

Gene clusters potentially associated with environmental adaptation, bioremediation, biocontrol, and plant-growth promotion in *Pseudomonas fragi* A13BB

Function	Gene	Gene Product
copper resistance	<i>copG</i>	copG protein
	<i>copD</i>	copper resistance protein
	<i>copZ</i>	copper chaperone
	<i>cueA</i>	copper-translocating P-type ATPase
	<i>mo</i>	multicopper oxidase
	<i>ct</i>	copper tolerance protein
	<i>clfA</i>	multidrug resistance transporter, Bcr/CfIA family
	<i>ccmH</i>	cytochrome c heme lyase subunit CcmH
	<i>ccmF</i>	cytochrome c heme lyase subunit CcmF
	<i>cusS</i>	copper sensory histidine kinase CusS
	<i>cusR</i>	copper-sensing two-component system response regulator CusR
	<i>cutE</i>	copper homeostasis protein
	<i>corC</i>	magnesium and cobalt efflux protein CorC
cobalt-zinc-cadmium resistance	<i>trMer</i>	transcriptional regulator; MerR family
	<i>czcR</i>	cobalt-zinc-cadmium resistance protein
	<i>fp</i>	probable Co/Zn/Cd efflux system membrane fusion protein
	<i>czrR</i>	DNA-binding heavy metal response regulator
	<i>hmhk</i>	heavy metal sensor histidine kinase
	<i>cadR</i>	Cd(II)/Pb(II)-responsive transcriptional regulator
	<i>hmrR</i>	heavy metal resistance transcriptional regulator HmrR
quininate degradation	<i>quiB2</i>	3-dehydroquininate dehydratase II
biphenyl degradation	<i>bphC</i>	2,3-dihydroxybiphenyl 1,2-dioxygenase
	<i>bphF</i>	4-hydroxy-2-oxovalerate aldolase
n-phenylalkanoic acid degradation	<i>fadA</i>	3-ketoacyl-CoA thiolase
	<i>fadB</i>	enoyl-CoA hydratase
	<i>fadD</i>	long-chain-fatty-acid--CoA ligase
	<i>phaJ1</i>	enoyl-CoA hydratase, R-specific
	<i>fadB2</i>	delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase
	<i>fadB3</i>	3-hydroxyacyl-CoA dehydrogenase
	<i>fadB4</i>	3-hydroxybutyryl-CoA epimerase
benzoate degradation	<i>benB</i>	benzoate 1,2-dioxygenase beta subunit
	<i>benA</i>	benzoate 1,2-dioxygenase alpha subunit
	<i>benC</i>	benzoate 1,2-dioxygenase, ferredoxin reductase component
	<i>benD</i>	1,2-dihydroxycyclohexa-3,5-diene-1-carboxylate dehydrogenase
	<i>benE2</i>	benzoate transport protein
	<i>benR</i>	benABC operon transcriptional activator BenR
p-hydroxybenzoate degradation	<i>pobA</i>	p-hydroxybenzoate hydroxylase
	<i>pcaK</i>	4-hydroxybenzoate transporter
beta-ketoadipate pathway of aromatic compound degradation	<i>catA</i>	catechol 1,2-dioxygenase
	<i>catB</i>	muconate cycloisomerase
	<i>catC</i>	muconolactone isomerase
	<i>catD</i>	beta-ketoadipate enol-lactone hydrolase
	<i>catEA</i>	3-oxoadipate CoA-transferase subunit A
	<i>catEB</i>	3-oxoadipate CoA-transferase subunit B
	<i>catA2</i>	catechol 1,2-dioxygenase 1
	<i>pcaR</i>	Pca regulon regulatory protein PcaR
	<i>pcaH</i>	protocatechuate 3,4-dioxygenase beta chain
	<i>pcaG</i>	protocatechuate 3,4-dioxygenase alpha chain
	<i>pcaB</i>	3-carboxy-cis,cis-muconate cycloisomerase
	<i>pcaC</i>	4-carboxymuconolactone decarboxylase
	<i>pcaI</i>	succinyl-CoA:3-ketoacid-coenzyme A transferase subunit A
	<i>pcaJ</i>	succinyl-CoA:3-ketoacid-coenzyme A transferase subunit B
	<i>pcaT</i>	dicarboxylic acid transporter PcaT

homogentisate pathway of aromatic compound degradation	<i>hmgA</i>	homogentisate 1,2-dioxygenase
	<i>hppd</i>	4-hydroxyphenylpyruvate dioxygenase
	<i>mai</i>	maleylacetoacetate isomerase
	<i>faa</i>	fumarylacetoacetase
	<i>aaa</i>	aromatic-amino-acid aminotransferase
	<i>hmgR</i>	transcriptional regulator, IclR family
gentisate degradation	<i>fhf</i>	fumarylacetoacetate hydrolase family protein
	<i>mai</i>	maleylacetoacetate isomerase
	<i>pca</i>	4-hydroxybenzoate transporter
glutathione-dependent pathway of formaldehyde detoxification	<i>frmA</i>	S-(hydroxymethyl)glutathione dehydrogenase
	<i>frmB</i>	S-formylglutathione hydrolase
	<i>frmF</i>	transcriptional regulator, LysR family, in formaldehyde detoxification operon
glutathione-dependent xenobiotic degradation	<i>gstZ</i>	glutathione S-transferase, zeta
	<i>gst</i>	glutathione S-transferase
	<i>gstU</i>	glutathione S-transferase, unnamed subgroup
	<i>gloA</i>	lactoylglutathione lyase
	<i>gloB</i>	hydroxyacylglutathione hydrolase
	<i>sam1</i>	SAM-dependent methyltransferase
	<i>gsr</i>	glutathione reductase
	<i>gpx</i>	glutathione peroxidase
	<i>grx3</i>	glutaredoxin 3
	<i>grx</i>	glutaredoxin
	<i>gshA</i>	glutamate--cysteine ligase
	<i>gshB</i>	glutathione synthetase
	<i>glt</i>	gamma-glutamyltranspeptidase
choline and betaine uptake, and betaine biosynthesis	<i>betA</i>	choline dehydrogenase
	<i>betB</i>	betaine aldehyde dehydrogenase
	<i>betT</i>	high-affinity choline uptake protein BetT
	<i>soxA</i>	sarcosine oxidase alpha subunit
	<i>soxB</i>	sarcosine oxidase beta subunit
	<i>soxD</i>	sarcosine oxidase delta subunit
	<i>soxG</i>	sarcosine oxidase gamma subunit
	<i>gbcA</i>	GbcA Glycine betaine demethylase subunit A
	<i>gbcB</i>	GbcB Glycine betaine demethylase subunit B
nitrogen metabolism	<i>norR</i>	anaerobic nitric oxide reductase transcription regulator NorR
	<i>glnE</i>	glutamate-ammonia-ligase adenyltransferase
	<i>amt</i>	ammonium transporter
	<i>gs1</i>	glutamine synthetase type I
	<i>glnD</i>	[Protein-P _{II}] uridylyltransferase
	<i>gltB</i>	glutamate synthase [NADPH] large chain
	<i>gltD</i>	glutamate synthase [NADPH] small chain
	<i>gogat</i>	ferredoxin-dependent glutamate synthase
ferric ion uptake	<i>pvsA</i>	vibrio ferritin ligase/carboxylase protein PvsA
	<i>pvsB</i>	vibrio ferritin amide bond forming protein PvsB
	<i>pvsC</i>	vibrio ferritin membrane-spanning transport protein PvsC
	<i>pvsD</i>	vibrio ferritin amide bond forming protein PvsD
	<i>feat</i>	iron-chelator utilization protein
	<i>iutA</i>	aerobactin siderophore receptor IutA
sulphur metabolism	<i>ssuA</i>	alkanesulfonates-binding protein
	<i>ssuF</i>	organosulfonate utilization protein SsuF
	<i>ssuC</i>	alkanesulfonates transport system permease protein
	<i>dde</i>	probable dibenzothiophene desulfurization enzyme
	<i>pc</i>	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components
	<i>td</i>	alpha-ketoglutarate-dependent taurine dioxygenase

	<i>ars</i>	arylsulfatase
	<i>trxR</i>	thioredoxin reductase
	<i>tpx</i>	thiol peroxidase, Tpx-type
	<i>bcp</i>	thiol peroxidase, Bcp-type
	<i>ahpC</i>	alkyl hydroperoxide reductase subunit C-like protein
	<i>as</i>	arylsulfatase
phosphate metabolism	<i>phoU</i>	phosphate transport system regulatory protein
	<i>phoR</i>	phosphate regulon sensor protein
	<i>phoB</i>	phosphate regulon transcriptional regulatory protein
	<i>ppk</i>	polyphosphate kinase
	<i>ppx</i>	exopolyphosphatase
	<i>phn-reg</i>	phosphonate uptake and metabolism regulator, LysR-family
	<i>phoA</i>	alkaline phosphatase
	<i>phnW</i>	2-aminoethylphosphonate:pyruvate aminotransferase
	<i>phnX</i>	phosphonoacetaldehyde hydrolase
	<i>phoH</i>	phosphate starvation-inducible protein
	<i>thB</i>	NAD(P) transhydrogenase subunit beta
	<i>phoQ</i>	response regulator in two-component regulatory system with PhoQ
	<i>th2</i>	soluble pyridine nucleotide transhydrogenase
	<i>lat</i>	low-affinity inorganic phosphate transporter
	<i>napi</i>	sodium-dependent phosphate transporter