

Table 3. Annotated genome of *Blochmannia floridanus* (Bfl) (GenBank/EMBL/DDBJ accession no. BX248583)

Bfl gene number	Gene name*	Start	End	Product	EC1	EC2	EC3	Cluster of orthologous genes (COG) no.	COG category
Bfl001	gidA	1	1905	glucose inhibited division protein				COG0445	D
Bfl002	atpB	2294	3112	ATP synthase subunit A	EC:3.6.3.14			COG0356	C
Bfl003	atpE	3181	3420	ATP synthase subunit C	EC:3.6.3.14			COG0636	C
Bfl004	atpF	3490	3975	ATP synthase subunit B	EC:3.6.3.14			COG0711	C
Bfl005	atpH	3976	4521	ATP synthase delta subunit	EC:3.6.3.14			COG0712	C
Bfl006	atpA	4543	6084	ATP synthase alpha subunit	EC:3.6.3.14			COG0056	C
Bfl007	atpG	6110	6976	ATP synthase gamma subunit	EC:3.6.3.14			COG0224	C
Bfl008	atpD	7006	8400	ATP synthase beta subunit	EC:3.6.3.14			COG0055	C
Bfl009	atpC	8460	8876	ATP synthase epsilon subunit	EC:3.6.3.14			COG0355	C
Bfl010	glmU	9010	10407	UDP-N-acetylglucosamine pyrophosphorylase	EC:2.7.7.23			COG1207	M
Bfl011	thdF	11961	10537	GTPase for tRNA modification and thiophene and furan oxidation				COG0486	R
Bfl012	yidC	13740	12064	putative Preprotein translocase subunit YidC				COG0706	R
Bfl013	yidD	14000	13776	Uncharacterized conserved protein				COG0759	S
Bfl014	rnpA	14326	13964	RNase P, protein component	EC:3.1.26.5			COG0594	L
Bfl015	rpmH	14514	14374	50s ribosomal protein l34				COG0230	J
Bfl016	dnaN	14731	15834	DNA polymerase III beta-subunit	EC:2.7.7.7			COG0592	L
Bfl017	gyrB	16096	18516	DNA gyrase subunit B	EC:5.99.1.3			COG0187	L
Bfl018	ibpA	18765	19175	heat shock protein A				COG0071	O
Bfl019	Bfl019	20356	19346	probable transmembrane protein				COG0628	P
Bfl020	glyQ	20794	21699	glycine-tRNA synthetase, alpha subunit	EC:6.1.1.14			COG0752	J
Bfl021	glyS	21725	23710	glycine-tRNA synthetase, beta subunit	EC:6.1.1.14			COG0751	J
Bfl022	sodA	24389	23766	manganese superoxide dismutase	EC:1.15.1.1			COG0605	P
Bfl023	prlC	24707	26794	oligopeptidase A	EC:3.4.24.70			COG0339	E
Bfl024	pitA	28562	26943	putative low-affinity inorganic phosphate transporter				COG0306	P
Bfl025	ubiA	28887	29741	4-hydroxybenzoate octaprenyl transferase	EC:2.5.1.-			COG0382	H

Bfl gene number	Gene name*	Start	End	Product	EC1	EC2	EC3	Cluster of orthologous genes (COG) no.	COG category
Bfl026	zur	30382	29903	zinc uptake regulation protein				COG0735	P
Bfl027	dnaB	30665	32065	replicative DNA helicase	EC:3.6.1.-			COG0305	L
Bfl028	ssb	32202	32678	single-strand DNA-binding protein				COG0629	L
Bfl029	yjcE	33060	34706	putative sodium/hydrogen exchanger family protein				COG0025	P
Bfl030	gltP	35103	36392	proton glutamate symport protein				COG1301	C
Bfl031	yjgF	36994	36578	putative translation initiation inhibitor				COG0251	S
Bfl032	argI	38105	37062	ornithine carbamoyltransferase	EC:2.1.3.3			COG0078	E
Bfl033	valS	41260	38360	valyl-tRNA synthetase	EC:6.1.1.9			COG0525	J
Bfl034	holC	41718	41257	DNA polymerase III, chi subunit	EC:2.7.7.7			COG2927	L
Bfl035	pepA	43352	41838	cytosol aminopeptidase	EC:3.4.11.1			COG0260	E
Bfl036	yjgP	43484	44596	putative inner membrane protein				COG0795	R
Bfl037	yjgQ	44598	45680	putative inner membrane protein				COG0795	R
Bfl038	yidZ	46615	45692	putative LysR-family transcriptional regulator				COG0583	K
Bfl039	tRNA-Leu5	46904	46985	tRNA-Leu anticodon CAA					
Bfl040	Bfl040	47224	47880	putative manganese transport system ATP-binding protein				COG1121	P
Bfl041	Bfl041	47930	48793	putative manganese transport system permease protein				COG1108	S
Bfl042	yhbG	49828	49103	probable ABC transport protein, ATP-binding component				COG1137	R
Bfl043	yhbN	50347	49841	conserved hypothetical protein				COG1934	S
Bfl044	yrbK	50936	50328	possible exported protein				COG3117	S
Bfl045	yrbA	51122	51376	conserved hypothetical protein				COG0271	T
Bfl046	murA	51431	52693	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	EC:2.5.1.7			COG0766	M
Bfl047	degQ	54183	52798	serine protease	EC:3.4.21.-			COG0265	O
Bfl048	yhcB	54803	54393	conserved hypothetical protein				COG3105	J
Bfl049	rplM	55306	55725	50S ribosomal subunit protein L13				COG0102	J
Bfl050	rpsI	55796	56188	30S ribosomal subunit protein S9				COG0103	J
Bfl051	yraP	56943	56365	possible lipoprotein				COG2823	S
Bfl052	yraL	57241	58146	conserved hypothetical protein				COG0313	R
Bfl053	mpB	58173	58584	regulatory RNA; RNase P RNA component, M1 RNA, processes tRNA, 4.5S RNA					

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Bfl054	yqjA	58900	59466	putative membrane protein				COG0586	R
Bfl055	tRNA-Met3	59570	59497	tRNA-Met anticodon CAT					
Bfl056	rpoD	61550	59697	RNA polymerase sigma-70 factor				COG0568	K
Bfl057	dnaG	63476	61710	DNA primase	EC:2.7.7.-			COG0358	L
Bfl058	rpsU	63837	63622	30S ribosomal subunit protein S21				COG0828	J
Bfl059	gcp	64010	65071	possible glycoprotease	EC:3.4.24.57			COG0533	O
Bfl060	ygiH	65733	65143	putative membrane protein				COG0344	S
Bfl061	folB	65861	66229	dihydroneopterin aldolase, also has dihydroneopterin triphosphate 2'-epimerase activity	EC:4.1.2.25			COG1539	H
Bfl062	cca	68011	66776	tRNA nucleotidyltransferase	EC:2.7.7.25			COG0617	J
Bfl063	rfaE	68185	69624	ADP-heptose synthase	EC:2.7.-.-			COG2870	G
Bfl064	yqjC	70039	69770	conserved hypothetical protein				COG2960	S
Bfl065	ribB	70261	70902	3,4-dihydroxy-2-butanone 4-phosphate synthase				COG0108	H
Bfl066	plsC	71182	71916	1-acyl-glycerol-3-phosphate acyltransferase	EC:2.3.1.51			COG0204	I
Bfl067	metC	73197	72022	beta-cystathionase	EC:4.4.1.8			COG0626	E
Bfl068	tRNA-Phe	73366	73294	tRNA-Phe anticodon GAA					
Bfl069	cutA	74061	73702	periplasmic divalent cation tolerance protein CutA				COG1324	P
Bfl070	mopB	74437	74730	GroES protein				COG0234	O
Bfl071	mopA	74787	76430	GroEL protein				COG0459	O
Bfl072	efp	76578	77141	elongation factor P (EF-P)				COG0231	J
Bfl073	yjeP	80439	77182	putative membrane protein				COG3264	S
Bfl074	psd	81411	80515	phosphatidylserine decarboxylase proenzyme	EC:4.1.1.65			COG0688	I
Bfl075	orn	81932	82474	oligoribonuclease	EC:3.1.-.-			COG1949	F
Bfl076	tRNA-Gly2	82596	82669	tRNA-Gly anticodon GCC					
Bfl077	yjeE	82974	83477	putative nucleotide-binding protein				COG0802	R
Bfl078	amiB	83491	84750	N-acetylmuramoyl-L-alanine amidase	EC:3.5.1.28			COG0860	M
Bfl079	miaA	84768	85739	tRNA delta-2-isopentenylpyrophosphate (IPP) transferase	EC:2.5.1.8			COG0324	J
Bfl080	hflX	86066	87184	HflX protein, putative GTP-binding protein				COG2262	R
Bfl081	hflK	87413	88735	HflK protein				COG0330	O

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Bfl082	hflC	88740	89765	HflC protein	EC:3.4.-.-			COG0330	O
Bfl083	purA	89881	91197	adenylosuccinate synthetase	EC:6.3.4.4			COG0104	F
Bfl084	yjfH	91405	92169	probable tRNA/rRNA methyltransferase	EC:2.1.1.-			COG0566	J
Bfl085	rpsF	92399	92761	30S ribosomal subunit protein S6				COG0360	J
Bfl086	rpsR	92839	93075	30S ribosomal subunit protein S18				COG0238	J
Bfl087	rplI	93152	93637	50S ribosomal subunit protein L9				COG0359	J
Bfl088	cysQ	93801	94589	cysQ protein				COG1218	P
Bfl089	ytfM	94765	96539	pseudogene of putative exported protein				COG0729	M
Bfl090	ytfN	96536	100396	putative exported protein				COG2911	S
Bfl091	ppa	101022	100483	inorganic pyrophosphatase	EC:3.6.1.1			COG0221	C
Bfl092	ispB	102159	101185	octaprenyl-diphosphate synthase	EC:2.5.1.-			COG0142	H
Bfl093	rplU	102286	102669	50S ribosomal subunit protein L21				COG0261	J
Bfl094	rpmA	102659	102916	50S ribosomal subunit protein L27				COG0211	J
Bfl095	yhbZ	103318	104235	probable GTP-binding protein				COG0536	R
Bfl096	greA	104321	104809	transcription elongation factor, cleaves 3' nucleotide of paused mRNA				COG0782	K
Bfl097	ftsJ	105196	105816	cell division protein 23S rRNA methyltransferase FtsJ	EC:2.1.1.-			COG0293	D
Bfl098	ftsH	105868	107802	cell division protein FtsH	EC:3.4.24.-			COG0465	O
Bfl099	folP	107925	108770	dihydropteroate synthase	EC:2.5.1.15			COG0294	H
Bfl100	mrsA	108772	110130	PGM/PMM-family protein	EC:5.4.2.2			COG1109	G
Bfl101	tRNA-Leu4	110685	110768	tRNA-Leu anticodon GAG					
Bfl102	tRNA-Met2	110836	110909	tRNA-Met anticodon CAT					
Bfl103	nusA	111377	112882	transcription pausing; L factor				COG0195	K
Bfl104	infB	112933	115626	protein chain initiation factor 2				COG0532	J
Bfl105	rbfA	115697	116050	ribosome-binding factor A (P15B protein)				COG0858	J
Bfl106	truB	116087	116854	tRNA pseudouridine 5S synthase	EC:4.2.1.70			COG0130	J
Bfl107	rpsO	116984	117256	30S ribosomal subunit protein S15				COG0184	J
Bfl108	pnp	117421	119514	polynucleotide phosphorylase, member of mRNA degradosome	EC:2.7.7.8			COG1185	J

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Bfl109	deaD	119755	121218	Cold-shock DEAD-box protein A, inducible ATP-independent RNA helicase				COG0513	L
Bfl110	holD	121590	121997	DNA polymerase III, psi subunit	EC:2.7.7.7			COG3050	L
Bfl111	thrA	122444	124900	aspartokinase I/homoserine dehydrogenase I	EC:2.7.2.4	EC:1.1.1.3		COG0527	E
Bfl112	thrB	124937	125872	homoserine kinase	EC:2.7.1.39			COG0083	E
Bfl113	thrC	125876	127207	threonine synthase	EC:4.2.99.2			COG0498	E
Bfl114	dnaK	127463	129394	DnaK protein (heat shock protein 70)				COG0443	O
Bfl115	dnaJ	129526	130659	DnaJ protein				COG0484	O
Bfl116	rpsT	131019	130753	30S ribosomal protein S20				COG0268	J
Bfl117	ribF	131171	132106	riboflavin biosynthesis protein RibF	EC:2.7.1.26	EC:2.7.7.2		COG0196	H
Bfl118	ileS	132130	134991	isoleucyl-tRNA synthetase	EC:6.1.1.5			COG0060	J
Bfl119	lspA	135013	135474	lipoprotein signal peptidase	EC:3.4.23.36			COG0597	N
Bfl120	lytB	135590	136492	pseudogene of LytB protein				COG0761	M
Bfl121	dapB	136567	137391	dihydrodipicolinate reductase	EC:1.3.1.26			COG0289	E
Bfl122	carA	137577	138725	carbamoyl-phosphate synthase small chain	EC:6.3.5.5			COG0505	E
Bfl123	carB	138746	142012	carbamoyl-phosphate synthase large chain	EC:6.3.5.5			COG0458	E
Bfl124	folA	142060	142566	dihydrofolate reductase type I	EC:1.5.1.3			COG0262	H
Bfl125	apaH	143440	142622	bis(5'-nucleosyl)-tetrphosphatase	EC:3.6.1.41			COG0639	T
Bfl126	ksgA	144369	143554	dimethyladenosine transferase	EC:2.1.1.-			COG0030	J
Bfl127	pdxA	145378	144350	pyridoxal phosphate biosynthetic protein PdxA				COG1995	H
Bfl128	surA	146651	145371	survival protein SurA precursor	EC:5.2.1.8			COG0760	O
Bfl129	imp	149157	146701	organic solvent tolerance protein precursor				COG1452	M
Bfl130	leuD	149950	149336	3-isopropylmalate dehydratase subunit 1	EC:4.2.1.33			COG0066	E
Bfl131	leuC	151384	149984	3-isopropylmalate dehydratase subunit 2	EC:4.2.1.33			COG0065	E
Bfl132	leuB	152490	151396	3-isopropylmalate dehydrogenase	EC:1.1.1.85			COG0473	E
Bfl133	leuA	154073	152514	2-isopropylmalate synthase	EC:4.1.3.12			COG0119	E
Bfl134	yabC	154460	155425	putative S-adenosyl methionine adenytransferase	EC:2.1.1.-			COG0275	M
Bfl135	ftsL	155428	155739	cell division protein FtsL				COG3116	M
Bfl136	ftsI	155840	157525	penicillin-binding protein 3 precursor				COG0768	M

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Bfl137	murE	157557	159056	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	EC:6.3.2.13			COG0769	M
Bfl138	murF	159076	160464	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanyl ligase	EC:6.3.2.15			COG0770	M
Bfl139	mraY	160449	161546	phospho-N-acetylmuramoyl-pentapeptide transferase	EC:2.7.8.13			COG0472	M
Bfl140	murD	161558	162892	UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase	EC:6.3.2.9			COG0771	M
Bfl141	ftsW	162965	164071	cell division protein FtsW				COG0772	D
Bfl142	murG	164094	165176	UDP-N-acetylglucosamine:N-acetylmuramyl- (pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase	EC:2.4.1.-			COG0707	M
Bfl143	murC	165206	166648	UDP-N-acetylmuramate:alanine ligase	EC:6.3.2.8			COG0773	M
Bfl144	ftsQ	166732	167562	cell division protein FtsQ				COG1589	M
Bfl145	ftsA	167555	168817	cell division protein FtsA				COG0849	D
Bfl146	ftsZ	168893	170068	cell division protein FtsZ				COG0206	D
Bfl147	lpxC	170136	171032	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	EC:3.5.1.-			COG0774	M
Bfl148	secA	171410	173932	preprotein translocase SecA subunit				COG0653	N
Bfl149	dksA	174973	175434	dosage-dependent dnaK suppressor protein				COG1734	T
Bfl150	folK	175495	175989	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase	EC:2.7.6.3			COG0801	H
Bfl151	lpdA	178012	176600	dihydrolipoamide dehydrogenase	EC:1.8.1.4			COG1249	C
Bfl152	aceF	179418	178141	dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase	EC:2.3.1.12			COG0508	C
Bfl153	aceE	182111	179433	pyruvate dehydrogenase E1 component	EC:1.2.4.1			COG2609	C
Bfl154	mrcB	182581	184923	penicillin-binding protein 1b; peptidoglycan synthetase	EC:2.4.2.-	EC:3.4.-.-		COG0744	M
Bfl155	yadR	185120	185479	conserved hypothetical protein				COG0316	S
Bfl156	pyrG	185911	187563	CTP synthetase	EC:6.3.4.2			COG0504	F
Bfl157	eno	187652	188995	enolase	EC:4.2.1.11			COG0148	G
Bfl158	cysJ	189377	191209	sulfite reductase (NADPH) flavoprotein beta subunit	EC:1.8.1.2			COG0369	P
Bfl159	cysI	191209	192918	sulfite reductase (NADPH) hemoprotein alpha subunit	EC:1.8.1.2			COG0155	P

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Bfl160	cysH	192957	193697	3'-phosphoadenosine 5'-phosphosulfate sulfotransferase	EC:1.8.99.4			COG0175	E
Bfl161	cysG	193837	195222	siroheme synthase	EC:2.1.1.107	EC:1.-.-.-	EC:4.99.1.-	COG0007	H
Bfl162	cysD	195282	196199	ATP sulfurylase (ATP:sulfate adenyltransferase) subunit 2	EC:2.7.7.4			COG0175	E
Bfl163	cysN	196218	197660	ATP sulfurylase (ATP:sulfate adenyltransferase) subunit 1	EC:2.7.7.4			COG2895	J
Bfl164	cysC	197664	198296	adenosine 5-phosphosulfate kinase	EC:2.7.1.25			COG0529	P
Bfl165	ygbQ	198470	198775	conserved hypothetical protein				COG2919	R
Bfl166	ygbP	199342	199461	pseudogene of 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	EC:2.7.7.60			COG1211	I
Bfl167	nlpD	200374	201321	lipoprotein NlpD precursor				COG0739	M
Bfl168	alaS	201467	204142	alanyl-tRNA synthetase	EC:6.1.1.7			COG0013	J
Bfl169	csrA	204306	204503	carbon storage regulator				COG1551	T
Bfl170	tRNA-Ser4	204652	204742	tRNA-Ser anticodon GCT					
Bfl171	tRNA-Arg4	204800	204873	tRNA-Arg anticodon ACG					
Bfl172	ffh	205013	206386	4.5S-RNP protein, GTP binding export factor, part of signal recognition particle with 4.5 RNA				COG0541	N
Bfl173	rpsP	206462	206710	30S ribosomal subunit protein S16				COG0228	J
Bfl174	rimM	206757	207314	16S rRNA processing protein				COG0806	J
Bfl175	trmD	207348	208094	tRNA(guanine-N1)methyltransferase	EC:2.1.1.31			COG0336	J
Bfl176	rplS	208123	208476	50S ribosomal subunit protein L19				COG0335	J
Bfl177	aroF	208858	209943	phospho-2-dehydro-3-deoxyheptonate aldolase, tyr-sensitive	EC:4.1.2.15			COG0722	E
Bfl178	tyrA	209950	211083	chorismate mutase/prephenate dehydrogenase	EC:1.3.1.12	EC:5.4.99.5		COG0287	E
Bfl179	pheA	212052	211156	prephenate dehydratase	EC:4.2.1.51			COG1605	E
Bfl180	yfiO	212889	212149	putative lipoprotein				COG0457	R
Bfl181	rluD	213012	213977	pseudouridine synthase (pseudouridines 1911, 1915, 1917 in 23S RNA)	EC:4.2.1.70			COG0564	J
Bfl182	clpB	214168	216786	ATP-dependent protease, Hsp 100, part of novel multi-chaperone system with DnaK, DnaJ, and GrpE				COG0542	O
Bfl183	murB	216984	218021	UDP-N-acetylenolpyruvoylglucosamine reductase	EC:1.1.1.158			COG0812	M
Bfl184	birA	218136	218960	bifunctional protein: biotin operon repressor and biotin-	EC:6.3.4.15			COG0340	K

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				[acetyl-CoA carboxylase] synthetase					
Bfl185	tRNA-Thr3	219918	219989	tRNA-Thr anticodon TGT					
Bfl186	tRNA-Tyr	220004	220085	tRNA-Tyr anticodon GTA					
Bfl187	tRNA-Gly1	220138	220209	tRNA-Gly anticodon TCC					
Bfl188	tRNA-Thr2	220246	220317	tRNA-Thr anticodon GGT					
Bfl189	bfr	220512	220982	bacterioferritin				COG2193	P
Bfl190	rpsJ	221115	221426	30S ribosomal subunit protein S10				COG0051	J
Bfl191	rplC	221527	222186	50S ribosomal subunit protein L3				COG0087	J
Bfl192	rplD	222183	222821	50S ribosomal subunit protein L4				COG0088	J
Bfl193	rplW	222830	223129	50S ribosomal subunit protein L23				COG0089	J
Bfl194	rplB	223151	223981	50S ribosomal subunit protein L2				COG0090	J
Bfl195	rpsS	224008	224289	30S ribosomal subunit protein S19				COG0185	J
Bfl196	rplV	224342	224671	50S ribosomal subunit protein L22				COG0091	J
Bfl197	rpsC	224731	225438	30S ribosomal subunit protein S3				COG0092	J
Bfl198	rplP	225456	225857	50S ribosomal subunit protein L16				COG0197	J
Bfl199	rpmC	225862	226062	50S ribosomal subunit protein L29				COG0255	J
Bfl200	rpsQ	226109	226366	30S ribosomal subunit protein S17				COG0186	J
Bfl201	rplN	226450	226821	50S ribosomal subunit protein L14				COG0093	J
Bfl202	rplX	226853	227173	50S ribosomal subunit protein L24				COG0198	J
Bfl203	rplE	227197	227769	50S ribosomal subunit protein L5				COG0094	J
Bfl204	rpsN	227775	228080	30S ribosomal subunit protein S14				COG0199	J
Bfl205	rpsH	228132	228527	30S ribosomal subunit protein S8				COG0096	J
Bfl206	rplF	228550	229095	50S ribosomal subunit protein L6				COG0097	J
Bfl207	rplR	229150	229503	50S ribosomal subunit protein L18				COG0256	J
Bfl208	rpsE	229516	230049	30S ribosomal subunit protein S5				COG0098	J
Bfl209	rpmD	230055	230231	50S ribosomal subunit protein L30				COG1841	J
Bfl210	rplO	230238	230681	50S ribosomal subunit protein L15				COG0200	J
Bfl211	secY	230690	232045	preprotein translocase subunit secY				COG0201	N
Bfl212	rpmJ	232091	232207	50S ribosomal subunit protein L36				COG0257	J

Bfl gene number	Gene name*	Start	End	Product	EC1	EC2	EC3	Cluster of orthologous genes (COG) no.	COG category
Bfl213	rpsM	232287	232643	30S ribosomal subunit protein S13				COG0099	J
Bfl214	rpsK	232707	233099	30S ribosomal subunit protein S11				COG0100	J
Bfl215	rpsD	233135	233758	30S ribosomal subunit protein S4				COG0522	J
Bfl216	rpoA	233794	234789	DNA-directed RNA polymerase alpha chain	EC:2.7.7.6			COG0202	K
Bfl217	rpIQ	234854	235231	50S ribosomal subunit protein L17				COG0203	J
Bfl218	fnt	236277	235306	methionyl-tRNA formyltransferase	EC:2.1.2.9			COG0223	J
Bfl219	def	236831	236304	polypeptide deformylase	EC:3.5.1.31			COG0242	J
Bfl220	yrdC	237099	237668	conserved hypothetical protein				COG0009	J
Bfl221	aroE	237684	238568	shikimate 5-dehydrogenase	EC:1.1.1.25			COG0169	E
Bfl222	5SrRNA	238664	238785	5S rRNA					
Bfl223	gloB	239591	238821	probable hydroxyacylglutathione hydrolase	EC:3.1.2.6			COG0491	R
Bfl224	rnhA	240144	239641	ribonuclease H	EC:3.1.26.4			COG0328	L
Bfl225	dnaQ	240201	240977	DNA polymerase III epsilon subunit	EC:2.7.7.7			COG0847	L
Bfl226	lpcA	241132	241713	phosphoheptose isomerase	EC:5.-.-.			COG0279	G
Bfl227	tRNA-Thr1	241865	241937	tRNA-Thr anticodon CGT					
Bfl228	ahpC	242632	242033	alkyl hydroperoxide reductase C22 protein	EC:1.6.4.-			COG0450	O
Bfl229	queA	242932	243993	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	EC:5.-.-.			COG0809	J
Bfl230	tgt	244122	245258	queuine tRNA-ribosyltransferase; tRNA-guanine transglycosylase	EC:2.4.2.29			COG0343	J
Bfl231	yajC	245301	245648	preprotein translocase YajC subunit				COG1862	S
Bfl232	secD	245653	247527	protein-export membrane protein SecD				COG0342	N
Bfl233	secF	247568	248470	protein-export membrane protein SecF				COG0341	N
Bfl234	ribD	248862	249998	bifunctional pyrimidine deaminase/reductase in pathway of riboflavin synthesis	EC:3.5.4.26	EC:1.1.1.193		COG0117	H
Bfl235	ribH	250136	250615	6,7-dimethyl-8-ribityllumazine synthase (riboflavin synthase beta chain)	EC:2.5.1.9			COG0054	H
Bfl236	nusB	250640	251056	transcription termination; L factor				COG0781	K
Bfl237	pgpA	251094	251570	phosphatidylglycerophosphatase A	EC:3.1.3.27			COG1267	I
Bfl238	dxs	253479	251626	1-deoxyxylulose-5-phosphate synthase	EC:4.1.3.7			COG1154	H

Bfl gene number	Gene name*	Start	End	Product	EC1	EC2	EC3	Cluster of orthologous genes (COG) no.	COG category
Bfl239	thiI	254257	255735	thiamine biosynthesis protein ThiI				COG0301	H
Bfl240	yajR	257057	255873	putative MFS family transporter				COG0477	G
Bfl241	cyoE	258063	257182	protohaeme IX farnesyltransferase (haeme O biosynthesis)	EC:2.5.1.-			COG0109	H
Bfl242	cyoD	258396	258094	cytochrome O ubiquinol oxidase subunit CyoD				COG3125	C
Bfl243	cyoC	258991	258401	cytochrome o ubiquinol oxidase subunit III	EC:1.10.3.-			COG1845	C
Bfl244	cyoB	260939	258975	cytochrome o ubiquinol oxidase subunit I	EC:1.10.3.-			COG0843	C
Bfl245	cyoA	261893	261009	cytochrome o ubiquinol oxidase subunit II	EC:1.10.3.-			COG1622	C
Bfl246	clpP	262722	263351	ATP-dependent Clp protease proteolytic subunit	EC:3.4.21.92			COG0740	O
Bfl247	clpX	263539	264819	ATP-dependent Clp protease ATP-binding subunit ClpX				COG1219	O
Bfl248	yggX	265176	264937	conserved hypothetical protein				COG2924	S
Bfl249	mutY	266297	265230	A/G-specific adenine glycosylase	EC:3.2.2.-			COG1194	L
Bfl250	yqgF	267389	266961	putative endonuclease involved in recombination				COG0816	R
Bfl251	yqgE	267967	267386	putative transcriptional regulator				COG1678	R
Bfl252	metK	269533	268376	S-adenosylmethionine synthetase	EC:2.5.1.6			COG0192	H
Bfl253	speB	269924	270835	agmatine ureohydrolase	EC:3.5.3.11			COG0010	E
Bfl254	pgk	271177	272379	phosphoglycerate kinase	EC:2.7.2.3			COG0126	G
Bfl255	fba	272472	273548	fructose 1,6-bisphosphate aldolase	EC:4.1.2.13			COG0191	G
Bfl256	rpiA	273801	274469	ribose 5-phosphate isomerase	EC:5.3.1.6			COG0120	G
Bfl257	ygfA	275194	274607	putative ligase				COG0212	H
Bfl258	ygfE	275633	275289	conserved hypothetical protein				COG3027	S
Bfl259	ubiH	276061	277245	2-octaprenyl-6-methoxyphenol hydroxylase	EC:1.14.13.-			COG0654	H
Bfl260	ygfZ	278759	277749	putative aminomethyltransferase				COG0354	R
Bfl261	prfB	279048	280145	peptide chain release factor 2 (RF-2)				COG1186	J
Bfl262	lysS	280221	281678	lysyl-tRNA synthetase	EC:6.1.1.6			COG1190	J
Bfl263	lysA	281804	283081	diaminopimelate decarboxylase	EC:4.1.1.20			COG0019	E
Bfl264	ygdP	283319	283795	conserved hypothetical protein	EC:3.6.1.-			COG0494	L
Bfl265	lgt	283950	284804	prolipoprotein diacylglyceryl transferase	EC:2.4.99.-			COG0682	M
Bfl266	recC	285021	288440	exonuclease V, subunit	EC:3.1.11.5			COG1330	L
Bfl267	recD	290416	288494	exonuclease V, alpha chain	EC:3.1.11.5			COG0507	L

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Bfl268	recB	294249	290623	exonuclease V, beta chain	EC:3.1.11.5			COG1074	L
Bfl269	dapD	295209	294367	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	EC:2.3.1.117			COG2171	E
Bfl270	map	296016	295222	methionine aminopeptidase	EC:3.4.11.18			COG0024	J
Bfl271	rpsB	296283	296978	30S ribosomal protein S2				COG0052	J
Bfl272	tsf	297058	297867	elongation factor Ts (EF-Ts)				COG0264	J
Bfl273	pyrH	298001	298732	uridine 5'-monophosphate kinase	EC:2.7.4.-			COG0528	F
Bfl274	frt	298800	299366	ribosome recycling factor				COG0233	J
Bfl275	dxr	299486	300661	1-deoxy-D-xylulose 5-phosphate reductoisomerase	EC:1.1.1.-			COG0743	I
Bfl276	uppS	300736	301488	undecaprenyl pyrophosphate synthetase	EC:2.5.1.31			COG0020	I
Bfl277	cdsA	301540	302406	phosphatidate cytidyltransferase	EC:2.7.7.41			COG0575	I
Bfl278	yaeL	302432	303820	putative membrane-associated Zn-dependent protease	EC:3.4.24.-			COG0750	M
Bfl279	yaeT	303837	306302	outer membrane protein precursor				COG0729	M
Bfl280	hlpA	306394	306900	histone-like protein, located in outer membrane				COG2825	L
Bfl281	lpxD	306928	308037	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	EC:2.3.1.-			COG1044	M
Bfl282	fabZ	308041	308496	(3R)-hydroxymyristol acyl carrier protein dehydrase	EC:4.2.1.-			COG0764	I
Bfl283	lpxA	308500	309288	acyl-[acyl-carrier-protein]:UDP-N- acetylglucosamine O-acyltransferase	EC:2.3.1.129			COG1043	M
Bfl284	lpxB	309315	310469	lipid-A-disaccharide synthase	EC:2.4.1.182			COG0763	M
Bfl285	rnhB	310493	311110	ribonuclease HII	EC:3.1.26.4			COG0164	L
Bfl286	dnaE	311183	314683	DNA polymerase III, alpha chain	EC:2.7.7.7			COG0587	L
Bfl287	accA	314706	315665	acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	EC:6.4.1.2			COG0825	I
Bfl288	mesJ	315871	317466	cell cycle protein MesJ				COG0037	R
Bfl289	proS	319333	317588	prolyl-tRNA synthetase	EC:6.1.1.15			COG0442	J
Bfl290	yaeD	319544	320070	pseudogene of conserved hypothetical protein				COG0241	E
Bfl291	accC	321577	320225	acetyl CoA carboxylase, biotin carboxylase subunit	EC:6.3.4.14			COG0439	I
Bfl292	accB	322030	321596	acetylCoA carboxylase, BCCP subunit, carrier of biotin				COG0511	I

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Bfl293	aroQ	322506	322066	3-dehydroquinate dehydratase II				COG0757	E
Bfl294	mreB	322853	323896	rod shape-determining protein MreB				COG1077	D
Bfl295	mreC	323987	324805	rod shape-determining protein MreC				COG1792	M
Bfl296	mreD	324845	325333	rod shape-determining protein MreD				COG2891	M
Bfl297	tldD	325620	327092	TldD protein				COG0312	R
Bfl298	pmbA	327138	328481	putative PmbA protein				COG0312	R
Bfl299	lon	328887	331223	Lon protease	EC:3.4.21.53			COG0466	O
Bfl300	apt	331775	332326	adenine phosphoribosyltransferase	EC:2.4.2.7			COG0503	F
Bfl301	dnaX	332391	334016	DNA polymerase III subunit gamma	EC:2.7.7.7			COG2812	L
Bfl302	adk	334622	335302	adenylate kinase	EC:2.7.4.3			COG0563	F
Bfl303	ybbF	336046	335303	UDP-2,3-diacetylglucosamine hydrolase	EC:3.6.1.-			COG2908	M
Bfl304	cysS	336243	337667	cysteinyl-tRNA synthetase	EC:6.1.1.16			COG0215	J
Bfl305	fold	338554	337664	FoID bifunctional protein [includes: methylenetetrahydrofolate dehydrogenase; methenyltetrahydrofolate cyclohydrolase	EC:1.5.1.5	EC:3.5.4.9		COG0190	H
Bfl306	tRNA-Arg3	338731	338804	tRNA-Arg anticodon TCT					
Bfl307	ytfF	338935	339897	putative membrane protein				COG0697	R
Bfl308	mrdB	341089	339974	rod shape-determining membrane protein; cell elongation in e phase				COG0772	D
Bfl309	mrdA	342966	341107	penicillin-binding protein 2				COG0768	M
Bfl310	ybeB	343366	343061	conserved hypothetical protein				COG0799	S
Bfl311	holA	344675	343641	DNA polymerase III, delta subunit	EC:2.7.7.7			COG1466	L
Bfl312	rlpB	345364	344753	rare lipoprotein B precursor				COG2980	M
Bfl313	leuS	347912	345309	leucyl-tRNA synthetase	EC:6.1.1.4			COG0495	J
Bfl314	Int	349649	348081	apolipoprotein N-acyltransferase	EC:2.3.1.-			COG0815	M
Bfl315	ybeX	350561	349686	haemolysin-related protein				COG1253	R
Bfl316	ybeY	351064	350603	conserved hypothetical protein				COG0319	S
Bfl317	phoL	352168	351161	PhoH-like ATP-binding protein				COG1702	T
Bfl318	ubiF	352518	353711	putative monooxygenase	EC:1.14.13.-			COG0654	H

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Bfl319	tRNA-Gln	353907	353836	tRNA-Gln anticodon TTG					
Bfl320	tRNA-Leu3	354041	353960	tRNA-Leu anticodon TAG					
Bfl321	tRNA-Met1	354170	354097	tRNA-Met anticodon CAT					
Bfl322	nagA	355509	354355	N-acetylglucosamine-6-phosphate deacetylase	EC:3.5.1.25			COG1820	G
Bfl323	nagB	356327	355524	glucosamine-6-phosphate isomerase	EC:3.5.99.6			COG0363	G
Bfl324	glnS	356593	358263	glutaminyl-tRNA synthetase	EC:6.1.1.18			COG0008	J
Bfl325	fldA	358897	358370	flavodoxin 1				COG0716	C
Bfl326	pgm	359724	361370	phosphoglucomutase	EC:5.4.2.2			COG0033	G
Bfl327	sdhC	362199	362594	succinate dehydrogenase cytochrome b-556 subunit	EC:1.3.99.1			COG2009	C
Bfl328	sdhD	362582	362929	succinate dehydrogenase hydrophobic membrane anchor protein	EC:1.3.99.1			COG2142	C
Bfl329	sdhA	362932	364740	succinate dehydrogenase flavoprotein subunit	EC:1.3.99.1			COG1053	C
Bfl330	sdhB	364754	365482	succinate dehydrogenase iron-sulfur protein	EC:1.3.99.1			COG0479	C
Bfl331	sucA	365626	368538	2-oxoglutarate dehydrogenase E1 component	EC:1.2.4.2			COG0567	C
Bfl332	sucB	368546	369862	dihydrolipoamide succinyltransferase component (E2)	EC:2.3.1.61			COG0508	C
Bfl333	sucC	369959	371158	succinyl-CoA synthetase beta chain	EC:6.2.1.5			COG0045	C
Bfl334	sucD	371161	372051	succinyl-CoA synthetase alpha chain	EC:6.2.1.5			COG0074	C
Bfl335	tolQ	372131	372880	TolQ protein				COG0811	N
Bfl336	tolR	372843	373271	tolR protein				COG0848	N
Bfl337	tolA	373293	374597	tolA protein				COG3064	N
Bfl338	tolB	374679	376061	tolB protein precursor				COG0823	N
Bfl339	pal	376113	376637	peptidoglycan-associated lipoprotein precursor				COG2885	N
Bfl340	ybgF	376643	377443	putative exported protein				COG1729	S
Bfl341	ybhE	378604	377588	conserved hypothetical protein				COG2706	R
Bfl342	gpmA	378754	379452	phosphoglycerate mutase 1	EC:5.4.2.1			COG0588	G
Bfl343	ybhL	379588	380298	putative permease				COG0670	R
Bfl344	ychF	381457	380411	putative ATP/GTP-binding protein				COG0012	R
Bfl345	pth	382176	381583	peptidyl-tRNA hydrolase	EC:3.1.1.29			COG0193	J
Bfl346	prsA	383272	382328	ribose-phosphate pyrophosphokinase	EC:2.7.6.1			COG0462	F

Bfl gene number	Gene name*	Start	End	Product	EC1	EC2	EC3	Cluster of orthologous genes (COG) no.	COG category
Bfl347	ipk	384036	383269	isopentenyl monophosphate kinase	EC:2.7.1.148			COG1947	S
Bfl348	prfA	384855	385931	peptide chain release factor 1 (RF-1)				COG0216	J
Bfl349	hemK	385928	386773	putative protoporphyrinogen oxidase	EC:2.1.1.-			COG2890	R
Bfl350	kdsA	386930	387766	2-dehydro-3-deoxyphosphooctonate aldolase	EC:4.1.2.16			COG2877	E
Bfl351	thrS	388653	389885	threonyl-tRNA synthetase	EC:6.1.1.3			COG0441	J
Bfl352	infC	389909	390436	translation initiation factor IF-3				COG0290	J
Bfl353	rpml	390531	390728	50S ribosomal subunit protein L35				COG0291	J
Bfl354	rplT	390826	391182	50S ribosomal subunit protein L20				COG0292	J
Bfl355	pheS	391286	392293	phenylalanyl-tRNA synthetase alpha chain	EC:6.1.1.20			COG0016	J
Bfl356	pheT	392329	394740	phenylalanyl-tRNA synthetase beta chain	EC:6.1.1.20			COG0072	J
Bfl357	lplA	394844	395857	lipoate-protein ligase A	EC:6.-.-			COG0095	H
Bfl358	sufA	396027	396410	putative HesB-like domain				COG0316	S
Bfl359	sufB	396424	397926	putative ABC transporter sufB				COG0719	R
Bfl360	sufC	397993	398730	probable ATP-dependent transporter sufC				COG0396	R
Bfl361	sufD	398714	400015	required for stability of iron-sulfur component of FhuF				COG0719	R
Bfl362	sufS	400012	401247	selenocysteine lyase	EC:4.4.1.16			COG0520	E
Bfl363	ynhA	401291	401722	conserved hypothetical protein				COG2166	R
Bfl364	lpp	402058	401822	major outer membrane lipoprotein				COG4238	M
Bfl365	tRNA-Val2	402258	402185	tRNA-Val anticodon GAC					
Bfl366	ribE	402614	403222	riboflavin synthase alpha chain	EC:2.5.1.9			COG0307	H
Bfl367	ydhD	403359	403694	conserved hypothetical protein				COG0278	O
Bfl368	rnt	404376	403705	ribonuclease T	EC:3.1.13.-			COG0847	L
Bfl369	slyA	404931	405365	transcriptional regulator SlyA				COG1846	K
Bfl370	pdxH	405628	406272	pyridoxamine 5'-phosphate oxidase	EC:1.4.3.5			COG0259	H
Bfl371	tyrS	406416	407684	tyrosyl-tRNA synthetase	EC:6.1.1.1			COG0162	J
Bfl372	nth	408370	407729	endonuclease III	EC:4.2.99.18			COG0177	L
Bfl373	fumC	409803	408457	fumarate hydratase class II	EC:4.2.1.2			COG0114	C
Bfl374	eaeH	409944	411986	putative adhesin					R
Bfl375	ubiX	412666	412067	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	EC:4.1.1.-			COG0163	H

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Bfl376	kdsB	413506	412730	3-deoxy-manno-octulosonate cytidyltransferase	EC:2.7.7.38			COG1212	M
Bfl377	ycaR	413688	413503	conserved hypothetical protein				COG2835	S
Bfl378	lpxK	414751	413750	tetraacyldisaccharide 4'-kinase	EC:2.7.1.130			COG1663	N
Bfl379	msbA	416502	414751	probable transport ATP-binding protein MsbA				COG1132	R
Bfl380	rpsA	418705	416978	30S ribosomal protein S1				COG0539	J
Bfl381	cmk	419514	418816	cytidylate kinase	EC:2.7.4.14			COG0283	F
Bfl382	aroA	420936	419635	3-phosphoshikimate 1-carboxyvinyltransferase	EC:2.5.1.19			COG0128	E
Bfl383	serC	422155	421058	phosphoserine aminotransferase	EC:2.6.1.52			COG1932	H
Bfl384	serS	423649	422339	seryl-tRNA synthetase	EC:6.1.1.11			COG0172	J
Bfl385	lolA	424784	424152	outer membrane lipoprotein carrier protein precursor				COG2834	M
Bfl386	ftsK	427235	424881	cell division protein FtsK				COG1674	D
Bfl387	trxB	427554	428525	thioredoxin reductase	EC:1.6.4.5			COG0492	O
Bfl388	infA	428649	428867	initiation factor IF-1				COG0361	J
Bfl389	oprC	431104	428942	outer membrane protein OprC				COG1629	N
Bfl390	yqeI	431534	432172	hypothetical protein				COG3710	S
Bfl391	mltE	433207	432452	membrane-bound lytic murein transglycosylase E	EC:3.2.1.-			COG0741	M
Bfl392	trmU	433593	434702	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	EC:2.1.1.61			COG0482	R
Bfl393	purB	434941	436326	adenylosuccinate lyase	EC:4.3.2.2			COG0015	F
Bfl394	lolE	437679	436429	ABC transporter integral membrane subunit				COG4591	M
Bfl395	lolD	438413	437706	ABC transporter ATP-binding subunit				COG1136	M
Bfl396	yefU	439620	438403	ABC transporter integral membrane subunit				COG4591	M
Bfl397	yefM	440303	439737	putative lipoprotein				COG3417	S
Bfl398	yefF	440895	440539	putative protein kinase C inhibitor				COG0537	F
Bfl399	yefH	441781	441002	putative deoxyribonuclease	EC:3.1.21.-			COG0084	R
Bfl400	holB	442801	441800	DNA polymerase III, delta prime subunit	EC:2.7.7.7			COG0470	L
Bfl401	tmk	443448	442813	thymidylate kinase	EC:2.7.4.9			COG0125	F
Bfl402	pabC	444440	443622	4-amino-4-deoxychorismate lyase	EC:4.-.-			COG0115	E
Bfl403	acpP	444803	444567	acyl carrier protein				COG0236	I

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Bfl404	fabG	445674	444940	3-oxoacyl-[acyl-carrier protein] reductase	EC:1.1.1.100			COG1028	R
Bfl405	fabD	446678	445713	malonyl CoA-acyl carrier protein transacylase	EC:2.3.1.39			COG0331	I
Bfl406	fabH	447663	446707	3-oxoacyl-[acyl-carrier-protein] synthase III	EC:2.3.1.41			COG0332	I
Bfl407	plsX	448709	447675	fatty acid/phospholipid synthesis protein PlsX				COG0416	I
Bfl408	rpmF	448900	448730	50S ribosomal protein L32				COG0333	J
Bfl409	rluC	450316	449348	ribosomal large subunit pseudouridine synthase C	EC:4.2.1.70			COG0564	J
Bfl410	rne	450736	452868	ribonuclease E	EC:3.1.4.-			COG1530	J
Bfl411	htrB	453267	454193	lipid A biosynthesis lauroyl acyltransferase	EC:2.3.1.-			COG1560	N
Bfl412	ybiS	454314	455209	pseudogene of putative exported protein				COG1376	S
Bfl413	tRNA-Leu2	455378	455296	tRNA-Leu anticodon TAA					
Bfl414	tRNA-Cys	455468	455398	tRNA-Cys anticodon GCA					
Bfl415	pgsA	456443	455871	phosphatidylglycerophosphate synthetase	EC:2.7.8.5			COG0558	I
Bfl416	tRNA-Lys2	456857	456786	tRNA-Lys anticodon CTT					
Bfl417	tRNA-Ser3	457082	456999	tRNA-Ser anticodon TGA					
Bfl418	yccK	457230	457559	putative sulfite reductase	EC:1.8.99.3			COG2920	R
Bfl419	yccV	457762	458079	conserved hypothetical protein				COG3785	S
Bfl420	fabA	458444	458962	D-3-hydroxydecanoyl-(acyl carrier-protein)	EC:4.2.1.60			COG0764	I
Bfl421	asnS	459061	460473	asparaginyl-tRNA synthetase	EC:6.1.1.22			COG0017	J
Bfl422	aspC	460603	461823	aspartate aminotransferase	EC:2.6.1.1			COG1448	E
Bfl423	ycbL	462523	461888	conserved hypothetical protein				COG0491	R
Bfl424	fabI	463402	462617	enoyl-[acyl-carrier-protein] reductase (NADH)	EC:1.3.1.9			COG0623	I
Bfl425	ribA	464182	464781	GTP cyclohydrolase II	EC:3.5.4.25			COG0807	H
Bfl426	trpE	465508	467073	anthranilate synthase component I	EC:4.1.3.27			COG0147	E
Bfl427	trpG	467081	467662	anthranilate synthase component II	EC:4.1.3.27			COG0512	E
Bfl428	trpD	467677	468699	anthranilate phosphoribosyltransferase	EC:2.4.2.18			COG0512	E
Bfl429	trpC	468711	470087	indole-3-glycerol phosphate synthase	EC:4.1.1.48	EC:5.3.1.24		COG0134	E
Bfl430	trpB	470124	471320	tryptophan synthase beta chain	EC:4.2.1.20			COG0133	E
Bfl431	trpA	471317	472132	tryptophan synthase alpha chain	EC:4.2.1.20			COG0159	E
Bfl432	tonB	473616	472837	TonB protein				COG0810	M

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Bfl433	cls	473951	475426	cardiolipin synthetase	EC:2.7.8.-			COG1502	I
Bfl434	tdk	476183	475605	thymidine kinase	EC:2.7.1.21			COG1435	F
Bfl435	xthA	477241	478044	exodeoxyribonuclease III	EC:3.1.11.2			COG0708	L
Bfl436	sppA	478172	480049	protease IV, a signal peptide peptidase	EC:3.4.21.-			COG0616	N
Bfl437	gapA	480436	481437	glyceraldehyde 3-phosphate dehydrogenase A	EC:1.2.1.12			COG0057	G
Bfl438	dsbB	481718	482242	disulfide bond formation protein B				COG1495	O
Bfl439	minC	482387	483103	septum site determining protein MinC				COG0850	D
Bfl440	minD	483114	483938	septum site determining protein MinD				COG2894	D
Bfl441	minE	483945	484247	cell division topological specificity factor				COG0851	D
Bfl442	yeaZ	484963	484301	conserved hypothetical protein				COG1214	O
Bfl443	pabB	485126	486511	para-aminobenzoate synthase component I	EC:4.1.3.-			COG0147	E
Bfl444	yoaE	488134	486575	putative membrane protein				COG0861	P
Bfl445	manX	488572	489561	PTS system, mannose-specific IIAB component	EC:2.7.1.69			COG2893	G
Bfl446	manY	489677	490492	phosphotransferase enzyme II, C component				COG3715	G
Bfl447	manZ	490505	491377	phosphotransferase enzyme II, D component				COG3716	G
Bfl448	cspC	491758	491549	cold shock-like protein CspC				COG1278	T
Bfl449	zwf	494125	492629	glucose 6-phosphate dehydrogenase	EC:1.1.1.49			COG0364	G
Bfl450	pykA	494615	496081	pyruvate kinase A	EC:2.7.1.40			COG0469	G
Bfl451	yebA	497569	496178	conserved hypothetical protein				COG0739	M
Bfl452	aspS	499511	497781	aspartyl-tRNA synthetase	EC:6.1.1.12			COG0173	J
Bfl453	argS	499941	501692	arginyl-tRNA synthetase	EC:6.1.1.19			COG0018	J
Bfl454	mviN	503270	501714	virulence factor MviN				COG0728	R
Bfl455	yceL	503795	505000	putative membrane transporter				COG0477	G
Bfl456	tRNA-Ser2	505261	505174	tRNA-Ser anticodon GGA					
Bfl457	tRNA-Ser1	505721	505634	tRNA-Ser anticodon CGA					
Bfl458	tRNA-Asn	505969	505897	tRNA-Asn anticodon GTT					
Bfl459	gutQ	507023	506043	putative phosphosugar binding protein				COG0517	R
Bfl460	yeeX	507763	507437	conserved hypothetical protein				COG2926	S
Bfl461	sbcB	508047	509552	exodeoxyribonuclease I	EC:3.1.11.1			COG2925	L

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Bfl462	hisG	509860	510759	ATP phosphoribosyltransferase	EC:2.4.2.17			COG0040	E
Bfl463	hisD	510764	512077	histidinol dehydrogenase	EC:1.1.1.23			COG0141	E
Bfl464	hisC	512074	513144	histidinol-phosphate aminotransferase	EC:2.6.1.9			COG0079	E
Bfl465	hisB	513168	514241	imidazoleglycerol-phosphate dehydratase; histidinol phosphatase	EC:3.1.3.15	EC:4.2.1.19		COG0131	E
Bfl466	hisH	514238	514828	glutamine amidotransferase, subunit with HisF	EC:2.4.2.-			COG0118	E
Bfl467	hisA	514835	515590	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase	EC:5.3.1.16			COG0106	E
Bfl468	hisF	515560	516336	imidazole glycerol phosphate synthase, subunit with HisH	EC:4.1.3.-			COG0107	E
Bfl469	hisI	516330	516971	phosphoribosyl-AMP cyclohydrolase / phosphoribosyl-ATP pyrophosphohydrolase	EC:3.5.4.19	EC:3.6.1.31		COG0140	E
Bfl470	gnd	518526	517102	6-phosphogluconate dehydrogenase, decarboxylating	EC:1.1.1.44			COG0362	G
Bfl471	metG	518883	520520	methionyl-tRNA synthetase	EC:6.1.1.10			COG0143	J
Bfl472	folE	521340	520675	GTP cyclohydrolase I	EC:3.5.4.16			COG0302	H
Bfl473	rplY	521617	521928	50s ribosomal protein L25				COG1825	J
Bfl474	ddlA	523025	521961	D-alanine:D-alanine ligase A	EC:6.3.2.4			COG1181	M
Bfl475	omp	524270	523140	outer membrane protein				COG3203	N
Bfl476	gyrA	527292	524704	DNA gyrase subunit A	EC:5.99.1.3			COG0188	L
Bfl477	ubiG	527499	528236	3-demethylubiquinone-9 3-methyltransferase	EC:2.1.1.64			COG2227	H
Bfl478	nrdA	528624	530909	ribonucleoside-diphosphate reductase I alpha chain	EC:1.17.4.1			COG0209	F
Bfl479	nrdB	530938	532068	ribonucleoside-diphosphate reductase I beta chain	EC:1.17.4.1			COG0208	F
Bfl480	yfaE	532043	532330	putative ferredoxin				COG0633	C
Bfl481	nuoN	533956	532442	NADH dehydrogenase I chain N	EC:1.6.5.3			COG1007	C
Bfl482	nuoM	535561	534032	NADH dehydrogenase I chain M	EC:1.6.5.3			COG1008	C
Bfl483	nuoL	537483	535606	NADH dehydrogenase I chain L	EC:1.6.5.3			COG1009	C
Bfl484	nuoK	537782	537480	NADH dehydrogenase I chain k	EC:1.6.5.3			COG0713	C
Bfl485	nuoJ	538333	537782	NADH dehydrogenase I chain J	EC:1.6.5.3			COG0839	C
Bfl486	nuoI	538908	538363	NADH dehydrogenase I chain I	EC:1.6.5.3			COG1143	C
Bfl487	nuoH	539903	538935	NADH dehydrogenase I chain H	EC:1.6.5.3			COG1005	C

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Bfl488	nuoG	542725	539900	NADH dehydrogenase I chain G	EC:1.6.5.3			COG1034	C
Bfl489	nuoF	544175	542838	NADH dehydrogenase I chain F	EC:1.6.5.3			COG1894	C
Bfl490	nuoE	544642	544178	NADH dehydrogenase I chain E	EC:1.6.5.3			COG1905	C
Bfl491	nuoCD	546523	544733	NADH dehydrogenase I chain C; chain D	EC:1.6.5.3			COG0649	C
Bfl492	nuoB	547324	546653	NADH dehydrogenase I chain B	EC:1.6.5.3			COG0377	C
Bfl493	nuoA	547761	547330	NADH dehydrogenase I chain A	EC:1.6.5.3			COG0838	C
Bfl494	folC	549446	548199	folypolyglutamate synthase	EC:6.3.2.17	EC:6.3.2.12		COG0285	H
Bfl495	accD	550403	549540	acetyl-CoA carboxylase beta subunit	EC:6.4.1.2			COG0777	I
Bfl496	truA	551280	550522	tRNA pseudouridine synthase A	EC:4.2.1.70			COG0101	J
Bfl497	pdxB	552555	551437	erythronate-4-phosphate dehydrogenase	EC:1.1.1.-			COG0111	C
Bfl498	fabB	554051	552834	3-oxoacyl-[acyl-carrier-protein] synthase I	EC:2.3.1.41			COG0304	I
Bfl499	yfcB	554680	555591	conserved hypothetical protein	EC:2.1.1.72			COG2890	R
Bfl500	aroC	555595	556668	chorismate synthase	EC:4.6.1.4			COG0082	E
Bfl501	tRNA-Arg2	556932	556861	tRNA-Arg anticodon CCT					
Bfl502	mntH	558390	557152	manganese transport protein MntH				COG1914	P
Bfl503	nupC	558663	559877	nucleoside permease NupC				COG1972	F
Bfl504	gltX	561718	560267	glutamyl-tRNA synthetase	EC:6.1.1.17			COG0008	J
Bfl505	tRNA-Val1	561940	561868	tRNA-Val anticodon TAC					
Bfl506	tRNA-Lys1	562056	561984	tRNA-Lys anticodon TTT					
Bfl507	lig	563944	562160	DNA ligase	EC:6.5.1.2			COG0272	L
Bfl508	cysK	564242	565186	cysteine synthase A	EC:4.2.99.8			COG0031	E
Bfl509	ptsH	565535	565807	phosphocarrier protein HPr				COG1925	G
Bfl510	ptsI	565839	567563	phosphoenolpyruvate-protein phosphotransferase	EC:2.7.3.9			COG1080	G
Bfl511	cysA	568739	567687	sulphate transport ATP-binding protein CysA				COG1118	P
Bfl512	cysW	569626	568769	sulphate transport system permease protein CysW				COG4208	P
Bfl513	cysU	570464	569628	sulphate transport system permease protein CysU				COG0555	P
Bfl514	cysP	571503	570469	thiosulphate-binding protein precursor				COG1613	P
Bfl515	talA	572171	573142	transaldolase A	EC:2.2.1.2			COG0176	G
Bfl516	tktA	573156	575150	transketolase	EC:2.2.1.1			COG0021	G

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Bfl517	dapE	575233	576387	succinyl-diaminopimelate desuccinylase	EC:3.5.1.18			COG0624	E
Bfl518	dapA	577859	576981	dihydrodipicolinate synthase	EC:4.2.1.52			COG0329	E
Bfl519	bcp	578340	578819	bacterioferritin comigratory protein				COG1225	O
Bfl520	upp	579510	578884	uracil phosphoribosyltransferase	EC:2.4.2.9			COG0035	F
Bfl521	ureG	580938	580309	putative urease accessory protein G				COG0378	F
Bfl522	ureF	581714	581031	putative urease accessory protein F				COG0830	F
Bfl523	ureC	583716	582013	putative urease structural subunit C (alpha)	EC:3.5.1.5			COG0804	F
Bfl524	ureB	584030	583719	putative urease structural subunit B (beta)	EC:3.5.1.5			COG0832	F
Bfl525	ureA	584368	584066	putative urease structural subunit A (gamma)	EC:3.5.1.5			COG0831	F
Bfl526	ureD	585245	584385	putative urease accessory protein D				COG0829	F
Bfl527	guaA	586991	585411	GMP synthase (glutamine-hydrolyzing)	EC:6.3.5.2			COG0518	F
Bfl528	guaB	588525	587056	inosine-5'-monophosphate dehydrogenase	EC:1.1.1.205			COG0516	F
Bfl529	mgo	588920	590494	probable malate:quinone oxidoreductase (malate dehydrogenase (acceptor))	EC:1.1.99.16			COG0579	R
Bfl530	engA	592011	590554	putative GTP-binding protein				COG1160	R
Bfl531	hisS	593408	592107	histidyl-tRNA synthetase	EC:6.1.1.21			COG0124	J
Bfl532	gcpE	594331	593566	pseudogene of GcpE protein (protein E)				COG0821	M
Bfl533	ndk	596452	596042	nucleoside diphosphate kinase	EC:2.7.4.6			COG0105	F
Bfl534	nifS	597951	596764	putative L-cysteine desulfurase	EC:4.4.1.-			COG1104	E
Bfl535	suhB	598453	599277	putative myo-inositol-1(or 4)-monophosphatase	EC:3.1.3.25			COG0483	G
Bfl536	glyA	600630	599386	serine hydroxymethyltransferase	EC:2.1.2.1			COG0112	E
Bfl537	yfhC	601183	600704	putative cytosine/adenosine deaminase	EC:3.5.4.1			COG0590	F
Bfl538	acpS	601704	601327	holo-[acyl-carrier protein] synthase	EC:2.7.8.7			COG0736	I
Bfl539	pdxJ	602444	601701	putative pyridoxal phosphate biosynthetic protein				COG0854	H
Bfl540	rnc	603368	602670	ribonuclease III	EC:3.1.26.3			COG0571	K
Bfl541	lepB	604501	603503	signal peptidase I	EC:3.4.21.89			COG0681	N
Bfl542	lepA	606344	604545	GTP-binding protein LepA				COG0481	N
Bfl543	ung	606597	607262	uracil-DNA glycosylase	EC:3.2.2.-			COG0692	L
Bfl544	grpE	608081	607494	heat shock protein GrpE				COG0576	O

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Bfl545	yfjB	608206	609087	probable inorganic polyphosphate/ATP-NAD kinase	EC:2.7.1.23			COG0061	R
Bfl546	smpA	609173	609520	small membrane protein A				COG2913	S
Bfl547	yfjG	610048	609605	conserved hypothetical protein				COG2867	S
Bfl548	smpB	610196	610642	small protein B; putative tmRNA-binding protein				COG0691	O
Bfl549	tmRNA	611082	610694	tmRNA					
Bfl550	emrE	611253	611582	emrE protein (methyl viologen resistance protein C) (ethidium resistance protein)				COG2076	P
Bfl551	pssA	611675	613060	phosphatidylserine synthase (CDP-diacylglycerol-serine O-phosphatidyltransferase)	EC:2.7.8.8			COG1502	I
Bfl552	23SrRNA	616171	613128	23S rRNA					
Bfl553	tRNA-Glu	616408	616337	tRNA-Glu anticodon TTC					
Bfl554	16SrRNA	618033	616478	16S rRNA					
Bfl555	purH	618462	620111	phosphoribosylaminoimidazolecarboxamide formyltransferase, IMP cyclohydrolase and MGS-like domain	EC:2.1.2.3	EC:3.5.4.10		COG0138	F
Bfl556	rpoC	624491	620229	DNA-directed RNA polymerase, beta-prime-subunit	EC:2.7.7.6			COG0086	K
Bfl557	rpoB	628634	624606	DNA-directed RNA polymerase, beta-subunit	EC:2.7.7.6			COG0085	K
Bfl558	rplL	629221	628841	50S ribosomal subunit protein L7/L12				COG0222	J
Bfl559	rplJ	629813	629316	50S ribosomal subunit protein L10				COG0244	J
Bfl560	rplA	630838	630131	50S ribosomal subunit protein L1				COG0081	J
Bfl561	rplK	631275	630835	50S ribosomal subunit protein L11				COG0080	J
Bfl562	nusG	631928	631383	transcription antitermination protein NusG				COG0250	K
Bfl563	secE	632304	631930	preprotein translocase SecE subunit				COG0690	N
Bfl564	tuf	633643	632459	elongation factor Tu (EF-Tu)	EC:3.6.1.48			COG0050	J
Bfl565	fusA	635872	633743	elongation factor G (EF-G)	EC:3.6.1.48			COG0480	J
Bfl566	rpsG	636453	635980	30S ribosomal subunit protein S7				COG0049	J
Bfl567	rpsL	636975	636601	30S ribosomal subunit protein S12				COG0048	J
Bfl568	pabA	638311	637730	para-aminobenzoate synthase, glutamine amidotransferase component II	EC:4.1.3.-			COG0512	E

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Bfl569	trpS	639475	638471	tryptophanyl-tRNA synthetase	EC:6.1.1.2			COG0180	J
Bfl570	rpe	640399	639719	ribulose-phosphate 3-epimerase	EC:5.1.3.1			COG0036	G
Bfl571	aroB	641790	640696	3-dehydroquinate synthase	EC:4.6.1.3			COG0337	E
Bfl572	aroK	642392	641835	shikimate kinase I	EC:2.7.1.71			COG0703	E
Bfl573	yhgI	643461	644078	conserved hypothetical protein				COG0694	O
Bfl574	asd	645359	644244	aspartate-semialdehyde dehydrogenase	EC:1.2.1.11			COG0136	E
Bfl575	yhgN	645579	646172	putative inner membrane protein				COG2095	S
Bfl576	yigL	647322	646522	putative hydrolase of the HAD superfamily				COG0561	R
Bfl577	corA	648511	647567	magnesium and cobalt transport protein				COG0598	P
Bfl578	yigB	649628	648900	putative hydrolase of the HAD superfamily				COG1011	R
Bfl579	dapF	650481	649651	diaminopimelate epimerase	EC:5.1.1.7			COG0253	E
Bfl580	hemC	650907	651842	prophobilinogen deaminase	EC:4.3.1.8			COG0181	H
Bfl581	hemD	651868	652611	uroporphyrinogen III synthase	EC:4.2.1.75			COG1587	H
Bfl582	tRNA-Pro	652786	652713	tRNA-Pro anticodon TGG					
Bfl583	tRNA-Leu1	652885	652799	tRNA-Leu anticodon CAG					
Bfl584	tRNA-His	652988	652916	tRNA-His anticodon GTG					
Bfl585	tRNA-Arg1	653133	653060	tRNA-Arg anticodon CCG					
Bfl586	rho	654689	653430	transcription termination factor Rho				COG1158	K
Bfl587	trxA	655399	655058	thioredoxin I, redox factor				COG0526	O
Bfl588	ilvC	657021	655543	ketol-acid reductoisomerase	EC:1.1.1.86			COG0059	E
Bfl589	ilvA	658643	657099	threonine deaminase	EC:4.2.1.16			COG1171	E
Bfl590	ilvD	660538	658682	dihydroxyacid dehydratase	EC:4.2.1.9			COG0129	E
Bfl591	ilvE	661540	660617	branched-chain amino-acid aminotransferase	EC:2.6.1.42			COG0115	E
Bfl592	ilvM	661847	661611	acetolactate synthase II, small subunit	EC:4.1.3.18			COG0440	E
Bfl593	ilvG	663556	661892	acetolactate synthase II, large subunit	EC:4.1.3.18			COG0028	E
Bfl594	tRNA-Trp	664046	663975	tRNA-Trp anticodon CCA					
Bfl595	tRNA-Asp	664177	664104	tRNA-Asp anticodon GTC					
Bfl596	tRNA-Ala	664314	664242	tRNA-Ala anticodon TGC					
Bfl597	metF	666003	665107	5,10 methylenetetrahydrofolate reductase	EC:1.7.99.5			COG0685	E

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Bfl598	metB	667310	666153	cystathionine gamma-synthase	EC:4.2.99.9			COG0626	E
Bfl599	rpmE	667721	667500	50S ribosomal protein L31				COG0254	J
Bfl600	fpr	668321	669070	ferredoxin--NADP reductase	EC:1.18.1.2			COG1018	C
Bfl601	tpiA	669260	670048	triosephosphate isomerase	EC:5.3.1.1			COG0149	G
Bfl602	pfkA	671076	670114	6-phosphofructokinase	EC:2.7.1.11			COG0205	G
Bfl603	cysE	672145	671411	serine acetyltransferase	EC:2.3.1.30			COG1045	E
Bfl604	gpsA	673232	672231	glycerol-3-phosphate dehydrogenase	EC:1.1.1.94			COG0240	C
Bfl605	grxC	673941	673675	glutaredoxin 3				COG0695	O
Bfl606	yibN	674412	673969	putative Rhodanese-related sulfurtransferases				COG0607	P
Bfl607	rfaD	674838	675773	ADP-L-Glycero-D-mannoheptose-6-epimerase	EC:5.1.3.20			COG0451	M
Bfl608	rfaF	675817	676872	ADP-heptose; lipopolysaccharide heptosyltransferase II	EC:2.4.1.-			COG0859	M
Bfl609	rfaC	676893	677873	lipopolysaccharide heptosyltransferase I	EC:2.4.1.-			COG0859	M
Bfl610	kdtA	678180	679472	3-deoxy-D-manno-octulosonic-acid transferase	EC:2.4.99.-			COG1519	M
Bfl611	rpmG	679688	679527	50S ribosomal subunit protein L33				COG0267	J
Bfl612	rpmB	679936	679697	50S ribosomal subunit protein L28				COG0227	J
Bfl613	dut	680447	680902	deoxyuridine 5'-triphosphate nucleotidohydrolase	EC:3.6.1.23			COG0756	F
Bfl614	yicC	681103	681975	putative stress-induced protein				COG1561	S
Bfl615	Bfl615	682523	682957	putative transcription regulator protein				COG1846	R
Bfl616	gmk	683158	683790	guanylate kinase	EC:2.7.4.8			COG0194	F
Bfl617	rpoZ	683827	684009	DNA-directed RNA polymerase omega chain	EC:2.7.7.6			COG1758	K
Bfl618	glnA	684080	685501	glutamine synthetase	EC:6.3.1.2			COG0174	E
Bfl619	polA	688468	685637	DNA polymerase I	EC:2.7.7.7			COG0749	L
Bfl620	yigC	690798	689299	putative oxidoreductase	EC:4.1.1.-			COG0043	S
Bfl621	aarF	692543	690906	ubiquinone biosynthesis protein				COG0661	R
Bfl622	ubiE	693869	693105	ubiquinone/menaquinone biosynthesis methyltransferase UbiE	EC:2.1.1.-			COG2226	H
Bfl623	rumC	695451	693976	putative membrane protein				COG1322	S
Bfl624	udp	696377	695562	uridine phosphorylase	EC:2.4.2.3			COG2820	F
Bfl625	metE	698735	696426	5-methyltetrahydropteroyltryglutamate-homocysteine S-	EC:2.1.1.14			COG0620	E

Bfl gene number	Gene name*	Start	End	Product	EC1	EC2	EC3	Cluster of orthologous genes (COG) no.	COG category
				methyltransferase					
Bfl626	rpoH	699829	698978	RNA polymerase sigma-32 factor				COG0568	K
Bfl627	ftsY	701089	700163	cell division protein FtsY				COG0552	N
Bfl628	yhhF	701183	701773	putative methyltransferase	EC:2.1.1.-			COG0742	L
Bfl629	pgi	703581	701905	glucose-6-phosphate isomerase	EC:5.3.1.9			COG0166	G
Bfl630	metA	704748	703858	homoserine O-succinyltransferase	EC:2.3.1.46			COG1897	E
Bfl631	tRNA-Ile	705085	705012	tRNA-Ile anticodon GAT					

*Pseudogenes are in shadowed boxes.