

Additional File 3:

Genes of *Arthrobacter* sp. Rue61a, grouped according to functions, as discussed in the text

Table S3.1: Genes of *Arthrobacter* sp. Rue61a presumed to be involved in osmoprotection.

Locus_tag	Gene symbol	Predicted protein product	EC #
ARUE_c02780	<i>proP1</i>	proline/betaine transporter, MF superfamily	
ARUE_c04460		betaine/carnitine/choline transporter, BCCT family	
ARUE_c04830		choline oxidase	1.1.3.17
ARUE_c04840	<i>gbsA</i>	betaine aldehyde dehydrogenase	1.2.1.8
ARUE_c05460	<i>proP2</i>	proline/betaine transporter, MF superfamily	
ARUE_c06090	<i>yehY</i>	ABC-type putative osmoprotectant uptake system, permease protein	
ARUE_c06100	<i>opuCA1</i>	ABC-type glycine betaine/carnitine/choline transport system, ATP-binding protein	
ARUE_c06110	<i>opuBB</i>	ABC-type glycine betaine/carnitine/choline transport system, permease protein	
ARUE_c06120	<i>osmF</i>	osmoprotectant uptake system, substrate-binding protein	
ARUE_c08620	<i>treS1</i>	trehalose synthase	5.4.99.16
ARUE_c08830	<i>otsB</i>	trehalose-6-phosphate phosphatase	3.1.3.12
ARUE_c08840	<i>otsA</i>	trehalose-6-phosphate synthase	2.4.1.15
ARUE_c16900	<i>trkA1</i>	Trk system potassium uptake protein, dinucleotide-binding regulatory component	
ARUE_c16910	<i>trkA2</i>	Trk system potassium uptake protein, dinucleotide-binding regulatory component	
ARUE_c17450	<i>gltB</i>	glutamate synthase [NADPH/NADH], alpha subunit	1.4.1.13 or 1.4.1.14
ARUE_c17460	<i>gltD</i>	glutamate synthase [NADPH/NADH], beta subunit	1.4.1.13 or 1.4.1.14
ARUE_c19080	<i>proP3</i>	proline/betaine transporter, MF superfamily	
ARUE_c25180	<i>proA</i>	gamma-glutamyl phosphate reductase	1.2.1.41
ARUE_c25190	<i>proB</i>	glutamate 5-kinase	2.7.2.11
ARUE_c25470	<i>mscS</i>	putative mechanosensitive ion channel protein	
ARUE_c29680	<i>proX</i>	glycine betaine/choline-binding protein of an ABC-type transport system	
ARUE_c29690	<i>proZ</i>	ABC-type proline/glycine betaine transport system, permease component	
ARUE_c29700	<i>proW</i>	ABC-type proline/glycine betaine transport system, permease component	
ARUE_c29710	<i>opuCA2</i>	glycine betaine/carnitine/choline transport system, OpuCA-like ATP-binding protein	
ARUE_c30460	<i>treZ</i>	malto-oligosyltrehalose trehalohydrolase	3.2.1.141
ARUE_c30470	<i>treY</i>	maltooligosyl trehalose synthase	5.4.99.15
ARUE_c34610	<i>gdh</i>	homooligomeric NADP ⁺ -specific glutamate dehydrogenase	
ARUE_c34640	<i>trkH</i>	TrkH-like potassium uptake protein, ion-conducting transmembrane component	
ARUE_c34650	<i>trkA3</i>	Trk system potassium uptake protein, dinucleotide-binding regulatory component	
ARUE_c34660	<i>proC</i>	pyrroline-5-carboxylate reductase	1.5.1.2
ARUE_c39590	<i>proP4</i>	proline/betaine transporter, MF superfamily	
ARUE_c39800		ABC-type transporter, substrate binding component	

ARUE_c39810		ABC-type proline/betaine transporter, permease component	
ARUE_c39820		ABC-type transporter, permease component	
ARUE_c39830	<i>opuCA3</i>	glycine betaine/carnitine/choline transporter, OpuCA-like ATP-binding protein	
ARUE_c40470	<i>proP5</i>	proline/betaine transporter, MF superfamily	
ARUE_c41530	<i>mscL</i>	large conductance mechanosensitive ion channel protein	
ARUE_c42120	<i>treS2</i>	trehalose synthase	5.4.99.16
ARUE_232p00510	<i>trkH</i>	TrkH-type potassium uptake protein	

Table S3.2: Genes of *Arthrobacter* sp. Rue61a possibly involved in formation of reactive oxygen species and in protection against oxidative stress.

Locus_tag	Gene symbol	Predicted protein product	EC #
ARUE_c00400	<i>puo</i>	putrescine oxidase	1.4.3.10
ARUE_c00520		putative sugar alcohol dehydrogenase or oxidase/alditol oxidase	
ARUE_c01660		FAD/FMN-containing dehydrogenase or oxidase	
ARUE_c04530		N,N-dimethylglycine oxidase	1.5.3.10
ARUE_c04810		acyl-coenzyme A oxidase	1.3.3.6
ARUE_c04830		choline oxidase	1.1.3.17
ARUE_c04860		putative molybdopterin oxidoreductase, sulfite oxidase family	
ARUE_c05480		Cu ²⁺ -containing amine oxidase	
ARUE_c06000	<i>ydbD</i>	putative Mn catalase	1.11.1.6
ARUE_c06400	<i>gpx</i>	glutathione peroxidase	1.11.1.9
ARUE_c07090		acyl-coenzyme A dehydrogenase/oxidase family protein	
ARUE_c09150		acyl-coenzyme A dehydrogenase/oxidase family protein	
ARUE_c09600		putative multicopper oxidase family protein	
ARUE_c11380	<i>soxA1</i>	putative monomeric sarcosine oxidase	1.5.3.1
ARUE_c11870		OsmC family stress protein or peroxiredoxin	
ARUE_c14160		acyl-coenzyme A dehydrogenase/oxidase family protein	
ARUE_c14890		putative molybdopterin oxidoreductase, sulfite oxidase family	
ARUE_c16720–16730		putative cytochrome d ubiquinol oxidase	1.10.2.-
ARUE_c17720		pyranose 2-oxidase	1.1.3.10
ARUE_c17930		pyranose 2-oxidase	1.1.3.10
ARUE_c19520		pyridoxine 5'-phosphate oxidase-like protein	
ARUE_c19630		putative multicopper oxidase family protein	
ARUE_c19980	<i>katE</i>	catalase	1.11.1.6
ARUE_c21130	<i>soxA2</i>	putative monomeric sarcosine oxidase oxidase	
ARUE_c21770		putative uncharacterized peroxidase	
ARUE_c22440	<i>sodaA</i>	superoxide dismutase	1.15.1.1
ARUE_c22940		acyl-coenzyme A dehydrogenase/oxidase family protein	
ARUE_c23620	<i>ctaE</i>	putative cytochrome oxidase subunit III	1.9.3.1
ARUE_c25860		putative peroxiredoxin, AhpE-like	1.11.1.15
ARUE_c26720		putative peroxiredoxin (PRX), BCP subfamily	1.11.1.15
ARUE_c26880	<i>nadB</i>	L-aspartate oxidase	1.4.3.16
ARUE_c29070	<i>hemG</i>	protoporphyrinogen oxidase	1.3.3.4
ARUE_c29170	<i>thiO</i>	putative glycine oxidase/D-amino acid oxidase	
ARUE_c32080	<i>katA</i>	catalase	1.11.1.6
ARUE_c35300–35310		putative xanthine dehydrogenase/xanthine oxidase	1.17.1.4/ 1.17.3.2
ARUE_c35390	<i>uox</i>	urate oxidase	1.7.3.3
ARUE_c36380		putative peroxiredoxin (PRX), BCP subfamily	1.11.1.15
ARUE_c36580		pyridoxine 5'-phosphate oxidase family protein	
ARUE_c36630		FAD/FMN-containing dehydrogenase or oxidase	
ARUE_c36760	<i>soxR</i>	redox-sensitive transcription factor SoxR	
ARUE_c37540		alkylhydroperoxidase like protein, AhpD family	
ARUE_c37570		Cu ²⁺ -containing primary amine oxidase	1.4.3.4
ARUE_c39110		putative sulfite oxidase	1.8.3.1
ARUE_c39620–39650	<i>soxBDAG</i>	sarcosine oxidase	1.5.3.1
ARUE_c41520	<i>xyoA</i>	putative xylitol oxidase	1.1.3.41
ARUE_232p00320		putative multicopper oxidase family protein	
ARUE_232p00590		multicopper oxidase	

ARUE_232p01420	<i>thiO/thiG</i>	bifunctional protein ThiO/ThiG (ThiG, amino acid oxidase)	
ARUE_113p00040-00060	<i>meqABC</i>	quinaldine 4-oxidase	
ARUE_113p00140		putative Fe/Mn superoxide dismutase	1.15.1.1

Table S3.3: Genes of *Arthrobacter* sp. Rue61a presumed to be involved in acquisition of iron.

Locus_tag	Gene symbol	Predicted protein product	EC #
ARUE_c02640	<i>rhbB</i>	L-2,4-diaminobutyrate decarboxylase	4.1.1.86
ARUE_c02650		putative lysine/ornithine N-monooxygenase	
ARUE_c02660		putative acetyltransferase	
ARUE_c02670	<i>rhbF</i>	rhizobactin siderophore biosynthesis protein	
ARUE_c03570		ABC-type Fe ³⁺ -hydroxamate transporter, extracellular iron-siderophore binding protein	
ARUE_c03580		siderophore interacting protein with a ferredoxin reductase-like (FNR-like) domain structure	
ARUE_c03590		Fe ³⁺ -siderophore ABC transporter, transmembrane subunit	
ARUE_c03600		Fe ³⁺ -siderophore ABC transporter, transmembrane subunit	
ARUE_c03610		Fe ³⁺ -siderophore ABC transporter, ATP-binding protein	
ARUE_c05260		Fe ³⁺ -siderophore ABC transporter, ATP-binding protein	
ARUE_c05270		Fe ³⁺ -siderophore ABC transporter, transmembrane subunit	
ARUE_c05280		Fe ³⁺ -siderophore ABC transporter, transmembrane subunit	
ARUE_c05290		Fe ³⁺ -siderophore binding protein, FhuD family	
ARUE_c07040		putative Fe ³⁺ transport system, SfuC-like ATP binding protein	3.6.3.30
ARUE_c07050		putative Fe ³⁺ -transport system, SfuB-like permease protein	3.6.3.30
ARUE_c07060		putative Fe ³⁺ -binding extracellular protein, SfuA-/FbpA-like	3.6.3.30
ARUE_c09470		siderophore interacting protein with a ferredoxin reductase-like (FNR-like) domain structure	
ARUE_c21680		Fe ³⁺ -siderophore ABC transporter, ATP-binding protein	
ARUE_c21690		Fe ³⁺ -siderophore binding protein, FhuD family	
ARUE_c21700		Fe ³⁺ -hydroxamate ABC transporter, permease subunit	
ARUE_c27860	<i>fur1</i>	ferric uptake regulation protein Fur	
ARUE_c32070	<i>fur2</i>	ferric uptake regulation protein Fur	
ARUE_c38950		siderophore interacting protein with a ferredoxin reductase-like (FNR-like) domain structure	
ARUE_c38960		Fe ³⁺ -siderophore ABC transporter, ATP-binding protein	
ARUE_c38970		Fe ³⁺ -siderophore ABC transporter, permease subunit	
ARUE_c38980		Fe ³⁺ -siderophore ABC transporter, permease subunit	
ARUE_c38990		Fe ³⁺ -siderophore binding protein, FepB family	
ARUE_c39970		Fe ³⁺ -siderophore ABC transporter, ATP-binding protein, CeuD family	
ARUE_c39980		Fe ³⁺ -siderophore ABC transporter, permease subunit, CeuC family	
ARUE_c39990		Fe ³⁺ -siderophore ABC transporter, permease subunit, CeuB family	
ARUE_c40000		siderophore binding protein (FatB), CeuA family	

Table S3.4: Genes of *Arthrobacter* sp. Rue61a presumed to be involved in response to heavy metal ions.

Locus_tag	Gene symbol	Predicted protein product	EC #
ARUE_c00900		putative NAD(P)H:flavin oxidoreductase/NAD(P)H nitroreductase	
ARUE_c03850	<i>czcD</i>	putative cation (cobalt-zinc-cadmium) efflux transporter	
ARUE_c19540		putative heavy-metal-translocating P-type ATPase	
ARUE_c26820		putative anion permease, ArsB/NhaD superfamily	
ARUE_c33070		putative NAD(P)H:flavin oxidoreductase/NAD(P)H nitroreductase	
ARUE_c37620	<i>arsC1</i>	putative arsenate reductase ArsC	1.20.4.1
ARUE_c37630	<i>arsC2</i>	putative arsenate reductase ArsC	1.20.4.1
ARUE_c37660	<i>arsC3</i>	putative arsenate reductase ArsC	1.20.4.1
ARUE_c41610		possible chromate reductase; YieF/ChrR-like NAD(P)H-dependent FMN reductase	
ARUE_c42390		heavy-metal-associated domain (HMA) -containing protein; possible copper chaperone	
ARUE_c42400	<i>copA</i>	putative heavy metal-translocating (Cu ⁺ /Ag ⁺) P-type ATPase, CopA-like	
ARUE_232p00330		putative major facilitator superfamily transporter; NreB-like	
ARUE_232p00400	<i>copC</i>	putative copper resistance protein CopC	
ARUE_232p00430	<i>czcD</i>	cation (cobalt-zinc-cadmium) efflux transporter CzcD	
ARUE_232p00560		putative Cd ²⁺ /Zn ²⁺ /Pb ²⁺ -translocating P-type ATPase	
ARUE_232p00610		putative ACR3-type arsenite efflux pump	
ARUE_232p00710		putative Cd ²⁺ /Zn ²⁺ /Pb ²⁺ -translocating P-type ATPase	
ARUE_232p00780		putative copper-translocating P-type ATPase	
ARUE_232p00800	<i>merA</i>	putative mercuric reductase MerA	1.16.1.1

Table S3.5: Genes of *Arthrobacter* sp. Rue61a possibly involved in resistance to bacitracin.

Locus_tag	Predicted protein product
ARUE_c22050	putative permease component of ABC transport system
ARUE_c22060	ATPase component of putative ABC-type peptide antibiotic transport system; BcrA subfamily
ARUE_c26540	putative sensor histidine kinase
ARUE_c26550	putative response regulator responding to cell wall stress/antimicrobial peptides
ARUE_c26560	ATPase component of ABC-type antimicrobial peptide transport system; BceA-like
ARUE_c26570	permease protein of ABC transporter
ARUE_c34930	ATPase component of ABC-type antimicrobial peptide transport system; BceA-like
ARUE_c34940	putative permease protein of ABC-type transport system
ARUE_c43020	putative response regulator containing a CheY-like signal receiver domain and LuxR-C-like HTH DNA-binding domain
ARUE_c43030	putative sensor histidine kinase
ARUE_c43040	putative permease component of ABC-type transport system
ARUE_c43050	ATPase component of putative antimicrobial peptides ABC transporter; BcrA-like
ARUE_c43130	putative response regulator containing a CheY-like signal receiver domain and LuxR-C-like HTH DNA-binding domain
ARUE_c43140	putative signal transduction histidine kinase
ARUE_c43150	putative ABC transporter, permease protein
ARUE_c43160	ATPase component of putative ABC transporter

Table S3.6: Genes of *Arthrobacter* sp. Rue61a involved in the metabolism of aromatic and N-heterocyclic compounds (see also Additional File 4 for Figures of pathways).

Locus_tag	Gene symbol	Predicted protein product	EC #
ARUE_c02440	<i>styA2B</i>	putative styrene monooxygenase, StyA2B-like	
ARUE_c02450	<i>styA1</i>	putative oxygenase component, StyA1-like	
ARUE_c05840	<i>hpaC</i>	flavin reductase; putative reductase component of 4-hydroxyphenylacetate 3-monooxygenase	
ARUE_c05860	<i>hpaB</i>	putative 4-hydroxyphenylacetate 3-monooxygenase oxygenase component (HpaB)	1.14.14.-
ARUE_c24100	<i>vanB</i>	VanB-like reductase component (flavin-iron/sulfur protein) of oxygenase system	
ARUE_c24110	<i>vanA</i>	vanillate O-demethylase oxygenase component VanA	1.14.13.82
ARUE_c33590	<i>paaG</i>	putative ring 1,2-epoxyphenylacetyl-CoA isomerase, oxepin-CoA-forming	
ARUE_c33600	<i>paaE</i>	ring 1,2-phenylacetyl-CoA epoxidase component	
ARUE_c33610	<i>paaD</i>	ring 1,2-phenylacetyl-CoA epoxidase component	
ARUE_c33620	<i>paaC</i>	ring 1,2-phenylacetyl-CoA epoxidase component	
ARUE_c33630	<i>paaB</i>	ring 1,2-phenylacetyl-CoA epoxidase component	
ARUE_c33640	<i>paaA</i>	ring 1,2-phenylacetyl-CoA epoxidase component	
ARUE_c33800	<i>paaI</i>	phenylacetic acid degradation protein, thioesterase PaaI	
ARUE_c33810	<i>paaK</i>	phenylacetate-coenzyme A ligase	
ARUE_c40570	<i>hpcH</i>	4-hydroxy-2-oxo-heptane-1,7-dioate aldolase HpcH	4.1.2.-
ARUE_c40580	<i>hpcG</i>	2-oxo-hepta-3-ene-1,7-dioic acid hydratase HpcG	4.2.1.-
ARUE_c40590	<i>hpcB</i>	3,4-dihydroxyphenylacetate 2,3-dioxygenase HpcB	1.13.11.2
ARUE_c40600	<i>hpcC</i>	5-carboxymethyl-2-hydroxy-muconate semialdehyde dehydrogenase HpcC	1.2.1.60
ARUE_c40620	<i>hpaG</i>	4-hydroxyphenylacetate degradation bifunctional isomerase/decarboxylase HpaG	4.1.1.67, 5.3.3.-
ARUE_c41200	<i>pobA</i>	4-hydroxybenzoate hydroxylase PobA	1.14.13.2
ARUE_c41720		putative 2-aminobenzoyl-CoA monooxygenase/reductase	1.14.13.40
ARUE_c41730		anthranilate-CoA ligase	6.2.1.32
ARUE_c41790	<i>pcaR</i>	Pca regulon regulatory protein PcaR	
ARUE_c41800	<i>pcaJ</i>	3-oxoadipate CoA-transferase subunit B	2.8.3.6
ARUE_c41810	<i>pcaI</i>	3-oxoadipate CoA-transferase subunit A	2.8.3.6
ARUE_c41820	<i>pcaF</i>	beta-ketoadipyl-CoA thiolase PcaF	2.3.1.174
ARUE_c41830	<i>pcaC</i>	4-carboxymuconolactone decarboxylase PcaC	4.1.1.44
ARUE_c41840	<i>pcaD</i>	3-oxoadipate enol lactone hydrolase PcaD	3.1.1.24
ARUE_c41850	<i>pcaB</i>	3-carboxy-cis,cis-muconate cycloisomerase PcaB	5.5.1.2
ARUE_c41860	<i>pcaG</i>	protocatechuate 3,4-dioxygenase alpha chain	1.13.11.3
ARUE_c41870	<i>pcaH</i>	protocatechuate 3,4-dioxygenase beta chain	1.13.11.3
ARUE_c41880	<i>hpd</i>	4-hydroxyphenylpyruvate dioxygenase Hpd	1.13.11.27
ARUE_113p00030		putative XdhC protein	
ARUE_113p00040	<i>meqA</i>	quinaldine 4-oxidase, small subunit	1.3.99.-
ARUE_113p00050	<i>meqB</i>	quinaldine 4-oxidase, medium subunit	1.3.99.-
ARUE_113p00060	<i>meqC</i>	quinaldine 4-oxidase, large subunit	1.3.99.-
ARUE_113p00070	<i>meqD</i>	1H-4-oxoquinaldine 3-monooxygenase	1.14.13.-
ARUE_113p00080	<i>meqE</i>	1H-3-hydroxy-4-oxoquinaldine 2,4-dioxygenase	1.13.11.48
ARUE_113p00090	<i>meqF</i>	N-acetylanthranilate amidase	3.5.1.13
ARUE_113p00160	<i>meqR1</i>	transcriptional regulator	
ARUE_113p00210		putative acyl-CoA thioesterase	3.1.2.-
ARUE_113p00220		anthranilate CoA ligase	6.2.1.32
ARUE_113p00230		putative 2-aminobenzoyl-CoA monooxygenase/reductase	1.14.13.40
ARUE_113p00240	<i>meqR2</i>	transcriptional regulator	