Table S3. Content of reconstructed TF and RNA regulons in the Bacillales.

Regulon name [1] / ***Target regulated operons***	**TF locus tag** / ***Locus tag for a target operon***	*Bacillus subtilis sstr. 168*	*Bacillus amyloliquefaciens FZB42*	*Bacillus pumilus SAFR-032*	*Bacillus licheniformis DSM 13*	*Anoxybacillus flavithermus WK1*	*Geobacillus kaustophilus HTA426*	*Bacillus cereus ATCC 14579*	*Bacillus halodurans C-125*	*Bacillus clausii KSM-K16*	*Oceanobacillus iheyensis HTE831*	*Paenibacillus sp. JDR-2*	**Regulated Metabolic pathway or Biological process** / **Functional role of a target operon**	**Experimental Evidence**	**Reference (NCBI PMID)**
TF regulons															
HrcA regulon	**hrcA**	+	+	+	+	+	+	+	+	+	+	+	**Heat-shock**		
hrcA-grpE-dnaK	*BSU25490*	+	+	+	+	+	+	+	+	+	+	+	Heat-shock response (chaperons)	exp.	8113175
groES-groEL	*BSU06020*	+	+	+	+	+	+	+	+	+	+	+	Heat-shock response (chaperons)	exp.	8576042
htpG	*BH1007*	-	-	-	-	0	0	0	+	+	+	+	Heat-shock response (chaperons)	-	
LexA regulon	**lexA**	+	+	+	+	+	+	+	+	+	+	+	**SOS regulon**	-	
lexA	*BSU17850*	+	+	+	+	+	+	+	+	+	+	+	SOS regulon repressor	exp.	9555905
yneAB-ynzC-tkt-yneEF	*BSU17870*	+	+	+	+	+	+	+	+	+	+	0	ABC transport protein, sugar-binding component yneA; site-specific r	exp.	16267290
uvrBA	*BSU35170*	+	+	+	+	+	+	+	+	+	+	-	Excinuclease ABC subunits B, A	exp.	16267290
yqjW	*BSU23710*	+	+	+	-	0	0	0	+	+	0	+	DNA polymerase IV	exp.	16267290
dnaE-ytsJ	*BSU29230*	+	+	+	+	-	-	-	-	-	+	-	DNA polymerase III, alpha subunit; Malate dehydrogenase	exp.	16267290
pcrA-ligA-yerH	*BSU06610*	+	+	+	+	-	-	-	-	-	-	-	ATP-dependent DNA helicase; NAD-dependent DNA ligase; Putative	exp.	16267290
parEC	*BSU18090*	+	+	+	-	+	+	+	+	+	+	+	DNA topoisomerase IV subunit B; DNA topoisomerase IV subunit A	exp.	16267290
uvrC	*BSU28490*	+	+	+	-	-	-	+	-	-	-	+	Excinuclease ABC subunit C	exp.	16267290
yhjD	*BSU10470*	+	+	+	+	0	0	0	+	0	+	+	Unknown conserved protein	exp.	16267290
recA	*BSU16940*	+	+	+	+	-	+	+	+	+	+	+	Recombination protein A	exp.	9555905
addBA	*BC1137*	-	-	-	-	-	+	+	0	0	+	+	ATP-dependent nuclease, subunit B, subunitA	-	
hupA	*BSU22790*	+	+	+	+	-	-	-	-	-	-	-	DNA-binding protein HBsu	-	
ytrHI	*BSU29239*	+	+	+	+	-	-	-	-	-	-	-	Sporulation membrane proteins	-	
sda	*BSU25690*	+	+	+	+	+	+	-	+	-	0	-	Sporulation inhibitor	exp.	16267290
BPUM_2882	*BPUM_2882*	0	0	+	+	0	0	0	+	0	0	0	Hypothetical protein	-	
xkdA	*BSU12500*	+	+	+	+	+	+	0	0	0	+	0	Phage-like element PBSX protein	exp.	16267290
yolD-uvrX	*BSU21510*	+	-	0	+	0	0	0	0	0	0	0	Hypothetical protein; UV-damage repair protein	exp.	16267290
yqhHG	*BSU24580*	+	+	-	-	+	-	-	-	-	+	-	Uncharacterized ATP-dependent helicase, SNF2 family	-	
vsr	*Pjdr2_4666*	0	0	0	0	0	0	0	0	0	-	+	DNA mismatch endonuclease Vsr	-	
ruvAB	*BSU27740*	+	+	+	+	-	+	+	-	+	+	+	Holliday junction DNA helicase motor protein; Holliday junction DNA	exp.	16267290
dinB	*BSU05630*	+	+	0	0	0	0	0	0	0	0	0	Nuclease inhibitor	exp.	16267290

ykvR	*BSU13800*	+	+	0	0	0	0	0	0	0	-	0	Hypothetical protein	exp.	16267290
aprX	*BSU17260*	+	+	-	-	0	-	0	-	0	-	-	Alkaline serine protease	exp.	16267290
ypuD	*BSU23300*	+	+	+	+	0	0	0	0	0	0	0	Hypothetical protein	exp.	16267290
tagC	*BSU35770*	+	0	0	0	0	0	0	0	0	0	0	Polyglycerol phosphate assembly and export	exp.	8969214
ybaK-cwlD	*BSU01520*	+	-	-	-	-	-	-	-	-	-	-	Hypothetical protein; N-acetylmuramoyl-L-alanine amidase	exp.	16267290
uvrX	*OB1361*	0	0	0	0	0	0	0	0	0	+	0	DNA-damage repair protein	-	
Rex regulon	**rex (ydiH)**	+	+	+	+	+	+	+	+	+	+	+	**Anaerobic metabolism**	-	
ldh-lctP	*BSU03050*	+	+	+	+	+	+	+	+	+	+	0	L-lactate dehydrogenase; L-lactate permease	exp.	16207915
yjlC-ndh	*BSU12280*	+	+	0	+	0	0	-	0	0	0	+	Hypothetical protein; NADH dehydrogenase	exp.	16207915
cydABCD-yxkO	*BSU38760*	+	+	+	-	0	0	-	-	0	-	0	Cytochrome bd ubiquinol oxidase (subunit I); cytochrome bd ubiquin	exp.	16207915
yumB	*BSU32100*	-	-	-	+	+	+	-	-	-	-	+	NADH dehydrogenase, paralog yjlD	-	
ywcJ	*BSU38060*	+	0	0	+	0	0	+	0	0	0	0	Formate/nitrate family transporter	exp.	16207915
pflBA	*BLi02132*	0	0	+	0	+	0	+	0	0	0	-	Pyruvate-formate lyase; Pyruvate-formate lyase-activating enzyme	-	
yndGHJ	*BPUM_1837*	-	-	+	+	0	0	+	0	0	-	-	Hypothetical protein	-	
adh	*BLi04290*	0	0	0	+	+	0	+	0	0	0	0	Alcohol dehydrogenase	-	
ABC1842	*ABC1842*	0	0	0	0	0	0	0	0	+	+	0	NADH dehydrogenase	-	
qoxABCD	*Aflv_0272*	-	+	-	-	+	-	+	+	-	+	0	Cytochrome aa3 quinol oxidase	-	
ydbI	*BSU04480*	+	+	-	-	0	0	0	0	0	0	0	Hypothetical protein	-	
OB2241-putP	*OB2241*	0	0	0	0	0	0	0	0	0	+	0	Pantothenate permease	-	
nadABC	*Pjdr2_0068*	-	-	-	-	-	-	-	-	-	0	+	NAD biosynthesis	-	
nasA	*BLi00365*	-	-	0	+	0	-	0	0	-	0	0	Nitrate transporter	-	
adh2	*BC2220*	0	-	0	0	0	0	+	0	0	0	0	Alcohol dehydrogenase	-	
nirS	*GK0767*	0	0	0	0	0	+	0	0	0	0	0	Nitrate reductase	-	
naoX	*Pjdr2_2160*	0	0	0	0	0	0	0	0	0	0	+	FAD-dependent pyridine nucleotide-disulphide oxidoreductase	-	
coxAB	*OB1745*	0	0	0	0	-	-	0	-	0	+	0	Cytochrome c oxidase (b(o/a)3-type) chain II; Cytochrome c oxidase	-	
Fnr regulon	**fnr**	+	+	0	+	+	+	+	+	0	0	+	**Anaerobic metabolism**	-	
narK-fnr	*BSU37320*	+	+	0	+	-	-	+	-	-	0	-	Nitrite extrusion protein; transcriptional regulator (FNR/CRP family)	exp.	16428414
narGHJI	*BSU37280*	+	+	-	+	0	-	-	0	-	0	0	Nitrate reductase	exp.	16428414
arfM	*BSU37290*	+	+	0	+	0	0	0	+	0	0	0	Anaerobic respiration and fermentation modulator	exp.	11698370
ldh-lctP	*BSU03050*	+	+	-	+	-	+	+	+	-	-	0	L-lactate dehydrogenase; L-lactate permease	-	
naoX	*Pjdr2_2160*	0	0	0	0	0	0	0	0	0	0	+	FAD-dependent pyridine nucleotide-disulphide oxidoreductase	-	
ywcJ	*BSU38060*	+	0	0	+	0	0	0	0	0	0	0	Formate/nitrate family transporter	-	
adh	*BLi04290*	0	0	0	+	-	0	+	0	0	0	0	Alcohol dehydrogenase	-	
coxAB	*BH0740*	0	0	0	0	-	-	0	+	0	-	0	Transcriptional regulator (Crp family, AMP-binding protein; nitric oxid	-	
LicR regulon	**licR**	+	+	+	+	0	0	+	0	+	+	0	**Betta-glucosides metabolism**	-	
licBCAH	*BSU38590*	+	+	+	-	0	0	-	0	+	+	0	Beta-glucosides-specific PTS system; 6-phospho-beta-glucosidase	exp.	10438772
licR	*BSU38600*	-	-	-	-	0	0	-	0	+	+	0	Transcriptiolan regulator of beta-glucosides utilization operon	-	
ManR regulon	**manR**	+	+	0	+	0	0	0	0	0	0	0	**Mannose utilization**	-	

manR	*BSU12000*	+	+	0	-	0	0	0	0	0	0	0	Transcriptiolan regulator of mannose utilization operon	exp.	20139185
manPA	*BSU12010*	+	+	0	+	0	0	0	0	0	0	0	Mannose utilization	exp.	20139185
MtlR regulon	**mtlR**	+	+	+	+	+	+	0	+	+	+	+	**Mannilol utilization**	-	
mtlAFD	*BSU03981*	+	+	+	+	+	+	0	+	-	+	+	Mannitol utilization	exp.	20444094
mtlR	*BSU04160*	+	+	+	-	+	+	0	+	-	+	+	Transcriptiolan regulator of mannitol utilization operon		
BirA regulon	**birA**	+	+	+	+	+	+	+	+	+	+	+	**Biotin methabolism**	-	
bioWAFDBI	*BSU30240*	+	+	+	+	+	+	+	+	0	0	+	Biotin biosynthesis	exp.	8892842
bioY2-yhfTS	*BSU10370*	+	+	+	+	0	0	+	0	+	+	+	Biotin ECF transporter; Long-chain-fatty-acid--CoA ligase; 3-ketoacyl	-	
bioY1	*BSU32030*	+	+	+	+	+	+	+	+	+	+	0	Biotin ECF transporter	-	
FruR regulon	**fruR**	+	+	+	+	+	+	+	+	+	+	0	**Fructose methabolism**	-	
fruRKA	*BSU14380*	+	+	+	+	+	+	+	+	+	+	0	Fructose utilization	-	
TreR regulon	**treR**	+	+	+	+	+	+	+	+	+	0	0	**Trehalose utilization**	-	
trePAR	*BSU07800*	+	+	+	+	+	+	+	+	+	0	0	Trehalose utilization	exp.	8755887
GntR regulon	**gntR**	+	0	0	+	0	0	0	0	0	+	0	**D-gluconate utilization**	-	
gntRKPZ	*BSU40050*	+	0	0	+	0	0	0	0	0	+	0	Gluconate utilization	exp.	7476858
YtrA regulon	**ytrA**	+	+	+	+	+	+	+	0	0	0	0	**Ramoplanin resistance**	-	
ytrABC	*BSU30460*	+	+	+	+	+	+	+	0	0	0	0	ABC efflux transporter; induced by Ramoplanin antibiotic	exp.	10986249
ywoBCD	*BSU36500*	+	0	0	0	0	0	0	0	0	0	0	Hypotetical transmembrane protein, drug resistance transporter	-	
ytrEF	*BSU30420*	+	+	+	+	0	0	0	0	0	0	0	ABC efflux transporter; induced by Ramoplanin antibiotic	exp.	10986249
ExuR regulon	**exuR**	+	+	+	+	0	0	0	0	0	0	0	**Hexuronate utilization**	-	
uxaC--exuM-yjmCD-uxuA-yjmF-exuTR-ux	*BSU12300*	+	+	+	+	0	0	0	0	0	0	0	Hexuronate utilization	exp.	9882655
LacR (GanR) regulon	**ganR**	+	0	+	+	0	0	0	+	+	0	0	**Galactan utilization**	-	
ganR	*BSU34170*	+	0	+	+	0	0	0	-	-	0	0	Transcriptiolan regulator of galactan utilization operon	-	
cycB-ganPQAB	*BSU34160*	+	0	+	+	-	0	0	+	+	0	0	Cyclodextrin ABC transporter; beta-1,4-galactooligomerase; arabinog	exp.	9287030
NtdR regulon	**ntdR**	+	0	+	+	0	0	0	0	0	0	0	**Neotrehalosadiamine utilization**	-	
ntdABC	*BSU10550*	+	0	+	+	0	0	0	0	0	0	0	NTD biosynthesis	exp.	14612444
ntdR	*BSU10560*	+	0	+	+	0	0	0	0	0	0	0	NTD biosynthesis operon regulator	-	
GlvR regulon	**glvR**	+	+	0	+	0	0	0	0	0	0	0	**Maltose utilization**	-	
glvARC	*BSU08180*	+	+	0	+	0	0	0	0	0	0	0	Maltose utilization	exp.	11489864
CggR regulon	**cggR**	+	+	+	+	+	+	+	+	+	+	+	**Fructose-1,6-bisphosphate metabolism**	-	
cggR-gapA-pgk-tpiA-pgm-eno	*BSU33950*	+	+	+	+	+	+	+	+	+	+	+	Glycolysis	exp.	12622823
ArgR regulon	**argR**	+	+	+	+	+	+	+	+	+	+	+	**Arginine metabolism**	-	
argCJBD-carAB-argF	*BSU11190*	+	+	+	+	+	+	+	+	+	+	+	Arginine biosynthesis	exp.	7565595
argGH	*BSU29450*	+	+	+	+	+	+	+	+	+	+	+	Arginine biosynthesis	-	
Aflv_0223	*Aflv_0223*	0	0	0	0	+	+	+	0	0	0	+	Amino acid acetyltransferase (GNAT family)	-	
artPQM	*BSU23980*	+	+	+	+	0	0	+	+	0	0	-	Arginine ABC transporter	-	
arcABDC	*BLi04163*	0	0	0	+	0	0	+	0	0	0	0	Arginine catabolism	-	
rocABC	*BSU37780*	+	-	-	-	-	-	+	-	-	+	-	Arginine utilization	exp.	7565595

rocDEF	*BSU40340*	+	-	+	-	-	-	-	-	-	+	-	Arginine utilization	exp.	9383188
Fur regulon	**fur**	+	+	+	+	+	+	+	+	+	+	+	**Iron metabolism**	-	
ykuNOP	*BSU14150*	+	+	+	+	+	0	+	0	+	0	+	Flavodoxin; BNR repeat domain protein; Flavodoxin; 2,3,4,5-tetrahyd	exp.	12354229
yfhC	*BSU08480*	+	+	+	+	0	0	+	+	+	+	-	Nitroreductase	exp.	12354229
yusV	*BSU32940*	+	+	+	+	+	-	-	+	0	+	+	Iron(III) dicitrate transport ATP-binding protein (TC 3.A.1.14.1)	exp.	12354229
yclNOPQ	*BSU03800*	+	+	+	+	0	0	+	+	+	+	0	Ferrichrome ABC transporter	exp.	12354229
yfiZ-yfhA	*BSU08450*	+	0	0	+	+	+	0	0	0	0	+	ABC-type Fe3+-siderophore transport system, permease component	exp.	12354229
yfiY	*BSU08440*	+	0	+	0	0	0	0	+	0	0	+	ABC-type Fe3+-siderophore transport system, periplasmic iron-bindi	exp.	12354229
feuABC-ybbA	*BSU01630*	+	+	+	+	0	0	+	0	+	+	+	Fe-bacillibactin transport system; Trilactonehydrolase	exp.	12354229
fhuBGC	*BSU33310*	+	+	+	+	+	+	+	+	+	+	+	Ferrichrome transport system permease protein; Ferrichrome transpo	exp.	12354229
fhuD	*BSU33320*	+	+	+	+	0	0	0	0	0	0	+	Ferrichrome ABC superfamily ATP binding cassette transporter, bind	exp.	12354229
asbABCDEF	*BC1978*	0	0	0	0	0	0	+	0	+	0	0	Anthrachelin biosynthesis	-	
sidABCDEFG	*BH2624*	0	0	+	+	0	0	0	+	0	0	0	Siderophore biosynthesis	-	
yetG	*BSU07150*	+	0	0	0	0	0	0	+	+	0	0	Antibiotic biosynthesis monooxygenase domain containing protein	exp.	21873409
ycgT	*BSU03270*	+	+	+	+	+	-	+	+	+	+	+	Thioredoxin reductase	exp.	12354229
dhbACEBF	*BSU32000*	+	+	+	+	0	0	0	0	0	+	0	Siderophore biosynthesis	exp.	12354229
fbpC (mgrC ypbR upstream)	*BSU22030 (u*	+	+	+	+	0	0	0	0	0	0	0	Fur-regulated basic proteins	exp.	18697947
fbpAB (ydbN)	*BSU04530*	+	+	+	+	0	0	0	0	0	0	0	Fur-regulated basic proteins	exp.	18697947
yxeB	*BSU39610*	+	+	0	+	0	0	0	0	+	+	+	Fe3+-hydroxamate ABC transporter substrate-binding protein	exp.	12354229
ywjAB	*BSU37230*	+	+	+	0	0	0	+	0	0	0	+	Multidrug resistance ABC transporter ATP-binding and permease pro	exp.	12354229
nikABCDE	*BLi02811*	0	0	+	+	0	0	0	+	0	0	0	Nickel transport system (nickel-binding protein); nickel transport syste	-	
feoAB	*BLi04266*	0	0	0	+	+	-	+	0	0	0	0	Fe2+ transport system protein A	-	
yhfQ	*BSU10330*	+	+	0	+	0	0	0	0	0	0	+	Heme ABC type transporter	exp.	12354229
efeUOB (ywbLMN)	*BSU38280*	+	0	0	0	0	0	0	0	0	0	+	Ferrous iron transport	exp.	12354229
OB3390	*OB3390*	0	0	0	0	0	0	0	0	0	+	+	Iron-siderophore binding lipoprotein	-	
futC	*BH0512*	0	0	0	0	0	0	0	+	0	0	0	Ferric iron ABC transporter, ATP-binding protein	-	
futAB	*BH0513*	0	0	0	0	0	0	0	+	0	0	0	Ferric iron ABC transporter, binding protein and permease protein	-	
fer	*BSU23040*	+	+	+	0	+	-	+	-	-	0	-	Ferredoxin	-	
fur	*BSU23520*	-	-	-	+	-	-	+	+	-	-	+	Transcription regulator	-	
miaB-ymcA	*BSU17010*	+	+	-	+	-	-	-	-	-	-	-	TRNA-i(6)A37 thiotransferase enzyme; Uncharacterized protein invol	-	
yuiI	*BSU32010*	+	+	0	+	0	0	0	0	0	0	+	Trilactone hydrolase [bacillibactin] siderophore	exp.	12354229
btr	*BSU01640*	+	+	+	-	0	0	0	0	+	0	+	Transcriptional regulator of Fe-bacillibactin uptake, AraC family	exp.	12354229
nasEF	*BSU03290*	+	-	-	-	0	-	-	-	-	0	0	Assimilatory nitrite reductase (subunit); uroporphyrin-III C-methyltran	exp.	12354229
yoaJ (exlX)	*BSU18630*	+	0	0	+	0	0	0	0	0	0	0	Extracellular endoglucanase precursor	exp.	12354229
yfmCDEF	*BSU07520*	+	0	0	0	0	0	+	+	+	0	0	Ferrichrome ABC transporter (binding protein)	exp.	12354229
yumC	*BSU32110*	+	+	+	-	-	-	-	-	-	+	-	Ferredoxin--NAD(+) reductase	-	
MntR regulon	**mntR**	+	+	+	+	+	+	+	+	+	+	+	**Manganase transport**	-	
mntABCD	*BSU30770*	+	0	+	+	+	0	0	+	+	+	+	Manganese ABC transporter	exp.	10760146

mntH	*BSU04360*	+	+	+	+	0	+	+	0	0	0	+	Manganese transport protein MntH	exp.	10760146
feoAB1B2	*BC0709*	0	0	-	0	-	-	+	0	0	0	0	Ferrous iron transport	-	
Zur regulon	**zur**	+	+	+	+	+	+	+	+	+	+	+	**Zinc transport**	-	
yciC	*BSU03360*	+	+	+	+	+	0	+	+	+	+	+	Putitative GTPase	exp.	9811636
yciAB	*BSU03340*	+	0	0	+	0	0	0	+	0	-	0	GTP cyclohydrolase I type 2; D-alanyl-D-alanine carboxypeptidase	exp.	12426338
adcABC	*BSU02850*	+	+	+	+	+	+	+	+	+	+	+	Zinc ABC transporter	exp.	9811636
zur	*BSU25100*	-	-	-	-	+	+	+	+	+	+	-	Zinc uptake regulation protein	-	
pgp	*BLi01934*	0	0	0	+	0	0	+	0	+	+	0	Putative GTPases	-	
rpmE2 (L31p)	*BSU30700*	+	+	+	+	0	0	-	-	-	-	0	50S ribosomal protein L31 type B	exp.	15049826
rpmGB (L33p)	*BLi02553*	0	-	+	+	+	0	+	0	0	+	0	50S ribosomal protein L33 paralog	-	
rpsN2 (S14p)	*BSU08880*	+	-	+	+	0	0	+	0	0	+	0	30S ribosomal protein S14 paralog	exp.	19648245
zinT	*BSU26830*	+	0	0	0	0	0	0	0	+	+	0	Candidate zinc-binding lipoprotein	-	
NiaR regulon	**niaR**	+	+	+	+	+	+	+	+	+	0	0	**NAD metabolism**	-	
nadBCA	*BSU27870*	+	+	+	+	+	+	+	+	+	0	-	Nicotinate ribonucleotide biosynthesis	exp.	18276644
nifS-niaR	*BSU27880*	+	+	+	+	+	+	+	+	+	0	0	Cysteine desulfurase; Transcriptional repressor	exp.	18276644
niaY	*BH3254*	0	0	-	0	0	0	0	+	+	0	0	Predicted nicotinate-regulated transporter NiaY	-	
niaP (yceI)	*BSU02950*	+	+	0	+	-	+	+	0	0	0	-	Niacin uptake	exp.	18276644
PerR regulon	**perR**	+	+	+	+	+	+	+	+	+	+	+	**H2O2 stress-response**	-	
perR	*BSU08730*	+	+	+	+	+	+	+	+	+	+	-	H2O2 stress-response transcriptional regulator	exp.	12029044
fur	*BSU23520*	+	+	+	+	+	+	+	+	+	+	+	Iron metabolism transcription regulator	exp.	12029044
hemAXCDBL	*BSU28170*	+	+	+	+	-	-	+	+	-	+	+	Uroporphyrinogen III biosynthesis	exp.	11532148
ahpCF	*BSU40090*	+	+	0	+	+	+	+	0	0	0	+	Alkyl hydroperoxide reductase	exp.	11532148
zosA (ykvW)	*BSU13850*	+	+	+	+	0	0	+	+	+	0	-	Zinc uptake ATPase	exp.	12426338
czcD	*Aflv_0372*	0	0	0	0	+	+	0	-	0	0	+	Co/Zn/Cd efflux system component	-	
katA	*BSU08820*	+	+	+	+	0	0	+	0	+	+	-	Catalase	exp.	11532148
ypzK	*BSU23240*	-	-	+	+	-	+	-	-	0	+	0	GCN5-related N-acetyltransferase (GNAT) domain protein	-	
spxA	*BSU11500*	+	+	+	+	+	+	+	-	-	+	0	RNAP transcription regulator	exp.	17158660
mrgA	*BSU32990*	+	+	0	+	0	0	0	0	0	0	0	Non-specific DNA-binding protein Dps / Iron-binding ferritin-like antio	exp.	11532148
dps	*BC5044*	-	-	-	0	-	-	+	0	0	-	-	Non-specific DNA-binding protein Dps	-	
yybE	*RBAM_0242*	0	+	0	+	0	0	0	0	0	0	+	HTH-transcriptional regulator	-	
Aflv_2437-Aflv_2436	*Aflv_2437*	0	0	0	0	+	+	0	0	0	0	0	Hypothetical protein; Predicted Zn peptidase	-	
yozI	*BSU18870*	+	0	0	0	0	0	0	0	0	0	0	Hypothetical protein	-	
plsC	*BSU09540*	-	-	-	-	-	0	+	-	0	0	-	1-acyl-sn-glycerol-3-phosphate acyltransferase	-	
yoaA	*OB2645*	-	-	-	-	0	0	-	-	-	+	-	Uncharacterized N-acetyltransferase	-	
yxbB	*BH1951*	0	0	0	0	0	0	0	+	0	0	0	Putative sugardehydrogenase	-	
OB0178	*OB0178*	0	0	0	0	0	0	0	0	0	+	0	Hypothetical protein	-	
trxB	*Pjdr2_0784*	-	-	-	-	-	-	-	-	-	-	+	Thioredoxin reductase	-	
Pjdr2_5937	*Pjdr2_5937*	0	-	0	0	0	+	+	0	0	+	+	Membrane protein	-	

XylR regulon	**xylR**	+	+	+	+	0	+	0	+	+	+	+	**Xylose metabolism**	-	
xylAB	*BSU17600*	+	+	+	+	0	+	0	+	+	+	+	Xylose utilization	exp.	7966270
xylR	*BSU17590*	+	+	+	+	0	+	0	+	-	+	+	Transcriptional regulator of xylose metabolism regulon	-	
xynPB	*BSU17570*	+	+	+	-	0	0	0	+	-	+	-	Xyloside transporter; xylan 1,4-beta-xylosidase	exp.	9973552
OB3123-OB3122-OB3121	*OB3123*	0	0	0	0	0	0	0	+	0	+	-	Predicted beta-xyloside ABC transporter	-	
BH3678-BH3679	*BH3678*	0	0	0	0	0	0	0	+	0	0	-	Sensor histidine kinase; two-component response regulator	-	
gunAB	*BLi01880*	0	0	-	+	0	0	0	0	0	0	0	Putative endo-1,4-glucanase; putative cellulose 1,4-beta-cellobiosida	-	
BLi03540-BLi03541-yurM-xylS-bglI	*BLi03540*	0	0	0	+	0	0	0	0	-	0	0	Possible xylosidase ABC transporter; Alpha-xylosidase; Beta-glucosi	-	
xynA	*BH2120*	0	0	0	0	0	0	0	+	0	0	-	Endo-1,4-beta-xylanase A	-	
xylF	*GK1881*	0	0	0	-	-	+	0	0	0	0	-	D-xylose ABC transporter (substrate-bindin protein)	-	
GltC regulon	**gltC**	+	+	+	+	+	+	0	0	0	0	0	**Glutamate metsbolism**	-	
gltAB	*BSU18450*	+	+	+	+	+	+	0	-	-	-	-	Glutamate synthase	exp.	7559359
gltC	*BSU18460*	+	+	+	+	+	+	0	0	0	0	0	Transcription activator	exp.	7559359
CtsR regulon	**ctsR**	+	+	+	+	+	+	+	+	+	+	+	**Heat-shock response**	-	
ctsR-mscAB-clpC-radA-disA	*BSU00830*	+	+	+	+	+	+	+	+	+	+	+	Transcription regulator; mscB induser; tyrosine kinase; ATPase for cl	exp.	9987115
clpE	*BSU13700*	+	+	+	+	-	+	-	+	+	+	-	ATP-dependent Clp protease ATP-binding subunit	exp.	10320580
clpP	*BSU34540*	+	+	+	+	+	+	+	+	+	+	+	ATP-dependent Clp protease proteolytic subunit	exp.	10320580
ywrO	*RBAM_0331*	-	+	0	-	0	0	-	0	0	0	-	General stress protein 14 (NAD(P)H dehydrogenase)	-	
sspI	*BLi03018*	-	-	-	+	-	-	-	+	-	-	-	Small acid-soluble spore protein SspI	-	
clpB	*GK0799*	0	0	0	0	+	+	+	0	0	0	0	Chaperone	-	
HSP16.4	*BC2214*	0	0	0	0	0	0	+	0	0	0	0	Heat shock protein HSP.16.4	-	
BC4452	*BC4452*	0	0	0	0	0	0	+	0	0	0	0	Hypothetical protein	-	
GlnR regulon	**glnR**	+	+	+	+	+	+	+	0	0	+	+	**Nitrogen excess response**	-	
glnRA	*BSU17450*	+	+	+	+	+	+	+	0	-	+	-	Transcriptional regulator; glutamine synthetase	exp.	1346263
tnrA	*BSU13310*	+	-	+	+	+	+	0	0	-	-	+	Transcriptional regulator	exp.	16547045
ureABC	*BSU36660*	+	+	0	0	0	+	0	0	0	0	+	Urease	exp.	9287005
nrgA	*BSU36510*	-	-	-	-	-	-	+	-	-	0	-	Ammonium transporter	-	
alsT	*BC5051*	0	0	0	0	0	0	+	0	0	0	0	Sodium/proton-dependent alanine carrier protein	-	
gltP	*BC1432*	0	0	0	0	0	0	+	0	0	0	0	Glutamate-aspartate carrier protein	-	
TnrA regulon	**tnrA**	+	+	+	+	+	+	0	+	+	+	+	**Nitrogen assimilation**	-	
tnrA	*BSU13310*	+	+	+	+	+	-	0	+	+	-	+	Transcriptional regulator	exp.	16547045
glnRA	*BSU17450*	+	+	+	+	+	-	0	+	-	+	-	Transcriptional regulator; glutamine synthetase	exp.	8799114
gabP	*BSU06310*	+	+	0	-	0	0	-	0	0	0	0	Gamma-aminobutyrate (GABA) permease	exp.	8951816
oppABCDF	*BSU11430*	+	+	-	+	+	+	0	+	+	0	+	Oligopeptide ABC transporter	exp.	12823818
ywlFG	*BSU36920*	+	+	-	-	-	-	-	-	-	-	-	Ribose 5-phosphate isomerase B; hypothetical protein	exp.	12823818
pucABCDE	*BSU32510*	+	-	0	0	0	-	-	-	+	0	+	Xanthine dehydrogenase	-	
pucJKLM	*BSU32430*	+	0	0	0	0	0	0	+	-	0	+	Xanthine permease; xanthine permease; uricase; urate oxidase strut	exp.	12823818
pucH	*BSU32410*	+	+	0	-	0	0	0	0	+	0	+	Allantoinase	-	

yurHG	*BSU32530*	-	-	-	+	0	0	0	-	-	0	+	Allantonate amidohydrolase; serene-pyruvate/alanine-glyoxylate ami	-	
ABC3747-45	*ABC3747*	0	0	0	0	0	0	0	0	+	0	+	Hypothetical ABC transporter	-	
nasBC	*BSU03320*	+	+	-	+	0	+	-	+	+	0	+	Assimilatory nitrate reductase	exp.	7836289
nasDEF	*BSU03300*	+	+	0	+	0	+	-	+	+	0	+	Nitrite reductase; uroporphyrin-III C-methyltransferase	exp.	7836289
nasA	*BSU03330*	+	+	0	0	0	0	0	0	+	0	0	Nitrate transporter	exp.	7836289
ykoLM	*BSU13330*	+	+	+	-	0	0	0	0	0	0	0	Hypothetical protein; transcriptional regulator	exp.	10671441
ykzB	*BSU13320*	+	+	0	0	+	+	0	0	0	0	0	Hypothetical protein	exp.	10671441
ycsFGI-kipIAR-lipC	*BSU04070*	+	+	+	+	0	-	-	-	-	-	-	LamB/YcsF family protein; putative branched chain amino acids trans	exp.	9334321
nrgAB	*BSU36510*	+	+	+	+	+	+	0	+	+	0	+	Ammonium transporter; nitrogen-regulated PII-like protein	exp.	8799114
pucR	*BSU32420*	+	+	+	+	0	0	0	+	-	0	+	Transcriptional regulator of purine degradation operon	exp.	12823818
argCJBD-carAB-argF	*BSU11190*	+	+	+	+	-	-	-	-	-	-	-	Argenine biosynthesis	-	
glnA2	*GK1637*	0	0	0	0	+	+	0	+	+	0	0	Glutamine synthetase type I	-	
ureABC	*BSU36660*	+	+	0	0	0	+	0	+	0	0	+	Urease	-	
urtABCDE	*GK1937*	0	0	0	0	0	+	0	+	0	0	+	Urea ABC transporter	-	
pucI-ywoF	*BSU36470*	+	+	+	+	0	0	0	0	-	0	0	Allantion permease; putitative pectate lyase	-	
gltAB	*BSU18450*	+	+	+	+	-	-	0	-	-	-	-	Glutamate synthase (large subunit); glutamate synthase (small subu	exp.	11029411
gltC	*BSU18460*	+	+	+	+	-	-	0	0	0	0	0	Transcription activator	-	
yoyD-yodF	*BSU19579*	+	+	+	+	0	0	0	0	0	0	0	Hypothetical protein; Na+/metabolite permease	exp.	12823818
yuiABC	*BSU32090*	+	+	+	+	-	-	-	+	-	-	-	Hypothetical protein; hypothetical protein; cell wall-cinding protein	-	
nagABRCP	*BLi04348*	-	+	-	+	0	-	-	+	-	+	-	N-acetylglucoseamine utilization	-	
ydaB	*BSU04170*	+	+	+	+	0	0	0	0	0	0	0	Long-chain-fatty-acid--CoA ligase	-	
ilvBHC-leuABCD	*BSU28310*	+	+	-	-	-	-	-	+	-	+	-	Branched-chain amino acid biosynthesis	exp.	15547269
alsT	*BSU18120*	+	+	0	+	0	0	0	+	-	0	0	Sodium:alanine symporter	exp.	12823818
thyA-dfrA	*BSU21820*	-	-	-	-	+	-	-	-	-	+	+	Thymidylate synthase; dihydrofolate reductase	-	
ilvD	*BSU21870*	-	-	+	+	+	+	-	-	-	0	-	Dihydroxy-acid dehydratase	-	
yumC	*BSU32110*	+	+	-	-	-	-	-	+	-	-	-	Ferredoxin--NADP reductase 2	-	
pel	*BSU07560*	+	+	0	+	0	0	0	0	0	0	0	Pectate lyase	exp.	12823818
arcD	*BLi03438*	0	0	0	+	0	0	0	+	+	0	0	Arginine/ornithine antiporter	-	
rapJ	*BSU02820*	+	+	+	+	0	0	0	0	0	0	0	Response regulator aspartate phosphatase	-	
gsiC-dppBCD-ABC0569-ABC0570-ABC0	*ABC0565*	0	0	-	-	-	0	0	-	+	-	0	Oligopeptide transporter; hypothetical protein; acetylornithine deacet	-	
braB	*BSU29600*	+	+	0	+	0	0	0	0	0	0	0	Branched chain amino acid-Na+ symporter	-	
yqzL-recO	*BSU25280*	+	+	+	+	-	+	-	+	-	-	-	DNA recombination and repair protein	-	
gltT	*BH3820*	0	0	-	-	-	0	-	+	-	+	0	H+/sodium-glutmate symporter	-	
glnB-BLi01175	*BLi01176*	0	0	0	+	0	0	0	0	0	+	0	Nitrogen regulatory PII protein; ammonium transporter	-	
ywdIJK	*BSU37930*	+	+	-	-	0	0	-	0	0	0	-	Hypothetical protein; purine/ pyrimidine permease; hypothetical prote	exp.	12823818
ysnE	*BSU28330*	+	+	+	0	0	0	0	+	0	0	0	Putative acetyltransferase	-	
oppXYBZA	*OB2615*	0	0	0	0	0	0	0	+	+	+	0	Oligopeptide ABC transporter	-	
yclG	*BSU03680*	+	+	+	+	0	0	0	0	0	0	0	Pectate lyase family protein	-	

yclF	*BSU03670*	+	+	+	-	-	0	0	0	0	0	0	Di-tripeptide-proton ABC symporter	-	
ykgA	*BSU13020*	-	+	+	+	0	0	0	0	-	-	0	Arginine deiminase	-	
BLi02962	*BLi02962*	0	0	+	+	-	-	-	0	0	0	0	Branched-chain amino acid aminotransferase	-	
pgsBCAE	*BSU35900*	+	-	+	-	0	0	0	0	0	0	0	Polyglutamate synthesis	-	
yrbD	*BSU27810*	+	0	0	0	0	0	0	0	+	0	0	Sudium/proton-alanine transporter	-	
yvgT	*BSU33460*	+	+	-	-	-	-	-	-	-	0	-	Membrane protein	-	
glnQHMP	*BSU27430*	+	-	-	0	-	-	-	0	-	0	+	Glutamine ABC transporter	exp.	12823818
yccC	*BSU02690*	+	-	-	0	0	0	0	0	0	0	0	L-asparaginase	exp.	11914346
yttA	*BSU30360*	+	+	0	0	0	0	0	0	0	0	0	Hypothetical protein	exp.	12823818
ywrD	*BSU36100*	+	+	0	+	0	0	0	0	0	0	+	Gamma-glutamyltransferase	exp.	12823818
yxkC	*BSU38850*	+	-	0	0	0	0	0	0	0	0	0	Hypothetical protein	exp.	12823818
yycCBA	*BSU40470*	+	-	-	+	0	0	0	0	0	+	0	Hypothetical protein; cyanate MFS transporter	exp.	12823818
degU	*BSU35490*	+	-	+	-	-	-	0	-	-	-	-	Transcription regulator	exp.	18502860
BglR regulon	**bglR**	**+**	**+**	**+**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**Beta-glucoside catabolism**	-	
bglR	*BSU40130*	+	+	+	0	0	0	0	0	0	0	0	Transcription regulator	-	
bglA	*BSU40110*	+	+	+	0	0	0	0	0	0	0	0	Aryl-phospho-beta-glucosidase	-	
RbsR regulon	**rbsR**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**Ribose utilization**	-	
rbsRKDACB	*BSU35910*	+	+	+	+	+	+	+	+	+	+	+	Ribose utilization	-	
ScrR regulon	**scrR**	**0**	**+**	**0**	**+**	**0**	**0**	**0**	**0**	**+**	**0**	**+**	**Sucrose utilization**	-	
scrR	*RBAM_0318*	0	+	0	+	0	0	0	0	-	0	+	Sucrose operon transcription regulator	-	
sacC	*RBAM_0318*	0	+	0	+	-	0	0	0	+	0	+	Sucrose-6-phosphate hydrolase	-	
ywbF	*RBAM_0318*	0	+	0	+	0	0	0	0	0	0	0	Sucrose permease	-	
sacHGF	*ABC3117*	0	0	0	+	0	0	0	0	+	0	+	ABC sugar transporter	-	
MsmR regulon	**msmR**	**+**	**+**	**+**	**+**	**0**	**0**	**0**	**+**	**0**	**0**	**0**	**Alpha-galactosides utilization**	-	
msmREFG-melA	*BSU30260*	+	+	+	+	0	0	0	+	-	0	-	multiple sugar ABC transporter; alpha-galactosidase	-	
MdxR regulon	**mdxR**	**+**	**0**	**0**	**+**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**Maltodextrin utilization**	-	
mdxEFG-malAKL-pgcM	*BSU34610*	+	0	0	+	0	0	0	0	0	0	0	Maltodextrin utilization	-	
mdxD	*BSU34610*	+	0	0	+	-	0	-	-	-	-	0	Intracellular maltogenic amylase	-	
NrdR regulon	**nrdR**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**Deoxyribonucleotide biosynthesis**	-	
nrdIEF-ymaB	*BSU17370*	+	+	+	+	0	0	+	0	+	0	+	Ribonucleotide reductase; ribonucleotide-diphosphate reductase;puta	-	
nrdJ	*BH2810*	0	0	0	0	0	+	0	+	0	0	+	Ribonucleoside-diphosphate reductase	-	
nrdAB	*BH0501*	0	0	0	0	+	+	0	+	0	+	0	Ribonucleotide-diphosphate reductase	-	
PurR regulon	**purR**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**Purine biosynthesis**	-	
purA	*BSU40420*	+	+	+	+	+	+	+	+	+	+	+	Adenylosuccinate synthase	exp.	9393704
purR-yabJ	*BSU00470*	+	+	+	+	-	+	+	+	+	+	+	Transcription regulator; endoribonuclease L-PSP	exp.	9393704
guaC	*BSU32130*	+	+	0	+	0	0	+	0	+	+	0	Guanosine 5'-monophosphate oxidoreductase	exp.	11591660
nusB-folD	*BSU24320*	+	+	+	+	-	+	+	+	-	-	-	Transcription termination factor; 5,10-methylene-tetrahydrofolate deh	exp.	11591660
glyA	*BSU36900*	+	+	+	+	+	+	+	+	+	-	-	Serine hydroxymethyltransferase	exp.	11591660

pbuO	*BSU29990*	+	+	+	+	0	0	0	0	0	0	0	Xanthine/uracil/thiamine/ascorbate permease	exp.	11591660
steT	*BSU12860*	+	+	+	+	-	0	-	0	0	0	0	Serine/threonine exchanger SteT	-	
purEKBCSQLFMNHD	*BSU06420*	+	+	+	+	+	+	+	+	+	+	-	IMP biosynthesis	exp.	9393704
pbuG	*BSU06370*	+	+	+	+	+	+	+	+	+	+	0	Hypoxanthine/guanine permease	exp.	11591660
xpt-pbuX	*BSU22070*	+	+	+	+	0	0	+	+	+	-	-	Xanthine phosphoribosyltransferase; xanthine permease	exp.	11591660
gcvTBA	*BSU24570*	-	-	+	+	+	+	-	+	+	+	0	Glycine cleavage system protein T (aminomethyltransferase); Glycin	-	
ABC2870-68	*ABC2870*	0	0	0	0	0	0	0	0	+	+	0	N-acetyl-L, L-diaminopimelate deacetylase; membrane protein; hypo	-	
BH1470	*BH1470*	0	0	0	0	+	-	-	+	0	0	-	NAD(FAD)-utilizing dehydroganase	-	
OB2790	*OB2790*	0	0	0	0	0	0	0	0	0	+	0	Aminobenzoyl-glutamate transport protein pump; hypothetical protei	-	
MurR regulon	**murR**	**+**	**0**	**+**	**+**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**Muropeptide rescue pathway**	-	
murQR-ybbF-amiE-nagZ-ybbC	*BSU01700*	+	-	+	+	0	0	-	-	-	-	0	N-acetylmuramic acid-6-phosphate etherase; tramscriptional regulat	-	
MhqR regulon	**mhqR**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**0**	**+**	**+**	**+**	**2-Methylhydroquinone and catechol resistance (thiol stress)**	-	
mhqED	*BSU19570*	+	+	+	+	0	0	+	0	-	0	+	Glyoxalase/bleomycin resistance protein/dioxygenase; Carboxyleste	exp.	17725564
mhqNOP	*BSU05480*	+	+	+	+	0	0	+	0	+	+	-	Oxygen-insensitive NAD(P)H nitroreductase / Dihydropteridine reduc	exp.	17725564
ywrF	*BSU36080*	-	-	-	+	0	0	+	-	-	-	+	Flavin reductase domain protein FMN-binding	-	
ywrF	*ABC0534*	0	0	+	+	0	0	0	-	+	-	0	Putative multimeric flavodoxin	-	
mhqA	BSU12870	+	+	+	+	0	0	0	0	0	0	0	Lactoylglutathione lyase	exp.	17725564
mhqR	*BSU13670*	-	-	-	+	+	-	+	0	+	-	+	MarR transcriptional regulator	-	
azoR2	*BSU33540*	+	+	+	-	0	-	+	-	0	0	0	FMN-dependent NADH-azoreductase	exp.	17725564
BC5037	*BC5037*	0	0	0	0	+	+	0	0	+	0	-	Pirin	-	
CymR	**cymR**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**Cysteine metabolism**	-	
cysK	*BSU00730*	+	+	+	+	+	+	+	+	+	+	+	Cysteine synthase(O-acetyl-L-serine sulfhydrylase)	exp.	16513748
yrrT-mtn-mccA-yrhBC	*BSU27280*	+	+	+	+	+	+	+	-	-	-	+	Cysteine biosynthesis	exp.	16513748
cysJ-yvgQ	*BSU33440*	-	-	-	+	+	-	0	+	-	+	-	Sulfite reductase (NADPH)	-	
cysHP-sat-cysC-sumT-sirBC	*BSU15570*	-	+	-	-	+	-	-	+	+	+	-	Siroheme biosynthesis	-	
yhcL	*BSU09130*	+	-	0	+	0	0	+	0	+	+	+	Sodium-cystine symporter	exp.	16513748
ytmI-tcyJKLMN-ytmO-ytnIJ-rbfK-ytnLM	*BSU29390*	+	+	0	0	0	0	0	0	0	0	+	Putative N-acetyltransferase; sulfur-containing amino acid ABC trans	exp.	16109943
yxeKLMNOPQ	*BSU39520*	+	+	+	0	0	0	0	0	0	0	0	Putative monooxygenase; putative acetyltransferase; amino acid AB	exp.	16513748
ydbM	*BSU04520*	+	+	+	+	0	-	0	-	-	+	-	Putative acyl-CoA dehydrogenase	exp.	16513748
ssuBACD	*BSU08830*	+	-	0	-	0	0	+	0	0	0	+	Aliphatic sulfonate ABC transporter (ATP-binding protein); aliphatic s	exp.	16513748
subI-cysTWA	*Pjdr2_4823*	0	0	0	0	0	0	+	+	-	0	+	Sulfate ABC transporter	-	
ytlI	*BSU29400*	+	+	0	0	0	0	0	0	0	0	0	Transcriptional regulator, LysR family	exp.	16513748
cysL	*BSU37650*	-	-	-	+	+	-	-	0	0	-	0	Regulator of sulfur assimilation, activates cysJI expression	-	
NsrR regulon	**nsrR**	**+**	**+**	**+**	**+**	**0**	**+**	**0**	**+**	**+**	**+**	**0**	**Nitrosative stress**	-	
hmp	*BSU13040*	+	+	+	+	0	+	-	+	+	+	-	Flavohemoprotein	exp.	16885456
nsrR	*BSU09380*	-	-	+	+	0	+	0	+	+	+	0	NO-dependent transcription regulator	-	
nasDEF	*BSU03300*	+	+	+	+	0	-	-	-	-	0	-	Nitrite reductase; uroporphyrin-III C-methyltransferase	exp.	16885456
HisR regulon	**hisR**	**+**	**+**	**+**	**+**	**+**	**+**	**0**	**+**	**+**	**+**	**+**	**Histidine metabolism**	-	

yuiF	*BSU32040*	+	+	+	+	+	0	-	+	+	+	0	Histidine permease	-	
hisZGDBHAFI	*BSU34930*	+	+	+	+	+	+	-	+	+	+	+	Histidine biosynthesis	-	
Btr regulon	**btr**	+	+	+	+	0	0	0	0	+	0	0	**Fe-bacillibactin uptake**	-	
feuABC	*BSU01630*	+	+	+	+	0	-	-	-	+	-	-	Iron-uptake system	exp.	17725565
ybbA	*BSU01600*	+	+	-	-	0	0	0	0	0	-	0	Putative ferri-bacillibactin esterase	exp.	17725565
yuiI	*BSU32010*	-	-	0	+	0	0	-	0	+	-	0	Putative ferri-bacillibactin esterase	-	
ArsR regulon	**arsR**	+	0	0	0	0	0	+	+	+	+	0	**Arsenic resistance**	-	
arsR	*BSU25810*	+	0	0	0	0	0	+	+	+	+	0	Arsenical resistance operon repressor	exp.	9537360
yqcK	*BSU25800*	+	-	0	0	0	0	+	0	+	+	0	Putative lactoylglutathione lyase	exp.	9537360
arsB	*BSU25790*	+	0	0	0	0	-	+	0	0	0	0	Arsenite efflux transporter	exp.	9537360
aseRA	*BSU05330*	-	-	0	-	-	-	0	-	+	-	0	Arsenic resistance transcription regulator; arsenite efflux transporter	-	
arsC	*BSU25780*	+	0	0	-	0	-	0	-	+	-	0	Arsenate reductase	exp.	9537360
BH2995	*BH2995*	0	0	0	0	0	0	0	+	0	0	0	FAD dependent oxidoreductase	-	
AseR regulon	**aseR**	+	+	0	+	+	+	0	+	+	+	0	**Arsenic resistance**	-	
aseRA	*BSU05330*	+	+	0	+	+	+	0	+	+	+	0	Arsenic resistance transcription regulator; arsenite efflux transporter	exp.	15948947
arsC	*BSU25780*	-	0	0	+	0	+	0	+	+	+	0	Arsenate reductase	-	
arsB	*BSU25790*	-	0	0	0	0	+	-	0	-	-	0	Arsenite efflux transporter	-	
CzrA regulon	**crzA**	+	+	+	+	+	+	+	0	+	+	+	**Zn(II), Cd(II), Cu(II), Co(II) and Ni(II) resistence**	-	
czcDO	*BSU26650*	+	+	0	+	0	+	+	-	+	+	+	Cation diffusion facilitator family transporter; CzcD accessory protein	exp.	15948947
cadA	*BSU33490*	+	+	+	+	+	0	-	-	0	0	+	P-type ATPase Cd(II) transporter	exp.	15948947
czrA	*BSU19120*	-	-	-	-	+	+	-	-	+	+	-	Multiple metal-sensing transcriptional repressor	-	
SdpR regulon	**sdpR**	+	0	+	+	+	+	+	0	+	+	+	**SdpC antitoxin system involved in sporulation**	-	
sdpRI	*BSU33790*	+	0	+	+	+	+	+	0	+	+	+	Transcriptional regulator of SdpC resistance operon; integral membra	exp.	16469701
YwrC regulon	**ywrC**	+	+	+	+	0	0	0	0	0	0	+	**Metal efflux transporter**	-	
ywrCBA	*BSU36110*	+	+	+	+	0	-	0	-	-	-	+	Transcription regulator; transporter from the chromate efflux transpor	-	
GlcR regulon	**glcR**	+	+	0	+	0	0	0	+	0	+	+		-	
glcR-ywpJ	*BSU36300*	+	+	0	+	0	0	0	+	0	+	-	Transcription regulator; hydrolase	-	
LevR regulon	**levR**	+	0	0	+	0	0	0	0	0	0	0	**Levan utilization**	-	
levDEFG-sacC	*BSU27070*	+	0	0	+	0	0	0	0	0	0	0	Phosphotransferase system; levanase	exp.	8057358
RocR regulon	**rocR**	+	+	+	+	0	+	+	+	+	0	0	**Arginine and ornithine utilization**	-	
rocR	*BSU40350*	+	+	+	+	0	+	+	+	+	0	0	Transcriptional activator of arginine utilization operon	exp.	7540694
rocABC	*BSU37780*	+	+	+	-	-	+	-	+	-	-	0	Arginine utilization	exp.	12634342
rocDEF	*BSU40340*	+	+	+	+	-	+	-	+	+	-	-	Arginine utilization	exp.	7540694
rocG	*BSU37790*	+*	-	-	-	-	+	-	+	-	-	-	NAD-specific glutamate dehydrogenase	exp.	12634342
AcoR regulon	**acoR**	+	+	+	+	0	0	+	+	0	0	0	**Acetoin dehydrogenase**	-	
acoABCL	*BSU08060*	+	+	+	+	0	0	+	+	-	0	0	Acetoin dehydrogenase complex	exp.	11274109
BkdR regulon	**bkdR**	+	+	+	+	+	+	+	+	+	+	0	**Isoleucine and valine utilization**	-	
ptb-bcd-buk-lpdV-bkdAABB	*BSU24090*	+	+	+	+	+	+	+	+	+	+	-	Phosphate butyryltransferase; leucine dehydrogenase; branched-cha	exp.	10094682

bkdR	*BSU24100*	+	+	+	+	+	+	+	-	-	+	0	Sigma-L-dependent transcriptional regulator	-	
GmuR	**gmuR**	+	+	+	+	0	+	0	+	0	0	0	**Glucomannan utilization**	-	
gmuBACDREFG	*BSU05810*	+	+	+	+	0	+	0	+	-	-	0	PTS system, cellobiose-specific enzyme II, B component; PTS syste	exp.	18177310
CcpN regulon	**ccpN**	+	+	+	+	+	+	+	+	+	+	0	**Gluconeogenesis**	-	
gapB	*BSU29020*	+	+	+	+	+	+	+	+	+	+	0	Glyceraldehyde-3-phosphate dehydrogenase	exp.	17011578
pckA	*BSU30560*	+	+	+	+	+	+	+	+	+	+	0	Phosphoenolpyruvate carboxykinase (ATP)	exp.	17011578
CcpB regulon	**ccpB**	+	+	0	0	0	0	0	0	0	0	0	**Catabolite repression**	-	
gntRKPZ	*BSU40050*	+	0	0	-	0	0	0	0	0	-	0	Gluconate utilization	exp.	9457849
xylAB	*BSU17600*	+	+	-	-	-	-	-	-	-	-	-	Xylose utilization	exp.	9457849
BglZ regulon	**bglZ**	+	+	+	+	0	0	+	0	0	0	0	**Beta-glucoside catabolism**	-	
bglC	*BSU03410*	+	+	+	+	0	-	0	0	0	0	0	Aryl-phospho-beta-D-glucosidase	-	
bglZ (ykvZ)	*BSU13870*	+	+	+	-	0	0	+	0	0	0	0	Transcriptional regulator, LacI family	-	
BC2618	*BC2618*	0	0	0	0	0	0	+	0	0	0	0	Hydrolase (HAD superfamily)	-	
CitR regulon	**citR**	+	+	0	+	0	0	0	0	+	0	0	**Citrate synthase**	-	
citA	*BSU09940*	+	+	0	+	0	0	0	0	+	0	0	Citrate synthase I	exp.	8045899
citR	*BSU09930*	+	+	0	+	0	0	0	0	+	0	0	Transcriptional regulator	-	
GltR regulon	**gltR**	+	0	0	0	0	0	0	0	0	0	+		-	
gltR	*BSU26670*	+	0	0	0	0	0	0	0	0	0	+	Transcription regulator	exp.	9023181
Pjdr2_3124	*Pjdr2_3124*	0	0	0	0	0	0	0	0	0	0	+	Major facilitator (MFS) superfamily protein	-	
yrpB	*BSU26800*	+	-	-	-	0	0	-	-	0	-	+	2-nitropropane dioxygenase	-	
YtlI regulon	**ytlI**	+	+	0	0	0	0	0	0	0	0	0	**L-cystine transporter**	-	
ytmI-tcyJKLMN-ytmO-ytnIJ-rbfK-ytnLM	*BSU29390*	+	+	0	0	0	0	0	0	0	0	-	Putative N-acetyltransferase; L-cystine ABC transporter; putative mo	exp.	16109943
ytlI	*BSU29400*	+	+	0	0	0	0	0	0	0	0	0	Transcriptional regulator, LysR family	exp.	16109943
CysL regulon	**cysL**	+	+	+	+	+	+	0	0	0	+	0	**Sulfate, sulfite, or thiosulfate**	-	
cysL	*BSU37650*	+	+	+	+	+	+	0	0	0	+	0	Transcriptional regulator	exp.	12169591
cysJI	*BSU33440*	+	+	+	+	+	+	0	-	-	+	-	Sulfite reductase	exp.	12169591
YetL regulon	**yetL**	+	+	0	0	0	0	0	0	0	0	0	**Flavonoids response**	-	
yetL	*BSU07220*	+	+	0	0	0	0	0	0	0	0	0	Transcriptional regulator	exp.	19329649
yetM	*BSU07230*	+	+	0	0	0	0	0	0	0	0	0	Putative FAD-dependent monooxgenase	exp.	19329649
OhrR regulon	**ohrR**	+	+	+	+	0	+	+	0	0	+	+	**Organic hydroperoxide resistance**	-	
ohrR	*BSU13150*	-	-	-	-	0	-	+	0	0	+	-	Transcriptional regulator, MarR family	-	
ohrA	*BSU13140*	+	+	+	+	0	+	+	0	0	+	+	Organic hydroperoxide resistance protein	exp.	11418552
tpx-trxB	*BSU29490*	-	-	-	-	-	-	-	-	-	-	+	Thioredoxin reductase; thiol peroxidase	-	
CitT regulon	**citT**	+	+	+	+	0	0	+	+	+	+	0	**Citrate transport**	-	
citM	*BSU07610*	+	+	+	+	0	0	0	+	+	+	0	Citrate/Mg2+ transporter	exp.	10972810
tctCBA	*OB3249*	0	0	0	0	0	0	0	0	0	+	0	Tricarboxylate transporter	-	
citH	*BC0562*	0	0	0	0	0	0	+	0	0	0	0	Ca2+/citrate complex secondary transporter	-	
DctR regulon	**dctR**	+	+	+	0	0	+	0	0	0	0	0	**C4-dicarboxylate transport**	-	

dctA	*BSU04470*	+	+	+	0	0	+	0	0	0	0	0	C4-dicarboxylate transporter for succinate, fumurate, malate and oxaloace	exp.	10708364
DeoR regulon	**deoR**	+	+	+	+	0	0	+	0	0	0	0	**Deoxynucleoside utilization**	-	
dra-nupC-pdp	*BSU39420*	+	+	+	+	0	0	+	0	0	0	0	Deoxyribose-phosphate aldolase; pyrimidine-nucleoside Na+(H+) co	exp.	10714997
FadR regulon	**fadR**	+	+	+	+	+	+	+	+	+	+	0	**Fatty acid degradation**	-	
lcfB	*BSU10270*	+	+	+	+	+	0	0	0	0	0	0	Long-chain fatty-acid-CoA ligase	exp.	17189250
fadHG	*BSU14060*	+	+	+	+	+	+	-	+	-	0	0	Probable 2,4-dienoyl-CoA reductase	exp.	17189250
fadNAE	*BSU32840*	+	+	+	+	-	+	+	+	+	+	-	Fatty acid degradation	exp.	17189250
fadF-acdA-rpoE	*BSU37180*	+	+	+	+	+	+	+	+	+	+	-	Fatty acid degradation	exp.	17189250
mmgABC	*BSU24170*	-	-	+	+	+	+	+	+	+	-	-	Fatty acid degradation	-	
fadRB-etfBA	*BSU28550*	+	+	+	+	+	+	+	+	+	+	-	Transcriptional regulator of fatty acids degradation (TetR/AcrR family	exp.	17189250
Aflv_1606	*Aflv_1606*	0	0	0	0	+	+	0	0	+	+	0	Zn-dependent hydrolase	-	
LmrA regulon	**lmrA**	+	+	0	0	0	0	0	0	0	0	0	**Multidrug resistance**	-	
lmrAB	*BSU02680*	+	+	-	-	0	0	0	0	0	0	0	Transcriptional repressor of multidrug resistance regulon; lincomycin	exp.	17483215
qdoR	*BSU39990*	+	-	-	-	0	0	0	0	0	0	0	Transcriptional regulator of multidrug resistance regulon	exp.	17483215
qodI-yxaH	*BSU39980*	+	0	-	0	0	0	0	-	0	0	0	Quercetin 2,3-dioxygenase; putative transporter	exp.	17483215
QdoR regulon	**yxaF**	+	+	+	+	0	0	0	0	0	0	0	**Multidrug resistance**	-	
lmrAB	*BSU02680*	+	+	-	+	0	0	0	0	0	0	0	Transcriptional repressor of multidrug resistance regulon; lincomycin	exp.	17483215
qdoR	*BSU39990*	+	-	-	+	0	0	0	0	0	0	0	Transcriptional regulator of multidrug resistance regulon	exp.	17483215
qodI-yxaH	*BSU39980*	+	0	+	0	0	0	0	-	0	0	0	Quercetin 2,3-dioxygenase; putative transporter	exp.	17483215
FatR regulon	**fatR**	+	+	+	+	0	0	0	0	0	0	0	**Toxic fatty acid stress response**	-	
fatR-cypB	*BSU27170*	+	+	+	+	0	0	0	0	0	0	0	Transcriptional regulator for cytochrome P450 102A3, TetR family; C	exp.	11734890
AnsR regulon	**ansR**	+	+	+	+	0	0	+	0	0	0	0	**Asparagine degradation**	-	
ansR	*BSU23580*	+	+	+	+	0	0	+	0	0	0	0	Transcriptional regulator	exp.	11914346
ansAB	*BSU23590*	+	+	+	+	-	0	+	0	0	0	0	Asparagine degradation	exp.	11914346
BltR regulon	**bltR**	+	+	+	0	0	0	0	+	0	0	0	**Multidrug transporter**	-	
bltD	*BSU26600*	+	+	0	0	0	0	0	0	0	-	0	Spermine/spermidine acetyltransferase	exp.	7608059
blt	*BSU26590*	+	-	-	0	0	0	-	0	-	0	-	Multidrug resistance protein, major facilitator (MFS) superfamily	exp.	7608059
ydhB	*BSU05690*	-	+	-	0	0	0	-	0	0	0	-	Hypothetical secreted protein	-	
yrkN	*BPUM_1819*	-	-	+	0	0	0	0	0	0	0	0	Possible acetyltransferase	-	
BH4045	*BH4045*	0	0	0	0	0	0	0	+	0	0	0	MATE family multidrug export protein	-	
NagR regulon	**nagR**	+	+	+	+	0	+	+	+	+	+	0	**N-acetylglucosamine utilization**	-	
nagABR	*BSU35010*	+	+	+	+	0	+	+	+	+	+	0	N-acetylglucosamine utilization	exp.	21602348
nagP	*BSU07700*	+	+	+	+	0	0	-	+	0	0	-	PTS system, N-acetylglucosamine-specific IIBC component	exp.	21602348
murQ2	*BLi04351*	0	0	0	+	0	0	0	0	0	0	0	N-acetylmuramic acid-6-phosphate etherase	-	
LutR (LldR) regulon	**lldR**	+	+	+	+	+	+	+	+	+	+	0	**L-lactate utilization**	-	
lutABC	*BSU34050*	+	+	+	+	+	+	+	+	+	+	0	L-lactate dehydrogenase	exp.	19201793
lutR	*BSU34180*	+	+	-	+	-	-	-	-	-	+	0	Transcriptional regulator	-	
lutP	*BSU34190*	+	+	0	+	+	+	0	+	+	+	0	L-lactate permease	-	

FrlR regulon	**frlR**	+	+	0	0	0	0	0	0	0	0	0	**Fructoselysine utilization**	-	
frlR	*BSU32560*	+	+	0	0	0	0	0	0	0	0	0	Transcription regulator	exp.	21398478
frlB	*BSU32610*	+	+	0	0	0	0	0	0	0	0	0	Fructoselysine-6-P-deglycase	exp.	21398478
yurJ	*BSU32550*	+	+	0	0	0	0	0	0	0	0	0	Putative fructoselysine ABC transporter (ATP-binding protein)	-	
frlONMD	*BSU32600*	+	+	0	0	0	0	0	0	0	0	0	Putative fructoselysine ABC transporter; fructoselysine kinase	exp.	21398478
YhcF regulon	**yhcF**	+	+	0	0	0	0	+	+	+	0	+	**Antibiotics resistance**	-	
yhcEFGHI	*BSU09080*	+	+	0	-	0	0	+	+	0	0	+	Putative integral inner membrane; transcriptional regulator (GntR fam	-	
bcrAB	*ABC1458*	0	0	-	-	0	0	+	0	+	-	-	Bacitracin transport	-	
GabR regulon	**gabR**	+	+	+	+	0	0	0	0	0	0	0	**Gamma-aminobutyrate utilization**	-	
gabTD	*BSU03900*	+	+	+	+	-	0	-	-	0	0	0	4-aminobutyrate aminotransferase; succinate-semialdehyde dehydro	exp.	15223311
BH0994	*BH0994*	0	0	+	+	-	0	0	-	0	-	0	Amino acid transporter	-	
gabR	*BSU03890*	+	+	+	+	0	0	0	0	0	0	0	Transcriptional regulator of gamma-aminobutyrate utilization	exp.	15223311
YcxD regulon	**ycxD**	+	+	+	+	0	0	0	0	0	0	+	**Hypothetical drug/metabolite efflux transporter**	-	
ycxD	*BSU03560*	+	+	+	+	0	0	0	0	0	0	+	Transcriptional regulator, GntR (MocR/GabR) family	-	
ycxC	*BSU03550*	+	+	+	+	0	0	0	0	0	0	+	DMT superfamily drug/metabolite transporter	-	
YhdI / YdeL regulon	**yhdI**	+	+	0	+	0	0	+	0	0	0	0		-	
ydhI	*BSU09480*	+	0	0	+	0	0	+	0	0	0	0	Transcription regulator	-	
ydhJ	*BSU09490*	+	0	0	+	0	-	+	-	-	-	0	Acetyltransferase	-	
ydeL	*BSU05240*	+	+	0	0	0	0	+	0	0	0	0	Transcription regulator	-	
ydeK	*BSU05230*	+	+	0	0	0	0	+	0	0	0	0	Hypothetical efflux transporter, DMT family	-	
YdfD / YisV regulon	**ydfD / yisV**	+	0	0	0	0	0	+	+	+	0	+	**Hypothetical efflux transporter**	-	
ydfD	*BSU05370*	+	0	0	0	0	0	+	0	0	0	0	Transcription regulator	-	
ydfC	*BSU05360*	+	0	0	0	0	0	+	0	-	0	0	Drug/metabolite transporter, DMT superfamily	-	
yisV	*BSU10880*	+	0	0	0	0	0	+	+	+	0	+	Transcription regulator	-	
yisU	*BSU10870*	+	0	-	0	0	0	+	+	+	0	+	Hypothetical efflux transporter, LysE family	-	
BmrR regulon	**bmrR**	+	0	0	+	0	0	0	0	0	0	0	**Multidrug transporter**	-	
bmr-bmrR	*BSU24010*	+	0	0	-	0	0	0	0	0	0	0	Multidrug transporter (MFS family); transcriptional regulator	exp.	7961792
BLi02783	*BLi02783*	0	0	0	+	0	0	0	0	0	0	0	Flavoredoxin	-	
YdfL regulon	**ydfL**	+	0	0	+	0	0	+	+	0	0	0	**Multidrug transporter**	-	
BC1615	*BC1615*	0	0	0	+	0	0	+	0	-	0	0	Na+ driven multidrug efflux pump	-	
ydfK	*BSU05450*	+	0	0	0	0	0	0	0	0	0	0	Putative integral inner membrane protein	-	
BH0429	*BH0429*	0	0	0	-	0	-	0	+	0	0	0	Putative trasporter	-	
RmgR regulon	**rmgR**	+	0	+	+	0	0	0	+	+	+	+	**Rhamnogalacturonan utilization**	-	
yteP-urhG2-yteSTU	*BSU30135*	+	0	+	+	0	0	0	+	+	+	+	Rhamnogalaturonan utilization	-	
uxaAB	*ABC1153*	0	0	0	0	0	0	0	+	+	0	0	Altronate hydrolase; altronate oxidoreductase	-	
BH0493-pelX	*BH0493*	0	0	0	0	0	0	0	+	0	0	0	Putative uronate isomerase; exopolygalacturonate lyase	-	
pglR	*OB2088*	0	0	0	0	0	0	0	0	0	+	0	Polygalacturonase	-	
xylB	*OB2087*	0	0	0	0	0	0	0	0	+	+	0	Xylosidase/arabinosidase	-	

rhgT	*OB2084*	0	0	0	0	0	0	0	0	0	+	0	Rhamnogalacturonan acetylesterase	-	
RhgR regulon	**rhgR**	**+**	**0**	**0**	**+**	**0**	**0**	**0**	**0**	**0**	**0**	**+**	**Rhamnogalacturonan utilization**	-	
yesOPQ	*BSU06970*	+	0	0	+	0	0	0	-	-	0	+	Rhamnose oligosaccharide ABC transporter	-	
urhG1-yesSTUVWXYZ	*BSU07000*	+	0	0	+	0	0	0	0	0	0	0	Rhamnogalacturonan utilization	-	
KipR regulon	**kipR**	**+**	**+**	**+**	**+**	**0**	**+**	**+**	**+**	**0**	**0**	**0**	**Initiation of developmental transcription at the onset of sporulat**	-	
ycsFGI-kipIAR-lipC	*BSU04050*	+	+	+	+	0	+	+	+	-	-	-	LamB/YcsF family protein; putative branched chain amino acids trans	exp.	9334321
AdaA regulon	**adaA**	**+**	**+**	**0**	**+**	**0**	**0**	**+**	**0**	**+**	**0**	**+**	**Adaptative response to DNA alkylation**	-	
adaAB	*BSU01810*	+	+	0	+	0	-	+	0	+	-	+	Methylphosphotriester-DNA alkyltransferase and transcriptional regu	exp.	8376346
alkA	*BSU01800*	+	0	0	0	0	0	+	0	+	0	+	DNA-3-methyladenine glycosylase II	exp.	8376346
exoA	*BSU40880*	-	+	0	0	0	-	-	0	-	-	-	Exodeoxyribonuclease III	-	
Pjdr2_5361	*Pjdr2_5361*	0	0	0	0	0	0	0	0	0	0	+	Short-chain dehydrogenase/reductase	-	
CcpC regulon	**ccpC**	**+**	**+**	**+**	**+**	**0**	**0**	**+**	**0**	**0**	**+**	**0**	**TCA cycle**	-	
ccpC	*BSU14140*	+	-	+	+	0	0	-	0	0	+	0	Transcriptional repressor of citB and citZ	exp.	11985717
citB	*BSU18000*	+	+	+	+	-	-	+	-	-	+	-	Aconitase A	exp.	10656796
citZ-icd-mdh	*BSU29140*	+	+	-	-	-	-	-	-	-	-	-	Citrate cycle	exp.	10656796
YdfI regulon	**ydfI**	**+**	**+**	**0**	**+**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**Metabolite transport**	-	
ydfJ	*BSU05430*	+	+	0	+	0	0	0	0	0	0	0	RND superfamily transporter	exp.	15941986
BceR regulon	**bceR**	**+**	**+**	**+**	**+**	**0**	**+**	**0**	**+**	**+**	**+**	**0**	**Bacitracin resistance**	-	
bceAB	*BSU30380*	+	+	+	+	0	+	-	+	+	+	0	ABC transporter involved in bacitracin resistance	exp.	12890034
AlsR regulon	**alsR**	**+**	**+**	**+**	**+**	**0**	**0**	**+**	**0**	**0**	**0**	**0**	**Alpha-acetolactate biosynthesis**	-	
alsR	*BSU36020*	+	+	+	+	0	0	-	0	0	0	0	Transcription regulator	exp.	22178965
alsSD	*BSU36010*	+	+	+	+	0	0	-	0	0	0	0	Acetolactate synthase ;alpha-acetolactate decarboxylase	exp.	22178965
GudR regulon	**gudR**	**+**	**0**	**0**	**+**	**0**	**0**	**0**	**0**	**+**	**+**	**0**	**D-glucarate/galactarate utilization**	-	
gudR	*BSU02500*	+	0	0	+	0	0	0	0	+	+	0	Transcription regulator	exp.	12044674
garD	*BSU02510*	+	0	0	+	0	0	0	0	0	0	0	D-galactarate dehydratase	exp.	12044674
ycbCD-gudD	*BSU02460*	+	0	0	+	0	0	0	0	+	+	0	Glucarate utilization	exp.	12044674
gudP	*BSU02480*	+	0	0	+	0	0	0	0	0	0	0	Glucarate transporter	exp.	12044674
ABC0466	*ABC0466*	0	0	0	0	0	0	0	0	+	0	0	Putative glucarate dehydratese		
ABC0469-67	*ABC0469-67*	0	0	0	0	0	0	0	0	+	+	0	Predictid D-glucarateTTT family transporter	-	
DesR regulon	**desR**	**+**	**+**	**+**	**+**	**0**	**0**	**0**	**0**	**+**	**+**	**0**	**Cold shock**	-	
des-desKR	*BSU036870*	+	+	+	+	0	0	0	0	+	+	0	Delta 5 - fatty acid desaturase; two-component system	exp.	11285232
YvfU regulon	**yvfU**	**+**	**0**	**0**	**+**	**0**	**0**	**0**	**0**	**+**	**0**	**+**		-	
yvfRSTU	*BSU34090*	+	0	0	+	0	0	0	0	+	0	+	ABC transporter (ATP binding protein); ABC transporter (permease);	-	
CssR regulon	**cssR**	**+**	**+**	**+**	**+**	**0**	**0**	**0**	**0**	**0**	**+**	**0**	**Protein secretion stress**	-	
cssRS	*BSU33010*	+	+	+	+	0	0	0	0	0	+	0	Two-component system of protein secretion stress regulon	exp.	12270824
htrB	*BSU33000*	+	+	+	+	0	0	-	-	-	+	0	HtrA-like serine protease	exp.	12270824
htrA	*BSU12900*	+	+	+	+	0	0	0	0	0	0	0	Probable serine protease	exp.	12270824
FapR regulon	**fapR**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**Fatty-acid biosynthesis**	-	

fabHA-F	*BSU11330*	+	+	+	+	+	+	+	+	+	+	+	3-oxoacyl-(acyl carrier protein) synthase III; 3-oxoacyl-(acyl-carrier-p	exp.	12737802
fapR-plsX-fabDG-acpA-rnc	*BSU15880*	+	+	+	+	0	+	+	+	+	+	+	Fatty-acid biosynthesis	exp.	12737802
fabI	*BSU11720*	+	+	+	+	+	+	+	+	+	+	0	Enoyl-(acyl carrier protein) reductase	exp.	12737802
fabHB	*BSU10170*	+	+	0	+	0	0	+	+	0	0	+	3-oxoacyl-(acyl carrier protein) synthase III	exp.	12737802
plsC	*BSU09540*	+	+	+	+	-	-	+	-	-	-	-	1-acyl-sn-glycerol-3-phosphate acyltransferase	exp.	12737802
BPUM_0755	*BPUM_0755*	0	0	+	0	0	0	+	0	0	0	0	Bifunctional nucleotide sugar epimerase/hydrolase	-	
Pjdr2_4960	*Pjdr2_4960*	0	+	0	0	0	0	0	0	0	0	+	Putative beta-ketoacyl-acyl carrier protein synthase II	-	
accBC-yqhY	*BSU24350*	-	-	-	+	-	-	+	-	-	+	-	Acetyl-CoA carboxylase biotin carboxyl carrier subunit; acetyl-CoA ca	-	
ComA regulon	**comA**	**+**	**+**	**+**	**+**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**Late competence genes, production of degradative enzymes an**	-	
srfAAAB	*BSU03480*	+	+	+	+	0	0	0	0	0	0	0	Surfactin synthetase	exp.	8387999
srfACAD	*BSU03510*	+	+	+	+	0	0	0	0	0	0	0	Surfactin synthetase	exp.	8387999
BPUM_0322-23	*BPUM_0322*	0	0	0	+	0	0	0	0	0	0	0	Nonribosomal peptide synthetase	-	
degQ	*BSU31720*	+	+	+	+	0	0	0	0	0	0	0	Degradation enzyme regulation protein	exp.	1901055
rapC-phrC	*BSU03770*	+	+	0	0	0	0	0	0	0	0	0	Response regulator aspartate phosphatase; secreted regulator of the	exp.	15968044
rapA-phrA	*BSU12430*	+	+	0	0	0	0	0	0	0	0	0	Response regulator aspartate phosphatase; secreted regulator of the	exp.	1378051
rapF-phrF	*BSU37470*	+	-	-	-	0	0	0	0	0	0	0	Response regulator aspartate phosphatase; secreted regulator of the	exp.	15968044
rapE-phrE	*BSU25830*	+	0	0	-	0	0	0	0	0	0	0	Response regulator aspartate phosphatase; secreted regulator of the	exp.	10629174
pel	*BSU07560*	+	-	0	-	0	0	0	0	0	0	0	Pectate lyase	exp.	16091051
RhaR regulon	**rhaR**	**+**	**0**	**0**	**+**	**0**	**0**	**0**	**+**	**0**	**+**	**+**	**Rhamnose utilization**	-	
rhaEW-rhaR-rhaBMA	*BSU31220*	+	0	0	+	0	0	0	+	-	+	+	Rhamnose utilization	-	
rhaY	*OB0494*	0	0	0	-	0	0	0	0	-	+	0	Predicted L-rhamnose permease	-	
rhaL	*BLi03559*	0	0	0	+	0	0	0	0	0	0	0	Predicted L-rhamnose isomerase	-	
IolR1 regulon	**iolR1**	**+**	**0**	**0**	**+**	**0**	**+**	**0**	**+**	**0**	**0**	**+**	**Inositol utilization**	-	
GK1894-93-iolIDEBCAJ	*GK1894*	-	-	0	-	0	+	0	-	-	0	+	Putative inositol ABC transporter; Inositol utilization	-	
iolR1 (degA)	*BSU10840*	-	0	0	-	0	-	0	+	0	0	+	Transcriptional regulator of inositol utilization, LacI family	-	
yrbE	*BSU27770*	+	0	0	0	0	0	0	+	0	0	+	Predicted inositol derivative dehydrogenase	-	
iolX	*BSU10850*	+	0	0	+	0	+	0	+	-	0	0	Scyllo-inositol dehydrogenase	-	
GK1899-96	*GK1899*	0	0	0	0	0	+	0	+	-	0	-	Predicted inositol derivative dehydrogenases	-	
BH2222	*BH2222*	0	0	0	-	0	0	0	+	-	0	0	Na+:myo-inositol cotransporter	-	
IolR regulon	**iolR**	**+**	**+**	**0**	**+**	**0**	**0**	**0**	**0**	**+**	**0**	**0**	**Myo-inositol catabolism**	-	
iolABCDEFGHIJ	*BSU39760*	+	+	0	+	0	-	0	-	+	0	-	Inositol utilization	exp.	9887260
iolRS	*BSU39770*	+	+	0	+	0	0	0	0	+	0	0	Transcriptional regulator of mio-inositol utilisation; Oxidoreductase	exp.	9887260
YisR regulon	**yisR**	**+**	**+**	**+**	**+**	**+**	**+**	**0**	**0**	**0**	**0**	**0**	**Multidrug resistance**	-	
yisQ	*BSU10820*	+	+	+	+	+	+	-	-	0	0	-	Na+-driven multidrug efflux pump	-	
AraR regulon	**araR**	**+**	**+**	**+**	**+**	**+**	**+**	**0**	**+**	**0**	**+**	**+**	**Arabinose utilization**	-	
araFGH	*GK1910*	0	0	0	-	0	+	0	-	-	0	-	L-arabinose ABC transporter	-	
abnA	*BSU28810*	+	+	0	-	0	0	0	0	0	0	0	Arabinan endo-1,5-alpha-L-arabinosidase	exp.	14973026
araE	*BSU33960*	+	+	+	+	0	0	0	0	0	+	0	L-arabinose-proton symporter	exp.	10417639

araR	*BSU33970*	+	+	+	+	+	+	0	+	0	+	+	Transcriptional regulator of arabinose metabolism, GntR family	exp.	10417639
xsa	*BSU28510*	+	+	0	0	0	0	0	+	-	0	0	Alpha-L-arabinofuranosidase	exp.	14973026
araABDLMNPQ-abfA	*BSU28720*	+	+	+	+	+	+	0	-	+	+	+	Arabinose utilization	exp.	10417639
araK	*BPUM_2329*	0	0	+	+	0	0	0	0	0	0	+	Alternative L-ribulokinase	-	
CsoR regulon	**csoR**	+	+	+	+	+	+	+	+	+	+	+	**Copper efflux**	-	
copA	*BSU33500*	+	+	+	+	+	+	+	+	+	+	+	Copper-transporting ATPase	exp.	18048925
copZ	*BSU33510*	+	+	+	+	+	+	+	+	+	+	+	Copper insertion chaperone and transporter component	exp.	18048925
csoR	*BSU33520*	-	-	-	-	+	+	-	-	-	+	+	Repressor of copper utilisation	-	
ydhK	*BSU05790*	+	-	0	0	0	-	0	0	+	+	+	Hypothetical protein	-	
Pjdr2_3010-11	*Pjdr2_3010*	0	0	0	0	0	-	0	0	0	0	+	Two component system	-	
YcnK regulon	**ycnK**	+	+	0	+	0	0	0	0	0	0	0	**Copper import**	-	
ycnKJI	*BSU03960*	+	+	-	+	0	0	-	0	0	0	-	Transcriptional regulator of copper import, DeoR family; putative cop	exp.	19168619
YczG regulon	**yczG**	+	+	+	+	0	0	+	0	0	0	0	**Aromatic compound detoxification**	-	
ycnE-nfrA2	*BSU03870*	+	+	-	+	0	0	-	-	0	0	0	Putative monooxygenase; NAD(P)H-dependent nitro/flavin reductase	-	
BC1999	*BC1999*	0	0	0	0	0	0	+	0	0	0	0	Uncharacterized oxidoreductase	-	
yczG	*BSU03880*	+	+	-	+	0	0	+	0	0	0	0	Transcriptional regulator, ArsR family	-	
YfmP regulon	**yfmP**	+	+	+	+	0	0	+	0	0	0	+	**Metal efflux**	-	
yfmPO	*BSU07390*	+	+	+	+	0	-	+	0	0	0	+	Transcriptional regulator of metal efflux transporter expression, MerR	exp.	14663075
HxlR regulon	**hxlR**	+	+	+	+	0	0	0	0	0	+	+	**Ribulose monophosphate pathway**	-	
hxlAB	*BSU03460*	+	+	+	+	0	0	0	0	0	+	+	Ribulose monophosphate pathway	exp.	10572115
YtcD regulon	**ytcD**	+	+	+	+	0	0	0	0	0	0	+		-	
ytcD	*BSU29030*	+	+	+	+	0	0	0	0	0	0	+	Transcriptional regulator, HxlR family	-	
ytbDE	*BSU29040*	+	+	+	+	0	0	0	0	0	0	+	Putative efflux transporter, MFS family; putative aldo/keto reductase	-	
BLi02841	*BLi02841*	-	0	0	+	0	0	0	0	0	0	0	Putative peptidase	-	
SinR regulon	**sinR**	+	+	+	+	0	0	0	+	0	0	0	**Biofilm formation**	-	
epsA-O	*BSU34370*	+	+	+	+	0	0	0	0	0	0	0	Exopolysaccaride production	exp.	16430695
yqxM-sipW-tasA	*BSU24640*	+	+	+	+	0	0	0	+	0	0	-	Lipoprotein for biofilm formation; signal peptidase I, required for TasA	exp.	15661000
slrR	*BSU34380*	+	+	+	+	0	0	0	0	0	0	0	Transcriptional repressor of cell separation and motility/antirepressor	exp.	18647168
YybR/YdeP regulon	**yybR/ydeP**	+	+	+	+	0	0	+	+	+	+	+	**Oxidative stress**	-	
yybR(ydeP)	*BSU40540 (E*	+	+	-	+	0	0	+	+	+	+	+	Transcriptional regulator, HxlR family	-	
ykfO	*BSU07830*	+	+	-	+	0	0	+	-	0	-	+	Putative NAD(P)H nitroreductase	-	
ppaC	*BSU04550*	+	+	-	0	0	0	-	0	-	-	-	Putative manganese-dependent inorganic pyrophosphatase	-	
ydeQ	*BSU05300*	+	0	0	0	0	0	0	0	0	0	0	Putative NAD(P)H oxidoreductase	-	
ABC0785	*ABC0785*	0	0	0	0	0	0	-	0	+	0	0	Putative nitroreductase	-	
OB0355-56	*OB0355*	0	-	0	0	0	0	-	0	0	+	-	Putative oxidoreductase; NADH-dependent FMN reductase	-	
BH0738	*BH0738*	0	0	-	0	0	0	0	+	-	0	0	Zinc-containing alcohol dehydrogenase/quinone oxidoreductase (NA	-	
YodB/CatR regulon	**yodB/catR**	+	+	+	+	+	0	+	+	0	+	+	**Oxidative stress**	-	
catDE	*BSU08230*	+	+	+	+	0	0	-	+	-	-	+	Catechol-2,3-dioxygenase	exp.	20639328

ribBD	*BPUM_3531*	0	0	+	0	0	0	+	0	0	0	+	Riboflavin biosynthesis	-	
ytkL	*BSU29410*	-	-	-	-	-	-	-	-	-	-	+	Metal-dependent hydrolase	-	
yodC	*BSU19550*	+	+	+	+	+	0	+	+	0	0	0	Putative NAD(P)H nitroreductase	exp.	17158660
yodB	*BSU19540*	+	+	+	+	+	0	+	-	0	0	+	Transcriptional regulator of oxidative stress, HxlR family	-	
BLi02273	*BLi02273*	0	0	-	+	0	-	0	-	-	0	0	Putative oxidoreductase	-	
spxA	*BSU11500*	+	+	+	+	-	-	+	-	-	-	0	RNA polymerase-binding transcriptional regulator of oxidative stress	exp.	17158660
azoR1	*BSU19230*	+	0	0	+	0	0	-	-	0	0	+	FMN-dependent NADH-azoreductase	exp.	18208493
azoR2	*BC2194*	-	-	-	-	0	-	+	-	0	0	0	FMN-dependent NADH-azoreductase	-	
catR	*BSU33680*	-	-	-	+	0	0	+	-		-	-	Transcriptional regulator of oxidative stress response, HxlR family	-	
PadR regulon	**padR**	+	+	+	+	0	0	0	0	0	0	0	**Phenolic acid stress response**	-	
yveFG-padC	*BSU34420*	+	+	+	+	0	0	0	0	0	0	0	Phenolic acid decarboxylase	exp.	21685295
padR	*BSU08340*	-	-	+	-	0	0	0	0	0	0	0	Transcriptional regulator of phenolic acid stress response, PadR fam	-	
YdfF regulon	**ydfF**	+	0	0	+	0	0	0	+	+	0	0		-	
ydfE	*BSU05380*	+	0	0	+	0	0	0	+	+	0	0	Putative flavoprotein	-	
ydfF	*BSU05390*	+	0	0	+	0	0	0	+	+	0	0	Transcriptional regulator, ArsR family	-	
ABC3713	*ABC3713*	0	0	0	+	0	0	0	0	+	0	0	Predicted carboxyphosphonoenolpyruvate phosphonomutase	-	
YybA regulon	**yybA**	+	+	0	+	0	0	0	+	+	+	+	**Polyamine homeostasis**	-	
yybA	*BSU40710*	+	+	0	+	0	0	0	+	+	+	+	Transcriptional regulator, MarR family	-	
paiA	*BSU32150*	+	+	0	+	0	0	0	+	+	+	0	N1-spermidine/spermine acetyltransferase	-	
paiB	*BSU32140*	+	0	0	+	0	0	0	0	0	0	0	Putative FMN-binding protein	-	
yyaS	*BSU40730*	+	+	0	+	0	0	0	+	0	0	0	Putative integral inner membrane protein	-	
yyaT	*BSU40720*	+	+	0	0	0	0	0	0	-	0	+	Putative N-acetyltransferase	-	
BsdA regulon	**bsdA**	+	+	0	+	0	0	0	0	0	0	0	**Salicylic acid resistance**	-	
bsdBCD1D2	*BSU03630*	+	+	0	+	0	0	0	0	0	0	0	4-hydroxybenzoate decarboxylase	exp.	17295427
bsdA	*BSU03790*	+	+	0	+	0	0	0	0	0	0	0	Transcriptional regulator of salicylic acid resistance, LysR family	-	
YuaC regulon	**yuaC**	+	+	+	+	0	0	0	0	+	0	0	**Osmotic stress response**	-	
gbsAB	*BSU31050*	+	+	+	+	0	0	0	0	+	0	0	Betaine aldehyde dehydrogenase; alcohol dehydrogenase	-	
YhgD regulon	**yhgD**	+	+	+	+	+	+	+	+	0	0	+		-	
yhgDE	*BSU10150*	+	+	+	+	+	+	+	+	0	0	-	Transcriptional regulator, TetR/AcrR family; Predicted membrane pro	-	
KdgR regulon	**kdgR**	+	0	+	+	0	0	0	0	0	0	0	**Pectin utilization**	-	
kdgRKAT	*BSU22120*	+	0	+	+	0	0	0	0	0	0	0	Galacturonate utilization	exp.	17322190
kduID	*BSU22130*	+	0	+	+	0	0	0	-	-	-	-	Galacturonate utilization	exp.	17322190
GamR regulon	**gamR**	+	0	0	+	0	0	0	+	+	+	0	**Predicted glucosamine utilization**	-	
licH-ywbABC	*BLi00335*	0	0	0	+	0	0	0	+	+	+	0	6-phospho-beta-glucosidase; PTS system, cellobiose specific	-	
chiA	*BH0916*	0	0	0	-	0	0	-	+	-	-	-	Chitinase	-	
gamAP	*BSU02360*	+	0	0	0	0	0	0	0	0	0	0	Glucosamine-6-phosphate deaminase; Glucosamine-specific PTS sy	-	
gamR	*BSU02370*	+	0	0	+	0	0	0	-	-	+	0	Predicted transcriptional regulator of glucosamine utilization, GntR fa	-	
BH0913	*BH0913*	0	0	0	+	0	0	-	+	+	+	0	Cellobiose phosphotransferase system YdjC-like protein	-	

YvbF/YvaV regulon	**YvbF/YvaV**	+	+	+	+	0	0	0	0	+	0	0	**Osmoregulated choline transport**	-	
yvbF	*BSU33840*	+	+	0	0	0	0	0	0	0	0	0	Transcriptional regulator of choline transport, MarR family	-	
yvbA	*BSU33740*	+	+	+	+	0	0	0	0	-	0	0	Transcriptional regulator of choline transport, MarR family	-	
opuCA-CB-CC-CD	*BSU33830*	+	+	0	0	0	0	0	0	0	0	0	Osmotically activated choline ABC transporter	-	
opuBA-BB-BC-BB	*BSU33730*	+	+	+	+	0	0	0	0	-	0	-	Osmotically activated L-carnitine/crotonobetaine/gamma-butyrobetai	-	
CcpA regulon	**ccpA**	+	+	+	+	+	+	+	+	+	+	+	**Carbon catabolite repression**	-	
cimH	*BSU38770*	+	+	0	-	0	0	0	0	0	0	0	L-Malate Citrate symporter (TC 2.A.24.2.4)	exp.	10666464
mutBA-BH2954	*GK2371*	0	0	0	0	+	+	0	-	0	0	0	Methylmalonyl-CoA mutase, small subunit; Methylmalonyl-CoA muta	-	
ABC0302	*ABC0302*	0	0	0	-	0	0	0	0	+	+	0	Predicted transcriptional repressor of the hexuronate utilization oper	-	
amyE	*BSU03040*	+	+	0	0	0	0	0	0	0	0	0	Alpha-amylase precursor	exp.	15773986
licT-bglP1	*BSU39080*	-	-	-	-	0	0	0	+	+	0	0	Beta-glucoside bgl operon antiterminator, BglG family; PTS system,	-	
ylbBC	*BSU14950*	+	+	+	+	-	-	-	-	-	-	-	CBS domain protein; Uncharacterized secreted protein with SCP do	-	
mrp	*BSU01540*	+	+	+	+	+	-	+	-	-	-	-	Scaffold protein for [4Fe-4S] cluster assembly ApbC, MRP-like	-	
lplBC-upgB	*ABC1135*	0	0	0	0	0	0	0	+	+	0	+	Transmembrane lipoprotein; Polysaccharide ABC transporter perme	-	
gntRKPZ	*BSU40050*	+	0	0	+	0	0	0	0	+	+	0	Gluconate operon transcriptional repressor; Gluconokinase; Glucona	exp.	15773986
yqgQ-glcK	*BSU24850*	+	-	+	-	+	-	+	-	-	-	-	Hypothetical Cytosolic Protein; Glucokinase	-	
kdgRKAT	*BSU22120*	+	0	+	+	0	0	0	0	0	0	0	Transcriptional regulator of pectin utilization, LacI family; 2-dehydro-3	exp.	10666464
BH3448-46	*BH3448*	0	0	0	+	0	-	0	+	0	0	+	ABC-type sugar transport system, periplasmic component; Two-com	-	
yesOPQR-rhgR-yesTUVWXYZ	*BSU06970*	+	0	0	+	0	0	0	0	0	0	+	Intracellular unsaturated galacturonyl hydrolase; transcriptional regul	-	
manR	*BSU12000*	+	+	0	+	0	0	0	0	0	0	0	Transcriptional regulator of mannose utilization, BglG family	exp.	20139185
citST	*BSU07580*	+	+	-	+	0	0	+	+	+	-	0	Sensor kinase CitA, DpiB; Transcriptional regulatory protein	exp.	16842348
BH3680-82-xynB-BH3684	*BH3680*	0	0	0	0	0	0	0	+	0	+	+	Predicted beta-xyloside ABC transporter, substrate-binding compone	-	
levDEFG-sacC	*BSU27070*	+	0	0	+	0	0	0	0	0	+	0	Fructose-specific PTS-system; Levanase	exp.	7592486
sdcS	*ABC3994*	0	0	0	+	0	0	0	0	+	+	0	Sodium:dicarboxylate cotransporter; di- and tricarboxylate transporte	-	
yhaR	*BSU09880*	+	+	-	+	-	-	-	0	0	0	0	Enoyl-CoA hydratase	-	
citMII	*BH0745*	0	0	+	0	0	0	0	+	+	0	0	Magnesium citrate secondary transporter	-	
cspD	*BSU21930*	+	+	-	+	-	-	-	0	0	0	0	Cold-shock protein, molecular chaperone, RNA-helicase co-factor	-	
nirC	*BSU38060*	+	0	0	-	+	0	+	0	0	0	0	Formate/nitrite family of transporters	-	
ABC3348-gatABC	*ABC3348*	0	0	0	0	0	0	0	+	+	+	0	Predicted galactitol operon regulator (transcriptional antiterminator),	-	
citH	*BSU39060*	+	+	0	0	0	0	+	0	0	0	0	Ca2+/citrate complex secondary transporter	-	
ywcBA	*BSU38230*	-	0	-	-	0	+	-	0	+	+	0	Hypothetical Membrane Spanning Protein; Putative sodium:proline s	-	
ccpC	*BSU14140*	+	+	-	-	0	-	+	-	-	-	0	CBS domain containing protein; Transcriptional repressor of citB and	exp.	11985717
dagA	*BSU18610*	-	0	0	+	0	0	0	+	0	+	-	Putative amino acid transporter	-	
licR	*BSU38600*	-	-	+	+	0	0	0	0	-	-	0	Transcriptional antiterminator of lichenan operon, BglG family	-	
araE	*OB2796*	+	+	+	+	0	0	0	0	0	+	0	Arabinose-proton symporter	exp.	12949161
yxjC-scoAB-yxjF	*BSU39000*	+	+	0	0	0	0	-	0	+	0	0	D-beta-hydroxybutyrate permease; Butyrate-acetoacetate CoA-trans	exp.	10666464
tctCBA	*ABC1013*	0	0	0	+	0	0	0	0	+	+	0	Tricarboxylate transpor	-	
uxuA-fabG	*BH0701*	0	0	0	+	0	0	0	+	0	+	0	Mannonate dehydratase; D-mannonate oxidoreductase	-	

dctPMQ-BH0704	*BH0705*	0	0	0	-	0	0	0	+	-	+	0	TRAP-type C4-dicarboxylate transport system; Alpha-glucosidase	-	
abnA	*BSU28810*	+	+	0	+	0	0	0	0	0	0	0	Arabinan endo-1,5-alpha-L-arabinosidase	exp.	17827291
dctA	*BSU04470*	+	+	+	0	0	0	0	0	0	0	0	C4-dicarboxylate transport protein	exp.	10708364
ganB	*BSU34120*	+	0	0	+	0	0	0	+	0	0	0	Arabinogalactan endo-1,4-beta-galactosidase precursor	-	
phoPR	*BSU29110*	+	+	-	+	-	-	-	-	-	-	-	Alkaline phosphatase synthesis transcriptional regulatory protein Pho	exp.	16452408
rmgR	*BSU30150*	-	0	-	-	0	0	0	+	+	0	-	Transcriptional regulator of rhamnogalacturonides utilization, AraC fa	-	
trePAR	*BSU07800*	+	+	+	+	-	-	+	+	-	0	0	PTS system, trehalose-specific enzyme II, BC component; Trehalose	exp.	10666464
msmX	*ABC1514*	+	+	+	+	+	-	0	+	+	+	0	Maltose/maltodextrin transport ATP-binding protein	exp.	10666464
cstA	*BSU28710*	+	+	+	+	0	0	0	0	0	0	0	Carbon starvation-induced membrane protein	-	
nupC-pdp	*BSU39430*	+	+	+	+	-	0	0	0	0	0	0	Pyrimidine-nucleoside Na+(H+) cotransporter; Pyrimidine-nucleoside	-	
galT	*BSU38190*	+	+	+	+	0	-	0	-	+	0	-	Galactose-1-phosphate uridylyltransferase	exp.	10666464
galKE	*BSU39410*	-	+	+	+	0	-	0	-	+	0	-	Galactokinase; UDP-glucose 4-epimerase	-	
ywfI	*BSU37670*	+	+	+	+	-	-	-	-	+	-	-	Predicted heme peroxidase involved in anaerobic stress response	-	
glcDF	*BSU28680*	+	+	-	+	+	-	-	-	-	-	0	Glycolate oxidase, subunit GlcD; Predicted glycolate oxidase iron-sul	-	
sucCD	*BSU16090*	+	+	+	+	-	-	-	-	-	-	-	Succinyl-CoA ligase [ADP-forming]	-	
ykoM	*BSU13340*	+	+	+	+	0	0	0	0	0	0	0	Putative transcriptional regulator, MarR family	-	
acoABCL	*BSU08060*	+	+	+	+	0	0	-	-	-	0	0	Acetoin dehydrogenase E1 component alpha-subunit; Acetoin dehyd	exp.	10666464
ylbP	*BSU15100*	+	+	+	+	0	0	0	-	+	+	0	Uncharacterized N-acetyltransferase	-	
araR	*BSU39970*	+	+	+	+	-	-	0	-	0	+	-	Transcriptional repressor of arabinoside utilization operon, GntR fam	-	
hutPHUIGM	*BSU39340*	+	+	0	0	0	+	+	+	-	0	0	Histidine utilization	exp.	8144455
cccA	*BSU25190*	+	+	+	+	-	-	-	-	-	-	-	Membrane-attached cytochrome c550	exp.	11361075
glvARC	*BSU08180*	+	+	-	+	0	0	0	0	+	0	0	Maltose utilization	exp.	11489864
dapA-eutG	*ABC0222*	0	0	+	+	0	0	0	0	+	0	0	Dihydrodipicolinate synthase family; Alcohol dehydrogenase	-	
kdgT-hop-pdxA	*ABC0308*	0	0	+	+	0	0	0	0	+	+	-	2-keto-3-deoxygluconate permease (KDG permease); Candidate typ	-	
bglPH	*BSU39270*	+	+	+	+	0	0	0	0	0	0	0	Aryl-phospho-beta-glucoside utilization	exp.	8626332
citM	*BSU07610*	+	+	+	+	0	-	-	-	-	0	0	Mg(2+) Citrate transporter (TC 2.A.11.1.1)	exp.	10666464
abnB	*BSU39330*	+	+	-	+	0	0	0	+	+	0	0	Alpha-N-arabinofuranosidase 2	-	
licBCAH	*BSU38590*	+	+	+	+	0	0	0	0	0	0	0	lichenan-,cellobiose-specific PTS system; 6-phospho-beta-glucosida	exp.	10559165
araFGH	*ABC0409*	0	0	0	+	-	+	-	+	+	0	-	L-arabinose ABC transporter	-	
gatCAB	*BSU06670*	+	+	+	+	-	-	-	-	-	-	-	Aspartyl/Glutamyl -tRNA amidotransferase subunit C; Aspartyl/Glutar	-	
yqgX	*BSU24790*	+	+	+	+	-	-	-	+	+	-	-	Similar to Hydroxyacylglutathione hydrolase, but in an organism lacki	-	
glpTQ	*BSU02140*	+	+	+	+	0	0	+	0	0	0	0	MFS family major facilitator transporter, glycerol-3-phosphate:cation	-	
drm-punA	*BSU23500*	+	+	+	+	+	-	+	-	-	-	-	Phosphopentomutase; Purine nucleoside phosphorylase	-	
acuABC	*BSU29690*	+	+	+	+	+	-	-	-	-	-	-	Acetyltransferase AcuA, acetyl-CoA synthetase inhibitor; Component	exp.	7913927
apbA-yllA	*BSU15110*	+	+	+	+	-	-	-	-	+	-	-	2-dehydropantoate 2-reductase; Hypothetical membrane spanning p	-	
BPUM_3238-36-pmi	*BSU35790*	+	-	+	0	0	+	0	+	0	-	-	Predicted beta-glucoside-regulated ABC transport system; Mannose-	-	
cycB-ganPQA	*BSU34160*	+	0	+	+	-	0	-	+	+	0	-	Maltose/maltodextrin ABC transporter; Beta-galactosidase	-	
ytcPQ	*BSU30170*	+	0	+	+	0	0	0	+	+	-	-	ABC superfamily ATP binding cassette transporter, membrane protei	-	

bglS	*BSU39070*	+	+	+	0	0	0	0	+	0	0	-	Endo-beta-1,3-1,4 glucanase (Licheninase)	exp.	8245831
xynPB	*BSU17570*	+	+	+	0	0	0	0	0	+	-	-	Putative H+-xyloside symporter; Beta-xylosidase	exp.	9973552
kduID	*BSU22130*	+	0	+	+	0	0	0	+	+	-	-	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase; 2-deoxy-D-g	-	
ackA	*BSU29470*	+	+	+	+	+	-	-	-	-	-	0	Acetate kinase	exp.	8226682
lrgAB	*BSU28910*	+	+	+	+	0	0	+	0	0	0	-	Penicillin resistance	-	
glsA1-glnT	*BSU02430*	+	+	+	+	0	0	-	+	0	-	-	Glutaminase; Glutamine permease	-	
sdhCAB-ysmA	*BSU28450*	+	+	+	+	-	-	+	-	-	+	-	Succinate dehydrogenase cytochrome b558 subunit; Succinate dehy	-	
citZ-icd-mdh	*BSU29140*	+	+	+	+	+	-	-	-	+	-	-	Citrate synthase (si); Isocitrate dehydrogenase [NADP]; Malate dehy	exp.	12100558
fruRKA	*BSU14380*	+	+	+	+	+	-	+	-	-	-	0	Transcriptional repressor of the fructose operon, DeoR family; Tagat	-	
yqgY	*BSU24780*	+	+	+	+	-	-	-	-	+	+	+	Uncharacterized short membrane protein	-	
yqgW	*BSU24800*	+	+	+	+	-	-	-	+	+	-	0	Alkaliphily related protein	-	
uxaC-exuM-yjmCD-uxuA-yjmF-exuTR-uxa	*BSU12300*	+	+	+	+	0	0	0	0	+	0	-	Uronate isomerase; Melibiose carrier protein, Na+/melibiose symport	exp.	10666464
msmREFG-melA	*BSU30260*	+	+	+	+	0	0	0	+	-	0	-	MSM (multiple sugar metabolism) operon regulatory protein; Multiple	-	
gmuBACDREFG	*BSU05810*	+	+	+	+	0	+	0	+	+	+	0	PTS system, cellobiose-specific IIB component; PTS system, cellobi	exp.	18223082
pta	*BSU37660*	+	+	+	+	-	-	-	+	+	-	0	Phosphate acetyltransferase	exp.	10559153
xylAB	*BSU17600*	+	+	+	+	0	+	0	+	+	-	-	Xylose isomerase; Xylulose kinase	exp.	15773986
acoR	*BSU08100*	+	+	+	+	0	0	+	+	0	0	0	Transcriptional activator of acetoin dehydrogenase operon AcoR	exp.	11274109
ndk	*BSU22720*	+	+	+	+	+	+	-	0	+	-	-	Nucleoside diphosphate kinase	-	
yvfVWY	*BSU34050*	+	+	-	+	+	+	+	+	+	+	0	Predicted L-lactate dehydrogenase, Fe-S oxidoreductase subunit; Pr	-	
lutR	*BSU34180*	+	+	-	-	+	+	-	+	-	-	0	Lactate-responsive regulator LldR in Firmicutes, GntR family	-	
ganR	*BSU34170*	-	-	0	+	0	0	0	+	-	0	0	Galactose operon repressor, GalR-LacI family of transcriptional regul	-	
lctP	*BH1831*	0	0	0	0	+	0	0	+	+	+	0	L-lactate permease	-	
odhAB	*BSU19370*	+	+	+	+	0	+	+	+	+	+	+	2-oxoglutarate dehydrogenase E1 component; 2-oxoglutarate dehyd	-	
sacPA	*BSU38050*	+	+	+	+	+	-	+	+	0	0	0	PTS sucrose-specific enzyme IIBC component; Sucrose-6-phosphat	-	
sacK	*BC0773*	0	0	0	0	+	0	+	+	0	0	0	Fructokinase	-	
lcfA	*BSU28560*	+	+	+	+	+	-	-	+	-	-	-	Long-chain-fatty-acid--CoA ligase	exp.	10666464
sigL	*BSU34200*	+	+	+	+	+	+	+	-	+	+	0	DNA-directed RNA polymerase sigma subunit SigL	exp.	16166551
mtlR	*BSU04160*	+	+	+	+	+	+	0	+	-	+	+	mannitol regulator	-	
mtlAFD	*BSU03981*	+	+	+	+	+	+	0	+	-	+	+	PTS family mannitol-permease II, BC component; Mannitol operon a	-	
rbsRKDACB	*BSU35910*	+	+	+	-	+	-	+	-	+	+	-	Ribose operon repressor, LacI family transcriptional regulator; Ribok	exp.	7592460
iolABCDEFGHIJ	*BSU39760*	+	+	0	+	0	-	+	+	+	+	-	Methylmalonate-semialdehyde dehydrogenase [inositol]; 5-deoxy-glu	exp.	10666464
araABDLMNPQ-abfA	*BSU27310*	+	+	+	+	-	-	0	+	+	+	-	L-arabinose isomerase; Ribulokinase; L-ribulose-5-phosphate 4-epim	exp.	12949161
xsa	*BSU28510*	+	+	-	-	0	0	0	-	+	-	-	Alpha-N-arabinofuranosidase 2???	-	
ilvBHC-leuABCD	*BSU28310*	+	+	-	-	-	-	-	-	-	+	-	Acetolactate synthase large subunit; Acetolactate synthase small sub	exp.	15916605
dat	*BLi02962*	0	0	+	+	+	+	+	0	0	0	0	Branched-chain amino acid aminotransferase	-	
acsA	*BSU29680*	+	+	+	+	+	-	-	+	+	+	+	Acetyl-coenzyme A synthetase	exp.	7913927
glpFK	*BSU09280*	+	-	+	+	-	+	+	+	+	+	0	Glycerol uptake facilitator protein; Glycerol kinase	exp.	11929549
mmgABCDE-prpB	*BSU24170*	+	+	+	+	+	+	-	+	+	+	-	3-ketoacyl-CoA thiolase [isoleucine degradation]; 3-hydroxybutyryl-C	exp.	8759838

yngIHHBGFE	*BSU18250*	+	+	+	+	-	+	-	+	+	-	0	Long-chain fatty-acid-CoA ligase; Biotin carboxylase of methylcroton	-	
CodY regulon	**codY**	+	+	+	+	+	+	+	+	+	+	+	**Global regulator of nutrient limitation and amino acid metabolis**	-	
acuABC	*BSU29690*	+	+	+	+	+	+	+	-	-	+	-	Acetyltransferase AcuA, acetyl-CoA synthetase inhibitor; Component	-	
acsA	*BSU29680*	+	+	+	+	+	+	+	-	-	-	-	Acetyl-coenzyme A synthetase	exp.	10231480
gltO	*BPUM_0421*	0	0	+	-	+	0	+	+	+	+	0	Proton/sodium-glutamate symport protein	-	
srfAAAB-comS-srfACAD	*BSU03480*	+	+	+	+	0	0	0	0	0	0	0	Surfactin synthetase	exp.	8830686
serA	*BSU23070*	+	+	+	+	+	+	0	-	-	-	-	D-3-phosphoglycerate dehydrogenase	-	
opuE	*BSU06660*	+	+	+	+	0	0	+	0	0	0	0	Sodium/proline symporter	-	
comK	*BSU10420*	+	+	+	+	0	-	-	0	0	+	0	Competence transcription factor	exp.	8830686
yuiABC	*BSU32090*	+	+	+	-	+	+	0	-	0	0	0	Conserved hypothetical proteins	-	
BH3439	*BH3439*	0	0	0	+	0	0	+	+	+	-	0	Sodium/proline symporter	-	
yocS	*BSU19350*	+	+	+	+	0	0	0	-	-	+	0	Sodium-dependent transporter	-	
ilvA	*BSU21770*	+	+	+	+	+	-	-	-	-	0	-	Threonine dehydratase biosynthetic	exp.	12618455
dppABCDE	*BSU12920*	+	+	+	+	0	0	0	0	-	+	0	Dipeptide-binding ABC transporter	exp.	8793880
lutABC	*BSU34050*	-	-	+	-	-	-	+	+	-	-	0	Predicted L-lactate dehydrogenase	-	
lutR	*BSU34180*	-	-	+	-	+	-	-	+	-	+	0	Transcriptional regulator of L-lactate utilization, GntR family	-	
lutP	*BSU34190*	-	-	0	-	+	-	0	+	-	-	0	L-lactate permease	-	
spo0A	*BSU24220*	-	-	+	-	+	+	+	+	-	-	-	Stage 0 sporulation two-component response regulator (Spo0A)	-	
yuxJ-pbpD-yuxK	*BSU31480*	+	+	-	+	0	0	0	0	-	0	0	MFS family major facilitator transporter; Multimodular transpeptidase	-	
liuR-Aflv_1280-81	*Aflv_1279*	0	0	0	0	+	+	0	0	0	0	0	Predicted transcriptional regulator LiuR of leucine degradation pathw	-	
ytcI	*BSU29560*	-	-	-	+	-	-	+	+	+	+	-	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases	-	
ycjHGF	*BSU11860*	+	+	+	-	+	+	-	-	-	-	0	Putative acetyl esterase YjcH; RNA ligase/cyclic nucleotide phospho	-	
sspOP	*BSU17990*	+	+	+	+	-	-	-	-	-	+	-	Small, acid-soluble spore protein	-	
oppABCDF	*BSU11430*	+	+	+	+	+	-	+	+	+	0	0	Oligopeptide ABC transporter	-	
dat	*BPUM_2473*	0	0	+	+	+	-	+	0	0	0	0	Branched-chain amino acid aminotransferase	-	
gatCAB	*BSU06670*	+	+	+	+	-	-	-	-	-	-	-	Aspartyl-tRNA(Asn) amidotransferase	-	
amhX	*BSU03010*	+	+	0	+	0	-	+	0	0	-	0	Amidohydrolase amhX	-	
ilvD	*BSU21870*	+	+	+	+	-	-	-	-	-	0	-	Dihydroxy-acid dehydratase	exp.	12618455
hom-thrCB	*BSU32260*	+	+	-	+	+	-	-	-	-	-	-	Threonine biosynthesis	-	
ackA	*BSU29470*	+	+	+	+	-	-	-	-	-	-	0	Acetate kinase	exp.	16995897
spoIIQ	*BSU36550*	+	+	+	+	-	-	-	-	0	-	-	Stage II sporulation protein related to metaloproteases (SpoIIQ)	-	
hpr	*BSU09990*	+	-	+	-	+	-	-	+	-	0	0	Transcriptional repressor of sporulation and extracellular protein, Ma	-	
ilvBHC-leuABCD	*BSU28310*	+	+	-	-	-	-	-	-	-	+	-	Leucine, isoleucine and valine biosynthesis	exp.	15228537
citB	*BSU18000*	+	+	+	+	-	-	-	-	-	-	-	Aconitate hydratase @ 2-methylisocitrate dehydratase	exp.	12591885
fadNAE	*BSU32840*	-	+	-	+	-	-	+	+	-	-	-	Enoyl-CoA hydratase [isoleucine degradation] / 3-hydroxyacyl-CoA d	-	
spoVS	*BSU16980*	+	+	-	-	+	-	+	-	-	-	-	Stage V sporulation protein required for dehydratation of the spore c	-	
yoyD-yodF	*BSU19579*	+	+	+	+	0	0	0	0	0	0	0	Hypothetical protein; SSS family solute:sodium (Na+) symporter	-	
kapD	*BSU31470*	+	+	-	+	0	-	+	0	0	0	0	KapD, inhibitor of KinA pathway to sporulation	-	

spoVG	*BSU00490*	+	-	-	-	-	+	+	-	-	-	-	Stage V sporulation protein G required for spore cortex synthesis	-	
opuBA-BB-BC-BB	*BSU33730*	+	+	0	0	0	0	0	0	0	0	0	Choline ABC transport system	-	
opuCA-CB-CC-CD	*BSU33830*	+	+	-	+	0	0	0	0	-	0	-	Osmotically activated L-carnitine/choline ABC transporter,	-	
kinE-ogt	*BSU13530*	+	+	-	-	+	-	0	0	0	0	0	Sporulation kinase E; Methylated-DNA--protein-cysteine methyltrans	-	
yaaC	*BSU00080*	-	-	+	+	-	-	+	-	-	-	0	Conserved hypothetical protein	-	
cueR	*BSU09560*	+	-	+	+	-	0	0	0	0	0	-	Transcriptional regulator, MerR family	-	
yhdT	*BSU09590*	+	-	+	+	0	0	0	0	0	0	0	Hemolysins and related proteins containing CBS domains	-	
yocR	*BSU19340*	+	+	0	+	0	0	0	-	0	0	0	Putative sodium-dependent transporter	-	
BH2374-73	*BH2374*	0	0	0	0	+	-	+	+	0	0	-	2-oxoglutarate oxidoreductase, alpha subunit; 2-oxoglutarate oxidore	-	
nupNOPQ	*BSU31540*	+	+	+	-	-	-	-	0	-	-	-	Guanosine ABC transport system	exp.	21926227
ykzI-suhB	*BSU14660*	-	-	-	-	+	-	+	-	-	-	+	Hypothetical protein; Inositol-1-monophosphatase	-	
ybgE	*BSU02390*	+	+	+	-	0	0	0	-	-	-	-	Branched-chain amino acid aminotransferase	exp.	12618455
murQR-ybbF-amiE-nagZ-ybbC	*BSU01700*	+	-	+	+	0	0	-	-	-	-	0	Muropeptide rescue pathway	-	
sshCAB	*BSU28450*	-	+	+	+	-	-	-	-	-	-	-	Succinate dehydrogenase	-	
yslB	*BSU28460*	-	+	+	+	-	-	-	-	-	-	-	Predicted hydrocarbon binding protein (V4R domain)	-	
ytkC	*BSU30640*	+	+	-	+	0	0	0	0	0	0	0	Hypothetical membrane protein	-	
ndk	*BSU22730*	-	-	-	+	-	-	-	-	-	+	-	Nucleoside diphosphate kinase	-	
rocR	*BSU40350*	+	-	-	+	0	0	+	-	-	0	0	Transcriptional activator of arginine utilization, Fis family	-	
lcfA	*BSU28560*	-	-	-	-	+	-	+	-	-	+	-	Long-chain-fatty-acid--CoA ligase	-	
ylmA	*BSU15340*	+	+	-	+	-	-	0	0	0	0	-	Putative ABC transporter, ATP-binding protein	exp.	18083814
ybxG	*BSU02060*	+	+	-	+	0	0	-	0	0	0	0	Amino acid permease	-	
hutPHUIGM	*BSU39340*	+	+	0	0	0	-	+	-	-	0	0	Histidine utilization	exp.	8682780
iscS-thiI	*BSU29590*	+	+	-	+	-	-	-	-	-	-	-	Thiamine biosynthesis	-	
bacABCDE-mtnE	*BSU37740*	+	+	-	-	-	-	0	0	-	-	-	Bacilysin biosynthesis	exp.	21709425
gabP	*BSU06310*	+	-	+	0	0	0	+	0	0	0	0	Gamma-aminobutyrate (GABA) permease	exp.	8951816
braB	*BSU29600*	+	+	+	0	0	0	0	0	0	0	0	Branched-chain amino acid transport system carrier protein	-	
metE2	*BSU38950*	+	+	+	-	0	0	0	0	0	0	0	Methionine synthase II (cobalamin-independent)	-	
citR	*BSU09430*	+	+	0	+	0	0	0	0	-	0	0	Transcriptional regulator of citrate synthase, LysR family	-	
metIC	*BSU11870*	+	-	+	-	-	-	-	-	-	0	-	Cystathionine gamma-synthase; Cystathionine beta-lyase	-	
metA	*BSU21910*	-	-	-	-	+	-	-	-	-	+	-	Homoserine O-succinyltransferase	-	
Aflv_2134	*Aflv_2134*	0	0	0	0	+	-	+	0	0	0	0	Uncharacterized membrane protein	-	
yppF	*BSU22260*	-	-	0	-	+	-	+	0	0	0	0	Hypothetical protein	-	
citZ-icd-mdh	*BSU29140*	+	+	+	+	+	+	-	-	-	+	-	Citrate synthase (si); Isocitrate dehydrogenase [NADP]; Malate dehy	-	
glnQHMP	*BSU27430*	+	+	-	0	0	-	-	0	-	0	-	Glutamine ABC transporter	-	
ycgA	*BSU03020*	-	+	+	0	0	0	0	0	0	-	0	Putative integral inner membrane protein	-	
glnB-amt	*BLi01176*	0	0	0	+	0	0	0	0	0	+	0	Nitrogen regulatory protein P-II; Ammonium transporter	-	
ABC3160	*ABC3160*	0	0	0	+	0	0	0	0	+	0	0	Hypothetical protein	-	
yjcL	*BSU11900*	+	0	0	+	0	0	0	0	0	0	0	Putative integral membrane protein	-	

yjnA	*BSU12400*	+	+	0	0	0	0	0	0	0	0	0	Putative integral membrane protein	-	
glnRA	*BSU17450*	-	+	-	-	+	-	-	-	-	-	-	Transcriptional regulator of nitrogen excess response, MerR family;	-	
azlCD	*RBAM_2677*	0	-	-	-	+	+	-	-	-	-	-	Branched-chain amino acid transport	-	
pta	*BSU37660*	-	-	-	-	-	-	-	+	+	-	0	Phosphate acetyltransferase	-	
ureABC	*BSU36660*	+	+	0	0	0	-	0	-	0	0	-	Urease	exp.	9287005
yhaA	*BSU10070*	+	-	-	+	-	0	0	0	0	-	0	N-acyl-L-amino acid amidohydrolase	-	
appDFABC	*Aflv_0356*	0	0	-	-	+	0	0	-	-	+	0	Oligopeptide ABC transporter	-	
glnHPQ	*Aflv_2792*	0	0	0	0	+	+	0	0	-	+	0	Glutamine ABC transporter	-	
putBCPR	*BSU03200*	+	+	-	+	0	+	+	-	-	-	0	Proline utilization	exp.	21840319
phoB	*BSU09410*	+	-	-	0	0	0	+	0	0	0	0	Alkaline phosphatase	-	
nasDEF	*BSU03300*	+	+	-	-	0	-	-	-	-	0	-	Nitrite reductase	-	
yhdGH	*BSU09460*	+	+	0	-	0	0	0	0	-	0	0	Amino acid transporter	exp.	21097623
frlBO-yurNM-frlD	*BSU32610*	+	+	0	0	0	0	0	0	0	0	0	Fructoselysine utilization	-	
gamR	*BSU02370*	+	0	0	-	0	0	0	-	+	-	0	Predicted transcriptional regulator of glucosamine utilization, GntR fa	-	
mcpC	*BSU13950*	+	-	-	-	-	-	-	+	0	0	0	Methyl-accepting chemotaxis protein McpC	-	
glnA2	*Aflv_1403*	0	0	0	0	+	-	0	-	+	0	0	Glutamine synthetase type I	-	
pelB	*BPUM_3515*	0	0	-	+	0	0	0	+	-	0	0	Pectate lyase precursor	-	
ywcBA	*BSU38230*	-	0	-	-	0	+	+	0	-	-	0	Hypothetical Membrane Spanning Protein; SSS family solute:sodium	-	
oppA2	*BH0031*	0	0	0	0	0	0	0	+	-	+	0	Oligopeptide ABC transporter, periplasmic oligopeptide-binding prote	-	
serC	*BSU10020*	-	+	-	-	+	-	-	-	-	0	-	Phosphoserine aminotransferase	-	
alaRT	*BSU31410*	-	-	-	+	+	-	-	-	-	0	-	Transcriptional regulator of alanine metabolism, Lrp/AsnC family; Asp	-	
yuaE	*BSU31030*	+	+	-	-	0	0	0	0	0	0	0	Hypothetical protein	-	
yuaFG	*BSU31020*	+	+	-	0	0	-	-	-	-	-	-	Hypothetical membrane protein	-	
yfmB	*BSU07530*	-	-	+	+	0	0	0	0	0	0	0	Hypothetical protein	-	
rocDEF	*BSU40340*	+	-	-	+	-	-	-	-	-	-	-	Arginine utilization	-	
glpQ	*BLi04156*	0	0	0	+	0	0	0	-	0	+	-	Glycerophosphoryl diester phosphodiesterase, periplasmic	-	
amyS	*BLi00656*	0	0	0	+	0	0	+	0	0	0	0	Cytoplasmic alpha-amylase	-	
cotR	*BSU34530*	+	+	0	0	0	0	0	0	0	0	0	Putative sporulation hydrolase	-	
ispA	*BSU13190*	+	-	+	-	0	0	0	0	0	0	0	S8 family serine protease precursor	-	
gltT	*BSU10220*	-	-	+	+	0	0	0	0	0	0	0	Proton/sodium-glutamate symport protein	-	
yqjP	*BSU23790*	-	-	-	-	+	-	+	-	0	0	0	Zinc metallohydrolase, metallo-beta-lactamase family	-	
yusZ	*BSU32980*	+	-	-	+	-	0	-	0	0	0	0	Oxidoreductase, short-chain dehydrogenase/reductase	-	
gltAB	*BSU18450*	-	-	-	-	-	-	0	+	-	+	-	Glutamate synthase [NADPH]	-	
yhjCB	*BSU10450*	+	+	0	0	0	0	-	0	0	0	0	Hypothetical protein; Na+/solute symporter	-	
rok	*BSU14240*	+	+	-	-	0	0	0	0	0	0	0	ComK repressor	-	
adeC	*BSU14520*	+	-	-	-	+	-	0	0	0	0	0	Adenine deaminase	-	
glyP	*BPUM_0735*	0	0	-	+	0	0	-	+	-	-	0	Sodium/glycine symporter GlyP	-	
gltP	*BSU02340*	-	+	+	-	0	0	0	0	0	0	0	Proton/glutamate symport protein @ Proton/aspartate symport protei	-	

RBAM_038050	*RBAM_0380*	0	+	0	0	0	0	+	0	0	0	0	Acetyltransferase, GNAT family protein	-	
tdh-kbl	*BSU16990*	-	+	+	-	0	0	-	-	0	-	0	L-threonine 3-dehydrogenase; 2-amino-3-ketobutyrate coenzyme A l	-	
dppCB-oppDF	*BH0030*	0	0	0	0	0	0	0	+	-	+	0	Oligopeptide ABC transporter	-	
gldA	*RBAM_0026*	0	+	-	-	0	0	0	0	-	+	0	Glycerol dehydrogenase	-	
gltZ	*BLi03198*	0	0	0	+	0	0	0	0	0	+	0	Proton/glutamate symport protein @ Sodium/glutamate symport prot	-	
yclF	*BSU03670*	-	-	+	-	-	+	0	0	0	0	0	POT family proton (H+)-dependent oligopeptide transporter	-	
chi	*OB0791*	0	0	0	-	0	0	0	+	+	-	-	Chitinase	-	
pdaB	*BSU01570*	-	-	-	+	+	-	-	-	-	-	-	Probable polysaccharide deacetylase	-	
argGH	*OB3129*	-	-	-	-	-	-	+	-	-	+	-	Argininosuccinate synthase; Argininosuccinate lyase	-	
slp	*BSU14620*	+	+	-	-	0	0	0	-	0	0	0	Peptidoglycan-associated protein	-	
ushA	*Aflv_2607*	0	0	0	0	+	0	0	-	-	0	+	5'-nucleotidase	-	
Pjdr2_3723-17	*Pjdr2_3723*	0	0	0	0	0	0	0	0	0	0	+	Oligopeptide ABC transporter	-	
crnA-Pjdr2_6137-33-wrbA-codA	*Pjdr2_6138*	0	0	0	0	0	0	0	0	-	0	+	Creatine degradation	-	
odhAB	*BSU19370*	-	-	-	-	0	-	+	+	-	-	-	2-oxoglutarate dehydrogenase E1 component; 2-oxoglutarate dehyd	-	
GutR regulon	**gutR**	**+**	**+**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**Sorbitol utilization**	-	
gutBP	*BSU06150*	+	+	0	0	0	0	0	0	0	0	0	Sorbitol utilization	exp.	11118449
MalR regulon	**malR**	**+**	**+**	**+**	**+**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**Malate utilization**	-	
ywkAB	*BSU37050*	+	+	+	+	0	0	0	0	0	0	0	Malate dehydrogenase; Malate permease	exp.	12949160
maeN	*BSU31580*	+	0		+	0	0	-	0	-	0	0	Malate Na(+) symporter	exp.	12949159
yflS	*BSU07570*	+	+	0	-	0	0	0	0	0	0	0	Putative malate transporter	exp.	12949159
YbzH regulon	**ybzH**	**+**	**+**	**0**	**+**	**0**	**0**	**0**	**0**	**+**	**0**	**0**	**Hypothetical efflux transporter**	-	
ybzH	*BSU01889*	+	+	0	+	0	0	0	0	+	0	0	Transcriptional regulator, ArsR family	-	
ybcL	*BSU01890*	+	+	0	+	0	0	0	0	+	0	0	Putative efflux transporter	-	
PutR regulon	**putR**	**+**	**+**	**+**	**+**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**Proline utilization**	-	
putBCPR	*BSU03200*	+	+	+	+	0	0	0	0	0	0	0	Proline utilization	exp.	21840319
GlnL regulon	**glnL**	**+**	**+**	**+**	**+**	**0**	**0**	**+**	**+**	**0**	**0**	**0**	**Glutamine utilization; Aspartate utilization**	-	
glsA1-glnT	*BSU02430*	+	+	+	+	0	0	+	+	0	-	-	Glutamine utilization	exp.	15995196
gltT-ansB1	*BPUM_3019*	0	0	+	0	0	0	+	0	0	0	0	Glutamine utilization	-	
gudB	*BH2718*	0	0	0	0	0	0	0	+	0	0	0	Glutamate dehydrogenase	-	
LiaR regulon	**liaR**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**Cell wall-active antibiotics stress response**		
liaIHFSR	*BSU33130*	+	+	+	+	+	+	+	+	+	+	+	Cell wall-active antibiotics stress response	exp.	17660417
liaG	*BSU33110*	+	+	+	+	0	0	0	+	0	0	+	Inhibitor of LiaR-dependent gene expression LiaF	exp.	17660417
YrkD regulon	**yrkD**	**+**	**+**	**+**	**+**	**+**	**+**	**+**	**0**	**0**	**+**	**0**	**Hypothetical substance detoxification pathway**	-	
yrkEFHIJ	*BSU26540*	+	+	+	+	+	+	+	0	0	+	0	Putative sulfur reduction protein; Rhodanese-like domain protein; Zn	-	
RBAM_005440	*RBAM_0054*	0	+	+	+	+	+	+	0	0	0	0	Rhodanese-like domain protein	-	
ydfQ	*BLi02789*	0	0	0	+	0	0	0	0	0	0	0	Thioredoxin	-	
BLi02788-yvqC-hmt2-BLi02785	*BLi02788*	0	-	0	+	+	+	0	0	0	0	0	Two-component system; Sulfide-quinone reductase; Rhodanese-like	-	
Aflv_1299-1300	*Aflv_1299*	0	0	0	0	+	+	+	0	0	0	0	CoA-disulfide reductase (EC 1.8.1.14) / Rhodanese domain protein;	-	

grx	*GK2075*	0	0	0	0	+	+	0	0	0	0	0	Predicted glutaredoxin	-	
yrkD	*BSU26550*	+	+	+	+	+	+	+	0	0	+	0	Transcriptional regulator, RcnR family	-	
GK2072	*GK2072*	0	0	0	0	0	+	0	0	0	0	0	Rhodanese-like domain protein	-	
Aflv_1540	*Aflv_1540*	0	0	0	0	+	0	0	0	0	0	0	Rhodanese-like domain protein	-	
Aflv_1298	*Aflv_1298*	0	0	0	0	+	0	0	0	0	0	0	Rhodanese-like domain protein	-	
LytT regulon	**lytT**	+	+	+	+	0	0	+	0	0	0	0	**Cell integrity protection**		
lrgAB	*BSU28910*	+	+	+	+	0	0	+	0	0	0	0	Inhibits the expression or activity of extracellular murein hydrolases b	-	
YwbI regulon	**ywbI**	+	+	+	+	0	0	0	0	0	0	+	**Cell integrity protection**	-	
ywbI	*BSU38310*	+	+	+	-	-	-	-	0	0	-	0	Transcriptional regulator, LysR family	-	
cidA-lrgB	*BSU38320*	+	+	+	+	0	0	-	0	0	0	+	Increases the activity of extracellular murein hydrolases possibly by r	-	
YvcP regulon	**yvcP**	+	0	0	0	0	0	0	+	+	0	+	**Bacitracin resistance**		
yvcRS	*BSU34690*	+	0	0	0	0	0	0	+	+	0	+	Putative antibiotics resistance ABC transport system	exp.	14651641
YizB regulon	**yizB**	+	+	+	+	0	0	+	0	0	0	0			
yizB-yitQR	*BSU11079*	+	0	0	0	0	0	0	0	0	+	0	Transcription regulator, PadR family; Predicted membrane protein	-	
RNA-elements regulons															
TPP regulon	**TPP**												**Thiamine biosynthesis**	-	
thiT	*BSU30990*	+	+	+	+	0	0	+	+	0	+	0	Substrate-specific component ThiT of thiamin ECF transporter	-	
thiC	*BSU08790*	+	+	+	+	+	+	+	+	0	0	+	Thiamin biosynthesis protein ThiC	-	
thiY2-COG0011-thiX2Z2-COG0084	*Pjdr2_3510*	0	0	0	0	0	0	+	0	0	0	+	Thiamin ABC transporter; TatD-related deoxyribonuclease, COG008	-	
tenAI-thiOSGFD	*BSU11650*	+	+	+	+	+	+	+	+	+	+	-	4-amino-5-aminomethyl-2-methylpyrimidine hydrolase TenA; Thiamin	exp.	12464185
ykoFEDC	*BSU13240*	+	+	+	+	+	+	0	0	+	+	0	Thiamin-regulated ECF transporter for HydroxyMethylPyrimidine	-	
ylmB	*BSU15350*	+	+	0	0	0	-	0	+	+	0	-	N-formyl-4-amino-5-aminomethyl-2-methylpyrimidine deformylase (E	-	
Cobalamin regulon	**Cobalamin**												**Cobalamin biosynthesis**	-	
btuFCD-pduO	*BSU33180*	+	-	-	-	+	+	0	+	-	0	+	Vitamin B12 ABC transporter; Cob(I)alamin adenosyltransferase Pdu	exp.	14704351
cbiWMNQOHXJCDETLFGAP-cobT-cysG	*Aflv_2185*	0	0	0	0	+	+	0	0	0	0	0	Cobalt ECF transporter; Cobalamin biosynthesis	-	
cbiB-cobDUSC-X-cblTS	*Aflv_1044*	0	0	0	0	+	+	0	+	0	0	+	Cobalamin biosynthesis	-	
metE	*BSU13180*	-	-	+	+	0	0	+	+	+	0	+	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransfera	-	
achX	*BH0798*	0	0	0	0	0	0	0	+	0	0	0	Predicted thioesterase	-	
nrdAB	*Aflv_0393*	0	0	0	0	+	+	0	+	0	-	0	Ribonucleotide reductase of class Ia (aerobic)	-	
Pjdr2_2684-88	*Pjdr2_2684*	0	0	0	0	0	0	0	0	0	0	+	S-layer domain protein; Hypothetical protein; B12-regulated ECF tran	-	
FMN regulon	**FMN**												**Riboflavin biosynthesis**	-	
ribU	*BSU23050*	+	+	+	+	0	+	+	0	0	+	0	Substrate-specific component RibU of riboflavin ECF transporter	exp.	15808508
impX	*ABC3060*	0	0	0	0	0	0	0	0	+	0	+	Predicted riboflavin transporter, EamA family	-	
ribDEBAHT	*BSU23270*	+	+	+	+	+	+	+	+	+	+	+	Riboflavin biosynthesis	exp.	12464185
Lysine regulon	**Lysine**												**Lysine biosynthesis**	-	
lysC	*BSU28470*	+	+	+	+	0	0	+	+	0	0	-	Aspartokinase	exp.	14523230
lysW	*BH3449*	0	0	0	0	0	0	0	+	+	+	0	Predicted lysine transporter, NhaC family	-	
lysA	*BSU23380*	-	-	-	-	-	-	-	+	+	-	-	Diaminopimelate decarboxylase	-	

lysP	*BC3052*	0	0	0	0	0	0	+	0	0	0	+	Lysine-specific permease	-	
yvsH	*BSU33330*	+	+	+	+	+	+	+	0	0	0	0	Putative lysine permease	-	
dapA	*BSU1742*	0	0	0	0	0	0	0	+	+	+	0	Dihydrodipicolinate synthase	-	
SAM regulon	**SAM**												**Methionine biosynthesis**	-	
metNPQ	*BSU32750*	+	+	+	+	+	+	+	+	+	+	-	Methionine ABC transporter	exp.	14990259
metK	*BSU30550*	+	+	+	+	+	+	+	+	+	+	-	S-adenosylmethionine synthetase	-	
mtnKA	*BSU13560*	+	+	+	+	+	+	+	0	0	0	-	5-methylthioribose kinase; Methylthioribose-1-phosphate isomerase	exp.	10094622
rbsBAC	*BPUM_3498*	0	0	+	0	+	+	+	0	0	0	-	Ribose ABC transport system	-	
mtnWXBD	*BSU13590*	+	+	+	+	+	+	+	0	0	0	-	2,3-diketo-5-methylthiopentyl-1-phosphate enolase; 2-hydroxy-3-ket	exp.	16091040
metQ2N2P2	*BC0198*	0	0	0	0	0	0	+	0	0	+	0	Methionine ABC transporter	-	
metN1P1Q1	*ABC0876*	0	0	0	+	0	0	0	0	+	+	0	Methionine ABC transporter	-	
OB3328	*OB3328*	0	-	-	-	0	0	0	0	+	+	0	Predicted alcohol dehydrogenase, iron-type	-	
metN3P3Q3	*BLi00972*	-	-	0	+	0	0	+	0	+	+	0	Methionine ABC transporter	-	
acy	*BC3176*	0	0	0	0	0	0	+	0	+	+	0	N-acyl-L-amino acid amidohydrolase	-	
metE	*BSU13180*	+	+	-	-	0	0	-	-	+	0	-	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransfer	-	
BH0835	*BH0835*	0	0	0	0	0	0	0	+	0	+	0	Uncharacterized protein	-	
OB3078	*OB3078*	0	0	0	0	0	0	0	0	0	+	0	Predicted sulfonate monooxygenase	-	
yoaDCB	*BSU18560*	+	+	0	0	0	0	0	0	0	0	0	Hydroxypyruvate reductase; Sugar kinase similar to xylulokinase, FG	exp.	18039762
metY2	*OB2640*	0	0	0	0	0	0	0	0	0	+	0	O-acetylhomoserine sulfhydrylase / O-succinylhomoserine sulfhydryl	-	
oppBCDFA	*BC0207*	0	0	0	0	0	0	+	0	0	0	0	Oligopeptide transport	-	
BC0395	*BC0395*	0	0	0	0	0	0	+	0	0	0	0	Putative formamidase	-	
bhmT	*OB0691*	0	0	0	0	0	0	0	0	0	+	0	Betaine--homocysteine S-methyltransferase	-	
oppA1	*BC0216*	0	0	0	0	0	0	+	0	0	0	0	Oligopeptide ABC transporter, periplasmic oligopeptide-binding prote	-	
metY	*Aflv_2473*	0	0	-	0	-	-	0	-	-	+	-	O-acetylhomoserine sulfhydrylase / O-succinylhomoserine sulfhydryl	-	
ssuE	*OB3079*	0	0	0	0	0	0	0	-	-	+	-	FMN reductase	-	
metT	*BC1434*	0	-	0	-	0	0	+	0	0	0	0	Methionine transporter MetT	-	
mtsA	*BC2624*	0	0	0	0	0	0	+	0	0	0	0	Substrate-specific component MtsA of methionine-regulated ECF tra	-	
OB2779-soxA	*OB2779*	0	0	0	0	0	0	0	0	0	+	0	Possible carboxymuconolactone decarboxylase family protein; Diben	-	
ywbC	*BSU38370*	-	-	-	-	0	+	-	-	-	0	-	Lactoylglutathione lyase and related lyases	-	
cysHP-sat-cysCG-sirBC	*BSU15570*	+	+	+	+	-	+	+	-	-	-	-	Reduction of sulfate to sulfite	exp.	19779461
metE3	*BSU38960*	+	0	0	0	0	0	0	0	0	0	0	Putative methionine synthase II (cobalamin-independent)	exp.	18039762
metE2	*BSU38950*	+	+	+	+	0	0	0	0	+	+	0	Putative methionine synthase II (cobalamin-independent)	exp.	18039762
metIC	*BSU11870*	+	+	+	+	+	+	+	+	+	0	+	Cystathionine gamma-synthase; Cystathionine beta-lyase	exp.	11832514
metF	*BSU11010*	+	+	+	+	+	+	+	+	+	0	0	5,10-methylenetetrahydrofolate reductase / Homolog of homocystein	exp.	16091040
metH	*BLi01192*	0	0	+	+	+	+	+	+	+	0	-	5-methyltetrahydrofolate--homocysteine methyltransferase	-	
Glycine regulon	**Glycine**												**Glycine metabolism**	-	
gcvTP1P2	*BSU24570*	+	+	+	+	+	+	-	+	+	+	0	Glycine cleavage system	exp.	15472076
glyP	*BC2317*	0	0	-	-	0	0	+	-	-	-	0	Sodium/glycine symporter GlyP	-	

ydgF	*RBAM_0369*	0	+	+	0	0	0	0	0	0	0	0	D-serine/D-alanine/glycine transporter	-	
Purine regulon	**Purine**												**Purine metabolism**	-	
nupG	*BSU39020*	+	+	0	+	0	0	+	0	0	-	0	Nucleoside permease NupG	-	
pbuG	*BSU06370*	+	+	+	+	+	+	+	+	+	+	+	Hypoxanthine/guanine permease PbuG	exp.	12923093
purEKBCSQLFMNHD	*BSU06420*	+	+	+	+	+	+	+	+	+	+	+	AMP biosynthesis	exp.	14718920
xpt-pbuX	*BSU22070*	+	+	+	+	0	0	+	+	+	+	+	Xanthine phosphoribosyltransferase; Xanthine permease	exp.	12787499
guaA	*BSU06360*	-	-	-	-	+	+	+	+	-	+	-	GMP synthase [glutamine-hydrolyzing]	-	
pbuE	*BSU05800*	+	+	+	0	0	0	-	0	0	-	0	Purine base efflux pump	exp.	14718920
pbuO	*BSU29990*	-	-	-	-	0	0	0	0	0	0	+	Hypoxanthine/guanine permease PbuO	-	
yczH	*BSU04020*	0	0	-	0	+	0	-	0	0	0	0	Dienelactone hydrolase family protein	-	
adeC	*BSU14520*	-	-	-	-	+	-	0	-	-	-	+	Adenine deaminase	-	
guaD	*BH0746*	0	0	0	0	0	0	0	+	0	0	-	5-methylthioadenosine/S-adenosylhomocysteine deaminase	-	
yfmC-yufNO	*BC3792*	-	-	-	0	-	-	+	0	-	-	0	Transcriptional regulator, GntR family; Predicted nucleoside ABC tra	-	
PreQ1 regulon	**PreQ1**												**Queuosine biosynthesis**	-	
queCDEF	*BSU13720*	+	+	+	+	+	+	+	+	+	+	+	Queuosine biosynthesis	exp.	17384645
ypdP	*BSU21980*	-	-	-	-	-	0	0	0	+	+	-	Putative preQ0 transporter	-	
queT	*BC1599*	0	0	0	0	-	0	+	0	0	+	0	Substrate-specific component QueT (COG4708) of predicted queuos	-	
glmS regulon	**glmS**												**Amino sugar metabolism**	-	
glmS	*BSU01780*	+	+	+	+	+	+	+	+	+	+	+	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]	exp.	15029187
PyrR regulon	**PyrR**												**Pyrimidine metabolism**	-	
pyrR	*BSU15470*	+	+	+	+	+	+	+	+	+	+	+	Uracil phosphoribosyltransferase / Pyrimidine operon regulatory prot	exp.	11726695
pyrP	*BSU15480*	+	+	+	+	+	+	+	+	+	+	-	Uracil permease	exp.	11726695
pyrBC-carAB-pyKDFE	*BSU15490*	+	+	+	+	+	+	+	+	+	+	+	UMP biosynthesis	exp.	11726695
BC5442	*BC5442*	0	0	0	0	0	0	+	0	0	0	0	Major facilitator superfamily (MFS) transport protein	-	
ydaO-yuaA regulon	**ydaO-yuaA**												**Cell wall metabolism; Osmotic stress response**	-	
ydaO	*BSU04320*	+	+	+	+	0	+	+	0	0	0	+	Putative metabolite transporter, COG0531	exp.	20511502
ktrAB	*BSU31090*	+	-	0	-	0	0	0	+	-	+	+	Potassium uptake	exp.	20511502
kdpABCD	*BC0753*	0	0	0	0	+	0	+	0	0	0	+	Potassium transport; Osmosensitive K+ channel histidine kinase Kdp	-	
BPUM_0421	*BPUM_0421*	0	0	+	+	0	0	0	0	0	0	0	Sodium:dicarboxylate symporter family protein, COG1301	-	
kamA	*Pjdr2_5396*	0	0	0	0	0	0	0	-	0	0	+	Lysine 2,3-aminomutase	-	
Pjdr2_0116	*Pjdr2_0116*	0	0	0	0	0	0	0	0	0	0	+	Cell wall-associated hydrolase, COG0791	-	
ykkC-yxkD regulon	**ykkC-yxkD**												**Multidrug resistance**	-	
ykkCD	*BSU13090*	+	+	+	+	0	0	-	+	+	+	+	Quaternary ammonium compound-resistance protein	-	
yxkD	*BSU38840*	+	+	0	+	0	0	0	0	0	0	0	Membrane protein, putative	-	
ykoK regulon	**ykoK**												**Magnesium uptake**	-	
mgtE	*BSU13300*	+	+	+	+	-	0	0	+	+	-	0	Magnesium transporter	exp.	15096624
sapB	*BH3225*	0	0	0	0	0	0	-	+	-	0	-	Peptide transport system permease protein sapB (TC 3.A.1.5.5)	-	
ylbH regulon	**ylbH**													-	

ylbH-coaD	*BSU15010*	+	+	+	+	+	+	+	+	-	+	+	Ribosomal RNA small subunit methyltransferase D; Phosphopanteth	-	
yybP-ykoY regulon	**yybP-ykoY**													-	
ykoY	*BSU13440*	+	+	+	+	+	+	+	+	+	+	0	Membrane protein TerC, possibly involved in tellurium resistance	-	
BC0827-ykoX	*BC0827*	-	-	-	-	0	+	+	0	0	0	0	Hypothetical protein	-	
yybP	*BSU40560*	+	0	+	+	0	0	-	0	0	0	-	Putative secreted protein	-	
yrzF	*ABC3139*	0	0	-	-	0	0	0	0	+	+	0	Predicted Ser/Thr protein kinase	-	
L10_leader regulon	**L10_leader**												**Ribosome biogenesis**	-	
rplJL	*BSU01040*	+	+	+	+	+	+	+	+	+	+	+	Ribosomal proteins	-	
L13_leader regulon	**L13_leader**												**Ribosome biogenesis**	-	
rplM-rpsI	*BSU01490*	+	+	+	+	+	+	+	-	-	+	-	Ribosomal proteins	-	
L19_leader regulon	**L19_leader**												**Ribosome biogenesis**	-	
rplS	*BSU16040*	+	+	+	+	+	+	+	+	+	+	-	Ribosomal proteins	-	
L20_leader regulon	**L20_leader**												**Ribosome biogenesis**	-	
infC-rpmI-rplT	*BSU28870*	+	+	-	+	+	-	+	+	+	+	+	Ribosomal proteins	-	
L21_leader regulon	**L21_leader**												**Ribosome biogenesis**	-	
rpuI-ysxB-rpmA	*BSU27960*	+	+	+	+	+	+	+	+	+	+	+	Ribosomal proteins	-	
T-box (Ala) regulon	**T-box (Ala)**												**Amino acid metabolism**	-	
alaS	*BSU27410*	+	+	+	+	+	+	+	+	+	+	-	Alanyl-tRNA synthetase	-	
T-box (Asn) regulon	**T-box (Asn)**												**Amino acid metabolism**	-	
hisS-aspS	*BSU27560*	+	+	-	+	+	-	-	+	+	-	-	Histidyl-tRNA synthetase; Aspartyl-tRNA synthetase	-	
asnA	*BC1746*	0	0	0	0	0	0	+	0	0	0	0	Aspartate--ammonia ligase	-	
asnS2	*BC4559*	0	0	0	0	0	0	+	0	0	0	0	Asparaginyl-tRNA synthetase	-	
T-box (Cys) regulon	**T-box (Cys)**												**Amino acid metabolism**	-	
cysES	*BSU00930*	+	+	+	+	+	+	+	+	+	+	+	Serine acetyltransferase; Cysteinyl-tRNA synthetase;	-	
T-box (Gly) regulon	**T-box (Gly)**												**Amino acid metabolism**	-	
glyQS	*BSU25270*	+	+	+	+	0	0	0	+	-	+	+	Glycyl-tRNA synthetase	exp.	15890195
glyS	*Aflv_2771*	0	0	0	0	+	+	0	0	0	0	0	Glycyl-tRNA synthetase	-	
T-box (Ile) regulon	**T-box (Ile)**												**Amino acid metabolism**	-	
ileS	*BSU15430*	+	+	+	+	+	+	+	+	+	+	0	Isoleucyl-tRNA synthetase	-	
ileS2	*BC2164*	0	0	0	0	0	0	+	0	0	+	-	Isoleucyl-tRNA synthetase	-	
ilvBHC-leuABCD-ilvA	*BSU28310*	-	-	-	-	-	-	+	-	-	+	-	Branched-chain amino acid biosynthesis	-	
brnQ	*BC1441*	0	0	0	0	0	0	+	0	0	0	0	Branched-chain amino acid transport	-	
Pjdr2_4149	*Pjdr2_4149*	0	0	0	0	0	0	0	0	0	0	+	GCN5-related N-acetyltransferase	-	
T-box (Leu) regulon	**T-box (Leu)**												**Amino acid metabolism**	-	
leuS	*BSU30320*	+	+	+	+	+	+	+	+	+	+	+	Leucyl-tRNA synthetase	-	
ilvBHC-leuABCD	*BSU28310*	+	+	+	+	+	+	-	+	+	-	+	Branched-chain amino acid biosynthesis	exp.	8606198
yvbW	*BSU34010*	+	+	+	+	0	0	0	0	0	0	0	Amino acid permease	-	
yuaI-OB1272	*OB1271*	-	0	-	-	0	-	-	-	-	+	-	Acetyltransferase, GNAT family; Predicted acetyltransferase	-	

yocR	*BC2170*	0	0	0	0	0	0	+	0	0	0	0	Sodium-dependent leucine transporter	-	
T-box (Phe) regulon	**T-box (Phe)**												**Amino acid metabolism**	-	
pheST	*BSU28640*	+	+	+	+	+	+	+	+	+	+	+	Phenylalanyl-tRNA synthetase	-	
T-box (Pro) regulon	**T-box (Pro)**												**Amino acid metabolism**	-	
proI	*BSU23800*	+	+	+	+	+	+	-	+	+	+	+	Pyrroline-5-carboxylate reductase	exp.	21233158
proBA	*BSU13120*	+	+	+	+	+	+	0	+	+	+	+	Glutamate 5-kinase; Gamma-glutamyl phosphate reductase	exp.	21233158
proS2	*BPUM_0197*	0	0	+	0	0	0	+	0	0	+	-	Prolyl-tRNA synthetase	-	
proS	*BSU16570*	-	-	-	-	-	-	-	-	-	0	+	Prolyl-tRNA synthetase	-	
T-box (Ser) regulon	**T-box (Ser)**												**Amino acid metabolism**	-	
serS	*BSU00130*	+	+	+	+	+	+	+	+	-	+	-	Seryl-tRNA synthetase	-	
serA	*BSU23070*	-	-	-	-	-	-	0	+	+	-	-	D-3-phosphoglycerate dehydrogenase	-	
serS2	*ABC1428*	0	0	0	0	0	0	0	0	+	0	+	Seryl-tRNA synthetase	-	
T-box (Thr) regulon	**T-box (Thr)**												**Amino acid metabolism**	-	
thrS	*BSU28950*	+	+	+	+	+	+	+	+	+	+	+	Threonyl-tRNA synthetase	exp.	9826762
thrZ	*BSU37560*	+	0	+	+	0	0	+	0	+	0	+	Threonyl-tRNA synthetase	exp.	8288542
hom-thrCB	*BSU32260*	-	-	-	-	-	-	+	-	-	-	-	Threonine biosynthesis	-	
ykbA	*BSU12860*	-	-	-	-	-	0	+	0	0	0	0	Amino acid transporter	-	
brnQ	*BC4550*	0	0	0	0	0	0	+	0	0	0	0	Threonine transporter	-	
T-box (Trp) regulon	**T-box (Trp)**												**Amino acid metabolism**	-	
trpS	*BSU11420*	+	+	+	+	+	+	+	+	+	+	+	Tryptophanyl-tRNA synthetase	-	
trpEGDCFBA	*BC1232*	-	-	-	-	-	-	+	-	-	+	-	Tryptophan biosynthesis	-	
rtpA-ycbK	*BSU02530*	+	0	0	+	0	0	0	0	0	0	0	Anti-TRAP regulator; Permeases of the drug/metabolite transporter (	exp.	10706627
yhdH	*BC1430*	0	0	0	0	0	0	+	0	0	0	0	Sodium-dependent tryptophan transporter	-	
T-box (Tyr) regulon	**T-box (Tyr)**												**Amino acid metabolism**	-	
tyrS	*BSU29670*	+	+	+	+	+	+	+	0	0	+	+	Tyrosyl-tRNA synthetase	exp.	1735721
tyrZ	*BSU38460*	+	0	0	+	0	0	0	+	+	0	0	Tyrosyl-tRNA synthetase	-	
aroF-hisC-tyrA-aroE	*BC2941*	-	-	-	-	-	-	+	-	-	-	-	Tyrosine biosynthesis	-	
phhA-phs	*BC4352*	0	0	0	0	0	0	+	0	0	0	0	Phenylalanine-4-hydroxylase; Pterin-4-alpha-carbinolamine dehydrat	-	
aroA	*BC2942*	0	0	0	0	0	0	+	0	0	0	0	Chorismate mutase I / 2-keto-3-deoxy-D-arabino-heptulosonate-7-ph	-	
tyrT	*BC4121*	0	0	0	0	0	0	+	0	0	+	0	Predicted tyrosine transporter, NhaC family	-	
T-box (Val) regulon	**T-box (Val)**												**Amino acid metabolism**	-	
valS	*BSU28090*	+	+	+	+	+	+	+	+	+	+	0	Valyl-tRNA synthetase	exp.	9098041

When the gene is present in the genome, the background colors denote the presence (green, '+') or absence (red , '-') of a TFBS in its upstream region; empty crossings ('0') denote the absence of an orthologous gene in the genome.