA23_c16580	1784786	1784112	putative phospholipase/carboxylesterase	COG0400	R	320	433	-113
RCA23_c16590	1785406	1784783	HhH-GPD superfamily base excision DNA repair protein	COG0122	L	201	319	-118
RCA23_c16600	1786128	1785397	precorrin-6A reductase CobK	COG2099	H	207	313	-106
RCA23_c16610	1787144	1786125	cobalamin (vitamin B12) biosynthesis CbiDprotein CbiD	COG1903	H	234	296	-62
RCA23_c16620	1787265	1788116	uroporphyrinogen-III C-methyltransferase CobA	COG0007	H	228	319	-91
RCA23_c16630	1788113	1789378	cobyrinic acid A,C-diamide synthase CobB	COG1797	H	219	233	-14
RCA23_c16640	1789397	1790620	putative major facilitator superfamily transporter			279	340	-61
RCA23_c16650	1791369	1790629	hypothetical protein	COG1562	I	196	257	-61
RCA23_c16660	1792730	1791366	cysteinyl-tRNA synthase CysS	COG0215	J	268	283	-15
RCA23_c16670	1792939	1794108	aspartate aminotransferase AspC	COG0436	E	174	265	-91
RCA23_c16680	1794310	1795845	trimethylamine methyltransferase MttB	COG5598	H	206	357	-151
RCA23_c16690	1797683	1795869	ABC transporter ATP-binding protein Uup	COG0488	R	291	374	-83
RCA23_c16700	1798221	1797715	hypothetical protein	COG3176	R	334	381	-47
RCA23_c16710	1798563	1798961	peptide methionine sulfoxide reductase MsrB	COG0229	O	307	366	-59
RCA23_c16720	1799290	1798958	hypothetical protein, lipoprotein	COG2913	J	179	299	-120
RCA23_c16730	1799541	1800038	hypothetical protein	COG1399	R	327	476	-149

RCA23_c16740	1800483	1801568	fatty acid/phospholipid synthesis protein PlsX	COG0416	I	370	356	14
RCA23_c16750	1801571	1802533	3-oxoacyl-[acyl-carrier-protein] synthase FabH	COG0332	I	321	335	-14
RCA23_c16760	1802638	1802916	integration host factor alpha subunit IhfA	COG0776	L	908	657	251
RCA23_c16770	1802922	1803605	hypothetical protein, MerR family regulatory protein	COG0789	K	363	366	-3
RCA23_c16790	1803802	1804875	deoxyguanosinetriphosphate triphosphohydrolase-like prote	COG0717	F	284	273	11
RCA23_c16800	1805746	1805078	putative segregation and condesation protein B	COG1386	K	292	333	-41
RCA23_c16810	1806524	1805739	hypothetical protein, segregation and condensation protein	COG1354	S	264	347	-83
RCA23_c16820	1807519	1806524	beta-hexosaminidase NagZ	COG1472	G	233	290	-57
RCA23_c16830	1808420	1807533	hypothetical protein			203	222	-19
RCA23_c16840	1810236	1808491	arginyl-tRNA synthase	COG0018	J	357	365	-8
RCA23_c16850	1811427	1810285	deoxyguanosinetriphosphate triphosphohydrolase-like prote	COG0232	F	269	313	-44
RCA23_c16860	1811504	1811830	putative iron-sulfur insertion protein erpA	COG0316	S	581	371	210
RCA23_c16870	1811876	1812664	exodeoxyribonuclease III	COG0708	L	439	421	18
RCA23_c16880	1813149	1812685	putative cytochrome B561	COG3038	C	276	347	-71
RCA23_c16890	1813755	1813333	putative dnak suppressor protein dksA	COG1734	T	459	450	9
RCA23_c16900	1813911	1814750	hypothetical protein	COG0714	R	623	506	117
RCA23_c16910	1814970	1816151	hypothetical protein	COG3825	S	326	385	-59
RCA23_c16920	1816264	1816953	putative peptidase, M48 family	COG0501	O	364	324	40
RCA23_c16930	1817481	1816948	hypothetical protein			233	300	-67
RCA23_c16940	1818677	1817481	putative ribosomal RNA large subunit methyltransferase	COG1092	R	266	302	-36
RCA23_c16950	1818800	1820605	phosphogluconate dehydratase Edd	COG0129	E	268	330	-62
RCA23_c16960	1820631	1821248	KHG/KDPG aldolase Eda	COG0800	G	181	211	-30
RCA23_c16970	1821507	1821208	hypothetical protein			267	405	-138
RCA23_c16980	1824217	1821497	glutamate-ammonia-ligase adenylyltransferase GlnE	COG1391	O	227	331	-104
RCA23_c16990	1824296	1824769	hypothetical protein	COG2606	S	270	333	-63
RCA23_c17000	1824858	1825280	hypothetical protein			1.898	707	1.191
RCA23_c17010	1825558	1825782	hypothetical protein			304	243	61
RCA23_c17020	1826061	1825840	hypothetical protein			247	200	47
RCA23_c17030	1827217	1826054	putative aromatic-ring-hydroxylating dioxygenase	COG4638	P	320	342	-22
RCA23_c17040	1827932	1827375	putative acetolactate synthase small subunit IlvH	COG0440	E	419	452	-33

RCA23_c17050	1829695	1827944	acetolactate synthase isozyme large subunit IlvI	COG0028	E	380	318	62
RCA23_c17060	1830055	1831023	hypothetical membrane protein, porin-like			724	550	174
RCA23_c17070	1831298	1832551	TRAP dicarboxylate transporter, subunit DctP	COG4663	Q	407	376	31
RCA23_c17080	1832674	1833531	TRAP dicarboxylate transporter, subunit DctQ	COG4665	Q	711	490	221
RCA23_c17090	1833543	1835897	TRAP dicarboxylate transporter, subunit DctM	COG4664	Q	337	395	-58
RCA23_c17100	1836779	1835958	putative arginyl-tRNA--protein transferase Ate	COG2935	O	448	457	-9
RCA23_c17110	1840606	1836959	vitamin B12-dependent ribonucleotide reductase NrdJ	COG0209	F	477	377	100
RCA23_c17120	1840806	1841066	hypothetical protein			175	144	31
RCA23_c17140	1841706	1841278	hypothetical protein DUF192	COG1430	S	474	371	103
RCA23_c17150	1842275	1841745	cold shock protein	COG1278	K	334	425	-91
RCA23_c17160	1843096	1842491	pyridoxine/pyridoxamine 5'-phosphate oxidase PdxH	COG0259	H	276	337	-61
RCA23_c17170	1843179	1843967	enoyl-[acyl-carrier-protein] reductase FabI	COG0623	I	385	443	-58
RCA23_c17180	1844001	1844504	xanthine phosphoribosyltransferase Gpt	COG0503	F	270	379	-109
RCA23_c17190	1844553	1845488	pyrimidine-specific ribonucleoside hydrolase RihA	COG1957	F	181	247	-66
RCA23_c17200	1845485	1846876	hypothetical protein UPF0061	COG0397	S	227	261	-34
RCA23_c17210	1846923	1848170	putative sodium/hydrogen exchanger	COG0025	P	328	487	-159
RCA23_c17220	1848192	1848626	ferric uptake regulator protein Fur	COG0735	P	556	482	74
RCA23_c17230	1848619	1849494	putative S-adenosylmethionine uptake transporter	COG0697	G	301	356	-55
RCA23_c17240	1849532	1850851	enolase Eno	COG0148	G	302	407	-105
RCA23_c17250	1852135	1851050	anhydro-N-acetylmuramic acid kinase AnmK	COG2377	O	202	334	-132
RCA23_c17260	1852202	1853452	tyrosyl-tRNA synthase TyrS	COG0162	J	477	463	14
RCA23_c17270	1853449	1854615	aspartate aminotransferase AspC	COG0436	E	258	354	-96
RCA23_c17280	1854680	1856539	hypothetical protein	COG0760	O	297	306	-9
RCA23_c17290	1856545	1858056	anthranilate synthase component TrpE	COG0147	E	224	249	-25
RCA23_c17300	1858187	1859110	protein soxG	COG0491	R	323	315	8
RCA23_c17310	1859114	1860058	protein soxH	COG0491	R	362	449	-87
RCA23_c17320	1861293	1860073	5-aminolevulinate synthase HemA	COG0156	H	337	393	-56
RCA23_c17330	1861747	1861295	sulfide dehydrogenase flavoprotein chain SoxF	COG3439	S	404	468	-64
RCA23_c17340	1862211	1861777	domain of unknown function DUF1791	COG1416	S	351	361	-10
RCA23_c17350	1863325	1862297	sulfite oxidase cytochrome subunit SoxD	COG3474	C	410	350	60

RCA23_c17360	1864577	1863309	sulfite oxidase molybdopterin subunit SoxC	COG2041	R	409	366	43
RCA23_c17370	1866311	1864608	sulfur oxidation protein SoxB	COG0737	F	518	409	109
RCA23_c17380	1867248	1866412	diheme cytochrome c	COG3258	C	536	298	238
RCA23_c17390	1867605	1867276	protein SoxZ			570	470	100
RCA23_c17400	1868053	1867631	protein SoxY	COG5501	S	301	243	58
RCA23_c17410	1868532	1868083	cytochrome c	COG2010	C	404	363	41
RCA23_c17420	1869206	1868649	thioredoxin SoxW	COG2143	O	639	479	160
RCA23_c17430	1869959	1869219	cytochrome c-type biogenesis protein SoxV	COG0785	O	588	396	192
RCA23_c17440	1870030	1870389	protein SoxS			435	382	53
RCA23_c17450	1870466	1870801	HTH-type transcriptional regulator, ArsR family	COG0640	K	321	345	-24
RCA23_c17460	1870811	1871866	putative soxT, transmembrane protein DUF395	COG2391	R	242	311	-69
RCA23_c17470	1872074	1873135	hypothetical protein DUF395	COG2391	R	383	379	4
RCA23_c17480	1874065	1873184	NAD-binding protein	COG2084	I	184	255	-71
RCA23_c17490	1875045	1874071	glyoxylate reductase GyaR	COG1052	C	161	206	-45
RCA23_c17500	1876573	1875236	glutamyl-tRNA(Gln) amidotransferase subunit A	COG0154	J	174	225	-51
RCA23_c17510	1877949	1876570	TRAP dicarboxylate transporter, subunit DctM	COG4664	Q	358	314	44
RCA23_c17520	1878581	1877964	TRAP dicarboxylate transporter, subunit DctQ	COG4665	Q	460	318	142
RCA23_c17530	1879745	1878651	TRAP dicarboxylate transporter, subunit DctP	COG4663	Q	421	267	154
RCA23_c17540	1880759	1880388	hypothetical protein			351	196	155
RCA23_c17550	1883014	1881539	glycerol kinase GlpK	COG0554	C	190	274	-84
RCA23_c17560	1883797	1883087	ribosomal RNA large subunit methyltransferase J	COG0293	J	286	438	-152
RCA23_c17570	1884919	1883804	putative Ppx/GppA phosphatase family protein	COG0248	F	321	343	-22
RCA23_c17580	1885166	1885453	hypothetical protein			298	453	-155
RCA23_c17590	1885491	1886417	hypothetical protein	COG0685	E	250	310	-60
RCA23_c17600	1886430	1887494	pterin domain containing enzyme	COG1410	E	257	263	-6
RCA23_c17610	1888307	1887537	HpcH/HpaI aldolase family protein	COG3836	G	262	427	-165
RCA23_c17620	1888466	1889464	glucokinase Glk	COG0837	G	320	380	-60
RCA23_c17630	1889451	1890644	hypothetical protein DUF1006	COG3214	S	188	320	-132
RCA23_c17640	1893859	1890659	reductive dehalogenase	COG1018	C	279	315	-36
RCA23_c17650	1894859	1893852	hypothetical protein, XdhC and CoxI	COG1975	O	205	328	-123

RCA23_c17660	1895830	1894940	2-hydroxy-3-oxopropionate reductase GlxR	COG2084	I	232	253	-21
RCA23_c17670	1896292	1897032	3-hydroxybutyrate dehydrogenase	COG1028	I	356	301	55
RCA23_c17680	1897074	1898861	dihydroxy-acid dehydratase IlvD	COG0129	E	259	298	-39
RCA23_c17690	1898872	1899720	fumarylacetoacetate hydrolase	COG0179	Q	276	301	-25
RCA23_c17700	1899793	1900119	hypothetical protein			128	158	-30
RCA23_c17710	1900591	1900169	nucleoside diphosphate kinase Ndk	COG0105	F	455	256	199
RCA23_c17720	1900744	1902597	hypothetical protein			97	96	1
RCA23_c17730	1902629	1904470	ABC transporter ATP-binding protein	COG0488	R	222	265	-43
RCA23_c17740	1904463	1905104	MarC family integral membrane protein	COG2095	U	403	394	9
RCA23_c17750	1905138	1905722	hypothetical protein	COG3577	R	305	350	-45
RCA23_c17760	1906191	1905760	putative DNA polymerase III chi subunit, HolC	COG2927	L	209	241	-32
RCA23_c17770	1907713	1906223	cytosol aminopeptidase PepA	COG0260	E	268	371	-103
RCA23_c17780	1907835	1908953	puative permease, YjgP/YjgQ family	COG0795	R	524	334	190
RCA23_c17790	1908950	1910047	puative permease, YjgP/YjgQ family	COG0795	R	326	382	-56
RCA23_c17800	1910078	1912183	putative organic solvent tolerance protein	COG1452	M	375	389	-14
RCA23_c17810	1912196	1913395	hypothetical protein, SurA	COG0760	O	287	313	-26
RCA23_c17820	1913462	1914475	4-hydroxythreonine-4-phosphate dehydrogenase PdxA	COG1995	H	207	256	-49
RCA23_c17830	1914465	1915301	dimethyladenosine transferase KsgA	COG0030	J	179	238	-59
RCA23_c17840	1916086	1915556	hypothetical protein			300	334	-34
RCA23_c17850	1917167	1916316	modification methylase, hemK family	COG2890	J	353	442	-89
RCA23_c17860	1918213	1917164	peptide chain release factor 1	COG0216	J	222	312	-90
RCA23_c17870	1918660	1918274	hypothetical protein	COG4446	S	205	218	-13
RCA23_c17880	1919709	1918672	agmatinase SpeB	COG0010	E	232	318	-86
RCA23_c17890	1919932	1920441	alpha/beta hydrolase			162	268	-106
RCA23_c17900	1921451	1920480	agmatinase SpeB	COG0010	E	226	300	-74
RCA23_c17910	1922618	1921452	hippurate hydrolase HipO	COG1473	R	195	320	-125
RCA23_c17920	1922668	1923480	protein MazG	COG3956	R	366	371	-5
RCA23_c17930	1923546	1924556	ABC transporter periplasmic iron-binding protein FutA	COG1840	P	270	407	-137
RCA23_c17940	1925179	1924631	putative peptidyl-prolyl cis-trans isomerase Ppi	COG0652	O	284	433	-149
RCA23_c17950	1925684	1925172	putative peptidyl-prolyl cis-trans isomerase Ppi	COG0652	O	415	489	-74

RCA23_c17960	1925805	1926983	phosphoglycerate kinase Pgk	COG0126	G	223	274	-51
RCA23_c17970	1927091	1927984	fructose-bisphosphate aldolase class 1	COG3588	G	219	411	-192
RCA23_c17980	1928074	1928373	hypothetical protein, septum formation initiator	COG2919	D	299	324	-25
RCA23_c17990	1928491	1929489	pyruvate dehydrogenase E1 component alpha subunit Pdh	COG1071	C	443	418	25
RCA23_c18000	1929493	1930863	pyruvate dehydrogenase E1 component beta subunit PdhB	COG0022	C	414	346	68
RCA23_c18010	1930874	1932154	dihydrolipoyllysine-residue acetyltransferase PdhC	COG0508	C	253	284	-31
RCA23_c18020	1933034	1932237	serine acetyltransferase CysE	COG1045	E	711	414	297
RCA23_c18030	1934250	1933132	putative gene transfer agent protein			109	156	-47
RCA23_c18040	1935148	1934639	putative gene transfer agent large terminase part 1	COG5323	S	8	55	-47
RCA23_c18050	1936044	1935133	putative gene transfer agent large terminase part 2	COG5323	S	121	191	-70
RCA23_c18060	1937543	1936392	aminodeoxychorismate lyase	COG1559	R	246	282	-36
RCA23_c18070	1938774	1937545	3-oxoacyl-[acyl-carrier-protein] synthase FabF	COG0304	I	379	520	-141
RCA23_c18080	1939180	1938947	acyl carrier protein AcpP	COG0236	I	739	630	109
RCA23_c18090	1940136	1939399	3-oxoacyl-[acyl-carrier-protein] reductase FabG	COG1028	I	252	290	-38
RCA23_c18100	1941123	1940194	malonyl CoA-acyl carrier protein transacylase	COG0331	I	204	295	-91
RCA23_c18110	1941409	1941774	30S ribosomal protein S6	COG0360	J	443	354	89
RCA23_c18120	1941788	1942015	30S ribosomal protein S18	COG0238	J	560	410	150
RCA23_c18130	1942052	1942645	50S ribosomal protein L9	COG0359	J	546	404	142
RCA23_c18140	1944185	1942854	trigger factor (TF)	COG0544	O	758	494	264
RCA23_c18160	1944635	1944973	nitrogen regulatory protein P-II 1	COG0347	E	931	485	446
RCA23_c18170	1945000	1946403	glutamine synthase GlnA type I	COG0174	E	786	431	355
RCA23_c18190	1947274	1946483	hypothetical protein			262	401	-139
RCA23_c18180	1947253	1948665	dimethylpropiothetin dethiomethylase DddP	COG0006	E	254	366	-112
RCA23_c18200	1949338	1948739	Biotin transporter BioY	COG1268	R	244	323	-79
RCA23_c18210	1949882	1949370	hypothetical protein			250	326	-76
RCA23_c18220	1949991	1951268	adenylosuccinate lyase PurB	COG0015	F	256	334	-78
RCA23_c18230	1951352	1951684	putative nitrile hydratase, beta subunit			324	231	93
RCA23_c18240	1951681	1951938	hypothetical protein			218	264	-46
RCA23_c18250	1951938	1952600	nitrile hydratase alpha subunit NthA			166	214	-48
RCA23_c18260	1952597	1953469	hypothetical protein DUF6 transmembrane	COG0697	G	213	283	-70

RCA23_c18270	1953462	1954361	putative lipid A biosynthesis lauroyl acyltransferase	COG1560	M	347	371	-24
RCA23_c18280	1955107	1954409	hypothetical protein	COG5429	S	489	407	82
RCA23_c18290	1955215	1957980	aconitate hydratase AcnA	COG1048	C	388	396	-8
RCA23_c18300	1958697	1958161	cytochrome c biogenesis protein CcmG	COG0526	O	243	314	-71
RCA23_c18310	1959609	1958839	cytochrome c-type biogenesis protein CcmC	COG0755	O	314	515	-201
RCA23_c18320	1960296	1959640	cytochrome c-type biogenesis protein CcmB	COG2386	O	273	384	-111
RCA23_c18330	1960907	1960293	cytochrome c biogenesis ATP-binding export protein CcmA	COG4133	O	227	402	-175
RCA23_c18340	1961264	1960911	hypothetical protein	COG3737	S	379	432	-53
RCA23_c18350	1962232	1961264	protein export membrane protein SecF	COG0341	U	436	416	20
RCA23_c18360	1963867	1962236	protein export membrane protein SecD	COG0342	U	300	327	-27
RCA23_c18370	1964193	1963912	putative immunogenic membrane protein YajC	COG1862	U	415	411	4
RCA23_c18380	1964441	1965733	seryl-tRNA synthase SerS	COG0172	J	267	313	-46
RCA23_c18390	1966135	1967112	hypothetical protein, alpha/beta hydrolase-like	COG2267	I	57	33	24
RCA23_c18400	1968740	1967283	GTP-binding protein EngA	COG1160	R	288	375	-87
RCA23_c18410	1970103	1968790	putative quinoprotein	COG1520	S	242	318	-76
RCA23_c18420	1970807	1970169	hypothetical protein DUF2133	COG4649	S	207	259	-52
RCA23_c18430	1971036	1972271	RND efflux transporter, MFP subunit	COG0845	M	278	245	33
RCA23_c18440	1972307	1975867	RND efflux transporter, permease protein	COG0841	V	413	402	11
RCA23_c18450	1977696	1975885	ABC transporter ATP-binding protein	COG5265	O	384	385	-1
RCA23_c18460	1979340	1977742	hypothetical protein, peptidoglycan-binding protein domain	COG1652	S	241	344	-103
RCA23_c18470	1980799	1979921	protein RarD	COG2962	R	792	473	319
RCA23_c18480	1981500	1980901	superoxide dismutase SodB	COG0605	P	814	669	145
RCA23_c18490	1982152	1981604	sarcosine oxidase subunit SoxG	COG4583	E	434	445	-11
RCA23_c18500	1985156	1982145	sarcosine oxidase alpha subunit SoxA	COG0404	E	308	339	-31
RCA23_c18510	1985553	1985224	sarcosine oxidase subunit SoxD	COG4311	E	215	300	-85
RCA23_c18520	1986862	1985618	sarcosine oxidase beta subunit SoxB	COG0665	E	258	354	-96
RCA23_c18530	1987085	1988227	cytochrome c-type biogenesis protein CycH	COG4235	O	177	223	-46
RCA23_c18540	1988224	1988700	hypothetical protein	COG0816	L	177	338	-161
RCA23_c18550	1988697	1988945	hypothetical protein DUF1289	COG3313	R	234	344	-110
RCA23_c18560	1989819	1989013	hypothetical protein			204	305	-101

RCA23_c18570	1990628	1989810	hypothetical protein DUF81	COG0730	R	187	292	-105
RCA23_c18580	1991653	1990628	tRNA-dihydrouridine synthase Dus	COG0042	J	192	241	-49
RCA23_c18590	1992384	1991857	putative peroxiredoxin (thioredoxin reductase)	COG0678	O	16	6	10
RCA23_c18600	1993473	1992418	benzaldehyde dehydrogenase	COG1012	C	10	6	4
RCA23_c18610	1994144	1993836	hypothetical protein			22	7	15
RCA23_c18620	1995454	1994423	hypothetical protein	COG2130	R	336	356	-20
RCA23_c18630	1995676	1996863	MFS-type transporter	COG2814	G	221	315	-94
RCA23_c18640	1996989	1997762	sorbitol dehydrogenase	COG1028	I	202	295	-93
RCA23_c18650	1997773	1999044	6-hydroxynicotinate 3-monooxygenase	COG0654	H	179	183	-4
RCA23_c18660	1999655	1999212	hypothetical protein			176	334	-158
RCA23_c18670	2001036	1999702	glycerate kinase	COG2379	G	170	266	-96
RCA23_c18680	2001093	2001482	putative carboxymuconolactone decarboxylase	COG0599	S	406	540	-134
RCA23_c18690	2001563	2003575	2,4-dienoyl-CoA reductase [NADPH]	COG1902	C	246	338	-92
RCA23_c18700	2005239	2003572	thiamine pyrophosphate protein	COG0028	E	182	231	-49
RCA23_c18710	2006314	2005394	rffG/rfbB: dTDP-glucose 4,6-dehydratase	COG1088	M	332	308	24
RCA23_c18720	2007489	2006419	hypothetical protein			322	352	-30
RCA23_c18730	2007506	2009269	choline dehydrogenase BetA	COG2303	E	198	304	-106
RCA23_c18740	2010131	2009487	succinyl-CoA:3-ketoacid-coenzyme A transferase subunit S	COG2057	I	338	422	-84
RCA23_c18750	2010826	2010131	succinyl-CoA:3-ketoacid-coenzyme A transferase subunit S	COG1788	I	799	597	202
RCA23_c18760	2011295	2011669	hypothetical membrane protein			419	471	-52
RCA23_c18770	2012857	2011751	putative dimethyl sulfoniopropionate demethylase DmdA	COG0404	E	288	455	-167
RCA23_c18780	2013130	2015229	hydantoin utilization protein A	COG0145	E	214	300	-86
RCA23_c18790	2015226	2016950	hydantoin utilization protein B	COG0146	E	190	304	-114
RCA23_c18800	2016951	2018159	FAD dependent oxidoreductase	COG0665	E	250	294	-44
RCA23_c18810	2018159	2018995	hypothetical protein, 3-beta hydroxysteroid dehydrogenase	COG0451	M	280	321	-41
RCA23_c18820	2019084	2019956	hypothetical protein, serine/threonine-protein kinase	COG1262	S	160	199	-39
RCA23_c18830	2021104	2019980	hypothetical protein	COG0457	R	168	236	-68
RCA23_c18840	2022102	2021257	hypothetical protein DUF1989	COG3665	S	128	236	-108
RCA23_c18850	2022203	2023267	putative diaminopropionate ammonia-lyase	COG1171	E	156	175	-19
RCA23_c18860	2023267	2024406	hypothetical protein, metallopeptidase M24	COG0006	E	270	264	6

RCA23_c18870	2024408	2025154	hypothetical protein, Asp/Glu/hydantoin racemase	COG3473	Q	224	239	-15
RCA23_c18880	2025960	2025172	putative 3-oxoadipate enol-lactonase 2, alpha/beta hydrolas	COG0596	R	268	310	-42
RCA23_c18890	2026549	2025953	hypothetical protein DUF1185			387	557	-170
RCA23_c18900	2027634	2026561	limonene 1,2-monooxygenase LimB	COG2141	C	291	316	-25
RCA23_c18910	2029075	2027600	aldehyde dehydrogenase, cytosolic	COG1012	C	197	267	-70
RCA23_c18920	2030336	2029185	ABC transporter, spermidine/putrescine import, permease p	COG1177	E	398	447	-49
RCA23_c18930	2031682	2030432	ABC transporter, spermidine/putrescine import, permease p	COG1176	E	339	358	-19
RCA23_c18940	2032842	2031745	ABC transporter, spermidine/putrescine import, substrate bi	COG0687	E	397	254	143
RCA23_c18950	2034010	2032913	ABC transporter, spermidine/putrescine import, ATP-binding	COG3842	E	529	415	114
RCA23_c18960	2034377	2034865	putative nitrilotriacetate monooxygenase component B	COG1853	R	273	303	-30
RCA23_c18970	2034990	2035700	hypothetical protein, DUF268			334	290	44
RCA23_c18980	2036599	2035859	hypothetical protein DUF28	COG0217	S	633	385	248
RCA23_c18990	2038600	2036810	sodium/sulphate symporter	COG0471	P	338	413	-75
RCA23_c19000	2039486	2038578	hypothetical protein	COG0697	G	338	439	-101
RCA23_c19010	2040307	2039483	hypothetical protein	COG1692	S	237	351	-114
RCA23_c19020	2040825	2040358	osmotically inducible OsmC-like protein	COG1764	O	222	392	-170
RCA23_c19030	2043111	2041045	3-hydroxyacyl-CoA dehydrogenase, NAD-binding	COG1250	I	224	311	-87
RCA23_c19040	2044071	2043151	putative transcriptional regulator	COG0703	E	205	334	-129
RCA23_c19050	2044508	2044068	thioesterase-like protein	COG0824	R	238	311	-73
RCA23_c19060	2045700	2044510	benzoyl-CoA oxygenase component A	COG0369	P	188	277	-89
RCA23_c19070	2047239	2045734	benzoyl-CoA oxygenase component B	COG3396	S	320	346	-26
RCA23_c19080	2048905	2047250	benzoyl-CoA-dihydrodiol lyase BoxC	COG1024	I	315	360	-45
RCA23_c19090	2049492	2049049	hypothetical protein DUF309			204	271	-67
RCA23_c19100	2050211	2049489	alpha/beta hydrolase	COG0596	R	179	279	-100
RCA23_c19110	2051839	2050304	benzoate-coenzyme A ligase	COG0318	I	187	281	-94
RCA23_c19120	2052630	2052070	putative 5-formyltetrahydrofolate cyclo-ligase family protein	COG0212	H	187	344	-157
RCA23_c19130	2054000	2052627	magnesium transporter MgtE	COG2239	P	255	384	-129
RCA23_c19140	2054072	2055358	guanine deaminase GuaD	COG0402	F	196	307	-111
RCA23_c19150	2056765	2055422	putative hydroxydechloroatrazine ethylaminohydrolase	COG0402	F	189	260	-71
RCA23_c19160	2057582	2056758	putative inositol monophosphatase family protein	COG0483	G	194	271	-77

RCA23_c19170	2057984	2057688	putative helix-turn-helix protein	COG1396	K	318	258	60
RCA23_c19180	2058365	2059330	putative alcohol dehydrogenase	COG0604	C	268	331	-63
RCA23_c19190	2059441	2060259	putative inner membrane protein	COG0670	R	1.541	607	934
RCA23_c19200	2060615	2061193	hypothetical protein			1.346	656	690
RCA23_c19210	2061960	2061328	putative N-acetylmuramoyl-L-alanine amidase amiD	COG3023	V	151	239	-88
RCA23_c19220	2062550	2062017	hypothetical protein			243	299	-56
RCA23_c19230	2064075	2062591	glutamyl-tRNA(Gln) amidotransferase subunit A	COG0154	J	294	350	-56
RCA23_c19240	2064362	2064075	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit	COG0721	J	232	432	-200
RCA23_c19250	2064883	2064449	putative deaminase	COG0590	F	205	227	-22
RCA23_c19260	2064947	2065729	putative ribosomal large subunit pseudouridine synthase B	COG1187	J	199	273	-74
RCA23_c19270	2066811	2065744	molybdate ABC transporter, ATP-binding protein ModC	COG4148	P	209	359	-150
RCA23_c19280	2067494	2066808	molybdate ABC transporter, pemease protein ModB	COG4149	P	241	332	-91
RCA23_c19290	2068318	2067491	molybdate ABC transporter, substrate binding protein ModA	COG0725	P	231	310	-79
RCA23_c19300	2068328	2068789	hypothetical protein, NUDIX hydrolase	COG0494	L	206	453	-247
RCA23_c19310	2068866	2069288	hypothetical protein DUF1178	COG5319	S	451	394	57
RCA23_c19320	2069388	2070611	aspartokinase LysC	COG0527	E	283	299	-16
RCA23_c19330	2070626	2072872	phosphoenolpyruvate-protein phosphotransferase PstI	COG3605	T	212	271	-59
RCA23_c19340	2073508	2073008	hypothetical protein, acetyltransferase-like	COG3153	R	164	260	-96
RCA23_c19350	2073581	2074186	hypothetical protein	COG1853	R	202	219	-17
RCA23_c19360	2075848	2074217	putative sulfate transporter	COG0659	P	264	369	-105
RCA23_c19370	2076031	2076906	methylthioadenosine phosphorylase MtnP	COG0005	F	204	304	-100
RCA23_c19380	2076963	2077523	adenine phosphoribosyltransferase Apt	COG0503	F	276	337	-61
RCA23_c19390	2078104	2077520	ribosomal-protein-alanine acetyltransferase RimJ	COG1670	J	240	287	-47
RCA23_c19400	2079370	2078108	uncharacterized zinc protease YmxG	COG0612	R	351	418	-67
RCA23_c19410	2080752	2079367	threonine synthase ThrC	COG0498	E	301	345	-44
RCA23_c19420	2081473	2080763	hypothetical protein, SURF1	COG3346	S	421	448	-27
RCA23_c19430	2082328	2081525	cytochrome c oxidase subunit 3	COG1845	C	694	471	223
RCA23_c19440	2082916	2082347	cytochrome c oxidase assembly protein CtaG	COG3175	O	694	524	170
RCA23_c19450	2084033	2083098	protoheme IX farnesyltransferase CtaB	COG0109	O	436	515	-79
RCA23_c19460	2084904	2084056	cytochrome c oxidase subunit 2 precursor	COG1622	C	794	480	314

RCA23_c19470	2085093	2086514	protein TldD	COG0312	R	190	276	-86
RCA23_c19480	2086648	2087799	SMF family protein	COG0758	L	160	264	-104
RCA23_c19490	2087889	2090483	DNA topoisomerase TopA	COG0550	L	240	343	-103
RCA23_c19500	2091332	2090493	fructose-bisphosphate aldolase Fba	COG0191	G	226	349	-123
RCA23_c19510	2092171	2091329	5-deoxy-glucuronate isomerase IolB	COG3718	G	378	459	-81
RCA23_c19520	2093164	2092175	5-dehydro-2-deoxygluconokinase IolC	COG0524	G	203	302	-99
RCA23_c19530	2095038	2093167	3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase IolD	COG3962	E	218	303	-85
RCA23_c19540	2096366	2095143	hypothetical protein DUF989	COG3748	S	398	405	-7
RCA23_c19550	2096731	2096378	5-hydroxyisourate hydrolase UraH	COG2351	R	330	328	2
RCA23_c19560	2096794	2098206	uric acid degradation bifunctional protein PucL	COG3195	S	210	248	-38
RCA23_c19570	2099161	2098337	putative allantoin catabolism protein YlbA	COG3257	R	252	300	-48
RCA23_c19580	2099379	2100608	sarcosine oxidase beta subunit SoxB	COG0665	E	248	344	-96
RCA23_c19590	2100622	2100909	sarcosine oxidase subunit SoxD	COG4311	E	235	330	-95
RCA23_c19600	2100906	2103860	sarcosine oxidase alpha subunit SoxA	COG0404	E	185	228	-43
RCA23_c19610	2103853	2104413	sarcosine oxidase subunit SoxG	COG4583	E	217	262	-45
RCA23_c19620	2105450	2104446	putative HTH-type transcriptional regulator, AraC family	COG4977	K	207	326	-119
RCA23_c19630	2105519	2106172	putative DNA-binding protein	COG1396	K	275	407	-132
RCA23_c19640	2106599	2106183	putative membrane protein			218	337	-119
RCA23_c19650	2107064	2107477	hypothetical protein			576	510	66
RCA23_c19660	2108227	2107835	hypothetical protein, thioesterase	COG2050	Q	412	379	33
RCA23_c19670	2108892	2108230	hypothetical protein, calcineurin-like phosphoesterase-like	COG1407	R	271	407	-136
RCA23_c19680	2111360	2108931	putative DEAD/DEAH box helicase	COG1201	R	207	359	-152
RCA23_c19690	2112302	2111400	bidunctional enzyme FolD	COG0190	H	301	440	-139
RCA23_c19700	2114064	2112388	formate--tetrahydrofolate ligase Fhs	COG2759	F	356	344	12
RCA23_c19710	2114959	2114357	hypothetical protein			275	383	-108
RCA23_c19720	2116937	2115018	cell division protease FtsH	COG0465	O	464	415	49
RCA23_c19730	2118254	2117031	tRNA(Ile)-lysidine synthase TilS	COG0037	D	188	268	-80
RCA23_c19740	2119039	2118251	hypothetical protein	COG1729	S	214	219	-5
RCA23_c19750	2119539	2119039	peptidoglycan-associated lipoprotein Pal	COG2885	M	189	256	-67
RCA23_c19760	2120916	2119594	Tol-Pal system beta propeller repeat protein TolB	COG0823	U	269	322	-53

RCA23_c19770	2121908	2120913	hypothetical protein, TolA-like			194	283	-89
RCA23_c19780	2122520	2122056	biopolymer transport protein TolR	COG0848	U	204	389	-185
RCA23_c19790	2123204	2122530	biopolymer transport protein TolQ	COG0811	U	243	362	-119
RCA23_c19800	2123640	2123296	acyl-CoA thioester hydrolase	COG0824	R	206	269	-63
RCA23_c19810	2124311	2123682	hypothetical protein			225	325	-100
RCA23_c19820	2125447	2124398	holliday junction ATP-dependent DNA helicase RuvB	COG2255	L	212	330	-118
RCA23_c19830	2126118	2125444	holliday junction ATP-dependent DNA helicase RuvA	COG0632	L	241	443	-202
RCA23_c19840	2126621	2126115	crossover junction endodeoxyribonuclease RuvC	COG0817	L	211	426	-215
RCA23_c19850	2128058	2127186	putative ribosomal protein L11 methyltransferase	COG2264	J	199	331	-132
RCA23_c19860	2128842	2128189	peptide methionine sulfoxide reductase MsrA	COG0225	O	470	535	-65
RCA23_c19870	2130139	2128931	hypothetical protein, major facilitator superfamily transporter			568	531	37
RCA23_c19880	2130289	2131452	L-lactate dehydrogenase IldD	COG1304	C	384	429	-45
RCA23_c19890	2133377	2131542	BCCT family transporter involved in DMSP uptake	COG1292	M	415	398	17
RCA23_c19900	2134841	2133696	putative MFS-type transporter			335	395	-60
RCA23_c19910	2134970	2135605	50S ribosomal protein L25	COG1825	J	907	573	334
RCA23_c19920	2135732	2136418	peptidyl-tRNA hydrolase Pth	COG0193	J	315	395	-80
RCA23_c19930	2136415	2137437	hypothetical protein	COG4427	S	189	250	-61
RCA23_c19940	2137439	2137810	hypothetical protein	COG3651	S	233	303	-70
RCA23_c19950	2139068	2137836	tryptophan synthase beta chain TrpB	COG0133	E	369	326	43
RCA23_c19960	2139789	2139151	N-(5'-phosphoribosyl)anthranilate isomerase TrpF	COG0135	E	185	217	-32
RCA23_c19970	2140121	2139786	hypothetical protein			393	402	-9
RCA23_c19980	2140422	2140141	integration host factor beta subunit IhfB	COG0776	L	601	452	149
RCA23_c19990	2142345	2140684	30S ribosomal protein S1	COG0539	J	695	460	235
RCA23_c20000	2142605	2142934	hypothetical protein			405	426	-21
RCA23_c20010	2143968	2142946	hypothetical protein, lacI family HTH-type regulatory protein	COG1609	K	159	288	-129
RCA23_c20020	2144050	2145192	putative phytanoyl-CoA dioxygenase	COG5285	Q	353	567	-214
RCA23_c20030	2146137	2145199	aldo/keto reductase	COG0667	C	253	316	-63
RCA23_c20040	2146855	2146184	cytidylate kinase Cmk	COG0283	F	198	213	-15
RCA23_c20050	2148201	2146852	3-phosphoshikimate 1-carboxyvinyltransferase AroA	COG0128	E	215	383	-168
RCA23_c20060	2148997	2148275	tRNA (guanine-N(7)-)-methyltransferase TrmB	COG0220	R	237	310	-73

RCA23_c20070	2150223	2149042	S-adenosylmethionine synthase MetK	COG0192	H	360	341	19
RCA23_c20080	2151767	2150271	apolipoprotein N-acyltransferase Lnt	COG0815	M	237	319	-82
RCA23_c20090	2152641	2151742	putative magnesium and cobalt efflux protein	COG1253	R	383	427	-44
RCA23_c20100	2153141	2152638	hypothetical protein UPF0054	COG0319	R	368	393	-25
RCA23_c20110	2154136	2153138	PhoH-like protein	COG1702	T	275	401	-126
RCA23_c20120	2155564	2154233	RNA modification enzyme, MiaB family	COG0621	J	275	292	-17
RCA23_c20130	2155629	2156543	hypothetical protein			513	459	54
RCA23_c20140	2156986	2156552	putative ferric uptake regulator family protein	COG0735	P	537	555	-18
RCA23_c20150	2157143	2157652	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase FabA	COG0764	I	376	331	45
RCA23_c20160	2157667	2158896	3-oxoacyl-[acyl-carrier-protein] synthase FabB	COG0304	I	361	339	22
RCA23_c20170	2158901	2159689	enoyl-[acyl-carrier-protein] reductase FabI	COG0623	I	292	375	-83
RCA23_c20180	2160715	2159738	threo-3-hydroxyaspartate ammonia-lyase SRY	COG1171	E	167	199	-32
RCA23_c20190	2161402	2160719	2-haloalkanoic acid dehalogenase	COG1011	R	258	323	-65
RCA23_c20200	2161460	2162248	3-oxoadipate enol-lactonase CatD	COG0596	R	289	372	-83
RCA23_c20210	2162268	2163494	putative tetracycline resistance protein, class C	COG2814	G	193	322	-129
RCA23_c20220	2163510	2164649	NAD/mycothiol-dependent formaldehyde dehydrogenase	COG1062	C	189	249	-60
RCA23_c20230	2164704	2165945	D-galactonate dehydratase DgoD	COG4948	M	320	382	-62
RCA23_c20240	2168433	2165986	dimethylglycine dehydrogenase	COG0404	E	269	340	-71
RCA23_c20250	2170044	2168488	trimethylamine methyltransferase MttB	COG5598	H	270	344	-74
RCA23_c20260	2170193	2170597	hypothetical protein	COG0607	P	248	216	32
RCA23_c20270	2170629	2171999	uncharacterized aminotransferase	COG0161	H	325	341	-16
RCA23_c20280	2172154	2173251	aminomethyltransferase, mitochondrial	COG0404	E	364	312	52
RCA23_c20290	2173265	2173630	glycine cleavage system protein GcvH	COG0509	E	591	456	135
RCA23_c20300	2173679	2176525	glycine dehydrogenase GcvP	COG1003	E	291	292	-1
RCA23_c20310	2177847	2176510	D-amino acid dehydrogenase small subunit DadA	COG0665	E	184	266	-82
RCA23_c20320	2177927	2178970	putrescine ABC transport system putrescine-binding peripla	COG0687	E	343	375	-32
RCA23_c20330	2180246	2179164	putrescine ABC transport system ATP-binding protein PotG	COG3842	E	257	331	-74
RCA23_c20340	2181058	2180243	putrescine ABC transport system permease protein PotI	COG1177	E	470	610	-140
RCA23_c20350	2181888	2181055	putrescine ABC transport system permease protein PotB	COG1176	E	607	570	37
RCA23_c20360	2183133	2181934	rieske 2Fe-2S domain protein	COG4638	P	465	415	50

RCA23_c20370	2184561	2183245	TRAP dicarboxylate transporter, subunit DctM	COG1593	G	441	547	-106
RCA23_c20380	2185139	2184558	TRAP dicarboxylate transporter, subunit DctQ	COG3090	G	521	546	-25
RCA23_c20390	2186242	2185214	TRAP dicarboxylate transporter, subunit DctP	COG1638	G	328	358	-30
RCA23_c20400	2186550	2187362	putative phytanoyl-CoA dioxygenase	COG5285	Q	167	221	-54
RCA23_c20410	2188449	2187382	putative phenylacetic acid degradation NADH oxidoreducta	COG1018	C	203	273	-70
RCA23_c20420	2188902	2188462	phenylacetate-CoA oxygenase, subunit PaaD	COG2151	R	161	250	-89
RCA23_c20430	2189696	2188944	phenylacetate-CoA oxygenase, subunit PaaC	COG3396	S	230	299	-69
RCA23_c20440	2189986	2189696	phenylacetate-CoA oxygenase, subunit PaaB	COG3460	Q	272	347	-75
RCA23_c20450	2190999	2190007	phenylacetate-CoA oxygenase, subunit PaaA	COG3396	S	292	384	-92
RCA23_c20460	2191871	2191050	phenylacetic acid degradation operon negative regulatory p	COG3327	K	194	338	-144
RCA23_c20470	2193916	2191868	phenylacetic acid degradation protein PaaZ	COG1012	C	200	257	-57
RCA23_c20480	2194006	2194791	putative enoyl-CoA hydratase PaaG	COG1024	I	157	198	-41
RCA23_c20490	2194793	2195233	acyl-coenzyme A thioesterase PaaI	COG2050	Q	207	193	14
RCA23_c20500	2195230	2196432	beta-ketoadipyl CoA thiolase PaaJ	COG0183	I	159	218	-59
RCA23_c20510	2196443	2197726	phenylacetate-CoA ligase PaaK	COG1541	H	258	377	-119
RCA23_c20520	2197730	2198344	putative HTH-type transcriptional regulator, TetR family	COG1309	K	255	313	-58
RCA23_c20530	2198826	2198341	3-dehydroquinate dehydratase AroQ	COG0757	E	480	484	-4
RCA23_c20540	2200260	2198869	tyrosine decarboxylase	COG0076	E	256	302	-46
RCA23_c20550	2200544	2201383	putative short chain dehydrogenase	COG0300	R	180	216	-36
RCA23_c20560	2202389	2201403	hypothetical protein, acetyltransferase-like	COG1247	M	188	325	-137
RCA23_c20570	2202793	2202455	protein CsaA	COG0073	R	280	393	-113
RCA23_c20580	2203601	2202786	pyrroline-5-carboxylate reductase ProC	COG0345	E	179	341	-162
RCA23_c20590	2204138	2203635	hypothetical protein DUF1790	COG5465	S	484	467	17
RCA23_c20600	2204711	2204427	hypothetical protein DUF526	COG2960	S	356	344	12
RCA23_c20610	2204859	2205740	prolipoprotein diacylglyceryl transferase Lgt	COG0682	M	217	274	-57
RCA23_c20620	2205707	2206798	hypothetical protein DUF185	COG1565	S	183	256	-73
RCA23_c20630	2206795	2207550	multi-copper polyphenol oxidoreductase laccase	COG1496	S	267	296	-29
RCA23_c20640	2208728	2207769	hypothetical protein			176	115	61
RCA23_c20650	2209482	2208988	leucine-responsive regulatory protein Lrp	COG1522	K	252	363	-111
RCA23_c20660	2209668	2210609	thioredoxin reductase TrxB	COG0492	O	277	273	4

RCA23_c20670	2210930	2212633	bifunctional sulfate adenylyltransferase / adenylyl-sulfate kir	COG2046	P	237	293	-56
RCA23_c20680	2213026	2212808	hypothetical protein DUF1150			755	497	258
RCA23_c20690	2213444	2213028	small heat shock protein IbpA	COG0071	O	739	516	223
RCA23_c20700	2213600	2213815	hypothetical protein DUF465	COG5481	S	416	481	-65
RCA23_c20710	2213872	2214354	N5-carboxyaminoimidazole ribonucleotide mutase PurE	COG0041	F	324	250	74
RCA23_c20720	2214347	2215408	N5-carboxyaminoimidazole ribonucleotide synthase PurK	COG0026	F	192	252	-60
RCA23_c20730	2216205	2215438	hypothetical protein	COG1075	R	302	371	-69
RCA23_c20740	2217963	2216314	chaperonin GroEL	COG0459	O	1.092	481	611
RCA23_c20750	2218302	2218015	chaperonin GroS	COG0234	O	1.580	549	1.031
RCA23_c20760	2218533	2219483	hypothetical protein			272	228	44
RCA23_c20770	2219687	2220529	hypothetical protein			311	282	29
RCA23_c20780	2220548	2221510	hypothetical protein			256	251	5
RCA23_c20790	2221605	2222753	creatinase	COG0006	E	207	242	-35
RCA23_c20800	2222847	2223821	putative membrane lipoprotein			262	439	-177
RCA23_c20810	2224547	2223837	hypothetical protein DUF261	COG5482	S	192	370	-178
RCA23_c20820	2224600	2225517	putative manganese-dependent inorganic pyrophosphatase	COG1227	C	323	325	-2
RCA23_c20830	2225535	2226407	hypothetical protein, HAD family hydrolase	COG0647	G	261	348	-87
RCA23_c20840	2226492	2226935	putative MaoC-like dehydratase	COG2030	I	300	344	-44
RCA23_c20850	2226997	2227944	riboflavin biosynthesis protein RibF	COG0196	H	281	423	-142
RCA23_c20860	2227941	2228405	hypothetical protein UPF0260	COG2983	S	370	349	21
RCA23_c20870	2228409	2229458	low specificity L-threonine aldolase ItaE	COG2008	E	279	242	37
RCA23_c20880	2230157	2229510	hypothetical protein, 2-hydroxychromene-2-carboxylate isor	COG3917	Q	254	239	15
RCA23_c20890	2230217	2231236	ribose-phosphate pyrophosphokinase Prs	COG0462	F	351	337	14
RCA23_c20900	2231567	2231247	hypothetical protein			339	407	-68
RCA23_c20910	2232095	2231688	ATP synthase epsilon chain AtpC	COG0355	C	217	213	4
RCA23_c20920	2233519	2232095	ATP synthase beta subunit AtpD	COG0055	C	765	423	342
RCA23_c20930	2234405	2233536	ATP synthase gamma chain AtpG	COG0224	C	785	455	330
RCA23_c20940	2235953	2234418	ATP synthase alpha subunit AtpA	COG0056	C	653	400	253
RCA23_c20950	2236520	2235954	ATP synthase delta chain AtpH	COG0712	C	742	430	312
RCA23_c20960	2237506	2236745	hypothetical protein			238	284	-46

RCA23_c20970	2237568	2238365	hydroxyacylglutathione hydrolase GloB	COG0491	R	203	292	-89
RCA23_c20980	2238504	2240834	ATP-dependent Clp protease ATP-binding subunit ClpA	COG0542	O	394	338	56
RCA23_c20990	2243121	2240878	hypothetical protein, OmpA	COG1360	N	305	321	-16
RCA23_c21000	2244303	2243131	hypothetical protein			257	346	-89
RCA23_c21010	2244901	2244371	putative cation transport protein ChaC	COG3703	P	210	316	-106
RCA23_c21020	2245169	2246512	hypothetical protein	COG1357	S	297	248	49
RCA23_c21030	2247465	2246560	protein TyrC	COG0287	E	207	274	-67
RCA23_c21040	2248547	2247462	histidinol-phosphate aminotransferase HisC	COG0079	E	204	333	-129
RCA23_c21050	2249402	2248746	30S ribosomal protein S4	COG0522	J	558	359	199
RCA23_c21060	2251712	2249745	cold-shock DEAD box protein A	COG0513	L	271	328	-57
RCA23_c21070	2252217	2251846	hypothetical protein DUF393	COG3011	S	295	410	-115
RCA23_c21080	2254594	2252333	vitamin B12-dependent ribonucleoside-diphosphate reducta	COG0209	F	354	420	-66
RCA23_c21090	2254754	2255152	hypothetical protein	COG5458	S	170	273	-103
RCA23_c21100	2255830	2255156	ATP-phosphoribosyltransferase HisG	COG0040	E	238	409	-171
RCA23_c21110	2256873	2255827	ATP phosphoribosyltransferase regulatory subunit HisZ	COG3705	E	159	258	-99
RCA23_c21120	2258375	2256870	histidyl-tRNA synthase HisS	COG0124	J	253	369	-116
RCA23_c21130	2258424	2258699	hypothetical protein	COG2900	S	209	308	-99
RCA23_c21140	2262238	2258738	DNA polymerase III 1 alpha subunit DnaE	COG0587	L	327	386	-59
RCA23_c21150	2262629	2263969	xanthine dehydrogenase XdhA	COG4630	F	236	242	-6
RCA23_c21160	2263966	2266269	xanthine dehydrogenase XdhB	COG4631	F	224	287	-63
RCA23_c21170	2266266	2267186	xanthine dehydrogenase accessory protein XdhC	COG1975	O	208	245	-37
RCA23_c21180	2267183	2268688	sugar ABC transporter, ATP-binding protein	COG3845	R	202	224	-22
RCA23_c21190	2268675	2269760	sugar ABC transporter, permease protein	COG4603	R	330	307	23
RCA23_c21200	2269741	2270742	ABC transporter permease protein	COG1079	R	283	408	-125
RCA23_c21210	2270770	2271849	putative basic membrane protein	COG1744	R	455	356	99
RCA23_c21220	2271933	2273012	putative FAD dependent oxidoreductase	COG0665	E	164	201	-37
RCA23_c21230	2275563	2273065	dimethylglycine dehydrogenase	COG0404	E	264	326	-62
RCA23_c21240	2275772	2276626	pantothenate synthase PanC	COG0414	H	240	384	-144
RCA23_c21250	2276623	2277435	3-methyl-2-oxobutanoate hydroxymethyltransferase PanB	COG0413	H	307	438	-131
RCA23_c21260	2277469	2277984	hypothetical protein	COG3807	S	226	318	-92

RCA23_c21270	2280010	2277986	peptidyl-dipeptidase Dcp	COG0339	E	227	267	-40
RCA23_c21280	2281046	2279997	molybdopterin biosynthesis protein MoeB	COG0476	H	211	292	-81
RCA23_c21290	2281504	2281043	deoxyuridine 5'-triphosphate nucleotidohydrolase Dut	COG0756	F	194	283	-89
RCA23_c21300	2282691	2281501	coenzyme A biosynthesis bifunctional protein CoaBC	COG0452	H	292	263	29
RCA23_c21310	2283626	2282748	RNA polymerase sigma-32 factor RpoH	COG0568	K	992	490	502
RCA23_c21320	2283716	2284249	bifunctional adenosylcobalamin biosynthesis protein CobP	COG2087	H	179	216	-37
RCA23_c21330	2284246	2284818	putative phosphoglycerate mutase family protein	COG0406	G	125	238	-113
RCA23_c21340	2284882	2285307	hypothetical protein, glutathione S-transferase	COG0625	O	225	320	-95
RCA23_c21350	2285323	2285757	glutathione S-transferase family protein			215	332	-117
RCA23_c21360	2285829	2286233	magnesium chelatase-like protein	COG0606	O	225	250	-25
RCA23_c21370	2286230	2287420	magnesium chelatase	COG0606	O	163	269	-106
RCA23_c21380	2288109	2287342	putative transmembrane protein			338	385	-47
RCA23_c21390	2289026	2288109	putative sulfite exporter TauE/SafE	COG0730	R	370	455	-85
RCA23_c21400	2290274	2289135	branched-chain amino acid transporter, permease compone	COG1079	R	267	471	-204
RCA23_c21410	2291340	2290279	branched-chain amino acid transporter, permease compone	COG4603	R	290	336	-46
RCA23_c21420	2292916	2291381	ABC transporter ATP-binding protein	COG3845	R	317	388	-71
RCA23_c21430	2293990	2292992	putative ABC transporter, periplasmic substrate-binding pro	COG1744	R	354	382	-28
RCA23_c21440	2294587	2294177	hypothetical protein, acetyltransferase-like	COG0456	R	209	279	-70
RCA23_c21450	2295161	2294598	NifU-like protein	COG0694	O	409	435	-26
RCA23_c21460	2295762	2295250	putative universal stress protein	COG0589	T	518	514	4
RCA23_c21470	2296878	2295862	tryptophanyl-tRNA synthase TrpS	COG0180	J	372	400	-28
RCA23_c21480	2296952	2297626	hypothetical protein, rhomboid protease	COG0705	R	167	212	-45
RCA23_c21490	2299173	2297638	virulence factor MviN homolg	COG0728	R	237	404	-167
RCA23_c21500	2301938	2299170	uridylyltransferase GlnD	COG2844	O	288	413	-125
RCA23_c21510	2303131	2301941	hypothetical protein	COG0683	E	173	274	-101
RCA23_c21520	2303164	2304075	putative tetrapyrrole methylase	COG0313	R	201	203	-2
RCA23_c21530	2304080	2304448	hypothetical protein UPF0102	COG0792	L	245	322	-77
RCA23_c21540	2304547	2305485	glutathione synthase GshB	COG0189	H	319	394	-75
RCA23_c21550	2306330	2305503	putative esterase/lipase	COG0657	I	327	376	-49
RCA23_c21560	2306806	2306327	NusB-like protein NusB	COG0781	K	272	421	-149

RCA23_c21570	2307324	2306803	6,7-dimethyl-8-ribityllumazine synthase RibH	COG0054	H	240	301	-61
RCA23_c21580	2308460	2307324	riboflavin biosynthesis protein RibB	COG0108	H	374	499	-125
RCA23_c21590	2309051	2308464	riboflavin synthase alpha chain RibE	COG0307	H	371	609	-238
RCA23_c21600	2309210	2310511	putative capsule polysaccharide export protein	COG3562	M	318	279	39
RCA23_c21610	2310600	2311748	putative polysaccharide export protein	COG1596	M	203	186	17
RCA23_c21620	2311750	2313762	putative capsule polysaccharide export protein	COG3563	M	150	241	-91
RCA23_c21630	2314853	2313759	riboflavin biosynthesis protein RibD	COG0117	H	190	222	-32
RCA23_c21640	2315317	2314850	transcriptional repressor NrdR	COG1327	K	348	414	-66
RCA23_c21650	2317485	2315515	RNA polymerase sigma factor RpoD	COG0568	K	608	437	171
RCA23_c21660	2319548	2317602	DNA primase DnaG	COG0358	L	355	423	-68
RCA23_c21670	2320108	2319557	sarcosine oxidase subunit SoxG	COG4583	E	231	384	-153
RCA23_c21680	2323031	2320101	sarcosine oxidase alpha subunit SoxA	COG0404	E	196	307	-111
RCA23_c21690	2323270	2323034	sarcosine oxidase subunit SoxD	COG4311	E	308	398	-90
RCA23_c21700	2324611	2323358	sarcosine oxidase beta subunit SoxB	COG0665	E	245	350	-105
RCA23_c21710	2325416	2324724	phosphatidylserine decarboxylase proenzyme Psd	COG0688	I	550	425	125
RCA23_c21720	2325810	2325421	diacylglycerol kinase	COG0818	M	881	641	240
RCA23_c21730	2327399	2325807	putative sulfatase	COG2194	R	919	638	281
RCA23_c21740	2328122	2327421	hypothetical protein, CDP-alcohol phosphatidyltransferase-l	COG1183	I	809	632	177
RCA23_c21750	2328718	2328254	hypothetical protein	COG0671	I	526	430	96
RCA23_c21760	2329421	2328897	hypothetical protein	COG2194	R	558	446	112
RCA23_c21770	2330356	2329541	hypothetical protein, DUF1705	COG2194	R	624	467	157
RCA23_c21780	2331919	2330483	glutamate dehydrogenase GluD	COG0334	E	314	332	-18
RCA23_c21790	2332495	2331998	hypothetical protein			258	365	-107
RCA23_c21800	2333529	2332585	2-hydroxy-3-oxopropionate reductase GarR	COG2084	I	329	359	-30
RCA23_c21810	2333544	2334782	reductive dehalogenase	COG1600	C	264	315	-51
RCA23_c21820	2334839	2335750	pirin	COG1741	R	430	440	-10
RCA23_c21830	2336333	2335734	transcriptional regulator	COG1309	K	274	419	-145
RCA23_c21840	2336413	2336667	hypothetical protein			261	359	-98
RCA23_c21850	2336787	2338076	homoserine dehydrogenase Hom	COG0460	E	298	326	-28
RCA23_c21860	2338209	2339174	fructose-1,6-bisphosphatase class II	COG1494	G	221	267	-46

RCA23_c21870	2339176	2340912	putative single-stranded-DNA-specific exonuclease	COG0608	L	211	311	-100
RCA23_c21890	2341884	2341321	sulfopyruvate decarboxylase beta subunit ComE	COG0028	E	560	522	38
RCA23_c21900	2342362	2341886	sulfopyruvate decarboxylase alpha subunit ComD	COG4032	R	797	611	186
RCA23_c21910	2343377	2342394	zinc-type alcohol dehydrogenase	COG1063	E	316	480	-164
RCA23_c21920	2344144	2343386	gluconate 5-dehydrogenase Gno	COG1028	I	200	301	-101
RCA23_c21930	2345464	2344148	histidinol dehydrogenase HisD	COG0141	E	306	379	-73
RCA23_c21940	2345518	2346576	HTH-type transcriptional regulator, LacI family	COG1609	K	291	268	23
RCA23_c21950	2347369	2346614	HTH-type transcriptional regulator, IclR family	COG1414	K	263	354	-91
RCA23_c21960	2347514	2349115	alcohol dehydrogenase AlkJ	COG2303	E	278	286	-8
RCA23_c21970	2349149	2349817	integral membrane protein TerC	COG0861	P	322	278	44
RCA23_c21980	2349936	2351048	putative TRAP transporter, DctP subunit	COG4663	Q	464	312	152
RCA23_c21990	2351168	2353642	TRAP transporter, DctM/DctQ subunit	COG4664	Q	296	253	43
RCA23_c22000	2355428	2353818	trimethylamine methyltransferase	COG5598	H	411	403	8
RCA23_c22010	2356156	2355458	putative HAD-family hydrolase	COG0546	R	278	354	-76
RCA23_c22020	2356437	2356156	hypothetical protein			306	534	-228
RCA23_c22030	2356766	2356512	hypothetical protein			187	301	-114
RCA23_c22040	2357079	2356789	hypothetical protein			143	183	-40
RCA23_c22050	2357261	2357656	hypothetical protein	COG5349	S	172	246	-74
RCA23_c22060	2357741	2358352	hypothetical protein, NUDIX hydrolase	COG0494	L	185	264	-79
RCA23_c22070	2359231	2358332	hypothetical protein			240	315	-75
RCA23_c22080	2360146	2359235	putative fatty acid desaturase	COG3239	I	238	271	-33
RCA23_c22090	2360233	2361102	putative helix-turn-helix protein	COG1396	K	271	380	-109
RCA23_c22100	2361854	2361099	short chain dehydrogenase	COG1028	I	199	337	-138
RCA23_c22110	2363320	2361851	putative 3-hydroxyacyl-CoA dehydrogenase	COG1250	I	222	316	-94
RCA23_c22130	2364364	2363357	hypothetical protein, DUF849	COG3246	S	198	375	-177
RCA23_c22120	2364345	2365316	transcriptional regulator, AraC family	COG4977	K	181	300	-119
RCA23_c22140	2366365	2365322	protein Tas	COG0667	C	249	289	-40
RCA23_c22150	2366465	2367088	hypothetical protein	COG4544	S	139	266	-127
RCA23_c22160	2367182	2368417	putative MFS-type transporter	COG2211	G	250	323	-73
RCA23_c22170	2368475	2370187	methionyl-tRNA synthase MetG	COG0143	J	246	334	-88

RCA23_c22190	2370689	2372218	integrase			GI 8	337	236	101
RCA23_c22200	2372685	2372215	integrase	COG4974	L	GI 8	417	345	72
RCA23_c22210	2373139	2373477	putative nucleotidyl transferase	COG1210	M	GI 8	343	199	144
RCA23_c22220	2375142	2374411	hypothetical protein			GI 8	371	226	145
RCA23_c22230	2375873	2375142	hypothetical protein			GI 8	424	250	174
RCA23_c22240	2376433	2375873	putative replication factor C, small subunit	COG2256	L	GI 8	578	315	263
RCA23_c22250	2377432	2376614	hypothetical protein			GI 8	378	220	158
RCA23_c22260	2377643	2378410	hypothetical protein			GI 8	363	260	103
RCA23_c22270	2380540	2379620	ParB-like nuclease	COG1475	K	GI 8	484	357	127
RCA23_c22280	2380679	2383024	cadmium-transporting ATPase CadA	COG2217	P	GI 8	160	160	0
RCA23_c22290	2383190	2383600	hypothetical protein	COG3034	S	GI 8	193	223	-30
RCA23_c22300	2384025	2383591	putative lipoprotein signal peptidase	COG0597	M	GI 8	324	287	37
RCA23_c22310	2384826	2384065	putative ZIP zinc transporter	COG0428	P	GI 8	206	270	-64
RCA23_c22320	2385290	2384874	hypothetical protein DUF411	COG3019	R	GI 8	365	300	65
RCA23_c22330	2385943	2385320	SCO-like protein	COG1999	R	GI 8	251	222	29
RCA23_c22340	2386320	2385943	hypothetical protein	COG2847	S	GI 8	208	146	62
RCA23_c22350	2387089	2386430	hypothetical protein	COG1651	O	GI 8	162	177	-15
RCA23_c22360	2387511	2387086	hypothetical protein, disulfide bond formation protein	COG1495	O	GI 8	213	286	-73
RCA23_c22370	2388080	2387508	SCO-like protein	COG1999	R	GI 8	225	229	-4
RCA23_c22380	2388277	2388705	putative HTH-type transcriptional regulator	COG0789	K	GI 8	204	271	-67
RCA23_c22390	2388708	2389034	hypothetical protein UPF0060	COG1742	S	GI 8	176	169	7
RCA23_c22400	2389105	2389329	hypothetical protein			GI 8	272	193	79
RCA23_c22410	2390264	2389434	hypothetical protein			GI 8	84	88	-4
RCA23_c22420	2392406	2391699	transposase	COG3316	L	GI 8	2	3	-1
RCA23_c22430	2393515	2392478	MORN motif precursor	COG4642	S	GI 8	283	186	97
RCA23_c22440	2394592	2393885	transposase	COG3316	L	GI 8	8	0	8
RCA23_c22450	2394953	2394711	hypothetical protein			GI 8	13	0	13
RCA23_c22460	2395528	2395211	hypothetical protein			GI 8	2.261	1.424	837
RCA23_c22470	2396464	2395883	hypothetical protein	COG3295	S	GI 8	42	18	24
RCA23_c22480	2397201	2396467	hypothetical protein			GI 8	64	18	46

RCA23_c22490	2397865	2397518	hypothetical protein			GI 8	0	0	0
RCA23_c22500	2398105	2398617	transcriptional regulator, LuxR family	COG2197	T	GI 8	24	14	10
RCA23_c22510	2399503	2398796	hypothetical protein	COG3316	L	GI 8	5	1	4
RCA23_c22520	2401019	2399598	hypothetical protein, HTH-type transcriptional regulator, Lux	COG5616	S	GI 8	40	75	-35
RCA23_c22530	2401309	2402388	cysteine synthase CysK	COG0031	E	GI 8	64	75	-11
RCA23_c22540	2402668	2402847	hypothetical protein			GI 8	137	182	-45
RCA23_c22550	2402904	2403158	hypothetical protein			GI 8	135	123	12
RCA23_c22560	2403266	2403550	hypothetical protein			GI 8	150	154	-4
RCA23_c22570	2403731	2404039	hypothetical protein			GI 8	67	62	5
RCA23_c22580	2404165	2404464	hypothetical protein	COG5470	S	GI 8	91	36	55
RCA23_c22590	2404900	2406312	coniferyl aldehyde dehydrogenase CalB	COG1012	C	GI 8	349	196	153
RCA23_c22600	2407339	2406443	regulatory protein NocR	COG0583	K	GI 8	256	176	80
RCA23_c22610	2407478	2408791	sn-glycerol-3-phosphate-binding periplasmic protein UgpB	COG1653	G	GI 8	431	258	173
RCA23_c22620	2408867	2409748	sn-glycerol-3-phosphate transport system permease protei	COG1175	G	GI 8	568	361	207
RCA23_c22630	2409790	2410626	sn-glycerol-3-phosphate transport system permease protei	COG0395	G	GI 8	590	318	272
RCA23_c22640	2410634	2411680	sn-glycerol-3-phosphate import ATP-bindingprotein UgpC	COG3839	G	GI 8	527	263	264
RCA23_c22650	2411680	2412570	putative glycerophosphoryl diester phosphodiesterase	COG0584	C	GI 8	368	259	109
RCA23_c22660	2414704	2413001	aerobic glycerol-3-phosphate dehydrogenase GlpD	COG0578	C	GI 8	212	146	66
RCA23_c22670	2416422	2414794	hypothetical protein, Na+/Pi-cotransporter	COG1283	P	GI 8	144	136	8
RCA23_c22680	2417269	2416478	hypothetical protein, calcineurin-like phosphoesterase-like	COG1409	R	GI 8	166	115	51
RCA23_c22690	2418075	2417266	ABC transporter permease protein	COG0395	G	GI 8	173	119	54
RCA23_c22700	2418965	2418072	ABC transporter permease protein	COG1175	G	GI 8	166	109	57
RCA23_c22710	2420318	2419050	ABC transporter extracellular solute-binding protein	COG1653	G	GI 8	305	157	148
RCA23_c22720	2421380	2420382	ABC transporter ATP-binding protein	COG3839	G	GI 8	233	135	98
RCA23_c22730	2422258	2421398	HTH-type transcriptional regulator, DeoR family	COG1349	K	GI 8	194	176	18
RCA23_c22740	2422599	2423399	HAD-superfamily hydrolase, subfamily IIB	COG0561	R	GI 8	192	150	42
RCA23_c22750	2423921	2424865	putative inner membrane transporter	COG0697	G	GI 8	285	181	104
RCA23_c22760	2424987	2426117	soluble aldose sugar dehydrogenase YliI	COG2133	G	GI 8	223	155	68
RCA23_c22770	2426301	2427080	putative FKBP-type peptidyl-prolyl cis-trans isomerase	COG0545	O	GI 8	37	48	-11
RCA23_c22780	2427117	2427665	putative NnrU family protein	COG4094	S	GI 8	65	34	31

RCA23_c22790	2428870	2429508	hypothetical protein			GI 8	23	19	4
RCA23_c22800	2429684	2430973	putative adenine methyltransferase	COG0863	L	GI 8	71	54	17
RCA23_c22810	2430970	2431335	hypothetical protein			GI 8	33	23	10
RCA23_c22820	2431343	2432776	phage uncharacterised protein	COG5410	S	GI 8	38	24	14
RCA23_c22830	2433238	2434899	hypothetical protein, resolvase-like	COG1961	L	GI 8	34	19	15
RCA23_c22840	2435361	2436626	putative prophage integrase	COG0582	L	GI 8	0	3	-3
RCA23_c22850	2436623	2437081	hypothetical protein, putative phage-like protein			GI 8	0	0	0
RCA23_c22860	2437153	2437380	hypothetical protein	COG3311	K	GI 8	15	3	12
RCA23_c22870	2437482	2437922	hypothetical protein			GI 8	3	3	0
RCA23_c22880	2438000	2439085	hypothetical protein			GI 8	85	61	24
RCA23_c22890	2439085	2440413	DNA polymerase III	COG5545	R	GI 8	168	114	54
RCA23_c22900	2440954	2441754	hypothetical protein, periplasmic binding protein-like	COG2998	H	GI 8	14	7	7
RCA23_c22910	2441772	2441930	hypothetical protein			GI 8	126	134	-8
RCA23_c22920	2442714	2442007	transposase	COG3316	L	GI 8	1	0	1
RCA23_c22930	2444420	2443158	molybdopterin biosynthesis protein MoeA	COG0303	H	GI 8	53	66	-13
RCA23_c22940	2444914	2444417	molybdopterin-guanine dinucleotide biosynthesis protein Mc	COG1763	H	GI 8	82	88	-6
RCA23_c22950	2445231	2444911	hypothetical protein, MobA-like	COG0746	H	GI 8	207	166	41
RCA23_c22960	2446280	2445228	formate dehydrogenase family accessory protein FdhD	COG1526	C	GI 8	171	128	43
RCA23_c22970	2447181	2446738	molybdopterin-converting factor subunit MoaE	COG0314	H	GI 8	65	59	6
RCA23_c22980	2447430	2447185	molybdopterin-converting factor subunit MoaD	COG1977	H	GI 8	163	66	97
RCA23_c22990	2448117	2447674	transposase	COG3328	L	GI 8	158	124	34
RCA23_c23000	2449773	2448766	molybdenum cofactor biosynthesis protein MoaA	COG2896	H	GI 8	105	125	-20
RCA23_c23010	2450390	2450662	transposase			GI 8	163	189	-26
RCA23_c23020	2451451	2450738	ABC transporter, ATP-binding cassette protein	COG3839	G	GI 8	113	81	32
RCA23_c23030	2452152	2451448	ABC transporter, permease protein	COG4662	H	GI 8	107	61	46
RCA23_c23040	2453771	2452395	formate dehydrogenase, gamma subunit FdhI	COG2864	C	GI 8	213	101	112
RCA23_c23050	2454447	2453854	formate dehydrogenase, iron-sulfur subunit FdhB	COG0437	C	GI 8	155	92	63
RCA23_c23060	2457355	2454461	formate dehydrogenase alpha subunit FdhA	COG0243	C	GI 8	116	75	41
RCA23_c23070	2457663	2457472	putative twin-arginine translocation pathway signal sequence domain			GI 8	62	49	13
RCA23_c23080	2458323	2457718	hypothetical protein, cytoplasmic chaperon TorD	COG3381	R	GI 8	126	84	42

RCA23_c23090	2458949	2458320	hypothetical protein			GI 8	196	135	61
RCA23_c23100	2459476	2458946	putative molybdopterin-guanine dinucleotide biosynthesis protein A			GI 8	117	86	31
RCA23_c23110	2459807	2461798	hypothetical protein, 4Fe-4S ferredoxin-like	COG1148	C	GI 8	51	69	-18
RCA23_c23120	2462517	2461792	hypothetical protein			GI 8	81	65	16
RCA23_c23130	2462613	2462804	hypothetical protein			GI 8	89	131	-42
RCA23_c23140	2462805	2463860	hypothetical protein, Mrp/NBP35 family protein	COG0489	D	GI 8	86	65	21
RCA23_c23150	2463857	2464570	hypothetical protein	COG0340	H	GI 8	67	78	-11
RCA23_c23160	2464572	2465081	hypothetical protein			GI 8	92	92	0
RCA23_c23170	2466057	2465644	putative phage terminase			GI 8	15	22	-7
RCA23_c23180	2467057	2466350	transposase	COG3316	L	GI 8	1	1	0
RCA23_c23190	2467131	2467988	putative phage helicase	COG3378	R	GI 8	70	48	22
RCA23_c23200	2468581	2468237	hypothetical protein			GI 8	73	97	-24
RCA23_c23210	2468997	2470031	putative pyridoxal 4-dehydrogenase	COG0667	C	GI 8	57	17	40
RCA23_c23220	2470845	2470078	2-dehydro-3-deoxy-D-gluconate 5-dehydrogenase KduD	COG1028	I	GI 8	75	17	58
RCA23_c23230	2471994	2470855	putative L-rhamnonate dehydratase rhamD	COG4948	M	GI 8	64	17	47
RCA23_c23240	2472826	2471987	ureidoglycolate lyase	COG0179	Q	GI 8	90	30	60
RCA23_c23250	2473812	2472823	D-3-phosphoglycerate dehydrogenase	COG1052	C	GI 8	68	18	50
RCA23_c23260	2474558	2473809	uncharacterized oxidoreductase	COG1028	I	GI 8	35	19	16
RCA23_c23270	2474872	2474555	putative rhamnose mutarotase RhaM	COG3254	S	GI 8	51	30	21
RCA23_c23280	2475636	2474872	putative acetoacetate decarboxylase Adc	COG4689	Q	GI 8	88	30	58
RCA23_c23290	2476659	2475637	uncharacterized oxidoreductase	COG0673	R	GI 8	77	19	58
RCA23_c23300	2477416	2476673	transcriptional regulator, GntR family	COG2186	K	GI 8	81	23	58
RCA23_c23310	2478408	2477413	putative ribose ABC transport system, permease protein Rb	COG1172	G	GI 8	111	41	70
RCA23_c23320	2479472	2478405	putative ribose ABC transport system, permease protein Rb	COG1172	G	GI 8	87	30	57
RCA23_c23330	2480980	2479472	ribose import ABC transporter, ATP-binding protein RbsA	COG1129	G	GI 8	68	26	42
RCA23_c23340	2482093	2481056	putative rhamnose ABC transport system, substrate-binding	COG1879	G	GI 8	47	36	11
RCA23_c23350	2482310	2483446	galactonate dehydratase	COG4948	M	GI 8	46	19	27
RCA23_c23360	2483461	2484276	xylose isomerase-like	COG1082	G	GI 8	66	19	47
RCA23_c23370	2484419	2484691	putative aldo/keto reductase	COG0667	C	GI 8	56	23	33
RCA23_c23380	2484851	2485741	amidohydrolase	COG3618	R	GI 8	75	36	39

RCA23_c23390	2486071	2486280	hypothetical protein			GI 8	58	21	37
RCA23_c23400	2487635	2486928	transposase	COG3316	L	GI 8	31	25	6
RCA23_c23410	2488060	2487743	L-rhamnose mutarotase RhaM	COG3254	S	GI 8	80	22	58
RCA23_c23420	2489347	2488439	ureidoglycolate lyase	COG0179	Q	GI 8	23	20	3
RCA23_c23430	2490360	2489458	dihydrodipicolinate synthase DapA	COG0329	E	GI 8	43	31	12
RCA23_c23440	2491404	2490508	amidohydrolase	COG3618	R	GI 8	67	20	47
RCA23_c23450	2492228	2491446	3-ketoacyl-(acyl-carrier-protein) reductase FabG	COG1028	I	GI 8	85	52	33
RCA23_c23460	2493559	2492393	L-rhamnonate dehydratase RhmD	COG4948	M	GI 8	28	27	1
RCA23_c23470	2494711	2493587	polyamine ABC transporter, ATP-binding protein PotA	COG3842	E	GI 8	14	8	6
RCA23_c23480	2495571	2494786	polyamine ABC transporter, permease protein	COG1177	E	GI 8	22	19	3
RCA23_c23490	2496561	2495575	polyamine ABC transporter, permease protein	COG1176	E	GI 8	21	7	14
RCA23_c23500	2497743	2496676	polyamine ABC transporter, substrate binding protein	COG0687	E	GI 8	13	9	4
RCA23_c23510	2498385	2498131	hypothetical protein			GI 8	21	11	10
RCA23_c23520	2498724	2498401	hypothetical protein			GI 8	12	4	8
RCA23_c23530	2499506	2498760	uncharacterized oxidoreductase	COG1028	I	GI 8	31	16	15
RCA23_c23540	2500818	2499526	L-rhamnonate dehydratase	COG4948	M	GI 8	25	20	5
RCA23_c23550	2501838	2500861	ribose ABC transport system, permease protein RbsC	COG1172	G	GI 8	5	21	-16
RCA23_c23560	2502656	2501835	ribose import ABC transporter, ATP-binding protein RbsA	COG1129	G	GI 8	17	16	1
RCA23_c23570	2503752	2502640	ribose import ABC transporter, substrate binding protein Rb	COG1879	G	GI 8	14	13	1
RCA23_c23580	2503924	2504961	HTH-type transcriptional regulator, GntR family	COG1609	K	GI 8	18	19	-1
RCA23_c23590	2505104	2505304	hypothetical protein	COG3311	K	GI 8	39	9	30
RCA23_c23600	2506163	2506816	putative DNA-binding protein	COG1396	K	GI 8	29	12	17
RCA23_c23610	2507367	2508263	glutamine amidotransferase-like protein GlxB	COG0067	E	GI 8	41	12	29
RCA23_c23620	2508265	2508942	glutamate synthase alpha subunit GlxC	COG0070	E	GI 8	20	3	17
RCA23_c23630	2508954	2510294	glutamate synthase large subunit GlxD	COG0069	E	GI 8	18	6	12
RCA23_c23640	2510364	2511698	glutamine synthase GlnA type III	COG0174	E	GI 8	17	8	9
RCA23_c23650	2512409	2513053	hypothetical protein			GI 8	48	23	25
RCA23_c23660	2513221	2514510	methyltrasnferase	COG0863	L	GI 8	66	37	29
RCA23_c23670	2514507	2514890	hypothetical protein			GI 8	38	17	21
RCA23_c23680	2514880	2516313	putative terminase, large subunit	COG5410	S	GI 8	31	15	16

RCA23_c23690	2516395	2516823	hypothetical protein, DUF2924			GI 8	42	22	20
RCA23_c23700	2516820	2518436	hypothetical protein, resolvase-like	COG1961	L	GI 8	19	21	-2
RCA23_c23720	2520249	2518873	signal transduction histidine kinase	COG0642	T		324	351	-27
RCA23_c23730	2521684	2520269	mercuric reductase MerA	COG1249	C		253	349	-96
RCA23_c23740	2522418	2521687	hypothetical protein	COG0398	S		532	524	8
RCA23_c23750	2522803	2523192	putative ribonuclease P	COG0594	J		226	280	-54
RCA23_c23760	2523189	2523428	hypothetical protein DUF37	COG0759	S		269	308	-39
RCA23_c23770	2523749	2523964	hypothetical protein				216	397	-181
RCA23_c23780	2524020	2524874	tRNA 2-thiocytidine biosynthesis protein TtcA	COG0037	D		246	264	-18
RCA23_c23790	2524928	2525959	putative diguanylate phosphodiesterase	COG2200	T		373	385	-12
RCA23_c23800	2526067	2527851	inner membrane protein OxaA	COG0706	U		371	367	4
RCA23_c23810	2527853	2528602	hypothetical protein, molybdenum cofactor sulfurase	COG3217	R		301	323	-22
RCA23_c23820	2528599	2529249	putative GTP-binding protein EngB	COG0218	R		261	317	-56
RCA23_c23830	2529343	2530209	acetylglutamate kinase ArgB	COG0548	E		288	298	-10
RCA23_c23840	2530224	2531015	putative fatty acid hydroxylase	COG3000	I		407	521	-114
RCA23_c23850	2531012	2531632	hypothetical protein	COG1148	C		236	288	-52
RCA23_c23860	2531644	2532126	hypothetical protein, phosphogylcerate mutase	COG2062	T		239	338	-99
RCA23_c23870	2532914	2532150	glutamate/glutamine/aspartate/asparagine transport ATP-bi	COG1126	E		530	458	72
RCA23_c23880	2534220	2532928	glutamate/glutamine/aspartate/asparagine transport system	COG0765	E		785	600	185
RCA23_c23890	2535391	2534222	glutamate/glutamine/aspartate/asparagine transport system	COG4597	E		312	250	62
RCA23_c23900	2536594	2535548	glutamate/glutamine/aspartate/asparagine-binding protein E	COG0834	E		743	471	272
RCA23_c23910	2537482	2536778	ATP chaperone protein	COG5387	O		326	440	-114
RCA23_c23920	2538147	2537479	putative phosphoglycerate phosphatase	COG0546	R		309	416	-107
RCA23_c23930	2539190	2538144	ribosomal large subunit pseudouridine synthase C	COG0564	J		228	289	-61
RCA23_c23940	2539558	2539181	putative ccrb-like protein	COG0239	D		321	383	-62
RCA23_c23950	2540903	2539590	replication-associated recombination protein A	COG2256	L		230	384	-154
RCA23_c23960	2541581	2540970	HTH-type transcriptional regulator, LuxR family	COG2197	T		227	315	-88
RCA23_c23970	2542163	2541810	50S ribosomal protein L17	COG0203	J		383	328	55
RCA23_c23980	2543490	2542336	DNA-directed RNA polymerase alpha subunit RpoA	COG0202	K		941	507	434
RCA23_c23990	2543849	2543460	30S ribosomal protein S11	COG0100	J		1.196	675	521

RCA23_c24000	2544228	2543860	30S ribosomal protein S13	COG0099	J	1.607	755	852
RCA23_c24010	2545048	2544407	adenylate kinase Adk	COG0563	F	470	419	51
RCA23_c24020	2546403	2545045	preprotein translocase subunit SecY	COG0201	U	515	462	53
RCA23_c24030	2546975	2546508	50S ribosomal protein L15	COG0200	J	648	387	261
RCA23_c24040	2547397	2547209	50S ribosomal protein L30	COG1841	J	495	458	37
RCA23_c24050	2548008	2547409	30S ribosomal protein S5	COG0098	J	562	385	177
RCA23_c24060	2548445	2548086	50S ribosomal protein L18	COG0256	J	613	407	206
RCA23_c24070	2548990	2548457	50S ribosomal protein L6	COG0097	J	960	459	501
RCA23_c24080	2549392	2549000	30S ribosomal protein S8	COG0096	J	851	363	488
RCA23_c24090	2549710	2549405	30S ribosomal protein S14	COG0199	J	1.103	430	673
RCA23_c24100	2550282	2549722	50S ribosomal protein L5	COG0094	J	1.295	531	764
RCA23_c24110	2550587	2550282	50S ribosomal protein L24	COG0198	J	1.045	441	604
RCA23_c24120	2550957	2550589	50S ribosomal protein L14	COG0093	J	1.214	626	588
RCA23_c24130	2551255	2551025	30S ribosomal protein S17	COG0186	J	1.128	542	586
RCA23_c24140	2551467	2551261	50S ribosomal protein L29	COG0255	J	919	575	344
RCA23_c24150	2551692	2552312	hypothetical protein			491	514	-23
RCA23_c24160	2552703	2552407	50S ribosomal protein L23	COG0089	J	913	531	382
RCA23_c24170	2553317	2552700	50S ribosomal protein L4	COG0088	J	843	572	271
RCA23_c24180	2554045	2553314	50S ribosomal protein L3	COG0087	J	919	565	354
RCA23_c24190	2554368	2554060	30S ribosomal protein S10	COG0051	J	561	460	101
RCA23_c24200	2555649	2554474	elongation factor Tu (EF-Tu)	COG0050	J	41	15	26
RCA23_c24210	2557851	2555734	elongation factor FusA	COG0480	J	997	541	456
RCA23_c24220	2558343	2557873	30S ribosomal protein S7	COG0049	J	558	374	184
RCA23_c24230	2558583	2558356	30S ribosomal protein S12	COG0048	J	966	883	83
RCA23_c24240	2559706	2559092	hypothetical protein	COG1072	H	197	222	-25
RCA23_c24250	2560443	2559703	ABC transporter ATP-binding protein	COG1129	G	377	332	45
RCA23_c24260	2561552	2560479	ABC tansporter permease protein	COG1172	G	316	328	-12
RCA23_c24270	2562676	2561672	putative ABC transporter periplasmic binding protein	COG1879	G	376	304	72
RCA23_c24280	2562858	2564048	putative transcriptional repressor	COG1940	K	257	274	-17
RCA23_c24290	2564800	2564060	hypothetical protein, acyl-CoA thioesterase-like	COG2755	E	330	432	-102

RCA23_c24300	2564921	2565451	ABC transporter ATP-binding protein	COG1136	V		271	378	-107
RCA23_c24310	2565448	2567970	putative ABC transporter permease protein	COG3127	Q		212	276	-64
RCA23_c24320	2568328	2569251	hypothetical protein, gylcosyl transferase family 2	COG0463	M		218	237	-19
RCA23_c24330	2570639	2569266	aminotransferase class-III	COG0161	H		358	316	42
RCA23_c24340	2571879	2570683	putative ectoine utilization protein EutD	COG0006	E		406	426	-20
RCA23_c24350	2572018	2572968	putative integral membrane proein DUF6				260	386	-126
RCA23_c24360	2573067	2574635	4-coumarate--CoA ligase	COG0318	I		229	302	-73
RCA23_c24370	2575672	2574737	hypothetical protein	COG0679	R		315	415	-100
RCA23_c24380	2576572	2575760	hypothetical protein DUF125	COG1814	S		191	301	-110
RCA23_c24390	2577015	2576587	transcriptional regulator, AsnC family	COG1522	K		269	276	-7
RCA23_c24400	2577133	2578062	arginase ArcA	COG0010	E		294	304	-10
RCA23_c24410	2578064	2579122	ornithine cyclodeaminase ArcB	COG2423	E		294	233	61
RCA23_c24420	2579119	2582481	bifunctional protein PutA	COG4230	C		254	302	-48
RCA23_c24430	2583144	2582581	hypothetical protein				459	415	44
RCA23_c24440	2583406	2583128	hypothetical protein				349	222	127
RCA23_c24460	2583863	2583615	hypothetical protein				249	201	48
RCA23_c24450	2583834	2585051	creatinase	COG0006	E		209	197	12
RCA23_c24470	2585998	2585276	putative hydrolase	COG0596	R		44	43	1
RCA23_c24480	2587548	2585995	glycine betaine/L-proline transport system permease protei	COG4176	E		108	62	46
RCA23_c24490	2588600	2587545	glycine betaine/L-proline transport ATP-binding protein Pro	COG4175	E		112	59	53
RCA23_c24500	2589635	2588670	glycine betaine-binding periplasmic protein ProX	COG2113	E		102	46	56
RCA23_c24510	2589879	2590763	putative HTH-type transcriptional regluator, LysR family	COG0583	K		244	166	78
RCA23_c24520	2591855	2590770	D-cysteine desulfhydrase DcyD	COG2515	E		285	248	37
RCA23_c24530	2591995	2592351	hypothetical protein				794	435	359
RCA23_c24540	2593298	2592375	high-affinity zinc uptake system protein ZnuA	COG4531	P		270	294	-24
RCA23_c24550	2593355	2593870	zinc uptake regulator	COG0735	P		213	353	-140
RCA23_c24560	2593867	2594616	zinc import ATP-binding protein ZnuC	COG1121	P		361	352	9
RCA23_c24570	2594616	2595410	high-affinity zinc uptake system membrane protein ZnuB	COG1108	P		234	351	-117
RCA23_c24580	2595534	2597435	4-hydroxyphenylpyruvate dioxygenase Hpd	COG3185	E		358	304	54
RCA23_c24590	2598436	2598104	hypothetical protein			GI 9	626	538	88

RCA23_c24600	2598748	2598503	hypothetical protein			GI 9	0	3	-3
RCA23_c24610	2599041	2599844	hypothetical protein	COG1028	I	GI 9	169	138	31
RCA23_c24620	2599863	2600606	hypothetical protein	COG1402	R	GI 9	102	95	7
RCA23_c24630	2601568	2600642	putative gluconolactonase	COG3386	G	GI 9	198	166	32
RCA23_c24640	2602967	2602047	ribokinase RbsK	COG0524	G	GI 9	266	185	81
RCA23_c24650	2603416	2602964	ribose ABC transporter protein RbsD	COG4154	G	GI 9	233	166	67
RCA23_c24660	2604556	2603489	putative ribose ABC transporter, ATP-binding protein RbsA	COG3839	G	GI 9	298	217	81
RCA23_c24670	2604859	2606439	putative ribose ABC transporter, substrate binding protein R	COG1653	G	GI 9	236	184	52
RCA23_c24680	2606509	2607615	putative ribose ABC transporter, permease protein RbsC	COG1175	G	GI 9	314	141	173
RCA23_c24690	2607617	2608534	putative ribose ABC transporter, permease protein RbsC	COG0395	G	GI 9	231	152	79
RCA23_c24700	2610024	2608537	hypothetical protein, L-fucose isomerase-like			GI 9	155	137	18
RCA23_c24710	2610626	2610162	sugar isomerase	COG0794	M	GI 9	162	121	41
RCA23_c24720	2612206	2610716	xylulose kinase XylB	COG1070	G	GI 9	199	157	42
RCA23_c24730	2613273	2612203	aminopeptidase SgcX	COG1363	G	GI 9	223	193	30
RCA23_c24740	2614073	2613270	photosystem I biogenesis protein BtpA	COG0434	R	GI 9	253	182	71
RCA23_c24750	2614166	2615188	pyridoxal 4-dehydrogenase Pld	COG0667	C	GI 9	294	224	70
RCA23_c24760	2615185	2616021	putative amidohydrolase	COG3618	R	GI 9	205	195	10
RCA23_c24770	2616791	2616009	putative carbohydrate kinase, pfkB family	COG0524	G	GI 9	131	162	-31
RCA23_c24780	2617753	2616854	xylose isomerase family protein	COG4952	M	GI 9	185	163	22
RCA23_c24790	2618529	2617822	putative HTH-type transcriptional regulator, GntR family	COG1802	K	GI 9	254	163	91
RCA23_c24800	2620064	2618739	mandelate racemase/muconate lactonizing enzyme	COG4948	M	GI 9	222	159	63
RCA23_c24810	2620722	2621792	fatty acid desaturase	COG3239	I	GI 9	209	154	55
RCA23_c24820	2622254	2621892	hypothetical protein			GI 9	16	5	11
RCA23_c24830	2623076	2622369	transposase	COG3316	L	GI 9	43	27	16
RCA23_c24840	2624076	2623558	transporter, LysE family	COG1280	E	GI 9	0	1	-1
RCA23_c24850	2624531	2624851	hypothetical protein			GI 9	26	35	-9
RCA23_c24860	2625998	2624925	putative transporter, periplasmic binding protein	COG2358	R	GI 9	8	1	7
RCA23_c24870	2626948	2627676	ribitol 2-dehydrogenase RbtD	COG4221	R	GI 9	50	26	24
RCA23_c24880	2631855	2628631	hypothetical protein			GI 9	26	16	10
RCA23_c24890	2631920	2634466	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltra	COG0457	R	GI 9	52	46	6

RCA23_c24900	2636319	2635342	putative phage integrase	COG4974	L	GI 9	100	70	30
RCA23_c24920	2636842	2638131	D-alanyl-D-alanine carboxypeptidase DacC	COG1686	M		251	324	-73
RCA23_c24930	2638132	2638746	thymidylate kinase Tmk	COG0125	F		197	301	-104
RCA23_c24940	2638743	2639867	hypothetical protein, DNA polymerase III delta subunit	COG2812	L		192	277	-85
RCA23_c24950	2639864	2640652	TatD family deoxyribonuclease	COG0084	L		240	435	-195
RCA23_c24960	2640649	2641437	hypothetical protein, metallo-beta-lactamase	COG1235	R		292	403	-111
RCA23_c24970	2641439	2642368	membrane transport protein	COG0679	R		307	401	-94
RCA23_c24980	2643457	2642372	FAD dependent oxidoreductase	COG0665	E		183	305	-122
RCA23_c24990	2643645	2645834	UvrABC system protein B	COG0556	L		246	358	-112
RCA23_c25000	2647627	2645909	hypothetical protein				553	485	68
RCA23_c25010	2648247	2647642	hypothetical protein				444	381	63
RCA23_c25020	2648732	2648331	hypothetical protein				640	595	45
RCA23_c25030	2650370	2648796	lysyl-tRNA synthase LysS	COG1384	J		506	461	45
RCA23_c25040	2650510	2650884	hypothetical protein				359	434	-75
RCA23_c25050	2652333	2650876	putative D-Ala-D-Ala carboxypeptidase 3 (S13) family prote	COG2027	M		272	431	-159
RCA23_c25060	2652562	2653368	hypothetical protein				240	271	-31
RCA23_c25070	2653967	2653365	nicotinic acid mononucleotide adenyltransferase NadD	COG1057	H		207	270	-63
RCA23_c25080	2654128	2655756	ABC transporter, ATP-binding cassette protein, ChvD famil	COG0488	R		488	465	23
RCA23_c25090	2655999	2656205	cold shock protein CspA	COG1278	K		304	373	-69
RCA23_c25100	2657646	2656327	glutamyl-tRNA synthase 1	COG0008	J		276	321	-45
RCA23_c25110	2659351	2657714	glutamine-dependent NAD(+) synthase NadE	COG0171	H		286	411	-125
RCA23_c25120	2659555	2660997	putative phosphatidylinositol-4-phosphate 5-kinase	COG4642	S		504	467	37
RCA23_c25130	2661772	2661011	hypothetical protein	COG1028	I		216	333	-117
RCA23_c25140	2661935	2663500	2-isopropylmalate synthase LeuA	COG0119	E		392	420	-28
RCA23_c25150	2663641	2664678	rod shape-determining protein MreB	COG1077	D		324	359	-35
RCA23_c25160	2664709	2665593	rod shape-determining protein MreC	COG1792	M		222	292	-70
RCA23_c25170	2665590	2666129	hypothetical protein				310	423	-113
RCA23_c25180	2666126	2668078	penicillin-binding protein 2	COG0768	M		309	352	-43
RCA23_c25190	2668075	2669226	rod shape-determining protein RodA	COG0772	D		498	483	15
RCA23_c25200	2669223	2670152	glyoxylate/hydroxypyruvate reductase GhrA	COG0111	H		293	472	-179

RCA23_c25210	2670938	2670162	hypothetical protein			226	269	-43
RCA23_c25220	2671545	2670925	hypothetical protein	COG1573	L	248	272	-24
RCA23_c25230	2671592	2672890	Na+/H+ antiporter NhaA	COG3004	P	338	391	-53
RCA23_c25240	2673062	2673721	capsule polysaccharide export protein KpsT	COG1134	G	568	561	7
RCA23_c25250	2673699	2675342	capsule polysaccharide export protein KpsE	COG3524	M	361	359	2
RCA23_c25270	2675994	2675545	hypothetical protein	COG1832	R	412	456	-44
RCA23_c25280	2676353	2675997	ferredoxin PetF	COG0633	C	421	371	50
RCA23_c25290	2677702	2676350	selenium binding protein			596	556	40
RCA23_c25300	2679228	2677789	aldehyde dehydrogenase	COG1012	C	264	321	-57
RCA23_c25310	2680435	2679296	CoA-transferase family III protein involved in DMSP degrad	COG1804	C	268	406	-138
RCA23_c25320	2680698	2681036	nitrogen regulatory protein P-II 2	COG0347	E	654	505	149
RCA23_c25330	2681036	2682373	ammonium transporter	COG0004	P	507	419	88
RCA23_c25340	2682887	2682426	homoprotocatechuate degradative operon repressor	COG1846	K	311	282	29
RCA23_c25350	2683007	2684515	5-carboxymethyl-2-hydroxymuconic semialdehyde dehydro	COG1012	C	402	427	-25
RCA23_c25360	2684539	2685522	3,4-dihydroxyphenylacetate 2,3-dioxygenase HpaD	COG0346	E	355	344	11
RCA23_c25370	2686538	2685534	3-carboxy-cis,cis-muconate cycloisomerase PcaB	COG0015	F	222	260	-38
RCA23_c25380	2687377	2686535	hypothetical protein DUF849	COG3246	S	286	319	-33
RCA23_c25390	2687930	2687370	protocatechuate 3,4-dioxygenase alpha chain PcaG	COG3485	Q	216	313	-97
RCA23_c25400	2688658	2687930	protocatechuate 3,4-dioxygenase beta chain PcaH	COG3485	Q	172	217	-45
RCA23_c25410	2689041	2688655	4-carboxymuconolactone decarboxylase PcaC	COG0599	S	193	228	-35
RCA23_c25420	2689451	2689260	hypothetical protein			343	373	-30
RCA23_c25430	2689498	2690184	transcriptional regulatory protein	COG0745	T	365	418	-53
RCA23_c25440	2690190	2691731	two component signal transduction histidine kinase ChvG	COG0642	T	479	455	24
RCA23_c25450	2691980	2691744	hypothetical protein			545	451	94
RCA23_c25460	2694029	2692536	Na(+)-phosphate symporter Pit	COG0306	P	375	421	-46
RCA23_c25470	2694422	2694246	hypothetical protein			625	496	129
RCA23_c25480	2695336	2694491	2-dehydro-3-deoxyphosphooctonate aldolase KdsA	COG2877	M	308	347	-39
RCA23_c25490	2695480	2696481	arabinose 5-phosphate isomerase KdsD	COG0794	M	281	328	-47
RCA23_c25500	2697297	2696491	3-deoxy-manno-octulosonate cytidylyltransferase KdsB	COG1212	M	476	394	82
RCA23_c25510	2698445	2697384	hypothetical protein			122	146	-24

RCA23_c25520	2703372	2698459	bacterial surface protein			86	44	42
RCA23_c25530	2703948	2706137	catalase-peroxidase KatG	COG0376	P	267	267	0
RCA23_c25540	2706353	2707432	hypothetical protein	COG2067	I	134	138	-4
RCA23_c25550	2707908	2707480	thioesterase/thiol ester dehydrase-isomerase	COG0824	R	50	135	-85
RCA23_c25560	2709059	2707905	iron-containing alcohol dehydrogenase	COG1454	C	136	190	-54
RCA23_c25570	2710310	2709075	hypothetical protein	COG1960	I	224	359	-135
RCA23_c25580	2710403	2710906	nodulation protein N-like protein	COG2030	I	274	303	-29
RCA23_c25590	2710903	2711943	putative phosphotransferase, eukaryotic acyl-CoA dehydrog	COG3173	R	286	369	-83
RCA23_c25600	2711940	2712548	putative HTH-type transcriptional regulator, TetR family	COG1309	K	280	365	-85
RCA23_c25610	2712623	2714713	fatty acid oxidation complex alpha subunit FadJ	COG1250	I	230	283	-53
RCA23_c25620	2714718	2715914	acyl-CoA dehydrogenase	COG1960	I	529	366	163
RCA23_c25630	2715918	2717012	acyl-CoA dehydrogenase	COG1960	I	266	245	21
RCA23_c25640	2717231	2717998	hypothetical protein, MarR family			285	270	15
RCA23_c25650	2718086	2719246	acyl-CoA dehydrogenase	COG1960	I	495	432	63
RCA23_c25660	2720282	2719305	quinone oxidoreductase (1.6.5.5.)	COG0604	C	467	472	-5
RCA23_c25670	2720400	2720990	hypothetical protein			218	348	-130
RCA23_c25680	2721719	2720952	putative DNA repair protein RecO	COG1381	L	297	529	-232
RCA23_c25690	2722155	2721823	hypothetical protein	COG5447	S	328	366	-38
RCA23_c25700	2723060	2722152	GTP-binding protein Era	COG1159	R	435	524	-89
RCA23_c25710	2723740	2723057	ribonuclease 3	COG0571	K	271	398	-127
RCA23_c25720	2724636	2723767	signal peptidase I	COG0681	U	348	422	-74
RCA23_c25730	2725101	2724688	holo-[acyl-carrier-protein] synthase AcpS	COG0736	I	188	392	-204
RCA23_c25740	2725841	2725098	pyridoxine 5'-phosphate synthase PdxJ	COG0854	H	284	320	-36
RCA23_c25750	2726515	2725865	hypothetical protein DUF2062	COG3216	S	343	410	-67
RCA23_c25760	2728673	2726508	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase	COG0317	T	439	454	-15
RCA23_c25770	2729039	2728686	DNA-directed RNA polymerase subunit omega	COG1758	K	1.123	669	454
RCA23_c25780	2729719	2729135	putative 2-amino-4-hydroxy-6-hydroxymethyldihydropteridin	COG0801	H	399	370	29
RCA23_c25790	2729822	2730388	hypothetical protein DUF88	COG1432	S	663	386	277
RCA23_c25800	2730453	2731418	4-hydroxy-3-methylbut-2-enyl diphosphate reductase IspH	COG0761	I	269	305	-36
RCA23_c25810	2731411	2731998	hypothetical protein, methyltransferase	COG2227	H	203	289	-86

RCA23_c25820	2731991	2732443	ribonuclease H	COG0328	L		255	386	-131
RCA23_c25830	2732467	2732703	hypothetical protein				262	428	-166
RCA23_c25840	2733584	2732700	methionyl-tRNA formyltransferase Fmt	COG0223	J		177	313	-136
RCA23_c25850	2734084	2733590	peptide deformylase Def	COG0242	J		298	457	-159
RCA23_c25860	2734710	2734081	peptide deformylase Def	COG0242	J		400	459	-59
RCA23_c25870	2734743	2735909	aminotransferase	COG1168	E		342	372	-30
RCA23_c25880	2736272	2735922	hypothetical protein				315	306	9
RCA23_c25890	2737133	2736360	precorrin-4 C(11)-methyltransferase CobM	COG2875	H		269	297	-28
RCA23_c25900	2738971	2737130	precorrin-3B C(17)-methyltransferase CobJ	COG1010	H		190	309	-119
RCA23_c25910	2739663	2738962	precorrin-2 C(20)-methyltransferase CobI	COG2243	H		215	381	-166
RCA23_c25920	2740859	2739660	precorrin-6Y C(5,15)-methyltransferase CobL	COG2242	H		190	368	-178
RCA23_c25930	2741494	2740856	precorrin-8X methylmutase CobH	COG2082	H		243	357	-114
RCA23_c25940	2742653	2741541	sirohydrochlorin cobaltochelatase CbiX	COG2138	S		330	408	-78
RCA23_c25950	2743257	2744771	methyltransferase, FkbM family	COG3774	M		151	145	6
RCA23_c25960	2744880	2745842	hypothetical protein, glutathione S-transferase	COG0435	O		555	486	69
RCA23_c25970	2745920	2746291	hypothetical protein DUF1636	COG5469	S		250	284	-34
RCA23_c25980	2746291	2747238	threonine-phosphate decarboxylase CobC	COG0079	E		212	334	-122
RCA23_c25990	2747235	2748140	cobalamin biosynthesis protein CobD	COG1270	H		288	321	-33
RCA23_c26000	2748210	2749349	putative peptidoglycan-binding lytic murein transglycosylase	COG2951	M		269	370	-101
RCA23_c26010	2752960	2749505	putative chromosome partition protein smc	COG1196	D		238	324	-86
RCA23_c26020	2753354	2753145	hypothetical protein				402	371	31
RCA23_c26030	2753524	2754378	hypothetical protein	COG1028	I		304	334	-30
RCA23_c26040	2754434	2755204	hypothetical protein DUF81	COG0730	R		615	430	185
RCA23_c26050	2755268	2756272	50S ribosomal protein L2	COG0090	J		670	458	212
RCA23_c26060	2756318	2756554	30S ribosomal protein S19	COG0185	J		875	505	370
RCA23_c26070	2756558	2756938	50S ribosomal protein L22	COG0091	J		1.115	598	517
RCA23_c26080	2756938	2757657	30S ribosomal protein S3	COG0092	J		748	364	384
RCA23_c26090	2757702	2758082	50S ribosomal protein L16	COG0197	J		391	269	122
RCA23_c26100	2758763	2758521	hypothetical protein			GI 10	525	482	43
RCA23_c26120	2760596	2759328	hypothetcial protein	COG0666	R	GI 10	10	9	1

RCA23_c26130	2761026	2760724	transcriptional regulator			GI 10	245	94	151
RCA23_c26140	2761304	2761564	hypothetical protein			GI 10	158	107	51
RCA23_c26150	2762158	2761697	hypothetical protein, UPF0311			GI 10	298	163	135
RCA23_c26160	2762238	2762687	transcriptional regulator, MarR family	COG1846	K	GI 10	324	211	113
RCA23_c26170	2762756	2764528	long-chain-fatty-acid-CoA-ligase	COG0318	I	GI 10	171	159	12
RCA23_c26180	2765853	2764525	TRAP dicarboxylate transporter, subunit DctM	COG1593	G	GI 10	163	218	-55
RCA23_c26190	2766366	2765854	TRAP dicarboxylate transporter, subunit DctQ			GI 10	225	194	31
RCA23_c26200	2767464	2766427	TRAP dicarboxylate transporter, subunit DctP	COG1638	G	GI 10	171	138	33
RCA23_c26210	2768296	2767511	3-hydroxybutyryl-CoA dehydratase Crt	COG1024	I	GI 10	128	207	-79
RCA23_c26220	2768372	2769280	metal-dependent hydrolase	COG2159	R	GI 10	381	230	151
RCA23_c26230	2769438	2770715	FAD dependent monooxygenase	COG0654	H	GI 10	204	180	24
RCA23_c26240	2772437	2770791	arylsulfatase	COG3119	P	GI 10	137	165	-28
RCA23_c26250	2772940	2772434	transcriptional regulator, MarR family	COG1846	K	GI 10	149	189	-40
RCA23_c26260	2773067	2774122	putative transporter, periplasmic binding protein	COG2358	R	GI 10	113	141	-28
RCA23_c26270	2774186	2776480	TRAP transporter, 4TM/12TM fusion protein	COG4666	R	GI 10	256	221	35
RCA23_c26280	2778081	2776852	hypothetical protein, UPF0261	COG5441	S	GI 10	500	428	72
RCA23_c26290	2779513	2778236	gamma-glutamylputrescine synthase PuuA	COG0174	E	GI 10	493	386	107
RCA23_c26300	2780750	2779515	cytochrome P450	COG2124	Q	GI 10	546	377	169
RCA23_c26310	2781471	2780740	glutamine amidotransferase class-I	COG0518	F	GI 10	630	421	209
RCA23_c26320	2782504	2781536	tripartite tricarboxylate transporter (TTT) protein TctC	COG3181	S	GI 10	491	360	131
RCA23_c26330	2783997	2782504	tripartite tricarboxylate transporter (TTT) protein TctA	COG3333	S	GI 10	471	384	87
RCA23_c26340	2784742	2784008	hypothetical protein, transmembrane			GI 10	794	831	-37
RCA23_c26350	2786274	2784739	gamma-glutamyl-gamma-aminobutyraldehyde dehydrogena	COG1012	C	GI 10	526	374	152
RCA23_c26360	2786992	2787321	hypothetical protein			GI 10	20	18	2
RCA23_c26370	2787569	2787901	hypothetical protein			GI 10	52	13	39
RCA23_c26380	2787903	2788388	hypothetical protein			GI 10	18	11	7
RCA23_c26390	2789043	2790062	putative fucosyltransferase			GI 10	54	41	13
RCA23_c26400	2790398	2790138	integrase	COG2801	L	GI 10	156	153	3
RCA23_c26410	2791528	2790497	putative extracellular solute-binding protein	COG1840	P	GI 10	271	192	79
RCA23_c26420	2792889	2791498	two-component system, sensor histidine kinase protein	COG0642	T	GI 10	137	118	19

RCA23_c26430	2793554	2792886	two-component system, response regulator protein	COG0745	T	GI 10	214	156	58
RCA23_c26440	2793656	2794624	tripartite tricarboxylate transporter (TTT) protein TctC	COG3181	S	GI 10	713	468	245
RCA23_c26450	2794624	2795112	tripartite tricarboxylate transporter (TTT) protein TctB			GI 10	634	402	232
RCA23_c26460	2795114	2796619	tripartite tricarboxylate transporter (TTT) protein TctA	COG3333	S	GI 10	592	369	223
RCA23_c26470	2796621	2797979	hypothetical protein			GI 10	474	353	121
RCA23_c26480	2797972	2798277	hypothetical protein			GI 10	592	419	173
RCA23_c26490	2798419	2798775	transposase A			GI 10	341	254	87
RCA23_c26510	2799713	2799357	hypothetical protein			GI 10	1	0	1
RCA23_c26520	2800934	2801293	hypothetical protein	COG1709	K	GI 10	0	4	-4
RCA23_c26530	2802543	2802343	hypothetical protein			GI 10	0	0	0
RCA23_c26540	2806319	2802786	putative RTX toxin and hemolysin-type calcium binding protein			GI 10	1	2	-1
RCA23_c26550	2809639	2806427	putative RTX toxin and hemolysin-type calcium binding protein			GI 10	89	22	67
RCA23_c26560	2809943	2811319	type I secretion outer membrane protein, TolC family	COG1538	M	GI 10	267	163	104
RCA23_c26570	2811316	2813484	type I secretion system ATP-binding component	COG2274	V	GI 10	378	289	89
RCA23_c26580	2813500	2814810	type I RTX secretion system membrane fusion protein, HlyD	COG1566	V	GI 10	493	289	204
RCA23_c26590	2814853	2815215	hypothetical protein			GI 10	680	516	164
RCA23_c26600	2815394	2815645	hypothetical protein			GI 10	1.043	506	537
RCA23_c26610	2815655	2815879	hypothetical protein			GI 10	1.033	554	479
RCA23_c26620	2815898	2816089	hypothetical protein			GI 10	1.041	460	581
RCA23_c26630	2816211	2817194	hypothetical protein DUF2125			GI 10	666	361	305
RCA23_c26640	2817683	2818480	Asp/Glu racemase	COG3473	Q	GI 10	500	349	151
RCA23_c26650	2818577	2819731	cystathionine beta-lyase	COG0626	E	GI 10	549	536	13
RCA23_c26660	2820022	2821635	deoxyribodipyrimidine photo-lyase PhrB	COG0415	L	GI 10	921	514	407
RCA23_c26670	2821821	2822804	hypothetical protein	COG3380	R	GI 10	564	376	188
RCA23_c26680	2823798	2822806	O-sialoglycoprotein endopeptidase Gcp	COG0533	O	GI 10	284	330	-46
RCA23_c26690	2824420	2823791	Sua5/YciO/YrdC/YwlC family protein	COG0009	J	GI 10	299	317	-18
RCA23_c26700	2825070	2824417	putative glycoprotease family protein	COG1214	O	GI 10	294	484	-190
RCA23_c26710	2825579	2825061	hypothetical protein UPF0079	COG0802	R	GI 10	267	388	-121
RCA23_c26720	2825795	2826562	xylose isomerase family protein	COG3622	G	GI 10	264	388	-124
RCA23_c26730	2826823	2828073	putative phage integrase	COG0582	L	GI 10	171	127	44

RCA23_c26740	2828066	2828713	hypothetical protein			GI 10	240	116	124
RCA23_c26750	2828793	2828993	putative prophage regulatory protein	COG3311	K	GI 10	75	92	-17
RCA23_c26760	2828990	2829565	hypothetical protein			GI 10	99	70	29
RCA23_c26770	2829691	2831313	DNA polymerase	COG0749	L	GI 10	144	96	48
RCA23_c26780	2832293	2831898	hypothetical protein			GI 10	65	51	14
RCA23_c26790	2833890	2832826	hypothetical protein, snoaL-like polyketide cyclase	COG5485	R	GI 10	73	81	-8
RCA23_c26800	2834472	2834092	hypothetical protein			GI 10	105	69	36
RCA23_c26810	2834841	2834566	glyoxalase/bleomycin resistance protein/dioxygenase superfamily protein			GI 10	58	114	-56
RCA23_c26820	2835971	2834964	hypothetical protein			GI 10	55	74	-19
RCA23_c26830	2836859	2835975	putative ABC transporter permease protein	COG0395	G	GI 10	92	82	10
RCA23_c26840	2837837	2836863	putative ABC transporter permease protein	COG1175	G	GI 10	79	120	-41
RCA23_c26850	2839229	2837985	putative ABC transporter extracellular solute binding protein	COG1653	G	GI 10	74	71	3
RCA23_c26860	2839509	2840555	ABC transporter ATP-binding protein	COG3839	G	GI 10	64	75	-11
RCA23_c26870	2840606	2841937	histidinol dehydrogenase HisD	COG0141	E	GI 10	55	65	-10
RCA23_c26880	2841934	2842959	hypothetical protein, snoaL-like polyketide cyclase	COG5485	R	GI 10	39	67	-28
RCA23_c26890	2842980	2843720	short chain dehydrogenase	COG1028	I	GI 10	32	52	-20
RCA23_c26900	2843720	2844733	putative HTH-type transcriptional regulator LacI family	COG1609	K	GI 10	46	72	-26
RCA23_c26910	2844730	2845731	hypothetical protein, snoaL-like polyketide cyclase			GI 10	44	75	-31
RCA23_c26920	2845728	2846693	hypothetical protein			GI 10	58	93	-35
RCA23_c26930	2846826	2847896	hypothetical protein, 2-hydroxypropyl-CoM lyase-like	COG0620	E	GI 10	53	79	-26
RCA23_c26940	2847893	2848561	hypothetical protein, alpha/beta hydrolase-like	COG0596	R	GI 10	80	90	-10
RCA23_c26950	2848567	2849259	hypothetical protein	COG0684	H	GI 10	49	85	-36
RCA23_c26960	2850269	2851174	3-hydroxyisobutyrate dehydrogenase MmsB	COG2084	I	GI 10	171	236	-65
RCA23_c26970	2851171	2852874	dihydroxy-acid dehydratase IlvD	COG0129	E	GI 10	91	124	-33
RCA23_c26980	2852884	2854224	hypothetical protein	COG4091	E	GI 10	80	132	-52
RCA23_c26990	2854264	2855901	putative choline (or alcohol) dehydrogenase	COG2303	E	GI 10	82	154	-72
RCA23_c27000	2855926	2857404	aldehyde dehydrogenase	COG1012	C	GI 10	132	164	-32
RCA23_c27010	2858020	2857418	transporter, LysE family	COG1280	E	GI 10	78	82	-4
RCA23_c27020	2859546	2858080	TRAP dicarboxylate transporter, subunit DctM	COG4664	Q	GI 10	186	208	-22
RCA23_c27030	2860109	2859546	TRAP dicarboxylate transporter, subunit DctQ	COG4665	Q	GI 10	193	194	-1

RCA23_c27040	2861235	2860195	TRAP dicarboxylate transporter, subunit DctP	COG4663	Q	GI 10	219	154	65
RCA23_c27050	2862106	2861444	transcriptional regulator, LysR family	COG0583	K	GI 10	265	258	7
RCA23_c27060	2864132	2863029	mandelate racemase/muconate lactonizing enzyme	COG4948	M	GI 10	75	142	-67
RCA23_c27070	2865241	2864129	Zn-dependant oxidoreductase	COG0604	C	GI 10	72	182	-110
RCA23_c27090	2866870	2865992	HTH-type transcriptional regulator, LysR family	COG0583	K	GI 10	109	112	-3
RCA23_c27100	2866984	2867739	class II aldolase	COG0235	G	GI 10	127	145	-18
RCA23_c27110	2867742	2868770	fatty acid desaturase	COG3239	I	GI 10	59	122	-63
RCA23_c27120	2868772	2869620	3-methyl-2-oxobutanoate hydroxymethyltransferase PanB	COG0413	H	GI 10	113	150	-37
RCA23_c27130	2869651	2869959	putative rieske [2Fe-2S] protein	COG2146	P	GI 10	181	173	8
RCA23_c27150	2871527	2870697	hypothetical protein	COG1396	K		597	445	152
RCA23_c27160	2872169	2873122	arginase family protein	COG0010	E		371	394	-23
RCA23_c27170	2873972	2873130	hypothetical protein	COG1082	G		609	538	71
RCA23_c27180	2874311	2875399	putative HTH-type transcriptional regulator, AraC family	COG2169	F		277	286	-9
RCA23_c27190	2876347	2875367	hypothetical protein. fatty acid desaturase	COG3239	I		497	509	-12
RCA23_c27200	2878323	2876440	AMP-dependent synthase / ligase	COG0318	I		392	482	-90
RCA23_c27210	2880212	2878422	ABC transporter ATP-binding protein	COG1132	V		279	330	-51
RCA23_c27220	2880650	2881150	spore coat family protein				310	326	-16
RCA23_c27230	2881370	2882092	PapD-like chaperone involved in fimbrial biogenesis	COG3121	N		313	228	85
RCA23_c27240	2882279	2884033	fimbrial biogenesis outer membrane usher protein	COG3188	N		235	333	-98
RCA23_c27250	2884043	2884906	fimbrial biogenesis outer membrane usher protein	COG3188	N		320	412	-92
RCA23_c27260	2885061	2885357	hypothetical protein				275	288	-13
RCA23_c27280	2886473	2885598	hypothetical protein	COG0697	G		437	532	-95
RCA23_c27290	2890851	2886601	DNA-directed RNA polymerase beta subunit RpoC	COG0086	K		605	404	201
RCA23_c27300	2895044	2890911	DNA-directed RNA polymerase beta subunit RpoB	COG0085	K		596	421	175
RCA23_c27310	2895693	2895316	50S ribosomal protein L7/L12	COG0222	J		1.149	666	483
RCA23_c27320	2896250	2895762	50S ribosomal protein L10	COG0244	J		1.251	786	465
RCA23_c27330	2897346	2896648	50S ribosomal protein L1	COG0081	J		541	451	90
RCA23_c27340	2897821	2897348	50S ribosomal protein L11	COG0080	J		723	502	221
RCA23_c27350	2898476	2897928	transcription antitermination protein NusG	COG0250	K		711	380	331
RCA23_c27360	2898893	2898627	preprotein translocase, subunit SecE	COG0690	U		366	293	73

RCA23_c27370	2899800	2898895	hypothetical protein			315	334	-19
RCA23_c27430	2905830	2905985	hypothetical protein			433	427	6
RCA23_c27440	2906449	2906021	hypothetical protein, transmembrane			477	559	-82
RCA23_c27450	2907137	2906511	hypothetical protein			166	344	-178
RCA23_c27460	2908720	2907134	putative acetolactate synthase isozyme 1 large subunit	COG0028	E	255	334	-79
RCA23_c27470	2910168	2908720	putative cation transporter	COG0168	P	535	514	21
RCA23_c27480	2911228	2910209	GTP cyclohydrolase FolE	COG1469	S	454	382	72
RCA23_c27490	2912575	2911334	O-succinylhomoserine sulfhydrylase MetZ	COG0626	E	484	552	-68
RCA23_c27500	2912751	2913443	hypothetical protein	COG0625	O	355	420	-65
RCA23_c27510	2914130	2913531	putative intracellular septation protein	COG2917	D	725	845	-120
RCA23_c27520	2915048	2914146	hypothetical protein	COG0697	G	373	538	-165
RCA23_c27530	2916226	2915045	putative cell division protein	COG0552	U	244	359	-115
RCA23_c27540	2918008	2916323	NADH-quinone oxidoreductase subunits E/F (fused)	COG1894	C	257	373	-116
RCA23_c27550	2919686	2918133	exodeoxyribonuclease 7 large subunit XseA	COG1570	L	243	310	-67
RCA23_c27560	2919757	2921019	phosphoribosylamine--glycine ligase PurD	COG0151	F	245	400	-155
RCA23_c27570	2921398	2921075	hypothetical protein, ferredoxin	COG0633	C	495	375	120
RCA23_c27580	2921502	2921894	hypothetical protein	COG0587	L	158	249	-91
RCA23_c27590	2923443	2921956	periplasmic serine protease DO-like	COG0265	O	449	643	-194
RCA23_c27600	2924668	2923781	putative protein hflC	COG0330	O	553	459	94
RCA23_c27610	2925849	2924668	protein HflK	COG0330	O	588	454	134
RCA23_c27620	2927271	2925913	glutathione reductase Gor	COG1249	C	302	406	-104
RCA23_c27630	2928055	2927336	ribose-5-phosphate isomerase A	COG0120	G	357	434	-77
RCA23_c27640	2928355	2928125	hypothetical protein			300	310	-10
RCA23_c27650	2928419	2929792	L-serine dehydratase SdaB	COG1760	E	239	300	-61
RCA23_c27660	2929823	2930707	putative integral membrane protein	COG0697	G	437	492	-55
RCA23_c27670	2931346	2930672	hypothetical protein, thiamine pyrophosphokinase	COG1564	H	326	453	-127
RCA23_c27680	2931480	2931917	hypothetical protein			176	341	-165
RCA23_c27690	2932339	2933484	hypothetical protein			512	344	168
RCA23_c27700	2933779	2933552	hypothetical protein			335	362	-27
RCA23_c27710	2935071	2933779	adenylosuccinate synthase PurA	COG0104	F	436	466	-30

RCA23_c27720	2935313	2935666	preprotein translocase, SecG subunit SecG			324	415	-91
RCA23_c27730	2935819	2937462	CTP synthase	COG0504	F	449	408	41
RCA23_c27740	2937481	2937774	hypothetical protein, DUF1330	COG5470	S	276	315	-39
RCA23_c27750	2937874	2938227	hypothetical protein DUF1332	COG4103	S	274	238	36
RCA23_c27760	2938232	2938948	hypothetical protein	COG3221	P	184	292	-108
RCA23_c27770	2939027	2939800	amino acid transport ATP-binding protein	COG4598	E	412	570	-158
RCA23_c27780	2939834	2940547	putative amino acid transport extracellular solute binding pr	COG0834	E	476	436	40
RCA23_c27790	2940762	2941547	putative ABC transporter inner membrane component	COG4215	E	351	411	-60
RCA23_c27800	2941544	2942347	putative amino acid transport permease protein	COG4160	E	271	371	-100
RCA23_c27810	2942344	2943621	gamma-glutamylputrescine synthase PuuA	COG0174	E	366	351	15
RCA23_c27820	2943682	2944383	hypothetical protein, glutamine amidotransferase class I	COG0518	F	410	506	-96
RCA23_c27830	2944380	2945732	gamma-glutamylputrescine synthase PuuA	COG0174	E	319	376	-57
RCA23_c27840	2945725	2947029	gamma-glutamylputrescine oxidoreductase PuuB	COG0665	E	194	296	-102
RCA23_c27850	2947227	2948594	aminotransferase class III	COG0161	H	481	435	46
RCA23_c27860	2949102	2948632	putative PHB synthesis repressor protein	COG5394	S	616	440	176
RCA23_c27870	2949760	2949338	hypothetical protein			962	483	479
RCA23_c27880	2951592	2949850	poly(R)-hydroxyalkanoic acid synthase PhaC	COG3243	I	772	600	172
RCA23_c27890	2951693	2952952	polyhydroxyalkanoate depolymerase PhaZ	COG4553	I	424	429	-5
RCA23_c27900	2952949	2953992	putative ribosome biogenesis GTPase RsgA	COG1162	R	273	335	-62
RCA23_c27910	2954694	2953999	hypothetical protein, alpha/beta hydrolase-like	COG0596	R	295	397	-102
RCA23_c27920	2955122	2954814	hypothetical protein			640	594	46
RCA23_c27930	2955968	2955144	hypothetical protein, alpha/beta hydrolase-like	COG0596	R	489	563	-74
RCA23_c27940	2956110	2958059	threonyl-tRNA synthase ThrS	COG0441	J	302	309	-7
RCA23_c27950	2958494	2958111	hypothetical protein, ArsC	COG1393	P	275	345	-70
RCA23_c27960	2959802	2958891	thymidylate synthase	COG1351	F	515	437	78
RCA23_c27970	2959890	2960318	putative glyoxalase/bleomycin resistance protein/dioxygena	COG0346	E	379	413	-34
RCA23_c27980	2960315	2961049	hypothetical protein			489	471	18
RCA23_c27990	2961528	2961043	putative transcriptional regulatorm marR family	COG1846	K	717	600	117
RCA23_c28000	2961866	2961600	hypothetical protein DUF339	COG2938	S	807	701	106
RCA23_c28010	2962255	2961863	hypothetical protein, DNA binding	COG1813	K	611	550	61

RCA23_c28020	2962344	2963546	aspartate aminotransferase AatA	COG0436	E	538	517	21
RCA23_c28030	2963696	2963965	hypothetical protein			520	538	-18
RCA23_c28040	2965311	2963962	multidrug resistance protein NorM	COG0534	V	289	371	-82
RCA23_c28050	2965347	2967407	DNA topoisomerase 4 subunit B	COG0187	L	401	416	-15
RCA23_c28060	2967432	2967866	hypothetical protein	COG3238	S	246	456	-210
RCA23_c28070	2968865	2967876	putative malate/L-lactate dehydrogenase	COG2055	C	232	307	-75
RCA23_c28080	2969623	2968946	lipoprotein-releasing system ATP-binding protein LolD	COG1136	V	324	503	-179
RCA23_c28090	2970938	2969616	lipoprotein-releasing system transmembrane protein, lolC/E	COG4591	M	391	420	-29
RCA23_c28100	2972322	2970991	prolyl-tRNA synthase ProS	COG0442	J	552	522	30
RCA23_c28110	2972479	2973552	hypothetical protein DUF20	COG0628	R	376	457	-81
RCA23_c28120	2973581	2974198	hypothetical protein	COG0593	L	404	491	-87
RCA23_c28130	2974261	2976429	polyphosphate kinase Ppk	COG0855	P	432	474	-42
RCA23_c28140	2976502	2978046	putative phosphatase	COG0248	F	329	415	-86
RCA23_c28150	2978758	2978078	hypothetical protein, DnaJ	COG1076	O	357	406	-49
RCA23_c28160	2979420	2978806	hypothetical protein			360	363	-3
RCA23_c28170	2981568	2979442	methylmalonyl-CoA mutase McmA	COG1884	I	438	453	-15
RCA23_c28180	2981692	2982117	hypothetical protein			443	452	-9
RCA23_c28190	2984179	2982182	biotin carboxylase AccC	COG4770	I	463	438	25
RCA23_c28200	2984788	2984429	hypothetical protein			688	418	270
RCA23_c28210	2986426	2984807	propionyl-CoA carboxylase beta chain, mitochondrial precu	COG4799	I	431	395	36
RCA23_c28220	2986614	2987720	putative major facilitator superfamily transporter	COG2814	G	324	367	-43
RCA23_c28230	2987752	2989146	hypothetical protein	COG3800	R	268	299	-31
RCA23_c28240	2990629	2989175	betaine aldehyde dehydrogenase BetB	COG1012	C	271	382	-111
RCA23_c28250	2991519	2990626	hypothetical protein	COG0697	G	358	670	-312
RCA23_c28260	2992971	2991571	TRAP dicarboxylate transporter, subunit DctM	COG1593	G	456	452	4
RCA23_c28270	2993600	2992971	TRAP dicarboxylate transporter, subunit DctQ	COG4665	Q	526	453	73
RCA23_c28280	2994698	2993682	TRAP dicarboxylate transporter, subunit DctP	COG1638	G	773	495	278
RCA23_c28290	2995125	2994823	transcriptional regulator, LacI family	COG1609	K	194	295	-101
RCA23_c28300	2996093	2995341	hypothetical protein, DUF81 family	COG0730	R	642	487	155
RCA23_c28310	2997240	2996074	serine--glyoxylate aminotransferase SgaA	COG0075	E	671	457	214

RCA23_c28320	2997311	3000124	D-lactate dehydrogenase Dld	COG0277	C	433	316	117
RCA23_c28330	3000108	3000872	hypothetical protein			591	406	185
RCA23_c28340	3002359	3000869	AMP-binding enzyme	COG0318	I	627	378	249
RCA23_c28350	3003741	3002356	succinate-semialdehyde dehydrogenase SucD	COG1012	C	714	387	327
RCA23_c28360	3005263	3003773	hypothetical protein	COG3333	S	551	345	206
RCA23_c28370	3005815	3005270	hypothetical protein			566	428	138
RCA23_c28380	3006899	3005886	putative tripartite tricarboxylate transporter family receptor	COG3181	S	478	291	187
RCA23_c28390	3008174	3007812	putative ETC complex I subunit			483	380	103
RCA23_c28450	3014946	3014311	sulfoxide reductase heme-binding subunit YedZ	COG2717	S	606	414	192
RCA23_c28460	3015970	3015032	sulfoxide reductase catalytic subunit YedY	COG2041	R	699	498	201
RCA23_c28470	3016084	3016839	3-oxoacyl-[acyl-carrier-protein] reductase FabG	COG1028	I	217	388	-171
RCA23_c28480	3017484	3016816	putative haloacid dehalogenase-like hydrolase	COG0637	R	241	355	-114
RCA23_c28490	3020158	3017549	chaperone protein ClpB	COG0542	O	571	466	105
RCA23_c28500	3020382	3021098	orotidine 5'-phosphate decarboxylase PyrF	COG0284	F	231	360	-129
RCA23_c28510	3021376	3021095	hypothetical protein			303	257	46
RCA23_c28520	3022266	3021376	SPFH domain/band 7 family protein	COG0330	O	332	320	12
RCA23_c28530	3022399	3023655	DNA polymerase IV	COG0389	L	244	376	-132
RCA23_c28540	3024583	3023660	putative N-formylglutamate amidohydrolase	COG3741	E	220	384	-164
RCA23_c28560	3026236	3025031	hypothetical protein, phenylacetate-coenzyme A ligase	COG1541	H	354	468	-114
RCA23_c28570	3027095	3026262	high-affinity branched-chain amino acid transporter ATP-bin	COG0410	E	388	363	25
RCA23_c28580	3028426	3027146	hypothetical protein	COG0683	E	356	266	90
RCA23_c28590	3029567	3028491	high-affinity branched-chain amino acid transporter permea	COG4177	E	514	348	166
RCA23_c28600	3030631	3029630	high-affinity branched-chain amino acid transporter permea	COG0559	E	662	420	242
RCA23_c28610	3031517	3030699	high-affinity branched-chain amino acid transporter ATP-bin	COG0411	E	616	480	136
RCA23_c28620	3033530	3031569	putative long-chain-fatty-acid-CoA ligase	COG1022	I	540	469	71
RCA23_c28630	3034611	3033706	tRNA pseudouridine synthase B	COG0130	J	444	471	-27
RCA23_c28650	3035184	3034663	ribosome-binding factor A	COG0858	J	390	589	-199
RCA23_c28640	3035183	3035992	dihydrodipicolinate synthase DapA	COG0289	E	232	307	-75
RCA23_c28660	3036242	3036039	hypothetical protein DUF1674	COG5508	S	308	405	-97
RCA23_c28670	3036304	3037596	putative ribosomal RNA small subunit methyltransferase B	COG0144	J	319	342	-23

RCA23_c28680	3037762	3039378	hypothetical protein, heparinase II/III	COG5360	S	307	415	-108
RCA23_c28690	3039420	3041006	bifunctional purine biosynthesis protein PurH	COG0138	F	334	417	-83
RCA23_c28700	3041008	3041490	signal peptidase II	COG0597	M	444	466	-22
RCA23_c28710	3041564	3042898	uncharacterized zinc protease y4wA	COG0612	R	259	271	-12
RCA23_c28720	3042895	3044199	uncharacterized zinc protease y4wB	COG0612	R	343	387	-44
RCA23_c28730	3044234	3046045	DNA mismatch repair protein MutL	COG0323	L	277	394	-117
RCA23_c28740	3046042	3047181	putative RmuC family protein	COG1322	S	453	493	-40
RCA23_c28750	3047826	3047176	transcriptional activator ChrR	COG3806	T	328	336	-8
RCA23_c28760	3048473	3047823	RNA polymerase sigma factor SigK	COG1595	K	815	442	373
RCA23_c28770	3048595	3049896	hypothetical protein	COG2907	R	645	423	222
RCA23_c28780	3049893	3050648	hypothetical protein DUF1365	COG3496	S	321	368	-47
RCA23_c28790	3050645	3051886	hypothetical protein	COG2211	G	246	374	-128
RCA23_c28800	3051883	3052434	hypothetical protein			338	406	-68
RCA23_c28810	3052441	3053175	putative short chain dehydrogenase	COG4221	R	338	412	-74
RCA23_c28820	3054242	3053181	saccharopine dehydrogenase (NAD+,L-lysine-forming)	COG3288	C	244	380	-136
RCA23_c28830	3054838	3054239	putative glutathione S-transferase	COG0625	O	410	462	-52
RCA23_c28840	3055518	3054859	putative phosphoglycerate mutase family protein	COG0406	G	408	433	-25
RCA23_c28850	3055678	3058473	formate dehydrogenase Fdh	COG3383	R	256	355	-99
RCA23_c28860	3059684	3058476	hypothetical protein	COG1357	S	149	173	-24
RCA23_c28870	3059845	3060351	hypothetical protein DUF1643	COG4333	S	165	251	-86
RCA23_c28880	3060348	3061232	haloacetate dehalogenase DehH	COG0596	R	216	302	-86
RCA23_c28890	3061378	3061647	30S ribosomal protein S15	COG0184	J	532	436	96
RCA23_c28900	3061763	3062671	hypothetical protein, DUF6 transmembrane protein	COG0697	G	291	363	-72
RCA23_c28910	3062837	3064972	polyribonucleotide nucleotidyltransferase Pnp	COG1185	J	566	452	114
RCA23_c28920	3065297	3066739	aldehyde dehydrogenase	COG1012	C	367	317	50
RCA23_c28930	3067514	3066870	ribosomal large subunit pseudouridine synthase A	COG0564	J	330	420	-90
RCA23_c28940	3067641	3068903	protein OtnG			239	284	-45
RCA23_c28950	3068952	3069767	hypothetical protein, DUF940 putative lipoprotein			460	502	-42
RCA23_c28960	3069770	3070432	hypothetical protein			502	397	105
RCA23_c28970	3070451	3071461	UDP-glucose 4-epimerase GalE	COG1087	M	409	393	16

RCA23_c28980	3072918	3071458	putative FAD linked oxidase	COG0277	C	266	432	-166
RCA23_c28990	3073207	3074703	signal recognition particle protein Ffh	COG0541	U	323	360	-37
RCA23_c29000	3074735	3075031	putative chorismate mutase type II	COG1605	E	471	593	-122
RCA23_c29010	3075077	3075463	30S ribosomal protein S16	COG0228	J	454	521	-67
RCA23_c29020	3075599	3076204	ribosome maturation factor RimM	COG0806	J	531	440	91
RCA23_c29030	3076201	3076983	tRNA (guanine-N(1)-)-methyltransferase TrmD	COG0336	J	262	287	-25
RCA23_c29040	3077274	3077645	50S ribosomal protein L19	COG0335	J	1.180	564	616
RCA23_c29050	3077657	3077878	50S ribosomal protein L31	COG0254	J	843	515	328
RCA23_c29060	3078055	3078864	ATPase MipZ	COG1192	D	467	427	40
RCA23_c29070	3079793	3078861	fructokinase	COG0524	G	353	434	-81
RCA23_c29080	3080009	3081187	P-hydroxybenzoate hydroxylase PobA	COG0654	H	481	429	52
RCA23_c29090	3081251	3082447	kynureninase KynU	COG3844	E	389	318	71
RCA23_c29100	3083041	3083694	HTH-type transcriptional regulator, GntR family	COG1802	K	449	308	141
RCA23_c29110	3083761	3084600	hypothetical protein, glutathione S-transferase	COG0625	O	529	404	125
RCA23_c29120	3084701	3085639	L-threonine 3-dehydrogenase	COG0451	M	348	353	-5
RCA23_c29130	3085650	3086444	enoyl-CoA hydratase	COG1024	I	185	255	-70
RCA23_c29140	3087386	3086463	enoyl-CoA hydratase	COG1250	I	205	333	-128
RCA23_c29150	3088163	3087396	3-hydroxyacyl-CoA dehydrogenase FadN	COG1028	I	242	312	-70
RCA23_c29160	3088298	3088942	hypothetical protein			381	386	-5
RCA23_c29170	3089925	3088969	integrase	COG4974	L	458	427	31
RCA23_c29180	3090052	3091107	hypothetical protein, porin-like			520	390	130
RCA23_c29190	3091254	3093845	leucyl-tRNA synthase LeuS	COG0495	J	433	380	53
RCA23_c29200	3093904	3094302	hypothetical protein DUF2159			571	462	109
RCA23_c29210	3094299	3095324	hypothetical protein			274	392	-118
RCA23_c29220	3095325	3095912	hypothetical protein, glutathione S-transferase	COG0625	O	500	442	58
RCA23_c29230	3097108	3095885	hypothetical protein	COG2081	R	237	270	-33
RCA23_c29240	3098243	3097311	hypothetical protein, porin			1.707	409	1.298
RCA23_c29250	3098481	3099143	hypothetical protein, alanine racemase-like	COG0325	R	273	282	-9
RCA23_c29260	3099644	3099150	hypothetical protein, YkuD	COG3786	S	218	327	-109
RCA23_c29270	3100696	3099641	GTP cyclohydrolase II RibA	COG0807	H	321	376	-55

RCA23_c29280	3100840	3101526	response regulator receiver protein	COG0745	T	801	648	153
RCA23_c29290	3102576	3101779	2-oxo-hepta-3-ene-1,7-dioic acid hydratase HpcG	COG3971	Q	378	339	39
RCA23_c29300	3103430	3102573	fumarylacetoacetate hydrolase family protein	COG0179	Q	416	428	-12
RCA23_c29310	3103834	3103427	5-carboxymethyl-2-hydroxymuconate isomerase	COG3232	E	367	337	30
RCA23_c29320	3104009	3104446	homoprotocatechuate degradation operon regulator HpaR	COG1846	K	513	682	-169
RCA23_c29330	3104443	3105903	4-hydroxyphenylacetate 3-monooxygenase oxygenase com	COG2368	Q	396	413	-17
RCA23_c29340	3106978	3105926	ABC sugar transporter, ATPase subunit	COG3839	G	417	427	-10
RCA23_c29350	3108378	3106966	mannitol 2-dehydrogenase MtlK	COG0246	G	541	470	71
RCA23_c29360	3109277	3108384	transcriptional regulator, AraC family	COG2207	K	845	568	277
RCA23_c29370	3110179	3109343	ABC sugar transporter, permease protein	COG0395	G	673	486	187
RCA23_c29380	3111128	3110190	ABC sugar transporter, permease protein	COG1175	G	627	368	259
RCA23_c29390	3112520	3111240	ABC transporter, periplasmic substrate-binding protein	COG1653	G	482	349	133
RCA23_c29400	3113045	3113410	putative flavohemoglobin / bacterial hemoglobin	COG1017	C	172	151	21
RCA23_c29410	3113570	3113848	hypothetical protein			357	239	118
RCA23_c29420	3115053	3113854	Na+/H+ antiporter NhaA	COG3004	P	869	651	218
RCA23_c29430	3115555	3115160	hypothetical protein			343	377	-34
RCA23_c29440	3116046	3115633	hypothetical protein DUF55	COG2947	S	575	446	129
RCA23_c29450	3116318	3116046	protein YciI	COG2350	S	444	407	37
RCA23_c29460	3117283	3116318	glycerol-3-phosphate dehydrogenase GpsA	COG0240	C	295	365	-70
RCA23_c29470	3117383	3118087	hypothetical protein, uroporophyrinogen-III synthase HemD	COG1587	H	261	373	-112
RCA23_c29480	3118112	3119260	hypothetical protein	COG3264	M	297	444	-147
RCA23_c29490	3119271	3120746	hypothetical protein, HemY	COG3898	S	255	322	-67
RCA23_c29500	3121065	3120736	transcriptional regulatory protein, Ars family	COG0640	K	351	449	-98
RCA23_c29510	3122055	3121183	magnesium-chelatase subunit BchO	COG0596	R	368	539	-171
RCA23_c29520	3123707	3122055	magnesium-chelatase subunit BchD	COG1240	H	228	347	-119
RCA23_c29530	3124716	3123709	magnesium-chelatase subunit BchI	COG1239	H	259	357	-98
RCA23_c29540	3125459	3124713	spheroidene monooxygenase CrtA			327	471	-144
RCA23_c29550	3125514	3127076	phytoene dehydrogenase CrtI	COG1233	Q	248	310	-62
RCA23_c29560	3127073	3128113	phytoene synthase CrtB	COG1562	I	282	412	-130
RCA23_c29570	3129022	3128114	hydroxyneurosporene dehydrogenase CrtC			315	427	-112

RCA23_c29580	3130449	3129025	methoxyneurosporene dehydrogenase CrtD	COG1233	Q	258	382	-124
RCA23_c29590	3130597	3131511	geranylgeranyl pyrophosphate synthase CrtE	COG0142	H	317	337	-20
RCA23_c29600	3131511	3132656	hydroxyneurosporene methyltransferase CrtF			351	342	9
RCA23_c29610	3132720	3133685	2-desacetyl-2-hydroxyethyl bacteriochlorophyllide A dehydr	COG1063	E	357	361	-4
RCA23_c29620	3133682	3134686	chlorophyllide reductase BchX	COG1348	P	519	502	17
RCA23_c29630	3134679	3136250	chlorophyllide reductase BchY			341	319	22
RCA23_c29640	3136250	3137710	chlorophyllide reductase subunit BchZ	COG2710	C	536	488	48
RCA23_c29650	3137707	3137940	protein PufQ			537	427	110
RCA23_c29660	3138087	3138242	light-harvesting protein B-870 beta chain PufB			6.978	500	6.478
RCA23_c29670	3138259	3138411	light-harvesting protein B-870 alpha chain PufA			6.270	527	5.743
RCA23_c29680	3138531	3139361	reaction center protein L chain PufL			874	581	293
RCA23_c29690	3139375	3140298	reaction center protein M chain PufM			677	578	99
RCA23_c29700	3140323	3140562	protein PufX			968	617	351
RCA23_c29710	3140748	3142640	1-deoxy-D-xylulose-5-phosphate synthase Dxs	COG1154	H	354	396	-42
RCA23_c29720	3143177	3142659	isopentenyl-diphosphate delta-isomerase Idi	COG1443	I	410	573	-163
RCA23_c29730	3144355	3143177	geranylgeranyl reductase BchP	COG0644	C	323	416	-93
RCA23_c29740	3145650	3144358	bacteriochlorophyll synthase 44.5 kDa chain			331	411	-80
RCA23_c29750	3146546	3145647	bacteriochlorophyll synthase BchG	COG0382	H	279	365	-86
RCA23_c29760	3146699	3147133	cytochrome c-551	COG3474	C	2.610	694	1.916
RCA23_c29770	3148204	3147191	uroporphyrinogen decarboxylase HemE	COG0407	H	678	490	188
RCA23_c29780	3148383	3149273	porphobilinogen deaminase HemC	COG0181	H	296	376	-80
RCA23_c29790	3149254	3150213	hypothetical protein, NmrA-like	COG0702	M	262	383	-121
RCA23_c29800	3151424	3150210	5-aminolevulinate synthase HemA	COG0156	H	552	474	78
RCA23_c29810	3152220	3151414	hypothetical protein			439	465	-26
RCA23_c29820	3153347	3152220	aerobic Mg-protoporphyrin IX monomethyl ester oxidative cyclase AcsF			646	487	159
RCA23_c29830	3153640	3153344	hypothetical protein			666	516	150
RCA23_c29840	3154124	3153657	hypothetical protein			392	356	36
RCA23_c29850	3154768	3154130	hypothetical protein			466	594	-128
RCA23_c29860	3155600	3154827	reaction center protein PuhA			424	380	44
RCA23_c29870	3157046	3155619	protein PucC			416	549	-133

RCA23_c29880	3157708	3157043	magnesium-protoporphyrin O-methyltransferase BchM	COG2227	H	353	470	-117
RCA23_c29890	3158604	3157708	light-independent protochlorophyllide reductase iron-sulfur	COG1348	P	615	601	14
RCA23_c29900	3162147	3158638	magnesium-chelatase subunit BchH	COG1429	H	346	408	-62
RCA23_c29910	3163717	3162173	light-independent protochlorophyllide reductase subunit Bch	COG2710	C	379	421	-42
RCA23_c29920	3164946	3163714	light-independent protochlorophyllide reductase subunit Bch	COG2710	C	243	340	-97
RCA23_c29930	3165482	3164994	2-vinyl bacteriochlorophyllide hydratase BchF			606	518	88
RCA23_c29940	3165800	3166510	putative transcriptional regulator PpaA			654	578	76
RCA23_c29950	3166571	3167995	transcriptional regulator PpsR	COG3829	K	507	360	147
RCA23_c29960	3168781	3168005	hypothetical protein	COG5012	R	383	415	-32
RCA23_c29970	3169806	3169207	transcriptional regulator protein FixJ	COG4566	T	571	377	194
RCA23_c29980	3170351	3169872	peripheral-type benzodiazepine receptor/signal transductio	COG3476	T	659	589	70
RCA23_c29990	3170538	3170972	hypothetical protein, integral membrane proteins YeeE/Yed	COG2391	R	475	462	13
RCA23_c30000	3171010	3171402	hypothetical protein, integral membrane proteins YeeE/Yed	COG2391	R	439	527	-88
RCA23_c30010	3171440	3172324	putative beta-lactamase hydrolase-like protein	COG0491	R	519	451	68
RCA23_c30020	3172386	3172811	hypothetical protein	COG3453	S	400	482	-82
RCA23_c30030	3172854	3174578	sulphate transporter	COG0659	P	577	541	36
RCA23_c30040	3174623	3176065	amidase	COG0154	J	392	412	-20
RCA23_c30050	3176200	3176790	hypothetical protein			555	390	165
RCA23_c30060	3176778	3177194	aminoglycoside phosphotransferase Aph			655	451	204
RCA23_c30070	3177342	3178808	hypothetical protein	COG2885	M	447	429	18
RCA23_c30080	3179766	3178849	chaperone protein DnaJ	COG0484	O	337	327	10
RCA23_c30090	3181980	3180073	chaperone protein DnaK	COG0443	O	2.596	868	1.728
RCA23_c30100	3182136	3182774	putative alpha-ketoglutarate-dependent dioxygenase AlkB	COG3145	L	444	449	-5
RCA23_c30110	3183607	3182780	putative ABC-2 type transporter	COG1682	G	559	435	124
RCA23_c30120	3183719	3184516	3'(2'),5'-bisphosphate nucleotidase CysQ	COG1218	P	487	424	63
RCA23_c30130	3184712	3185623	UTP-glucose-1-phosphate uridylyltransferase GalU	COG1210	M	100	76	24
RCA23_c30140	3185671	3186672	hypothetical protein	COG0463	M	29	29	0
RCA23_c30150	3186755	3187789	hypothetical protein			61	22	39
RCA23_c30160	3187804	3189483	hypothetical protein beta-1,6-N-acetylglucosaminyltransferases			64	40	24
RCA23_c30170	3189485	3190912	hypothetical protein			83	93	-10

RCA23_c30180	3191373	3190909	nitrogen regulatory protein PtsN	COG1762	G	462	459	3
RCA23_c30190	3191964	3191398	putative sigma 54 modulation protein	COG1544	J	716	558	158
RCA23_c30200	3192915	3192157	lipopolysaccharide export system ATP-binding protein LptB	COG1137	R	444	438	6
RCA23_c30210	3193403	3192915	putative lipopolysaccharide export system protein LptA	COG1934	S	280	352	-72
RCA23_c30220	3194020	3193412	hypothetical protein			689	490	199
RCA23_c30230	3194662	3194048	putative 3'-5'-exonuclease	COG0349	J	741	509	232
RCA23_c30240	3194850	3195968	glycine amidinotransferase	COG1834	E	521	526	-5
RCA23_c30250	3196817	3196053	hypothetical protein	COG4123	R	631	493	138
RCA23_c30260	3197481	3196918	hypothetical protein, metal-dependent phosphohydrolase	COG1896	R	457	580	-123
RCA23_c30270	3197634	3199025	S-adenosyl-L-homocysteine hydrolase AhcY	COG0499	H	603	490	113
RCA23_c30280	3199890	3199339	photosynthetic apparatus regulatory protein RegA	COG4567	T	407	550	-143
RCA23_c30290	3200570	3199947	protein SenC	COG1999	R	543	578	-35
RCA23_c30300	3200649	3202016	sensor histidine kinase RegB	COG0642	T	358	402	-44
RCA23_c30310	3202073	3203299	hypothetical protein			342	444	-102
RCA23_c30320	3203450	3204445	hypothetical protein, aminoglycoside phosphotransferase	COG3178	R	494	540	-46
RCA23_c30330	3204445	3205107	hypothetical protein, nucleotidyl transferase	COG1208	M	458	486	-28
RCA23_c30340	3205100	3208018	double-strand break repair protein AddB	COG3893	L	333	483	-150
RCA23_c30350	3208015	3211371	double-strand break repair helicase AddA	COG1074	L	483	495	-12
RCA23_c30360	3211430	3211750	thioredoxin TrxA	COG3118	O	926	781	145
RCA23_c30370	3211858	3212415	ATP-dependent protease HslV	COG5405	O	570	616	-46
RCA23_c30380	3212412	3213719	ATP-dependent hsl protease ATP-binding subunit HslU	COG1220	O	505	486	19
RCA23_c30390	3213757	3214968	MFS-type transporter	COG2814	G	450	609	-159
RCA23_c30400	3215543	3214965	hypothetical protein, Smr protein/MutS2	COG2840	S	359	384	-25
RCA23_c30410	3216574	3215546	putative lytic murein transglycosylase	COG2821	M	516	462	54
RCA23_c30420	3217245	3216571	hypothetical protein, TIM44	COG4395	S	603	469	134
RCA23_c30430	3217333	3217791	putative cytoplasmic membrane protein FxsA	COG3030	R	1.292	879	413
RCA23_c30440	3217847	3218353	protein-export protein SecB	COG1952	U	980	584	396
RCA23_c30450	3219045	3218350	DNA polymerase III subunit epsilon	COG0847	L	740	456	284
RCA23_c30460	3219631	3219038	dephospho-CoA kinase CoaE	COG0237	H	607	420	187
RCA23_c30470	3221043	3219628	shikimate 5-dehydrogenase AroE	COG0169	E	384	325	59

RCA23_c30480	3222030	3223286	transcription termination factor Rho	COG1158	K	799	587	212
RCA23_c30490	3223296	3224582	tRNA modification GTPase MnmE	COG0486	R	677	610	67
RCA23_c30500	3224597	3226456	tRNA uridine 5-carboxymethylaminomethyl modification enz	COG0445	D	754	479	275
RCA23_c30510	3226453	3227076	ribosomal RNA small subunit methyltransferase G	COG0357	M	923	624	299
RCA23_c30520	3227063	3227839	chromosome-partitioning protein ParA	COG1192	D	715	536	179
RCA23_c30530	3227913	3228749	chromosome-partitioning protein ParB	COG1475	K	590	401	189
RCA23_c30540	3229894	3228746	oxygen-independent coproporphyrinogen III oxidase HemN	COG0635	H	502	365	137
RCA23_c30550	3230502	3229894	nucleoside-triphosphatase RdgB	COG0127	F	443	404	39
RCA23_c30560	3231212	3230502	ribonuclease PH	COG0689	J	433	583	-150
RCA23_c30570	3231309	3232340	heat-inducible transcription repressor HrcA	COG1420	K	677	565	112
RCA23_c30580	3232347	3232901	protein GrpE	COG0576	O	715	541	174
RCA23_c30590	3235734	3232948	DNA mismatch repair protein MutS	COG0249	L	382	470	-88
RCA23_c30600	3235847	3238102	NADP-dependent malic enzyme MaeB	COG0281	C	751	604	147
RCA23_c30610	3238099	3238974	pfkB family carbohydrate kinase	COG0524	G	385	437	-52
RCA23_c30620	3239064	3239972	putative aminotransferase class IV	COG0115	E	420	511	-91
RCA23_c30630	3239969	3240679	hypothetical protein, branched-chain-amino-acid aminotransferase-like			281	358	-77
RCA23_c30640	3241914	3240697	argininosuccinate synthase ArgG	COG0137	E	456	465	-9
RCA23_c30650	3242076	3243311	threonine dehydratase, biosynthetic	COG1171	E	565	492	73
RCA23_c30660	3243760	3243320	putative NUDIX hydrolase	COG0494	L	859	585	274
RCA23_c30670	3243841	3244851	heat shock protein 33	COG1281	O	563	552	11
RCA23_c30680	3244832	3245428	putative NUDIX hydrolase	COG0494	L	312	397	-85
RCA23_c30690	3245425	3246585	hypothetical protein, poly A polymerase	COG0617	J	231	347	-116
RCA23_c30700	3246667	3248505	ABC transporter ATP-binding/permease protein	COG1132	V	582	671	-89
RCA23_c30710	3248505	3249719	hypothetical protein	COG2265	J	472	532	-60
RCA23_c30720	3249726	3250487	ion transport protein			613	593	20
RCA23_c30730	3250547	3251041	hypothetical protein	COG3034	S	812	587	225
RCA23_c30740	3251589	3251068	hypothetical protein, SCP-like extracellular protein	COG2340	S	495	433	62
RCA23_c30750	3251740	3252339	hypothetical protein	COG1376	S	713	514	199
RCA23_c30760	3253788	3252730	ferrochelatase HemH	COG0276	H	912	584	328
RCA23_c30770	3254654	3253839	hypothetical protein			409	512	-103

RCA23_c30780	3254684	3255250	hypothetical protein, ComF/GntX family	COG1040	R	415	446	-31
RCA23_c30790	3255612	3255869	glutaredoxin GrxC	COG0695	O	580	614	-34
RCA23_c30800	3255866	3256708	putative carbon-nitrogen hydrolase	COG0388	R	467	593	-126
RCA23_c30810	3256692	3257135	putative HTH-type transcriptional regulator, MarR family	COG1846	K	401	502	-101
RCA23_c30820	3257890	3257132	3-demethylubiquinone-9 3-O-methyltransferase UbiG	COG2227	H	394	398	-4
RCA23_c30830	3257891	3258916	proline iminopeptidase Pip	COG0596	R	482	453	29
RCA23_c30840	3259000	3259989	putative peptide transport system permease protein	COG0601	E	927	665	262
RCA23_c30850	3259998	3261185	putative peptide transport system permease protein	COG1173	E	830	594	236
RCA23_c30860	3261190	3262836	peptide transport system ATP-binding protein	COG1123	R	405	486	-81
RCA23_c30870	3262914	3264458	putative periplasmic peptide-binding protein	COG0747	E	501	416	85
RCA23_c30880	3264952	3265524	hypothetical protein UPF0090	COG0779	S	735	510	225
RCA23_c30890	3265524	3267137	transcription elongation protein NusA	COG0195	K	693	541	152
RCA23_c30900	3267138	3267740	hypothetical protein DUF448	COG2740	K	467	523	-56
RCA23_c30910	3267775	3270240	translation initiation factor IF-2	COG0532	J	419	390	29
RCA23_c30920	3270924	3270526	putative mutator MutT protein	COG1051	F	388	382	6
RCA23_c30930	3272138	3270921	arginine biosynthesis bifunctional protein ArgJ	COG1364	E	357	419	-62
RCA23_c30940	3272976	3272143	putative peptidylprolyl isomerase	COG0760	O	441	438	3
RCA23_c30950	3273165	3275849	protein translocase subunit SecA	COG0653	U	662	490	172
RCA23_c30960	3276115	3277296	putative O-acetyltransferase OatA	COG1835	I	719	508	211
RCA23_c30970	3278383	3277550	hypothetical protein	COG4922	S	341	243	98
RCA23_c30980	3278502	3278876	hypothetical protein, transcriptional regulator-like	COG1733	K	257	195	62
RCA23_c30990	3278997	3280049	UDP-glucoronate 5'-epimerase LspL	COG0451	M	224	174	50
RCA23_c31000	3281732	3280023	hypothetical protein			214	200	14
RCA23_c31010	3283201	3281858	phosphoglucosamine mutase GlmM	COG1109	G	394	488	-94
RCA23_c31020	3284844	3283315	putative ubiquinone biosynthesis protein UbiB	COG0661	R	400	432	-32
RCA23_c31030	3285621	3284845	ubiquinone/menaquinone biosynthesis methyltransferase U	COG2226	H	488	408	80
RCA23_c31040	3285680	3286531	formamidopyrimidine-DNA glycosylase MutM	COG0266	L	369	371	-2
RCA23_c31050	3286594	3287370	enoyl-CoA hydratase/isomerase	COG1024	I	637	567	70
RCA23_c31060	3287519	3287782	30S ribosomal protein S20	COG0268	J	521	411	110