

Taxon	RefSeqID	Function
<i>Pseudomonas</i> sp. ATCC13985	WP009049534.1	hypothetical protein
<i>Pseudomonas</i> sp. ATCC13985	WP004884175.1	cysteine synthase CysM
<i>Pseudomonas</i> sp. ATCC13985	WP008047384.1	arginine-ornithine antiporter
<i>Pseudomonas</i> sp. ATCC13985	WP016702134.1	IclR family transcriptional regulator
<i>Pseudomonas</i> sp. ATCC13985	WP009048342.1	BapA prefix-like domain-containing protein
<i>Pseudomonas</i> sp. ATCC13985	WP016705331.1	TerC family protein
<i>Pseudomonas</i> sp. ATCC13985	WP016702548.1	LLM class flavin-dependent oxidoreductase
<i>Pseudomonas</i> sp. ATCC13985	WP007920721.1	DUF2931 family protein
<i>Pseudomonas</i> sp. ATCC13985	WP009050262.1	cobyrinate a,c-diamide synthase
<i>Pseudomonas</i> sp. ATCC13985	WP019581841.1	SCP2 domain-containing protein
<i>Pseudomonas</i> sp. ATCC13985	YP235760.1	arginine-ornithine antiporter
<i>Pseudomonas</i> sp. ATCC13985	WP016974961.1	UDP-N-acetylmuramate-L-alanine ligase
<i>Pseudomonas</i> sp. ATCC13985	WP016701734.1	GNAT family N-acetyltransferase
<i>Pseudomonas</i> sp. ATCC13985	WP009042593.1	type I secretion C-terminal target domain-containing protein
<i>Pseudomonas</i> sp. ATCC13985	WP007920721.1	DUF2931 family protein
<i>Pseudomonas</i> sp. ATCC13985	WP019362126.1	hypothetical protein
<i>Pseudomonas</i> sp. ATCC13985	WP005792167.1	GlxA family transcriptional regulator
<i>Pseudomonas</i> sp. ATCC13985	WP009051431.1	transcriptional regulator
<i>Pseudomonas</i> sp. ATCC13985	WP076565591.1	copper-translocating P-type ATPase
<i>Pseudomonas</i> sp. ATCC13985	WP016704202.1	exodeoxyribonuclease V subunit beta
<i>Pseudomonas</i> sp. ATCC13985	WP012722383.1	TonB-dependent receptor family protein
<i>Arthrobacter</i> sp. KBS0702	WP019875756.1	serine esterase
<i>Arthrobacter</i> sp. KBS0702	WP011774166.1	histidine kinase
<i>Arthrobacter</i> sp. KBS0702	WP018760130.1	peptide chain release factor N(5)-glutamine methyltransferase
<i>Arthrobacter</i> sp. KBS0702	WP018774671.1	DUF4129 domain-containing protein
<i>Arthrobacter</i> sp. KBS0702	WP017831488.1	hypothetical protein
<i>Arthrobacter</i> sp. KBS0702	WP011775442.1	succinyl-diaminopimelate desuccinylase
<i>Arthrobacter</i> sp. KBS0702	WP018773675.1	30S ribosomal protein S5
<i>Pseudomonas</i> sp. KBS0707	WP011168094.1	hypothetical protein
<i>Pseudomonas</i> sp. KBS0707	YP235546.1	methylcrotonoyl-CoA carboxylase
<i>Pseudomonas</i> sp. KBS0707	YP236973.1	glycerol kinase GlpK
<i>Pseudomonas</i> sp. KBS0707	WP007243709.1	carbamoyl-phosphate synthase large subunit
<i>Pseudomonas</i> sp. KBS0707	NP792266.1	FAD-dependent oxidoreductase
<i>Pseudomonas</i> sp. KBS0707	YP237338.1	serine hydroxymethyltransferase
<i>Pseudomonas</i> sp. KBS0707	YP233146.1	tryptophan synthase subunit beta
<i>Pseudomonas</i> sp. KBS0707	YP234694.1	Ice nucleation protein
<i>Pseudomonas</i> sp. KBS0707	WP011077862.1	IS5-like element ISPsy2 family transposase
<i>Pseudomonas</i> sp. KBS0707	WP020800276.1	ribonucleotide-diphosphate reductase subunit beta
<i>Pseudomonas</i> sp. KBS0707	WP005733560.1	RNA-directed DNA polymerase
<i>Pseudomonas</i> sp. KBS0707	YP237619.1	elongation factor G
<i>Pseudomonas</i> sp. KBS0707	WP003179755.1	aspartate-semialdehyde dehydrogenase
<i>Pseudomonas</i> sp. KBS0707	NP793271.1	hypothetical protein
<i>Janthinobacterium</i> sp. KBS0711	WP020656832.1	valine-tRNA ligase
<i>Janthinobacterium</i> sp. KBS0711	WP010399297.1	alpha-hydroxy-acid oxidizing protein
<i>Janthinobacterium</i> sp. KBS0711	WP010393863.1	mechanosensitive ion channel family protein
<i>Janthinobacterium</i> sp. KBS0711	WP010395693.1	DNA gyrase subunit A
<i>Janthinobacterium</i> sp. KBS0711	WP010394527.1	GTPase
<i>Janthinobacterium</i> sp. KBS0711	WP009239942.1	SufS family cysteine desulfurase
<i>Janthinobacterium</i> sp. KBS0711	WP013236088.1	cytochrome c oxidase subunit II
<i>Janthinobacterium</i> sp. KBS0711	WP017875079.1	electron transfer flavoprotein-ubiquinone oxidoreductase
<i>Janthinobacterium</i> sp. KBS0711	WP020701617.1	flagellar type III secretion system pore protein FlpP
<i>Janthinobacterium</i> sp. KBS0711	WP020701147.1	ribonucleotide-diphosphate reductase subunit beta
<i>Janthinobacterium</i> sp. KBS0711	WP008450068.1	chemotaxis response regulator protein-glutamate methylesterase
<i>Janthinobacterium</i> sp. KBS0711	WP018059363.1	methionine-tRNA ligase
<i>Janthinobacterium</i> sp. KBS0711	WP020702753.1	30S ribosomal protein S2
<i>Janthinobacterium</i> sp. KBS0711	WP018058636.1	sulfate ABC transporter permease subunit CysW
<i>Janthinobacterium</i> sp. KBS0711	WP019923632.1	bacterioferritin
<i>Janthinobacterium</i> sp. KBS0711	WP019139956.1	ABC transporter ATP-binding protein
<i>Janthinobacterium</i> sp. KBS0711	WP005664034.1	F0F1 ATP synthase subunit alpha
<i>Janthinobacterium</i> sp. KBS0711	WP020704252.1	methionine adenosyltransferase
<i>Janthinobacterium</i> sp. KBS0711	WP010394499.1	c-type cytochrome biogenesis protein CcsB
<i>Janthinobacterium</i> sp. KBS0711	WP010397062.1	aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme
<i>Janthinobacterium</i> sp. KBS0711	WP008446499.1	cation acetate symporter
<i>Janthinobacterium</i> sp. KBS0711	WP008120030.1	urea ABC transporter substrate-binding protein
<i>Janthinobacterium</i> sp. KBS0711	WP010399469.1	HAMP domain-containing protein
<i>Janthinobacterium</i> sp. KBS0711	WP010399755.1	acetolactate synthase 3 catalytic subunit
<i>Janthinobacterium</i> sp. KBS0711	WP020201433.1	iron-sulfur cluster assembly protein IscA
<i>Janthinobacterium</i> sp. KBS0711	WP017878982.1	amino-acid N-acetyltransferase
<i>Janthinobacterium</i> sp. KBS0711	WP008452953.1	ethanolamine ammonia-lyase subunit EutB
<i>Janthinobacterium</i> sp. KBS0711	WP010462720.1	ABC transporter permease
<i>Janthinobacterium</i> sp. KBS0711	WP010401750.1	leucine-tRNA ligase
<i>Janthinobacterium</i> sp. KBS0711	WP010393918.1	cytochrome-c oxidase, cbb3-type subunit III
<i>Janthinobacterium</i> sp. KBS0711	WP007858097.1	sugar ABC transporter substrate-binding protein
<i>Janthinobacterium</i> sp. KBS0711	WP020655683.1	30S ribosomal protein S3
<i>Janthinobacterium</i> sp. KBS0711	WP010394894.1	RNA polymerase sigma factor RpoH
<i>Janthinobacterium</i> sp. KBS0711	WP013232709.1	fructose-bisphosphate aldolase class II

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<i>Curtobacterium</i> sp. KBS0715	WP015889560.1	acyl-CoA dehydrogenase
<i>Curtobacterium</i> sp. KBS0715	WP017886488.1	sigma-70 family RNA polymerase sigma factor
<i>Curtobacterium</i> sp. KBS0715	WP018760995.1	helix-turn-helix domain-containing protein
<i>Curtobacterium</i> sp. KBS0715	WP017886379.1	molecular chaperone DnaK
<i>Curtobacterium</i> sp. KBS0715	WP017886367.1	AAA domain-containing protein
<i>Curtobacterium</i> sp. KBS0715	WP015488887.1	LacI family DNA-binding transcriptional regulator
<i>Curtobacterium</i> sp. KBS0715	WP014049992.1	helix-turn-helix domain-containing protein
<i>Curtobacterium</i> sp. KBS0715	WP017888530.1	DHA2 family efflux MFS transporter permease subunit
<i>Curtobacterium</i> sp. KBS0715	WP017887327.1	helix-turn-helix domain-containing protein
<i>Curtobacterium</i> sp. KBS0715	WP017888845.1	mannitol-1-phosphate 5-dehydrogenase
<i>Curtobacterium</i> sp. KBS0715	WP017888829.1	HAMP domain-containing protein
<i>Curtobacterium</i> sp. KBS0715	WP018191823.1	phosphate ABC transporter ATP-binding protein
<i>Curtobacterium</i> sp. KBS0715	WP017887958.1	NCS2 family permease
<i>Curtobacterium</i> sp. KBS0715	WP020098135.1	Gfo/Idh/MocA family oxidoreductase
<i>Curtobacterium</i> sp. KBS0715	WP005264067.1	gluconate transporter
<i>Curtobacterium</i> sp. KBS0715	WP017887197.1	phosphoribosyl-AMP cyclohydrolase
<i>Curtobacterium</i> sp. KBS0715	WP017887160.1	hypothetical protein
<i>Flavobacterium</i> sp. KBS0721	WP012023066.1	type IX secretion system membrane protein PorP/SprF
<i>Flavobacterium</i> sp. KBS0721	WP007809800.1	two-component sensor histidine kinase
<i>Oerskovia</i> sp. KBS0722	WP017544097.1	trypsin-like serine protease
<i>Oerskovia</i> sp. KBS0722	WP018171360.1	aminotransferase class III-fold pyridoxal phosphate-dependent enzyme
<i>Oerskovia</i> sp. KBS0722	WP014987154.1	nucleotidyltransferase domain-containing protein
<i>Oerskovia</i> sp. KBS0722	WP020388261.1	YccF domain-containing protein
<i>Oerskovia</i> sp. KBS0722	WP013772173.1	transcription-repair coupling factor
<i>Oerskovia</i> sp. KBS0722	WP015031728.1	cell division protein ZapE
<i>Oerskovia</i> sp. KBS0722	WP013885059.1	Na(+)/H(+) antiporter subunit C
<i>Oerskovia</i> sp. KBS0722	WP012865786.1	HAD-IIB family hydrolase
<i>Rhodococcus</i> sp. KBS0724	WP005263410.1	glutamate synthase large subunit
<i>Rhodococcus</i> sp. KBS0724	WP019746392.1	Ig-like domain repeat protein
<i>Rhodococcus</i> sp. KBS0724	WP005245084.1	cutinase family protein
<i>Burkholderia</i> sp. KBS0801	WP012372410.1	Ig-like domain repeat protein
<i>Burkholderia</i> sp. KBS0801	WP006400402.1	histone H1
<i>Burkholderia</i> sp. KBS0801	WP011694851.1	hemagglutinin
<i>Burkholderia</i> sp. KBS0801	WP012364521.1	hypothetical protein
<i>Burkholderia</i> sp. KBS0801	WP006763239.1	LysR family transcriptional regulator
<i>Burkholderia</i> sp. KBS0801	WP014726283.1	branched-chain amino acid ABC transporter substrate-binding protein
<i>Burkholderia</i> sp. KBS0801	YP109880.1	branched-chain amino acid ABC transporter substrate-binding protein
<i>Burkholderia</i> sp. KBS0801	YP109111.1	30S ribosomal protein S1
<i>Burkholderia</i> sp. KBS0801	WP006400141.1	ABC transporter permease
<i>Burkholderia</i> sp. KBS0801	YP107714.1	sodium:solute symporter family protein
<i>Burkholderia</i> sp. KBS0801	WP011353482.1	5-formyltetrahydrofolate cyclo-ligase
<i>Burkholderia</i> sp. KBS0801	WP012337267.1	aldehyde dehydrogenase family protein
<i>Burkholderia</i> sp. KBS0801	WP012217585.1	LysR family transcriptional regulator
<i>Burkholderia</i> sp. KBS0801	WP006498174.1	peptidase S8/S53 subtilisin kexin sedolisin