

Study set genes

Gene	Annotation	Known TF sites
aceB	malate synthase A	fruR , iclR
aldA	aldehyde dehydrogenase; NAD-linked	crp
ansB	periplasmic L-asparaginase II	crp , fnr
araB	L-ribulokinase	araC , crp
araE	low-affinity L-arabinose transport system proton symport protein	araC , crp
araF	L-arabinose-binding periplasmic protein	araC , crp
araJ	involved in either transport or processing of arabinose polymers	araC , crp
argA	N-acetylglutamate synthase; amino acid acetyltransferase	argR
argC	N-acetyl-gamma-glutamylphosphate reductase	argR
argD	acetylornithine delta-aminotransferase	argR
argG	argininosuccinate synthetase	argR
argI	ornithine carbamoyltransferase 1	argR
argR	repressor of arg regulon; cer-mediated site specific recombination	argR
aroF	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase (DAHP synthetase; tyrosine repressible)	tyrR
aroG	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase (DAHP synthetase; phenylalanine repressible)	tyrR
aroL	shikimate kinase II	tyrR
aroP	aromatic amino acid transport protein	tyrR
b1741	putative excinuclease subunit	lexA
carA	carbamoyl-phosphate synthetase; glutamine (small) subunit	argR , carP , purR
cdd	cytidine/deoxycytidine deaminase	crp , cytR
cirA	outer membrane receptor for iron-regulated colicin I receptor; porin; requires tonB gene product	fur
codB	cytosine permease/transport	purR
cpxR	transcriptional regulator in 2-component system	cpxR
crp	cyclic AMP receptor protein	crp
cvpA	membrane protein required for colicin V production	purR
cyaA	adenylate cyclase	crp

cydA	cytochrome d terminal oxidase; polypeptide subunit I	fnr
cynR	cyn operon positive regulator	cynR
cysB	positive transcriptional regulator for cysteine regulon	cysB
cysK	cysteine synthase A; O-acetylserine sulfhydrolase A	cysB
cytR	regulator for deo operon; udp; cdd; tsx; nupC; and nupG	crp , cytR
dadA	D-amino acid dehydrogenase subunit	crp
deoC	2-deoxyribose-5-phosphate aldolase	crp , cytR , deoR
dinG	probably ATP-dependent helicase	lexA
dinI	damage-inducible protein I	lexA
dmsA	anaerobic dimethyl sulfoxide reductase subunit A	modE , narL , fnr
dps	global regulator; starvation conditions	oxyR
edd	6-phosphogluconate dehydratase	fruR
epd	D-erythrose 4-phosphate dehydrogenase	fruR
fabA	beta-hydroxydecanoyl thioester dehydrase; trans-2-decenoyl-ACP isomerase	fadR , fabR
fadB	4-enzyme protein: 3-hydroxyacyl-CoA dehydrogenase; 3-hydroxybutyryl-CoA epimerase; delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase; enoyl-CoA hydratase	fadR
fadD	acyl-CoA synthetase; long-chain-fatty-acid--CoA ligase	fadR
fadL	transport of long-chain fatty acids; sensitivity to phage T2	fadR , ompR
fdhF	selenopolypeptide subunit of formate dehydrogenase H	fhfA
fdnG	formate dehydrogenase-N; nitrate-inducible; alpha subunit	fnr , narL , narP
fepA	outer membrane receptor for ferric enterobactin (enterochelin) and colicins B and D	fur
fepB	ferric enterobactin (enterochelin) binding protein; periplasmic component	fur
flhB	putative part of export apparatus for flagellar proteins	flhCD
flhD	regulator of flagellar biosynthesis; acting on class 2 operons; transcriptional initiation factor	crp , ompR
fliA	flagellar biosynthesis; alternative sigma factor 28; regulation of flagellar operons	flhCD
fliL	flagellar biosynthesis	flhCD
focA	probable formate transporter (formate channel 1)	fnr , narL
frdA	fumarate reductase; anaerobic; flavoprotein subunit	narL
fruB	PTS system; fructose-specific IIA/fpr component	fruR
ftsK	cell division protein	lexA

fumC	fumarase C= fumarate hydratase Class II; isozyme	soxS
fur	negative regulator	crp , fur , oxyR
galE	UDP-galactose-4-epimerase	crp , galR
galP	galactose-proton symport of transport system	galR
galR	repressor of galETK operon	galR
galS	mgI repressor; galactose operon inducer	galR
gcvA	positive regulator of gcv operon	gcvA
gcvT	aminomethyltransferase (T protein; tetrahydrofolate-dependent) of glycine cleavage system	gcvA , purR , crp
glmU	N-acetyl glucosamine-1-phosphate uridyltransferase	nagC
glnA	glutamine synthetase	ntrC
glnH	periplasmic glutamine-binding protein; permease	ntrC
glnL	histidine protein kinase sensor for GlnG regulator (nitrogen regulator II; NRII)	ntrC
glpA	sn-glycerol-3-phosphate dehydrogenase (anaerobic); large subunit	crp , glpR
glpD	sn-glycerol-3-phosphate dehydrogenase (aerobic)	crp , glpR
glpF	facilitated diffusion of glycerol	crp , glpR
glyA	serine hydroxymethyltransferase	metR , purR
guaB	IMP dehydrogenase	purR , crp
gyrA	DNA gyrase; subunit A; type II topoisomerase	cspA
hns	DNA-binding protein HLP-II (HU; BH2; HD; NS); pleiotropic regulator	cspA
htrA	periplasmic serine protease Do; heat shock protein HtrA	cpxR
hycA	transcriptional repression of hyc and hyp operons	fhIA , modE
hycB	probable small subunit of hydrogenase-3; iron-sulfur protein (part of formate hydrogenlyase (FHL) complex)	fhIA
iclR	repressor of aceBA operon	fadR , iclR
ilvB	acetolactate synthase I; valine-sensitive; large subunit	crp
ilvC	ketol-acid reductoisomerase	ilvY
katG	catalase; hydroperoxidase HPI(I)	oxyR
lacZ	beta-D-galactosidase	crp , lacI
lexA	regulator for SOS(lexA) regulon	lexA
malE	periplasmic maltose-binding protein; substrate recognition for transport and	crp ,

	chemotaxis	malT
malP	maltodextrin phosphorylase	malT
malS	alpha-amylase	crp , malT
malT	positive regulator of mal regulon	crp , mlc
manX	PTS enzyme IIAB; mannose-specific	crp , mlc
marR	multiple antibiotic resistance protein; repressor of mar operon	marR , marA
melA	alpha-galactosidase	crp , melR
metA	homoserine transsuccinylase	metJ , metR
metC	cystathionine beta-lyase (beta-cystathionase)	metJ
metE	tetrahydropteroyltriglutamate methyltransferase	metJ , metR
metF	5;10-methylenetetrahydrofolate reductase	metJ , metR
metH	B12-dependent homocysteine-N5-methyltetrahydrofolate transmethylase; repressor of metE and metF	metR
metJ	repressor of all met genes but metF	metJ
mlc	putative NAGC-like transcriptional regulator	mlc
moaA	molybdopterin biosynthesis; protein A	modE
modA	molybdate-binding periplasmic protein; permease	modE
mtlA	PTS system; mannitol-specific enzyme IIABC components	crp , fruR
mtr	tryptophan-specific transport protein	trpR , tyrR
nagB	glucosamine-6-phosphate deaminase	crp , nagC
napF	ferredoxin-type protein: electron transfer	fnr , narL , narP
narG	nitrate reductase 1; alpha subunit	fnr , narL
narK	nitrite extrusion protein	fnr , narL
ndh	respiratory NADH dehydrogenase	fnr
nirB	nitrite reductase (NAD(P)H) subunit	fnr , narL , narP
nrfA	periplasmic cytochrome c(552): plays a role in nitrite reduction	fnr , narL , narP
nupG	transport of nucleosides; permease protein	crp , cytR

ompA	outer membrane protein 3a (II*;G;d)	crp
ompC	outer membrane protein 1b (Ib;c)	ompR
ompF	outer membrane protein 1a (Ia;b;F)	ompR
ompR	response regulator (sensor; EnvZ) affecting transcription of ompC and ompF: outer membrane protein synthesis	crp
oxyR	activator; hydrogen peroxide-inducible genes	oxyR
pckA	phosphoenolpyruvate carboxykinase	crp , fruR
pdhR	transcriptional regulator for pyruvate dehydrogenase complex	pdhR
pfkA	6-phosphofructokinase I	fruR
phnC	ATP-binding component of phosphonate transport	phoB
phoB	positive response regulator for pho regulon; sensor is PhoR (or CreC)	phoB
phoE	outer membrane pore protein E (E;Ic;NmpAB)	phoB
polB	DNA polymerase II	lexA
ppiA	peptidyl-prolyl cis-trans isomerase A (rotamase A)	cpxR , crp , cytR
ppsA	phosphoenolpyruvate synthase	fruR
proP	low-affinity transport system; proline permease II	crp
pstS	high-affinity phosphate-specific transport system; periplasmic phosphate-binding protein	phoB
ptsH	PTS system protein HPr	crp , fruR , mlc
purA	adenylosuccinate synthetase	purR
purC	phosphoribosylaminoimidazole-succinocarboxamide synthetase = SAICAR synthetase	purR
purE	phosphoribosylaminoimidazole carboxylase = AIR carboxylase; catalytic subunit	purR
purH	phosphoribosylaminoimidazolecarboxamideformyltransferase = AICAR formyltransferase; IMP cyclohydrolase	purR
purL	phosphoribosylformyl-glycineamide synthetase = FGAM synthetase	purR
purM	phosphoribosylaminoimidazole synthetase = AIR synthetase	purR
purR	transcriptional repressor for pur regulon; glyA; glnB; prsA; speA	purR
purT	phosphoribosylglycinamide formyltransferase 2	purR
pykF	pyruvate kinase I (formerly F); fructose stimulated	fruR
pyrC	dihydro-ototase	purR
pyrD	dihydro-ototate dehydrogenase	purR
recA	DNA strand exchange and renaturation; DNA-dependent ATPase; DNA- and ATP-dependent coprotease	lexA
recN	protein used in recombination and DNA repair	lexA

rhaS	positive regulator for rhaBAD operon	crp , rhaR
rhaT	rhamnose transport	rhaS , crp
rpoH	RNA polymerase; sigma(32) factor; regulation of proteins induced at high temperatures	crp , cytR
ruvA	Holliday junction helicase subunit B; branch migration; repair	lexA
sodA	superoxide dismutase; manganese	fur , soxS
soxS	regulation of superoxide response regulon	soxR , soxS
srlA	PTS system; glucitol/sorbitol-specific IIC component; one of two	crp
sulA	suppressor of lon; inhibits cell division and ftsZ ring formation	lexA
tdcA	transcriptional activator of tdc operon	crp
tnaA	tryptophanase	crp
tonB	energy transducer; uptake of iron; cyanocobalamin; sensitivity to phages; colicins	fur
torC	trimethylamine N-oxide reductase; cytochrome c-type subunit	torR
trpE	anthranilate synthase component I	trpR
trpR	regulator for trp operon and aroH; trp aporepressor	trpR
tsx	nucleoside channel; receptor of phage T6 and colicin K	crp , cytR
tyrB	tyrosine aminotransferase; tyrosine repressible	tyrR
tyrP	tyrosine-specific transport system	tyrR
tyrR	transcriptional regulation of aroF; aroG; tyrA and aromatic amino acid transport	tyrR
udp	uridine phosphorylase	crp , cytR
ugpB	sn-glycerol 3-phosphate transport system; periplasmic binding protein	phoB
umuD	SOS mutagenesis; error-prone repair; processed to UmuD'; forms complex with UmuC	lexA
uvrA	excision nuclease subunit A	lexA
uvrB	DNA repair; excision nuclease subunit B	lexA
uvrD	DNA-dependent ATPase I and helicase II	lexA
uxuA	mannonate hydrolase	crp
yjiW	orf; hypothetical protein	lexA
zwf	glucose-6-phosphate dehydrogenase	soxS

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