Protein id	Swiss-Prot		Gene name	EcoGene name	GenBank GI number
	Entry name	Accession Number			
b0037	CAIC_ECOLI	P31552	caiC	EG11558	1786221
b0051	KSGA_ECOLI	P06992	ksgA	EG10523	1786236
b0110	AMPD_ECOLI	P13016	ampD	EG10041	1786300
b0126	YADF_ECOLI	P36857	yadF	EG12319	1786318
b0179	LPXD_ECOLI	P21645	lpxD	EG10316	1786376
b0323	ARCM_ECOLI	P77624	yahI	EG13593	1786516
b0363	YAIP_ECOLI	Q47536	yaiP	EG13298	1786560
b0394	YAJF_ECOLI	P23917	mak	EG11288	1786593
b0419	YAJO_ECOLI	P77735	yajO	EG13611	1786621
b0429	CYOD_ECOLI	P18403	cyoD	EG10181	1786632
b0430	CYOC_ECOLI	P18402	cyoC	EG10180	1786633
b0431	CYOB_ECOLI	P18401	cyoB	EG10179	1786634
b0452	TESB_ECOLI	P23911	tesB	EG10995	1786657
b0454	YBAZ_ECOLI	P75707	ybaZ	EG13254	1786659
b0476	AES_ECOLI	P23872	aes	EG11101	1786682
b0581	YBDK_ECOLI	P77213	ybdK	EG13644	1786795
b0630	LIPB_ECOLI	P30976	lipB	EG11591	1786848
b0714	END8_ECOLI	P50465	nei	EG13237	1786932
b0736	YBGC_ECOLI	P08999	ybgC	EG11110	1786957
b0772	YBHC_ECOLI	P46130	ybhC	EG12875	1786989
b0825	FSAA_ECOLI	P78055	fsaA	EG13471	1787046
b0859	YBJF_ECOLI	P75817	ybjF	EG13427	1787083
b0894	DMSA_ECOLI	P18775	dmsA	EG10232	1787121
b0909	YCAL_ECOLI	P43674	ycaL	EG13133	1787138
b0927	YCBL_ECOLI	P75849	ycbL	EG13704	1787158
b0948	YCBY_ECOLI	P75864	ycbY	EG13717	1787181
b1055	YCEA_ECOLI	P24188	yceA	EG11116	1787294
b1059	MTOX_ECOLI	P40874	solA	EG12669	1787298
b1119	YCFX_ECOLI	P75959	ycfX	EG13442	1787363
b1145	YMFK_ECOLI	P75974	ymfK	EG14249	1787391
b1183	UMUD_ECOLI	P04153	umuD	EG11057	1787431
b1200	YCGT_ECOLI	P76015	dhaK	EG13901	1787450
b1271	YCIK_ECOLI	P31808	yciK	EG11759	1787526
b1298	YCJL_ECOLI	P76038	ycjL	EG13909	1787556
b1409	YNBB_ECOLI	P76091	ynbB	EG13749	1787677
b1411	YNBD_ECOLI	P76093	ynbD	EG13751	1787679
b1498	YDEN_ECOLI	P77318	ydeN	EG13796	1787775
b1517	YNEB_ECOLI	P76143	lsrF	EG13810	1787796
b1542	YDFI_ECOLI	P77260	ydfI	EG13821	1787823
b1598	YDGD_ECOLI	P76176	ydgD	EG13925	1787882
b1606	YDGB_ECOLI	P52109	ydgB	EG13189	1787891
b1650	NEMA_ECOLI	P77258	nemA	EG13546	1787939
b1687	YDIJ_ECOLI	P77748	ydiJ	EG13969	1787977
b1710	BTUE_ECOLI	P06610	btuE	EG10129	1788003
b1737	PTCC_ECOLI	P17334	chbC	EG10141	1788032
b1748	ARGM_ECOLI	P77581	argM	EG13999	1788044
b1771	YDJG_ECOLI	P77256	ydjG	EG13483	1788070
b1773	YDJI_ECOLI	P77704	ydjI	EG13485	1788072
b1774	YDJJ_ECOLI	P77280	ydjJ	EG13486	1788073
b1802	YEAW_ECOLI	P76253	yeaW	EG13509	1788103

b1812	PABB_ECOLI	P05041	pabB	EG10683	1788114
b1829	HTPX_ECOLI	P23894	htpX	EG10462	1788133
b1917	YECC_ECOLI	P37774	yecC	EG12347	1788225
b2058	WCAB_ECOLI	P77558	wcaB	EG13570	1788371
b2096	GATY_ECOLI	P37192	gatY	EG12419	1788412
b2102	YEGX_ECOLI	P76421	yegX	EG14067	1788419
b2147	YEIA_ECOLI	P25889	yeiA	EG11289	1788469
b2255	YFBG_ECOLI	P77398	arnA	EG14091	1788589
b2267	ELAA_ECOLI	P52077	elaA	EG13184	1788602
b2299	YFCD_ECOLI	P76494	yfcD	EG14107	1788637
b2371	YFDE_ECOLI	P76518	yfdE	EG13284	1788714
b2374	YFDW_ECOLI	P77407	yfdW	EG14145	1788717
b2407	XAPA_ECOLI	P45563	xapA	EG20250	1788746
b2426	UCPA_ECOLI	P37440	ucpA	EG12133	1788766
b2458	EUTD_ECOLI	P77218	eutD	EG14188	1788800
b2468	AEGA_ECOLI	P37127	aegA	EG12409	1788811
b2482	HYFB_ECOLI	P23482	hyfB	EG11282	1788827
b2484	HYFD_ECOLI	P77416	hyfD	EG14212	1788829
b2486	HYFF_ECOLI	P77437	hyfF	EG14214	1788831
b2494	YFGC_ECOLI	P76568	yfgC	EG14199	1788840
b2495	YFGD_ECOLI	P76569	yfgD	EG14200	1788841
b2532	YFHQ_ECOLI	P77438	yfhQ	EG13452	1788881
b2638	YFJU_ECOLI	P52136	yfjU	EG13207	1788991
b2690	YQAB_ECOLI	P77475	yqaB	EG13530	1789046
b2736	YGBJ_ECOLI	Q46888	ygbJ	EG13104	1789092
b2738	YGBL_ECOLI	Q46890	ygbL	EG13106	1789094
b2776	YGCE_ECOLI	P55138	ygcE	EG13033	1789138
b2785	RUMA_ECOLI	P55135	rumA	EG11247	1789148
b2788	GUDX_ECOLI	Q46915	gudX	EG13168	1789151
b2794	YQCD_ECOLI	Q46920	yqcD	EG13173	1789158
b2836	AAS_ECOLI	P31119	aas	EG11679	1789201
b2872	YGEY_ECOLI	Q46805	ygeY	EG13055	1789236
b2873	YGEZ_ECOLI	Q46806	hyuA	EG13056	1789237
b2874	ARCL_ECOLI	Q46807	yqeA	EG13057	1789238
b2887	YGFT_ECOLI	Q46820	ygfT	EG13070	1789253
b2912	YGFA_ECOLI	P09160	ygfA	EG11158	1789278
b2917	SBM_ECOLI	P27253	yliK	EG11444	1789284
b2920	YGFH_ECOLI	P52043	ygfH	EG12973	1789287
b2930	YGGF_ECOLI	P21437	yggF	EG11245	1789298
b2936	YGGG_ECOLI	P25894	yggG	EG11291	1789305
b2979	GLCD_ECOLI	P52075	glcD	EG12997	1789351
b2999	Q46849	None	yghX	EG13008	1789373
b3015	YGIQ_ECOLI		ygiQ	EG13019	1789391
b3019	PARC_ECOLI	P20082	parC	EG10686	1789396
b3030	PARE_ECOLI	P20083	parE	EG10687	1789408
b3054	YGIF_ECOLI	P30871	ygiF	EG11603	1789434
b3114	TDCE_ECOLI	P42632	tdcE	EG12758	1789502
b3115	TDCD_ECOLI	P11868	tdcD	EG11172	1789503
b3137	AGAY_ECOLI	P42908	kbaY	EG12768	1789526
b3141	AGAI_ECOLI	P42912	agaI	EG12772	1789530
b3360	PABA_ECOLI	P00903	pabA	EG10682	1789760
b3374	YHFQ_ECOLI	P45543	frlD	EG12912	1789775

b3379	PHP_ECOLI	P45548	php	EG12917	1789780
b3551	BISC_ECOLI	P20099	bisC	EG10124	1789973
b3581	SGBH_ECOLI	P37678	sgbH	EG12285	1790006
b3583	SGBE_ECOLI	P37680	sgbE	EG12287	1790008
b3611	YIBN_ECOLI	P37688	yibN	EG12295	1790040
b3647	YICF_ECOLI	P25772	ligB	EG11334	1790079
b3678	YIDJ_ECOLI	P31447	yidJ	EG11705	1790112
b3683	PTIC_ECOLI	P31452	glvC	EG11710	1790117
b3718	YIEK_ECOLI	P31470	yieK	EG11728	1790155
b3784	WECA_ECOLI	P24235	rfe	EG10840	1790218
b3787	WECC_ECOLI	P27829	rffD	EG11452	2367284
b3794	WECG_ECOLI	P27836	rffM	EG11458	2367289
b3812	YIGB_ECOLI	P23306	yigB	EG11202	2367295
b3833	UBIE_ECOLI	P27851	ubiE	EG11473	2367307
b3862	YIHG_ECOLI	P32129	yihG	EG11833	1790293
b3879	YIHR_ECOLI	P32139	yihR	EG11844	1790311
b3881	YIHT_ECOLI	P32141	yihT	EG11846	1790314
b3882	YIHU_ECOLI	P32142	yihU	EG11847	1790315
b3883	YIHV_ECOLI	P32143	yihV	EG11848	1790316
b3932	HSLV_ECOLI	P31059	hslV	EG11676	1790367
b3946	FSAB_ECOLI	P32669	fsaB	EG11905	1790382
b3949	PTWC_ECOLI	P32672	frwC	EG11908	1790386
b4085	ALSE_ECOLI	P32719	alsE	EG11957	1790523
b4196	SGAH_ECOLI	P39304	ulaD	EG12496	1790640
b4198	SGAE_ECOLI	P39306	ulaF	EG12498	1790642
b4233	MPL_ECOLI	P37773	mpl	EG12440	1790680
b4301	SGCE_ECOLI	P39362	sgcE	EG12553	1790754
b4374	YJJG_ECOLI	P33999	yjjG	EG12115	1790833
b4379	YJJW_ECOLI	P39409	yjjW	EG12599	1790839
b4386	LPLA_ECOLI	P32099	lplA	EG11796	1790846

EFICAz predicted 4 digit EC number
6.2.1.3
2.1.1.48
3.5.1.28
4.2.1.1
2.3.1.129
2.7.2.2
2.4.1.12
2.7.1.2
1.1.1.274
1.9.3.1
1.9.3.1
1.9.3.1
3.1.2.2
2.1.1.63
3.1.1.3
6.3.2.2
6.3.4.15
3.2.2.23
3.1.2.23
3.1.1.11
2.2.1.2
2.1.1.35
1.7.2.3
3.4.24.84
3.1.2.6
2.1.1.72
2.8.1.1
1.5.3.1
2.7.1.2
3.4.21.88
3.4.21.88
2.7.1.29
1.1.1.125;1.3.1.9
3.4.19.9
2.7.7.41
3.1.3.48
3.1.6.1
4.1.2.13
1.1.1.11
3.4.21.19
1.3.1.9
1.6.99.1
1.1.2.4
1.11.1.9
2.7.1.69
2.6.1.11
1.1.1.274
4.1.2.13
1.1.1.14
1.14.15.7

4.1.3.27
3.4.24.84
3.6.3.25
2.3.1.30
4.1.2.13
3.2.1.17
1.3.3.1
2.1.2.9
6.2.1.22
5.3.3.2
5.1.99.4
5.1.99.4
2.4.2.1
1.3.1.56
2.3.1.8
1.4.1.13
1.6.5.3
1.6.5.3
1.6.5.3
3.4.24.84
1.20.4.1
2.1.1.34
1.20.4.1
5.4.2.6
1.1.1.31
4.1.2.17
2.7.1.53
2.1.1.35
4.2.1.40
3.5.4.16
1.2.1.31
3.4.13.3
3.5.2.2
2.7.2.2
1.4.1.13
6.3.3.2
5.4.99.2
3.1.2.1
3.1.3.11
3.4.24.84
1.1.2.4
3.1.1.45
1.97.1.4
5.99.1.3
5.99.1.3
3.6.1.28
2.3.1.54
2.7.2.1
4.1.2.13
3.5.99.6
4.1.3.27
2.7.1.4

3.1.8.1
1.7.2.3
4.1.1.23
4.1.2.17;5.1.3.4
2.8.1.1
6.5.1.2
3.1.6.1
2.7.1.69
3.5.99.6
2.7.8.13
1.1.1.22
2.4.1.187
3.1.3.18
2.1.1.64
2.3.1.51
5.1.3.3
4.1.2.40
1.1.1.31
2.7.1.15
3.4.25.1
2.2.1.2
2.7.1.69
5.1.3.1
4.1.1.23
5.1.3.4
6.3.2.8
5.1.3.1
3.1.3.18
1.97.1.4
6.3.4.15

Enzyme function description	Compon	
	SIT	PROSITE
Long-chain-fatty-acid--CoA ligase		
rRNA (adenine-N(6)-)-methyltransferase	SIT	PROSITE
N-acetylmuramoyl-L-alanine amidase		
Carbonate dehydratase	SIT	PROSITE
Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase		
Carbamate kinase	SIT	
Cellulose synthase (UDP-forming)		
Glucokinase		
2,5-didehydrogluconate reductase		
Cytochrome-c oxidase		
Cytochrome-c oxidase	SIT	
Cytochrome-c oxidase	SIT	
Palmitoyl-CoA hydrolase	SIT	
Methylated-DNA--[protein]-cysteine S-methyltransferase		
Triacylglycerol lipase	SIT	PROSITE
Glutamate--cysteine ligase		
Biotin--[acetyl-CoA-carboxylase] ligase		
DNA-formamidopyrimidine glycosylase	SIT	PROSITE
4-hydroxybenzoyl-CoA thioesterase	SIT	PROSITE
Pectinesterase	SIT	PROSITE
Transaldolase	SIT	
tRNA (uracil-5-)-methyltransferase	SIT	PROSITE
Trimethylamine-N-oxide reductase (cytochrome c)	SIT	
Ste24 endopeptidase		
Hydroxyacylglutathione hydrolase		
Site-specific DNA-methyltransferase (adenine-specific)		
Thiosulfate sulfurtransferase		
Sarcosine oxidase	SIT	
Glucokinase		
Repressor lexA		
Repressor lexA		
Glycerone kinase		
2-deoxy-D-gluconate 3-dehydrogenase;Enoyl-[acyl-carrier protein] reductase (NADH)		
Gamma-glutamyl hydrolase		
Phosphatidate cytidylyltransferase	SIT	PROSITE
Protein-tyrosine-phosphatase		
Arylsulfatase		
Fructose-bisphosphate aldolase		
D-arabinitol 4-dehydrogenase		
Glutamyl endopeptidase		
Enoyl-[acyl-carrier protein] reductase (NADH)		
NADPH dehydrogenase	SIT	
D-lactate dehydrogenase (cytochrome)		
Glutathione peroxidase		
Protein-N(pi)-phosphohistidine-sugar phosphotransferase	SIT	
Acetylornithine transaminase	SIT	
2,5-didehydrogluconate reductase		
Fructose-bisphosphate aldolase	SIT	
L-iditol 2-dehydrogenase		
Choline monooxygenase		

Anthranilate synthase	SIT	
Ste24 endopeptidase		
Sulfate-transporting ATPase		
Serine O-acetyltransferase	SIT	
Fructose-bisphosphate aldolase	SIT	PROSITE
Lysozyme		
Dihydroorotate oxidase	SIT	
Methionyl-tRNA formyltransferase		
[Citrate (pro-3S)-lyase] ligase		
Isopentenyl-diphosphate delta-isomerase		
Alpha-methylacyl-CoA racemase		
Alpha-methylacyl-CoA racemase		
Purine-nucleoside phosphorylase	SIT	
Cis-2,3-dihydrobiphenyl-2,3-diol dehydrogenase		
Phosphate acetyltransferase		
Glutamate synthase (NADPH)		
NADH dehydrogenase (ubiquinone)		
NADH dehydrogenase (ubiquinone)		
NADH dehydrogenase (ubiquinone)		
Ste24 endopeptidase		
Arsenate reductase (glutaredoxin)	SIT	
tRNA (guanosine-2'-O-)-methyltransferase		
Arsenate reductase (glutaredoxin)		
Beta-phosphoglucomutase		
3-hydroxyisobutyrate dehydrogenase		
L-fuculose-phosphate aldolase		
L-xylulokinase		
tRNA (uracil-5-)-methyltransferase	SIT	PROSITE
Glucarate dehydratase	SIT	
GTP cyclohydrolase I		
Aminoadipate-semialdehyde dehydrogenase		
Xaa-His dipeptidase		
Dihydropyrimidinase	SIT	
Carbamate kinase	SIT	
Glutamate synthase (NADPH)		
5-formyltetrahydrofolate cyclo-ligase		
Methylmalonyl-CoA mutase	SIT	PROSITE
Acetyl-CoA hydrolase		
Fructose-bisphosphatase		
Ste24 endopeptidase		
D-lactate dehydrogenase (cytochrome)		
Carboxymethylenebutenolidase		
Formate acetyltransferase activating enzyme		
DNA topoisomerase (ATP-hydrolyzing)	SIT	
DNA topoisomerase (ATP-hydrolyzing)	SIT	
Thiamine-triphosphatase		
Formate C-acetyltransferase	SIT	
Acetate kinase	SIT	
Fructose-bisphosphate aldolase	SIT	PROSITE
Glucosamine-6-phosphate deaminase	SIT	PROSITE
Anthranilate synthase	SIT	
Fructokinase		

Aryldialkylphosphatase	SIT	PROSITE
Trimethylamine-N-oxide reductase (cytochrome c)	SIT	
Orotidine-5'-phosphate decarboxylase		
L-fuculose-phosphate aldolase;L-ribulose-phosphate 4-epimerase	SIT	
Thiosulfate sulfurtransferase		
DNA ligase (NAD+)	SIT	PROSITE
Arylsulfatase		
Protein-N(pi)-phosphohistidine-sugar phosphotransferase	SIT	
Glucosamine-6-phosphate deaminase	SIT	PROSITE
Phospho-N-acetylmuramoyl-pentapeptide-transferase		
UDP-glucose 6-dehydrogenase		
mannosaminyltransferase		
Phosphoglycolate phosphatase		
3-demethylubiquinone-9 3-O-methyltransferase		
1-acylglycerol-3-phosphate O-acyltransferase		
Aldose 1-epimerase		
Tagatose-bisphosphate aldolase		
3-hydroxyisobutyrate dehydrogenase		
Ribokinase	SIT	
Proteasome endopeptidase complex		
Transaldolase	SIT	
Protein-N(pi)-phosphohistidine-sugar phosphotransferase		
Ribulose-phosphate 3-epimerase	SIT	PROSITE
Orotidine-5'-phosphate decarboxylase		
L-ribulose-phosphate 4-epimerase	SIT	
UDP-N-acetylmuramate--L-alanine ligase	SIT	
Ribulose-phosphate 3-epimerase	SIT	PROSITE
Phosphoglycolate phosphatase		
Formate acetyltransferase activating enzyme	SIT	PROSITE
Biotin--[acetyl-CoA-carboxylase] ligase		

ent of EFICAz responsible for the prediction		
CHIEF-FDR	**PFAM-FDR**	**Number of components**
CHIEF-FDR		1
CHIEF-FDR	PFAM-FDR	4
	PFAM-FDR	1
CHIEF-FDR	PFAM-FDR	4
CHIEF-FDR		1
CHIEF-FDR	PFAM-FDR	3
	PFAM-FDR	1
CHIEF-FDR	PFAM-FDR	2
CHIEF-FDR	PFAM-FDR	2
	PFAM-FDR	1
		1
		1
CHIEF-FDR	PFAM-FDR	3
	PFAM-FDR	1
		2
	PFAM-FDR	1
	PFAM-FDR	1
CHIEF-FDR	PFAM-FDR	4
		2
CHIEF-FDR	PFAM-FDR	4
		1
		2
		1
	PFAM-FDR	1
CHIEF-FDR		1
	PFAM-FDR	1
CHIEF-FDR		1
CHIEF-FDR		2
CHIEF-FDR	PFAM-FDR	2
	PFAM-FDR	1
CHIEF-FDR	PFAM-FDR	2
CHIEF-FDR		1
CHIEF-FDR	PFAM-FDR	2
	PFAM-FDR	1
CHIEF-FDR	PFAM-FDR	4
	PFAM-FDR	1
CHIEF-FDR		1
CHIEF-FDR		1
CHIEF-FDR		1
	PFAM-FDR	1
	PFAM-FDR	1
CHIEF-FDR		2
CHIEF-FDR		1
CHIEF-FDR		1
		1
CHIEF-FDR		2
	PFAM-FDR	1
CHIEF-FDR	PFAM-FDR	3
CHIEF-FDR		1
CHIEF-FDR		1

		1
	PFAM-FDR	1
CHIEF-FDR		1
		1
CHIEF-FDR	PFAM-FDR	4
CHIEF-FDR	PFAM-FDR	2
		1
CHIEF-FDR		1
	PFAM-FDR	1
CHIEF-FDR		1
CHIEF-FDR	PFAM-FDR	2
CHIEF-FDR		1
CHIEF-FDR	PFAM-FDR	3
CHIEF-FDR		1
CHIEF-FDR	PFAM-FDR	2
	PFAM-FDR	1
CHIEF-FDR		1
CHIEF-FDR		1
CHIEF-FDR		1
	PFAM-FDR	1
CHIEF-FDR	PFAM-FDR	3
	PFAM-FDR	1
CHIEF-FDR		1
CHIEF-FDR		1
CHIEF-FDR		1
	PFAM-FDR	1
CHIEF-FDR		1
		2
CHIEF-FDR	PFAM-FDR	3
	PFAM-FDR	1
	PFAM-FDR	1
	PFAM-FDR	1
CHIEF-FDR	PFAM-FDR	3
CHIEF-FDR	PFAM-FDR	3
	PFAM-FDR	1
CHIEF-FDR	PFAM-FDR	2
CHIEF-FDR	PFAM-FDR	4
CHIEF-FDR		1
	PFAM-FDR	1
	PFAM-FDR	1
CHIEF-FDR		1
CHIEF-FDR	PFAM-FDR	2
	PFAM-FDR	1
CHIEF-FDR	PFAM-FDR	3
CHIEF-FDR	PFAM-FDR	3
	PFAM-FDR	1
CHIEF-FDR	PFAM-FDR	3
CHIEF-FDR	PFAM-FDR	3
CHIEF-FDR	PFAM-FDR	4
		2
CHIEF-FDR	PFAM-FDR	3
	PFAM-FDR	1

		2
	PFAM-FDR	2
	PFAM-FDR	1
CHIEF-FDR	PFAM-FDR	3
CHIEF-FDR		1
CHIEF-FDR		3
CHIEF-FDR		1
CHIEF-FDR		2
		2
CHIEF-FDR	PFAM-FDR	2
CHIEF-FDR		1
CHIEF-FDR	PFAM-FDR	2
	PFAM-FDR	1
	PFAM-FDR	1
CHIEF-FDR		1
CHIEF-FDR	PFAM-FDR	2
CHIEF-FDR	PFAM-FDR	2
CHIEF-FDR		1
		1
CHIEF-FDR	PFAM-FDR	2
		1
CHIEF-FDR		1
CHIEF-FDR	PFAM-FDR	4
	PFAM-FDR	1
CHIEF-FDR	PFAM-FDR	3
CHIEF-FDR		2
CHIEF-FDR	PFAM-FDR	4
	PFAM-FDR	1
CHIEF-FDR	PFAM-FDR	4
	PFAM-FDR	1

KEGG annotation
probable crotonobetaine/carnitine-CoA ligase [EC:6.3.2.-]
dimethyladenosine transferase [EC:2.1.1.-]
ampD protein
putative carbonic anhydrase [EC:4.2.1.1]
UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase (firA protein) (rifampicin resistance protein) [EC:2.3.
carbamate kinase [EC:2.7.2.2]
hypothetical 44.7 kD protein in adhC-taua intergenic region
putative nitrate transport permease protein
hypothetical oxidoreductase in pgpA-ispA intergenic region
cytochrome o ubiquinol oxidase operon protein cyoD
cytochrome o ubiquinol oxidase subunit III [EC:1.10.3.-]
cytochrome o ubiquinol oxidase subunit I [EC:1.10.3.-]
acyl-CoA thioesterase II [EC:3.1.2.-]
hypothetical 14.4 kD protein in tesB-hha intergenic region
acetyl esterase [EC:3.1.1.-]
hypothetical 41.7 kD protein in nfnB-entD intergenic region
lipoate-protein ligase B (lipoate biosynthesis protein B) [EC:6.-.-.-]
endonuclease VIII [EC:3.2.-.-]
hypothetical 15.6 kD protein in cydB-tolQ intergenic region
putative pectinesterase
putative transaldolase [EC:4.1.2.-]
hypothetical RNA methyltransferase in potI-artJ intergenic region [EC:2.1.1.-]
anaerobic dimethyl sulfoxide reductase chain A precursor (DMSO reductase) [EC:1.8.99.-]
putative metalloprotease [EC:3.4.24.-]
hypothetical 23.8 kD protein in mukB-aspC intergenic region
putative oxidoreductase
hypothetical 40.0 kD protein in htrB-dinI intergenic region (ORF39.9)
putative sarcosine oxidase [EC:1.5.3.1]
hypothetical 33.0 kD protein in mfd-cobb intergenic region
putative phage repressor
umuD protein [EC:3.4.21.-]
putative dihydroxyacetone kinase
hypothetical oxidoreductase in btuR-sohB intergenic region [EC:1.-.-.-]
hypothetical 28.5 kD protein in sapA-aldH intergenic region
putative phosphatidate cytidiltransferase [EC:2.7.7.41]
hypothetical 49.6 kD protein in maoC-acpD intergenic region
putative sulfatase [EC:3.1.6.-]
hypothetical 31.9 kD protein in hipB-uxaB intergenic region [EC:4.2.1.-]
putative oxidoreductase
putative protease ydgD precursor [EC:3.4.21.-]
hypothetical oxidoreductase in pntA-rstA intergenic region [EC:1.-.-.-]
N-ethylmaleimide reductase (N-ethylmaleimide reducing enzyme) [EC:1.-.-.-]
hypothetical 113.2 kD protein in lpp-aroD intergenic region
vitamin B12 transport system substrate-binding protein
pts system, cellobiose-specific IIC component (EIIC-Cel) (cellobiose-permease IIC component) (phosphotransfera
succinylornithine transaminase (succinylornithine aminotransferase) (carbon starvation protein C) [EC:2.6.1.-]
probable oxidoreductase
putative aldolase
hypothetical zinc-type alcohol dehydrogenase-like protein in ansA-gapA intergenic region
putative dioxygenase alpha subunit yeaw [EC:1.14.1.-]

para-aminobenzoate synthase component I (adc synthase) [EC:4.1.3.-]
probable protease htpX (heat shock protein htpX) [EC:3.4.24.-]
putative polar amino acid transport system ATP-binding protein
putative colanic acid biosynthesis acetyltransferase wcaB [EC:2.3.1.-]
tagatose-bisphosphate aldolase gatY [EC:4.1.2.-]
putative autolytic lysozyme
hypothetical 45.3 kD protein in cdd-mglC intergenic region
putative transformylase
elaA protein
putative regulator
hypothetical 43.3 kD protein in evgS-glk intergenic region
putative enzyme
xanthosine phosphorylase [EC:2.4.2.-]
oxidoreductase ucpA [EC:1.-.-.-]
ethanolamine utilization protein eutI
putative oxidoreductase, Fe-S subunit
hydrogenase-4 component B [EC:1.-.-.-]
hydrogenase-4 component D [EC:1.-.-.-]
hydrogenase-4 component F [EC:1.-.-.-]
hypothetical protein
putative oxidoreductase
putative ATP synthase beta subunit [EC:2.1.1.-]
hypothetical protein
hypothetical 20.8 kD protein in gshA-csrA intergenic region
putative dehydrogenase [EC:1.1.-.-]
hypothetical 23.2 kD protein in prpB-rpoS intergenic region
hypothetical sugar kinase in cysJ-eno intergenic region
hypothetical RNA methyltransferase in relA-barA intergenic region [EC:2.1.1.-]
probable glucarate dehydratase 2 (GDH) [EC:4.2.1.40]
hypothetical 32.6 kD protein in syd-sdaC intergenic region
2-acylglycerophosphoethanolamine acyltransferase / acyl-acyl carrier protein synthetase (2-acyl-gpe acyltransferas
hypothetical 44.8 kD protein in kduI-lysS intergenic region
hypothetical protein
carbamate kinase [EC:2.7.2.2]
hypothetical 69.7 kD protein in kduI-lysS intergenic region
hypothetical 21.1 kD protein in ssr-serA intergenic region (O182)
methylmalonyl-CoA mutase [EC:5.4.99.2]
hypothetical 53.8 kD protein in sbm-fba intergenic region (O492)
hypothetical 34.3 kD protein in epd-cmtA intergenic region (ORF 1) (F321)
putative metalloprotease [EC:3.4.24.-]
glycolate oxidase subunit glcD [EC:1.1.3.15]
hypothetical protein
hypothetical protein
topoisomerase IV subunit [EC:5.99.1.-]
topoisomerase IV subunit B [EC:5.99.1.-]
hypothetical 48.4 kD protein in glnE-cca intergenic region (ORFXE)
keto-acid formate acetyltransferase (keto-acid formate-lyase) [EC:2.3.1.54]
propionate kinase [EC:2.7.2.-]
tagatose-bisphosphate aldolase agaY [EC:4.1.2.-]
putative galactosamine-6-phosphate isomerase (galactosamine-6-phosphate deaminase) [EC:5.3.1.-]
para-aminobenzoate synthase component II [EC:4.1.3.-]
hypothetical 28.3 kD protein in cysG-trpS intergenic region (O261)

phosphotriesterase homology protein
biotin sulfoxide reductase 1 (bds reductase 1) (bso reductase 1) [EC:1.-.-.-]
probable hexulose-6-phosphate synthase (HUMPS) (D-arabino 3-hexulose 6-phosphate formaldehyde lyase) [EC:
probable sugar isomerase sgbE [EC:5.1.3.4]
hypothetical 15.6 kD protein in secB-tdh intergenic region
hypothetical 63.2 kD protein in rph-gmk intergenic region
putative sulfatase [EC:3.1.6.-]
pts system, arbutin-like IIC component (phosphotransferase enzyme II, C component)
hypothetical 23.3 kD protein in tnaB-bglB intergenic region
undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase [EC:2.4.1.-]
UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase (UDP-mannaca dehydrogenase) [EC:1.1.1.-]
probable UDP-N-acetyl-D-mannosaminuronic acid transferase (UDP-mannaca transferase) [EC:2.4.1.-]
hypothetical 27.1 kD protein in xerC-uvrD intergenic region (ORF 238)
ubiquinone/menaquinone biosynthesis methlytransferase ubiE [EC:2.1.1.-]
hypothetical 36.3 kD protein in dsbA-polA intergenic region
hypothetical 34 kD protein in glnA-rbn intergenic region (F308)
hypothetical 32 kD protein in glnA-rbn intergenic region (F292)
putative dehydrogenase [EC:1.1.-.-]
hypothetical 31.9 kD protein in glnA-rbn intergenic region (O300)
heat shock protein hslV [EC:3.4.25.-]
fructose-6-phosphate aldolase 2 [EC:4.1.2.-]
pts system, fructose-like-2 IIC component (phosphotransferase enzyme II, C component)
hypothetical 26.1 kD protein in fdhF-phnP intergenic region (F231)
probable hexulose-6-phosphate synthase (HUMPS) (D-arabino 3-hexulose 6-phosphate formaldehyde lyase) [EC:
probable sugar isomerase sgaE [EC:5.1.3.4]
UDP-N-acetylmuramate: L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase [EC:6.3.2.-]
sgcE protein [EC:5.1.3.-]
hypothetical 25.3 kD protein in rimI-prfC intergenic region
hypothetical 31.5 kD protein in osmY-deoC intergenic region (F287)
lipoate-protein ligase A [EC:6.-.-.-]

Swiss-Prot annotation
Probable crotonobetaine/carnitine-CoA ligase (EC 6.3.2.-).
Dimethyladenosine transferase (EC 2.1.1.-) (S-adenosylmethionine-6-N', N'-adenosyl(rRNA) dimethyltransferase) (
AmpD protein.
Protein yadF.
UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase (EC 2.3.1.-) (FirA protein) (Rifampicin resistance pro
Carbamate kinase-like protein yahI.
Hypothetical protein yaiP.
Hypothetical protein yajF.
Hypothetical oxidoreductase yajO (EC 1.-.-.-).
Cytochrome O ubiquinol oxidase protein cyoD (Ubiquinol oxidase chain D).
Cytochrome O ubiquinol oxidase subunit III (EC 1.10.3.-) (Ubiquinol oxidase chain C).
Ubiquinol oxidase polypeptide I (EC 1.10.3.-) (Cytochrome O subunit 1) (Oxidase BO(3) subunit 1) (Cytochrome O
Acyl-CoA thioesterase II (EC 3.1.2.-) (TEII).
Hypothetical protein ybaZ.
Acetyl esterase (EC 3.1.1.-).
Hypothetical protein ybdK.
Lipoate-protein ligase B (EC 6.-.-.-) (Lipoate biosynthesis protein B).
Endonuclease VIII (EC 3.2.-.-).
Protein ybgC.
Putative lipoprotein ybHC precursor.
Fructose-6-phosphate aldolase 1 (EC 4.1.2.-).
Hypothetical RNA methyltransferase ybjF (EC 2.1.1.-).
Anaerobic dimethyl sulfoxide reductase chain A precursor (EC 1.8.99.-) (DMSO reductase).
Putative metalloprotease ycaL (EC 3.4.24.-).
Hypothetical protein ycbL.
Hypothetical protein ycbY.
Hypothetical UPF0176 protein yceA (ORF39.9).
N-methyl-L-tryptophan oxidase (EC 1.5.3.-) (MTOX).
Hypothetical protein ycfX.
Putative lambdoid prophage e14 repressor protein C2.
UmuD protein (EC 3.4.21.-) [Contains: UmuD' protein].
Hypothetical protein ycgT.
Hypothetical oxidoreductase yciK (EC 1.-.-.-).
Hypothetical protein ycjL.
Hypothetical protein ynbB.
Hypothetical protein ynbD.
Putative sulfatase ydeN precursor (EC 3.1.6.-).
Putative aldolase yneB (EC 4.2.1.-).
Hypothetical oxidoreductase ydfI (EC 1.-.-.-).
Putative protease ydgD precursor (EC 3.4.21.-).
Hypothetical oxidoreductase ydgB (EC 1.-.-.-).
N-ethylmaleimide reductase (EC 1.-.-.-) (N-ethylmaleimide reducing enzyme).
Hypothetical protein ydiJ.
Vitamin B12 transport periplasmic protein btuE.
PTS system, N,N'-diacetylchitobiose-specific IIC component (EIIC-Chb) (N,N'-diacetylchitobiose-permease IIC com
Succinylornithine transaminase (EC 2.6.1.-) (Succinylornithine aminotransferase) (Carbon starvation protein C).
Hypothetical oxidoreductase ydjG (EC 1.-.-.-).
Hypothetical protein ydjI.
Hypothetical zinc-type alcohol dehydrogenase-like protein ydjJ.
Putative dioxygenase alpha subunit yeaW (EC 1.14.1.-).

Para-aminobenzoate synthase component I (EC 4.1.3.-) (ADC synthase).
Probable protease htpX (EC 3.4.24.-) (Heat shock protein htpX).
Hypothetical amino-acid ABC transporter ATP-binding protein yecC.
Putative colanic acid biosynthesis acetyltransferase wcaB (EC 2.3.1.-).
Tagatose-1,6-bisphosphate aldolase gatY (EC 4.1.2.-) (TBPA).
Hypothetical protein yegX.
Hypothetical protein yeiA.
Hypothetical protein yfbG.
Protein elaA.
Putative Nudix hydrolase yfcD (EC 3.6.-.-).
Hypothetical protein yfdE.
Hypothetical protein yfdW.
Xanthosine phosphorylase (EC 2.4.2.-).
Oxidoreductase ucpA (EC 1.-.-.-).
Ethanolamine utilization protein eutD.
AegA protein.
Hydrogenase-4 component B (EC 1.-.-.-).
Hydrogenase-4 component D (EC 1.-.-.-).
Hydrogenase-4 component F (EC 1.-.-.-).
Hypothetical protein yfgC precursor.
Protein yfgD.
Hypothetical tRNA/rRNA methyltransferase yfhQ (EC 2.1.1.-).
Putative arsenate reductase (EC 1.20.4.1) (Arsenical pump modifier) (Fragment).
Hypothetical protein yqaB.
Hypothetical oxidoreductase ygbJ (EC 1.1.-.-).
Hypothetical aldolase class II protein ygbL.
Hypothetical sugar kinase ygcE.
23S rRNA (Uracil-5-)-methyltransferase rumA (EC 2.1.1.-) (23S rRNA(M- 5-U1939)-methyltransferase).
Glucarate dehydratase related protein (EC 4.2.1.-) (GDH-RP) (GlucDRP).
Hypothetical protein yqcD.
AAS bifunctional protein [Includes: 2-acylglycerophosphoethanolamine acyltransferase (2-acyl-GPE acyltransferase
Hypothetical protein ygeY.
Hypothetical hydrolase ygeZ (EC 3.-.-.-).
Carbamate kinase-like protein yqeA.
Hypothetical protein ygfT.
Hypothetical protein ygfA.
Sbm protein.
Hypothetical protein ygfH.
Hypothetical protein yggF.
Putative metalloprotease yggG (EC 3.4.24.-).
Glycolate oxidase subunit glcD.

Hypothetical protein ygiQ.
Topoisomerase IV subunit A (EC 5.99.1.-).
Topoisomerase IV subunit B (EC 5.99.1.-).
Hypothetical protein ygiF (ORFXE).
Keto-acid formate acetyltransferase (EC 2.3.1.-) (Keto-acid formate- lyase).
Propionate kinase (EC 2.7.2.-).
Tagatose-1,6-bisphosphate aldolase agaY (EC 4.1.2.-) (TBPA).
Putative galactosamine-6-phosphate isomerase (EC 5.3.1.-) (Galactosamine-6-phosphate deaminase).
Para-aminobenzoate synthase glutamine amidotransferase component II (EC 4.1.3.-).
Hypothetical sugar kinase yhfQ.

Phosphotriesterase homology protein.
Biotin sulfoxide reductase (EC 1.-.-.-) (BDS reductase) (BSO reductase).
Probable hexulose-6-phosphate synthase (EC 4.1.2.-) (HUMPS) (D-arabino 3-hexulose 6-phosphate formaldehyd
Probable sugar isomerase sgbE (EC 5.1.-.-).
Hypothetical protein yibN.
Hypothetical DNA ligase-like protein yicF.
Putative sulfatase yidJ (EC 3.1.6.-).
PTS system, arbutin-like IIC component (Phosphotransferase enzyme II, C component).
Hypothetical protein yieK.
Undecaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate transferase (EC 2.7.8.-) (UDP-GlcNAc:undeca
UDP-N-acetyl-D-mannosamine dehydrogenase (EC 1.1.1.-) (UDP-ManNAc dehydrogenase).
Probable UDP-N-acetyl-D-mannosaminuronic acid transferase (EC 2.4.1.-) (UDP-ManNAcA transferase).
Hypothetical protein yigB.
Ubiquinone/menaquinone biosynthesis methyltransferase ubiE (EC 2.1.1.-).
Hypothetical protein yihG.
Hypothetical protein yihR.
Hypothetical protein yihT.
Hypothetical oxidoreductase yihU (EC 1.1.-.-).
Hypothetical sugar kinase yihV.
ATP-dependent protease hslV (EC 3.4.25.-) (Heat shock protein hslV).
Fructose-6-phosphate aldolase 2 (EC 4.1.2.-).
PTS system, fructose-like-2 IIC component (Phosphotransferase enzyme II, C component).
D-allulose-6-phosphate 3-epimerase (EC 5.1.3.-).
Probable hexulose-6-phosphate synthase (EC 4.1.2.-) (HUMPS) (D-arabino 3-hexulose 6-phosphate formaldehyd
Probable sugar isomerase sgaE (EC 5.1.-.-).
UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase (EC 6.3.2.-) (Murein peptide lig
Protein sgcE (EC 5.1.3.-).
Hypothetical protein yjjG.
Hypothetical protein yjjW.
Lipoate-protein ligase A (EC 6.-.-.-).

(16S rRNA dimethylase) (High level kasugamycin resistance protein ksgA) (Kasugamycin dimethyltransferase).

otein).

) ubiquinol oxidase subunit 1) (Ubiquinol oxidase chain A).

nponent) (Phosphotransferase enzyme II, C component).

e); Acyl-acyl carrier protein synthetase (Acyl-ACP synthetase)].

e lyase).

prenyl-phosphate GlcNAc-1- phosphate transferase).

e lyase).

jase).

Protein id	Swiss-Prot		Gene name	EcoGene name	GenBank GI number
	Entry name	Accession Number			
b0030	YAAF_ECOLI	P22564	rihC	EG11082	1786213
b0037	CAIC_ECOLI	P31552	caiC	EG11558	1786221
b0039	CAIA_ECOLI	P31571	caiA	EG11560	1786223
b0051	KSGA_ECOLI	P06992	ksgA	EG10523	1786236
b0110	AMPD_ECOLI	P13016	ampD	EG10041	1786300
b0126	YADF_ECOLI	P36857	yadF	EG12319	1786318
b0144	YADB_ECOLI	P27305	yadB	EG11362	1786337
b0161	DEGP_ECOLI	P09376	degP	EG10463	1786356
b0179	LPXD_ECOLI	P21645	lpxD	EG10316	1786376
b0200	YAED_ECOLI	P31546	gmhB	EG11736	1786399
b0269	YAGF_ECOLI	P77596	yagF	EG13345	1786464
b0323	ARCM_ECOLI	P77624	yahI	EG13593	1786516
b0325	YAHK_ECOLI	P75691	yahK	EG13595	1786518
b0347	MHPA_ECOLI	P77397	mhpA	EG20273	1786543
b0348	MHPB_ECOLI	P54711	mhpB	EG20274	1786544
b0363	YAIP_ECOLI	Q47536	yaiP	EG13298	1786560
b0394	YAJF_ECOLI	P23917	mak	EG11288	1786593
b0419	YAJO_ECOLI	P77735	yajO	EG13611	1786621
b0429	CYOD_ECOLI	P18403	cyoD	EG10181	1786632
b0430	CYOC_ECOLI	P18402	cyoC	EG10180	1786633
b0431	CYOB_ECOLI	P18401	cyoB	EG10179	1786634
b0452	TESB_ECOLI	P23911	tesB	EG10995	1786657
b0454	YBAZ_ECOLI	P75707	ybaZ	EG13254	1786659
b0476	AES_ECOLI	P23872	aes	EG11101	1786682
b0493	YBBO_ECOLI	P77388	ybbO	EG13262	1786701
b0581	YBDK_ECOLI	P77213	ybdK	EG13644	1786795
b0599	YBDH_ECOLI	P45579	ybdH	EG12692	1786815
b0606	AHPF_ECOLI	P35340	ahpF	EG11385	1786823
b0608	YBDR_ECOLI	P77316	ybdR	EG13537	1786825
b0630	LIPB_ECOLI	P30976	lipB	EG11591	1786848
b0651	YBEK_ECOLI	P41409	rihA	EG12701	1786871
b0662	UBIF_ECOLI	P75728	ubiF	EG13658	1786883
b0676	NAGC_ECOLI	P15301	nagC	EG10636	1786891
b0714	END8_ECOLI	P50465	nei	EG13237	1786932
b0732	YBGG_ECOLI	P54746	ybgG	EG13236	1786952
b0736	YBGC_ECOLI	P08999	ybgC	EG11110	1786957
b0772	YBHC_ECOLI	P46130	ybhC	EG12875	1786989
b0777	BIOC_ECOLI	P12999	bioC	EG10119	1786994
b0790	YBHP_ECOLI	P75772	ybhP	EG13672	1787008
b0801	YBIC_ECOLI	P30178	ybiC	EG11581	1787020
b0825	FSAA_ECOLI	P78055	fsaA	EG13471	1787046
b0841	YBJG_ECOLI	P75806	ybjG	EG13676	1787064
b0851	NFSA_ECOLI	P17117	nfsA	EG11261	1787075
b0859	YBJF_ECOLI	P75817	ybjF	EG13427	1787083
b0894	DMSA_ECOLI	P18775	dmsA	EG10232	1787121
b0909	YCAL_ECOLI	P43674	ycaL	EG13133	1787138
b0927	YCBL_ECOLI	P75849	ycbL	EG13704	1787158
b0948	YCBY_ECOLI	P75864	ycbY	EG13717	1787181
b1008	YCDI_ECOLI	P75894	ycdI	EG13855	1787243
b1022	YCDQ_ECOLI	P75905	ycdQ	EG13863	1787259

b1055	YCEA_ECOLI	P24188	yceA	EG11116	1787294
b1059	MTOX_ECOLI	P40874	solA	EG12669	1787298
b1119	YCFX_ECOLI	P75959	ycfX	EG13442	1787363
b1126	POTA_ECOLI	P23858	potA	EG10749	1787370
b1145	YMFK_ECOLI	P75974	ymfK	EG14249	1787391
b1183	UMUD_ECOLI	P04153	umuD	EG11057	1787431
b1200	YCGT_ECOLI	P76015	dhaK	EG13901	1787450
b1212	HEMK_ECOLI	P37186	prmC	EG12424	1787463
b1271	YCIK_ECOLI	P31808	yciK	EG11759	1787526
b1298	YCJL_ECOLI	P76038	ycjL	EG13909	1787556
b1378	NIFJ_ECOLI	P52647	ydbK	EG13183	1787642
b1397	PAAJ_ECOLI	P77525	paaJ	EG13744	1787663
b1408	YNBA_ECOLI	P76090	ynbA	EG13748	1787676
b1409	YNBB_ECOLI	P76091	ynbB	EG13749	1787677
b1411	YNBD_ECOLI	P76093	ynbD	EG13751	1787679
b1439	YDCR_ECOLI	P77730	ydcR	EG13761	1787710
b1441	YDCT_ECOLI	P77795	ydcT	EG13763	1787712
b1494	PQQL_ECOLI	P31828	pqqL	EG11744	1787770
b1498	YDEN_ECOLI	P77318	ydeN	EG13796	1787775
b1511	YDEV_ECOLI	P77432	ydeV	EG13804	1787789
b1517	YNEB_ECOLI	P76143	lsrF	EG13810	1787796
b1525	YNEI_ECOLI	P76149	yneI	EG13817	1787805
b1539	YDFG_ECOLI	P39831	ydfG	EG12345	1787820
b1542	YDFI_ECOLI	P77260	ydfI	EG13821	1787823
b1580	RSPB_ECOLI	P38105	rspB	EG12452	1787863
b1594	MLC_ECOLI	P50456	dgsA	EG13156	1787878
b1598	YDGD_ECOLI	P76176	ydgD	EG13925	1787882
b1606	YDGB_ECOLI	P52109	ydgB	EG13189	1787891
b1647	YDHF_ECOLI	P76187	ydhF	EG13420	1787936
b1650	NEMA_ECOLI	P77258	nemA	EG13546	1787939
b1687	YDIJ_ECOLI	P77748	ydiJ	EG13969	1787977
b1694	YDIF_ECOLI	P37766	ydiF	EG12432	1787985
b1695	YDIO_ECOLI	P76200	ydiO	EG13974	1787986
b1710	BTUE_ECOLI	P06610	btuE	EG10129	1788003
b1737	PTCC_ECOLI	P17334	chbC	EG10141	1788032
b1748	ARGM_ECOLI	P77581	argM	EG13999	1788044
b1758	YNJF_ECOLI	P76226	ynjF	EG14008	1788055
b1771	YDJG_ECOLI	P77256	ydjG	EG13483	1788070
b1772	YDJH_ECOLI	P77493	ydjH	EG13484	1788071
b1773	YDJI_ECOLI	P77704	ydjI	EG13485	1788072
b1774	YDJJ_ECOLI	P77280	ydjJ	EG13486	1788073
b1781	YEAE_ECOLI	P76234	yeaE	EG13491	1788081
b1802	YEAW_ECOLI	P76253	yeaW	EG13509	1788103
b1812	PABB_ECOLI	P05041	pabB	EG10683	1788114
b1829	HTPX_ECOLI	P23894	htpX	EG10462	1788133
b1917	YECC_ECOLI	P37774	yecC	EG12347	1788225
b2033	WBBJ_ECOLI	P37750	wbbJ	EG11984	1788345
b2054	WCAF_ECOLI	P71240	wcaF	EG13574	1788367
b2058	WCAB_ECOLI	P77558	wcaB	EG13570	1788371
b2086	YEGS_ECOLI	P76407	yegS	EG14367	1788402
b2096	GATY_ECOLI	P37192	gatY	EG12419	1788412
b2099	YEGU_ECOLI	P76418	yegU	EG14064	1788416

b2100	YEGV_ECOLI	P76419	yegV	EG14065	1788417
b2102	YEGX_ECOLI	P76421	yegX	EG14067	1788419
b2147	YEIA_ECOLI	P25889	yeiA	EG11289	1788469
b2160	YEII_ECOLI	P33020	yeiI	EG12028	1788484
b2162	YEIK_ECOLI	P33022	rihB	EG12030	1788486
b2166	YEIC_ECOLI	P30235	yeiC	EG11646	1788491
b2172	YEIQ_ECOLI	P33029	yeiQ	EG12036	1788497
b2245	YFAU_ECOLI	P76469	yfaU	EG14083	1788578
b2254	ARNC_ECOLI	P77757	arnC	EG14090	1788588
b2255	YFBG_ECOLI	P77398	arnA	EG14091	1788589
b2267	ELAA_ECOLI	P52077	elaA	EG13184	1788602
b2290	YFBQ_ECOLI	P77727	yfbQ	EG14101	1788627
b2299	YFCD_ECOLI	P76494	yfcD	EG14107	1788637
b2371	YFDE_ECOLI	P76518	yfdE	EG13284	1788714
b2374	YFDW_ECOLI	P77407	yfdW	EG14145	1788717
b2379	YFDZ_ECOLI	P77434	yfdZ	EG14198	1788722
b2407	XAPA_ECOLI	P45563	xapA	EG20250	1788746
b2426	UCPA_ECOLI	P37440	ucpA	EG12133	1788766
b2453	EUTG_ECOLI	P76553	eutG	EG14183	1788795
b2458	EUTD_ECOLI	P77218	eutD	EG14188	1788800
b2467	YFFH_ECOLI	P37128	yffH	EG12410	1788810
b2468	AEGA_ECOLI	P37127	aegA	EG12409	1788811
b2482	HYFB_ECOLI	P23482	hyfB	EG11282	1788827
b2484	HYFD_ECOLI	P77416	hyfD	EG14212	1788829
b2486	HYFF_ECOLI	P77437	hyfF	EG14214	1788831
b2494	YFGC_ECOLI	P76568	yfgC	EG14199	1788840
b2495	YFGD_ECOLI	P76569	yfgD	EG14200	1788841
b2532	YFHQ_ECOLI	P77438	yfhQ	EG13452	1788881
b2538	HCAE_ECOLI	Q47139	hcaE	EG13456	1788888
b2539	HCAF_ECOLI	Q47140	hcaF	EG13457	1788889
b2541	HCAB_ECOLI	P77646	hcaB	EG13459	1788891
b2545	YPHC_ECOLI	P77360	yphC	EG13464	1788895
b2550	YPHH_ECOLI	P76586	yphH	EG13469	1788901
b2559	YFHC_ECOLI	P30134	tadA	EG11372	1788911
b2581	YFIF_ECOLI	P33635	yfiF	EG11786	1788935
b2638	YFJU_ECOLI	P52136	yfjU	EG13207	1788991
b2690	YQAB_ECOLI	P77475	yqaB	EG13530	1789046
b2711	NORW_ECOLI	P37596	norW	EG12450	1789065
b2736	YGBJ_ECOLI	Q46888	ygbJ	EG13104	1789092
b2738	YGBL_ECOLI	Q46890	ygbL	EG13106	1789094
b2739	YGBM_ECOLI	Q46891	ygbM	EG13107	1789095
b2774	YGCW_ECOLI	P76633	ygcW	EG13130	1789135
b2776	YGCE_ECOLI	P55138	ygcE	EG13033	1789138
b2785	RUMA_ECOLI	P55135	rumA	EG11247	1789148
b2788	GUDX_ECOLI	Q46915	gudX	EG13168	1789151
b2794	YQCD_ECOLI	Q46920	yqcD	EG13173	1789158
b2834	TAS_ECOLI	Q46933	tas	EG13093	1789199
b2836	AAS_ECOLI	P31119	aas	EG11679	1789201
b2840	YGEA_ECOLI	P03813	ygeA	EG11157	1789205
b2870	YGEW_ECOLI	Q46803	ygeW	EG13053	1789234
b2872	YGEY_ECOLI	Q46805	ygeY	EG13055	1789236
b2873	YGEZ_ECOLI	Q46806	hyuA	EG13056	1789237

b2874	ARCL_ECOLI	Q46807	yqeA	EG13057	1789238
b2878	YGFK_ECOLI	Q46811	ygfK	EG13061	1789243
b2887	YGFT_ECOLI	Q46820	ygfT	EG13070	1789253
b2902	YGFF_ECOLI	P52037	ygfF	EG12971	2367175
b2906	VISC_ECOLI	P25535	visC	EG11333	1789273
b2912	YGFA_ECOLI	P09160	ygfA	EG11158	1789278
b2917	SBM_ECOLI	P27253	yliK	EG11444	1789284
b2920	YGFH_ECOLI	P52043	ygfH	EG12973	1789287
b2927	E4PD_ECOLI	P11603	epd	EG10368	1789295
b2930	YGGF_ECOLI	P21437	yggF	EG11245	1789298
b2936	YGGG_ECOLI	P25894	yggG	EG11291	1789305
b2954	HAM1_ECOLI	P52061	rdgB	EG12982	1789324
b2979	GLCD_ECOLI	P52075	glcD	EG12997	1789351
b2999	Q46849	None	yghX	EG13008	1789373
b3003	YGHA_ECOLI	P25887	yghA	EG11292	1789378
b3011	YQHD_ECOLI	Q46856	yqhD	EG13014	1789386
b3015	YGIQ_ECOLI		ygiQ	EG13019	1789391
b3019	PARC_ECOLI	P20082	parC	EG10686	1789396
b3030	PARE_ECOLI	P20083	parE	EG10687	1789408
b3038	YGIC_ECOLI	P24196	ygiC	EG11165	1789416
b3039	YGID_ECOLI	P24197	ygiD	EG11166	1789417
b3052	RFAE_ECOLI	P76658	rfaE	EG13416	1789432
b3054	YGIF_ECOLI	P30871	ygiF	EG11603	1789434
b3114	TDCE_ECOLI	P42632	tdcE	EG12758	1789502
b3115	TDCD_ECOLI	P11868	tdcD	EG11172	1789503
b3137	AGAY_ECOLI	P42908	kbaY	EG12768	1789526
b3141	AGAI_ECOLI	P42912	agaI	EG12772	1789530
b3146	YRAL_ECOLI	P45528	yraL	EG12777	1789535
b3160	YHBW_ECOLI	P45529	yhbW	EG12792	1789551
b3187	ISPB_ECOLI	P19641	ispB	EG10017	1789578
b3234	DEGQ_ECOLI	P39099	degQ	EG12612	1789629
b3235	DEGS_ECOLI	P31137	degS	EG11652	1789630
b3271	YHDZ_ECOLI	P45769	yhdZ	EG12837	1789672
b3360	PABA_ECOLI	P00903	pabA	EG10682	1789760
b3374	YHFQ_ECOLI	P45543	frlD	EG12912	1789775
b3379	PHP_ECOLI	P45548	php	EG12917	1789780
b3380	YHFW_ECOLI	P45549	yhfW	EG12918	1789781
b3431	GLGX_ECOLI	P15067	glgX	EG10381	2367229
b3551	BISC_ECOLI	P20099	bisC	EG10124	1789973
b3575	YIAK_ECOLI	P37672	yiaK	EG12279	1790000
b3581	SGBH_ECOLI	P37678	sgbH	EG12285	1790006
b3583	SGBE_ECOLI	P37680	sgbE	EG12287	1790008
b3606	YIBK_ECOLI	P33899	yibK	EG11888	1790034
b3611	YIBN_ECOLI	P37688	yibN	EG12295	1790040
b3647	YICF_ECOLI	P25772	ligB	EG11334	1790079
b3656	YICI_ECOLI	P31434	yicI	EG11685	2367256
b3678	YIDJ_ECOLI	P31447	yidJ	EG11705	1790112
b3683	PTIC_ECOLI	P31452	glvC	EG11710	1790117
b3715	YIEH_ECOLI	P31467	yieH	EG11725	1790151
b3718	YIEK_ECOLI	P31470	yieK	EG11728	1790155
b3784	WECA_ECOLI	P24235	rfe	EG10840	1790218
b3787	WECC_ECOLI	P27829	rffD	EG11452	2367284

b3794	WECG_ECOLI	P27836	rffM	EG11458	2367289
b3812	YIGB_ECOLI	P23306	yigB	EG11202	2367295
b3833	UBIE_ECOLI	P27851	ubiE	EG11473	2367307
b3862	YIHG_ECOLI	P32129	yihG	EG11833	1790293
b3878	YIHQ_ECOLI	P32138	yihQ	EG11843	2367323
b3879	YIHR_ECOLI	P32139	yihR	EG11844	1790311
b3881	YIHT_ECOLI	P32141	yihT	EG11846	1790314
b3882	YIHU_ECOLI	P32142	yihU	EG11847	1790315
b3883	YIHV_ECOLI	P32143	yihV	EG11848	1790316
b3897	FRVR_ECOLI	P32152	frvR	EG11861	1790331
b3932	HSLV_ECOLI	P31059	hslV	EG11676	1790367
b3946	FSAB_ECOLI	P32669	fsaB	EG11905	1790382
b3949	PTWC_ECOLI	P32672	frwC	EG11908	1790386
b4085	ALSE_ECOLI	P32719	alsE	EG11957	1790523
b4180	YJFH_ECOLI	P39290	rlmB	EG12483	1790623
b4186	YJFC_ECOLI	P33222	yjfC	EG11812	1790629
b4187	AIDB_ECOLI	P33224	aidB	EG11811	1790630
b4196	SGAH_ECOLI	P39304	ulaD	EG12496	1790640
b4198	SGAE_ECOLI	P39306	ulaF	EG12498	1790642
b4233	MPL_ECOLI	P37773	mpl	EG12440	1790680
b4249	YJGI_ECOLI	P39333	yjgI	EG12528	2367365
b4297	YJHG_ECOLI	P39358	yjhG	EG12549	2367371
b4301	SGCE_ECOLI	P39362	sgcE	EG12553	1790754
b4340	YJIR_ECOLI	P39389	yjiR	EG12579	1790797
b4374	YJJG_ECOLI	P33999	yjjG	EG12115	1790833
b4379	YJJW_ECOLI	P39409	yjjW	EG12599	1790839
b4386	LPLA_ECOLI	P32099	lplA	EG11796	1790846
b4403	LAST_ECOLI	P37005	lasT	EG12309	1790865

EFICAz predicted 4 digit EC number
3.2.2
6.2.1
1.3.99
2.1.1
3.5.1
4.2.1
6.1.1
3.4.21
2.3.1
3.1.3
4.2.1
2.7.2
1.1.1
1.14.13
1.13.11
2.4.1
2.7.1
1.1.1
1.9.3
1.9.3
1.9.3
3.1.2
2.1.1
3.1.1
1.1.1
6.3.2
1.1.1
1.6.99
1.1.1
6.3.4
3.2.2
1.14.13
2.7.1
3.2.2
3.2.1
3.1.2
3.1.1
2.1.1
3.1.3;3.1.4
1.1.1
2.2.1
3.1.3
1.6.99
2.1.1
1.7.2
3.4.24
3.1.2
2.1.1
1.6.99
2.4.1

2.8.1
1.5.3
2.7.1
3.6.3
3.4.21
3.4.21
2.7.1
2.1.1
1.1.1
3.4.19
1.2.7
2.3.1
2.7.8
2.7.7
3.1.3
2.6.1
3.6.3
3.4.24
3.1.6
2.7.1
4.1.2
1.2.1
1.1.1
1.1.1
1.1.1
2.7.1
3.4.21
1.3.1
1.1.1
1.6.99
1.1.2
2.8.3
1.3.99
1.11.1
2.7.1
2.6.1
2.7.8
1.1.1
2.7.1
4.1.2
1.1.1
1.1.1
1.14.15
4.1.3
3.4.24
3.6.3
2.3.1
2.3.1
2.3.1
2.7.1
4.1.2
3.2.2

2.7.1
3.2.1
1.3.3
2.7.1
3.2.2
2.7.1
1.1.1
4.1.2
2.4.1
2.1.2
6.2.1
2.6.1
5.3.3
5.1.99
5.1.99
2.6.1
2.4.2
1.1.1
1.1.1
2.3.1
3.6.1
1.4.1
1.6.5
1.6.5
1.6.5
3.4.24
1.20.4
2.1.1
1.14.12
1.14.12
1.1.1;1.3.1
1.1.1
2.7.1
3.5.4
2.1.1
1.20.4
5.4.2
1.18.1
1.1.1
4.1.2
5.3.1
1.1.1
2.7.1
2.1.1
4.2.1
3.5.4
1.1.1
1.2.1;2.3.1
5.1.1
2.1.3
3.4.13
3.5.2

2.7.2
1.4.1
1.4.1
1.1.1
1.14.13
6.3.3
5.4.99
3.1.2
1.2.1
3.1.3
3.4.24
3.6.1
1.1.2
3.1.1
1.1.1;1.3.1
1.1.1
1.97.1
5.99.1
5.99.1
6.3.1
1.13.11
2.7.1;2.7.7
3.6.1
2.3.1
2.7.2
4.1.2
3.5.99
2.1.1
1.14.14
2.5.1
3.4.21
3.4.21
3.6.3
4.1.3
2.7.1
3.1.8
5.4.2
2.4.1;3.2.1
1.7.2
1.1.1
4.1.1
5.1.3
2.1.1
2.8.1
6.5.1
3.2.1
3.1.6
2.7.1
3.8.1
3.5.99
2.7.8
1.1.1

2.4.1
3.1.3
2.1.1
2.3.1
3.2.1
5.1.3
4.1.2
1.1.1
2.7.1
2.7.1
3.4.25
2.2.1
2.7.1
5.1.3
2.1.1
6.3.1
1.3.99
4.1.1
5.1.3
6.3.2
1.1.1
4.2.1
5.1.3
2.6.1
3.1.3
1.97.1
6.3.4
2.1.1

Enzyme function description
Hydrolases, glycosylases, hydrolyzing N-glycosyl compounds
Ligases, forming carbon-sulfur bonds, acid--thiol ligases
Oxidoreductases, acting on the CH-CH group of donors, with other acceptors
Transferases, transferring one-carbon groups, methyltransferases
Hydrolases, acting on carbon-nitrogen bonds, other than peptide bonds, in linear amides
Lyases, carbon-oxygen lyases, hydro-lyases
Ligases, forming carbon-oxygen bonds, ligases forming aminoacyl-tRNA and related compounds
Hydrolases, acting on peptide bonds (peptide hydrolases), serine endopeptidases
Transferases, acyltransferases, transferring groups other than amino-acyl groups
Hydrolases, acting on ester bonds, phosphoric monoester hydrolases
Lyases, carbon-oxygen lyases, hydro-lyases
Transferases, transferring phosphorous-containing groups, phosphotransferases with a carboxyl group as accepto
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor
Oxidoreductases, miscellaneous (requires further characterization), miscellaneous (requires further characterizatio
Oxidoreductases, acting on single donors with incorporation of molecular oxygen, with incorporation of two atoms o
Transferases, glycosyltransferases, hexosyltransferases
Transferases, transferring phosphorous-containing groups, phosphotransferases with an alcohol group as acceptor
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor
Oxidoreductases, acting on a heme group of donors, with oxygen as acceptor
Oxidoreductases, acting on a heme group of donors, with oxygen as acceptor
Oxidoreductases, acting on a heme group of donors, with oxygen as acceptor
Hydrolases, acting on ester bonds, thiolester hydrolases
Transferases, transferring one-carbon groups, methyltransferases
Hydrolases, acting on ester bonds, carboxylic ester hydrolases
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor
Ligases, forming carbon-nitrogen bonds, acid--D-amino-acid ligases (peptide synthases)
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor
Oxidoreductases, acting on NADH or NADPH, with other acceptors
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor
Ligases, forming carbon-nitrogen bonds, other carbon--nitrogen ligases
Hydrolases, glycosylases, hydrolyzing N-glycosyl compounds
Oxidoreductases, miscellaneous (requires further characterization), miscellaneous (requires further characterizatio
Transferases, transferring phosphorous-containing groups, phosphotransferases with an alcohol group as acceptor
Hydrolases, glycosylases, hydrolyzing N-glycosyl compounds
Hydrolases, glycosylases, glycosidases, i.e
Hydrolases, acting on ester bonds, thiolester hydrolases
Hydrolases, acting on ester bonds, carboxylic ester hydrolases
Transferases, transferring one-carbon groups, methyltransferases
Hydrolases, acting on ester bonds, phosphoric monoester hydrolases;Hydrolases, acting on ester bonds, phosphor
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor
Transferases, transferring aldehyde or ketone residues, transketolases and transaldolases
Hydrolases, acting on ester bonds, phosphoric monoester hydrolases
Oxidoreductases, acting on NADH or NADPH, with other acceptors
Transferases, transferring one-carbon groups, methyltransferases
Oxidoreductases, acting on other nitrogenous compounds as donors, with a cytochrome as acceptor
Hydrolases, acting on peptide bonds (peptide hydrolases), metalloendopeptidases
Hydrolases, acting on ester bonds, thiolester hydrolases
Transferases, transferring one-carbon groups, methyltransferases
Oxidoreductases, acting on NADH or NADPH, with other acceptors
Transferases, glycosyltransferases, hexosyltransferases

Transferases, transferring sulfur-containing groups, sulfurtransferases
Oxidoreductases, acting on the CH-NH group of donors, with oxygen as acceptor
Transferases, transferring phosphorous-containing groups, phosphotransferases with an alcohol group as accepto
Hydrolases, acting on acid anhydrides, in sulfonyl-containing anhydrides
Hydrolases, acting on peptide bonds (peptide hydrolases), serine endopeptidases
Hydrolases, acting on peptide bonds (peptide hydrolases), serine endopeptidases
Transferases, transferring phosphorous-containing groups, phosphotransferases with an alcohol group as acceptor
Transferases, transferring one-carbon groups, methyltransferases
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor
Hydrolases, acting on peptide bonds (peptide hydrolases), omega peptidases
Oxidoreductases, acting on the aldehyde or oxo group of donors, with an iron-sulfur protein as acceptor
Transferases, acyltransferases, transferring groups other than amino-acyl groups
Transferases, transferring phosphorous-containing groups, transferases for other substituted phosphate groups
Transferases, transferring phosphorous-containing groups, nucleotidyltransferases
Hydrolases, acting on ester bonds, phosphoric monoester hydrolases
Transferases, transferring nitrogenous groups, transaminases (aminotransferases)
Hydrolases, acting on acid anhydrides, in sulfonyl-containing anhydrides
Hydrolases, acting on peptide bonds (peptide hydrolases), metalloendopeptidases
Hydrolases, acting on ester bonds, sulfuric ester hydrolases
Transferases, transferring phosphorous-containing groups, phosphotransferases with an alcohol group as acceptor
Lyases, carbon-carbon lyases, aldehyde-lyases
Oxidoreductases, acting on the aldehyde or oxo group of donors, with NAD(+) or NADP(+) as acceptor
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor
Transferases, transferring phosphorous-containing groups, phosphotransferases with an alcohol group as acceptor
Hydrolases, acting on peptide bonds (peptide hydrolases), serine endopeptidases
Oxidoreductases, acting on the CH-CH group of donors, with NAD(+) or NADP(+) as acceptor
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor
Oxidoreductases, acting on NADH or NADPH, with other acceptors
Oxidoreductases, acting on the CH-OH group of donors, with a cytochrome as acceptor
Transferases, transferring sulfur-containing groups, coA-transferases
Oxidoreductases, acting on the CH-CH group of donors, with other acceptors

Transferases, transferring phosphorous-containing groups, phosphotransferases with an alcohol group as accepto
Transferases, transferring nitrogenous groups, transaminases (aminotransferases)
Transferases, transferring phosphorous-containing groups, transferases for other substituted phosphate groups
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor
Transferases, transferring phosphorous-containing groups, phosphotransferases with an alcohol group as accepto
Lyases, carbon-carbon lyases, aldehyde-lyases
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor
Oxidoreductases, miscellaneous (requires further characterization), miscellaneous (requires further characterizatio
Lyases, carbon-carbon lyases, oxo-acid-lyases
Hydrolases, acting on peptide bonds (peptide hydrolases), metalloendopeptidases
Hydrolases, acting on acid anhydrides, in sulfonyl-containing anhydrides
Transferases, acyltransferases, transferring groups other than amino-acyl groups
Transferases, acyltransferases, transferring groups other than amino-acyl groups
Transferases, acyltransferases, transferring groups other than amino-acyl groups
Transferases, transferring phosphorous-containing groups, phosphotransferases with an alcohol group as acceptor
Lyases, carbon-carbon lyases, aldehyde-lyases
Hydrolases, glycosylases, hydrolyzing N-glycosyl compounds

Transferases, transferring phosphorous-containing groups, phosphotransferases with an alcohol group as accepto
Hydrolases, glycosylases, glycosidases, i.e
Oxidoreductases, acting on the CH-CH group of donors, with oxygen as acceptor
Transferases, transferring phosphorous-containing groups, phosphotransferases with an alcohol group as accepto
Hydrolases, glycosylases, hydrolyzing N-glycosyl compounds
Transferases, transferring phosphorous-containing groups, phosphotransferases with an alcohol group as accepto
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor
Lyases, carbon-carbon lyases, aldehyde-lyases
Transferases, glycosyltransferases, hexosyltransferases
Transferases, transferring one-carbon groups, hydroxymethyl-, formyl- and related transferases
Ligases, forming carbon-sulfur bonds, acid--thiol ligases
Transferases, transferring nitrogenous groups, transaminases (aminotransferases)
Isomerases, intramolecular oxidoreductases, transposing C==C bonds
Isomerases, racemases and epimerases, acting on other compounds
Isomerases, racemases and epimerases, acting on other compounds
Transferases, transferring nitrogenous groups, transaminases (aminotransferases)
Transferases, glycosyltransferases, pentosyltransferases
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor
Transferases, acyltransferases, transferring groups other than amino-acyl groups
Hydrolases, acting on acid anhydrides, in phosphorous-containing anhydrides
Oxidoreductases, acting on the CH-NH(2) group of donors, with NAD(+) or NADP(+) as acceptor
Oxidoreductases, acting on NADH or NADPH, with a quinone or similar compound as acceptor
Oxidoreductases, acting on NADH or NADPH, with a quinone or similar compound as acceptor
Oxidoreductases, acting on NADH or NADPH, with a quinone or similar compound as acceptor
Hydrolases, acting on peptide bonds (peptide hydrolases), metalloendopeptidases
Oxidoreductases, acting on phosphorus or arsenic in donors, acting on phosphorus or arsenic in donors
Transferases, transferring one-carbon groups, methyltransferases
Oxidoreductases, miscellaneous (requires further characterization), miscellaneous (requires further characterizatic
Oxidoreductases, miscellaneous (requires further characterization), miscellaneous (requires further characterizatic
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor;Oxidoreductases, a
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor
Transferases, transferring phosphorous-containing groups, phosphotransferases with an alcohol group as accepto
Hydrolases, acting on carbon-nitrogen bonds, other than peptide bonds, in cyclic amidines
Transferases, transferring one-carbon groups, methyltransferases
Oxidoreductases, acting on phosphorus or arsenic in donors, acting on phosphorus or arsenic in donors
Isomerases, intramolecular transferases (mutases), phosphotransferases (phosphomutases)
Oxidoreductases, acting on iron-sulfur proteins as donors, with NAD(+) or NADP(+) as acceptor
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor
Lyases, carbon-carbon lyases, aldehyde-lyases
Isomerases, intramolecular oxidoreductases, interconverting aldoses and ketoses
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor
Transferases, transferring phosphorous-containing groups, phosphotransferases with an alcohol group as accepto
Transferases, transferring one-carbon groups, methyltransferases
Lyases, carbon-oxygen lyases, hydro-lyases
Hydrolases, acting on carbon-nitrogen bonds, other than peptide bonds, in cyclic amidines
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor
Oxidoreductases, acting on the aldehyde or oxo group of donors, with NAD(+) or NADP(+) as acceptor;Transferas
Isomerases, racemases and epimerases, acting on amino acids and derivatives
Transferases, transferring one-carbon groups, carboxyl- and carbamoyltransferases
Hydrolases, acting on peptide bonds (peptide hydrolases), dipeptidases
Hydrolases, acting on carbon-nitrogen bonds, other than peptide bonds, in cyclic amides

Transferases, transferring phosphorous-containing groups, phosphotransferases with a carboxyl group as accepto
Oxidoreductases, acting on the CH-NH(2) group of donors, with NAD(+) or NADP(+) as acceptor
Oxidoreductases, acting on the CH-NH(2) group of donors, with NAD(+) or NADP(+) as acceptor
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor
Oxidoreductases, miscellaneous (requires further characterization), miscellaneous (requires further characterizatio
Ligases, forming carbon-nitrogen bonds, cyclo-ligases
Isomerases, intramolecular transferases (mutases), transferring other groups
Hydrolases, acting on ester bonds, thiolester hydrolases
Oxidoreductases, acting on the aldehyde or oxo group of donors, with NAD(+) or NADP(+) as acceptor
Hydrolases, acting on ester bonds, phosphoric monoester hydrolases
Hydrolases, acting on peptide bonds (peptide hydrolases), metalloendopeptidases
Hydrolases, acting on acid anhydrides, in phosphorous-containing anhydrides
Oxidoreductases, acting on the CH-OH group of donors, with a cytochrome as acceptor
Hydrolases, acting on ester bonds, carboxylic ester hydrolases
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor;Oxidoreductases, ac
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor

Ligases, forming carbon-nitrogen bonds, acid--ammonia (or amide) ligases (amide synthases)
Oxidoreductases, acting on single donors with incorporation of molecular oxygen, with incorporation of two atoms o
Transferases, transferring phosphorous-containing groups, phosphotransferases with an alcohol group as acceptor
Hydrolases, acting on acid anhydrides, in phosphorous-containing anhydrides
Transferases, acyltransferases, transferring groups other than amino-acyl groups
Transferases, transferring phosphorous-containing groups, phosphotransferases with a carboxyl group as accepto
Lyases, carbon-carbon lyases, aldehyde-lyases
Hydrolases, acting on carbon-nitrogen bonds, other than peptide bonds, in other compounds
Transferases, transferring one-carbon groups, methyltransferases
Oxidoreductases, miscellaneous (requires further characterization), miscellaneous (requires further characterizatio

Hydrolases, acting on peptide bonds (peptide hydrolases), serine endopeptidases
Hydrolases, acting on peptide bonds (peptide hydrolases), serine endopeptidases
Hydrolases, acting on acid anhydrides, in sulfonyl-containing anhydrides
Lyases, carbon-carbon lyases, oxo-acid-lyases
Transferases, transferring phosphorous-containing groups, phosphotransferases with an alcohol group as accepto
Hydrolases, acting on ester bonds, phosphoric triester hydrolases
Isomerases, intramolecular transferases (mutases), phosphotransferases (phosphomutases)
Transferases, glycosyltransferases, hexosyltransferases;Hydrolases, glycosylases, glycosidases, i.e
Oxidoreductases, acting on other nitrogenous compounds as donors, with a cytochrome as acceptor
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor
Lyases, carbon-carbon lyases, carboxy-lyases
Isomerases, racemases and epimerases, acting on carbohydrates and derivatives
Transferases, transferring one-carbon groups, methyltransferases
Transferases, transferring sulfur-containing groups, sulfurtransferases

Hydrolases, glycosylases, glycosidases, i.e
Hydrolases, acting on ester bonds, sulfuric ester hydrolases
Transferases, transferring phosphorous-containing groups, phosphotransferases with an alcohol group as accepto
Hydrolases, acting on halide bonds, in C-halide compounds
Hydrolases, acting on carbon-nitrogen bonds, other than peptide bonds, in other compounds
Transferases, transferring phosphorous-containing groups, transferases for other substituted phosphate groups
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor

Transferases, glycosyltransferases, hexosyltransferases
Hydrolases, acting on ester bonds, phosphoric monoester hydrolases
Transferases, transferring one-carbon groups, methyltransferases
Transferases, acyltransferases, transferring groups other than amino-acyl groups
Hydrolases, glycosylases, glycosidases, i.e
Isomerases, racemases and epimerases, acting on carbohydrates and derivatives
Lyases, carbon-carbon lyases, aldehyde-lyases
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor
Transferases, transferring phosphorous-containing groups, phosphotransferases with an alcohol group as accepto
Transferases, transferring phosphorous-containing groups, phosphotransferases with an alcohol group as acceptor
Hydrolases, acting on peptide bonds (peptide hydrolases), threonine endopeptidases
Transferases, transferring aldehyde or ketone residues, transketolases and transaldolases
Transferases, transferring phosphorous-containing groups, phosphotransferases with an alcohol group as acceptor
Isomerases, racemases and epimerases, acting on carbohydrates and derivatives
Transferases, transferring one-carbon groups, methyltransferases
Ligases, forming carbon-nitrogen bonds, acid--ammonia (or amide) ligases (amide synthases)
Oxidoreductases, acting on the CH-CH group of donors, with other acceptors
Lyases, carbon-carbon lyases, carboxy-lyases
Isomerases, racemases and epimerases, acting on carbohydrates and derivatives
Ligases, forming carbon-nitrogen bonds, acid--D-amino-acid ligases (peptide synthases)
Oxidoreductases, acting on the CH-OH group of donors, with NAD(+) or NADP(+) as acceptor
Lyases, carbon-oxygen lyases, hydro-lyases
Isomerases, racemases and epimerases, acting on carbohydrates and derivatives
Transferases, transferring nitrogenous groups, transaminases (aminotransferases)
Hydrolases, acting on ester bonds, phosphoric monoester hydrolases

Ligases, forming carbon-nitrogen bonds, other carbon--nitrogen ligases
Transferases, transferring one-carbon groups, methyltransferases

	Component of EFICAz responsible for the prediction				
	SIT	**PROSITE**	**CHIEF-FDR**	**PFAM-FDR**	**Number of components**
	SIT	PROSITE		PFAM-FDR	3
			CHIEF-FDR		1
	SIT	PROSITE			2
	SIT	PROSITE	CHIEF-FDR	PFAM-FDR	4
				PFAM-FDR	1
	SIT	PROSITE	CHIEF-FDR	PFAM-FDR	4
			CHIEF-FDR	PFAM-FDR	2
				PFAM-FDR	1
			CHIEF-FDR		1
			CHIEF-FDR		1
	SIT	PROSITE	CHIEF-FDR	PFAM-FDR	4
	SIT				1
			CHIEF-FDR		1
n)			CHIEF-FDR	PFAM-FDR	2
of oxygen				PFAM-FDR	1
			CHIEF-FDR		1
r			CHIEF-FDR	PFAM-FDR	2
			CHIEF-FDR		1
				PFAM-FDR	1
	SIT				1
	SIT		CHIEF-FDR		2
	SIT		CHIEF-FDR	PFAM-FDR	3
			CHIEF-FDR	PFAM-FDR	2
	SIT	PROSITE			2
			CHIEF-FDR		1
				PFAM-FDR	1
	SIT			PFAM-FDR	2
	SIT				1
			CHIEF-FDR		1
				PFAM-FDR	1
	SIT	PROSITE		PFAM-FDR	3
n)				PFAM-FDR	1
r			CHIEF-FDR		1
	SIT	PROSITE	CHIEF-FDR	PFAM-FDR	4
				PFAM-FDR	1
	SIT	PROSITE			2
	SIT	PROSITE	CHIEF-FDR	PFAM-FDR	4
			CHIEF-FDR		1
ric diester hydrolases				PFAM-FDR	1
	SIT		CHIEF-FDR	PFAM-FDR	3
	SIT				1
				PFAM-FDR	1
				PFAM-FDR	1
	SIT	PROSITE			2
	SIT				1
				PFAM-FDR	1
			CHIEF-FDR		1
				PFAM-FDR	1
				PFAM-FDR	1
			CHIEF-FDR		1

				PFAM-FDR	1
	SIT		CHIEF-FDR		2
	SIT		CHIEF-FDR	PFAM-FDR	3
			CHIEF-FDR		1
				PFAM-FDR	1
			CHIEF-FDR	PFAM-FDR	2
r			CHIEF-FDR		1
			CHIEF-FDR		1
			CHIEF-FDR		1
				PFAM-FDR	1
			CHIEF-FDR		1
	SIT	PROSITE	CHIEF-FDR	PFAM-FDR	4
				PFAM-FDR	1
	SIT	PROSITE	CHIEF-FDR	PFAM-FDR	4
			CHIEF-FDR	PFAM-FDR	2
			CHIEF-FDR		1
			CHIEF-FDR		1
			CHIEF-FDR		1
			CHIEF-FDR	PFAM-FDR	2
r			CHIEF-FDR	PFAM-FDR	2
			CHIEF-FDR	PFAM-FDR	2
			CHIEF-FDR		1
			CHIEF-FDR		1
	SIT		CHIEF-FDR	PFAM-FDR	3
			CHIEF-FDR		1
r			CHIEF-FDR		1
				PFAM-FDR	1
				PFAM-FDR	1
			CHIEF-FDR		1
	SIT		CHIEF-FDR		2
			CHIEF-FDR		1
				PFAM-FDR	1
	SIT	PROSITE	CHIEF-FDR	PFAM-FDR	4
			CHIEF-FDR		1
	SIT		CHIEF-FDR		2
	SIT				1
				PFAM-FDR	1
			CHIEF-FDR		1
	SIT	PROSITE	CHIEF-FDR	PFAM-FDR	4
	SIT		CHIEF-FDR	PFAM-FDR	3
			CHIEF-FDR		1
			CHIEF-FDR		1
n)			CHIEF-FDR		1
	SIT				1
				PFAM-FDR	1
			CHIEF-FDR		1
			CHIEF-FDR		1
			CHIEF-FDR		1
	SIT		CHIEF-FDR		2
r				PFAM-FDR	1
	SIT	PROSITE	CHIEF-FDR	PFAM-FDR	4
			CHIEF-FDR	PFAM-FDR	2

SIT	PROSITE	CHIEF-FDR	PFAM-FDR	4
		CHIEF-FDR	PFAM-FDR	2
SIT				1
SIT	PROSITE	CHIEF-FDR	PFAM-FDR	4
SIT	PROSITE		PFAM-FDR	3
SIT	PROSITE	CHIEF-FDR	PFAM-FDR	4
SIT		CHIEF-FDR	PFAM-FDR	3
SIT				1
		CHIEF-FDR		1
		CHIEF-FDR		1
			PFAM-FDR	1
SIT		CHIEF-FDR		2
		CHIEF-FDR		1
		CHIEF-FDR	PFAM-FDR	2
		CHIEF-FDR		1
		CHIEF-FDR		1
SIT	PROSITE	CHIEF-FDR	PFAM-FDR	4
SIT		CHIEF-FDR		2
SIT		CHIEF-FDR	PFAM-FDR	3
SIT		CHIEF-FDR	PFAM-FDR	3
		CHIEF-FDR		1
SIT		CHIEF-FDR		2
		CHIEF-FDR		1
		CHIEF-FDR		1
		CHIEF-FDR		1
			PFAM-FDR	1
SIT		CHIEF-FDR	PFAM-FDR	3
			PFAM-FDR	1
SIT		CHIEF-FDR		2
SIT				1
SIT		CHIEF-FDR		2
		CHIEF-FDR		1
or		CHIEF-FDR		1
		CHIEF-FDR	PFAM-FDR	2
			PFAM-FDR	1
		CHIEF-FDR		1
		CHIEF-FDR		1
SIT				1
SIT				1
			PFAM-FDR	1
SIT				1
SIT		CHIEF-FDR		2
or		CHIEF-FDR	PFAM-FDR	2
SIT	PROSITE			2
SIT		CHIEF-FDR	PFAM-FDR	3
			PFAM-FDR	1
		CHIEF-FDR		1
ses, acyltransferases, transfer			PFAM-FDR	1
SIT	PROSITE		PFAM-FDR	3
		CHIEF-FDR	PFAM-FDR	2
			PFAM-FDR	1
		CHIEF-FDR		1

	SIT				1
				PFAM-FDR	1
	SIT		CHIEF-FDR	PFAM-FDR	3
			CHIEF-FDR		1
n)				PFAM-FDR	1
			CHIEF-FDR	PFAM-FDR	2
	SIT	PROSITE	CHIEF-FDR	PFAM-FDR	4
			CHIEF-FDR		1
	SIT		CHIEF-FDR	PFAM-FDR	3
				PFAM-FDR	1
				PFAM-FDR	1
	SIT				1
			CHIEF-FDR		1
			CHIEF-FDR	PFAM-FDR	2
cting on the CH			CHIEF-FDR		1
	SIT		CHIEF-FDR	PFAM-FDR	3
				PFAM-FDR	1
	SIT		CHIEF-FDR	PFAM-FDR	3
	SIT		CHIEF-FDR	PFAM-FDR	3
			CHIEF-FDR		1
of oxygen				PFAM-FDR	1
r;Transferases,			CHIEF-FDR	PFAM-FDR	2
				PFAM-FDR	1
	SIT		CHIEF-FDR	PFAM-FDR	3
	SIT	PROSITE	CHIEF-FDR	PFAM-FDR	4
	SIT	PROSITE	CHIEF-FDR	PFAM-FDR	4
	SIT	PROSITE			2
			CHIEF-FDR		1
n)				PFAM-FDR	1
	SIT	PROSITE	CHIEF-FDR	PFAM-FDR	4
				PFAM-FDR	1
				PFAM-FDR	1
			CHIEF-FDR		1
	SIT		CHIEF-FDR	PFAM-FDR	3
	SIT	PROSITE	CHIEF-FDR	PFAM-FDR	4
	SIT	PROSITE			2
			CHIEF-FDR	PFAM-FDR	2
			CHIEF-FDR		1
	SIT			PFAM-FDR	2
			CHIEF-FDR	PFAM-FDR	2
				PFAM-FDR	1
	SIT		CHIEF-FDR	PFAM-FDR	3
				PFAM-FDR	1
			CHIEF-FDR		1
	SIT	PROSITE	CHIEF-FDR		3
			CHIEF-FDR	PFAM-FDR	2
				PFAM-FDR	1
	SIT		CHIEF-FDR		2
				PFAM-FDR	1
	SIT	PROSITE			2
			CHIEF-FDR	PFAM-FDR	2
			CHIEF-FDR	PFAM-FDR	2

		CHIEF-FDR	PFAM-FDR	2
			PFAM-FDR	1
			PFAM-FDR	1
		CHIEF-FDR	PFAM-FDR	2
		CHIEF-FDR	PFAM-FDR	2
		CHIEF-FDR	PFAM-FDR	2
		CHIEF-FDR	PFAM-FDR	2
SIT		CHIEF-FDR		2
SIT		CHIEF-FDR		2
r		CHIEF-FDR		1
		CHIEF-FDR	PFAM-FDR	2
SIT				1
r		CHIEF-FDR		1
SIT	PROSITE	CHIEF-FDR	PFAM-FDR	4
			PFAM-FDR	1
		CHIEF-FDR		1
SIT	PROSITE			2
			PFAM-FDR	1
SIT		CHIEF-FDR	PFAM-FDR	3
SIT		CHIEF-FDR	PFAM-FDR	3
		CHIEF-FDR		1
SIT	PROSITE	CHIEF-FDR	PFAM-FDR	4
SIT	PROSITE	CHIEF-FDR	PFAM-FDR	4
		CHIEF-FDR		1
			PFAM-FDR	1
SIT	PROSITE	CHIEF-FDR	PFAM-FDR	4
			PFAM-FDR	1
			PFAM-FDR	1

KEGG annotation
hypothetical 32.6 kD protein in lytB-dapB intergenic region
probable crotonobetaine/carnitine-CoA ligase [EC:6.3.2.-]
probable carnitine operon oxidoreductase caiA [EC:1.3.99.-]
dimethyladenosine transferase [EC:2.1.1.-]
ampD protein
putative carbonic anhydrase [EC:4.2.1.1]
putative tRNA synthetase
protease do precursor [EC:3.4.21.-]
UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase (firA protein) (rifampicin resistance protein) [EC:2.3.
D-glycero-D-manno-heptose 1,7-bisphosphate phosphatase [EC:3.1.1.-]
hypothetical 69.4 kD protein in perR-argF intergenic region
carbamate kinase [EC:2.7.2.2]
hypothetical zinc-type alcohol dehydrogenase-like protein in betT-prpR intergenic region
3-(3-hydroxy-phenyl)propionate hydroxylase [EC:1.14.13.-]
2,3-dihydroxyphenylpropionate 1,2-dioxygenase [EC:1.13.11.-]
hypothetical 44.7 kD protein in adhC-taua intergenic region
putative nitrate transport permease protein
hypothetical oxidoreductase in pgpA-ispA intergenic region
cytochrome o ubiquinol oxidase operon protein cyoD
cytochrome o ubiquinol oxidase subunit III [EC:1.10.3.-]
cytochrome o ubiquinol oxidase subunit I [EC:1.10.3.-]
acyl-CoA thioesterase II [EC:3.1.2.-]
hypothetical 14.4 kD protein in tesB-hha intergenic region
acetyl esterase [EC:3.1.1.-]
putative oxidoreductase [EC:1.-.-.-]
hypothetical 41.7 kD protein in nfnB-entD intergenic region
hypothetical oxidoreductase in cstA-ahpC intergenic region [EC:1.1.-.-]
alkyl hydroperoxide reductase f52a protein [EC:1.6.4.-]
hypothetical zinc-type alcohol dehydrogenase-like protein in ahpF-rnk intergenic region
lipoate-protein ligase B (lipoate biosynthesis protein B) [EC:6.-.-.-]
hypothetical 33.8 kD protein in leuS-gltL intergenic region
2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase [EC:1.14.13.-]
N-acetylglucosamine repressor
endonuclease VIII [EC:3.2.-.-]
putative alpha-mannosidase
hypothetical 15.6 kD protein in cydB-tolQ intergenic region
putative pectinesterase
biotin synthesis protein bioC
hypothetical 28.8 kD protein in moaE-rhlE intergenic region
putative malate dehydrogenase, archaea type [EC:1.1.1.37]
putative transaldolase [EC:4.1.2.-]
hypothetical 22.4 kD protein in deoR-cmr intergenic region
oxygen-insensitive NADPH nitroreductase [EC:1.-.-.-]
hypothetical RNA methyltransferase in potI-artJ intergenic region [EC:2.1.1.-]
anaerobic dimethyl sulfoxide reductase chain A precursor (DMSO reductase) [EC:1.8.99.-]
putative metalloprotease [EC:3.4.24.-]
hypothetical 23.8 kD protein in mukB-aspC intergenic region
putative oxidoreductase
putative enzyme
hypothetical 50.8 kD protein in phoH-csgG intergenic region

hypothetical 40.0 kD protein in htrB-dinI intergenic region (ORF39.9)
putative sarcosine oxidase [EC:1.5.3.1]
hypothetical 33.0 kD protein in mfd-cobb intergenic region
spermidine/putrescine transport system ATP-binding protein
putative phage repressor
umuD protein [EC:3.4.21.-]
putative dihydroxyacetone kinase
hemK protein [EC:2.1.1.-]
hypothetical oxidoreductase in btuR-sohB intergenic region [EC:1.-.-.-]
hypothetical 28.5 kD protein in sapA-aldH intergenic region
pyruvate ferredoxin oxidoreductase [EC:1.2.7.-]
putative acetyl-CoA acetyltransferase [EC:2.3.1.-]
hypothetical protein
putative phosphatidate cytidiltransferase [EC:2.7.7.41]
hypothetical 49.6 kD protein in maoC-acpD intergenic region
multi modular. putative transcriptional regulator. also putative ATP-binding component of a transport system
putative spermidine/putrescine transport system ATP-binding protein
probable zinc protease pqqL [EC:3.4.99.-]
putative sulfatase [EC:3.1.6.-]
hypothetical sugar kinase in hipB-uxaB intergenic region
hypothetical 31.9 kD protein in hipB-uxaB intergenic region [EC:4.2.1.-]
putative aldehyde dehydrogenase [EC:1.2.1.-]
probable oxidoreductase in dcp-nohA intergenic region [EC:1.-.-.-]
putative oxidoreductase
starvation sensing protein rspB [EC:1.1.1.-]
MLC protein (making large colonies protein)
putative protease ydgD precursor [EC:3.4.21.-]
hypothetical oxidoreductase in pntA-rstA intergenic region [EC:1.-.-.-]
hypothetical protein
N-ethylmaleimide reductase (N-ethylmaleimide reducing enzyme) [EC:1.-.-.-]
hypothetical 113.2 kD protein in lpp-aroD intergenic region
hypothetical 56.2 kD protein in aroD-ppsA intergenic region
putative oxidoreductase
vitamin B12 transport system substrate-binding protein
pts system, cellobiose-specific IIC component (EIIC-Cel) (cellobiose-permease IIC component) (phosphotransfera
succinylornithine transaminase (succinylornithine aminotransferase) (carbon starvation protein C) [EC:2.6.1.-]
putative cytochrome oxidase
probable oxidoreductase
putative kinase
putative aldolase
hypothetical zinc-type alcohol dehydrogenase-like protein in ansA-gapA intergenic region
putative an aldehyde reductase
putative dioxygenase alpha subunit yeaw [EC:1.14.1.-]
para-aminobenzoate synthase component I (adc synthase) [EC:4.1.3.-]
probable protease htpX (heat shock protein htpX) [EC:3.4.24.-]
putative polar amino acid transport system ATP-binding protein
putative lipopolysaccharide biosynthesis O-acetyl transferase WbbJ [EC:2.3.1.-]
putative colanic acid biosynthesis acetyltransferase wcaF [EC:2.3.1.-]
putative colanic acid biosynthesis acetyltransferase wcaB [EC:2.3.1.-]
hypothetical 32.0 kD protein in ogrK-gatr intergenic region
tagatose-bisphosphate aldolase gatY [EC:4.1.2.-]
hypothetical protein

putative kinase
putative autolytic lysozyme
hypothetical 45.3 kD protein in cdd-mglC intergenic region
hypothetical 39.7 kD protein in nfo-fruA intergenic region
hypothetical 33.7 kD protein in nfo-fruA intergenic region
hypothetical 33.6 kD protein in nfo-fruA intergenic region
hypothetical 54.0 kD protein in fruK-bcr intergenic region
hypothetical protein
Putative glycosyl transferase [EC:2.-.-.-]
putative transformylase
elaA protein
putative aspartate aminotransferase [EC:2.6.1.1]
putative regulator
hypothetical 43.3 kD protein in evgS-glk intergenic region
putative enzyme
N-succinyldiaminopimelate aminotransferase [EC:2.6.1.17]
xanthosine phosphorylase [EC:2.4.2.-]
oxidoreductase ucpA [EC:1.-.-.-]
ethanolamine utilization protein eutG
ethanolamine utilization protein eutI
hypothetical 21.7 kD protein in tktB-narQ intergenic region
putative oxidoreductase, Fe-S subunit
hydrogenase-4 component B [EC:1.-.-.-]
hydrogenase-4 component D [EC:1.-.-.-]
hydrogenase-4 component F [EC:1.-.-.-]
hypothetical protein
putative oxidoreductase
putative ATP synthase beta subunit [EC:2.1.1.-]
digoxigenin alpha subunit [EC:1.14.1.-]
digoxigenin beta subunit [EC:1.14.1.-]
2,3-dihydroxy-2,3-dihydrophenylpropionate dehydrogenase [EC:1.3.1.-]
hypothetical zinc-type alcohol dehydrogenase-like protein in csiE-glyA intergenic region
hypothetical 44.8 kD protein in csiE-glyA intergenic region
hypothetical 20.0 kD protein in purL-dpj intergenic region (ORF178)
hypothetical tRNA/rRNA methyltransferase yfiF [EC:2.1.1.-]
hypothetical protein
hypothetical 20.8 kD protein in gshA-csrA intergenic region
flavorubredoxin reductase [EC:1.18.1.-]
putative dehydrogenase [EC:1.1.-.-]
hypothetical 23.2 kD protein in prpB-rpoS intergenic region
hypothetical 29.2 kD protein in mutS-rpoS intergenic region (O258)
putative oxidoreductase [EC:1.-.-.-]
hypothetical sugar kinase in cysJ-eno intergenic region
hypothetical RNA methyltransferase in relA-barA intergenic region [EC:2.1.1.-]
probable glucarate dehydratase 2 (GDH) [EC:4.2.1.40]
hypothetical 32.6 kD protein in syd-sdaC intergenic region
hypothetical protein
2-acylglycerophosphoethanolamine acyltransferase / acyl-acyl carrier protein synthetase (2-acyl-gpe acyltransfera
hypothetical 25.2 kD protein in lysR-araE intergenic region
hypothetical 40.2 kD protein in kduI-lysS intergenic region
hypothetical 44.8 kD protein in kduI-lysS intergenic region
hypothetical protein

carbamate kinase [EC:2.7.2.2]
putative oxidoreductase, Fe-S subunit
hypothetical 69.7 kD protein in kduI-lysS intergenic region
hypothetical oxidoreductase in bglA-gcvP intergenic region [EC:1.-.-.-]
visC protein [EC:1.-.-.-]
hypothetical 21.1 kD protein in ssr-serA intergenic region (O182)
methylmalonyl-CoA mutase [EC:5.4.99.2]
hypothetical 53.8 kD protein in sbm-fba intergenic region (O492)
D-erythrose 4-phosphate dehydrogenase (E4PDH) [EC:1.2.1.-]
hypothetical 34.3 kD protein in epd-cmtA intergenic region (ORF 1) (F321)
putative metalloprotease [EC:3.4.24.-]
hypothetical 21.0 kD protein in gshB-ansB intergenic region (O197)
glycolate oxidase subunit glcD [EC:1.1.3.15]
hypothetical protein
hypothetical oxidoreductase in hybA-exbD intergenic region [EC:1.-.-.-]
hypothetical oxidoreductase in metC-sufI intergenic region [EC:1.1.-.-]
hypothetical protein
topoisomerase IV subunit [EC:5.99.1.-]
topoisomerase IV subunit B [EC:5.99.1.-]
hypothetical 45.0 kD protein in tolC-ribB intergenic region (ORFA) (O386)
hypothetical 29.9 kD protein in tolC-ribB intergenic region (ORFC) (F271)
bifunctional D-glycero-beta-D-manno-heptose 7-phosphate kinase/D-glycero-beta-D-manno-heptose 1-phosphate
hypothetical 48.4 kD protein in glnE-cca intergenic region (ORFXE)
keto-acid formate acetyltransferase (keto-acid formate-lyase) [EC:2.3.1.54]
propionate kinase [EC:2.7.2.-]
tagatose-bisphosphate aldolase agaY [EC:4.1.2.-]
putative galactosamine-6-phosphate isomerase (galactosamine-6-phosphate deaminase) [EC:5.3.1.-]
hypothetical 31.3 kD protein in agaI-mtr intergenic region (F286)
hypothetical 37.1 kD protein in sohA-mtr intergenic region (O335)
octaprenyl-diphosphate synthase (octaprenyl pyrophosphate synthetase) [EC:2.5.1.-]
protease degQ precursor [EC:3.4.21.-]
protease degS precursor [EC:3.4.21.-]
putative polar amino acid transport system ATP-binding protein
para-aminobenzoate synthase component II [EC:4.1.3.-]
hypothetical 28.3 kD protein in cysG-trpS intergenic region (O261)
phosphotriesterase homology protein
hypothetical 44.6 kD protein in cysG-trpS intergenic region (F408)
glycogen operon protein glgX [EC:3.2.1.-]
biotin sulfoxide reductase 1 (bds reductase 1) (bso reductase 1) [EC:1.-.-.-]
putative malate dehydrogenase, archaea type [EC:1.1.1.37]
probable hexulose-6-phosphate synthase (HUMPS) (D-arabino 3-hexulose 6-phosphate formaldehyde lyase) [EC:
probable sugar isomerase sgbE [EC:5.1.3.4]
hypothetical tRNA/rRNA methyltransferase yibK [EC:2.1.1.-]
hypothetical 15.6 kD protein in secB-tdh intergenic region
hypothetical 63.2 kD protein in rph-gmk intergenic region
putative glycosyl hydrolase
putative sulfatase [EC:3.1.6.-]
pts system, arbutin-like IIC component (phosphotransferase enzyme II, C component)
hypothetical 24.7 kD protein in tnaB-bglB intergenic region
hypothetical 23.3 kD protein in tnaB-bglB intergenic region
undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase [EC:2.4.1.-]
UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase (UDP-mannaca dehydrogenase) [EC:1.1.1.-]

probable UDP-N-acetyl-D-mannosaminuronic acid transferase (UDP-mannaca transferase) [EC:2.4.1.-]
hypothetical 27.1 kD protein in xerC-uvrD intergenic region (ORF 238)
ubiquinone/menaquinone biosynthesis methlytransferase ubiE [EC:2.1.1.-]
hypothetical 36.3 kD protein in dsbA-polA intergenic region
putative glycosyl hydrolase
hypothetical 34 kD protein in glnA-rbn intergenic region (F308)
hypothetical 32 kD protein in glnA-rbn intergenic region (F292)
putative dehydrogenase [EC:1.1.-.-]
hypothetical 31.9 kD protein in glnA-rbn intergenic region (O300)
putative frv operon regulatory protein
heat shock protein hslV [EC:3.4.25.-]
fructose-6-phosphate aldolase 2 [EC:4.1.2.-]
pts system, fructose-like-2 IIC component (phosphotransferase enzyme II, C component)
hypothetical 26.1 kD protein in fdhF-phnP intergenic region (F231)
hypothetical tRNA/rRNA methyltransferase yjfH [EC:2.1.1.-]
hypothetical 45.0 kD protein in vacB-aidB intergenic region (O387)
aidB protein
probable hexulose-6-phosphate synthase (HUMPS) (D-arabino 3-hexulose 6-phosphate formaldehyde lyase) [EC:
probable sugar isomerase sgaE [EC:5.1.3.4]
UDP-N-acetylmuramate: L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase [EC:6.3.2.-]
hypothetical oxidoreductase in pyrL-argI intergenic region [EC:1.-.-.-]
hypothetical 70.0 kD protein in fecI-fimB intergenic region
sgcE protein [EC:5.1.3.-]
hypothetical 53.0 kD protein in iadA-mcrD intergenic region (F470)
hypothetical 25.3 kD protein in rimI-prfC intergenic region
hypothetical 31.5 kD protein in osmY-deoC intergenic region (F287)
lipoate-protein ligase A [EC:6.-.-.-]
hypothetical tRNA/rRNA methyltransferase lasT [EC:2.1.1.-]

Swiss-Prot annotation
Hypothetical protein yaaF.
Probable crotonobetaine/carnitine-CoA ligase (EC 6.3.2.-).
Crotonobetainyl-CoA dehydrogenase (EC 1.3.99.-) (Crotonobetainyl-CoA reductase).
Dimethyladenosine transferase (EC 2.1.1.-) (S-adenosylmethionine-6-N', N'-adenosyl(rRNA) dimethyltransferase) (
AmpD protein.
Protein yadF.
Hypothetical protein yadB.
Protease do precursor (EC 3.4.21.-).
UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase (EC 2.3.1.-) (FirA protein) (Rifampicin resistance pro
Hypothetical protein yaeD.
Hypothetical protein yagF.
Carbamate kinase-like protein yahI.
Zinc-type alcohol dehydrogenase-like protein yahK.
3-(3-hydroxy-phenyl)propionate hydroxylase (EC 1.14.13.-).
2,3-dihydroxyphenylpropionate 1,2-dioxygenase (EC 1.13.11.-).
Hypothetical protein yaiP.
Hypothetical protein yajF.
Hypothetical oxidoreductase yajO (EC 1.-.-.-).
Cytochrome O ubiquinol oxidase protein cyoD (Ubiquinol oxidase chain D).
Cytochrome O ubiquinol oxidase subunit III (EC 1.10.3.-) (Ubiquinol oxidase chain C).
Ubiquinol oxidase polypeptide I (EC 1.10.3.-) (Cytochrome O subunit 1) (Oxidase BO(3) subunit 1) (Cytochrome O
Acyl-CoA thioesterase II (EC 3.1.2.-) (TEII).
Hypothetical protein ybaZ.
Acetyl esterase (EC 3.1.1.-).
Hypothetical oxidoreductase ybbO (EC 1.-.-.-).
Hypothetical protein ybdK.
Hypothetical oxidoreductase ybdH (EC 1.1.-.-).
Alkyl hydroperoxide reductase subunit F (EC 1.6.4.-) (Alkyl hydroperoxide reductase F52A protein).
Hypothetical zinc-type alcohol dehydrogenase-like protein ybdR.
Lipoate-protein ligase B (EC 6.-.-.-) (Lipoate biosynthesis protein B).
Hypothetical protein ybeK.
2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase (EC 1.14.13.-).
N-acetylglucosamine repressor.
Endonuclease VIII (EC 3.2.-.-).
Hypothetical protein ybgG.
Protein ybgC.
Putative lipoprotein ybHC precursor.
Biotin synthesis protein bioC.
Hypothetical protein ybhP.
Hypothetical oxidoreductase ybiC (EC 1.1.1.-).
Fructose-6-phosphate aldolase 1 (EC 4.1.2.-).
Hypothetical protein ybjG.
Oxygen-insensitive NADPH nitroreductase (EC 1.-.-.-) (Modulator of drug activity A).
Hypothetical RNA methyltransferase ybjF (EC 2.1.1.-).
Anaerobic dimethyl sulfoxide reductase chain A precursor (EC 1.8.99.-) (DMSO reductase).
Putative metalloprotease ycaL (EC 3.4.24.-).
Hypothetical protein ycbL.
Hypothetical protein ycbY.
Putative NADH dehydrogenase/NAD(P)H nitroreductase ycdI (EC 1.-.-.-).
Hypothetical protein ycdQ.

Hypothetical UPF0176 protein yceA (ORF39.9).
N-methyl-L-tryptophan oxidase (EC 1.5.3.-) (MTOX).
Hypothetical protein ycfX.
Spermidine/putrescine transport ATP-binding protein potA.
Putative lambdoid prophage e14 repressor protein C2.
UmuD protein (EC 3.4.21.-) [Contains: UmuD' protein].
Hypothetical protein ycgT.
Protein methyltransferase hemK (EC 2.1.1.-) (Protein-glutamine N- methyltransferase hemK) (Protein-(glutamine-N
Hypothetical oxidoreductase yciK (EC 1.-.-.-).
Hypothetical protein ycjL.
Probable pyruvate-flavodoxin oxidoreductase (EC 1.2.7.-).
Probable beta-ketoadipyl CoA thiolase (EC 2.3.1.-).
Hypothetical protein ynbA.
Hypothetical protein ynbB.
Hypothetical protein ynbD.
Hypothetical protein ydcR.
Hypothetical ABC transporter ATP-binding protein ydcT.
Probable zinc protease pqqL (EC 3.4.99.-).
Putative sulfatase ydeN precursor (EC 3.1.6.-).
Hypothetical sugar kinase ydeV.
Putative aldolase yneB (EC 4.2.1.-).
Aldehyde-dehydrogenase like protein yneI (EC 1.2.1.-).
Probable oxidoreductase ydfG (EC 1.-.-.-).
Hypothetical oxidoreductase ydfI (EC 1.-.-.-).
Starvation sensing protein rspB (EC 1.1.1.-).
Mlc protein (Making large colonies protein).
Putative protease ydgD precursor (EC 3.4.21.-).
Hypothetical oxidoreductase ydgB (EC 1.-.-.-).
Hypothetical oxidoreductase ydhF (EC 1.-.-.-).
N-ethylmaleimide reductase (EC 1.-.-.-) (N-ethylmaleimide reducing enzyme).
Hypothetical protein ydiJ.
Hypothetical protein ydiF.
Hypothetical protein ydiO.
Vitamin B12 transport periplasmic protein btuE.
PTS system, N,N'-diacetylchitobiose-specific IIC component (EIIC-Chb) (N,N'-diacetylchitobiose-permease IIC com
Succinylornithine transaminase (EC 2.6.1.-) (Succinylornithine aminotransferase) (Carbon starvation protein C).
Hypothetical protein ynjF.
Hypothetical oxidoreductase ydjG (EC 1.-.-.-).
Hypothetical sugar kinase ydjH.
Hypothetical protein ydjI.
Hypothetical zinc-type alcohol dehydrogenase-like protein ydjJ.
Hypothetical protein yeaE.
Putative dioxygenase alpha subunit yeaW (EC 1.14.1.-).
Para-aminobenzoate synthase component I (EC 4.1.3.-) (ADC synthase).
Probable protease htpX (EC 3.4.24.-) (Heat shock protein htpX).
Hypothetical amino-acid ABC transporter ATP-binding protein yecC.
Putative lipopolysaccharide biosynthesis O-acetyl transferase wbbJ (EC 2.3.1.-).
Putative colanic acid biosynthesis acetyltransferase wcaF (EC 2.3.1.-).
Putative colanic acid biosynthesis acetyltransferase wcaB (EC 2.3.1.-).
Hypothetical protein yegS.
Tagatose-1,6-bisphosphate aldolase gatY (EC 4.1.2.-) (TBPA).
Hypothetical protein yegU.

Hypothetical sugar kinase yegV.
Hypothetical protein yegX.
Hypothetical protein yeiA.
Hypothetical sugar kinase yeiI.
Hypothetical protein yeiK.
Hypothetical sugar kinase yeiC.
Hypothetical oxidoreductase yeiQ (EC 1.-.-.-).
Hypothetical protein yfaU.
Glycosyl transferase arnC (EC 2.-.-.-) (Ara4N transferase) (Polymixin resistance protein pmrF).
Hypothetical protein yfbG.
Protein elaA.
Probable aminotransferase yfbQ (EC 2.6.1.-).
Putative Nudix hydrolase yfcD (EC 3.6.-.-).
Hypothetical protein yfdE.
Hypothetical protein yfdW.
Hypothetical aminotransferase yfdZ (EC 2.6.1.-).
Xanthosine phosphorylase (EC 2.4.2.-).
Oxidoreductase ucpA (EC 1.-.-.-).
Ethanolamine utilization protein eutG.
Ethanolamine utilization protein eutD.
Hypothetical protein yffH.
AegA protein.
Hydrogenase-4 component B (EC 1.-.-.-).
Hydrogenase-4 component D (EC 1.-.-.-).
Hydrogenase-4 component F (EC 1.-.-.-).
Hypothetical protein yfgC precursor.
Protein yfgD.
Hypothetical tRNA/rRNA methyltransferase yfhQ (EC 2.1.1.-).
3-phenylpropionate dioxygenase alpha subunit (EC 1.14.1.-) (Digoxigenin alpha subunit).
3-phenylpropionate dioxygenase beta subunit (EC 1.14.1.-) (Digoxigenin beta subunit).
2,3-dihydroxy-2,3-dihydro-phenylpropionate dehydrogenase (EC 1.3.1.-).
Hypothetical zinc-type alcohol dehydrogenase-like protein yphC.
Hypothetical protein yphH.
Hypothetical protein yfhC.
Hypothetical tRNA/rRNA methyltransferase yfiF (EC 2.1.1.-).
Putative arsenate reductase (EC 1.20.4.1) (Arsenical pump modifier) (Fragment).
Hypothetical protein yqaB.
Nitric oxide reductase FlRd-NAD(+) reductase (EC 1.18.1.-) (Flavorubredoxin reductase) (FlRd-reductase) (FlavoR
Hypothetical oxidoreductase ygbJ (EC 1.1.-.-).
Hypothetical aldolase class II protein ygbL.
Hypothetical protein ygbM.
Hypothetical oxidoreductase ygcW (EC 1.-.-.-).
Hypothetical sugar kinase ygcE.
23S rRNA (Uracil-5-)-methyltransferase rumA (EC 2.1.1.-) (23S rRNA(M- 5-U1939)-methyltransferase).
Glucarate dehydratase related protein (EC 4.2.1.-) (GDH-RP) (GlucDRP).
Hypothetical protein yqcD.
Tas protein.
AAS bifunctional protein [Includes: 2-acylglycerophosphoethanolamine acyltransferase (2-acyl-GPE acyltransferas
Hypothetical protein ygeA.
Hypothetical protein ygeW.
Hypothetical protein ygeY.
Hypothetical hydrolase ygeZ (EC 3.-.-.-).

Carbamate kinase-like protein yqeA.
Hypothetical protein ygfK.
Hypothetical protein ygfT.
Hypothetical oxidoreductase ygfF (EC 1.-.-.-).
Protein visC (EC 1.-.-.-).
Hypothetical protein ygfA.
Sbm protein.
Hypothetical protein ygfH.
D-erythrose 4-phosphate dehydrogenase (EC 1.2.1.-) (E4PDH).
Hypothetical protein yggF.
Putative metalloprotease yggG (EC 3.4.24.-).
HAM1 protein homolog.
Glycolate oxidase subunit glcD.

Hypothetical oxidoreductase yghA (EC 1.-.-.-).
Hypothetical oxidoreductase yqhD (EC 1.1.-.-).
Hypothetical protein ygiQ.
Topoisomerase IV subunit A (EC 5.99.1.-).
Topoisomerase IV subunit B (EC 5.99.1.-).
Hypothetical protein ygiC.
Hypothetical protein ygiD.
ADP-heptose synthase (EC 2.7.-.-).
Hypothetical protein ygiF (ORFXE).
Keto-acid formate acetyltransferase (EC 2.3.1.-) (Keto-acid formate- lyase).
Propionate kinase (EC 2.7.2.-).
Tagatose-1,6-bisphosphate aldolase agaY (EC 4.1.2.-) (TBPA).
Putative galactosamine-6-phosphate isomerase (EC 5.3.1.-) (Galactosamine-6-phosphate deaminase).
Hypothetical protein yraL.
Hypothetical protein yhbW.
Octaprenyl-diphosphate synthase (EC 2.5.1.-) (Octaprenyl pyrophosphate synthetase) (OPP synthetase).
Protease degQ precursor (EC 3.4.21.-).
Protease degS precursor (EC 3.4.21.-).
Hypothetical amino-acid ABC transporter ATP-binding protein yhdZ.
Para-aminobenzoate synthase glutamine amidotransferase component II (EC 4.1.3.-).
Hypothetical sugar kinase yhfQ.
Phosphotriesterase homology protein.
Hypothetical protein yhfW.
Glycogen operon protein glgX (EC 3.2.1.-).
Biotin sulfoxide reductase (EC 1.-.-.-) (BDS reductase) (BSO reductase).
Hypothetical oxidoreductase yiaK (EC 1.1.1.-).
Probable hexulose-6-phosphate synthase (EC 4.1.2.-) (HUMPS) (D-arabino 3-hexulose 6-phosphate formaldehyde
Probable sugar isomerase sgbE (EC 5.1.-.-).
Hypothetical tRNA/rRNA methyltransferase yibK (EC 2.1.1.-).
Hypothetical protein yibN.
Hypothetical DNA ligase-like protein yicF.
Putative family 31 glucosidase yicI.
Putative sulfatase yidJ (EC 3.1.6.-).
PTS system, arbutin-like IIC component (Phosphotransferase enzyme II, C component).
Hypothetical protein yieH.
Hypothetical protein yieK.
Undecaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate transferase (EC 2.7.8.-) (UDP-GlcNAc:undeca
UDP-N-acetyl-D-mannosamine dehydrogenase (EC 1.1.1.-) (UDP-ManNAc dehydrogenase).

Probable UDP-N-acetyl-D-mannosaminuronic acid transferase (EC 2.4.1.-) (UDP-ManNAcA transferase).
Hypothetical protein yigB.
Ubiquinone/menaquinone biosynthesis methyltransferase ubiE (EC 2.1.1.-).
Hypothetical protein yihG.
Putative family 31 glucosidase yihQ.
Hypothetical protein yihR.
Hypothetical protein yihT.
Hypothetical oxidoreductase yihU (EC 1.1.-.-).
Hypothetical sugar kinase yihV.
Putative frv operon regulatory protein.
ATP-dependent protease hslV (EC 3.4.25.-) (Heat shock protein hslV).
Fructose-6-phosphate aldolase 2 (EC 4.1.2.-).
PTS system, fructose-like-2 IIC component (Phosphotransferase enzyme II, C component).
D-allulose-6-phosphate 3-epimerase (EC 5.1.3.-).
Hypothetical tRNA/rRNA methyltransferase yjfH (EC 2.1.1.-).
Hypothetical protein yjfC.
AidB protein.
Probable hexulose-6-phosphate synthase (EC 4.1.2.-) (HUMPS) (D-arabino 3-hexulose 6-phosphate formaldehyd
Probable sugar isomerase sgaE (EC 5.1.-.-).
UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase (EC 6.3.2.-) (Murein peptide lig
Hypothetical oxidoreductase yjgI (EC 1.-.-.-).
Hypothetical protein yjhG.
Protein sgcE (EC 5.1.3.-).
Hypothetical protein yjiR.
Hypothetical protein yjjG.
Hypothetical protein yjjW.
Lipoate-protein ligase A (EC 6.-.-.-).
Hypothetical tRNA/rRNA methyltransferase lasT (EC 2.1.1.-).

(16S rRNA dimethylase) (High level kasugamycin resistance protein ksgA) (Kasugamycin dimethyltransferase).

otein).

ubiquinol oxidase subunit 1) (Ubiquinol oxidase chain A).

N5) MTase hemK) (M.EcoKHemKP).

nponent) (Phosphotransferase enzyme II, C component).

Rb reductase).

se); Acyl-acyl carrier protein synthetase (Acyl-ACP synthetase)]

e lyase).

prenyl-phosphate GlcNAc-1- phosphate transferase).

e lyase).

ase).