PhD 16 - Codes4strains

D-PhD16-3.1

Responsible Partner: Institut Pasteur

GENERAL INFORMATION

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Author	Mélanie HENNART & Sylvain BRISSE
Other contributors	Alexis Criscuolo
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cgMLST schemes for *Klebsiella pneumoniae* and *Escherichia coli*

Klebsiella pneumoniae:

As metric for the LIN code system, we use pairwise distances between the allele profiles. We first had to make a choice of which cgMLST scheme to use. In 2014, Bialek-Davenet et al (2) defined a cgMLST scheme of Klebsiella pneumoniae that included 634 highly conserved and syntenic genes. Here, we re-evaluated this cgMLST schema with our dataset, and removed five loci that were of low prevalence among this set of genomes; resulting in a cgMLST scheme of 629 gene loci. In addition, the loci templates were extended to include entire coding sequences of the corresponding genes.

The link to access the loci of the cgMLST scheme is: https://bigsdb.web.pasteur.fr/cgi-bin/bigsdb/bigsdb.pl?db=pubmlst_klebsiella_seqdef&page=schemeInfo&scheme_id=18

Below is the table is the loci and their length characteristics.

Locus	Standard length	Min length (setting)	Max length (setting)
rbsC_S	966	918	1014
rbsB_S	891	846	936
rbsK_S	930	885	975
yieP_S	702	666	738
polA_S	2793	2655	2931
engB_S	633	603	663
KP1_0026_S	507	483	531
hemN_S	1374	1305	1443
glnG_S	1410	1341	1479
glnL_S	1050	999	1101
glnA_S	1410	1341	1479
bipA_S	1824	1734	1914
rhaD_S	831	789	873
rhaA_S	1266	1203	1329
rhaB_S	1467	1395	1539
rhaS_S	837	795	879
rhaR_S	846	804	888
rhaT_S	1035	984	1086
sodA_S	627	597	657
KP1_0077_S	675	642	708
cpxA_S	1374	1305	1443
cpxR_S	699	666	732
cpxP_S	504	480	528
yijC_S	633	603	663
KP1_0118_S	360	342	378

trmA_S	1101	1047	1155
KP1_0120_S	123	117	129
btuB_S	1839	1749	1929
KP1_0122_S	852	810	894
ilvM_S	258	246	270
ilvE_S	930	885	975
ilvD_S	1851	1758	1944
ilvA_S	1488	1413	1563
ilvY_S	975	927	1023
cyaY_S	321	306	336
KP1_0167_S	204	195	213
dapF_S	828	786	870
KP1_0169_S	708	672	744
xerC_S	903	858	948
yigB_S	717	681	753
rhtB_S	621	591	651
pldB_S	993	945	1041
KP1_0183_S	801	762	840
yigM_S	900	855	945
metR_S	954	906	1002
udp_S	762	723	801
yigN_S	1449	1377	1521
ubiE_S	756	720	792
KP1_0193_S	606	576	636
ubiB_S	1641	1560	1722
tatA_S	300	285	315
tatB_S	537	510	564
tatC_S	780	741	819
tatD_S	792	753	831
rfaH_S	489	465	513
ubiD_S	1476	1404	1548
fre_S	702	666	738
fadA_S	1164	1107	1221
rsd_S	498	474	522
nudC_S	774	735	813
hemE_S	1065	1011	1119
nfi_S	672	639	705
KP1_0239_S	591	561	621
KP1_0241_S	273	261	285
KP1_0242_S	702	666	738
zraP_S	438	417	459
yjaB_S	462	438	486
metA_S	930	885	975
aceA_S	1320	1254	1386
aceK_S	1785	1695	1875

iclR_S	927	882	972
KP1_0299_S	417	396	438
KP1_0300_S	357	339	375
uvrA_S	2826	2685	2967
ssb_S	525	498	552
KP1_0375_S	321	306	336
cbpA_S	918	873	963
KP1_0378_S	699	666	732
KP1_0379_S	834	792	876
hmsS_S	450	429	471
efp_S	567	540	594
ecnA_S	132	126	138
ecnB_S	147	141	153
sugE_S	318	303	333
blc_S	534	507	561
frdD_S	390	372	408
hfq_S	309	294	324
hflX_S	1281	1218	1344
hflK_S	1263	1200	1326
hflC_S	1005	954	1056
KP1_0445_S	342	324	360
KP1_0446_S	198	189	207
KP1_0467_S	276	264	288
priB_S	168	159	177
KP1_0513_S	645	612	678
KP1_0514_S	1134	1077	1191
KP1_0515_S	1119	1065	1173
KP1_0516_S	1104	1050	1158
KP1_0517_S	741	705	777
KP1_0567_S	825	783	867
KP1_0568_S	888	843	933
KP1_0569_S	885	840	930
yjgB_S	1020	969	1071
yjjA_S	492	468	516
dnaC_S	738	702	774
dnaT_S	540	513	567
yjjB_S	489	465	513
yjjP_S	777	738	816
KP1_0775_S	1185	1125	1245
KP1_0776_S	882	837	927
fhuF_S	789	750	828
ycdT_S	1047	996	1098
mtr_S	354	336	372
holD_S	414	393	435
rimI_S	447	426	468

yjjG_S	678	645	711
prfC_S	1590	1512	1668
deoA_S	1323	1257	1389
deoB_S	1224	1164	1284
KP1_0801_S	720	684	756
lplA_S	1017	966	1068
smp_S	648	615	681
serB_S	993	945	1041
sms_S	1383	1314	1452
nadR_S	1233	1173	1293
yjjK_S	1668	1584	1752
creB_S	690	657	723
creC_S	1425	1353	1497
arcA_S	717	681	753
lasT_S	687	654	720
thrA_S	2505	2379	2631
thrB_S	930	885	975
yabF_S	534	507	561
kefC_S	1866	1773	1959
folA_S	480	456	504
apaH_S	849	807	891
apaG_S	378	360	396
ksgA_S	822	780	864
pdxA_S	990	942	1038
araD_S	696	663	729
araA_S	1503	1428	1578
araB_S	1710	1626	1794
araC_S	846	804	888
yabI_S	768	729	807
tbpA_S	945	897	993
yabN_S	1656	1575	1737
KP1_0882_S	159	153	165
setA_S	1185	1125	1245
gudP_S	1311	1245	1377
ilvI_S	1725	1638	1812
ilvH_S	522	495	549
fruR_S	1005	954	1056
KP1_0903_S	495	471	519
mraW_S	942	894	990
ftsL_S	366	348	384
ftsI_S	1767	1680	1854
mutT_S	393	375	411
yacG_S	195	186	204
KP1_0925_S	744	708	780
coaE_S	621	591	651

KP1_0927_S	132	126	138
guaC_S	1044	993	1095
ppdD_S	432	411	453
nadC_S	894	849	939
ampD_S	564	537	591
ampE_S	855	813	897
KP1_0935_S	951	903	999
KP1_0936_S	1407	1338	1476
lpdA_S	1428	1356	1500
KP1_0945_S	285	270	300
KP1_0946_S	816	777	855
hpt_S	549	522	576
yadG_S	927	882	972
yadH_S	771	732	810
yadI_S	441	420	462
KP1_0965_S	1248	1185	1311
folK_S	480	456	504
yadB_S	882	837	927
dksA_S	474	450	498
sfsA_S	717	681	753
map_S	795	756	834
tsf_S	852	810	894
pyrH_S	726	690	762
frr_S	558	531	585
ispC_S	1203	1143	1263
dkgB_S	804	765	843
yafC_S	906	861	951
KP1_1068_S	807	768	846
yafE_S	771	732	810
yafP_S	453	432	474
pepD_S	1458	1386	1530
gpt_S	459	438	480
frsA_S	1245	1182	1308
crl_S	399	381	417
KP1_1206_S	903	858	948
KP1_1207_S	642	609	675
KP1_1209_S	546	519	573
KP1_1211_S	867	825	909
KP1_1227_S	366	348	384
KP1_1228_S	696	663	729
tsx_S	885	840	930
yajI_S	540	513	567
nrdR_S	450	429	471
thiJ_S	600	570	630
apbA_S	912	867	957

KP1_1246_S	585	555	615
yajR_S	1365	1296	1434
KP1_1248_S	1179	1122	1236
KP1_1251_S	819	780	858
tig_S	1299	1236	1362
clpP_S	624	594	654
clpX_S	1275	1212	1338
lon_S	2463	2340	2586
hupB_S	273	261	285
ppiD_S	1875	1782	1968
KP1_1275_S	369	351	387
ptsG_S	315	300	330
lacI_S	1071	1017	1125
rpmE2_S	264	252	276
adk_S	645	612	678
hemH_S	963	915	1011
gsk_S	1305	1239	1371
ybaL_S	1677	1593	1761
fsr_S	1221	1161	1281
betA_S	1710	1626	1794
betB_S	1473	1401	1545
betT_S	2034	1932	2136
ykfE_S	528	501	555
KP1_1607_S	798	759	837
dcuC_S	1374	1305	1443
pagP_S	519	495	543
cspE_S	294	279	309
KP1_1612_S	384	366	402
ybeM_S	789	750	828
tatE_S	204	195	213
lipA_S	966	918	1014
ybeF_S	1005	954	1056
KP1_1623_S	468	444	492
KP1_1624_S	318	303	333
nadD_S	654	621	687
holA_S	1023	972	1074
rlpB_S	591	561	621
nagD_S	753	717	789
nagC_S	1221	1161	1281
nagA_S	1149	1092	1206
nagB_S	801	762	840
nagE_S	1956	1860	2052
glnS_S	1668	1584	1752
metH_S	309	294	324
KP1_1656_S	501	477	525

KP1_1657_S	333	318	348
fur_S	453	432	474
fldA_S	600	570	630
KP1_1661_S	363	345	381
ybfF_S	774	735	813
KP1_1663_S	693	660	726
cydA_S	1572	1494	1650
cydB_S	1140	1083	1197
KP1_1696_S	291	276	306
KP1_1697_S	405	384	426
tolQ_S	693	660	726
tolR_S	429	408	450
ybhA_S	819	780	858
ybhE_S	996	948	1044
KP1_1726_S	267	255	279
KP1_1727_S	306	291	321
KP1_1728_S	246	234	258
KP1_1729_S	1212	1152	1272
KP1_1730_S	735	699	771
KP1_1731_S	555	528	582
KP1_1732_S	366	348	384
KP1_1734_S	924	879	969
glnH_S	747	711	783
dps_S	504	480	528
ybiF_S	888	843	933
ompX_S	513	489	537
ybiP_S	1590	1512	1668
KP1_1803_S	126	120	132
mntR_S	474	450	498
ybiR_S	1113	1059	1167
potH_S	954	906	1002
potI_S	888	843	933
KP1_1853_S	489	465	513
KP1_1855_S	717	681	753
hcr_S	969	921	1017
hcp_S	1653	1572	1734
ybjE_S	900	855	945
ihfB_S	288	273	303
msbA_S	1749	1662	1836
KP1_1916_S	1230	1170	1290
ssuC_S	792	753	831
ssuD_S	1146	1089	1203
ssuA_S	963	915	1011
ssuE_S	576	549	603
pyrD_S	1038	987	1089

KP1_2044_S	738	702	774
ycdY_S	555	528	582
ycdZ_S	483	459	507
KP1_2047_S	546	519	573
KP1_2048_S	594	564	624
mdoC_S	1161	1104	1218
yceF_S	585	555	615
KP1_2077_S	522	495	549
plsX_S	1098	1044	1152
fabH_S	954	906	1002
fabD_S	930	885	975
fabG_S	735	699	771
fabF_S	1242	1179	1305
pabC_S	810	771	849
yceG_S	1023	972	1074
tmk_S	642	609	675
holB_S	1005	954	1056
ycfH_S	795	756	834
ptsG2_S	1434	1362	1506
KP1_2092_S	357	339	375
ycfQ_S	636	606	666
ycfS_S	960	912	1008
mfd_S	3447	3276	3618
ycfU_S	1209	1149	1269
ycfV_S	702	666	738
ycfW_S	1245	1182	1308
yeaE_S	885	840	930
KP1_2220_S	885	840	930
yeaA_S	414	393	435
KP1_2224_S	279	267	291
KP1_2225_S	345	327	363
spy_S	483	459	507
nadE_S	828	786	870
osmE_S	339	324	354
celA_S	321	306	336
celC_S	348	330	366
KP1_2532_S	336	321	351
ydgB_S	723	687	759
ydgI_S	1383	1314	1452
KP1_2535_S	951	903	999
KP1_2536_S	183	174	192
KP1_2672_S	945	897	993
KP1_2673_S	483	459	507
yneJ_S	879	837	921
yneI_S	894	849	939

yneH_S	927	882	972
KP1_2697_S	672	639	705
KP1_2700_S	1029	978	1080
KP1_2702_S	312	297	327
KP1_2703_S	756	720	792
gst_S	606	576	636
pdxY_S	861	819	903
tyrS_S	1275	1212	1338
pdxH_S	657	624	690
KP1_3049_S	324	309	339
anmK_S	1098	1044	1152
ydhM_S	600	570	630
nemA_S	1098	1044	1152
gloA_S	408	387	429
KP1_3065_S	348	330	366
ydhO_S	873	831	915
KP1_3289_S	759	723	795
pfkB_S	933	888	978
KP1_3291_S	285	270	300
chaC_S	681	648	714
chaB_S	231	219	243
chaA_S	1101	1047	1155
kdsA_S	855	813	897
ychQ_S	393	375	411
hemK_S	849	807	891
prfA_S	1083	1029	1137
KP1_3440_S	447	426	468
ycgM_S	660	627	693
KP1_3442_S	321	306	336
minC_S	699	666	732
minD_S	813	774	852
minE_S	270	258	282
fadD_S	1686	1602	1770
yeaY_S	582	552	612
yeaZ_S	696	663	729
KP1_3451_S	345	327	363
KP1_3486_S	384	366	402
holE_S	231	219	243
exoX_S	660	627	693
ptrB_S	2061	1959	2163
KP1_3490_S	660	627	693
yebG_S	348	330	366
purT_S	1179	1122	1236
msbB_S	975	927	1023
KP1_3501_S	1320	1254	1386

znuA_S	1071	1017	1125
znuC_S	753	717	789
znuB_S	786	747	825
ruvB_S	1011	960	1062
ruvA_S	612	582	642
ftnA_S	498	474	522
KP1_3536_S	240	228	252
tyrP_S	1212	1152	1272
KP1_3538_S	669	636	702
dapA4_S	882	837	927
KP1_3551_S	432	411	453
rcsA_S	624	594	654
KP1_3553_S	192	183	201
KP1_3554_S	225	213	237
yedI_S	912	867	957
mglA_S	1521	1446	1596
mglB_S	999	951	1047
galS_S	1023	972	1074
folE_S	669	636	702
yejE_S	1026	975	1077
KP1_3844_S	345	327	363
bcr_S	1197	1137	1257
rsuA_S	720	684	756
KP1_3852_S	636	606	666
KP1_3853_S	762	723	801
yejK_S	1008	957	1059
KP1_3855_S	228	216	240
yejM_S	1761	1674	1848
nuoF_S	1338	1272	1404
nuoE_S	501	477	525
nuoC_S	1809	1719	1899
nuoB_S	675	642	708
nuoA_S	447	426	468
yfcD_S	552	525	579
yfcF_S	639	609	669
yfcG_S	630	600	660
folX_S	363	345	381
accD_S	984	936	1032
dedA_S	660	627	693
truA_S	813	774	852
KP1_3958_S	1014	963	1065
pdxB_S	1137	1080	1194
KP1_3960_S	129	123	135
flk_S	978	930	1026
KP1_3965_S	282	267	297

yfcM_S	549	522	576
yfcA_S	810	771	849
mepA_S	825	783	867
aroC_S	1089	1035	1143
KP1_4022_S	900	855	945
KP1_4023_S	576	549	603
KP1_4024_S	450	429	471
ypeA_S	441	420	462
KP1_4027_S	141	135	147
amiA_S	873	831	915
hemF_S	900	855	945
hscB_S	516	492	540
iscA_S	324	309	339
KP1_4113_S	387	369	405
iscS_S	1215	1155	1275
iscR_S	492	468	516
yfhQ_S	735	699	771
suhB_S	804	765	843
glyA_S	1254	1191	1317
hmpA_S	1191	1131	1251
KP1_4132_S	339	324	354
yfhA_S	1338	1272	1404
yfhG_S	708	672	744
yfhK_S	1440	1368	1512
nadB_S	1620	1539	1701
yfiC_S	759	723	795
srmB_S	1332	1266	1398
yfiD_S	384	366	402
ung_S	690	657	723
grpE_S	591	561	621
ppnK_S	879	837	921
smpA_S	342	324	360
KP1_4196_S	291	276	306
KP1_4197_S	477	453	501
smpB_S	483	459	507
ygaH_S	336	321	351
emrR_S	501	477	525
emrA_S	1173	1116	1230
KP1_4281_S	1677	1593	1761
cbiQ_S	678	645	711
KP1_4452_S	282	267	297
KP1_4453_S	738	702	774
KP1_4455_S	795	756	834
KP1_4456_S	786	747	825
KP1_4457_S	726	690	762

pduW_S	1215	1155	1275
pduX_S	903	858	948
cobD_S	1077	1023	1131
amiC_S	1290	1227	1353
argA_S	1332	1266	1398
ppdA_S	468	444	492
thyA_S	795	756	834
lgt_S	876	834	918
ptsP_S	2247	2136	2358
ygdP_S	531	504	558
galR_S	1017	966	1068
KP1_4520_S	480	456	504
KP1_4521_S	774	735	813
KP1_4523_S	1428	1356	1500
KP1_4524_S	1401	1332	1470
dsbC_S	714	678	750
xerD_S	897	852	942
fldB_S	522	495	549
KP1_4612_S	411	390	432
KP1_4613_S	267	255	279
yqfA_S	660	627	693
KP1_4617_S	312	297	327
KP1_4618_S	729	693	765
KP1_4629_S	1203	1143	1263
pepP_S	1317	1251	1383
KP1_4632_S	585	555	615
KP1_4633_S	330	315	345
yggE_S	768	729	807
yggA_S	636	606	666
yggB_S	858	816	900
fbaA_S	1080	1026	1134
pgk_S	1164	1107	1221
epd_S	1029	978	1080
KP1_4652_S	501	477	525
endA_S	765	726	804
KP1_4654_S	807	768	846
gshB_S	951	903	999
KP1_4657_S	564	537	591
yqgF_S	417	396	438
KP1_4731_S	672	639	705
ygiC_S	1161	1104	1218
ygiD_S	792	753	831
ygiE_S	771	732	810
ribB_S	654	621	687
uppP_S	822	780	864

folB_S	387	369	405
KP1_4750_S	618	588	648
ureD_S	825	783	867
ureA_S	303	288	318
ureB_S	321	306	336
KP1_4812_S	501	477	525
ygjR_S	990	942	1038
ygjT_S	972	924	1020
ygjU_S	1248	1185	1311
KP1_4816_S	555	528	582
KP1_4822_S	384	366	402
KP1_4823_S	369	351	387
KP1_4824_S	306	291	321
KP1_4825_S	399	381	417
KP1_4826_S	297	282	312
KP1_4861_S	387	369	405
yraO_S	627	597	657
yraP_S	576	549	603
KP1_4865_S	1041	990	1092
yhbO_S	666	633	699
KP1_4868_S	444	423	465
KP1_4870_S	504	480	528
KP1_4871_S	525	498	552
yhbU_S	996	948	1044
yhbV_S	894	849	939
yhbW_S	1008	957	1059
yrbI_S	567	540	594
KP1_4921_S	576	549	603
yhbN_S	546	519	573
yhbG_S	726	690	762
rpoN_S	1434	1362	1506
yhbH_S	288	273	303
ptsN_S	489	465	513
KP1_4927_S	855	813	897
ptsO_S	273	261	285
KP1_4977_S	192	183	201
KP1_4978_S	1017	966	1068
KP1_4979_S	609	579	639
KP1_4980_S	453	432	474
accB_S	468	444	492
accC_S	1350	1284	1416
KP1_4984_S	243	231	255
prmA_S	882	837	927
KP1_4987_S	231	219	243
yrdA_S	555	528	582

KP1_4999_S	258	246	270
aroE_S	819	780	858
yrdC_S	618	588	648
yrdD_S	543	516	570
KP1_5003_S	474	450	498
smf_S	1125	1068	1182
def_S	510	486	534
KP1_5012_S	369	351	387
KP1_5015_S	990	942	1038
secY_S	1332	1266	1398
yheS_S	1905	1809	2001
yheT_S	1023	972	1074
KP1_5068_S	219	210	228
prkB_S	870	828	912
KP1_5070_S	405	384	426
crp_S	633	603	663
pabA_S	564	537	591
KP1_5075_S	603	573	633
KP1_5076_S	168	159	177
ppiA_S	570	543	597
yhfC_S	1188	1128	1248
nirD_S	327	312	342
cysG_S	1374	1305	1443
trpS_S	1005	954	1056
gph_S	762	723	801
rpe_S	678	645	711
dam_S	828	786	870
aroB_S	1095	1041	1149
aroK_S	522	495	549
glgA_S	1434	1362	1506
glgC_S	1296	1233	1359
glgX_S	1881	1788	1974
glgB_S	2187	2079	2295
asd_S	1155	1098	1212
pitA_S	1497	1422	1572
yhiO_S	336	321	351
uspA_S	438	417	459
yhiP_S	1473	1401	1545
KP1_5202_S	810	771	849
prlC_S	2043	1941	2145
KP1_5210_S	570	543	597
KP1_5213_S	1032	981	1083
KP1_5258_S	750	714	786
KP1_5259_S	936	891	981
KP1_5260_S	1281	1218	1344

tkrA_S	972	924	1020
KP1_5262_S	711	675	747
secB_S	468	444	492
grxC_S	252	240	264
yibN_S	432	411	453
yibO_S	1626	1545	1707
KP1_5307_S	1272	1209	1335
KP1_5309_S	948	900	996
sbp_S	990	942	1038
KP1_5367_S	246	234	258
glpF_S	852	810	894
glpK_S	1512	1437	1587
gltS_S	831	789	873
yicE_S	1401	1332	1470
atpF_S	465	441	489
atpE_S	240	228	252
atpB_S	816	777	855
atpI_S	453	432	474
gidB_S	624	594	654

Escherichia coli:
We have chosen the cgMLST scheme from EnteroBase (https://enterobase.warwick.ac.uk/species/ecoli/download_data, select the cells cgMLST V1 + HierCC V1 in the column scheme name), which includes 2513 loci. This choice was based on an assessment of existing schemes and their usage. The one from EnteroBase was published, and used for more than 153,043 genomes (present in EnteroBase), so that it is a *de facto* reference.

Attached below the table is the locis templates.

Locus	**Description**
AEJV01_03887 (-)	hypothetical protein
b0001 (thrL)	thr operon leader peptide
b0002 (thrA)	Bifunctional aspartokinase/homoserine dehydrogenase 1
b0003 (thrB)	homoserine kinase
b0004 (thrC)	L-threonine synthase
b0005 (yaaX)	DUF2502 family putative periplasmic protein
b0006 (yaaA)	peroxide resistance protein, lowers intracellular iron
b0008 (talB)	transaldolase B
b0009 (mog)	molybdochelatase incorporating molybdenum into molybdopterin
b0010 (satP)	succinate-acetate transporter
b0011 (yaaW)	UPF0174 family protein
b0013 (yaaI)	UPF0412 family protein
b0014 (dnaK)	chaperone Hsp70, with co-chaperone DnaJ
b0015 (dnaJ)	chaperone Hsp40, DnaK co-chaperone
b0018 (mokC)	regulatory protein for HokC, overlaps CDS of hokC
b0019 (nhaA)	sodium-proton antiporter

b0020 (nhaR)	transcriptional activator of nhaA
b0023 (rpsT)	30S ribosomal subunit protein S20
b0024 (yaaY)	uncharacterized protein
b0025 (ribF)	bifunctional riboflavin kinase/FAD synthetase
b0026 (ileS)	isoleucyl-tRNA synthetase
b0027 (lspA)	prolipoprotein signal peptidase (signal peptidase II)
b0028 (fkpB)	FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase)
b0029 (ispH)	4-hydroxy-3-methylbut-2-enyl diphosphate reductase, 4Fe-4S protein
b0030 (rihC)	ribonucleoside hydrolase 3
b0031 (dapB)	dihydrodipicolinate reductase
b0032 (carA)	carbamoyl phosphate synthetase small subunit, glutamine amidotransferase
b0033 (carB)	carbamoyl-phosphate synthase large subunit
b0034 (caiF)	cai operon transcriptional activator
b0035 (caiE)	stimulator of CaiD and CaiB enzyme activities
b0036 (caiD)	carnitinyl-CoA dehydratase
b0037 (caiC)	putative crotonobetaine/carnitine-CoA ligase
b0039 (caiA)	crotonobetaine reductase subunit II, FAD-binding
b0040 (caiT)	putative transporter
b0041 (fixA)	anaerobic carnitine reduction putative electron transfer flavoprotein subunit
b0042 (fixB)	putative electron transfer flavoprotein, NAD/FAD-binding domain and ETFP adenine nucleotide-binding domain-like protein
b0043 (fixC)	putative oxidoreductase
b0044 (fixX)	putative 4Fe-4S ferredoxin-type protein
b0046 (kefF)	potassium-efflux system ancillary protein for KefC, glutathione-regulated; quinone oxidoreductase, FMN-dependent
b0047 (kefC)	potassium:proton antiporter
b0048 (folA)	dihydrofolate reductase
b0050 (apaG)	protein associated with Co2+ and Mg2+ efflux
b0051 (rsmA)	16S rRNA m(6)A1518, m(6)A1519 dimethyltransferase, SAM-dependent
b0052 (pdxA)	4-hydroxy-L-threonine phosphate dehydrogenase, NAD-dependent
b0053 (surA)	peptidyl-prolyl cis-trans isomerase (PPIase)
b0054 (lptD)	LPS assembly OM complex LptDE, beta-barrel component
b0055 (djlA)	membrane-anchored DnaK co-chaperone, DNA-binding protein
b0058 (rluA)	dual specificity 23S rRNA pseudouridine(746), tRNA pseudouridine(32) synthase, SAM-dependent
b0059 (rapA)	RNA polymerase remodeling/recycling factor ATPase; RNA polymerase-associated, ATP-dependent RNA translocase
b0060 (polB)	DNA polymerase II
b0062 (araA)	L-arabinose isomerase
b0063 (araB)	L-ribulokinase
b0065 (yabI)	DedA family inner membrane protein
b0066 (thiQ)	thiamine, thiamine pyrophosphate ABC transporter ATPase; ThiBPQ thiamine, thiamine pyrophosphate importer

b0067 (thiP)	thiamine, thiamine pyrophosphate ABC transporter permease; ThiBPQ thiamine, thiamine pyrophosphate importer
b0068 (thiB)	thiamine-, thiamine pyrophosphate-, thiamine monophosphate-binding ABC transporter periplasmic protein; ThiBPQ thiamine, thiamine pyrophosphate importer
b0071 (leuD)	3-isopropylmalate dehydratase small subunit
b0072 (leuC)	3-isopropylmalate dehydratase large subunit
b0073 (leuB)	3-isopropylmalate dehydrogenase, NAD(+)-dependent
b0074 (leuA)	2-isopropylmalate synthase
b0075 (leuL)	leu operon leader peptide
b0076 (leuO)	global transcription factor
b0077 (ilvI)	acetolactate synthase 3 large subunit
b0078 (ilvH)	acetolactate synthase 3, small subunit, valine-sensitive
b0080 (cra)	transcriptional repressor-activator for carbon metabolism
b0081 (mraZ)	RsmH methytransferase inhibitor
b0082 (rsmH)	16S rRNA m(4)C1402 methyltransferase, SAM-dependent
b0083 (ftsL)	membrane bound cell division protein at septum containing leucine zipper motif
b0084 (ftsI)	transpeptidase involved in septal peptidoglycan synthesis (penicillin-binding protein 3)
b0085 (murE)	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate:meso-diaminopimelate ligase
b0086 (murF)	UDP-N-acetylmuramoyl-tripeptide:D-alanyl-D-alanine ligase
b0087 (mraY)	phospho-N-acetylmuramoyl-pentapeptide transferase
b0088 (murD)	UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase
b0089 (ftsW)	lipid II flippase; integral membrane protein involved in stabilizing FstZ ring during cell division
b0090 (murG)	N-acetylglucosaminyl transferase
b0091 (murC)	UDP-N-acetylmuramate:L-alanine ligase
b0092 (ddlB)	D-alanine:D-alanine ligase
b0093 (ftsQ)	divisome assembly protein, membrane anchored protein involved in growth of wall at septum
b0094 (ftsA)	ATP-binding cell division protein involved in recruitment of FtsK to Z ring
b0095 (ftsZ)	GTP-binding tubulin-like cell division protein
b0096 (lpxC)	UDP-3-O-acyl N-acetylglucosamine deacetylase
b0097 (secM)	regulator of secA translation
b0098 (secA)	preprotein translocase subunit, ATPase
b0101 (yacG)	DNA gyrase inhibitor
b0102 (zapD)	FtsZ stabilizer
b0103 (coaE)	dephospho-CoA kinase
b0104 (guaC)	GMP reductase
b0106 (hofC)	assembly protein in type IV pilin biogenesis, transmembrane protein
b0108 (ppdD)	putative prepilin peptidase-dependent pilin
b0109 (nadC)	quinolinate phosphoribosyltransferase
b0110 (ampD)	1,6-anhydro-N-acetylmuramyl-L-alanine amidase, Zn-dependent; murein amidase

b0111 (ampE)	ampicillin resistance inner membrane protein; putative signaling protein in beta-lactamase regulation
b0112 (aroP)	aromatic amino acid transporter
b0113 (pdhR)	pyruvate dehydrogenase complex repressor; autorepressor
b0114 (aceE)	pyruvate dehydrogenase, decarboxylase component E1, thiamine triphosphate-binding
b0115 (aceF)	pyruvate dehydrogenase, dihydrolipoyltransacetylase component E2
b0116 (lpd)	lipoamide dehydrogenase, E3 component is part of three enzyme complexes
b0118 (acnB)	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase
b0119 (yacL)	UPF0231 family protein
b0120 (speD)	S-adenosylmethionine decarboxylase
b0121 (speE)	spermidine synthase (putrescine aminopropyltransferase)
b0122 (yacC)	PulS_OutS family protein
b0123 (cueO)	multicopper oxidase (laccase)
b0125 (hpt)	hypoxanthine phosphoribosyltransferase
b0126 (can)	carbonic anhydrase
b0127 (yadG)	putative ABC superfamily transporter ATP-binding subunit
b0128 (yadH)	inner membrane putative ABC superfamily transporter permease
b0129 (yadI)	putative PTS Enzyme IIA
b0130 (yadE)	putative polysaccharide deacetylase lipoprotein
b0131 (panD)	aspartate 1-decarboxylase
b0133 (panC)	pantothenate synthetase
b0134 (panB)	3-methyl-2-oxobutanoate hydroxymethyltransferase
b0142 (folK)	2-amino-4-hydroxy-6-hydroxymethyldihyropteridine pyrophosphokinase
b0143 (pcnB)	poly(A) polymerase
b0144 (gluQ)	glutamyl-Q tRNA(Asp) synthetase
b0145 (dksA)	transcriptional regulator of rRNA transcription, DnaK suppressor protein
b0146 (sfsA)	sugar fermentation stimulation protein A
b0147 (ligT)	2'-5' RNA ligase
b0148 (hrpB)	putative ATP-dependent helicase
b0149 (mrcB)	fused glycosyl transferase and transpeptidase
b0151 (fhuC)	iron-hydroxamate transporter subunit
b0152 (fhuD)	iron-hydroxamate transporter subunit
b0153 (fhuB)	fused iron-hydroxamate transporter subunits of ABC superfamily: membrane components
b0154 (hemL)	glutamate-1-semialdehyde aminotransferase (aminomutase)
b0155 (clcA)	H(+)/Cl(-) exchange transporter
b0156 (erpA)	iron-sulfur cluster insertion protein
b0157 (yadS)	UPF0126 family inner membrane protein
b0158 (btuF)	vitamin B12 transporter subunit: periplasmic-binding component of ABC superfamily
b0159 (mtn)	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase
b0161 (degP)	serine endoprotease (protease Do), membrane-associated
b0162 (cdaR)	carbohydrate diacid regulon transcriptional regulator; autoregulator

b0163 (yaeH)	UPF0325 family protein
b0166 (dapD)	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase
b0167 (glnD)	uridylyltransferase
b0168 (map)	methionine aminopeptidase
b0169 (rpsB)	30S ribosomal subunit protein S2
b0170 (tsf)	translation elongation factor EF-Ts
b0171 (pyrH)	uridylate kinase
b0172 (frr)	ribosome recycling factor
b0173 (dxr)	1-deoxy-D-xylulose 5-phosphate reductoisomerase
b0174 (ispU)	undecaprenyl pyrophosphate synthase
b0175 (cdsA)	CDP-diglyceride synthase
b0176 (rseP)	inner membrane zinc RIP metalloprotease; RpoE activator, by degrading RseA; cleaved signal peptide endoprotease
b0177 (bamA)	BamABCDE complex OM biogenesis outer membrane pore-forming assembly factor
b0178 (skp)	periplasmic chaperone
b0179 (lpxD)	UDP-3-O-(3-hydroxymyristoyl)-glucosamine N-acyltransferase
b0180 (fabZ)	(3R)-hydroxymyristol acyl carrier protein dehydratase
b0181 (lpxA)	UDP-N-acetylglucosamine acetyltransferase
b0182 (lpxB)	tetraacyldisaccharide-1-P synthase
b0183 (rnhB)	ribonuclease HII, degrades RNA of DNA-RNA hybrids
b0184 (dnaE)	DNA polymerase III alpha subunit
b0185 (accA)	acetyl-CoA carboxylase, carboxytransferase, alpha subunit
b0187 (yaeR)	putative lyase
b0189 (rof)	modulator of Rho-dependent transcription termination
b0190 (yaeQ)	PDDEXK superfamily protein
b0191 (arfB)	alternative stalled-ribosome rescue factor B; peptidyl-tRNA hydrolase, ribosome-attached
b0192 (nlpE)	lipoprotein involved with copper homeostasis and adhesion
b0194 (proS)	prolyl-tRNA synthetase
b0195 (tsaA)	tRNA-Thr(GGU) m(6)t(6)A37 methyltransferase, SAM-dependent
b0196 (rcsF)	putative outer membrane protein
b0197 (metQ)	DL-methionine transporter subunit
b0198 (metI)	DL-methionine transporter subunit
b0199 (metN)	DL-methionine transporter subunit
b0209 (yafD)	endo/exonuclease/phosphatase family protein
b0211 (mltD)	putative membrane-bound lytic murein transglycosylase D
b0212 (gloB)	hydroxyacylglutathione hydrolase
b0213 (yafS)	putative S-adenosyl-L-methionine-dependent methyltransferase
b0214 (rnhA)	ribonuclease HI, degrades RNA of DNA-RNA hybrids
b0215 (dnaQ)	DNA polymerase III epsilon subunit
b0220 (ivy)	inhibitor of c-type lysozyme, periplasmic
b0221 (fadE)	acyl coenzyme A dehydrogenase
b0222 (gmhA)	D-sedoheptulose 7-phosphate isomerase
b0223 (yafJ)	putative amidotransfease
b0224 (yafK)	L,D-transpeptidase-related protein

b0231 (dinB)	DNA polymerase IV
b0234 (yafP)	putative acyl-CoA transferase
b0237 (pepD)	aminoacyl-histidine dipeptidase (peptidase D)
b0238 (gpt)	xanthine phosphoribosyltransferase; xanthine-guanine phosphoribosyltransferase
b0239 (frsA)	fermentation-respiration switch protein; PTS Enzyme IIA(Glc)-binding protein; pNP-butyrate esterase activity
b0241 (phoE)	outer membrane phosphoporin protein E
b0242 (proB)	gamma-glutamate kinase
b0243 (proA)	gamma-glutamylphosphate reductase
b0366 (tauB)	taurine transporter subunit
b0367 (tauC)	taurine transporter subunit
b0368 (tauD)	taurine dioxygenase, 2-oxoglutarate-dependent
b0369 (hemB)	5-aminolevulinate dehydratase (porphobilinogen synthase)
b0375 (yaiV)	putative transcriptional regulator
b0376 (ampH)	D-alanyl-D-alanine-carboxypeptidase/endopeptidase; penicillin-binding protein; weak beta-lactamase
b0377 (sbmA)	microcin B17 transporter
b0378 (yaiW)	putative lipoprotein
b0379 (yaiY)	DUF2755 family inner membrane protein
b0380 (yaiZ)	DUF2754 family putative inner membrane protein
b0381 (ddlA)	D-alanine-D-alanine ligase A
b0382 (iraP)	anti-RssB factor, RpoS stabilzer during Pi starvation; anti-adapter protein
b0383 (phoA)	bacterial alkaline phosphatase
b0384 (psiF)	PsiF family protein
b0386 (proC)	pyrroline-5-carboxylate reductase, NAD(P)-binding
b0388 (aroL)	shikimate kinase II
b0389 (yaiA)	OxyR-regulated conserved protein
b0390 (aroM)	AroM family protein
b0391 (yaiE)	UPF0345 family protein
b0393 (rdgC)	nucleoid-associated ssDNA and dsDNA binding protein; competitive inhibitor of RecA function
b0394 (mak)	manno(fructo)kinase
b0397 (sbcC)	exonuclease, dsDNA, ATP-dependent
b0398 (sbcD)	exonuclease, dsDNA, ATP-dependent
b0399 (phoB)	response regulator in two-component regulatory system with PhoR (or CreC)
b0400 (phoR)	sensory histidine kinase in two-component regulatory system with PhoB
b0401 (brnQ)	branched-chain amino acid transport system 2 carrier protein; LIV-II transport system for Ile, Leu, and Val
b0402 (proY)	proline-specific permease
b0403 (malZ)	maltodextrin glucosidase
b0404 (acpH)	acyl carrier protein (ACP) phosphodiesterase; ACP hydrolyase
b0405 (queA)	S-adenosylmethionine:tRNA ribosyltransferase-isomerase
b0406 (tgt)	tRNA-guanine transglycosylase

b0407 (yajC)	SecYEG protein translocase auxillary subunit
b0408 (secD)	SecYEG protein translocase auxillary subunit
b0409 (secF)	SecYEG protein translocase auxillary subunit
b0410 (yajD)	HNH nuclease family protein
b0411 (tsx)	nucleoside channel, receptor of phage T6 and colicin K
b0413 (nrdR)	Nrd regulon repressor
b0414 (ribD)	fused diaminohydroxyphosphoribosylaminopyrimidine deaminase and 5-amino-6-(5-phosphoribosylamino) uracil reductase
b0415 (ribE)	riboflavin synthase beta chain
b0416 (nusB)	transcription antitermination protein
b0417 (thiL)	thiamine monophosphate kinase
b0419 (yajO)	2-carboxybenzaldehyde reductase
b0420 (dxs)	1-deoxyxylulose-5-phosphate synthase, thiamine triphosphate-binding, FAD-requiring
b0421 (ispA)	geranyltranstransferase
b0422 (xseB)	exonuclease VII small subunit
b0423 (thiI)	tRNA s(4)U8 sulfurtransferase
b0424 (yajL)	oxidative-stress-resistance chaperone
b0425 (panE)	2-dehydropantoate reductase, NADPH-specific
b0426 (yajQ)	phage Phi6 host factor, ATP/GTP binding protein
b0428 (cyoE)	protoheme IX farnesyltransferase
b0429 (cyoD)	cytochrome o ubiquinol oxidase subunit IV
b0430 (cyoC)	cytochrome o ubiquinol oxidase subunit III
b0431 (cyoB)	cytochrome o ubiquinol oxidase subunit I
b0433 (ampG)	muropeptide transporter
b0434 (yajG)	putative lipoprotein
b0435 (bolA)	stationary-phase morphogene, transcriptional repressor for mreB; also regulator for dacA, dacC, and ampC
b0436 (tig)	peptidyl-prolyl cis/trans isomerase (trigger factor)
b0437 (clpP)	proteolytic subunit of ClpA-ClpP and ClpX-ClpP ATP-dependent serine proteases
b0438 (clpX)	ATPase and specificity subunit of ClpX-ClpP ATP-dependent serine protease
b0439 (lon)	DNA-binding ATP-dependent protease La
b0441 (ppiD)	periplasmic folding chaperone, has an inactive PPIase domain
b0443 (fadM)	long-chain acyl-CoA thioesterase III
b0444 (queC)	7-cyano-7-deazaguanine (preQ0) synthase; queuosine biosynthesis
b0445 (ybaE)	putative ABC superfamily transporter periplasmic-binding protein
b0446 (cof)	thiamine pyrimidine pyrophosphate hydrolase; HMP-PP phosphatase
b0447 (ybaO)	putative DNA-binding transcriptional regulator
b0448 (mdlA)	putative multidrug transporter subunit of ABC superfamily, ATP-binding component
b0449 (mdlB)	putative multidrug transporter subunit of ABC superfamily, ATP-binding component
b0451 (amtB)	ammonium transporter
b0452 (tesB)	acyl-CoA thioesterase 2
b0453 (ybaY)	outer membrane lipoprotein

b0454 (ybaZ)	excision repair protein, alkyltransferase-like protein ATL
b0456 (ybaA)	DUF1428 family protein
b0457 (ylaB)	putative membrane-anchored cyclic-di-GMP phosphodiesterase
b0458 (ylaC)	DUF1449 family inner membrane protein
b0459 (maa)	maltose O-acetyltransferase
b0460 (hha)	modulator of gene expression, with H-NS
b0461 (tomB)	Hha toxicity attenuator; conjugation-related protein
b0462 (acrB)	multidrug efflux system protein
b0463 (acrA)	multidrug efflux system
b0464 (acrR)	transcriptional repressor
b0465 (mscK)	mechanosensitive channel protein, intermediate conductance, K+ regulated
b0467 (priC)	primosomal replication protein N''
b0468 (ybaN)	DUF454 family inner membrane protein
b0469 (apt)	adenine phosphoribosyltransferase
b0470 (dnaX)	DNA polymerase III/DNA elongation factor III, tau and gamma subunits
b0471 (ybaB)	DNA-binding protein, putative nucleoid-associated protein
b0472 (recR)	gap repair protein
b0473 (htpG)	protein refolding molecular co-chaperone Hsp90, Hsp70-dependent; heat-shock protein; ATPase
b0474 (adk)	adenylate kinase
b0475 (hemH)	ferrochelatase
b0477 (gsk)	inosine/guanosine kinase
b0478 (ybaL)	inner membrane putative NAD(P)-binding transporter
b0481 (ybaK)	Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase
b0482 (ybaP)	TraB family protein
b0484 (copA)	copper transporter
b0485 (glsA)	glutaminase 1
b0486 (ybaT)	putative amino acid transporter
b0487 (cueR)	copper-responsive regulon transcriptional regulator
b0489 (qmcA)	PHB domain membrane-anchored putative protease
b0490 (fetA)	iron exporter, ATP-binding subunit, ABC transporter FetAB subunit; peroxide resistance protein
b0491 (fetB)	iron exporter permease subunit, ABC transporter FetAB; peroxide resistance protein
b0492 (ybbN)	DnaK co-chaperone, thioredoxin-like protein
b0493 (ybbO)	putative oxidoreductase
b0494 (tesA)	multifunctional acyl-CoA thioesterase 1; protease I; lysophospholipase L1
b0495 (ybbA)	putative ABC superfamily transporter ATP-binding subunit
b0496 (ybbP)	putative ABC transporter permease
b0503 (mnmH)	tRNA 2-selenouridine synthase, selenophosphate-dependent
b0521 (ybcF)	putative carbonate kinase
b0522 (purK)	N5-carboxyaminoimidazole ribonucleotide synthase
b0523 (purE)	N5-carboxyaminoimidazole ribonucleotide mutase
b0524 (lpxH)	UDP-2,3-diacylglucosamine pyrophosphohydrolase

b0526 (cysS)	cysteinyl-tRNA synthetase
b0528 (ybcJ)	ribosome-associated protein; putative RNA-binding protein
b0529 (folD)	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/5,10-methylene-tetrahydrofolate cyclohydrolase
b0571 (cusR)	response regulator in two-component regulatory system with CusS
b0577 (ybdG)	mechanosensitive channel protein, miniconductance
b0578 (nfsB)	dihydropteridine reductase, NAD(P)H-dependent, oxygen-insensitive
b0580 (ybdJ)	DUF1158 family putative inner membrane protein
b0592 (fepB)	iron-enterobactin transporter subunit
b0593 (entC)	isochorismate synthase 1
b0594 (entE)	2,3-dihydroxybenzoate-AMP ligase component of enterobactin synthase multienzyme complex
b0596 (entA)	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase
b0597 (entH)	enterobactin synthesis proofreading thioesterase
b0599 (ybdH)	putative oxidoreductase
b0600 (ybdL)	methionine aminotransferase, PLP-dependent
b0605 (ahpC)	alkyl hydroperoxide reductase, C22 subunit
b0606 (ahpF)	alkyl hydroperoxide reductase, F52a subunit, FAD/NAD(P)-binding
b0607 (uspG)	universal stress protein UP12
b0610 (rnk)	regulator of nucleoside diphosphate kinase
b0611 (rna)	ribonuclease I
b0612 (citT)	citrate:succinate antiporter
b0613 (citG)	2-(5''-triphosphoribosyl)-3'-dephosphocoenzyme-A synthase
b0614 (citX)	apo-citrate lyase phosphoribosyl-dephospho-CoA transferase
b0615 (citF)	citrate lyase, citrate-ACP transferase (alpha) subunit
b0616 (citE)	citrate lyase, citryl-ACP lyase (beta) subunit
b0617 (citD)	citrate lyase, acyl carrier (gamma) subunit
b0624 (flc)	fluoride efflux channel, dual topology membrane protein
b0627 (tatE)	TatABCE protein translocation system subunit
b0628 (lipA)	lipoate synthase
b0630 (lipB)	octanoyltransferase; octanoyl-[ACP]:protein N-octanoyltransferase
b0631 (ybeD)	UPF0250 family protein
b0632 (dacA)	D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 5)
b0633 (rlpA)	septal ring protein, suppressor of prc, minor lipoprotein
b0634 (mrdB)	cell wall shape-determining protein
b0635 (mrdA)	transpeptidase involved in peptidoglycan synthesis (penicillin-binding protein 2)
b0636 (rlmH)	23S rRNA m(3)Psi1915 pseudouridine methyltransferase, SAM-dependent
b0637 (rsfS)	ribosomal silencing factor
b0638 (cobC)	putative alpha-ribazole-5'-P phosphatase
b0639 (nadD)	nicotinic acid mononucleotide adenylyltransferase, NAD(P)-dependent
b0640 (holA)	DNA polymerase III, delta subunit
b0641 (lptE)	LPS assembly OM complex LptDE, lipoprotein component
b0642 (leuS)	leucyl-tRNA synthetase

b0643 (ybeL)	DUF1451 family protein
b0651 (rihA)	ribonucleoside hydrolase 1
b0653 (gltK)	glutamate, aspartate ABC transporter permease subunit
b0654 (gltJ)	glutamate, aspartate ABC transporter permease subunit
b0655 (gltI)	glutamate, aspartate binding protein, periplasmic; part of GltJKLI ABC transporter
b0658 (ybeX)	putative ion transport
b0659 (ybeY)	ssRNA-specific endoribonuclease; co-endoribonuclease working with RNase R in 16S rRNA 3' end maturation and quality control; rRNA transcription antitermination factor
b0660 (ybeZ)	PhoH-like heat shock protein
b0661 (miaB)	tRNA-i(6)A37 methylthiotransferase
b0662 (ubiF)	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol oxygenase
b0674 (asnB)	asparagine synthetase B
b0675 (umpH)	UMP phosphatase
b0676 (nagC)	N-acetylglucosamine-inducible nag divergent operon transcriptional repressor
b0677 (nagA)	N-acetylglucosamine-6-phosphate deacetylase
b0678 (nagB)	glucosamine-6-phosphate deaminase
b0679 (nagE)	fused N-acetyl glucosamine specific PTS enzyme: IIC, IIB, and IIA components
b0680 (glnS)	glutamyl-tRNA synthetase
b0682 (chiQ)	chitosugar-induced verified lipoprotein
b0683 (fur)	ferric iron uptake regulon transcriptional repressor; autorepressor
b0684 (fldA)	flavodoxin 1
b0685 (ybfE)	LexA-regulated protein, CopB family
b0686 (ybfF)	acyl-CoA esterase
b0687 (seqA)	negative modulator of initiation of replication
b0688 (pgm)	phosphoglucomutase
b0694 (kdpE)	response regulator in two-component regulatory system with KdpD
b0695 (kdpD)	fused sensory histidine kinase in two-component regulatory system with KdpE: signal sensing protein
b0696 (kdpC)	potassium translocating ATPase, subunit C
b0697 (kdpB)	potassium translocating ATPase, subunit B
b0698 (kdpA)	potassium translocating ATPase, subunit A
b0699 (ybfA)	DUF2517 family protein
b0707 (ybgA)	DUF1722 family protein
b0708 (phr)	deoxyribodipyrimidine photolyase, FAD-binding
b0709 (dtpD)	dipeptide and tripeptide permease D
b0710 (ybgI)	NIF3 family metal-binding protein
b0711 (ybgJ)	putative allophanate hydrolase, subunit 1
b0712 (ybgK)	putative allophanate hydrolase, subunit 2
b0713 (ybgL)	UPF0271 family protein
b0714 (nei)	endonuclease VIII/5-formyluracil/5-hydroxymethyluracil DNA glycosylase
b0715 (abrB)	regulator of aidB expression; inner membrane protein
b0720 (gltA)	citrate synthase

b0721 (sdhC)	succinate dehydrogenase, membrane subunit, binds cytochrome b556
b0722 (sdhD)	succinate dehydrogenase, membrane subunit, binds cytochrome b556
b0724 (sdhB)	succinate dehydrogenase, FeS subunit
b0726 (sucA)	2-oxoglutarate decarboxylase, thiamine triphosphate-binding
b0727 (sucB)	dihydrolipoyltranssuccinase
b0728 (sucC)	succinyl-CoA synthetase, beta subunit
b0729 (sucD)	succinyl-CoA synthetase, NAD(P)-binding, alpha subunit
b0733 (cydA)	cytochrome d terminal oxidase, subunit I
b0734 (cydB)	cytochrome d terminal oxidase, subunit II
b0735 (ybgE)	putative inner membrane protein in cydABX-ybgE operon
b0736 (ybgC)	acyl-CoA thioester hydrolase
b0737 (tolQ)	membrane spanning protein in TolA-TolQ-TolR complex
b0738 (tolR)	membrane spanning protein in TolA-TolQ-TolR complex
b0739 (tolA)	membrane anchored protein in TolA-TolQ-TolR complex
b0740 (tolB)	periplasmic protein
b0741 (pal)	peptidoglycan-associated outer membrane lipoprotein
b0742 (ybgF)	periplasmic TolA-binding protein
b0751 (pnuC)	nicotinamide riboside transporter
b0753 (ybgS)	putative periplasmic protein
b0755 (gpmA)	phosphoglyceromutase 1
b0756 (galM)	aldose 1-epimerase; type-1 mutarotase
b0757 (galK)	galactokinase
b0758 (galT)	galactose-1-phosphate uridylyltransferase
b0759 (galE)	UDP-galactose-4-epimerase
b0760 (modF)	fused molybdate transporter subunits of ABC superfamily: ATP-binding components
b0761 (modE)	transcriptional repressor for the molybdenum transport operon modABC
b0762 (acrZ)	AcrAB-TolC efflux pump accessory protein, membrane-associated
b0763 (modA)	molybdate transporter subunit
b0764 (modB)	molybdate transporter subunit
b0765 (modC)	molybdate transporter subunit
b0767 (pgl)	6-phosphogluconolactonase
b0772 (ybhC)	acyl-CoA thioesterase, lipoprotein
b0773 (ybhB)	kinase inhibitor homolog, UPF0098 family
b0774 (bioA)	7,8-diaminopelargonic acid synthase, PLP-dependent
b0775 (bioB)	biotin synthase
b0776 (bioF)	8-amino-7-oxononanoate synthase
b0777 (bioC)	malonyl-ACP O-methyltransferase, SAM-dependent
b0778 (bioD)	dethiobiotin synthetase
b0779 (uvrB)	excinulease of nucleotide excision repair, DNA damage recognition component
b0780 (ybhK)	putative NAD(P)-binding transferase
b0781 (moaA)	molybdopterin biosynthesis protein A
b0782 (moaB)	inactive molybdopterin adenylyltransferase
b0783 (moaC)	molybdopterin biosynthesis, protein C

b0784 (moaD)	molybdopterin synthase, small subunit
b0785 (moaE)	molybdopterin synthase, large subunit
b0786 (ybhL)	UPF0005 family inner membrane protein
b0789 (clsB)	cardiolipin synthase 2
b0790 (ybhP)	endo/exonuclease/phosphatase family protein
b0791 (ybhQ)	inner membrane protein
b0792 (ybhR)	inner membrane putative ABC superfamily transporter permease
b0793 (ybhS)	inner membrane putative ABC superfamily transporter permease
b0794 (ybhF)	putative transporter subunit of ABC superfamily: ATP-binding component
b0795 (ybhG)	putative membrane fusion protein (MFP) component of efflux pump, membrane anchor
b0796 (ybiH)	DUF1956 domain-containing tetR family putative transcriptional regulator
b0799 (dinG)	ATP-dependent DNA helicase
b0800 (ybiB)	putative family 3 glycosyltransferase
b0801 (ybiC)	putative dehydrogenase
b0802 (ybiJ)	DUF1471 family putative periplasmic protein
b0803 (ybiI)	DksA-type zinc finger protein
b0804 (ybiX)	Fe(II)-dependent oxygenase superfamily protein
b0806 (mcbA)	colanic acid mucoidy stimulation protein
b0807 (rlmF)	23S rRNA m(6)A1618 methyltransferase, SAM-dependent
b0808 (ybiO)	mechanosensitive channel protein, intermediate conductance
b0809 (glnQ)	glutamine transporter subunit
b0810 (glnP)	glutamine transporter subunit
b0811 (glnH)	glutamine transporter subunit
b0812 (dps)	Fe-binding and storage protein; stress-inducible DNA-binding protetin
b0813 (rhtA)	threonine and homoserine efflux system
b0814 (ompX)	outer membrane protein X
b0815 (ybiP)	putative EptAB family phosphoethanolamine transferase, inner membrane protein
b0817 (mntR)	Mn(2+)-responsive manganese regulon transcriptional regulator
b0818 (ybiR)	putative transporter
b0819 (ldtB)	L,D-transpeptidase linking Lpp to murein
b0822 (ybiV)	sugar phosphatase; preference for fructose-1-P, ribose-5-P and glucose-6-P
b0823 (ybiW)	putative pyruvate formate lyase
b0824 (ybiY)	putative pyruvate formate lyase activating enzyme
b0826 (moeB)	molybdopterin synthase sulfurylase
b0827 (moeA)	molybdopterin molybdenumtransferase; molybdopterin biosynthesis protein
b0828 (iaaA)	Isoaspartyl peptidase
b0829 (gsiA)	glutathione transporter ATP-binding protein, ABC superfamily
b0830 (gsiB)	glutathione periplasmic binding protein, ABC superfamily transporter
b0831 (gsiC)	glutathione transporter, permease component, ABC superfamily
b0832 (gsiD)	glutathione transporter, permease component, ABC superfamily
b0835 (rimO)	ribosomal protein S12 methylthiotransferase; radical SAM superfamily

b0836 (bssR)	repressor of biofilm formation by indole transport regulation
b0840 (deoR)	deoxyribose-5-phosphate-inducible deoxyribose operon transcriptional repressor; repressor of nupG and tsx
b0841 (ybjG)	undecaprenyl pyrophosphate phosphatase
b0842 (mdfA)	multidrug efflux system protein
b0843 (ybjH)	uncharacterized protein
b0844 (ybjI)	5-amino-6-(5-phospho-D-ribitylamino)uracil phosphatase; pyrimidine phosphatase; riboflavin synthesis
b0845 (ybjJ)	putative transporter
b0846 (rcdA)	transcriptional regulator of csgD and ybiJI; autoregulator
b0847 (ybjL)	putative transporter
b0848 (ybjM)	inner membrane protein
b0849 (grxA)	glutaredoxin 1, redox coenzyme for ribonucleotide reductase (RNR1a)
b0850 (ybjC)	DUF1418 family protein
b0852 (rimK)	ribosomal protein S6 modification protein
b0853 (ybjN)	negative regulator of motility; multicopy suppressor of coaA(Ts)
b0854 (potF)	putrescine transporter subunit: periplasmic-binding component of ABC superfamily
b0855 (potG)	putrescine transporter subunit: ATP-binding component of ABC superfamily
b0856 (potH)	putrescine transporter subunit: membrane component of ABC superfamily
b0857 (potI)	putrescine transporter subunit: membrane component of ABC superfamily
b0858 (ybjO)	DUF2593 family inner membrane protein
b0859 (rlmC)	23S rRNA m(5)U747 methyltransferase, SAM-dependent
b0861 (artM)	arginine transporter subunit
b0862 (artQ)	arginine transporter subunit
b0863 (artI)	arginine transporter subunit
b0864 (artP)	arginine transporter subunit
b0865 (ybjP)	lipoprotein
b0866 (ybjQ)	UPF0145 family protein
b0867 (amiD)	1,6-anhydro-N-acetylmuramyl-L-alanine amidase, Zn-dependent; OM lipoprotein
b0868 (ybjS)	putative NAD(P)H-dependent oxidoreductase with NAD(P)-binding Rossmann-fold domain
b0869 (ybjT)	putative NAD-dependent oxidoreductase
b0870 (ltaE)	L-allo-threonine aldolase, PLP-dependent
b0871 (poxB)	pyruvate dehydrogenase (pyruvate oxidase), thiamine triphosphate-binding, FAD-binding
b0872 (hcr)	HCP oxidoreductase, NADH-dependent
b0873 (hcp)	hybrid-cluster [4Fe-2S-2O] protein in anaerobic terminal reductases
b0874 (ybjE)	putative transporter
b0876 (ybjD)	putative OLD family ATP-dependent endonuclease; DUF2813 family protein
b0877 (ybjX)	DUF535 family protein
b0878 (macA)	macrolide transporter subunit, membrane fusion protein (MFP) component

b0879 (macB)	fused macrolide transporter subunits of ABC superfamily: ATP-binding component/membrane component
b0880 (cspD)	inhibitor of DNA replication, cold shock protein homolog
b0881 (clpS)	regulatory protein for ClpA substrate specificity
b0884 (infA)	translation initiation factor IF-1
b0885 (aat)	leucyl/phenylalanyl-tRNA-protein transferase
b0886 (cydC)	fused glutathione, cysteine exporter subunits of ABC superfamily: membrane component/ATP-binding component
b0887 (cydD)	fused glutathione, cysteine exporter subunits of ABC superfamily: membrane component/ATP-binding component
b0888 (trxB)	thioredoxin reductase, FAD/NAD(P)-binding
b0889 (lrp)	leucine-responsive global transcriptional regulator
b0890 (ftsK)	DNA translocase at septal ring sorting daughter chromsomes
b0891 (lolA)	lipoprotein chaperone
b0892 (rarA)	DNA-dependent ATPase involved in processing recombination intermediates at replication forks
b0893 (serS)	seryl-tRNA synthetase, also charges selenocysteinyl-tRNA with serine
b0894 (dmsA)	dimethyl sulfoxide reductase, anaerobic, subunit A
b0896 (dmsC)	dimethyl sulfoxide reductase, anaerobic, subunit C
b0898 (ycaD)	putative MFS-type transporter
b0902 (pflA)	[formate-C-acetyltransferase 1]-activating enzyme; pyruvate formate-lyase 1-activating enzyme
b0903 (pflB)	formate C-acetyltransferase 1, anaerobic; pyruvate formate-lyase 1
b0904 (focA)	formate channel
b0905 (ycaO)	ribosomal protein S12 methylthiotransferase accessory factor
b0906 (ycaP)	UPF0702 family putative inner membrane protein
b0907 (serC)	3-phosphoserine/phosphohydroxythreonine aminotransferase
b0908 (aroA)	5-enolpyruvylshikimate-3-phosphate synthetase
b0909 (ycaL)	putative peptidase-related chaperone
b0910 (cmk)	cytidylate kinase
b0911 (rpsA)	30S ribosomal subunit protein S1
b0912 (ihfB)	integration host factor (IHF), DNA-binding protein, beta subunit
b0914 (msbA)	fused lipid transporter subunits of ABC superfamily: membrane component/ATP-binding component
b0915 (lpxK)	lipid A 4'kinase
b0916 (ycaQ)	DUF1006 family protein with C-terminal wHTH domain
b0917 (ycaR)	peroxide and acid resistance protein, UPF0434 family
b0918 (kdsB)	3-deoxy-manno-octulosonate cytidylyltransferase
b0919 (ycbJ)	protein kinase-like domain protein
b0920 (ycbC)	DUF218 superfamily protein
b0921 (smtA)	putative S-adenosyl-L-methionine-dependent methyltransferase
b0922 (mukF)	chromosome condensin MukBEF, kleisin-like subunit, binds calcium
b0923 (mukE)	chromosome condensin MukBEF, MukE localization factor
b0924 (mukB)	chromosome condensin MukBEF, ATPase and DNA-binding subunit
b0925 (ldtD)	murein L,D-transpeptidase
b0926 (ycbK)	M15A protease-related family periplasmic protein
b0927 (ycbL)	putative metal-binding enzyme

b0928 (aspC)	aspartate aminotransferase, PLP-dependent
b0929 (ompF)	outer membrane porin 1a (Ia;b;F)
b0930 (asnS)	asparaginyl tRNA synthetase
b0931 (pncB)	nicotinate phosphoribosyltransferase
b0932 (pepN)	aminopeptidase N
b0935 (ssuD)	alkanesulfonate monooxygenase, FMNH(2)-dependent
b0936 (ssuA)	aliphatic sulfonate binding protein, SsuABC ABC transporter
b0945 (pyrD)	dihydro-orotate oxidase, FMN-linked
b0946 (zapC)	FtsZ stabilizer
b0947 (ycbX)	6-N-hydroxylaminopurine detoxification oxidoreductase
b0948 (rlmL)	fused 23S rRNA m(2)G2445 and m(7)G2069 methyltransferase, SAM-dependent
b0949 (uup)	putative transporter subunit of ABC superfamily: ATP-binding component
b0950 (pqiA)	paraquat-inducible, SoxRS-regulated inner membrane protein
b0951 (pqiB)	paraquat-inducible, SoxRS-regulated MCE domain protein
b0952 (pqiC)	DUF330 family putative lipoprotein
b0953 (rmf)	ribosome modulation factor
b0954 (fabA)	beta-hydroxydecanoyl thioester dehydrase
b0955 (ycbZ)	putative peptidase
b0956 (matP)	Ter macrodomain organizer matS-binding protein
b0957 (ompA)	outer membrane protein A (3a;II*;G;d)
b0958 (sulA)	SOS cell division inhibitor
b0961 (yccF)	DUF307 family inner membrane protein
b0962 (helD)	DNA helicase IV
b0963 (mgsA)	methylglyoxal synthase
b0964 (yccT)	UPF0319 family protein
b0965 (yccU)	putative CoA-binding protein
b0966 (hspQ)	heat shock protein involved in degradation of mutant DnaA; hemimethylated oriC DNA-binding protein
b0967 (rlmI)	23S rRNA m(5)C1962 methyltransferase, SAM-dependent
b0968 (yccX)	weak acylphosphatase
b0969 (tusE)	mnm(5)-s(2)U34-tRNA 2-thiolation sulfurtransferase
b0970 (yccA)	HflBKC-binding inner membrane protein, UPF0005 family
b0972 (hyaA)	hydrogenase 1, small subunit
b0973 (hyaB)	hydrogenase 1, large subunit
b0974 (hyaC)	hydrogenase 1, b-type cytochrome subunit
b0975 (hyaD)	hydrogenase 1 maturation protease
b0976 (hyaE)	putative HyaA chaperone
b0977 (hyaF)	protein involved in nickel incorporation into hydrogenase-1 proteins
b0995 (torR)	response regulator in two-component regulatory system with TorS
b0996 (torC)	trimethylamine N-oxide (TMAO) reductase I, cytochrome c-type subunit
b0999 (cbpM)	modulator of CbpA co-chaperone
b1000 (cbpA)	DnaK co-chaperone; curved DNA-binding protein
b1002 (agp)	glucose-1-phosphatase/inositol phosphatase

b1003 (yccJ)	uncharacterized protein
b1013 (rutR)	rut operon transcriptional repressor for
b1033 (ghrA)	glyoxylate/hydroxypyruvate reductase A
b1034 (ycdX)	alkaline phosphatase
b1035 (ycdY)	redox enzyme maturation protein (REMP) chaperone for YcdX
b1036 (ycdZ)	DUF1097 family inner membrane protein
b1037 (csgG)	curli production assembly/transport outer membrane lipoprotein
b1045 (ymdB)	O-acetyl-ADP-ribose deacetylase; RNase III inhibitor during cold shock; putative cardiolipin synthase C regulatory subunit
b1046 (clsC)	stationary phase cardiolipin synthase 3
b1047 (opgC)	osmoregulated periplasmic glucan succinylation membrane protein
b1048 (opgG)	osmoregulated periplasmic glucan (OPG) biosynthesis periplasmic protein
b1049 (opgH)	membrane glycosyltransferase; nutrient-dependent cell size regulator, FtsZ assembly antagonist
b1054 (lpxL)	lauryl-acyl carrier protein (ACP)-dependent acyltransferase
b1055 (yceA)	putative rhodanese-related sulfurtransferase
b1056 (yceI)	secreted protein
b1057 (yceJ)	putative cytochrome b561
b1059 (solA)	N-methyltryptophan oxidase, FAD-binding
b1060 (bssS)	biofilm regulator
b1061 (dinI)	DNA damage-inducible protein I
b1062 (pyrC)	dihydro-orotase
b1063 (yceB)	lipoprotein, DUF1439 family
b1065 (mdtH)	multidrug resistance efflux transporter conferring overexpression resistance to norfloxacin and enoxacin
b1066 (rimJ)	ribosomal-protein-S5-alanine N-acetyltransferase
b1067 (yceH)	UPF0502 family protein
b1069 (murJ)	putative peptidoglycan lipid II flippase
b1070 (flgN)	export chaperone for FlgK and FlgL
b1071 (flgM)	anti-sigma factor for FliA (sigma 28)
b1072 (flgA)	assembly protein for flagellar basal-body periplasmic P ring
b1073 (flgB)	flagellar component of cell-proximal portion of basal-body rod
b1074 (flgC)	flagellar component of cell-proximal portion of basal-body rod
b1075 (flgD)	flagellar hook assembly protein
b1076 (flgE)	flagellar hook protein
b1077 (flgF)	flagellar component of cell-proximal portion of basal-body rod
b1078 (flgG)	flagellar component of cell-distal portion of basal-body rod
b1079 (flgH)	flagellar protein of basal-body outer-membrane L ring
b1080 (flgI)	putative flagellar basal body protein
b1081 (flgJ)	flagellar rod assembly protein and murein hydrolase; flagellum-specific muramidase
b1082 (flgK)	flagellar hook-filament junction protein 1
b1083 (flgL)	flagellar hook-filament junction protein
b1084 (rne)	fused ribonucleaseE: endoribonuclease/RNA-binding protein/RNA degradosome binding protein
b1085 (yceQ)	uncharacterized protein

b1086 (rluC)	23S rRNA pseudouridine(955,2504,2580) synthase
b1087 (yceF)	Maf-like protein
b1088 (yceD)	DUF177 family protein
b1089 (rpmF)	50S ribosomal subunit protein L32
b1090 (plsX)	putative phosphate acyltransferase
b1091 (fabH)	3-oxoacyl-[acyl-carrier-protein] synthase III
b1092 (fabD)	malonyl-CoA-[acyl-carrier-protein] transacylase
b1093 (fabG)	3-oxoacyl-[acyl-carrier-protein] reductase
b1094 (acpP)	acyl carrier protein (ACP)
b1095 (fabF)	3-oxoacyl-[acyl-carrier-protein] synthase II
b1096 (pabC)	4-amino-4-deoxychorismate lyase component of para-aminobenzoate synthase multienzyme complex
b1097 (yceG)	septation protein, ampicillin sensitivity
b1098 (tmk)	thymidylate kinase
b1099 (holB)	DNA polymerase III, delta prime subunit
b1100 (ycfH)	putative DNase
b1103 (hinT)	purine nucleoside phosphoramidase, dadA activator protein
b1104 (ycfL)	uncharacterized protein
b1105 (lpoB)	OM lipoprotein stimulator of MrcB transpeptidase
b1106 (thiK)	thiamine kinase
b1107 (nagZ)	beta N-acetyl-glucosaminidase
b1108 (ycfP)	putative UPF0227 family esterase
b1109 (ndh)	respiratory NADH dehydrogenase 2/cupric reductase
b1110 (ycfJ)	uncharacterized protein
b1111 (ycfQ)	repressor for bhsA(ycfR)
b1112 (bhsA)	biofilm, cell surface and signaling protein
b1113 (ldtC)	L,D-transpeptidase linking Lpp to murein
b1114 (mfd)	transcription-repair coupling factor
b1115 (ycfT)	inner membrane protein
b1116 (lolC)	lipoprotein-releasing system transmembrane protein
b1117 (lolD)	outer membrane-specific lipoprotein transporter subunit
b1118 (lolE)	lipoprotein-releasing system transmembrane protein
b1119 (nagK)	N-acetyl-D-glucosamine kinase
b1123 (potD)	polyamine transporter subunit
b1124 (potC)	polyamine transporter subunit
b1126 (potA)	polyamine transporter subunit
b1128 (roxA)	50S ribosomal protein L16 arginine hydroxylase; 2-oxoglutarate oxygenase
b1129 (phoQ)	sensory histidine kinase in two-component regulatory system with PhoP
b1130 (phoP)	response regulator in two-component regulatory system with PhoQ
b1131 (purB)	adenylosuccinate lyase
b1132 (hflD)	putative lysogenization regulator
b1133 (mnmA)	tRNA(Gln,Lys,Glu) U34 2-thiouridylase, first step in mnm(5)-s(2)U34-tRNA synthesis

b1134 (nudJ)	bifunctional thiamine pyrimidine pyrophosphate hydrolase/thiamine pyrophosphate hydrolase
b1135 (rluE)	23S rRNA pseudouridine(2457) synthase
b1136 (icd)	e14 prophage; isocitrate dehydrogenase, specific for NADP+
b1174 (minE)	cell division topological specificity factor
b1175 (minD)	membrane ATPase of the MinC-MinD-MinE system
b1176 (minC)	cell division inhibitor
b1179 (ycgL)	UPF0745 family protein
b1180 (ycgM)	putative isomerase/hydrolase
b1181 (ycgN)	UPF0153 family cysteine cluster protein
b1185 (dsbB)	oxidoreductase that catalyzes reoxidation of DsbA protein disulfide isomerase I
b1186 (nhaB)	sodium:proton antiporter
b1187 (fadR)	fatty acid metabolism regulon transcriptional regulator
b1188 (ycgB)	SpoVR family stationary phase protein
b1189 (dadA)	D-amino acid dehydrogenase
b1190 (dadX)	alanine racemase, catabolic, PLP-binding
b1191 (cvrA)	putative cation/proton antiporter
b1192 (ldcA)	murein tetrapeptide carboxypeptidase; LD-carboxypeptidase A
b1193 (emtA)	lytic murein endotransglycosylase E
b1195 (ymgE)	UPF0410 family putative inner membrane protein
b1203 (ychF)	catalase inhibitor protein; ATPase, K+-dependent, ribosome-associated
b1204 (pth)	peptidyl-tRNA hydrolase
b1205 (ychH)	DUF2583 family putative inner membrane protein
b1206 (dauA)	C4-dicarboxylic acid transporter
b1207 (prs)	phosphoribosylpyrophosphate synthase
b1208 (ispE)	4-diphosphocytidyl-2-C-methylerythritol kinase
b1209 (lolB)	lipoprotein localization factor
b1210 (hemA)	glutamyl tRNA reductase
b1211 (prfA)	peptide chain release factor RF-1
b1212 (prmC)	N5-glutamine methyltransferase, modifies release factors RF-1 and RF-2
b1213 (ychQ)	SIRB family inner membrane protein
b1214 (ychA)	transglutaminase-like TPR-repeat protein
b1215 (kdsA)	3-deoxy-D-manno-octulosonate 8-phosphate synthase
b1216 (chaA)	calcium/sodium:proton antiporter
b1217 (chaB)	cation transport regulator
b1218 (chaC)	cation transport regulator
b1219 (ychN)	putative sulfur relay protein
b1220 (ychO)	putative invasin
b1221 (narL)	response regulator in two-component regulatory system with NarX (or NarQ)
b1222 (narX)	sensory histidine kinase in two-component regulatory system with NarL
b1223 (narK)	nitrate/nitrite transporter
b1225 (narH)	nitrate reductase 1, beta (Fe-S) subunit

b1226 (narJ)	molybdenum-cofactor-assembly chaperone subunit (delta subunit) of nitrate reductase 1
b1232 (purU)	formyltetrahydrofolate hydrolase
b1233 (ychJ)	UPF0225 family protein
b1234 (rssA)	putative patatin-like family phospholipase
b1235 (rssB)	PcnB-degradosome interaction factor; response regulator
b1236 (galU)	glucose-1-phosphate uridylyltransferase
b1237 (hns)	global DNA-binding transcriptional dual regulator H-NS
b1238 (tdk)	thymidine kinase/deoxyuridine kinase
b1241 (adhE)	fused acetaldehyde-CoA dehydrogenase/iron-dependent alcohol dehydrogenase/pyruvate-formate lyase deactivase
b1242 (ychE)	UPF0056 family inner membrane protein
b1243 (oppA)	oligopeptide transporter subunit
b1244 (oppB)	oligopeptide transporter subunit
b1245 (oppC)	oligopeptide transporter subunit
b1246 (oppD)	oligopeptide transporter subunit
b1247 (oppF)	oligopeptide transporter subunit
b1248 (yciU)	UPF0263 family protein
b1249 (clsA)	cardiolipin synthase 1
b1250 (kch)	voltage-gated potassium channel
b1251 (yciI)	putative DGPF domain-containing enzyme
b1252 (tonB)	membrane spanning protein in TonB-ExbB-ExbD transport complex
b1253 (yciA)	acyl-CoA esterase
b1254 (yciB)	IspA family inner membrane protein
b1255 (yciC)	UPF0259 family inner membrane protein
b1256 (ompW)	outer membrane protein W
b1260 (trpA)	tryptophan synthase, alpha subunit
b1261 (trpB)	tryptophan synthase, beta subunit
b1262 (trpC)	fused indole-3-glycerolphosphate synthetase/N-(5-phosphoribosyl)anthranilate isomerase
b1263 (trpD)	fused glutamine amidotransferase (component II) of anthranilate synthase/anthranilate phosphoribosyl transferase
b1264 (trpE)	component I of anthranilate synthase
b1265 (trpL)	trp operon leader peptide
b1266 (yciV)	PHP domain protein
b1267 (yciO)	putative RNA binding protein
b1269 (rluB)	23S rRNA pseudouridine(2605) synthase
b1270 (btuR)	cob(I)yrinic acid a,c-diamide adenosyltransferase
b1271 (yciK)	putative EmrKY-TolC system oxoacyl-(acyl carrier protein) reductase
b1272 (sohB)	inner membrane protein, S49 peptidase family protein
b1273 (yciN)	DUF2498 protein YciN
b1274 (topA)	DNA topoisomerase I, omega subunit
b1275 (cysB)	N-acetylserine-responsive cysteine regulon transcriptional activator; autorepressor
b1276 (acnA)	aconitate hydratase 1
b1277 (ribA)	GTP cyclohydrolase II

b1278 (pgpB)	phosphatidylglycerophosphatase B
b1279 (yciS)	DUF1049 family inner membrane protein, function unknown
b1280 (yciM)	envelope integrity maintenance protein; EnvC-interacting protein
b1281 (pyrF)	orotidine-5'-phosphate decarboxylase
b1282 (yciH)	initiation factor function partial mimic, SUI1 family
b1283 (osmB)	lipoprotein
b1284 (yciT)	global regulator of transcription; DeoR family
b1286 (rnb)	ribonuclease II
b1287 (yciW)	putative oxidoreductase
b1288 (fabI)	enoyl-[acyl-carrier-protein] reductase, NADH-dependent
b1290 (sapF)	antimicrobial peptide transport ABC system ATP-binding protein
b1291 (sapD)	antimicrobial peptide transport ABC system ATP-binding protein
b1292 (sapC)	antimicrobial peptide transport ABC transporter permease
b1293 (sapB)	antimicrobial peptide transport ABC transporter permease
b1294 (sapA)	antimicrobial peptide transport ABC transporter periplasmic binding protein
b1295 (ymjA)	DUF2543 family protein
b1304 (pspA)	regulatory protein for phage-shock-protein operon
b1305 (pspB)	psp operon transcription co-activator
b1306 (pspC)	psp operon transcription co-activator
b1307 (pspD)	peripheral inner membrane phage-shock protein
b1308 (pspE)	thiosulfate:cyanide sulfurtransferase (rhodanese)
b1321 (ycjX)	DUF463 family protein, putative P-loop NTPase
b1322 (ycjF)	UPF0283 family inner membrane protein
b1323 (tyrR)	aromatic amino acid biosynthesis and transport regulon transcriptional regulator; autorepressor; ATPase; phosphatase
b1324 (tpx)	lipid hydroperoxide peroxidase
b1325 (ycjG)	L-Ala-D/L-Glu epimerase
b1326 (mpaA)	murein peptide amidase A
b1329 (mppA)	murein tripeptide (L-ala-gamma-D-glutamyl-meso-DAP) transporter subunit
b1332 (ynaJ)	DUF2534 family putative inner membrane protein
b1333 (uspE)	stress-induced protein
b1334 (fnr)	oxygen-sensing anaerobic growth regulon transcriptional regulator; autorepressor
b1335 (ogt)	O-6-alkylguanine-DNA:cysteine-protein methyltransferase
b1340 (smrA)	DNA endonuclease
b1342 (ydaN)	putative Zn(II) transporter
b1343 (dbpA)	ATP-dependent RNA helicase, specific for 23S rRNA
b1344 (ttcA)	tRNA 2-thiocytidine biosynthesis protein
b1376 (uspF)	stress-induced protein, ATP-binding protein
b1378 (pfo)	pyruvate-flavodoxin oxidoreductase
b1380 (ldhA)	fermentative D-lactate dehydrogenase, NAD-dependent
b1381 (ydbH)	putative membrane-anchored protein, function unknown
b1382 (ynbE)	lipoprotein
b1412 (azoR)	NADH-azoreductase, FMN-dependent

b1413 (hrpA)	putative ATP-dependent helicase
b1418 (cybB)	cytochrome b561
b1422 (ydcI)	putative DNA-binding transcriptional regulator
b1423 (ydcJ)	putative metalloenzyme
b1424 (opgD)	osmoregulated periplasmic glucan (OPG) biosynthesis periplasmic protein
b1426 (ydcH)	DUF465 family protein
b1428 (ydcK)	uncharacterized protein
b1429 (tehA)	potassium-tellurite ethidium and proflavin transporter
b1430 (tehB)	tellurite, selenium methyltransferase, SAM-dependent; tellurite, selenium resistance protein
b1445 (ydcX)	DUF2566 family protein
b1446 (ydcY)	uncharacterized protein
b1448 (mnaT)	methionine N-acyltransferase; L-amino acid N-acyltransferase
b1473 (yddG)	aromatic amino acid exporter
b1476 (fdnI)	formate dehydrogenase-N, cytochrome B556 (gamma) subunit, nitrate-inducible
b1477 (yddM)	putative DNA-binding transcriptional regulator
b1479 (maeA)	malate dehydrogenase, (decarboxylating, NAD-requiring) (malic enzyme)
b1482 (osmC)	lipoyl-dependent Cys-based peroxidase, hydroperoxide resistance; salt-shock inducible membrane protein; peroxiredoxin
b1491 (yddW)	liprotein, glycosyl hydrolase homolog
b1492 (gadC)	glutamate:gamma-aminobutyric acid antiporter
b1521 (uxaB)	altronate oxidoreductase, NAD-dependent
b1524 (glsB)	glutaminase 2
b1528 (ydeA)	arabinose efflux transporter, arabinose-inducible
b1529 (marC)	UPF0056 family inner membrane protein
b1530 (marR)	transcriptional repressor of multiple antibiotic resistance
b1531 (marA)	multiple antibiotic resistance transcriptional regulator
b1532 (marB)	mar operon regulator, periplasmic
b1538 (dcp)	dipeptidyl carboxypeptidase II
b1539 (ydfG)	NADP-dependent 3-hydroxy acid dehydrogenase; malonic semialdehyde reductase
b1540 (rspR)	transcriptional repressor for rspAB
b1541 (ydfZ)	selenoprotein, function unknown
b1591 (dmsD)	twin-argninine leader-binding protein for DmsA and TorA
b1592 (clcB)	H(+)/Cl(-) exchange transporter
b1593 (ynfK)	putative dethiobiotin synthetase
b1594 (mlc)	glucosamine anaerobic growth regulon transcriptional repressor; autorepressor
b1595 (ynfL)	LysR family putative transcriptional regulator
b1596 (ynfM)	putative arabinose efflux transporter
b1597 (asr)	acid shock-inducible periplasmic protein
b1598 (ydgD)	putative peptidase
b1599 (mdtI)	multidrug efflux system transporter
b1600 (mdtJ)	multidrug efflux system transporter

b1602 (pntB)	pyridine nucleotide transhydrogenase, beta subunit
b1603 (pntA)	pyridine nucleotide transhydrogenase, alpha subunit
b1604 (ydgH)	DUF1471 family periplasmic protein
b1605 (ydgI)	putative arginine/ornithine antiporter transporter
b1606 (folM)	dihydromonapterin reductase, NADPH-dependent; dihydrofolate reductase isozyme
b1607 (ydgC)	GlpM family inner membrane protein
b1608 (rstA)	response regulator of RstAB two-component system, low Mg-responsive via PhoQP
b1609 (rstB)	sensory histidine kinase of RstAB two-component system, low Mg-responsive via PhoQP
b1610 (tus)	inhibitor of replication at Ter, DNA-binding protein
b1611 (fumC)	fumarate hydratase (fumarase C),aerobic Class II
b1613 (manA)	mannose-6-phosphate isomerase
b1614 (ydgA)	DUF945 family protein
b1620 (malI)	transcriptional repressor of Mal regulon
b1621 (malX)	fused maltose and glucose-specific PTS enzymes: IIB component, IIC component
b1622 (malY)	bifunctional beta-cystathionase, PLP-dependent/regulator of maltose regulon
b1623 (add)	adenosine deaminase
b1624 (ydgJ)	putative oxidoreductase
b1625 (cnu)	nucleoid-associated oriC-binding protein; H-NS and StpA stabilizing factor
b1626 (ydgK)	DUF2569 family inner membrane protein
b1627 (rsxA)	SoxR iron-sulfur cluster reduction factor component; inner membrane protein of electron transport complex
b1628 (rsxB)	SoxR iron-sulfur cluster reduction factor component; putative iron-sulfur protein
b1630 (rsxD)	SoxR iron-sulfur cluster reduction factor component; putative membrane protein of electron transport complex
b1631 (rsxG)	SoxR iron-sulfur cluster reduction factor component; putative membrane protein of electron transport complex
b1632 (rsxE)	SoxR iron-sulfur cluster reduction factor component; electron transport inner membrane NADH-quinone reductase
b1633 (nth)	DNA glycosylase and apyrimidinic (AP) lyase (endonuclease III)
b1634 (dtpA)	dipeptide and tripeptide permease A
b1636 (pdxY)	pyridoxamine kinase
b1637 (tyrS)	tyrosyl-tRNA synthetase
b1638 (pdxH)	pyridoxine 5'-phosphate oxidase
b1640 (anmK)	anhydro-N-acetylmuramic acid kinase
b1641 (slyB)	outer membrane lipoprotein
b1642 (slyA)	global transcriptional regulator
b1643 (ydhI)	DUF1656 family putative inner membrane efflux pump associated protein
b1644 (ydhJ)	putative membrane fusion protein (MFP) of YdhJK efflux pump
b1646 (sodC)	superoxide dismutase, Cu, Zn, periplasmic
b1647 (ydhF)	putative oxidoreductase

b1648 (ydhL)	DUF1289 family protein
b1649 (nemR)	transcriptional repressor for the nemRA-gloA operon, quinone-, glyoxal-, and HOCl-activated
b1650 (nemA)	chromate reductase, quinone reductase, FMN-linked; N-Ethylmaleimide reductase; old yellow enzyme
b1651 (gloA)	glyoxalase I, Ni-dependent
b1652 (rnt)	ribonuclease T (RNase T)
b1654 (grxD)	glutaredoxin-4
b1655 (mepH)	murein DD-endopeptidase, space-maker hydrolase
b1656 (sodB)	superoxide dismutase, Fe
b1657 (ydhP)	putative transporter
b1658 (purR)	transcriptional repressor, hypoxanthine-binding
b1659 (ydhB)	LysR family putative transcriptional regulator
b1660 (ydhC)	putative arabinose efflux transporter
b1661 (cfa)	cyclopropane fatty acyl phospholipid synthase (unsaturated-phospholipid methyltransferase)
b1662 (ribC)	riboflavin synthase, alpha subunit
b1663 (mdtK)	multidrug efflux system transporter
b1664 (ydhQ)	autotransporter adhesin-related protein
b1667 (ydhR)	putative monooxygenase
b1669 (ydhT)	FNR, Nar, NarP-regulated protein; putative subunit of YdhYVWXUT oxidoreductase complex
b1675 (ydhZ)	uncharacterized protein
b1676 (pykF)	pyruvate kinase I
b1677 (lpp)	murein lipoprotein
b1678 (ldtE)	murein L,D-transpeptidase
b1679 (sufE)	sulfur acceptor protein
b1680 (sufS)	cysteine desulfurase, stimulated by SufE; selenocysteine lyase, PLP-dependent
b1681 (sufD)	component of SufBCD Fe-S cluster assembly scaffold
b1682 (sufC)	SufBCD Fe-S cluster assembly scaffold protein, ATP-binding protein
b1683 (sufB)	component of SufBCD Fe-S cluster assembly scaffold
b1684 (sufA)	Fe-S cluster assembly protein
b1685 (ydiH)	uncharacterized protein
b1686 (menI)	1,4-dihydroxy-2-naphthoyl-CoA hydrolase
b1687 (ydiJ)	putative FAD-linked oxidoreductase
b1688 (ydiK)	UPF0118 family inner membrane protein
b1692 (ydiB)	quinate/shikimate 5-dehydrogenase, NAD(P)-binding
b1693 (aroD)	3-dehydroquinate dehydratase
b1702 (ppsA)	phosphoenolpyruvate synthase
b1703 (ppsR)	bifunctional regulatory protein: PEP synthase kinase and PEP synthase pyrophosphorylase
b1704 (aroH)	3-deoxy-D-arabino-heptulosonate-7-phosphate synthase, tryptophan repressible
b1705 (ydiE)	hemin uptake protein HemP homolog
b1706 (ydiU)	UPF0061 family protein
b1707 (ydiV)	anti-FlhD4C2 factor, inactive EAL family phosphodiesterase

b1708 (nlpC)	putative C40 clan peptidase lipoprotein
b1709 (btuD)	vitamin B12 transporter subunit : ATP-binding component of ABC superfamily
b1710 (btuE)	glutathione peroxidase
b1711 (btuC)	vitamin B12 transporter subunit: membrane component of ABC superfamily
b1712 (ihfA)	integration host factor (IHF), DNA-binding protein, alpha subunit
b1713 (pheT)	phenylalanine tRNA synthetase, beta subunit
b1714 (pheS)	phenylalanine tRNA synthetase, alpha subunit
b1715 (pheM)	phenylalanyl-tRNA synthetase operon leader peptide
b1716 (rplT)	50S ribosomal subunit protein L20
b1717 (rpmI)	50S ribosomal subunit protein L35
b1718 (infC)	translation initiation factor IF-3
b1719 (thrS)	threonyl-tRNA synthetase
b1722 (ydiY)	acid-inducible putative outer membrane protein
b1723 (pfkB)	6-phosphofructokinase II
b1724 (ydiZ)	uncharacterized protein
b1725 (yniA)	fructosamine kinase family protein
b1726 (yniB)	putative inner membrane protein
b1727 (yniC)	2-deoxyglucose-6-P phosphatase
b1728 (ydjM)	inner membrane protein regulated by LexA
b1729 (ydjN)	putative transporter
b1731 (cedA)	cell division modulator
b1733 (chbG)	chito-oligosaccharide deacetylase
b1736 (chbA)	N,N'-diacetylchitobiose-specific enzyme IIA component of PTS
b1738 (chbB)	N,N'-diacetylchitobiose-specific enzyme IIB component of PTS
b1739 (osmE)	osmotically-inducible lipoprotein
b1740 (nadE)	NAD synthetase, NH3/glutamine-dependent
b1742 (ves)	cold- and stress-inducible protein
b1744 (astE)	succinylglutamate desuccinylase
b1745 (astB)	succinylarginine dihydrolase
b1746 (astD)	succinylglutamic semialdehyde dehydrogenase
b1747 (astA)	arginine succinyltransferase
b1748 (astC)	succinylornithine transaminase, PLP-dependent
b1749 (xthA)	exonuclease III
b1751 (ydjY)	putative ferrodoxin-like lipoprotein
b1752 (ydjZ)	TVP38/TMEM64 family inner membrane protein
b1753 (ynjA)	carboxymuconolactone decarboxylase family protein
b1756 (ynjD)	putative ABC superfamily transporter ATP-binding subunit
b1757 (ynjE)	molybdopterin synthase sulfurtransferase
b1759 (nudG)	CTP pyrophosphohydrolase; also hydrolyzes 2-hydroxy-dATP, 8-hydroxy-dGTP, 5-hydroxy-CTP, dCTP and 5-methyl-dCTP
b1760 (ynjH)	DUF1496 family protein
b1761 (gdhA)	glutamate dehydrogenase, NADP-specific
b1764 (selD)	selenophosphate synthase
b1765 (ydjA)	putative oxidoreductase

b1766 (sppA)	protease IV (signal peptide peptidase)
b1767 (ansA)	cytoplasmic L-asparaginase 1
b1768 (pncA)	nicotinamidase/pyrazinamidase
b1777 (yeaC)	DUF1315 family protein
b1778 (msrB)	methionine sulfoxide reductase B
b1779 (gapA)	glyceraldehyde-3-phosphate dehydrogenase A
b1780 (yeaD)	D-hexose-6-phosphate epimerase-like protein
b1781 (yeaE)	aldo-keto reductase, methylglyoxal to acetol, NADPH-dependent
b1782 (mipA)	scaffolding protein for murein synthesizing machinery
b1787 (yeaK)	aminoacyl-tRNA editing domain protein
b1788 (yoaI)	uncharacterized protein
b1789 (yeaL)	UPF0756 family putative inner membrane protein
b1792 (yeaO)	DUF488 family protein
b1793 (yoaF)	DUF333 family outer membrane lipoprotein
b1804 (rnd)	ribonuclease D
b1805 (fadD)	acyl-CoA synthetase (long-chain-fatty-acid--CoA ligase)
b1806 (yeaY)	Slp family lipoprotein, RpoE-regulated
b1807 (tsaB)	tRNA(ANN) t(6)A37 threonylcarbamoyladenosine modification protein; binding partner and protease for TsaD
b1808 (yoaA)	putative ATP-dependent helicase, DinG family
b1809 (yoaB)	putative reactive intermediate deaminase
b1810 (yoaC)	DUF1889 family protein
b1811 (yoaH)	UPF0181 family protein
b1812 (pabB)	aminodeoxychorismate synthase, subunit I
b1813 (nudL)	putative CoA pyrophosphohydrolase, weak 3-phosphohydroxypyruvate phosphatase
b1815 (yoaD)	putative membrane-anchored cyclic-di-GMP phosphodiesterase, regulator of cellulose production
b1816 (yoaE)	putative membrane protein/conserved protein
b1817 (manX)	fused mannose-specific PTS enzymes: IIA component/IIB component
b1818 (manY)	mannose-specific enzyme IIC component of PTS
b1819 (manZ)	mannose-specific enzyme IID component of PTS
b1821 (mntP)	putative Mn(2+) efflux pump, mntR-regulated
b1822 (rlmA)	23S rRNA m(1)G745 methyltransferase, SAM-dependent
b1824 (yobF)	DUF2527 family heat-induced protein
b1825 (yebO)	putative inner membrane protein
b1826 (mgrB)	regulatory peptide for PhoPQ, feedback inhibition
b1827 (kdgR)	KDG regulon transcriptional repressor
b1829 (htpX)	putative endopeptidase
b1830 (prc)	carboxy-terminal protease for penicillin-binding protein 3
b1831 (proQ)	RNA chaperone, putative ProP translation regulator
b1832 (msrC)	free methionine-(R)-sulfoxide reductase
b1833 (yebS)	inner membrane protein
b1834 (yebT)	MCE domain protein
b1835 (rsmF)	16S rRNA m(5)C1407 methyltransferase, SAM-dependent
b1837 (yebW)	uncharacterized protein

b1839 (yebY)	DUF2511 family protein
b1840 (yebZ)	inner membrane protein
b1841 (yobA)	CopC family protein
b1842 (holE)	DNA polymerase III, theta subunit
b1843 (yobB)	C-N hydrolase family protein
b1844 (exoX)	exodeoxyribonuclease 10; DNA exonuclease X
b1845 (ptrB)	protease II
b1846 (yebE)	DUF533 family inner membrane protein
b1847 (yebF)	extracellular Colicin M immunity family protein
b1848 (yebG)	DNA damage-inducible protein regulated by LexA
b1849 (purT)	phosphoribosylglycinamide formyltransferase 2
b1850 (eda)	multifunctional 2-keto-3-deoxygluconate 6-phosphate aldolase and 2-keto-4-hydroxyglutarate aldolase and oxaloacetate decarboxylase
b1851 (edd)	6-phosphogluconate dehydratase
b1852 (zwf)	glucose-6-phosphate 1-dehydrogenase
b1853 (yebK)	putative DNA-binding transcriptional regulator
b1854 (pykA)	pyruvate kinase II
b1855 (lpxM)	myristoyl-acyl carrier protein (ACP)-dependent acyltransferase
b1856 (mepM)	murein DD-endopeptidase, space-maker hydrolase, septation protein
b1857 (znuA)	zinc transporter subunit: periplasmic-binding component of ABC superfamily
b1858 (znuC)	zinc transporter subunit: ATP-binding component of ABC superfamily
b1859 (znuB)	zinc transporter subunit: membrane component of ABC superfamily
b1860 (ruvB)	ATP-dependent DNA helicase, component of RuvABC resolvasome
b1861 (ruvA)	component of RuvABC resolvasome, regulatory subunit
b1863 (ruvC)	component of RuvABC resolvasome, endonuclease
b1864 (yebC)	UPF0082 family protein
b1865 (nudB)	dihydroneopterin triphosphate pyrophosphatase
b1866 (aspS)	aspartyl-tRNA synthetase
b1869 (yecN)	MAPEG family inner membrane protein
b1870 (cmoA)	carboxy-SAM synthase
b1871 (cmoB)	tRNA (cmo5U34)-carboxymethyltransferase, carboxy-SAM-dependent
b1874 (cutC)	copper homeostasis protein
b1875 (yecM)	putative metal-binding enzyme
b1876 (argS)	arginyl-tRNA synthetase
b1897 (otsB)	trehalose-6-phosphate phosphatase, biosynthetic
b1900 (araG)	fused L-arabinose transporter subunits of ABC superfamily: ATP-binding components
b1901 (araF)	L-arabinose transporter subunit
b1902 (ftnB)	ferritin B, putative ferrous iron reservoir
b1904 (yecR)	lipoprotein, function unknown
b1905 (ftnA)	ferritin iron storage protein (cytoplasmic)
b1906 (yecH)	DUF2492 family protein
b1907 (tyrP)	tyrosine transporter
b1908 (yecA)	UPF0149 family protein
b1912 (pgsA)	phosphatidylglycerophosphate synthetase

b1913 (uvrC)	excinuclease UvrABC, endonuclease subunit
b1914 (uvrY)	response regulator in two-component regulatory system with BarA
b1915 (yecF)	DUF2594 family protein
b1917 (yecC)	putative ABC superfamily transporter ATP-binding subunit
b1918 (yecS)	ABC family putative inner membrane permease
b1919 (dcyD)	D-cysteine desulfhydrase, PLP-dependent
b1920 (fliY)	cystine transporter subunit
b1922 (fliA)	RNA polymerase, sigma 28 (sigma F) factor
b1925 (fliS)	flagellar protein potentiates polymerization
b1927 (amyA)	cytoplasmic alpha-amylase
b1928 (yedD)	lipoprotein
b1929 (yedE)	UPF0394 family sulfur transport domain-containing inner membrane protein
b1930 (yedF)	putative TusA family sulfurtransferase
b1937 (fliE)	flagellar basal-body component
b1952 (dsrB)	uncharacterized protein
b1953 (yodD)	uncharacterized protein
b1957 (yodC)	uncharacterized protein
b1958 (yedI)	DUF808 family inner membrane protein
b1959 (yedA)	amino acid exporter for phenylalanine, threonine
b1960 (vsr)	DNA mismatch endonuclease of very short patch repair
b1961 (dcm)	DNA cytosine methyltransferase
b1969 (yedW)	response regulator family protein
b1970 (hiuH)	hydroxyisourate hydrolase
b1971 (yedY)	membrane-anchored, periplasmic TMAO, DMSO reductase
b1972 (yedZ)	inner membrane heme subunit for periplasmic YedYZ reductase
b1973 (zinT)	zinc and cadmium binding protein, periplasmic
b1976 (mtfA)	anti-repressor for DgsA(Mlc)
b1983 (yeeN)	UPF0082 family protein
b1987 (cbl)	ssuEADCB/tauABCD operon transcriptional activator
b1992 (cobS)	cobalamin synthase
b2007 (yeeX)	UPF0265 family protein
b2014 (plaP)	putrescine importer, low affinity
b2016 (yeeZ)	putative epimerase
b2065 (dcd)	2'-deoxycytidine 5'-triphosphate deaminase
b2066 (udk)	uridine/cytidine kinase
b2075 (mdtB)	multidrug efflux system, subunit B
b2077 (mdtD)	putative arabinose efflux transporter
b2078 (baeS)	sensory histidine kinase in two-component regulatory system with BaeR
b2079 (baeR)	response regulator in two-component regulatory system with BaeS
b2080 (yegP)	UPF0339 family protein
b2081 (yegQ)	putative peptidase
b2086 (yegS)	phosphatidylglycerol kinase, metal-dependent
b2097 (fbaB)	fructose-bisphosphate aldolase class I
b2099 (yegU)	ADP-ribosylglycohydrolase family protein

b2100 (yegV)	putative kinase
b2101 (yegW)	putative DNA-binding transcriptional regulator
b2103 (thiD)	bifunctional hydroxy-methylpyrimidine kinase/hydroxy-phosphomethylpyrimidine kinase
b2104 (thiM)	hydoxyethylthiazole kinase
b2105 (rcnR)	transcriptional repressor of rcnA
b2107 (rcnB)	periplasmic modulator of Ni and Co efflux
b2113 (mrp)	antiporter inner membrane protein
b2124 (yehS)	DUF1456 family protein
b2125 (yehT)	putative response regulator in two-component system withYehU
b2126 (yehU)	inner membrane putative sensory kinase in two-component system with YehT
b2128 (yehW)	inner membrane putative ABC superfamily transporter permease
b2129 (yehX)	putative ABC superfamily transporter ATP-binding subunit
b2130 (yehY)	inner membrane putative ABC superfamily transporter permease
b2131 (osmF)	putative ABC superfamily transporter periplasmic-binding protein
b2132 (bglX)	beta-D-glucoside glucohydrolase, periplasmic
b2133 (dld)	D-lactate dehydrogenase, FAD-binding, NADH independent
b2134 (pbpG)	D-alanyl-D-alanine endopeptidase
b2135 (yohC)	Yip1 family inner membrane protein
b2136 (yohD)	DedA family inner membrane protein
b2141 (yohJ)	UPF0299 family inner membrane protein
b2142 (yohK)	LrgB family inner membrane protein
b2143 (cdd)	cytidine/deoxycytidine deaminase
b2144 (sanA)	vancomycin high temperature exclusion protein, DUF218 superfamily protein
b2145 (yeiS)	DUF2542 family protein
b2146 (preT)	dihydropyrimidine dehydrogenase, NADH-dependent, subunit N
b2147 (preA)	dihydropyrimidine dehydrogenase, NADH-dependent, subunit C
b2148 (mglC)	methyl-galactoside transporter subunit
b2149 (mglA)	fused methyl-galactoside transporter subunits of ABC superfamily: ATP-binding components
b2150 (mglB)	methyl-galactoside transporter subunit
b2151 (galS)	galactose- and fucose-inducible galactose regulon transcriptional isorepressor; mgl operon transcriptional repressor; autorepressor
b2152 (yeiB)	DUF418 family putative inner membrane protein
b2153 (folE)	GTP cyclohydrolase I
b2156 (lysP)	lysine transporter
b2157 (yeiE)	putative DNA-binding transcriptional regulator
b2158 (yeiH)	UPF0324 family inner membrane protein
b2159 (nfo)	endonuclease IV with intrinsic 3'-5' exonuclease activity
b2160 (yeiI)	putative kinase
b2165 (psuG)	pseudouridine 5'-phosphate glycosidase
b2167 (fruA)	fused fructose-specific PTS enzymes: IIBcomponent/IIC components
b2168 (fruK)	fructose-1-phosphate kinase
b2169 (fruB)	fused fructose-specific PTS enzymes: IIA component/HPr component

b2171 (yeiP)	elongation factor P-like protein
b2172 (yeiQ)	putative NAD-dependent D-mannonate oxidoreductase
b2173 (yeiR)	Zn-stimulated GTPase involved in zinc homeostasis; mutants are cadmium and EDTA sensitive; Zn(2+) binding protein
b2174 (lpxT)	lipid A 1-diphosphate synthase; undecaprenyl pyrophosphate:lipid A 1-phosphate phosphotransferase
b2175 (mepS)	murein DD-endopeptidase, space-maker hydrolase, mutational suppressor of prc thermosensitivity, outer membrane lipoprotein
b2176 (rtn)	resistance protein for phages lambda and N4, putative membrane-anchored cyclic-di-GMP phosphodiesterase
b2177 (yejA)	microcin C transporter YejABEF, periplasmic binding protein; ABC family
b2178 (yejB)	microcin C transporter YejABEF, permease subunit; ABC family
b2179 (yejE)	microcin C transporter YejABEF, permease subunit; ABC family
b2180 (yejF)	microcin C transporter, ATP-binding subunit; ABC family
b2181 (yejG)	uncharacterized protein
b2182 (bcr)	bicyclomycin/cysteine/sulfonamide efflux transporter
b2183 (rsuA)	16S rRNA pseudouridine(516) synthase
b2184 (yejH)	putative ATP-dependent DNA or RNA helicase
b2185 (rplY)	50S ribosomal subunit protein L25
b2186 (yejK)	spermidine nucleoid-associated protein
b2187 (yejL)	UPF0352 family protein
b2188 (yejM)	essential inner membrane DUF3413 domain-containing protein; lipid A production and membrane permeability factor
b2193 (narP)	response regulator in two-component regulatory system with NarQ or NarX
b2194 (ccmH)	heme lyase, CcmH subunit
b2195 (dsbE)	periplasmic thioredoxin of cytochrome c-type biogenesis
b2196 (ccmF)	heme lyase, CcmF subunit
b2197 (ccmE)	periplasmic heme chaperone
b2198 (ccmD)	cytochrome c biogenesis protein
b2199 (ccmC)	heme exporter subunit
b2200 (ccmB)	heme exporter subunit
b2201 (ccmA)	heme exporter subunit
b2202 (napC)	quinol dehydrogenase, electron source for NapAB
b2203 (napB)	nitrate reductase, small, cytochrome C550 subunit, periplasmic
b2204 (napH)	ferredoxin-type protein essential for electron transfer from ubiquinol to periplasmic nitrate reductase (NapAB)
b2205 (napG)	ferredoxin-type protein essential for electron transfer from ubiquinol to periplasmic nitrate reductase (NapAB)
b2206 (napA)	nitrate reductase, periplasmic, large subunit
b2207 (napD)	assembly protein for periplasmic nitrate reductase
b2208 (napF)	ferredoxin-type protein, role in electron transfer to periplasmic nitrate reductase NapA
b2209 (eco)	ecotin, a serine protease inhibitor
b2210 (mqo)	malate dehydrogenase, FAD/NAD(P)-binding domain
b2211 (yojI)	microcin J25 efflux pump, TolC-dependent; fused ABC transporter permease and ATP-binding components

b2212 (alkB)	oxidative demethylase of N1-methyladenine or N3-methylcytosine DNA lesions
b2213 (ada)	fused DNA-binding transcriptional dual regulator/O6-methylguanine-DNA methyltransferase
b2214 (apbE)	putative thiamine-synthetic flavin transferase lipoprotein
b2216 (rcsD)	phosphotransfer intermediate protein in two-component regulatory system with RcsBC
b2217 (rcsB)	response regulator in two-component regulatory system with RcsC and YojN
b2218 (rcsC)	hybrid sensory kinase in two-component regulatory system with RcsB and YojN
b2225 (yfaP)	DUF2135 family protein, putative host defense protein
b2231 (gyrA)	DNA gyrase (type II topoisomerase), subunit A
b2232 (ubiG)	bifunctional 3-demethylubiquinone-9 3-methyltransferase/2-octaprenyl-6-hydroxy phenol methylase
b2234 (nrdA)	ribonucleoside-diphosphate reductase 1, alpha subunit
b2235 (nrdB)	ribonucleoside-diphosphate reductase 1, beta subunit, ferritin-like protein
b2236 (yfaE)	ferredoxin involved with ribonucleotide reductase diferric-tyrosyl radical (Y*) cofactor maintenance
b2237 (inaA)	acid-inducible Kdo/WaaP family putative kinase
b2239 (glpQ)	periplasmic glycerophosphodiester phosphodiesterase
b2240 (glpT)	sn-glycerol-3-phosphate transporter
b2241 (glpA)	sn-glycerol-3-phosphate dehydrogenase (anaerobic), large subunit, FAD/NAD(P)-binding
b2242 (glpB)	sn-glycerol-3-phosphate dehydrogenase (anaerobic), membrane anchor subunit
b2243 (glpC)	anaerobic sn-glycerol-3-phosphate dehydrogenase, C subunit, 4Fe-4S iron-sulfur cluster
b2249 (yfaY)	inactive PncC family protein
b2250 (yfaZ)	outer membrane protein, putative porin
b2251 (nudI)	nucleoside triphosphatase
b2252 (ais)	putative LPS core heptose(II)-phosphate phosphatase
b2253 (arnB)	uridine 5'-(beta-1-threo-pentapyranosyl-4-ulose diphosphate) aminotransferase, PLP-dependent
b2254 (arnC)	undecaprenyl phosphate-L-Ara4FN transferase
b2255 (arnA)	fused UDP-L-Ara4N formyltransferase/UDP-GlcA C-4'-decarboxylase
b2256 (arnD)	undecaprenyl phosphate-alpha-L-ara4FN deformylase
b2257 (arnT)	4-amino-4-deoxy-L-arabinose transferase
b2258 (arnF)	undecaprenyl phosphate-alpha-L-ara4N exporter; flippase ArnEF subunit
b2259 (pmrD)	inactive two-component system connector protein
b2260 (menE)	O-succinylbenzoate-CoA ligase
b2261 (menC)	O-succinylbenzoyl-CoA synthase
b2262 (menB)	dihydroxynaphthoic acid synthetase
b2263 (menH)	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase
b2264 (menD)	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase; SEPHCHC synthase

b2265 (menF)	isochorismate synthase 2
b2266 (elaB)	DUF883 family protein, putative membrane-anchored ribosome-binding protein
b2267 (elaA)	putative acyl-CoA transferase
b2268 (rbn)	RNase BN, tRNA processing enzyme
b2272 (yfbM)	DUF1877 family protein
b2276 (nuoN)	NADH:ubiquinone oxidoreductase, membrane subunit N
b2277 (nuoM)	NADH:ubiquinone oxidoreductase, membrane subunit M
b2278 (nuoL)	NADH:ubiquinone oxidoreductase, membrane subunit L
b2279 (nuoK)	NADH:ubiquinone oxidoreductase, membrane subunit K
b2280 (nuoJ)	NADH:ubiquinone oxidoreductase, membrane subunit J
b2281 (nuoI)	NADH:ubiquinone oxidoreductase, chain I
b2282 (nuoH)	NADH:ubiquinone oxidoreductase, membrane subunit H
b2283 (nuoG)	NADH:ubiquinone oxidoreductase, chain G
b2284 (nuoF)	NADH:ubiquinone oxidoreductase, chain F
b2285 (nuoE)	NADH:ubiquinone oxidoreductase, chain E
b2286 (nuoC)	NADH:ubiquinone oxidoreductase, fused CD subunit
b2287 (nuoB)	NADH:ubiquinone oxidoreductase, chain B
b2288 (nuoA)	NADH:ubiquinone oxidoreductase, membrane subunit A
b2289 (lrhA)	transcriptional repressor of flagellar, motility and chemotaxis genes
b2290 (alaA)	valine-pyruvate aminotransferase 2
b2291 (yfbR)	5'-nucleotidase
b2292 (yfbS)	putative transporter
b2293 (yfbT)	sugar phosphatas
b2294 (yfbU)	UPF0304 family protein
b2295 (yfbV)	UPF0208 family inner membrane protein
b2296 (ackA)	acetate kinase A and propionate kinase 2
b2297 (pta)	phosphate acetyltransferase
b2298 (yfcC)	putative inner membrane transporter, C4-dicarboxylate anaerobic carrier family
b2299 (yfcD)	putative NUDIX hydrolase
b2300 (yfcE)	phosphodiesterase activity on bis-pNPP
b2301 (yfcF)	glutathione S-transferase
b2302 (yfcG)	GSH-dependent disulfide bond oxidoreductase
b2303 (folX)	D-erythro-7,8-dihydroneopterin triphosphate 2'-epimerase and dihydroneopterin aldolase
b2304 (yfcH)	putative NAD-dependent nucleotide-sugar epimerase
b2306 (hisP)	histidine/lysine/arginine/ornithine transporter subunit
b2307 (hisM)	histidine/lysine/arginine/ornithine transporter subunit
b2308 (hisQ)	histidine/lysine/arginine/ornithine transporter permease subunit
b2309 (hisJ)	histidine/lysine/arginine/ornithine transporter subunit
b2311 (ubiX)	3-octaprenyl-4-hydroxybenzoate carboxy-lyase
b2312 (purF)	amidophosphoribosyltransferase
b2313 (cvpA)	colicin V production membrane protein
b2314 (dedD)	membrane-anchored periplasmic protein involved in septation
b2315 (folC)	bifunctional folylpolyglutamate synthase/dihydrofolate synthase

b2316 (accD)	acetyl-CoA carboxylase, beta (carboxyltransferase) subunit
b2317 (dedA)	DedA family inner membrane protein
b2318 (truA)	tRNA pseudouridine(38-40) synthase
b2319 (usg)	putative semialdehyde dehydrogenase
b2320 (pdxB)	erythronate-4-phosphate dehydrogenase
b2321 (flk)	putative flagella assembly protein
b2322 (yfcJ)	putative arabinose efflux transporter
b2323 (fabB)	3-oxoacyl-[acyl-carrier-protein] synthase I
b2324 (mnmC)	fused 5-methylaminomethyl-2-thiouridine-forming enzyme methyltransferase and FAD-dependent demodification enzyme
b2325 (yfcL)	uncharacterized protein
b2326 (epmC)	Elongation Factor P Lys34 hydroxylase
b2327 (yfcA)	UPF0721 family inner membrane protein
b2328 (mepA)	murein DD-endopeptidase
b2329 (aroC)	chorismate synthase
b2330 (prmB)	N5-glutamine methyltransferase
b2331 (smrB)	putative DNA endonuclease
b2340 (sixA)	phosphohistidine phosphatase
b2341 (fadJ)	fused enoyl-CoA hydratase and epimerase and isomerase/3-hydroxyacyl-CoA dehydrogenase
b2342 (fadI)	beta-ketoacyl-CoA thiolase, anaerobic, subunit
b2343 (yfcZ)	UPF0381 family protein
b2344 (fadL)	long-chain fatty acid outer membrane transporter
b2346 (mlaA)	ABC transporter maintaining OM lipid asymmetry, OM lipoprotein component
b2347 (yfdC)	putative inner membrane protein
b2377 (yfdY)	DUF2545 family putative inner membrane protein
b2378 (lpxP)	palmitoleoyl-acyl carrier protein (ACP)-dependent acyltransferase
b2379 (alaC)	valine-pyruvate aminotransferase 3
b2381 (ypdB)	response regulator activating yhjX; pyruvate-responsive YpdAB two-component system
b2382 (ypdC)	putative DNA-binding protein
b2384 (ypdE)	aminopeptidase
b2386 (fryC)	putative enzyme IIC component of PTS
b2387 (fryB)	putative enzyme IIB component of PTS
b2388 (glk)	glucokinase
b2389 (yfeO)	putative ion channel protein
b2390 (ypeC)	DUF2502 family putative periplasmic protein
b2392 (mntH)	manganese/divalent cation transporter
b2393 (nupC)	nucleoside (except guanosine) transporter
b2398 (yfeC)	DUF1323 family putative DNA-binding protein
b2399 (yfeD)	DUF1323 family putative DNA-binding protein
b2400 (gltX)	glutamyl-tRNA synthetase
b2410 (yfeH)	putative inorganic ion transporter
b2411 (ligA)	DNA ligase, NAD(+)-dependent
b2412 (zipA)	FtsZ stabilizer

b2413 (cysZ)	EI24 family inner membrane protein; putative sulfate transporter
b2414 (cysK)	cysteine synthase A, O-acetylserine sulfhydrolase A subunit
b2415 (ptsH)	phosphohistidinoprotein-hexose phosphotransferase component of PTS system (Hpr)
b2417 (crr)	glucose-specific enzyme IIA component of PTS
b2418 (pdxK)	pyridoxal-pyridoxamine kinase/hydroxymethylpyrimidine kinase
b2421 (cysM)	cysteine synthase B (O-acetylserine sulfhydrolase B)
b2422 (cysA)	sulfate/thiosulfate transporter subunit
b2423 (cysW)	sulfate/thiosulfate ABC transporter subunit
b2424 (cysU)	sulfate/thiosulfate ABC transporter permease
b2425 (cysP)	thiosulfate-binding protein
b2426 (ucpA)	furfural resistance protein, putative short-chain oxidoreductase
b2428 (murQ)	N-acetylmuramic acid 6-phosphate (MurNAc-6-P) etherase
b2431 (yfeX)	porphyrinogen oxidase, cytoplasmic
b2432 (yfeY)	RpoE-regulated lipoprotein
b2433 (yfeZ)	inner membrane protein
b2434 (ypeA)	putative acyl-CoA transferase
b2435 (amiA)	N-acetylmuramoyl-l-alanine amidase I
b2436 (hemF)	coproporphyrinogen III oxidase
b2438 (eutK)	putative ethanol utilization carboxysome structural protein
b2439 (eutL)	putative ethanol utilization carboxysome structural protein
b2461 (eutP)	putative P-loop NTPase ethanolamine utilization protein
b2462 (eutS)	putative ethanol utilization carboxysome structural protein
b2463 (maeB)	malic enzyme: putative oxidoreductase/putative phosphotransacetylase
b2464 (talA)	transaldolase A
b2466 (ypfG)	DUF1176 family protein
b2467 (nudK)	GDP-mannose pyrophosphatase
b2468 (aegA)	putative oxidoreductase, FeS binding subunit/NAD/FAD-binding subunit
b2470 (acrD)	aminoglycoside/multidrug efflux system
b2471 (yffB)	putative ArsC family reductase
b2472 (dapE)	N-succinyl-diaminopimelate deacylase
b2473 (ypfH)	palmitoyl-CoA esterase activity, uncertain physiological substrate
b2474 (tmcA)	elongator methionine tRNA (ac4C34) acetyltransferase
b2475 (ypfJ)	putative neutral zinc metallopeptidase
b2476 (purC)	phosphoribosylaminoimidazole-succinocarboxamide synthetase
b2477 (bamC)	BamABCDE complex OM biogenesis lipoprotein
b2478 (dapA)	dihydrodipicolinate synthase
b2479 (gcvR)	transcriptional repressor, regulatory protein accessory to GcvA
b2480 (bcp)	peroxiredoxin; thiol peroxidase, thioredoxin-dependent
b2493 (yfgO)	putative UPF0118 family inner membrane permease
b2494 (bepA)	periplasmic metalloprotease and chaperone for OM protein maintenance and assembly
b2495 (yfgD)	putative oxidoreductase
b2496 (hda)	ATPase regulatory factor involved in DnaA inactivation

b2497 (uraA)	uracil permease
b2498 (upp)	uracil phosphoribosyltransferase
b2499 (purM)	phosphoribosylaminoimidazole synthetase
b2500 (purN)	phosphoribosylglycinamide formyltransferase 1
b2501 (ppk)	polyphosphate kinase, component of RNA degradosome
b2502 (ppx)	exopolyphosphatase
b2504 (yfgG)	uncharacterized protein
b2505 (yfgH)	outer membrane integrity lipoprotein
b2506 (yfgI)	nalidixic acid resistance protein, putative periplasmic protein
b2507 (guaA)	GMP synthetase (glutamine aminotransferase)
b2508 (guaB)	IMP dehydrogenase
b2511 (der)	GTPase; multicopy suppressor of ftsJ
b2512 (bamB)	BamABCDE complex OM biogenesis lipoprotein
b2513 (yfgM)	putative anti-RcsB factor
b2514 (hisS)	histidyl tRNA synthetase
b2515 (ispG)	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase
b2516 (rodZ)	MreB assembly cytoskeletal protein
b2517 (rlmN)	dual specificity 23S rRNA m(2)A2503, tRNA m(2)A37 methyltransferase, SAM-dependent
b2518 (ndk)	multifunctional nucleoside diphosphate kinase and apyrimidinic endonuclease and 3'-phosphodiesterase
b2522 (sseB)	rhodanase-like enzyme, sulfur transfer from thiosulfate
b2523 (pepB)	aminopeptidase B
b2524 (iscX)	Iron binding protein associated with IscS; putative molecular adaptor of IscS function
b2525 (fdx)	[2Fe-2S] ferredoxin
b2527 (hscB)	HscA co-chaperone, J domain-containing protein Hsc56; IscU-specific chaperone HscAB
b2528 (iscA)	FeS cluster assembly protein
b2529 (iscU)	iron-sulfur cluster assembly scaffold protein
b2530 (iscS)	cysteine desulfurase (tRNA sulfurtransferase), PLP-dependent
b2531 (iscR)	isc operon transcriptional repressor; suf operon transcriptional activator; oxidative stress- and iron starvation-inducible; autorepressor
b2533 (suhB)	inositol monophosphatase
b2534 (yfhR)	putative S9 family prolyl oligopeptidase
b2535 (csiE)	stationary phase inducible protein
b2536 (hcaT)	putative 3-phenylpropionic transporter
b2543 (yphA)	DoxX family inner membrane protein
b2544 (yphB)	mutarotase superfamily protein, YphB family
b2545 (yphC)	putative Zn-dependent NAD(P)-binding oxidoreductase
b2547 (yphE)	putative sugar transporter subunit of ABC superfamily, ATP-binding component
b2550 (yphH)	putative DNA-binding transcriptional regulator
b2551 (glyA)	serine hydroxymethyltransferase
b2552 (hmp)	fused nitric oxide dioxygenase/dihydropteridine reductase 2
b2555 (yfhG)	putative outer membrane protein modulating the QseEF response

b2556 (glrK)	sensor protein kinase regulating glmY sRNA in two-component system with response regulator GlrR
b2557 (purL)	phosphoribosylformyl-glycineamide synthetase
b2558 (mltF)	membrane-bound lytic transglycosylase F, murein hydrolase
b2559 (tadA)	tRNA-specific adenosine deaminase
b2560 (pgpC)	phosphatidylglycerophosphatase C, membrane bound
b2561 (yfhH)	putative DNA-binding transcriptional regulator
b2562 (yfhL)	putative 4Fe-4S cluster-containing protein
b2563 (acpS)	holo-[acyl-carrier-protein] synthase 1
b2564 (pdxJ)	pyridoxine 5'-phosphate synthase
b2565 (recO)	gap repair protein
b2566 (era)	membrane-associated, 16S rRNA-binding GTPase
b2567 (rnc)	RNase III
b2568 (lepB)	leader peptidase (signal peptidase I)
b2569 (lepA)	back-translocating elongation factor EF4, GTPase
b2570 (rseC)	SoxR iron-sulfur cluster reduction factor component; with RsxABCDEG
b2571 (rseB)	anti-sigma E factor, binds RseA
b2572 (rseA)	anti-sigma factor
b2573 (rpoE)	RNA polymerase sigma E factor
b2575 (trmN)	tRNA1(Val) (adenine(37)-N6)-methyltransferase
b2576 (srmB)	ATP-dependent RNA helicase
b2577 (yfiE)	putative DNA-binding transcriptional regulator
b2578 (eamB)	cysteine and O-acetylserine exporter
b2580 (ung)	uracil-DNA-glycosylase
b2581 (yfiF)	putative methyltransferase
b2582 (trxC)	thioredoxin 2
b2583 (yfiP)	DTW domain protein
b2584 (pka)	protein lysine acetyltransferase
b2585 (pssA)	phosphatidylserine synthase (CDP-diacylglycerol-serine O-phosphatidyltransferase)
b2586 (yfiM)	putative lipoprotein
b2587 (kgtP)	alpha-ketoglutarate transporter
b2592 (clpB)	protein disaggregation chaperone
b2593 (yfiH)	UPF0124 family protein
b2594 (rluD)	23S rRNA pseudouridine(1911,1915,1917) synthase
b2595 (bamD)	BamABCDE complex OM biogenesis lipoprotein
b2597 (raiA)	cold shock protein associated with 30S ribosomal subunit
b2598 (pheL)	pheA gene leader peptide
b2599 (pheA)	chorismate mutase and prephenate dehydratase, P-protein
b2600 (tyrA)	fused chorismate mutase T/prephenate dehydrogenase
b2601 (aroF)	3-deoxy-D-arabino-heptulosonate-7-phosphate synthase, tyrosine-repressible
b2602 (yfiL)	lipoprotein
b2603 (yfiR)	putative periplasmic inhibitor of YfiN activity
b2605 (yfiB)	OM lipoprotein putative positive effector of YfiN activity
b2606 (rplS)	50S ribosomal subunit protein L19

b2607 (trmD)	tRNA m(1)G37 methyltransferase, SAM-dependent
b2608 (rimM)	16S rRNA processing protein
b2609 (rpsP)	30S ribosomal subunit protein S16
b2610 (ffh)	Signal Recognition Particle (SRP) component with 4.5S RNA (ffs)
b2611 (ypjD)	cytochrome c assembly protein family inner membrane protein
b2615 (nadK)	NAD kinase
b2616 (recN)	recombination and repair protein
b2617 (bamE)	lipoprotein component of BamABCDE OM biogenesis complex
b2618 (ratB)	UPF0125 family protein
b2619 (ratA)	toxic UPF0083 family protein inhibitor of 70S ribosome formation
b2620 (smpB)	trans-translation protein
b2664 (csiR)	transcriptional repressor of csiD
b2665 (ygaU)	uncharacterized protein
b2666 (yqaE)	cyaR sRNA-regulated protein
b2667 (ygaV)	tributyltin-inducible repressor of ygaVP
b2668 (ygaP)	DUF2892 family inner membrane rhodanese
b2669 (stpA)	DNA binding protein, nucleoid-associated
b2670 (alaE)	alanine exporter, alanine-inducible, stress-responsive
b2671 (ygaC)	uncharacterized protein
b2672 (ygaM)	DUF883 family protein, putative membrane-anchored ribosome-binding protein
b2673 (nrdH)	hydrogen donor for NrdEF electron transport system; glutaredoxin-like protein
b2675 (nrdE)	ribonucleoside-diphosphate reductase 2, alpha subunit
b2676 (nrdF)	ribonucleoside-diphosphate reductase 2, beta subunit, ferritin-like protein
b2677 (proV)	glycine betaine transporter subunit
b2678 (proW)	glycine betaine transporter subunit
b2679 (proX)	glycine betaine transporter subunit
b2682 (ygaZ)	putative L-valine exporter, norvaline resistance protein
b2683 (ygaH)	putative L-valine exporter, norvaline resistance protein
b2684 (mprA)	transcriptional repressor of microcin B17 synthesis and multidrug efflux
b2685 (emrA)	multidrug efflux system
b2686 (emrB)	multidrug efflux system protein
b2687 (luxS)	S-ribosylhomocysteine lyase
b2688 (gshA)	glutamate-cysteine ligase
b2689 (yqaA)	COG1238 family inner membrane protein
b2690 (yqaB)	fructose-1-P and 6-phosphogluconate phosphatase
b2696 (csrA)	pleiotropic regulatory protein for carbon source metabolism
b2697 (alaS)	alanyl-tRNA synthetase
b2698 (recX)	regulatory protein for RecA
b2699 (recA)	DNA recombination and repair protein; ssDNA-dependent ATPase; synaptase; ssDNA and dsDNA binding protein forming filaments; ATP-dependent homologous DNA strand exchanger; recombinase A; LexA autocleavage cofactor
b2700 (pncC)	nicotinamide-nucleotide amidohydrolase; NMN amidohydrolase

b2701 (mltB)	membrane-bound lytic murein transglycosylase B
b2708 (srlQ)	D-arabinose 5-phosphate isomerase
b2709 (norR)	anaerobic nitric oxide reductase DNA-binding transcriptional activator
b2710 (norV)	anaerobic nitric oxide reductase flavorubredoxin
b2711 (norW)	NADH:flavorubredoxin oxidoreductase
b2713 (hydN)	formate dehydrogenase-H, [4Fe-4S] ferredoxin subunit
b2722 (hycD)	hydrogenase 3, membrane subunit
b2723 (hycC)	hydrogenase 3, membrane subunit
b2724 (hycB)	hydrogenase 3, Fe-S subunit
b2725 (hycA)	regulator of the transcriptional regulator FhlA
b2726 (hypA)	protein involved in nickel insertion into hydrogenases 3
b2727 (hypB)	GTP hydrolase involved in nickel liganding into hydrogenases
b2728 (hypC)	hydrogenase maturation protein
b2729 (hypD)	hydrogenase maturation protein
b2730 (hypE)	carbamoyl dehydratase, hydrogenases 1,2,3 maturation protein
b2733 (mutS)	methyl-directed mismatch repair protein
b2741 (rpoS)	RNA polymerase, sigma S (sigma 38) factor
b2742 (nlpD)	activator of AmiC murein hydrolase activity, lipoprotein
b2743 (pcm)	L-isoaspartate protein carboxylmethyltransferase type II
b2744 (umpG)	broad specificity 5'(3')-nucleotidase and polyphosphatase
b2745 (truD)	tRNA(Glu) pseudouridine(13) synthase
b2746 (ispF)	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
b2747 (ispD)	4-diphosphocytidyl-2C-methyl-D-erythritol synthase
b2748 (ftsB)	cell division protein
b2749 (ygbE)	DUF3561 family inner membrane protein
b2750 (cysC)	adenosine 5'-phosphosulfate kinase
b2751 (cysN)	sulfate adenylyltransferase, subunit 1
b2752 (cysD)	sulfate adenylyltransferase, subunit 2
b2753 (iap)	aminopeptidase in alkaline phosphatase isozyme conversion
b2762 (cysH)	phosphoadenosine phosphosulfate reductase; PAPS reductase, thioredoxin dependent
b2763 (cysI)	sulfite reductase, beta subunit, NAD(P)-binding, heme-binding
b2764 (cysJ)	sulfite reductase, alpha subunit, flavoprotein
b2765 (queD)	6-pyruvoyl tetrahydrobiopterin synthase (PTPS)
b2777 (queE)	7-carboxy-7-deazaguanine synthase; queosine biosynthesis
b2779 (eno)	enolase
b2780 (pyrG)	CTP synthetase
b2781 (mazG)	nucleoside triphosphate pyrophosphohydrolase
b2784 (relA)	(p)ppGpp synthetase I/GTP pyrophosphokinase
b2785 (rlmD)	23S rRNA m(5)U1939 methyltransferase, SAM-dependent
b2786 (barA)	hybrid sensory histidine kinase, in two-component regulatory system with UvrY
b2790 (yqcA)	short-chain flavodoxin, FMN-binding
b2791 (truC)	tRNA(Ile1,Asp) pseudouridine(65) synthase
b2792 (yqcC)	DUF446 family protein
b2793 (syd)	SecY-interacting protein

b2794 (queF)	7-cyano-7-deazaguanine reductase (NADPH-dependent)
b2795 (ygdH)	UPF0717 family protein
b2796 (sdaC)	putative serine transporter
b2798 (ygdG)	Ssb-binding protein, misidentified as ExoIX
b2799 (fucO)	L-1,2-propanediol oxidoreductase
b2800 (fucA)	L-fuculose-1-phosphate aldolase
b2802 (fucI)	L-fucose isomerase
b2803 (fucK)	L-fuculokinase
b2804 (fucU)	L-fucose mutarotase
b2805 (fucR)	l-fucose operon activator
b2806 (rlmM)	23S rRNA C2498 2'-O-ribose methyltransferase, SAM-dependent
b2807 (ygdD)	UPF0382 family inner membrane protein
b2808 (gcvA)	glycine cleavage system transcriptional activator; autorepressor
b2809 (ygdI)	DUF903 family verified lipoprotein
b2811 (csdE)	CsdA-binding activator; Fe-S protein
b2812 (tcdA)	tRNA threonylcarbamoyladenosine dehydratase; sulfur acceptor for CsdA
b2813 (mltA)	membrane-bound lytic murein transglycosylase A
b2817 (amiC)	N-acetylmuramoyl-L-alanine amidase
b2818 (argA)	fused acetylglutamate kinase homolog (inactive)/amino acid N-acetyltransferase
b2819 (recD)	exonuclease V (RecBCD complex), alpha chain
b2820 (recB)	exonuclease V (RecBCD complex), beta subunit
b2821 (ptrA)	protease III
b2822 (recC)	exonuclease V (RecBCD complex), gamma chain
b2823 (ppdC)	putative prepilin peptidase-dependent protein
b2824 (ygdB)	DUF2509 family protein
b2825 (ppdB)	putative prepilin peptidase-dependent protein
b2826 (ppdA)	putative prepilin peptidase-dependent protein
b2827 (thyA)	thymidylate synthetase
b2828 (lgt)	phosphatidylglycerol-prolipoprotein diacylglyceryl transferase
b2829 (ptsP)	fused PTS enzyme: PEP-protein phosphotransferase (enzyme I)/GAF domain containing protein
b2830 (rppH)	RNA pyrophosphohydrolase
b2831 (mutH)	methyl-directed mismatch repair protein
b2832 (ygdQ)	UPF0053 family inner membrane protein
b2833 (ygdR)	DUF903 family verified lipoprotein
b2834 (tas)	putative NADP(H)-dependent aldo-keto reductase
b2835 (lplT)	lysophospholipid transporter
b2836 (aas)	fused 2-acylglycerophospho-ethanolamine acyl transferase/acyl-acyl carrier protein synthetase
b2837 (galR)	galactose-inducible d-galactose regulon transcriptional repressor; autorepressor
b2838 (lysA)	diaminopimelate decarboxylase, PLP-binding
b2839 (lysR)	transcriptional activator of lysA; autorepressor
b2840 (ygeA)	Asp/Glu_racemase family protein

b2841 (araE)	arabinose transporter
b2842 (kduD)	hexuronate dehydrogenase; hexuronate utilization in high osmolarity
b2843 (kduI)	hexuronate isomerase; hexuronate utilization in high osmolarity
b2844 (yqeF)	short chain acyltransferase
b2889 (idi)	isopentenyl diphosphate isomerase
b2892 (recJ)	ssDNA exonuclease, 5' --> 3'-specific
b2893 (dsbC)	protein disulfide isomerase II
b2894 (xerD)	site-specific tyrosine recombinase
b2895 (fldB)	flavodoxin 2
b2896 (cptA)	toxin of CptAB toxin-antitoxin pair
b2897 (sdhE)	flavinator of succinate dehydrogenase; antitoxin of CptAB toxin-antitoxin pair
b2898 (ygfZ)	iron-sulfur cluster repair protein, plumbagin resistance
b2899 (yqfA)	hemolysin III family HylIII inner membrane protein
b2900 (yqfB)	UPF0267 family protein
b2901 (bglA)	6-phospho-beta-glucosidase A
b2903 (gcvP)	glycine decarboxylase, PLP-dependent, subunit (protein P) of glycine cleavage complex
b2904 (gcvH)	glycine cleavage complex lipoylprotein
b2905 (gcvT)	aminomethyltransferase, tetrahydrofolate-dependent, subunit (T protein) of glycine cleavage complex
b2906 (ubiI)	2-octaprenylphenol hydroxylase, FAD-dependent
b2907 (ubiH)	2-octaprenyl-6-methoxyphenol hydroxylase, FAD/NAD(P)-binding
b2908 (pepP)	proline aminopeptidase P II
b2909 (ygfB)	UPF0149 family protein
b2910 (zapA)	FtsZ stabilizer
b2912 (fau)	5-formyltetrahydrofolate cyclo-ligase family protein
b2913 (serA)	D-3-phosphoglycerate dehydrogenase
b2914 (rpiA)	ribose 5-phosphate isomerase, constitutive
b2916 (argP)	transcriptional regulator for arginine transport and DNA replication genes; replication initiation inhibitor
b2922 (yggE)	oxidative stress defense protein
b2923 (argO)	arginine transporter
b2925 (fbaA)	fructose-bisphosphate aldolase, class II
b2926 (pgk)	phosphoglycerate kinase
b2927 (epd)	D-erythrose 4-phosphate dehydrogenase
b2935 (tktA)	transketolase 1, thiamine triphosphate-binding
b2936 (loiP)	Phe-Phe periplasmic metalloprotease, OM lipoprotein; low salt-inducible; heat shock protein that binds Era
b2937 (speB)	agmatinase
b2938 (speA)	biosynthetic arginine decarboxylase, PLP-binding
b2939 (yqgB)	uncharacterized protein
b2940 (yqgC)	uncharacterized protein
b2942 (metK)	S-adenosylmethionine synthetase
b2943 (galP)	D-galactose transporter
b2944 (yggI)	Zn-dependent metalloprotease-related protein

b2945 (endA)	DNA-specific endonuclease I
b2946 (rsmE)	16S rRNA m(3)U1498 methyltransferase, SAM-dependent
b2947 (gshB)	glutathione synthetase
b2948 (yqgE)	uncharacterized protein
b2949 (yqgF)	putative Holliday junction resolvase
b2950 (yggR)	putative PilT family AAA+ ATPase
b2951 (yggS)	UPF0001 family protein, PLP-binding
b2952 (yggT)	putative inner membrane protein; compensates for loss in K+ uptake
b2953 (yggU)	UPF0235 family protein
b2954 (rdgB)	dITP/XTP pyrophosphatase
b2955 (yggW)	HemN family putative oxidoreductase
b2957 (ansB)	periplasmic L-asparaginase 2
b2958 (yggN)	DUF2884 family putative periplasmic protein
b2959 (yggL)	DUF469 family protein
b2960 (trmI)	tRNA m(7)G46 methyltransferase, SAM-dependent
b2961 (mutY)	adenine DNA glycosylase
b2962 (yggX)	protein that protects iron-sulfur proteins against oxidative damage
b2963 (mltC)	membrane-bound lytic murein transglycosylase C
b2964 (nupG)	nucleoside transporter
b2966 (yqgA)	DUF554 family putative inner membrane protein
b2988 (gss)	fused glutathionylspermidine amidase/glutathionylspermidine synthetase
b2989 (yghU)	putative S-transferase
b2990 (hybG)	hydrogenase 2 accessory protein
b2991 (hybF)	protein involved with the maturation of hydrogenases 1 and 2
b2992 (hybE)	hydrogenase 2-specific chaperone
b2993 (hybD)	maturation protease for hydrogenase 2
b2994 (hybC)	hydrogenase 2, large subunit
b2995 (hybB)	putative hydrogenase 2 cytochrome b type component
b2996 (hybA)	hydrogenase 2 4Fe-4S ferredoxin-type component
b2997 (hybO)	hydrogenase 2, small subunit
b2998 (yghW)	DUF2623 family protein
b3001 (gpr)	L-glyceraldehyde 3-phosphate reductase
b3002 (yqhA)	UPF0114 family putative inner membrane protein
b3005 (exbD)	membrane spanning protein in TonB-ExbB-ExbD complex
b3006 (exbB)	membrane spanning protein in TonB-ExbB-ExbD complex
b3008 (metC)	cystathionine beta-lyase, PLP-dependent
b3010 (yqhC)	transcriptional activator of yqhD
b3011 (yqhD)	aldehyde reductase, NADPH-dependent
b3012 (dkgA)	2,5-diketo-D-gluconate reductase A
b3014 (yqhH)	outer membrane lipoprotein, Lpp paralog
b3017 (ftsP)	septal ring component that protects the divisome from stress; multicopy suppressor of ftsI(Ts)
b3018 (plsC)	1-acyl-sn-glycerol-3-phosphate acyltransferase
b3019 (parC)	DNA topoisomerase IV, subunit A
b3023 (ygiV)	transcriptional repressor for mcbR biofilm gene

b3024 (ygiW)	hydrogen peroxide and cadmium resistance periplasmic protein; stress-induced OB-fold protein
b3025 (qseB)	quorum sensing DNA-binding response regulator in two-component regulatory system with QseC
b3026 (qseC)	quorum sensing sensory histidine kinase in two-component regulatory system with QseB
b3028 (mdaB)	NADPH quinone reductase
b3029 (ygiN)	quinol monooxygenase
b3031 (yqiA)	acyl CoA esterase
b3032 (cpdA)	3',5' cAMP phosphodiesterase
b3033 (yqiB)	DUF1249 protein YqiB
b3034 (nudF)	ADP-ribose pyrophosphatase
b3035 (tolC)	transport channel
b3037 (ygiB)	DUF1190 family protein
b3038 (ygiC)	ATP-Grasp family ATPase
b3039 (ygiD)	4,5-DOPA-extradiol-dioxygenase
b3040 (zupT)	zinc transporter
b3041 (ribB)	3,4-dihydroxy-2-butanone-4-phosphate synthase
b3049 (glgS)	motility and biofilm regulator
b3052 (hldE)	fused heptose 7-phosphate kinase/heptose 1-phosphate adenyltransferase
b3053 (glnE)	fused deadenylyltransferase/adenylyltransferase for glutamine synthetase
b3054 (ygiF)	inorganic triphosphatase
b3055 (ygiM)	SH3 domain protein
b3056 (cca)	fused tRNA nucleotidyl transferase/2'3'-cyclic phosphodiesterase/2'nucleotidase and phosphatase
b3057 (bacA)	undecaprenyl pyrophosphate phosphatase
b3058 (folB)	bifunctional dihydroneopterin aldolase/dihydroneopterin triphosphate 2'-epimerase
b3059 (plsY)	putative glycerol-3-phosphate acyltransferase
b3061 (ttdA)	L-tartrate dehydratase, alpha subunit
b3062 (ttdB)	L-tartrate dehydratase, beta subunit
b3063 (ttdT)	L-tartrate/succinate antiporte
b3064 (tsaD)	tRNA(ANN) t(6)A37 threonylcarbamoyladenosine modification protein; glycation binding protein
b3065 (rpsU)	30S ribosomal subunit protein S21
b3066 (dnaG)	DNA primase
b3067 (rpoD)	RNA polymerase, sigma 70 (sigma D) factor
b3068 (mug)	G/U mismatch-specific DNA glycosylase; xanthine DNA glycosylase
b3070 (yqjH)	putative siderophore interacting protein
b3071 (yqjI)	PadR family putative transcriptional regulator
b3072 (aer)	fused signal transducer for aerotaxis sensory component/methyl accepting chemotaxis component
b3073 (patA)	putrescine:2-oxoglutaric acid aminotransferase, PLP-dependent
b3074 (ygjH)	putative tRNA binding protein; putative tRNA corner chaperone
b3075 (ebgR)	transcriptional repressor

b3076 (ebgA)	evolved beta-D-galactosidase, alpha subunit
b3077 (ebgC)	evolved beta-D-galactosidase, beta subunit; cupin superfamily
b3081 (fadH)	2,4-dienoyl-CoA reductase, NADH and FMN-linked
b3084 (rlmG)	23S rRNA m(2)G1835 methyltransferase, SAM-dependent
b3085 (ygjP)	putative metal dependent hydrolase
b3087 (ygjR)	putative NAD(P)-dependent dehydrogenase
b3088 (alx)	putative membrane-bound redox modulator
b3089 (sstT)	sodium:serine/threonine symporter
b3090 (ygjV)	Imp-YgjV family inner membrane protein
b3091 (uxaA)	altronate hydrolase
b3092 (uxaC)	uronate isomerase
b3093 (exuT)	hexuronate transporter
b3094 (exuR)	hexuronate regulon transcriptional repressor; autorepressor
b3095 (yqjA)	general envelope maintenance protein; DedA family inner membrane protein
b3096 (mzrA)	modulator of EnvZ/OmpR regulon
b3097 (yqjC)	DUF1090 family putative periplasmic protein
b3098 (yqjD)	membrane-anchored ribosome-binding protein
b3099 (yqjE)	DUF1469 family inner membrane protein
b3100 (yqjK)	uncharacterized protein
b3101 (yqjF)	putative quinol oxidase subunit
b3102 (yqjG)	putative S-transferase
b3105 (yhaJ)	LysR family putative transcriptional regulator
b3106 (yhaK)	redox-sensitive bicupin
b3107 (yhaL)	uncharacterized protein
b3113 (tdcF)	putative reactive intermediate deaminase
b3115 (tdcD)	propionate kinase/acetate kinase C, anaerobic
b3116 (tdcC)	L-threonine/L-serine transporter
b3117 (tdcB)	L-threonine dehydratase, catabolic
b3118 (tdcA)	tdc operon transcriptional activator
b3119 (tdcR)	L-threonine dehydratase operon activator protein
b3124 (garK)	glycerate kinase I
b3125 (garR)	tartronate semialdehyde reductase
b3126 (garL)	alpha-dehydro-beta-deoxy-D-glucarate aldolase
b3127 (garP)	putative (D)-galactarate transporter
b3147 (lpoA)	OM lipoprotein stimulator of MrcA transpeptidase
b3148 (yraN)	UPF0102 family protein
b3149 (diaA)	DnaA initiator-associating factor for replication initiation
b3150 (yraP)	outer membrane lipoprotein
b3151 (yraQ)	putative inner membrane permease
b3152 (yraR)	putative nucleoside-diphosphate-sugar epimerase
b3155 (yhbQ)	GIY-YIG nuclease superfamily protein
b3156 (yhbS)	putative acyl-CoA transferase
b3157 (yhbT)	SCP-2 sterol transfer family protein
b3158 (yhbU)	U32 peptidase family protein
b3159 (yhbV)	U32 peptidase family protein

b3160 (yhbW)	putative luciferase-like monooxygenase
b3161 (mtr)	tryptophan transporter of high affinity
b3162 (deaD)	ATP-dependent RNA helicase
b3163 (nlpI)	lipoprotein involved in osmotic sensitivity and filamentation
b3164 (pnp)	polynucleotide phosphorylase/polyadenylase
b3165 (rpsO)	30S ribosomal subunit protein S15
b3166 (truB)	tRNA pseudouridine synthase B: tRNA pseudouridine(55) synthase and putative tmRNA pseudouridine(342) synthase
b3167 (rbfA)	30s ribosome binding factor
b3168 (infB)	translation initiation factor IF-2
b3169 (nusA)	transcription termination/antitermination L factor
b3170 (rimP)	ribosome maturation factor for 30S subunits
b3172 (argG)	argininosuccinate synthetase
b3175 (secG)	preprotein translocase membrane subunit
b3176 (glmM)	phosphoglucosamine mutase
b3177 (folP)	7,8-dihydropteroate synthase
b3178 (ftsH)	protease, ATP-dependent zinc-metallo
b3179 (rlmE)	23S rRNA U2552 2'-O-ribose methyltransferase, SAM-dependent
b3180 (yhbY)	RNA binding protein associated with pre-50S ribosomal subunits
b3181 (greA)	transcript cleavage factor
b3182 (dacB)	D-alanyl-D-alanine carboxypeptidase
b3183 (obgE)	GTPase involved in cell partioning and DNA repair
b3184 (yhbE)	EamA family inner membrane putative transporter
b3185 (rpmA)	50S ribosomal subunit protein L27
b3186 (rplU)	50S ribosomal subunit protein L21
b3187 (ispB)	octaprenyl diphosphate synthase
b3188 (sfsB)	malPQ operon transcriptional activator
b3189 (murA)	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
b3190 (ibaG)	acid stress protein; putative transcriptional regulator, BolA family
b3191 (mlaB)	ABC transporter maintaining OM lipid asymmetry, cytoplasmic STAS component
b3192 (mlaC)	ABC transporter maintaining OM lipid asymmetry, periplasmic binding protein
b3193 (mlaD)	ABC transporter maintaining OM lipid asymmetry, anchored periplasmic binding protein
b3194 (mlaE)	ABC transporter maintaining OM lipid asymmetry, inner membrane permease protein
b3195 (mlaF)	ABC transporter maintaining OM lipid asymmetry, ATP-binding protein
b3196 (yrbG)	putative calcium/sodium:proton antiporter
b3197 (kdsD)	D-arabinose 5-phosphate isomerase
b3198 (kdsC)	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase
b3199 (lptC)	lipopolysaccharide export, IM-tethered periplasmic protein of the LptBFGC export complex
b3200 (lptA)	periplasmic LPS-binding protein
b3201 (lptB)	lipopolysaccharide export ABC transporter ATP-binding protein of the LptBFGC export complex

b3202 (rpoN)	RNA polymerase, sigma 54 (sigma N) factor
b3203 (hpf)	ribosome hibernation promoting factor HPF; stabilizes 70S dimers (100S)
b3204 (ptsN)	sugar-specific enzyme IIA component of PTS
b3205 (yhbJ)	adaptor protein RapZ for GlmZ/GlmY sRNA decay; glucosamine-6-phosphate regulated; NTPase
b3206 (npr)	phosphohistidinoprotein-hexose phosphotransferase component of N-regulated PTS system (Npr)
b3207 (yrbL)	Mg(2+)-starvation-stimulated protein
b3208 (mtgA)	biosynthetic peptidoglycan transglycosylase
b3209 (elbB)	isoprenoid biosynthesis protein with amidotransferase-like domain
b3210 (arcB)	aerobic respiration control sensor histidine protein kinase, cognate to two-component response regulators ArcA and RssB
b3211 (yhcC)	putative Fe-S oxidoreductase, Radical SAM superfamily protein
b3212 (gltB)	glutamate synthase, large subunit
b3213 (gltD)	glutamate synthase, 4Fe-4S protein, small subunit
b3221 (yhcH)	DUF386 family protein, cupin superfamily
b3222 (nanK)	N-acetylmannosamine kinase
b3223 (nanE)	putative N-acetylmannosamine-6-P epimerase
b3224 (nanT)	sialic acid transporter
b3225 (nanA)	N-acetylneuraminate lyase
b3226 (nanR)	transcriptional repressor of the nan operon, induced by sialic acid
b3228 (sspB)	ClpXP protease specificity enhancing factor
b3229 (sspA)	stringent starvation protein A, phage P1 late gene activator, RNAP-associated acid-resistance protein, inactive glutathione S-transferase homolog
b3230 (rpsI)	30S ribosomal subunit protein S9
b3231 (rplM)	50S ribosomal subunit protein L13
b3232 (yhcM)	putative AFG1-like family P-loop ATPase
b3233 (yhcB)	DUF1043 family inner membrane-anchored protein
b3234 (degQ)	serine endoprotease, periplasmic
b3235 (degS)	serine endoprotease, periplasmic
b3236 (mdh)	malate dehydrogenase, NAD(P)-binding
b3237 (argR)	l-arginine-responsive arginine metabolism regulon transcriptional regulator
b3238 (yhcN)	cadmium and peroxide resistance protein, stress-induced
b3239 (yhcO)	putative barnase inhibitor
b3240 (aaeB)	p-hydroxybenzoic acid efflux system component
b3241 (aaeA)	p-hydroxybenzoic acid efflux system component
b3242 (aaeX)	DUF1656 family putative inner membrane efflux pump associated protein
b3243 (aaeR)	transcriptional regulator for aaeXAB operon
b3244 (tldD)	putative peptidase
b3247 (rng)	ribonuclease G
b3248 (yhdE)	Maf-like protein
b3249 (mreD)	cell wall structural complex MreBCD transmembrane component MreD

b3250 (mreC)	cell wall structural complex MreBCD transmembrane component MreC
b3251 (mreB)	cell wall structural complex MreBCD, actin-like component MreB
b3252 (csrD)	targeting factor for csrBC sRNA degradation
b3253 (acuI)	putative acryloyl-CoA reductase
b3255 (accB)	acetyl CoA carboxylase, BCCP subunit
b3256 (accC)	acetyl-CoA carboxylase, biotin carboxylase subunit
b3257 (yhdT)	DUF997 family putative inner membrane protein
b3258 (panF)	pantothenate:sodium symporter
b3259 (prmA)	methyltransferase for 50S ribosomal subunit protein L11
b3260 (dusB)	tRNA-dihydrouridine synthase B
b3261 (fis)	global DNA-binding transcriptional dual regulator
b3262 (yhdJ)	DNA adenine methyltransferase, SAM-dependent
b3263 (yhdU)	putative membrane protein
b3279 (yrdA)	bacterial transferase hexapeptide domain protein
b3280 (yrdB)	DUF1488 family protein
b3281 (aroE)	dehydroshikimate reductase, NAD(P)-binding
b3282 (tsaC)	tRNA(ANN) t(6)A37 threonylcarbamoyladenosine modification protein, threonine-dependent ADP-forming ATPase
b3283 (yrdD)	putative DNA topoisomerase
b3284 (smg)	DUF494 family putative periplasmic protein
b3288 (fmt)	10-formyltetrahydrofolate:L-methionyl-tRNA(fMet) N-formyltransferase
b3289 (rsmB)	16S rRNA m(5)C967 methyltransferase, SAM-dependent
b3290 (trkA)	NAD-binding component of TrK potassium transporter
b3294 (rplQ)	50S ribosomal subunit protein L17
b3295 (rpoA)	RNA polymerase, alpha subunit
b3296 (rpsD)	30S ribosomal subunit protein S4
b3297 (rpsK)	30S ribosomal subunit protein S11
b3298 (rpsM)	30S ribosomal subunit protein S13
b3299 (rpmJ)	50S ribosomal subunit protein L36
b3300 (secY)	preprotein translocase membrane subunit
b3301 (rplO)	50S ribosomal subunit protein L15
b3302 (rpmD)	50S ribosomal subunit protein L30
b3303 (rpsE)	30S ribosomal subunit protein S5
b3304 (rplR)	50S ribosomal subunit protein L18
b3305 (rplF)	50S ribosomal subunit protein L6
b3306 (rpsH)	30S ribosomal subunit protein S8
b3307 (rpsN)	30S ribosomal subunit protein S14
b3308 (rplE)	50S ribosomal subunit protein L5
b3309 (rplX)	50S ribosomal subunit protein L24
b3310 (rplN)	50S ribosomal subunit protein L14
b3311 (rpsQ)	30S ribosomal subunit protein S17
b3312 (rpmC)	50S ribosomal subunit protein L29
b3313 (rplP)	50S ribosomal subunit protein L16
b3314 (rpsC)	30S ribosomal subunit protein S3

b3315 (rplV)	50S ribosomal subunit protein L22
b3316 (rpsS)	30S ribosomal subunit protein S19
b3317 (rplB)	50S ribosomal subunit protein L2
b3318 (rplW)	50S ribosomal subunit protein L23
b3319 (rplD)	50S ribosomal subunit protein L4
b3320 (rplC)	50S ribosomal subunit protein L3
b3321 (rpsJ)	30S ribosomal subunit protein S10
b3340 (fusA)	protein chain elongation factor EF-G, GTP-binding
b3342 (rpsL)	30S ribosomal subunit protein S12
b3343 (tusB)	mnm(5)-s(2)U34-tRNA synthesis 2-thiolation protein
b3344 (tusC)	mnm(5)-s(2)U34-tRNA synthesis 2-thiolation protein
b3345 (tusD)	sulfurtransferase for 2-thiolation step of mnm(5)-s(2)U34-tRNA synthesis
b3346 (yheO)	putative PAS domain-containing DNA-binding transcriptional regulator
b3347 (fkpA)	FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase)
b3348 (slyX)	phi X174 lysis protein
b3349 (slyD)	FKBP-type peptidyl prolyl cis-trans isomerase (rotamase)
b3351 (kefG)	potassium-efflux system ancillary protein for KefB, glutathione-regulated
b3352 (yheS)	putative transporter subunit of ABC superfamily: ATP-binding component
b3353 (yheT)	UPF0017 family putative hydrolase
b3354 (yheU)	UPF0270 family protein
b3355 (prkB)	putative phosphoribulokinase
b3356 (yhfA)	OsmC family protein
b3357 (crp)	cAMP-activated global transcription factor, mediator of catabolite repression
b3358 (yhfK)	putative transporter, FUSC superfamily inner membrane protein, tandem domains
b3360 (pabA)	aminodeoxychorismate synthase, subunit II
b3361 (fic)	stationary-phase adenosine monophosphate-protein transferase domain protein
b3362 (yhfG)	putative Fic-binding protein
b3363 (ppiA)	peptidyl-prolyl cis-trans isomerase A (rotamase A)
b3364 (tsgA)	putative transporter
b3365 (nirB)	nitrite reductase, large subunit, NAD(P)H-binding
b3366 (nirD)	nitrite reductase, NAD(P)H-binding, small subunit
b3367 (nirC)	nitrite transporter
b3368 (cysG)	fused siroheme synthase 1,3-dimethyluroporphyriongen III dehydrogenase and siroheme ferrochelatase/uroporphyrinogen methyltransferase
b3369 (yhfL)	small lipoprotein
b3384 (trpS)	tryptophanyl-tRNA synthetase
b3385 (gph)	phosphoglycolate phosphatase
b3386 (rpe)	D-ribulose-5-phosphate 3-epimerase
b3387 (dam)	DNA adenine methyltransferase
b3388 (damX)	cell division protein that binds to the septal ring

b3389 (aroB)	3-dehydroquinate synthase
b3390 (aroK)	shikimate kinase I
b3391 (hofQ)	DNA catabolic putative fimbrial transporter
b3392 (hofP)	DNA catabolic protein
b3393 (hofO)	DNA catabolic protein
b3394 (hofN)	DNA catabolic putative fimbrial assembly protein
b3395 (hofM)	DNA catabolic putative pilus assembly protein
b3396 (mrcA)	fused penicillin-binding protein 1a: murein transglycosylase/murein transpeptidase
b3397 (nudE)	adenosine nucleotide hydrolase; substrates include Ap3A, Ap2A, ADP-ribose, NADH
b3398 (yrfF)	inner membrane protein
b3399 (yrfG)	GMP/IMP nucleotidase
b3400 (hslR)	ribosome-associated heat shock protein Hsp15
b3401 (hslO)	heat shock protein Hsp33
b3402 (yhgE)	DUF4153 family putative inner membrane protein
b3403 (pck)	phosphoenolpyruvate carboxykinase
b3404 (envZ)	sensory histidine kinase in two-component regulatory system with OmpR
b3405 (ompR)	response regulator in two-component regulatory system with EnvZ
b3406 (greB)	transcript cleavage factor
b3407 (yhgF)	putative transcriptional accessory protein
b3408 (feoA)	ferrous iron transporter, protein A
b3409 (feoB)	fused ferrous iron transporter, protein B: GTP-binding protein/membrane protein
b3410 (feoC)	putative DNA-binding transcriptional regulator
b3412 (bioH)	pimeloyl-ACP methyl ester carboxylesterase
b3413 (gntX)	DNA catabolic protein
b3414 (nfuA)	Fe/S biogenesis protein; putative scaffold/chaperone for damaged Fe/S proteins
b3415 (gntT)	gluconate transporter, high-affinity GNT I system
b3418 (malT)	mal regulon transcriptional activator
b3424 (glpG)	rhomboid intramembrane serine protease
b3425 (glpE)	thiosulfate:cyanide sulfurtransferase (rhodanese)
b3426 (glpD)	sn-glycerol-3-phosphate dehydrogenase, aerobic, FAD/NAD(P)-binding
b3428 (glgP)	glycogen phosphorylase
b3429 (glgA)	glycogen synthase
b3430 (glgC)	glucose-1-phosphate adenylyltransferase
b3431 (glgX)	glycogen debranching enzyme
b3432 (glgB)	1,4-alpha-glucan branching enzyme
b3433 (asd)	aspartate-semialdehyde dehydrogenase, NAD(P)-binding
b3434 (yhgN)	UPF0056 family inner membrane protein
b3437 (gntK)	gluconate kinase 2
b3438 (gntR)	d-gluconate inducible gluconate regulon transcriptional repressor
b3439 (yhhW)	quercetinase activity in vitro
b3440 (yhhX)	putative oxidoreductase

b3448 (yhhA)	DUF2756 family protein
b3449 (ugpQ)	glycerophosphodiester phosphodiesterase, cytosolic
b3450 (ugpC)	glycerol-3-phosphate transporter subunit
b3451 (ugpE)	glycerol-3-phosphate transporter subunit
b3452 (ugpA)	glycerol-3-phosphate transporter subunit
b3454 (livF)	leucine/isoleucine/valine transporter subunit
b3455 (livG)	leucine/isoleucine/valine transporter subunit
b3456 (livM)	leucine/isoleucine/valine transporter subunit
b3457 (livH)	leucine/isoleucine/valine transporter subunit
b3459 (panM)	PanD autocleavage accelerator, panothenate synthesis
b3461 (rpoH)	RNA polymerase, sigma 32 (sigma H) factor
b3462 (ftsX)	inner membrane putative ABC superfamily transporter permease
b3463 (ftsE)	putative ABC superfamily transporter ATP-binding subunit
b3464 (ftsY)	Signal Recognition Particle (SRP) receptor
b3465 (rsmD)	16S rRNA m(2)G966 methyltransferase, SAM-dependent
b3466 (yhhL)	DUF1145 family protein
b3467 (yhhM)	DUF2500 family protein
b3468 (yhhN)	TMEM86 family putative inner membrane protein
b3469 (zntA)	zinc, cobalt and lead efflux system
b3470 (tusA)	mnm(5)-s(2)U34-tRNA 2-thiolation sulfurtransferase
b3471 (yhhQ)	DUF165 family inner membrane protein
b3472 (dcrB)	putative lipoprotein
b3473 (yhhS)	putative arabinose efflux transporter
b3474 (yhhT)	UPF0118 family putative transporter
b3475 (acpT)	4'-phosphopantetheinyl transferase
b3476 (nikA)	nickel-binding, heme-binding periplasmic protein
b3477 (nikB)	nickel transporter subunit
b3478 (nikC)	nickel transporter subunit
b3479 (nikD)	nickel transporter subunit
b3480 (nikE)	nickel transporter subunit
b3481 (nikR)	transcriptional repressor, Ni-binding
b3485 (yhhJ)	inner membrane putative ABC transporter permease
b3486 (rbbA)	ribosome-associated ATPase: ATP-binding protein/ATP-binding membrane protein
b3487 (yhiI)	putative membrane fusion protein (MFP) of efflux pump
b3494 (uspB)	universal stress (ethanol tolerance) protein B
b3495 (uspA)	universal stress global response regulator
b3496 (dtpB)	dipeptide and tripeptide permease B
b3497 (rsmJ)	16S rRNA m(2)G1516 methyltransferase, SAM-dependent
b3498 (prlC)	oligopeptidase A
b3499 (rlmJ)	23S rRNA m(6)A2030 methyltransferase, SAM-dependent
b3500 (gor)	glutathione oxidoreductase
b3503 (arsC)	arsenate reductase
b3506 (slp)	outer membrane lipoprotein
b3507 (dctR)	LuxR family putative transcriptional regulator
b3509 (hdeB)	acid-resistance protein

b3510 (hdeA)	stress response protein acid-resistance protein
b3511 (hdeD)	acid-resistance membrane protein
b3512 (gadE)	gad regulon transcriptional activator
b3515 (gadW)	transcriptional activator of gadA and gadBC; repressor of gadX
b3519 (treF)	cytoplasmic trehalase
b3520 (yhjB)	putative DNA-binding transcriptional response regulator
b3521 (yhjC)	LysR family putative transcriptional regulator
b3522 (yhjD)	inner membrane putative BrbK family alternate lipid exporter
b3523 (yhjE)	MFS superfamily sugar transport 1 family protein
b3524 (yhjG)	putative inner membrane-anchored periplasmic AsmA family protein
b3525 (yhjH)	cyclic-di-GMP phosphodiesterase, FlhDC-regulated
b3526 (kdgK)	2-dehydro-3-deoxygluconokinase
b3527 (yhjJ)	putative periplasmic M16 family chaperone
b3528 (dctA)	C4-dicarboxylic acid, orotate and citrate transporter
b3529 (yhjK)	cyclic-di-GMP phosphodiesterase
b3531 (bcsZ)	endo-1,4-D-glucanase
b3539 (yhjV)	putative transporter
b3541 (dppD)	dipeptide/heme transporter
b3542 (dppC)	dipeptide/heme transporter
b3543 (dppB)	dipeptide/heme transporter
b3544 (dppA)	dipeptide transporter
b3546 (eptB)	KDO phosphoethanolamine transferase, Ca(2+)-inducible
b3548 (yhjY)	autotransporter beta-domain protein
b3549 (tag)	3-methyl-adenine DNA glycosylase I, constitutive
b3550 (yiaC)	putative acyl-CoA transferase
b3551 (bisC)	biotin sulfoxide reductase
b3552 (yiaD)	multicopy suppressor of bamB; outer membrane lipoprotein
b3553 (ghrB)	glyoxylate/hydroxypyruvate reductase B
b3554 (yiaF)	barrier effect co-colonization resistance factor; DUF3053 family lipoprotein
b3555 (yiaG)	HTH_CROC1 family putative transcriptional regulator
b3559 (glyS)	glycine tRNA synthetase, beta subunit
b3560 (glyQ)	glycine tRNA synthetase, alpha subunit
b3561 (wecH)	O-acetyltransferase for enterobacterial common antigen
b3563 (yiaB)	YiaAB family inner membrane protein
b3565 (xylA)	D-xylose isomerase
b3590 (selB)	selenocysteinyl-tRNA-specific translation factor
b3591 (selA)	selenocysteine synthase
b3592 (yibF)	glutathione S-transferase homolog
b3598 (yibI)	DUF3302 family inner membrane protein
b3599 (mtlA)	fused mannitol-specific PTS enzymes: IIA components/IIB components/IIC components
b3600 (mtlD)	mannitol-1-phosphate dehydrogenase, NAD-dependent
b3601 (mtlR)	mannitol operon repressor
b3602 (yibL)	ribosome-associated DUF2810 family protein
b3603 (lldP)	L-lactate permease

b3604 (lldR)	dual role activator/repressor for lldPRD operon
b3605 (lldD)	L-lactate dehydrogenase, FMN-linked
b3606 (trmL)	tRNA Leu mC34,mU34 2'-O-methyltransferase, SAM-dependent
b3607 (cysE)	serine acetyltransferase
b3608 (gpsA)	glycerol-3-phosphate dehydrogenase (NAD+)
b3609 (secB)	protein export chaperone
b3610 (grxC)	glutaredoxin 3
b3611 (yibN)	putative rhodanese-related sulfurtransferase
b3612 (gpmM)	phosphoglycero mutase III, cofactor-independent
b3613 (envC)	activator of AmiB,C murein hydrolases, septal ring factor
b3614 (yibQ)	putative polysaccharide deacetylase
b3616 (tdh)	L-threonine 3-dehydrogenase, NAD(P)-binding
b3617 (kbl)	glycine C-acetyltransferase
b3619 (hldD)	ADP-L-glycero-D-mannoheptose-6-epimerase, NAD(P)-binding
b3620 (waaF)	ADP-heptose:LPS heptosyltransferase II
b3630 (waaP)	kinase that phosphorylates core heptose of lipopolysaccharide
b3631 (waaG)	glucosyltransferase I
b3633 (waaA)	3-deoxy-D-manno-octulosonic-acid transferase (KDO transferase)
b3634 (coaD)	pantetheine-phosphate adenylyltransferase
b3635 (mutM)	formamidopyrimidine/5-formyluracil/5-hydroxymethyluracil DNA glycosylase
b3636 (rpmG)	50S ribosomal subunit protein L33
b3637 (rpmB)	50S ribosomal subunit protein L28
b3639 (dfp)	fused 4'-phosphopantothenoylcysteine decarboxylase/phosphopantothenoylcysteine synthetase, FMN-binding
b3640 (dut)	deoxyuridinetriphosphatase
b3641 (slmA)	nucleoid occlusion factor, anti-FtsZ division inhibitor
b3642 (pyrE)	orotate phosphoribosyltransferase
b3644 (yicC)	UPF0701 family protein
b3646 (yicG)	UPF0126 family inner membrane protein
b3647 (ligB)	DNA ligase, NAD(+)-dependent
b3648 (gmk)	guanylate kinase
b3649 (rpoZ)	RNA polymerase, omega subunit
b3650 (spoT)	bifunctional (p)ppGpp synthetase II/guanosine-3',5'-bis pyrophosphate 3'-pyrophosphohydrolase
b3651 (trmH)	tRNA mG18-2'-O-methyltransferase, SAM-dependent
b3652 (recG)	ATP-dependent DNA helicase
b3653 (gltS)	glutamate transporter
b3654 (xanP)	xanthine permease
b3655 (yicH)	putative inner membrane-anchored periplasmic AsmA family protein
b3663 (yicN)	DUF1198 family protein
b3666 (uhpT)	hexose phosphate transporter
b3667 (uhpC)	membrane protein regulates uhpT expression
b3668 (uhpB)	sensory histidine kinase in two-component regulatory sytem with UhpA

b3669 (uhpA)	response regulator in two-component regulatory system wtih UhpB
b3670 (ilvN)	acetolactate synthase 1 small subunit
b3671 (ilvB)	acetolactate synthase 2 large subunit
b3672 (ivbL)	ilvB operon leader peptide
b3673 (emrD)	multidrug efflux system protein
b3674 (yidF)	putative Cys-type oxidative YidJ-maturating enzyme
b3675 (yidG)	inner membrane protein
b3676 (yidH)	DUF202 family inner membrane protein
b3685 (yidE)	putative transporter
b3686 (ibpB)	heat shock chaperone
b3687 (ibpA)	heat shock chaperone
b3688 (yidQ)	DUF1375 family outer membrane protein
b3689 (yidR)	DUF3748 family protein
b3697 (yidA)	sugar phosphate phosphatase; substrates include erythrose 4-P and mannose 1-P phosphatase
b3698 (yidB)	DUF937 family protein
b3699 (gyrB)	DNA gyrase, subunit B
b3700 (recF)	gap repair protein
b3701 (dnaN)	DNA polymerase III, beta subunit
b3702 (dnaA)	chromosomal replication initiator protein DnaA, DNA-binding transcriptional dual regulator
b3703 (rpmH)	50S ribosomal subunit protein L34
b3704 (rnpA)	protein C5 component of RNase P
b3705 (yidC)	membrane protein insertase
b3706 (mnmE)	tRNA U34 5-methylaminomethyl-2-thiouridine modification GTPase
b3710 (mdtL)	multidrug efflux system protein
b3712 (yieE)	phosphopantetheinyl transferase superfamily protein
b3713 (chrR)	chromate reductase, Class I, flavoprotein
b3725 (pstB)	phosphate transporter subunit
b3726 (pstA)	phosphate transporter subunit
b3727 (pstC)	phosphate transporter subunit
b3728 (pstS)	periplasmic phosphate binding protein, high-affinity
b3729 (glmS)	L-glutamine:D-fructose-6-phosphate aminotransferase
b3730 (glmU)	fused N-acetyl glucosamine-1-phosphate uridyltransferase/glucosamine-1-phosphate acetyl transferase
b3731 (atpC)	F1 sector of membrane-bound ATP synthase, epsilon subunit
b3732 (atpD)	F1 sector of membrane-bound ATP synthase, beta subunit
b3733 (atpG)	F1 sector of membrane-bound ATP synthase, gamma subunit
b3734 (atpA)	F1 sector of membrane-bound ATP synthase, alpha subunit
b3735 (atpH)	F1 sector of membrane-bound ATP synthase, delta subunit
b3736 (atpF)	F0 sector of membrane-bound ATP synthase, subunit b
b3737 (atpE)	F0 sector of membrane-bound ATP synthase, subunit c
b3738 (atpB)	F0 sector of membrane-bound ATP synthase, subunit a
b3739 (atpI)	ATP synthase, membrane-bound accessory factor
b3740 (rsmG)	16S rRNA m(7)G527 methyltransferase, SAM-dependent; glucose-inhibited cell-division protein

b3741 (mnmG)	5-methylaminomethyl-2-thiouridine modification at tRNA U34
b3742 (mioC)	FMN-binding protein MioC
b3743 (asnC)	transcriptional activator of asnA; autorepressor
b3744 (asnA)	asparagine synthetase A
b3745 (viaA)	stimulator of RavA ATPase activity; von Willebrand factor domain protein
b3746 (ravA)	hexameric AAA+ MoxR family ATPase, putative molecular chaperone
b3747 (kup)	potassium transporter
b3748 (rbsD)	putative cytoplasmic sugar-binding protein
b3750 (rbsC)	D-ribose transporter subunit
b3752 (rbsK)	ribokinase
b3753 (rbsR)	transcriptional repressor of ribose metabolism
b3754 (hsrA)	putative multidrug or homocysteine efflux system
b3755 (yieP)	putative transcriptional regulator
b3764 (yifE)	UPF0438 family protein
b3766 (ilvL)	ilvG operon leader peptide
b3769 (ilvM)	acetolactate synthase 2 small subunit
b3770 (ilvE)	branched-chain amino-acid aminotransferase
b3771 (ilvD)	dihydroxyacid dehydratase
b3772 (ilvA)	L-threonine dehydratase, biosynthetic; also known as threonine deaminase
b3774 (ilvC)	ketol-acid reductoisomerase, NAD(P)-binding
b3775 (ppiC)	peptidyl-prolyl cis-trans isomerase C (rotamase C)
b3779 (gpp)	guanosine pentaphosphatase/exopolyphosphatase
b3780 (rhlB)	ATP-dependent RNA helicase
b3781 (trxA)	thioredoxin 1
b3783 (rho)	transcription termination factor
b3784 (wecA)	UDP-GlcNAc:undecaprenylphosphate GlcNAc-1-phosphate transferase
b3785 (wzzE)	Entobacterial Common Antigen
b3786 (wecB)	UDP-N-acetyl glucosamine-2-epimerase
b3787 (wecC)	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase
b3788 (rffG)	dTDP-glucose 4,6-dehydratase
b3789 (rffH)	glucose-1-phosphate thymidylyltransferase
b3790 (wecD)	TDP-fucosamine acetyltransferase
b3791 (wecE)	TDP-4-oxo-6-deoxy-D-glucose transaminase
b3792 (wzxE)	O-antigen translocase
b3793 (wzyE)	putative ECA polysaccharide chain elongation protein
b3794 (wecG)	UDP-N-acetyl-D-mannosaminuronic acid transferase
b3795 (yifK)	putative APC family amino acid transporter
b3800 (aslB)	putative AslA-specific sulfatase-maturating enzyme
b3802 (hemY)	putative protoheme IX synthesis protein
b3804 (hemD)	uroporphyrinogen III synthase
b3805 (hemC)	hydroxymethylbilane synthase
b3806 (cyaA)	adenylate cyclase
b3807 (cyaY)	iron-dependent inhibitor of iron-sulfur cluster formation; frataxin; iron-binding and oxidizing protein

b3809 (dapF)	diaminopimelate epimerase
b3810 (yigA)	DUF484 family protein
b3811 (xerC)	site-specific tyrosine recombinase
b3812 (yigB)	5-amino-6-(5-phospho-D-ribitylamino)uracil phosphatase; pyrimidine phosphatase; riboflavin synthesis
b3813 (uvrD)	DNA-dependent ATPase I and helicase II
b3820 (yigI)	4HBT thioesterase family protein
b3821 (pldA)	outer membrane phospholipase A
b3822 (recQ)	ATP-dependent DNA helicase
b3823 (rhtC)	threonine efflux pump
b3824 (rhtB)	homoserine, homoserine lactone and S-methyl-methionine efflux pump
b3825 (pldB)	lysophospholipase L2
b3826 (yigL)	pyridoxal phosphate phosphatase
b3827 (yigM)	putative inner membrane EamA-like transporter
b3828 (metR)	methionine biosynthesis regulon transcriptional regulator
b3829 (metE)	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase
b3832 (rmuC)	DNA recombination protein
b3833 (ubiE)	bifunctional 2-octaprenyl-6-methoxy-1,4-benzoquinone methylase/S-adenosylmethionine:2-DMK methyltransferase
b3834 (ubiJ)	aerobic ubiquinone synthesis protein, SCP2 family protein
b3835 (ubiB)	regulator of octaprenylphenol hydroxylation, ubiquinone synthesis; regulator of 2'-N-acetyltransferase; putative ABC1 family protein kinase
b3836 (tatA)	TatABCE protein translocation system subunit
b3838 (tatB)	TatABCE protein translocation system subunit
b3839 (tatC)	TatABCE protein translocation system subunit
b3842 (rfaH)	transcription antitermination protein
b3843 (ubiD)	3-octaprenyl-4-hydroxybenzoate decarboxylase
b3844 (fre)	NAD(P)H-flavin reductase
b3845 (fadA)	3-ketoacyl-CoA thiolase (thiolase I)
b3846 (fadB)	fused 3-hydroxybutyryl-CoA epimerase/delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase/enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase
b3847 (pepQ)	proline dipeptidase
b3848 (yigZ)	UPF0029 family protein
b3849 (trkH)	potassium transporter
b3850 (hemG)	protoporphyrin oxidase, flavoprotein
b3856 (mobB)	molybdopterin-guanine dinucleotide biosynthesis protein B
b3857 (mobA)	molybdopterin-guanine dinucleotide synthase
b3858 (yihD)	DUF1040 protein YihD
b3859 (srkA)	stress response kinase A; MazF antagonist; Thr/Ser kinase involved in Cpx stress response
b3860 (dsbA)	periplasmic protein disulfide isomerase I
b3863 (polA)	fused DNA polymerase I 5'->3' polymerase/3'->5' exonuclease/5'->3' exonuclease

b3865 (yihA)	cell division GTP-binding protein
b3866 (yihI)	activator of Der GTPase
b3867 (hemN)	coproporphyrinogen III oxidase, SAM and NAD(P)H dependent, oxygen-independent
b3868 (glnG)	fused DNA-binding response regulator in two-component regulatory system with GlnL: response regulator/sigma54 interaction protein
b3869 (glnL)	sensory histidine kinase in two-component regulatory system with GlnG
b3870 (glnA)	glutamine synthetase
b3871 (typA)	GTP-binding protein
b3885 (yihX)	alpha-D-Glucose-1-P phosphatase, anomer-specific
b3886 (yihY)	BrkB family putative transporter, inner membrane protein
b3887 (dtd)	D-tyr-tRNA(Tyr) deacylase
b3888 (yiiD)	putative acetyltransferase
b3891 (fdhE)	formate dehydrogenase formation protein
b3892 (fdoI)	formate dehydrogenase-O, cytochrome b556 subunit
b3893 (fdoH)	formate dehydrogenase-O, Fe-S subunit
b3905 (rhaS)	transcriptional activator of rhaBAD and rhaT
b3906 (rhaR)	transcriptional activator of rhaSR
b3908 (sodA)	superoxide dismutase, Mn
b3910 (yiiM)	6-N-hydroxylaminopurine resistance protein
b3911 (cpxA)	sensory histidine kinase in two-component regulatory system with CpxR
b3912 (cpxR)	response regulator in two-component regulatory system with CpxA
b3915 (fieF)	ferrous iron and zinc transporter
b3916 (pfkA)	6-phosphofructokinase I
b3917 (sbp)	sulfate transporter subunit
b3918 (cdh)	CDP-diacylglycerol phosphotidylhydrolase
b3919 (tpiA)	triosephosphate isomerase
b3920 (yiiQ)	DUF1454 family putative periplasmic protein
b3921 (yiiR)	DUF805 family putative inner membrane protein
b3922 (yiiS)	UPF0381 family protein
b3923 (uspD)	stress-induced protein
b3924 (fpr)	ferredoxin-NADP reductase
b3925 (glpX)	fructose 1,6-bisphosphatase II
b3927 (glpF)	glycerol facilitator
b3928 (zapB)	FtsZ stabilizer; septal ring assembly factor, stimulates cell division
b3929 (rraA)	ribonuclease E (RNase E) inhibitor protein
b3930 (menA)	1,4-dihydroxy-2-naphthoate octaprenyltransferase
b3931 (hslU)	molecular chaperone and ATPase component of HslUV protease
b3932 (hslV)	peptidase component of the HslUV protease
b3933 (ftsN)	essential cell division protein
b3934 (cytR)	Anti-activator for CytR-CRP nucleoside utilization regulon
b3935 (priA)	Primosome factor n' (replication factor Y)
b3936 (rpmE)	50S ribosomal subunit protein L31
b3937 (yiiX)	putative lipid binding hydrolase, DUF830 family protein

b3938 (metJ)	transcriptional repressor, S-adenosylmethionine-binding
b3939 (metB)	cystathionine gamma-synthase, PLP-dependent
b3940 (metL)	Bifunctional aspartokinase/homoserine dehydrogenase 2
b3941 (metF)	5,10-methylenetetrahydrofolate reductase
b3942 (katG)	catalase-peroxidase HPI, heme b-containing
b3943 (yijE)	EamA-like transporter family protein
b3944 (yijF)	DUF1287 family protein
b3945 (gldA)	glycerol dehydrogenase, NAD+ dependent; 1,2-propanediol:NAD+ oxidoreductase
b3949 (frwC)	putative enzyme IIC component of PTS
b3950 (frwB)	putative enzyme IIB component of PTS
b3951 (pflD)	putative glycine radical domain-containing pyruvate formate-lyase
b3952 (pflC)	putative [formate-C-acetyltransferase 2]-activating enzyme; pyruvate formate-lyase 1-activating enzyme
b3953 (frwD)	putative enzyme IIB component of PTS
b3954 (yijO)	AraC family putative transcriptional activator
b3955 (eptC)	LPS heptose I phosphoethanolamine transferase
b3956 (ppc)	phosphoenolpyruvate carboxylase
b3957 (argE)	acetylornithine deacetylase
b3958 (argC)	N-acetyl-gamma-glutamylphosphate reductase, NAD(P)-binding
b3959 (argB)	acetylglutamate kinase
b3960 (argH)	argininosuccinate lyase
b3961 (oxyR)	oxidative and nitrosative stress transcriptional regulator
b3962 (sthA)	pyridine nucleotide transhydrogenase, soluble
b3963 (fabR)	transcriptional repressor of fabA and fabB
b3964 (yijD)	DUF1422 family inner membrane protein
b3965 (trmA)	tRNA m(5)U54 methyltransferase, SAM-dependent; tmRNA m(5)U341 methyltransferase
b3967 (murI)	glutamate racemase
b3972 (murB)	UDP-N-acetylenolpyruvoylglucosamine reductase, FAD-binding
b3973 (birA)	bifunctional biotin-[acetylCoA carboxylase] holoenzyme synthetase/DNA-binding transcriptional repressor, bio-5'-AMP-binding
b3974 (coaA)	pantothenate kinase
b3981 (secE)	preprotein translocase membrane subunit
b3982 (nusG)	transcription termination factor
b3983 (rplK)	50S ribosomal subunit protein L11
b3984 (rplA)	50S ribosomal subunit protein L1
b3985 (rplJ)	50S ribosomal subunit protein L10
b3986 (rplL)	50S ribosomal subunit protein L7/L12
b3987 (rpoB)	RNA polymerase, beta subunit
b3988 (rpoC)	RNA polymerase, beta prime subunit
b3990 (thiH)	tyrosine lyase, involved in thiamine-thiazole moiety synthesis
b3991 (thiG)	thiamine biosynthesis ThiGH complex subunit
b3992 (thiF)	adenylyltransferase, modifies ThiS C-terminus
b3993 (thiE)	thiamine phosphate synthase (thiamine phosphate pyrophosphorylase)

b3994 (thiC)	phosphomethylpyrimidine synthase
b3995 (rsd)	stationary phase protein, binds sigma 70 RNA polymerase subunit
b3996 (nudC)	NADH pyrophosphatase
b3997 (hemE)	uroporphyrinogen decarboxylase
b3998 (nfi)	endonuclease V; deoxyinosine 3' endonuclease
b3999 (yjaG)	DUF416 domain protein
b4000 (hupA)	HU, DNA-binding transcriptional regulator, alpha subunit
b4001 (yjaH)	DUF1481 family putative lipoprotein
b4002 (zraP)	Zn-dependent periplasmic chaperone
b4003 (zraS)	sensory histidine kinase in two-component regulatory system with ZraR
b4004 (zraR)	fused DNA-binding response regulator in two-component regulatory system with ZraS: response regulator/sigma54 interaction protein
b4005 (purD)	phosphoribosylglycinamide synthetase phosphoribosylamine-glycine ligase
b4006 (purH)	fused IMP cyclohydrolase/phosphoribosylaminoimidazolecarboxamide formyltransferase
b4012 (yjaB)	putative acetyltransferase
b4013 (metA)	homoserine O-transsuccinylase
b4015 (aceA)	isocitrate lyase
b4018 (iclR)	transcriptional repressor
b4019 (metH)	homocysteine-N5-methyltetrahydrofolate transmethylase, B12-dependent
b4020 (yjbB)	putative Na+/Pi-cotransporter
b4021 (pepE)	(alpha)-aspartyl dipeptidase
b4022 (rluF)	23S rRNA pseudouridine(2604) synthase
b4024 (lysC)	lysine-sensitive aspartokinase 3
b4025 (pgi)	glucosephosphate isomerase
b4026 (yjbE)	extracellular polysaccharide production threonine-rich protein
b4027 (yjbF)	extracellular polysaccharide production lipoprotein
b4030 (psiE)	phosphate starvation inducible protein
b4032 (malG)	maltose transporter subunit
b4033 (malF)	maltose transporter subunit
b4034 (malE)	maltose transporter subunit
b4035 (malK)	fused maltose transport subunit, ATP-binding component of ABC superfamily/regulatory protein
b4036 (lamB)	maltose outer membrane porin (maltoporin)
b4037 (malM)	maltose regulon periplasmic protein
b4039 (ubiC)	chorismate--pyruvate lyase
b4040 (ubiA)	p-hydroxybenzoate octaprenyltransferase
b4041 (plsB)	glycerol-3-phosphate O-acyltransferase
b4042 (dgkA)	diacylglycerol kinase
b4043 (lexA)	transcriptional repressor of SOS regulon
b4044 (dinF)	oxidative stress resistance protein; putative MATE family efflux pump; UV and mitomycin C inducible protein
b4045 (yjbJ)	stress-induced protein, UPF0337 family

b4046 (zur)	transcriptional repressor, Zn(II)-binding
b4050 (pspG)	phage shock protein G
b4051 (qorA)	quinone oxidoreductase, NADPH-dependent
b4052 (dnaB)	replicative DNA helicase
b4053 (alr)	alanine racemase, biosynthetic, PLP-binding
b4054 (tyrB)	tyrosine aminotransferase, tyrosine-repressible, PLP-dependent
b4055 (aphA)	acid phosphatase/phosphotransferase, class B, non-specific
b4056 (yjbQ)	thiamine phosphate synthase
b4057 (yjbR)	DUF419 family protein
b4058 (uvrA)	ATPase and DNA damage recognition protein of nucleotide excision repair excinuclease UvrABC
b4059 (ssb)	single-stranded DNA-binding protein
b4060 (yjcB)	putative inner membrane protein
b4062 (soxS)	superoxide response regulon transcriptional activator; autoregulator
b4065 (yjcE)	putative cation/proton antiporter
b4067 (actP)	acetate transporter
b4068 (yjcH)	DUF485 family inner membrane protein
b4069 (acs)	acetyl-CoA synthetase
b4070 (nrfA)	nitrite reductase, formate-dependent, cytochrome
b4071 (nrfB)	nitrite reductase, formate-dependent, penta-heme cytochrome c
b4072 (nrfC)	formate-dependent nitrite reductase, 4Fe4S subunit
b4073 (nrfD)	formate-dependent nitrite reductase, membrane subunit
b4074 (nrfE)	heme lyase (NrfEFG) for insertion of heme into c552, subunit NrfE
b4075 (nrfF)	heme lyase (NrfEFG) for insertion of heme into c552, subunit NrfF
b4076 (nrfG)	heme lyase (NrfEFG) for insertion of heme into c552, subunit NrfG
b4077 (gltP)	glutamate/aspartate:proton symporter
b4078 (yjcO)	Sel1 family TPR-like repeat protein
b4080 (mdtP)	outer membrane factor of efflux pump
b4081 (mdtO)	membrane translocase (MDR) of MdtNOP efflux pump, PET family
b4082 (mdtN)	membrane fusion protein of efflux pump
b4107 (yjdN)	metalloprotein superfamily protein
b4108 (yjdM)	zinc-ribbon family protein
b4111 (proP)	proline/glycine betaine transporter
b4112 (basS)	sensory histidine kinase in two-component regulatory system with BasR
b4113 (basR)	response regulator in two-component regulatory system with BasS
b4114 (eptA)	lipid A phosphoethanolamine transferase
b4115 (adiC)	arginine:agmatine antiporter
b4116 (adiY)	adi system transcriptional activator
b4117 (adiA)	arginine decarboxylase
b4123 (dcuB)	C4-dicarboxylate transporter, anaerobic; DcuS co-sensor
b4124 (dcuR)	response regulator in two-component regulatory system with DcuS
b4125 (dcuS)	sensory histidine kinase in two-component regulatory system with DcuR, regulator of anaerobic fumarate respiration
b4135 (yjdC)	putative transcriptional regulator

b4136 (dsbD)	fused thiol:disulfide interchange protein: activator of DsbC/conserved protein
b4137 (cutA)	divalent-cation tolerance protein, copper sensitivity
b4138 (dcuA)	C4-dicarboxylate antiporter
b4139 (aspA)	aspartate ammonia-lyase
b4140 (fxsA)	suppressor of F exclusion of phage T7
b4141 (yjeH)	putative transporter
b4142 (groS)	Cpn10 chaperonin GroES, small subunit of GroESL
b4143 (groL)	Cpn60 chaperonin GroEL, large subunit of GroESL
b4144 (yjeI)	DUF4156 family lipoprotein
b4146 (epmB)	EF-P-Lys34 lysylation protein; weak lysine 2,3-aminomutase
b4147 (efp)	polyproline-specific translation elongation factor EF-P
b4148 (sugE)	multidrug efflux system protein
b4149 (blc)	outer membrane lipoprotein (lipocalin), cell division and growth function
b4150 (ampC)	penicillin-binding protein; beta-lactamase, intrinsically weak
b4151 (frdD)	fumarate reductase (anaerobic), membrane anchor subunit
b4152 (frdC)	fumarate reductase (anaerobic), membrane anchor subunit
b4153 (frdB)	fumarate reductase (anaerobic), Fe-S subunit
b4154 (frdA)	fumarate reductase (anaerobic) catalytic and NAD/flavoprotein subunit
b4155 (epmA)	Elongation Factor P Lys34 lysyltransferase
b4159 (mscM)	mechanosensitive channel protein, miniconductance
b4160 (psd)	phosphatidylserine decarboxylase
b4161 (rsgA)	ribosome small subunit-dependent GTPase A
b4162 (orn)	oligoribonuclease
b4166 (queG)	epoxyqueuosine reductase, cobalamine-stimulated; queosine biosynthesis
b4167 (nnr)	bifunctional NAD(P)H-hydrate repair enzyme; C-terminal domain ADP-dependent (S)-NAD(P)H-hydrate dehydratase and N-terminal domain NAD(P)H-hydrate epimerase
b4168 (tsaE)	tRNA(ANN) t(6)A37 threonylcarbamoyladenosine modification protein; ADP binding protein
b4169 (amiB)	N-acetylmuramoyl-l-alanine amidase II
b4170 (mutL)	methyl-directed mismatch repair protein
b4171 (miaA)	delta(2)-isopentenylpyrophosphate tRNA-adenosine transferase
b4172 (hfq)	global sRNA chaperone; HF-I, host factor for RNA phage Q beta replication
b4173 (hflX)	GTPase, stimulated by 50S subunit binding
b4174 (hflK)	modulator for HflB protease specific for phage lambda cII repressor
b4175 (hflC)	modulator for HflB protease specific for phage lambda cII repressor
b4176 (yjeT)	DUF2065 family protein
b4177 (purA)	adenylosuccinate synthetase
b4178 (nsrR)	nitric oxide-sensitive repressor for NO regulon
b4179 (rnr)	exoribonuclease R, RNase R
b4180 (rlmB)	23S rRNA mG2251 2'-O-ribose methyltransferase, SAM-dependent
b4186 (yjfC)	ATP-Grasp family ATPase

b4187 (aidB)	DNA alkylation damage repair protein; flavin-containing DNA binding protein, weak isovaleryl CoA dehydrogenase
b4188 (yjfN)	DUF1471 family periplasmic protein
b4189 (bsmA)	bioflm peroxide resistance protein
b4190 (yjfP)	acyl CoA esterase
b4191 (ulaR)	transcriptional repressor for the L-ascorbate utilization (ula) divergent operon
b4192 (ulaG)	L-ascorbate 6-phosphate lactonase
b4193 (ulaA)	L-ascorbate-specific enzyme IIC permease component of PTS
b4194 (ulaB)	L-ascorbate-specific enzyme IIB component of PTS
b4195 (ulaC)	L-ascorbate-specific enzyme IIA component of PTS
b4196 (ulaD)	3-keto-L-gulonate 6-phosphate decarboxylase
b4197 (ulaE)	L-xylulose 5-phosphate 3-epimerase
b4198 (ulaF)	L-ribulose 5-phosphate 4-epimerase
b4199 (yjfY)	YhcN family protein, periplasmic
b4200 (rpsF)	30S ribosomal subunit protein S6
b4201 (priB)	primosomal protein N
b4202 (rpsR)	30S ribosomal subunit protein S18
b4203 (rplI)	50S ribosomal subunit protein L9
b4206 (ytfB)	OapA family protein
b4207 (fklB)	FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase)
b4209 (ytfE)	iron-sulfur cluster repair protein RIC
b4210 (ytfF)	DMT transporter family inner membrane protein
b4211 (qorB)	NAD(P)H:quinone oxidoreductase
b4212 (ytfH)	DUF24 family HxlR-type putative transcriptional regulator
b4214 (cysQ)	3'(2'),5'-bisphosphate nucleotidase
b4217 (ytfK)	DUF1107 family protein
b4218 (ytfL)	UPF0053 family inner membrane protein
b4219 (msrA)	methionine sulfoxide reductase A
b4220 (tamA)	translocation and assembly module for autotransporter export, outer membrane subunit
b4221 (tamB)	translocation and assembly module for autotransporter export, inner membrane subunit
b4222 (ytfP)	GGCT-like protein
b4226 (ppa)	inorganic pyrophosphatase
b4227 (ytfQ)	galactofuranose binding proteint: periplasmic-binding component of ABC superfamily
b4230 (ytfT)	inner membrane putative ABC superfamily sugar transporter permease
b4232 (fbp)	fructose-1,6-bisphosphatase I
b4233 (mpl)	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase
b4234 (yjgA)	ribosome-associated UPF0307 family protein
b4235 (pmbA)	putative antibiotic peptide MccB17 maturation peptidase
b4237 (nrdG)	anaerobic ribonucleotide reductase activating protein
b4238 (nrdD)	anaerobic ribonucleoside-triphosphate reductase
b4239 (treC)	trehalose-6-P hydrolase

b4240 (treB)	fused trehalose(maltose)-specific PTS enzyme: IIB component/IIC component
b4241 (treR)	trehalose 6-phosphate-inducible trehalose regulon transcriptional repressor
b4242 (mgtA)	magnesium transporter
b4244 (pyrI)	aspartate carbamoyltransferase, regulatory subunit
b4245 (pyrB)	aspartate carbamoyltransferase, catalytic subunit
b4246 (pyrL)	pyrBI operon leader peptide
b4255 (rraB)	protein inhibitor of RNase E
b4256 (yjgM)	putative acetyltransferase
b4258 (valS)	valyl-tRNA synthetase
b4259 (holC)	DNA polymerase III, chi subunit
b4260 (pepA)	multifunctional aminopeptidase A: a cyteinylglycinase, transcription regulator and site-specific recombination factor
b4261 (lptF)	lipopolysaccharide export ABC permease of the LptBFGC export complex
b4262 (lptG)	lipopolysaccharide export ABC permease of the LptBFGC export complex
b4322 (uxuA)	mannonate hydrolase
b4324 (uxuR)	fructuronate-inducible hexuronate regulon transcriptional repressor; autorepressor
b4352 (yjiA)	GTP-binding protein, putative GTPase
b4354 (yjiY)	putative transporter
b4358 (yjjN)	L-galactonate oxidoreductase
b4359 (opgB)	phosphoglycerol transferases I and II
b4360 (yjjA)	putative DUF2501 family periplasmic protein
b4361 (dnaC)	DNA biosynthesis protein
b4362 (dnaT)	DNA biosynthesis protein (primosomal protein I)
b4363 (yjjB)	DUF3815 family inner membrane protein
b4364 (yjjP)	DUF1212 family inner membrane protein
b4366 (bglJ)	bgl operon transcriptional activator
b4367 (fhuF)	ferric iron reductase involved in ferric hydroximate transport
b4371 (rsmC)	16S rRNA m(2)G1207 methyltransferase, SAM-dependent
b4372 (holD)	DNA polymerase III, psi subunit
b4373 (rimI)	ribosomal-protein-S18-alanine N-acetyltransferase
b4374 (yjjG)	dUMP phosphatase
b4376 (osmY)	periplasmic protein
b4377 (yjjU)	putative patatin-like family phospholipase
b4379 (yjjW)	putative pyruvate formate lyase activating enzyme
b4381 (deoC)	2-deoxyribose-5-phosphate aldolase, NAD(P)-linked
b4382 (deoA)	thymidine phosphorylase
b4383 (deoB)	phosphopentomutase
b4384 (deoD)	purine-nucleoside phosphorylase
b4386 (lplA)	lipoate-protein ligase A
b4387 (ytjB)	SMP_2 family putative membrane-anchored periplasmic protein
b4388 (serB)	3-phosphoserine phosphatase
b4389 (radA)	DNA repair protein

b4390 (nadR)	trifunctional protein: nicotinamide mononucleotide adenylyltransferase, ribosylnicotinamide kinase, transcriptional repressor
b4391 (yjjK)	putative transporter subunit of ABC superfamily: ATP-binding component
b4392 (slt)	lytic murein transglycosylase, soluble
b4393 (trpR)	transcriptional repressor, tryptophan-binding
b4395 (ytjC)	phosphatase
b4396 (rob)	right oriC-binding transcriptional activator, AraC family
b4397 (creA)	putative periplasmic protein
b4398 (creB)	response regulator in two-component regulatory system with CreC
b4399 (creC)	sensory histidine kinase in two-component regulatory system with CreB or PhoB, regulator of the CreBC regulon
b4400 (creD)	inner membrane protein
b4401 (arcA)	response regulator in two-component regulatory system with ArcB or CpxA
b4402 (yjjY)	uncharacterized protein
b4403 (yjtD)	putative methyltransferase
b4406 (yaeP)	UPF0253 family protein
b4407 (thiS)	immediate sulfur donor in thiazole formation
b4409 (blr)	beta-lactam resistance membrane protein; divisome-associated protein
b4410 (ecnA)	entericidin A membrane lipoprotein, antidote entericidin B
b4411 (ecnB)	entericidin B membrane lipoprotein
b4455 (hokA)	toxic polypeptide, small
b4461 (yfjD)	UPF0053 family inner membrane protein
b4469 (ygiQ)	Radical SAM superfamily protein
b4470 (yhaM)	putative L-serine dehydratase alpha chain
b4472 (yhdP)	DUF3971-AsmA2 domains protein
b4473 (smf)	DNA recombination-mediator A family protein
b4476 (gntU)	gluconate transporter, low affinity GNT 1 system
b4480 (hdfR)	flhDC operon transcriptional repressor
b4481 (wecF)	TDP-Fuc4NAc:lipidIIFuc4NAc transferase
b4483 (tatD)	quality control of Tat-exported FeS proteins; Mg-dependent cytoplasmic DNase
b4484 (cpxP)	inhibitor of the cpx response; periplasmic adaptor protein
b4485 (ytfR)	putative ABC superfamily sugar transporter ATP-binding subunit
b4502 (yeiW)	UPF0153 cysteine cluster protein
b4513 (kdpF)	potassium ion accessory transporter subunit
b4515 (cydX)	cytochrome d (bd-I) ubiquinol oxidase subunit X
b4522 (ymiA)	uncharacterized protein
b4523 (yciX)	uncharacterized protein
b4529 (ydbJ)	DUF333 family putative lipoprotein
b4535 (yniD)	uncharacterized protein
b4536 (yobH)	uncharacterized protein
b4537 (yecJ)	uncharacterized protein
b4542 (yohO)	putative membrane protein

b4544 (arnE)	undecaprenyl phosphate-alpha-L-ara4N exporter; flippase ArnEF subunit
b4546 (ypeB)	DUF3820 family protein
b4547 (ypfN)	putative membrane protein, UPF0370 family
b4551 (yheV)	DUF2387 family putative metal-binding protein
b4553 (ysaB)	uncharacterized protein
b4555 (yicS)	putative periplasmic protein
b4557 (yidD)	membrane protein insertion efficiency factor, inner membrane protein, UPF0161 family
b4558 (yifL)	putative lipoprotein
b4567 (yjjZ)	uncharacterized protein
b4568 (ytjA)	uncharacterized protein
b4592 (cbdX)	putative cytochrome bd-II oxidase subunit
b4595 (yciY)	uncharacterized protein
b4596 (yciZ)	uncharacterized protein
b4598 (yncL)	stress-induced small inner membrane enterobacterial protein
b4601 (ydgU)	stationary phase-induced protein
b4602 (ynhF)	stress response membrane
b4606 (ypfM)	stress-induced small enterobacterial protein
b4613 (dinQ)	UV-inducible membrane toxin, DinQ-AgrB type I toxin-antitoxin system
b4620 (yjbT)	putative periplasmic protein
b4637 (uof)	ryhB-regulated fur leader peptide
b4663 (azuC)	acid-inducible small membrane-associated protein
b4669 (ilvX)	uncharacterized protein
b4670 (yjeV)	uncharacterized protein
b4675 (yoaJ)	inner membrane-associated protein
b4676 (yoaK)	inner membrane-associated protein
b4678 (yoeI)	uncharacterized protein
b4680 (ypdK)	inner membrane protein
b4684 (yqfG)	uncharacterized protein
b4685 (yrbN)	uncharacterized protein
b4686 (yshB)	uncharacterized protein
b4687 (shoB)	toxic membrane protein
b4702 (mgtL)	regulatory leader peptide for mgtA
b4703 (pmrR)	putative membrane-bound BasS regulator
b4705 (mntS)	Mn(2)-response protein, MntR-repressed
C_RS24035 (fdoG)	formate dehydrogenase major subunit
C_RS24040 (-)	spermidine/putrescine ABC transporter substrate-binding protein
EAKF1_RS07940 (tsr)	methyl-accepting chemotaxis protein I, serine sensor receptor
ECs0267 (crl)	DNA-binding transcriptional regulator Crl
ECs4266 (glpR)	DNA-binding transcriptional repressor GlpR
ECs4518 (rph)	ribonuclease PH
ECs4702 (-)	acetolactate synthase 2 catalytic subunit
EFER_RS06010 (cydB)	cytochrome d ubiquinol oxidase subunit II
EFER_RS09440 (-)	hypothetical protein

NCTC12129_00311 (glgP)	starch phosphorylase
NCTC12129_01305 (argT)	lysine/arginine/ornithine transport system substrate-binding protein
NCTC12129_03460 (csdA)	cysteine sulfinate desulfinase
NCTC12129_03503 (-)	lysM domain protein
NCTC12130_00627 (-)	membrane protein