

organism	bgc	contig	gene	ann	replace_antismash_bg	ann_verbose	ann_acc	ann_percent_prot_id	notes
Bacillus cereus UW85	Pulcheriminic acid	Ga0417192_01	Bc_ctg1_118	pchE	Bc_Ga0417192_01_m03	pulcheriminic acid efflux transporter	CAB15514.1	52.8	
Bacillus cereus UW85	Pulcheriminic acid	Ga0417192_01	Bc_ctg1_119	pchB	Bc_Ga0417192_01_m03	mark-like regulator	CAB15513.1	53.3	
Bacillus cereus UW85	Pulcheriminic acid	Ga0417192_01	Bc_ctg1_120	pynA	Bc_Ga0417192_01_m03	mark-like regulator	NP_391385.1	42.2	
Bacillus cereus UW85	Pulcheriminic acid	Ga0417192_01	Bc_ctg1_121	cypC	Bc_Ga0417192_01_m03	cytochrome p450	CAB15511.1	73.9	
Bacillus cereus UW85	Pulcheriminic acid	Ga0417192_01	Bc_ctg1_122	pchC	Bc_Ga0417192_01_m03	cyclodipeptide synthase	CAB15512.1	63.3	
Bacillus cereus UW85	Bacillithiol - Locus 1	Ga0417192_01	Bc_ctg1_3901	ypjC	Bc_Ga0417192_01_m27	inner membrane protein	CAB14167.2	73	
Bacillus cereus UW85	Bacillithiol - Locus 1	Ga0417192_01	Bc_ctg1_3902	ypjD	Bc_Ga0417192_01_m27	oxidized nucleotide pyrophosphohydrolase	CAB14166.1	77.1	
Bacillus cereus UW85	Bacillithiol - Locus 1	Ga0417192_01	Bc_ctg1_3903	dnaB	Bc_Ga0417192_01_m27	4S)-4-hydroxy-2,3,4,5-tetrahydro-(2S)-dipicolinic acid (HTPA) dehydratase reductase	CAB14165.1	70.6	
Bacillus cereus UW85	Bacillithiol - Locus 1	Ga0417192_01	Bc_ctg1_3904	mgaA	Bc_Ga0417192_01_m27	methylglyoxal synthase	CAB14164.1	67.3	
Bacillus cereus UW85	Bacillithiol - Locus 1	Ga0417192_01	Bc_ctg1_3905	bshB1	Bc_Ga0417192_01_m27	N-acetyl-alpha-D-glucosaminyl L-malate deacetylase	CAB14163.2	59.1	
Bacillus cereus UW85	Bacillithiol - Locus 1	Ga0417192_01	Bc_ctg1_3906	bshA	Bc_Ga0417192_01_m27	N-acetyl-alpha-D-glucosaminyl L-malate synthase	CAB14162.1	61.8	
Bacillus cereus UW85	Bacillithiol - Locus 1	Ga0417192_01	Bc_ctg1_3907	cca	Bc_Ga0417192_01_m27	HRNA nucleotidyltransferase	CAB14161.1	41.8	
Bacillus cereus UW85	Bacillithiol - Locus 1	Ga0417192_01	Bc_ctg1_3908	bira	Bc_Ga0417192_01_m27	botin acetyl-Cox-carboxylase ligase	CAB14160.1	54.9	
Bacillus cereus UW85	Bacillithiol - Locus 1	Ga0417192_01	Bc_ctg1_3910	panB	Bc_Ga0417192_01_m27	ketopantoate hydrosynthettransferase	CAB14159.1	67	
Bacillus cereus UW85	Bacillithiol - Locus 1	Ga0417192_01	Bc_ctg1_3911	panC	Bc_Ga0417192_01_m27	panthothenate synthetase	CAB14158.1	55.9	
Bacillus cereus UW85	Bacillithiol - Locus 1	Ga0417192_01	Bc_ctg1_3912	panD	Bc_Ga0417192_01_m27	aspartate 1-decarboxylase	CAB14157.1	56.5	
Bacillus cereus UW85	Bacillithiol - Locus 2	Ga0417192_01	Bc_ctg1_356	yojF	NA	uncharacterized protein	O31858.1	53.8	
Bacillus cereus UW85	Bacillithiol - Locus 2	Ga0417192_01	Bc_ctg1_355	bcbB2	NA	N-acetyl-alpha-D-glucosaminyl L-malate deacetylase	CAB13838.2	56.1	
Bacillus cereus UW85	Bacillithiol - Locus 3	Ga0417192_01	Bc_ctg1_896	ykoQ	NA	2-dehydrogentoate 2-reductase	CAB13384.1	43.6	
Bacillus cereus UW85	Bacillithiol - Locus 3	Ga0417192_01	Bc_ctg1_895	bshC	NA	malate glucosamine cysteine ligase	CAB13385.2	42	
Bacillus cereus UW85	Petrobactin	Ga0417192_01	Bc_ctg1_4289	asbA	Bc_Ga0417192_01_m31	spermidine-citrate ligase	AAOAF7R52.1	91.7	
Bacillus cereus UW85	Petrobactin	Ga0417192_01	Bc_ctg1_4290	asbB	Bc_Ga0417192_01_m31	citryl-spermidine/3,4-dihydroxybenzoyl-citryl-spermidine:spermidine ligase	Q81RQ8.1	84	
Bacillus cereus UW85	Petrobactin	Ga0417192_01	Bc_ctg1_4291	asbC	Bc_Ga0417192_01_m31	3,4-dihydroxybenzoic acid-AMP ligase	Q81RQ7.1	92.2	
Bacillus cereus UW85	Petrobactin	Ga0417192_01	Bc_ctg1_4292	asbD	Bc_Ga0417192_01_m31	acyl carrier protein	AAOAJ01113.1	96.7	
Bacillus cereus UW85	Petrobactin	Ga0417192_01	Bc_ctg1_4293	asbE	Bc_Ga0417192_01_m31	petrobactin synthase	Q81RQ5.1	92.9	
Bacillus cereus UW85	Petrobactin	Ga0417192_01	Bc_ctg1_4294	asbF	Bc_Ga0417192_01_m31	3-dehydroshikimate dehydratase	Q81RQ4.1	88.9	
Bacillus cereus UW85	Bacillibactin	Ga0417192_01	Bc_ctg1_4639	pagR	Bc_Ga0417192_01_m32	transcriptional repressor (metal binding)	O31178.1	53.1	
Bacillus cereus UW85	Bacillibactin	Ga0417192_01	Bc_ctg1_4640	ykvS	Bc_Ga0417192_01_m32	uncharacterized protein	O31684.2	40.4	
Bacillus cereus UW85	Bacillibactin	Ga0417192_01	Bc_ctg1_4641	yhxK	Bc_Ga0417192_01_m32	MFS transporter	P37662.1	44.8	
Bacillus cereus UW85	Bacillibactin	Ga0417192_01	Bc_ctg1_4642	dhaB	Bc_Ga0417192_01_m32	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase	CAB15190.2	73.9	
Bacillus cereus UW85	Bacillibactin	Ga0417192_01	Bc_ctg1_4643	dhaC	Bc_Ga0417192_01_m32	isochorismate synthase	CAB15189.2	65.8	
Bacillus cereus UW85	Bacillibactin	Ga0417192_01	Bc_ctg1_4644	dhaE	Bc_Ga0417192_01_m32	2,3-dihydroxybenzoate-AMP ligase	CAB15188.1	74.4	
Bacillus cereus UW85	Bacillibactin	Ga0417192_01	Bc_ctg1_4645	dhaB	Bc_Ga0417192_01_m32	isochorismatase	CAB15187.1	57.1	
Bacillus cereus UW85	Bacillibactin	Ga0417192_01	Bc_ctg1_4646	dhaF	Bc_Ga0417192_01_m32	siderophore 2,3-dihydroxybenzoate-glycine-threonine trimeric ester bacillibactin synthetase	CAB15186.3	64.9	
Bacillus cereus UW85	Bacillibactin	Ga0417192_01	Bc_ctg1_4647	ybdZ	Bc_Ga0417192_01_m32	uncharacterized protein	C9H36.1	56.7	
Bacillus cereus UW85	Bacillibactin	Ga0417192_01	Bc_ctg1_4648	yhaA	Bc_Ga0417192_01_m32	MFS transporter	P54585.2	31.9	
Bacillus cereus UW85	Bacillibactin	Ga0417192_01	Bc_ctg1_4649	hetI	Bc_Ga0417192_01_m32	4'-phosphopantetheinyl transferase	P37695.2	32.1	
Bacillus cereus UW85	Bacillibactin	Ga0417192_01	Bc_ctg1_4650		Bc_Ga0417192_01_m32	hypothetical protein	WP_000959120.1	100	
Bacillus cereus UW85	Nicotinate - Locus 1	Ga0417192_01	Bc_ctg1_1410	nadA	NA	guinolinate synthetase	NP_390663.1	69.9	
Bacillus cereus UW85	Nicotinate - Locus 1	Ga0417192_01	Bc_ctg1_1411	nadC	NA	nicotinate-nucleotide pyrophosphorylase	NP_390664.1	44.6	
Bacillus cereus UW85	Nicotinate - Locus 1	Ga0417192_01	Bc_ctg1_1412	nadB	NA	aspartate oxidase	NP_390665.1	57.5	
Bacillus cereus UW85	Nicotinate - Locus 2	Ga0417192_01	Bc_ctg1_3016	pchB	NA	nicotinate phosphoribosyltransferase	NP_391053.1	68.7	
Bacillus cereus UW85	Kurstakin	Ga0417192_01	Bc_ctg1_4789	krsE	Bc_Ga0417192_01_m33	Major facilitator superfamily MFS_1	EEM74021.1	98.3	
Bacillus cereus UW85	Kurstakin	Ga0417192_01	Bc_ctg1_4790	krsA	Bc_Ga0417192_01_m33	NRPS	EEM74022.1	93.3	
Bacillus cereus UW85	Kurstakin	Ga0417192_01	Bc_ctg1_4791	krsB	Bc_Ga0417192_01_m33	NRPS	EEM74023.1	95.7	
Bacillus cereus UW85	Kurstakin	Ga0417192_01	Bc_ctg1_4792	krsC	Bc_Ga0417192_01_m33	NRPS	EEM74024.1	95.9	
Bacillus cereus UW85	Kurstakin	Ga0417192_01	Bc_ctg1_4793	krsD	Bc_Ga0417192_01_m33	4'-phosphopantetheinyl transferase	EEM74025.1	96	
Bacillus cereus UW85	Kurstakin	Ga0417192_01	Bc_ctg1_4794	krsD	Bc_Ga0417192_01_m33	type II thioesterase	EEM74026.1	92.1	
Bacillus cereus UW85	Zwittermicin/Kanosome	Ga0417192_02	Bc_ctg2_422	zmaA	Bc_Ga0417192_02_m03				
Bacillus cereus UW85	Zwittermicin/Kanosome	Ga0417192_02	Bc_ctg2_423	zmaB	Bc_Ga0417192_02_m03				
Bacillus cereus UW85	Zwittermicin/Kanosome	Ga0417192_02	Bc_ctg2_424	zmaC	Bc_Ga0417192_02_m03				
Bacillus cereus UW85	Zwittermicin/Kanosome	Ga0417192_02	Bc_ctg2_425	zmaD	Bc_Ga0417192_02_m03				
Bacillus cereus UW85	Zwittermicin/Kanosome	Ga0417192_02	Bc_ctg2_426	zmaE	Bc_Ga0417192_02_m03				
Bacillus cereus UW85	Zwittermicin/Kanosome	Ga0417192_02	Bc_ctg2_427	zmaF	Bc_Ga0417192_02_m03				
Bacillus cereus UW85	Zwittermicin/Kanosome	Ga0417192_02	Bc_ctg2_428	zmaF	Bc_Ga0417192_02_m03				
Bacillus cereus UW85	Zwittermicin/Kanosome	Ga0417192_02	Bc_ctg2_429	zmaG	Bc_Ga0417192_02_m03				
Bacillus cereus UW85	Zwittermicin/Kanosome	Ga0417192_02	Bc_ctg2_430	zmaH	Bc_Ga0417192_02_m03				
Bacillus cereus UW85	Zwittermicin/Kanosome	Ga0417192_02	Bc_ctg2_431	zmaI	Bc_Ga0417192_02_m03				
Bacillus cereus UW85	Zwittermicin/Kanosome	Ga0417192_02	Bc_ctg2_432	zmaJ	Bc_Ga0417192_02_m03				
Bacillus cereus UW85	Zwittermicin/Kanosome	Ga0417192_02	Bc_ctg2_433	zmaK	Bc_Ga0417192_02_m03				
Bacillus cereus UW85	Zwittermicin/Kanosome	Ga0417192_02	Bc_ctg2_434	zmaL	Bc_Ga0417192_02_m03				
Bacillus cereus UW85	Zwittermicin/Kanosome	Ga0417192_02	Bc_ctg2_435	zmaM	Bc_Ga0417192_02_m03				
Bacillus cereus UW85	Zwittermicin/Kanosome	Ga0417192_02	Bc_ctg2_436	zmaN	Bc_Ga0417192_02_m03				
Bacillus cereus UW85	Zwittermicin/Kanosome	Ga0417192_02	Bc_ctg2_437	zmaO	Bc_Ga0417192_02_m03				
Bacillus cereus UW85	Zwittermicin/Kanosome	Ga0417192_02	Bc_ctg2_438	zmaP	Bc_Ga0417192_02_m03				
Bacillus cereus UW85	Zwittermicin/Kanosome	Ga0417192_02	Bc_ctg2_439	zmaQ	Bc_Ga0417192_02_m03				
Bacillus cereus UW85	Zwittermicin/Kanosome	Ga0417192_02	Bc_ctg2_440	zmaS	Bc_Ga0417192_02_m03				
Bacillus cereus UW85	Zwittermicin/Kanosome	Ga0417192_02	Bc_ctg2_441	kabR	Bc_Ga0417192_02_m03				
Bacillus cereus UW85	Zwittermicin/Kanosome	Ga0417192_02	Bc_ctg2_442	kabA	Bc_Ga0417192_02_m03				
Bacillus cereus UW85	Zwittermicin/Kanosome	Ga0417192_02	Bc_ctg2_443	kabB	Bc_Ga0417192_02_m03				
Bacillus cereus UW85	Zwittermicin/Kanosome	Ga0417192_02	Bc_ctg2_444	kabC	Bc_Ga0417192_02_m03				
Bacillus cereus UW85	Zwittermicin/Kanosome	Ga0417192_02	Bc_ctg2_445	kabD	Bc_Ga0417192_02_m03				
Bacillus cereus UW85	Zwittermicin/Kanosome	Ga0417192_02	Bc_ctg2_446	zmaT	Bc_Ga0417192_02_m03				
Bacillus cereus UW85	Zwittermicin/Kanosome	Ga0417192_02	Bc_ctg2_447	zmaU	Bc_Ga0417192_02_m03				
Bacillus cereus UW85	Zwittermicin/Kanosome	Ga0417192_02	Bc_ctg2_448	zmaV	Bc_Ga0417192_02_m03				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1108	Fjoh_1075	Fj_NC_009441.1_m11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1109	Fjoh_1076	Fj_NC_009441.1_m11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1110	Fjoh_1077	Fj_NC_009441.1_m11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1111	Fjoh_1078	Fj_NC_009441.1_m11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1112	Fjoh_1079	Fj_NC_009441.1_m11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1113	Fjoh_1080	Fj_NC_009441.1_m11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1114	Fjoh_1081	Fj_NC_009441.1_m11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1115	Fjoh_1082	Fj_NC_009441.1_m11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1116	Fjoh_1083	Fj_NC_009441.1_m11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1117	Fjoh_1084	Fj_NC_009441.1_m11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1118	Fjoh_1085	Fj_NC_009441.1_m11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1119	Fjoh_1086	Fj_NC_009441.1_m11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1120	Fjoh_1087	Fj_NC_009441.1_m11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1121	Fjoh_1088	Fj_NC_009441.1_m11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1122	Fjoh_1089	Fj_NC_009441.1_m11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1123	Fjoh_1090	Fj_NC_009441.1_m11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1124	Fjoh_1091	Fj_NC_009441.1_m11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1125	Fjoh_1092	Fj_NC_009441.1_m11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1126	Fjoh_1093	Fj_NC_009441.1_m11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1127	Fjoh_1094	Fj_NC_009441.1_m11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1128	Fjoh_1095	Fj_NC_009441.1_m11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1129	Fjoh_1096	Fj_NC_009441.1_m11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1130	Fjoh_1097	Fj_NC_009441.1_m11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1131	Fjoh_1098	Fj_NC_009441.1_m11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1132	Fjoh_1100	Fj_NC_009441.1_m11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1133	Fjoh_1101	Fj_NC_009441.1_m11				

Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1134	darB	Fj_NC_009441.1_rn11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1135	darB	Fj_NC_009441.1_rn11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1136	darB	Fj_NC_009441.1_rn11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1137	Fjoh_1105	Fj_NC_009441.1_rn11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1138	Fjoh_1106	Fj_NC_009441.1_rn11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1139	Fjoh_1107	Fj_NC_009441.1_rn11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1140	Fjoh_1108	Fj_NC_009441.1_rn11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1141	Fjoh_1109	Fj_NC_009441.1_rn11				
Flavobacterium johnsoniae UW101	Flexirubin	NC_009441.1	Fj_ctg1_1142	Fjoh_1110	Fj_NC_009441.1_rn11				
Flavobacterium johnsoniae UW101	Fulvirigamide-like siderophore	NC_009441.1	Fj_ctg1_3250	Fjoh_3169	Fj_NC_009441.1_rn24	Lysine 4-hydroxylase			l-lys to (4R)-4-hydroxy-L-lys (stero-specif. hydroxyl on the gamma carbon)
Flavobacterium johnsoniae UW101	Fulvirigamide-like siderophore	NC_009441.1	Fj_ctg1_3251	Fjoh_3170	Fj_NC_009441.1_rn24	NAD(P)H nitroreductase			nitroreductase...will reduce a N
Flavobacterium johnsoniae UW101	Fulvirigamide-like siderophore	NC_009441.1	Fj_ctg1_3252	fulA	Fj_NC_009441.1_rn24	pyridoxal-dependent decarboxylase	QHG11726.1	50.8	strip the cooh off l-lys... makes cadaverine precursor
Flavobacterium johnsoniae UW101	Fulvirigamide-like siderophore	NC_009441.1	Fj_ctg1_3253	Fjoh_3172	Fj_NC_009441.1_rn24	Spermidine-citrate ligase, lucA-like siderophore synthesis protein			asbA (petrobactin), rhbC (rhizobactin), lucA (aerobactin) homologs; these all take citrate/citric acid and attach it to an NH2
Flavobacterium johnsoniae UW101	Fulvirigamide-like siderophore	NC_009441.1	Fj_ctg1_3254	fulB	Fj_NC_009441.1_rn24	monooxygenase	QHG11727.1	44.7	install hydroxyl on one of the NH2 ends (now NHOH)
Flavobacterium johnsoniae UW101	Fulvirigamide-like siderophore	NC_009441.1	Fj_ctg1_3255	fulD	Fj_NC_009441.1_rn24	ATP-dependent siderophore synthetase	QHG11730.1	42.3	put monomers together
Flavobacterium johnsoniae UW101	Fulvirigamide-like siderophore	NC_009441.1	Fj_ctg1_3256	Fjoh_3175	Fj_NC_009441.1_rn24	MATE family efflux transporter			transport
Flavobacterium johnsoniae UW101	Fulvirigamide-like siderophore	NC_009441.1	Fj_ctg1_3257	Fjoh_3176	Fj_NC_009441.1_rn24	acyl carrier protein			acp...load?
Flavobacterium johnsoniae UW101	Fulvirigamide-like siderophore	NC_009441.1	Fj_ctg1_3258	Fjoh_3177	Fj_NC_009441.1_rn24	Long-chain acyl-CoA synthetase			coA ligase...make acyl tail?
Flavobacterium johnsoniae UW101	Fulvirigamide-like siderophore	NC_009441.1	Fj_ctg1_3259	fulF	Fj_NC_009441.1_rn24	Acyl transferase	QHG11731.1	42.3	attach acyl tail
Pseudomonas koreensis C12	N-acetylglutaminylglutamine amide	Ga0417193_01	Pk_ctg1_1352	naggn, peptidase	Pk_Ga0417193_01_rn08	WAGON peptidase	NP_252151.1	78.9	
Pseudomonas koreensis C12	N-acetylglutaminylglutamine amide	Ga0417193_01	Pk_ctg1_1353	nagS	Pk_Ga0417193_01_rn08	acetyltransferase	NP_252150.1	73.9	
Pseudomonas koreensis C12	N-acetylglutaminylglutamine amide	Ga0417193_01	Pk_ctg1_1354	asnO	Pk_Ga0417193_01_rn08	glutamine amidotransferase	NP_252149.1	79.5	
Pseudomonas koreensis C12	Powderdine-like siderophore - chromophore NRPS locus	Ga0417193_01	Pk_ctg1_1541		Pk_Ga0417193_01_rn08				
Pseudomonas koreensis C12	Powderdine-like siderophore - chromophore NRPS locus	Ga0417193_01	Pk_ctg1_1542		Pk_Ga0417193_01_rn08				
Pseudomonas koreensis C12	Powderdine-like siderophore - chromophore NRPS locus	Ga0417193_01	Pk_ctg1_1543	pwdZ	Pk_Ga0417193_01_rn08	siderophore biosynthesis protein			
Pseudomonas koreensis C12	Powderdine-like siderophore - chromophore NRPS locus	Ga0417193_01	Pk_ctg1_1544	pwdS	Pk_Ga0417193_01_rn08	ferric regulator	CAK14554.1	75.6	
Pseudomonas koreensis C12	Powderdine-like siderophore - chromophore NRPS locus	Ga0417193_01	Pk_ctg1_1545	pwdA	Pk_Ga0417193_01_rn08	nrps - powderdine synthetase A	CAK14555.1	87.8	
Pseudomonas koreensis C12	Powderdine-like siderophore - chromophore NRPS locus	Ga0417193_01	Pk_ctg1_1546		Pk_Ga0417193_01_rn08		CAK14556.1	73	
Pseudomonas koreensis C12	Powderdine-like siderophore - chromophore NRPS locus	Ga0417193_01	Pk_ctg1_1547		Pk_Ga0417193_01_rn08				
Pseudomonas koreensis C12	Powderdine-like siderophore - chromophore NRPS locus	Ga0417193_01	Pk_ctg1_1548		Pk_Ga0417193_01_rn08				
Pseudomonas koreensis C12	Powderdine-like siderophore - chromophore NRPS locus	Ga0417193_01	Pk_ctg1_1549		Pk_Ga0417193_01_rn08				
Pseudomonas koreensis C12	Powderdine-like siderophore - chromophore NRPS locus	Ga0417193_01	Pk_ctg1_1550		Pk_Ga0417193_01_rn08				
Pseudomonas koreensis C12	Powderdine-like siderophore - chromophore NRPS locus	Ga0417193_01	Pk_ctg1_1551		Pk_Ga0417193_01_rn08				
Pseudomonas koreensis C12	Powderdine-like siderophore - chromophore NRPS locus	Ga0417193_01	Pk_ctg1_1552		Pk_Ga0417193_01_rn08				
Pseudomonas koreensis C12	Powderdine-like siderophore - chromophore NRPS locus	Ga0417193_01	Pk_ctg1_1553		Pk_Ga0417193_01_rn08				
Pseudomonas koreensis C12	Powderdine-like siderophore - chromophore NRPS locus	Ga0417193_01	Pk_ctg1_1554	dat	Pk_Ga0417193_01_rn08	diaminobutyrate-2-oxoglutarate aminotransferase	CAK16398.1	84.8	
Pseudomonas koreensis C12	Powderdine-like siderophore - chromophore NRPS locus	Ga0417193_01	Pk_ctg1_1555	mbtH	Pk_Ga0417193_01_rn11	mbtH family protein	WP_064591340.1	100	
Pseudomonas koreensis C12	Powderdine-like siderophore - chromophore NRPS locus	Ga0417193_01	Pk_ctg1_1556		Pk_Ga0417193_01_rn08	conserved hypothetical protein, putative signal peptide	CAK16000.1	54.2	
Pseudomonas koreensis C12	Powderdine-like siderophore - chromophore NRPS locus	Ga0417193_01	Pk_ctg1_1557		Pk_Ga0417193_01_rn08	putative cation ABC transporter, permease protein	CAK15999.1	85.9	
Pseudomonas koreensis C12	Powderdine-like siderophore - chromophore NRPS locus	Ga0417193_01	Pk_ctg1_1558		Pk_Ga0417193_01_rn08	putative cation ABC transporter, ATP-binding protein	CAK15998.1	81.1	
Pseudomonas koreensis C12	Powderdine-like siderophore - chromophore NRPS locus	Ga0417193_01	Pk_ctg1_1559		Pk_Ga0417193_01_rn08	putative cation ABC transporter, periplasmic cation-binding protein	CAK15997.1	83.9	
Pseudomonas koreensis C12	Powderdine-like siderophore - chromophore NRPS locus	Ga0417193_01	Pk_ctg1_1560		Pk_Ga0417193_01_rn08	conserved hypothetical protein	CAK15996.1	53.4	
Pseudomonas koreensis C12	Powderdine-like siderophore - chromophore NRPS locus	Ga0417193_01	Pk_ctg1_1561		Pk_Ga0417193_01_rn08	conserved hypothetical protein, putative signal peptide	CAK15995.1	72.4	
Pseudomonas koreensis C12	Powderdine-like siderophore - chromophore NRPS locus	Ga0417193_01	Pk_ctg1_1562		Pk_Ga0417193_01_rn08	conserved hypothetical protein	CAK15994.1	69	
Pseudomonas koreensis C12	Powderdine-like siderophore - chromophore NRPS locus	Ga0417193_01	Pk_ctg1_1563		Pk_Ga0417193_01_rn08	conserved hypothetical protein, putative membrane protein	CAK15993.1	72.7	
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2148		Pk_Ga0417193_01_rn11				
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2149		Pk_Ga0417193_01_rn11				
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2150		Pk_Ga0417193_01_rn11				
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2151		Pk_Ga0417193_01_rn11				
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2152		Pk_Ga0417193_01_rn11				
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2153		Pk_Ga0417193_01_rn11				
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2154		Pk_Ga0417193_01_rn11				
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2155		Pk_Ga0417193_01_rn11				
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2156		Pk_Ga0417193_01_rn11				
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2157		Pk_Ga0417193_01_rn11				
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2158		Pk_Ga0417193_01_rn11				
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2159		Pk_Ga0417193_01_rn11				
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2160		Pk_Ga0417193_01_rn11	ABC transporter substrate-binding protein	WP_116029632.1	99.7	
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2161		Pk_Ga0417193_01_rn11	hypothetical protein	WP_064591340.1	99.4	
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2162		Pk_Ga0417193_01_rn11	copper chaperone PcuJ/AJC	WP_077572416.1	100	
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2163		Pk_Ga0417193_01_rn11	SCO family protein	WP_008079652.1	100	
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2164	lokT	Pk_Ga0417193_01_rn11	RND efflux	QDF82261.1	86.5	
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2165	lokR	Pk_Ga0417193_01_rn11	luxR family regulator	QDF82260.1	88.3	
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2166		Pk_Ga0417193_01_rn11	hypothetical protein	WP_183404506.1		
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2167	lokA	Pk_Ga0417193_01_rn11	nrps	QDF82254.1	76.9	
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2168	lokB	Pk_Ga0417193_01_rn11	nrps	QDF82255.1	82.5	
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2169	lokC	Pk_Ga0417193_01_rn11	nrps	QDF82259.1	87.5	
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2170	macA	Pk_Ga0417193_01_rn11	macrolide-specific efflux protein	QDF82253.1	92.7	
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2171	macB	Pk_Ga0417193_01_rn11	macrolide export ATP-binding/permease protein	QDF82252.1	91.3	
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2172		Pk_Ga0417193_01_rn11				
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2173		Pk_Ga0417193_01_rn11				
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2174		Pk_Ga0417193_01_rn11				
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2175		Pk_Ga0417193_01_rn11				
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2176		Pk_Ga0417193_01_rn11				
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2177		Pk_Ga0417193_01_rn11				
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2178		Pk_Ga0417193_01_rn11				
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2179		Pk_Ga0417193_01_rn11				
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2180		Pk_Ga0417193_01_rn11				
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2181		Pk_Ga0417193_01_rn11				
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2182		Pk_Ga0417193_01_rn11				
Pseudomonas koreensis C12	Lokisin	Ga0417193_01	Pk_ctg1_2183		Pk_Ga0417193_01_rn11				
Pseudomonas koreensis C12	Powderdine-like siderophore - peptide backbone locus	Ga0417193_01	Pk_ctg1_3654	pwdA	Pk_Ga0417193_01_rn18				
Pseudomonas koreensis C12	Powderdine-like siderophore - peptide backbone locus	Ga0417193_01	Pk_ctg1_3655		Pk_Ga0417193_01_rn18				
Pseudomonas koreensis C12	Powderdine-like siderophore - peptide backbone locus	Ga0417193_01	Pk_ctg1_3656	RND efflux	Pk_Ga0417193_01_rn18				
Pseudomonas koreensis C12	Powderdine-like siderophore - peptide backbone locus	Ga0417193_01	Pk_ctg1_3657	RND efflux	Pk_Ga0417193_01_rn18				
Pseudomonas koreensis C12	Powderdine-like siderophore - peptide backbone locus	Ga0417193_01	Pk_ctg1_3658	RND efflux	Pk_Ga0417193_01_rn18				
Pseudomonas koreensis C12	Powderdine-like siderophore - peptide backbone locus	Ga0417193_01	Pk_ctg1_3659	pwdP	Pk_Ga0417193_01_rn18				
Pseudomonas koreensis C12	Powderdine-like siderophore - peptide backbone locus	Ga0417193_01	Pk_ctg1_3660		Pk_Ga0417193_01_rn18				
Pseudomonas koreensis C12	Powderdine-like siderophore - peptide backbone locus	Ga0417193_01	Pk_ctg1_3661		Pk_Ga0417193_01_rn18				
Pseudomonas koreensis C12	Powderdine-like siderophore - peptide backbone locus	Ga0417193_01	Pk_ctg1_3662		Pk_Ga0417193_01_rn18				
Pseudomonas koreensis C12	Powderdine-like siderophore - peptide backbone locus	Ga0417193_01	Pk_ctg1_3663	pwdE	Pk_Ga0417193_01_rn18				
Pseudomonas koreensis C12	Powderdine-like siderophore - peptide backbone locus	Ga0417193_01	Pk_ctg1_3664	fpvA	Pk_Ga0417193_01_rn18				
Pseudomonas koreensis C12	Powderdine-like siderophore - peptide backbone locus	Ga0417193_01	Pk_ctg1_3665	lpase	Pk_Ga0417193_01_rn18				
Pseudomonas koreensis C12	Powderdine-like siderophore - peptide backbone locus	Ga0417193_01	Pk_ctg1_3666	backbone NRPS	Pk_Ga0417193_01_rn18				
Pseudomonas koreensis C12	Powderdine-like siderophore - peptide backbone locus	Ga0417193_01	Pk_ctg1_3667	backbone NRPS	Pk_Ga0417193_01_rn18				
Pseudomonas koreensis C12	Powderdine-like siderophore - peptide backbone locus	Ga0417193_01	Pk_ctg1_3668	backbone NRPS	Pk_Ga0417193_01_rn18				
Pseudomonas koreensis C12	Powderdine-like siderophore - peptide backbone locus	Ga0417193_01	Pk_ctg1_3669		Pk_Ga0417193_01_rn18				
Pseudomonas koreensis C12	Powderdine-like siderophore - peptide backbone locus	Ga0417193_01	Pk_ctg1_3670		Pk_Ga0417193_01_rn18				
Pseudomonas koreensis C12	Powderdine-like siderophore - peptide backbone locus	Ga0417193_01	Pk_ctg1_3671		Pk_Ga0417193_01_rn18				
Pseudomonas koreensis C12	Powderdine-like siderophore - peptide backbone locus	Ga0417193_01	Pk_ctg1_3672		Pk_Ga0417193_01_rn18				
Pseudomonas koreensis C12	Powderdine-like siderophore - peptide backbone locus	Ga0417193_01	Pk_ctg1_3673		Pk_Ga0417193_01_rn18				
Pseudomonas koreensis C12	Powderdine-like siderophore - peptide backbone locus	Ga0417193_01	Pk_ctg1_3674		Pk_Ga0417193_01_rn18				

Pseudomonas koreensis C12	Pyoverdine-like siderophore - peptide backbone locus	Ga0417193_01	Pk_ctg1_3675		Pk_Ga0417193_01_rm18			
Pseudomonas koreensis C12	Pyoverdine-like siderophore - peptide backbone locus	Ga0417193_01	Pk_ctg1_3676		Pk_Ga0417193_01_rm18			
Pseudomonas koreensis C12	Pyoverdine-like siderophore - peptide backbone locus	Ga0417193_01	Pk_ctg1_3677		Pk_Ga0417193_01_rm18			
Pseudomonas koreensis C12	Pyoverdine-like siderophore - peptide backbone locus	Ga0417193_01	Pk_ctg1_3678		Pk_Ga0417193_01_rm18			
Pseudomonas koreensis C12	Koreenceine	Ga0417193_01	Pk_ctg1_4873	kecA	Pk_Ga0417193_01_rm24			
Pseudomonas koreensis C12	Koreenceine	Ga0417193_01	Pk_ctg1_4872	kecB	Pk_Ga0417193_01_rm24			
Pseudomonas koreensis C12	Koreenceine	Ga0417193_01	Pk_ctg1_4871	kecC	Pk_Ga0417193_01_rm24			
Pseudomonas koreensis C12	Koreenceine	Ga0417193_01	Pk_ctg1_4870	kecD	Pk_Ga0417193_01_rm24			
Pseudomonas koreensis C12	Koreenceine	Ga0417193_01	Pk_ctg1_4869	kecE	Pk_Ga0417193_01_rm24			
Pseudomonas koreensis C12	Koreenceine	Ga0417193_01	Pk_ctg1_4868	kecF	Pk_Ga0417193_01_rm24			
Pseudomonas koreensis C12	Koreenceine	Ga0417193_01	Pk_ctg1_4867	kecG	Pk_Ga0417193_01_rm24			
Pseudomonas koreensis C12	Koreenceine	Ga0417193_01	Pk_ctg1_4866	kecH	Pk_Ga0417193_01_rm24			
Pseudomonas koreensis C12	Koreenceine	Ga0417193_01	Pk_ctg1_4865	kecI	Pk_Ga0417193_01_rm24			
Pseudomonas koreensis C12	Koreenceine	Ga0417193_01	Pk_ctg1_4864	kecJ	Pk_Ga0417193_01_rm24			
Pseudomonas koreensis C12	Koreenceine	Ga0417193_01	Pk_ctg1_4863	kecK	Pk_Ga0417193_01_rm24			
Pseudomonas koreensis C12	Fragin-like	Ga0417193_01	Pk_ctg1_5433		Pk_Ga0417193_01_rm27			
Pseudomonas koreensis C12	Fragin-like	Ga0417193_01	Pk_ctg1_5434		Pk_Ga0417193_01_rm27			
Pseudomonas koreensis C12	Fragin-like	Ga0417193_01	Pk_ctg1_5435		Pk_Ga0417193_01_rm27			
Pseudomonas koreensis C12	Fragin-like	Ga0417193_01	Pk_ctg1_5436		Pk_Ga0417193_01_rm27			
Pseudomonas koreensis C12	Fragin-like	Ga0417193_01	Pk_ctg1_5437	hamA	Pk_Ga0417193_01_rm27			
Pseudomonas koreensis C12	Fragin-like	Ga0417193_01	Pk_ctg1_5438	hamC	Pk_Ga0417193_01_rm27			
Pseudomonas koreensis C12	Fragin-like	Ga0417193_01	Pk_ctg1_5439	hamD	Pk_Ga0417193_01_rm27			
Pseudomonas koreensis C12	Fragin-like	Ga0417193_01	Pk_ctg1_5440	hamE	Pk_Ga0417193_01_rm27			
Pseudomonas koreensis C12	Fragin-like	Ga0417193_01	Pk_ctg1_5441		Pk_Ga0417193_01_rm27			
Pseudomonas koreensis C12	Fragin-like	Ga0417193_01	Pk_ctg1_5442		Pk_Ga0417193_01_rm27			
Pseudomonas koreensis C12	Fragin-like	Ga0417193_01	Pk_ctg1_5443		Pk_Ga0417193_01_rm27			
Pseudomonas koreensis C12	Fragin-like	Ga0417193_01	Pk_ctg1_5444		Pk_Ga0417193_01_rm27			
Pseudomonas koreensis C12	Fragin-like	Ga0417193_01	Pk_ctg1_5445		Pk_Ga0417193_01_rm27			
Pseudomonas koreensis C12	Fragin-like	Ga0417193_01	Pk_ctg1_5446		Pk_Ga0417193_01_rm27			
Pseudomonas koreensis C12	Fragin-like	Ga0417193_01	Pk_ctg1_5447		Pk_Ga0417193_01_rm27			
Pseudomonas koreensis C12	Fragin-like	Ga0417193_01	Pk_ctg1_5448		Pk_Ga0417193_01_rm27			
Pseudomonas koreensis C12	Fragin-like	Ga0417193_01	Pk_ctg1_5449		Pk_Ga0417193_01_rm27			
Pseudomonas koreensis C12	Fragin-like	Ga0417193_01	Pk_ctg1_5450		Pk_Ga0417193_01_rm27			
Pseudomonas koreensis C12	Fragin-like	Ga0417193_01	Pk_ctg1_5451		Pk_Ga0417193_01_rm27			