

SUPPLEMENTARY MATERIAL

***Agrobacterium tumefaciens* ExoR Controls Acid Response Genes and Impacts Exopolysaccharide Synthesis, Horizontal Gene Transfer and Virulence Gene Expression**

Running Title: *Agrobacterium tumefaciens* ExoR Regulon

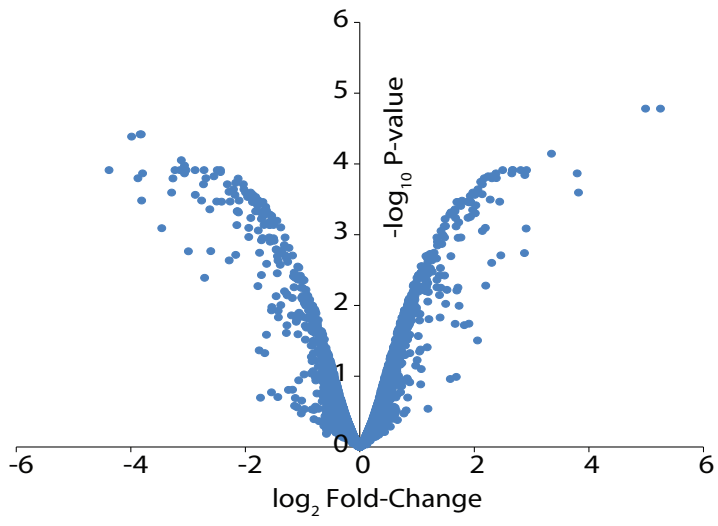
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- 1) Supplementary Figures – S1-S3
- 2) Supplementary Figure Legends
- 3) Supplementary Tables – S1-S3
- 4) Supplementary References

Fig S1

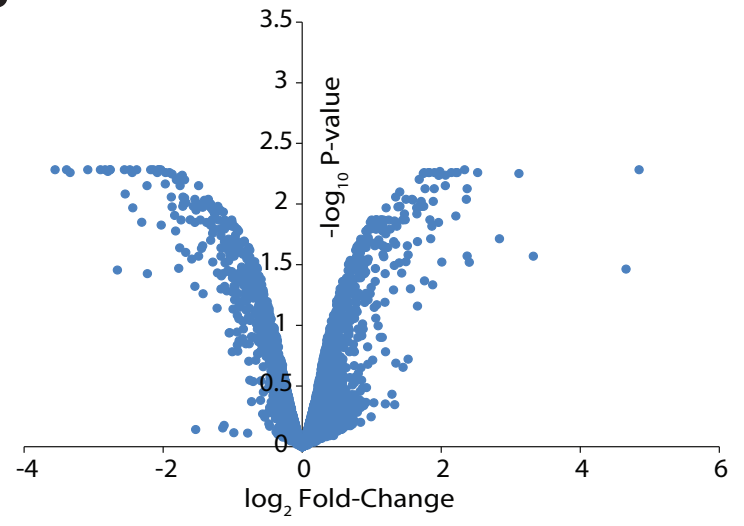
A

ΔexoR vs. wild-type



B

$\Delta\text{exoA}\Delta\text{exoR}$ vs. ΔexoA



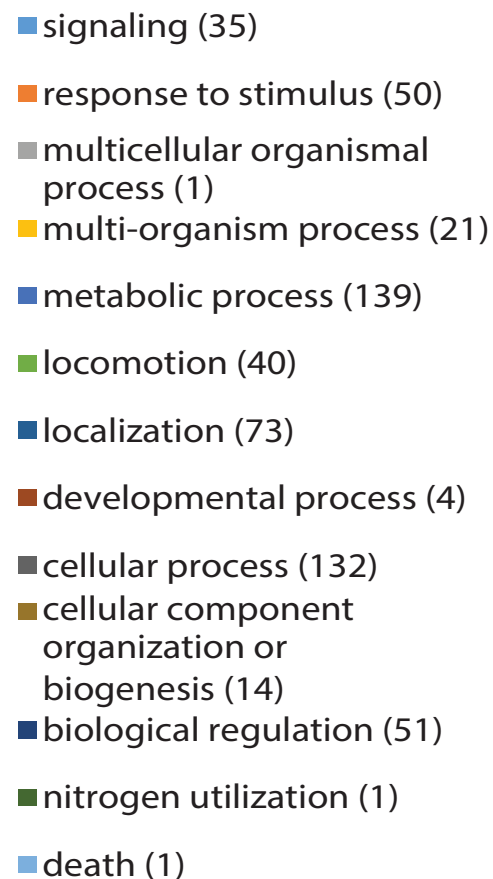
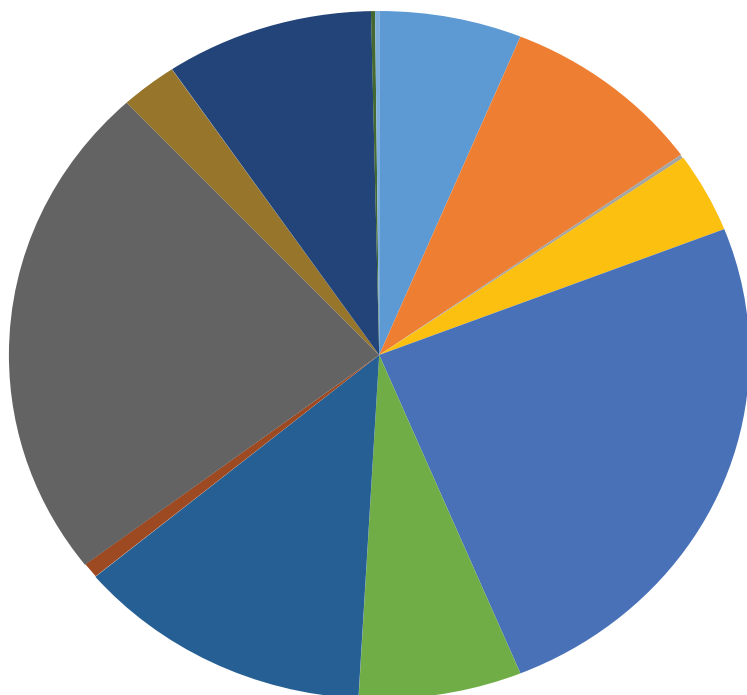
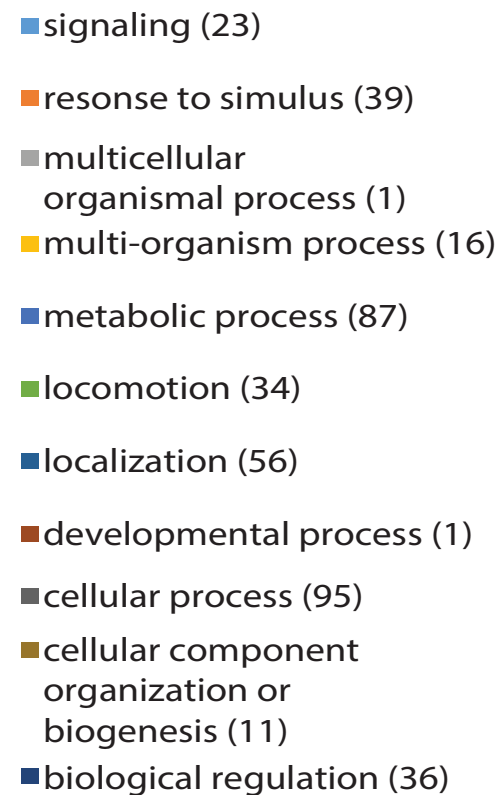
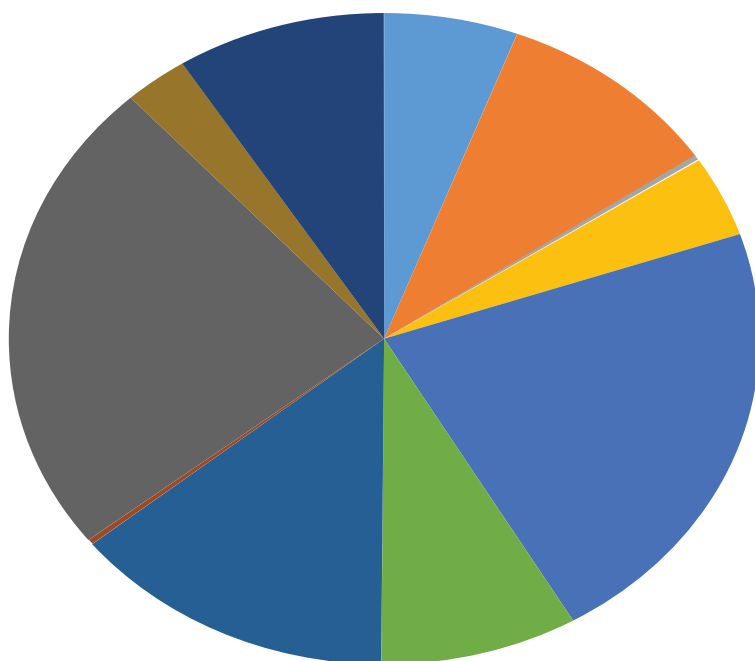
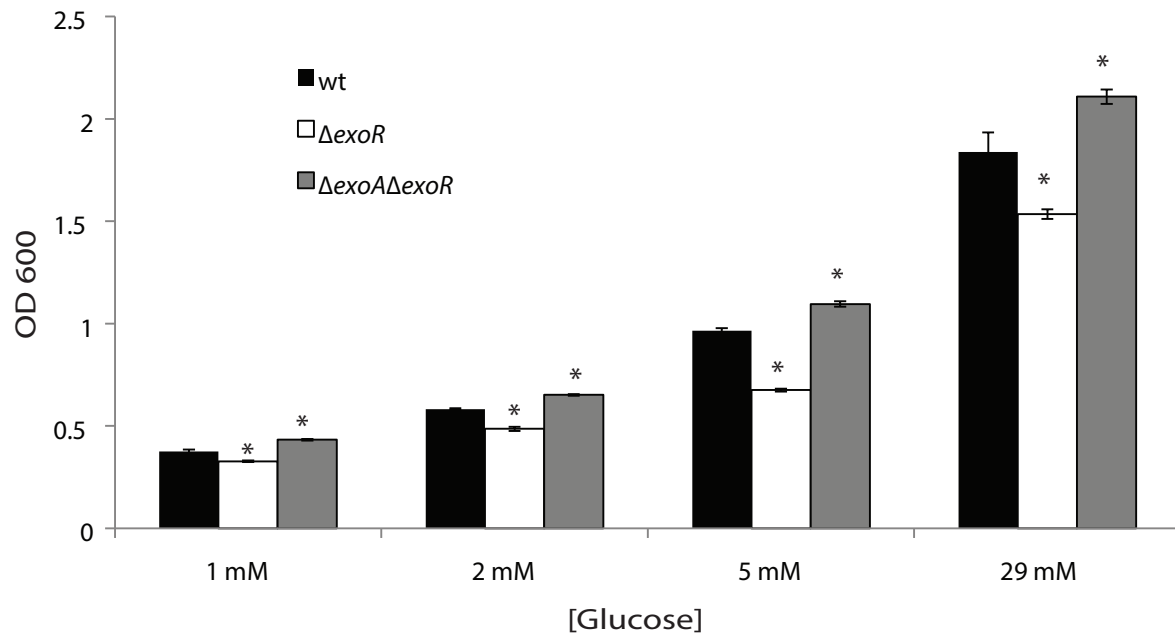
A*ΔexoR* vs. wild-type**B***ΔexoAΔexoR* vs. *ΔexoA*

Fig S3



Supplemental Figure 1: Volcano plots of each microarray analysis. (A), $\Delta exoR$ versus wild-type, (B), $\Delta exoA\Delta exoR$ versus $\Delta exoA$. Each point represents a single gene. The cut-off values for significant expression changes were a P-value of <0.05 and an M-value of ± 0.5 .

Supplemental Figure 2: GO Analysis of ExoR regulon by Blast2GO Fasta files containing nucleotide sequences corresponding to Atu numbers of significantly regulated genes were run through the Blast2GO software. The fasta file was first run through BLAST step, then through the GO-Mapping, Annotation, and InterPro Scan steps to generate a set of annotated genes. Not every sequence entered into the software was assigned to a GO group, and many sequences were assigned to more than one group, so the total number of GO-annotated genes does not correspond directly with the number of sequences in the fasta file. A combined graph was generated in the Cellular Processes category, and the pie chart represents Level 2 organization of the GO IDs in this category.

Supplemental Figure 3: Succinoglycan Over-production Leads to Decreased Growth Yields Strains were grown in minimal media (ATGN) with a range of glucose concentrations for 71 hours to determine growth yield differences. Asterisks denote a significant difference of the OD_{600} compared to wild-type at each time point ($p < 0.05$). Error bars represent standard deviation of the mean of three biological replicates.

Table S1: strains and plasmids used in this study

Strain/plasmid designation	Relevant features	Reference
<i>E. coli</i>		
DH5 α / λ pir	λ pir; cloning strain	(1)
TOP10 F'	Cloning strain	Invitrogen
S17-1/ λ pir	λ pir ; Tra ⁺ , cloning host	(2)
S17-1/ λ pir (pFD1)	<i>Himar1</i> conjugal donor	(3)
<i>Agrobacterium tumefaciens</i>		
C58	Nopaline type strain; pTiC58; pAtC58	(4)
PMM1	Δ exoR (Atu1715)	(5)
ERM91	C58 pTi-, pAtGm ^R	This study
ERM52	C58 plasmidless, aada+	(6)
PMM2	Δ exoA Δ exoR (Atu4053-1715)	(5)
PMM4	Δ flfE (Atu0574)	(7)
MLL2	Δ exoA (Atu4053)	(5)
BH101	Δ exoR Δ chvI (Atu1715-0034)	This study
BH102	Δ exoAR Δ exoR Δ chvI (Atu4053-1715-0034)	This study
BH103	Δ chvI (Atu0034)	This study
BH107	Δ chvG (Atu0033)	This study
BH108	Δ exoR Δ chvG (Atu1715-0033)	This study
BH109	Δ exoA Δ exoR Δ chvG (Atu4053-1715-0033)	This study
Plasmids		
pGEM-T Easy	PCR cloning vector, Amp ^R	Promega
pNPTS138	ColE1 suicide plasmid; <i>sacB</i> ; Km ^R	Gift of M. Alley
pSRKGm	Broad host range (BHR), P _{lac} expression vector; <i>lacIQ</i> ; Gm ^R	(8)
pRA301	Broad host range; promoterless <i>lacZ</i> ; Spc ^R	(9)
pJX160	pRA301 carrying <i>PflgE—lacZ</i> ; Spc ^R	(10)
pBH203	pNPTS138 carrying <i>chvI</i> SOE deletion fragment	This study
pBH204	pNPTS138 carrying <i>chvG</i> SOE deletion fragment	This study
pBH100	pSRKGm carrying <i>P_{lac}—chvI</i>	This study
pBH104	pSRKGm carrying <i>P_{lac}—chvG</i>	This study
pSW209	BHR, <i>PvirB—lacZ</i> , Km ^R , IncP relicon	S.C. Winans
pSW174	<i>virG</i> (includes intact P1 and P2)— <i>lacZ</i> , Spc ^R	(11)
pSW264	<i>virG</i> (includes only P2)— <i>lacZ</i>	(11)
pSW303	<i>virG</i> (includes intact P1 and 10-bp deletion of P2)— <i>lacZ</i>	(11)

Table S2: Oligonucleotides used in this study

Primer Name	Sequence 5' – 3'	Application
chvG delete P1	(SpeI) actagtTCGCCAGAAATCGGATATTCCCGT	<i>chvG</i> deletion
chvG delete P2	<i>aagcttggtagccaattc</i> CACGTATTAAGTCCTCACGCCCCG	
chvG delete P3	<i>gaattcggtagccaagctt</i> TGAACGCTTCAACCTGCATGCGAC	
chvG delete P4	(PstI) ctgcagTCCTGTCCATCGGTGGGATTTTCAT	
chvG comp 5'	(NdeI) catatgTTGAAGAAAACGCCGAAACC	<i>chvG</i> complementation
chvG comp 3'	(KpnI) ggtaccGTCGCATGCAGGTTGAAGCGTTCA	
chvI delete P1	(SpeI) actagtAGATTGCGGATGAACAGCGAATGC	<i>chvI</i> deletion
chvI delete P2	<i>aagcttggtagccaattc</i> CATGTAGTTGGTCTCCATCGTCAT	
chvI delete P3	<i>gaattcggtagccaagctt</i> TAAAGAAGCCGACTCAAGCAGAAG	
chvI delete P4	(SphI) gcatgcAATCGAGCAACAGATTGGCATCGG	
chvI comp 5'	(NdeI) catatgCAGACGATCGCGCTTGTGCGAC	<i>chvI</i> complementation
chvI comp 3'	(KpnI)ggtaccCTTCTGCTTGAGTCGGCTTCTTTA	
exoY qPCR fwd	AGACCAATCTGGAAGTCATCGCCA	Quantitative PCR
exoY qPCR rev	TGCGCTCGGTCTGGTAAAGAAGAT	
flgD qPCR fwd	AGACCAATCTGGAAGTCATCGCCA	
flgD qPCR rev	TGCGCTCGGTCTGGTAAAGAAGAT	
σ^{70} qPCR fwd	ATCTTTCGGATGACGCGGTCAA	
σ^{70} qPCR rev	TTGATGCCATATCGGACAGCA	
virG qPCR fwd	TGAGAGGTGAACCGTTGAAACACG	
virG qPCR rev	GATTGAACTGCTTGCTGTGCGGCTA	
rctB qPCR fwd	GGCCAAACACATTTCCGAAACG	
rctB qPCR rev	CGGAATGATTGGTGGTGGTTGA	
MarTDL2	GACACGGGCTCGANGNNCNTNGG	Touchdown PCR and sequencing
MarRSeq	CGGGTATCGCTCTTGAAGGGA	
MarLSeq	GGGAATCATTTGAAGGTTGGT	
MarTDR1	CAACCGTGGCGGGGNTNCNNGCNCNG	

Capital letter sequences anneal to their target sequences; lower case letters are sequences that have been engineered into the oligonucleotide but do not anneal with the genomic target sequence. Italicized sequences are complimentary to each other between paired primers. Restriction endonuclease cleavage sites are noted in parentheses.

All genes identified in two microarray experiments: Δ exoR vs. wild-type and Δ exoA Δ exoR vs. Δ exoA including agreement with acid regulon of Yuan, *et al. J. Bact.* 2008

Gene ID	Name	Product	Δ exoR vs. wt log ₂ FC	Δ exoR vs. wt p-value	Δ exoA Δ exoR vs. Δ exoA log ₂ FC	Δ exoA Δ exoR vs. Δ exoA p-value	acid regulon
Atu0562	<i>fliN</i>	flagellar motor switch protein FliN	-4.38	< 0.01	-3.34	0.01	
Atu0552	<i>flgG</i>	flagellar basal body rod protein FlgG	-3.99	< 0.01	-3.55	0.01	
Atu0555	<i>flgB</i>	flagellar basal body rod protein FlgB	-3.88	< 0.01	-3.39	0.01	
Atu0554	<i>flgC</i>	flagellar basal body rod protein FlgC	-3.84	< 0.01	-2.79	0.01	
Atu0553	<i>fliE</i>	flagellar hook-basal body protein FliE	-3.82	< 0.01	-2.23	0.04	
Atu0561	<i>fliM</i>	flagellar motor switch protein	-3.81	< 0.01	-2.44	0.01	
Atu0560	<i>motA</i>	flagellar motor protein MotA	-3.79	< 0.01	-2.83	0.01	
Atu0551	<i>flgA</i>	flagellar basal body P-ring biosynthesis protein FlgA	-3.46	< 0.01	-2.48	0.01	
Atu0545	<i>flaA</i>	flagella associated protein	-3.29	< 0.01	-3.08	0.01	*
Atu0584	-	hypothetical protein	-3.27	< 0.01	-2.55	0.01	
Atu0563	<i>fliG</i>	flagellar motor switch protein G	-3.23	< 0.01	-2.31	0.01	
Atu0549	-	hypothetical protein	-3.14	< 0.01	-2.03	0.01	
Atu0571	<i>motD</i>	chemotaxis MotD protein	-3.12	< 0.01	-2.90	0.01	
Atu0559	-	hypothetical protein	-3.06	< 0.01	-2.07	0.01	
Atu0585	-	hypothetical protein	-3.06	< 0.01	-2.76	0.01	
Atu4535	-	ABC transporter, substrate binding protein (amino acid)	-3.04	< 0.01	-2.38	0.01	
Atu0844	-	hypothetical protein	-3.00	< 0.01	-2.23	0.01	
Atu0892	-	hypothetical protein	-2.88	< 0.01	-2.76	0.01	
Atu0558	<i>flgF</i>	flagellar basal body rod protein FlgF	-2.87	< 0.01	-1.78	0.03	
Atu1715	<i>exoR</i>	exopolysaccharide production negative regulator	-2.76	< 0.01	-2.66	0.03	
Atu4547	<i>pcaI</i>	3-oxoadipate CoA-transferase subunit A	-2.73	< 0.01	-1.71	0.01	
Atu5117	-	hypothetical protein	-2.72	< 0.01			
Atu0557	<i>fliI</i>	flagellum-specific ATP synthase	-2.71	< 0.01	-1.54	0.01	
Atu4537	-	ABC transporter, membrane spanning protein (amino acid)	-2.69	< 0.01	-1.76	0.01	
Atu3977	<i>ina</i>	ice nucleation-like protein	-2.62	< 0.01	-1.91	0.01	*
Atu5118	-	hypothetical protein	-2.61	< 0.01			
Atu0568	-	hypothetical protein	-2.55	< 0.01	-1.67	0.01	
Atu1233	-	hypothetical protein	-2.50	< 0.01	-1.76	0.02	

Atu4542	<i>pcaD</i>	beta-ketoadipate enol-lactone hydrolase	-2.49	< 0.01	-1.69	0.01	
Atu5116	<i>rctB</i>	transcriptional regulator protein	-2.43	< 0.01			
Atu0565	-	hypothetical protein	-2.43	< 0.01	-2.06	0.01	
Atu4539	<i>pcaG</i>	protocatechuate 3,4-dioxygenase alpha chain	-2.42	< 0.01	-1.97	0.01	
Atu0543	<i>flaB</i>	hypothetical protein	-2.31	< 0.01	-2.44	0.01	*
Atu0574	<i>flgE</i>	flagellar hook protein FlgE	-2.29	< 0.01	-2.56	0.01	
Atu0569	<i>motB</i>	flagellar motor protein MotB	-2.28	< 0.01	-1.52	0.01	
Atu2223	<i>mcpA</i>	methyl-accepting chemotaxis protein	-2.27	< 0.01	-1.97	0.01	*
Atu4736	-	methyl-accepting chemotaxis protein	-2.21	< 0.01	-1.54	0.05	
Atu0514	-	methyl-accepting chemotaxis protein	-2.18	< 0.01	-1.76	0.01	
Atu4518	<i>livH</i>	ABC transporter, membrane spanning protein (branched chain amino acid)	-2.17	< 0.01	-1.81	0.01	
Atu0547	<i>flilL</i>	flagellar protein	-2.17	< 0.01	-1.51	0.01	
Atu0550	<i>flgl</i>	flagellar basal body P-ring protein	-2.15	< 0.01	-1.74	0.01	
Atu4531	<i>aroQ</i>	3-dehydroquinase dehydratase	-2.14	< 0.01	-1.22	0.01	
Atu4540	<i>pcaH</i>	protocatechuate 3,4-dioxygenase beta chain	-2.14	< 0.01	-1.71	0.01	
Atu0516	<i>cheY</i>	chemotaxis receiver protein	-2.13	< 0.01	-2.14	0.01	
Atu5161	-	hypothetical protein	-2.12	< 0.01			
Atu0515	-	hypothetical protein	-2.11	< 0.01	-1.87	0.01	*
Atu4519	<i>livJ</i>	ABC transporter, substrate binding protein (branched amino acid)	-2.04	< 0.01	-1.32	0.02	
Atu2394	<i>sinR</i>	regulator of biofilm formation, Fnr family			-2.03	0.01	*
Atu0520	<i>cheY</i>	chemotaxis receiver protein	-2.02	< 0.01	-2.08	0.01	*
Atu0519	<i>cheB</i>	chemotaxis-specific methylesterase	-1.99	< 0.01	-1.88	0.01	
Atu0482	-	polysaccharide deacetylase	-1.96	< 0.01	-1.29	0.01	*
Atu0700	-	two component sensor kinase	-1.94	< 0.01	-1.35	0.01	
Atu5172	<i>avhB11</i>	type IV secretion protein AvhB11	-1.94	< 0.01			
Atu0575	<i>flgK</i>	flagellar hook-associated protein FlgK	-1.91	< 0.01	-1.72	0.01	
Atu0373	-	methyl-accepting chemotaxis protein	-1.90	0.01	-2.18	0.01	*
Atu2173	<i>mcpA</i>	methyl-accepting chemotaxis protein	-1.87	< 0.01	-1.32	0.01	
Atu3198	-	ABC transporter, substrate binding protein (ribose)			-1.87	0.01	
Atu4549	<i>pcaF</i>	beta-ketoadipyl CoA thiolase	-1.87	< 0.01			
Atu0653	-	hypothetical protein	-1.85	< 0.01	-1.69	0.01	
Atu5170	<i>avhB9</i>	type IV secretion protein AvhB9	-1.82	< 0.01			
Atu5169	<i>avhB8</i>	type IV secretion protein AvhB8	-1.82	< 0.01			

Atu0521	<i>cheD</i>	chemoreceptor glutamine deamidase CheD	-1.79	< 0.01	-1.49	0.01	
Atu5165	<i>avhB4</i>	type IV secretion protein AvhB4	-1.79	< 0.01			
Atu5163	<i>avhB2</i>	type IV secretion protein AvhB2	-1.79	< 0.01			
Atu0681	-	hypothetical protein	-1.78	0.01	-1.04	0.03	
Atu4516	<i>livG</i>	ABC transporter, nucleotide binding/ATPase protein (branched chain amino acid)	-1.78	< 0.01	-1.32	0.01	
Atu4532	<i>aroE</i>	shikimate 5-dehydrogenase	-1.77	< 0.01			
Atu4538	<i>pcaB</i>	3-carboxy-cis,cis-muconate cycloisomerase	-1.77	< 0.01	-1.01	0.02	
Atu0566	-	hypothetical protein	-1.76	0.04			
Atu5164	<i>avhB3</i>	type IV secretion protein AvhB3	-1.75	< 0.01			
Atu5162	<i>avhB1</i>	type IV secretion protein AvhB1	-1.75	< 0.01			
Atu4548	<i>pcaJ</i>	3-oxoadipate CoA-transferase subunit B	-1.74	< 0.01	-1.29	0.01	
Atu0739	-	hypothetical protein	-1.72	0.01	-0.97	0.05	
Atu0570	-	chemotaxis protein	-1.72	< 0.01	-0.90	0.04	
Atu4536	-	ABC transporter, membrane spanning protein (amino acid)	-1.72	< 0.01	-1.32	0.01	
Atu0517	<i>cheA</i>	chemotaxis protein histidine kinase	-1.70	< 0.01	-1.54	0.01	
Atu5109	<i>traD</i>	conjugal transfer protein	-1.69	< 0.01			
Atu0577	<i>flaF</i>	flagellar biosynthesis regulatory protein FlaF	-1.69	< 0.01	-1.33	0.01	
Atu5167	<i>avhB6</i>	type IV secretion protein AvhB6	-1.69	< 0.01			
Atu5168	<i>avhB7</i>	type IV secretion protein AvhB7	-1.68	< 0.01			
Atu3121	<i>cspA</i>	cold shock protein			-1.67	0.02	*
Atu3122	-	cold shock protein			-1.72	0.01	
Atu3124	-	hypothetical protein			-1.17	0.03	
Atu8018	-	hypothetical protein	-1.67	< 0.01	-1.30	0.01	
Atu5110	<i>traC</i>	conjugal transfer protein	-1.67	< 0.01			
Atu0556	-	hypothetical protein	-1.66	0.05	-1.19	0.02	
Atu0895	-	ABC transporter, substrate binding protein	-1.64	< 0.01	-0.82	0.04	
Atu0548	<i>flgH</i>	flagellar basal body L-ring protein	-1.63	0.03	-1.53	0.01	
Atu5171	<i>avhB10</i>	type IV secretion protein AvhB10	-1.63	< 0.01			
Atu4596	-	hypothetical protein	-1.63	0.01	-1.59	0.03	
Atu5166	<i>avhB5</i>	type IV secretion protein AvhB5	-1.61	< 0.01			
Atu0567	<i>flaD</i>	flagellin protein FlaD	-1.58	< 0.01	-1.43	0.02	
Atu4517	<i>livM</i>	ABC transporter, membrane spanning protein (branched chain amino acid)	-1.58	< 0.01	-1.13	0.02	

Atu0572	-	hypothetical protein	-1.58	< 0.01	-1.51	0.01	
Atu4515	<i>livF</i>	ABC transporter, nucleotide binding/ATPase protein (branched chain amino acid)	-1.57	< 0.01	-1.29	0.01	
Atu3725	-	methyl-accepting chemotaxis protein	-1.56	< 0.01	-1.28	0.02	
Atu3975	<i>glf</i>	UDP-galactopyranose mutase	-1.54	0.01			
Atu4736	-	methyl-accepting chemotaxis protein			-1.54	0.05	
Atu0896	-	hypothetical protein	-1.54	< 0.01	-1.17	0.02	*
Atu3974	<i>ina</i>	ice nucleation-like protein	-1.54	0.01	-1.04	0.04	
Atu0893	-	ABC transporter, nucleotide binding/ATPase protein	-1.51	< 0.01	-0.69	0.04	
Atu0576	<i>flgL</i>	flagellar hook-associated protein FlgL	-1.51	< 0.01	-1.43	0.01	
Atu3252	<i>exuR</i>	GntR family transcriptional regulator			-1.56	0.01	
Atu3254	-	ABC transporter, nucleotide binding/ATPase protein (dicarboxylate)			-1.46	0.01	
Atu4472	-	hypothetical protein	-1.50	< 0.01			
Atu1559	-	hypothetical protein	-1.46	0.01	-1.01	0.04	
Atu2075	<i>cheW</i>	chemotaxis protein	-1.46	< 0.01	-1.18	0.01	
Atu0522	-	hypothetical protein	-1.46	< 0.01	-1.29	0.01	
Atu3504	-	ABC transporter, substrate binding protein (sulfate)	-1.45	< 0.01	-0.74	0.05	
Atu3976	-	hypothetical protein	-1.44	< 0.01	-0.81	0.05	
Atu2470	-	hypothetical protein			-1.45	0.02	*
Atu5108	<i>traG</i>	conjugal transfer coupling protein TraG	-1.44	< 0.01			
Atu5173	-	dehydrogenase	-1.43	< 0.01			
Atu1631	<i>rrpX</i>	two component response regulator	-1.43	0.01	-0.87	0.04	
Atu0646	<i>mcpA</i>	methyl-accepting chemotaxis protein A	-1.42	0.01			
Atu4597	-	ABC transporter, membrane spanning protein	-1.39	< 0.01	-0.98	0.05	
Atu0476	<i>aqpZ</i>	aquaporin Z	-1.38	0.01	-0.98	0.03	
Atu4447	-	ABC transporter, substrate binding protein (sorbitol)			-1.38	0.01	
Atu5022	-	hypothetical protein	-1.38	< 0.01	-1.13	0.02	
Atu0518	<i>cheR</i>	chemotaxis methyltransferase	-1.37	< 0.01	-1.21	0.01	
Atu1912	<i>mclA</i>	methyl-accepting chemotaxis protein	-1.32	< 0.01	-1.12	0.02	*
Atu4442	-	hypothetical protein	-1.31	0.01			
Atu5122	<i>fabG</i>	3-ketoacyl-(acyl-carrier-protein) reductase	-1.31	< 0.01			
Atu5119	-	two component response regulator	-1.31	< 0.01			
Atu4033	-	ABC transporter, substrate binding protein (sugar)			-1.28	0.03	
Atu4594	-	hypothetical protein	-1.28	0.02	-1.16	0.04	

Atu3365	-	hypothetical protein	-1.28	< 0.01			
Atu0587	<i>tagA</i>	teichoic acid biosynthesis protein	-1.28	0.01	-1.23	0.01	
Atu3838	-	hypothetical protein	-1.27	0.02			*
Atu5031	-	hypothetical protein	-1.27	0.01			
Atu0578	<i>flbT</i>	flagellar biosynthesis repressor FlbT	-1.26	< 0.01	-1.29	0.02	
Atu0115	-	hypothetical protein			-1.22	0.04	
Atu0116	-	hypothetical protein			-1.82	0.02	
Atu0117	-	hypothetical protein			-1.41	0.01	
Atu0118	-	hypothetical protein			-1.00	0.02	
Atu5114	-	hypothetical protein	-1.24	< 0.01			
Atu0523	<i>fliF</i>	flagellar MS-ring protein	-1.20	0.01			
Atu5021	-	hypothetical protein	-1.18	0.01	-0.94	0.03	
Atu0652	-	hypothetical protein			-1.20	0.01	
Atu5121	-	two component response regulator	-1.17	< 0.01			
Atu2744	-	C4-dicarboxylate binding protein			-1.17	0.02	*
Atu0872	<i>mcpC</i>	methyl-accepting chemotaxis protein	-1.16	< 0.01	-0.80	0.03	
Atu0579	<i>flgD</i>	flagellar basal body rod modification protein	-1.15	0.01	-1.32	0.01	
Atu0894	-	ABC transporter, membrane spanning protein	-1.15	< 0.01			
Atu4123	-	ABC transporter, substrate binding protein (branched chain amino acid)			-1.14	0.04	
Atu2228	-	GGDEF family protein	-1.13	< 0.01			
Atu3222	-	ABC transporter, substrate binding protein (ribose)			-1.12	0.02	
Atu0224	<i>ctpA</i>	components of type IV pilus, pilin subunit	-1.13	0.01	-1.26	0.01	
Atu3842	-	hypothetical protein	-1.11	0.02	-1.06	0.03	
Atu0542	<i>fla</i>	flagellin	-1.11	0.02	-1.02	0.02	
Atu5020	-	hypothetical protein	-1.09	< 0.01	-0.75	0.03	
Atu1469	-	hypothetical protein	-1.08	0.03			
Atu5124	<i>atrB</i>	glutamate-1-semialdehyde aminotransferase	-1.08	< 0.01			
Atu3116	-	oxidoreductase			-1.06	0.02	
Atu3031	-	hypothetical protein			-1.06	0.02	
Atu3032	-	hypothetical protein			-1.12	0.01	
Atu5513	<i>cspA</i>	cold shock protein			-1.06	0.02	
Atu0387	<i>mcpA</i>	methyl-accepting chemotaxis protein	-1.07	< 0.01	-1.05	0.02	*
Atu5442	-	methyl-accepting chemotaxis protein	-1.06	0.01			

Atu1139	-	hypothetical protein	-1.05	0.01	-1.05	0.02	*
Atu4593	<i>hpaG</i>	2-hydroxyhepta-2,4-diene-1, 7-dioate isomerase/5-carboxymethyl-2-oxo-hex-3-ene-1, 7-dioate decarboxylase	-1.04	< 0.01	-0.64	0.03	
Atu5361	<i>aqpZ</i>	aquaporin Z	-1.03	0.01			
Atu0309	-	hypothetical protein	-1.03	0.01			
Atu3687	-	TonB-dependent receptor	-1.02	0.01			
Atu2416	<i>glnA</i>	glutamine synthetase	-1.02	< 0.01			
Atu0984	<i>pepN</i>	aminopeptidase N	-1.02	0.01	-1.00	0.02	
Atu0183	<i>dapB</i>	dihydrodipicolinate reductase	-1.00	0.01			
Atu3338	<i>thuE</i>	ABC transporter, substrate binding protein (trehalose/maltose)			-0.85	0.04	
Atu3339	<i>thuF</i>	ABC transporter, membrane spanning protein (trehalose/maltose)			-0.98	0.03	
Atu3352	-	ABC transporter, substrate binding protein (sugar)			-1.02	0.03	
Atu3371	-	ABC transporter, nucleotide binding/ATPase protein (sugar)			-1.02	0.02	
Atu4410	<i>napC</i>	periplasmic nitrate reductase, cytochrome c-type protein	-1.00	0.01	-0.91	0.02	
Atu5023	-	hypothetical protein	-1.00	0.01			
Atu1126	<i>moaE</i>	molybdopterin converting factor, large subunit			-1.01	0.01	
Atu2370	-	hypothetical protein			-1.01	0.01	
Atu2224	<i>aldA</i>	aldehyde dehydrogenase			-1.00	0.04	*
Atu5123	<i>atrC</i>	acetolactate synthase catalytic subunit	-0.99	< 0.01			
Atu0526	<i>mclA</i>	methyl-accepting chemotaxis protein	-0.99	0.01	-0.94	0.02	
Atu1257	-	GGDEF family protein	-0.97	< 0.01			
Atu0580	<i>fliQ</i>	flagellar biosynthesis protein FliQ	-0.97	0.01	-0.75	0.02	
Atu3868	-	hypothetical protein	-0.95	0.02			
Atu2571	<i>acpP</i>	acyl carrier protein	-0.95	0.03			
Atu4667	-	ABC transporter, nucleotide binding/ATPase protein	-0.95	0.01			*
Atu3367	-	TRAP dicarboxylate transporter, DctM subunit	-0.95	0.01	-1.61	0.01	
Atu3832	-	hypothetical protein	-0.95	0.01			
Atu0544	-	hypothetical protein	-0.93	0.02	-0.87	0.03	*
Atu0477	-	hypothetical protein	-0.93	0.01			
Atu3298	<i>dctA</i>	C4-dicarboxylate transporter DctA			-0.93	0.04	
Atu3546	-	hypothetical protein	-0.92	0.01	-0.59	0.04	

Atu1717	<i>fadL</i>	long-chain fatty acid transport protein			-0.94	0.02	*
Atu0768	<i>coxA</i>	cytochrome-c oxidase chain I			-0.92	0.02	
Atu0771	<i>coxC</i>	cytochrome c oxidase subunit III			-0.96	0.02	*
Atu2238	<i>fbcB</i>	ubiquinol-cytochrome c reductase cytochrome b subunit			-0.92	0.02	
Atu2239	<i>fbcF</i>	ubiquinol-cytochrome C reductase iron-sulfur subunit			-0.76	0.03	
Atu2572	<i>acd</i>	acyl-CoA dehydrogenase	-0.91	0.01			
Atu1853	-	hypothetical protein			-0.91	0.02	
Atu0707	-	LuxR family transcriptional regulator	-0.90	0.01			
Atu4408	<i>napA</i>	nitrate reductase catalytic subunit	-0.90	0.02	-0.81	0.05	
Atu2136	<i>parA</i>	chromosome partitioning protein	-0.89	0.01	-0.84	0.04	
Atu2573	-	hypothetical protein	-0.88	0.01	-0.97	0.02	
Atu2489	-	hypothetical protein	-0.87	0.01	-0.89	0.04	
Atu2575	-	mannosidase	-0.86	0.01	-0.98	0.02	
Atu3575	<i>xylH</i>	ABC transporter, membrane spanning protein (xylose)			-0.85	0.03	*
Atu3503	-	ABC transporter, membrane spanning protein	-0.85	0.04			
Atu1577	-	ABC transporter, substrate binding protein (amino acid)	-0.84	0.01	-1.13	0.01	*
Atu0530	<i>galE</i>	UDP-galactose 4-epimerase	-0.84	0.02			
Atu1789	-	lipoprotein			-0.83	0.02	
Atu2601	<i>malE</i>	ABC transporter, substrate binding protein (maltose)			-0.83	0.03	
Atu4546	<i>pcaR</i>	IcIR family transcriptional regulator	-0.83	0.02			
Atu1769	<i>glnB</i>	nitrogen regulatory protein PII	-0.83	0.04			
Atu3244	-	GGDEF family protein	-0.83	< 0.01			
Atu2354	-	MarR family transcriptional regulator	-0.83	0.02	-1.09	0.02	
Atu3076	<i>uraA</i>	uracil transport protein	-0.83	0.01			
Atu4409	<i>napB</i>	periplasmic nitrate reductase small subunit	-0.82	< 0.01			
Atu1451	<i>hflx</i>	GTP-binding protein HFLX	-0.81	0.02			
Atu0223	<i>ctpB</i>	components of type IV pilus, prepilin peptidase	-0.81	0.03			
Atu4687	-	ABC transporter, substrate binding protein (amino acid)			-0.81	0.04	*
Atu1620	<i>tpiA</i>	triosephosphate isomerase	-0.81	0.02	-0.60	0.05	
Atu0343	<i>barA</i>	two component sensor kinase/response regulator hybrid	-0.81	0.05			
Atu2757	<i>glnK</i>	nitrogen regulatory protein PII	-0.80	0.02			

Atu0887	-	acetyltransferase	-0.79	0.01			*
Atu4407	<i>napD</i>	periplasmic nitrate reductase, NapD protein	-0.79	0.02	-0.91	0.04	
Atu0885	-	hypothetical protein	-0.79	0.01			
Atu0683	<i>groES</i>	co-chaperonin GroES	-0.78	0.02			
Atu4530	-	TetR family transcriptional regulator	-0.78	0.01			
Atu6094	-	hypothetical protein	-0.78	0.01			
Atu4406	<i>napF</i>	periplasmic nitrate reductase, ferredoxin-like protein	-0.78	0.02			
Atu2504	-	GntR family transcriptional regulator	-0.78	0.02			
Atu2229	-	ABC transporter, substrate binding protein (amino acid)	-0.77	0.02			
Atu2574	-	hypothetical protein	-0.77	0.01			
Atu3533	-	ABC transporter, substrate binding protein (sugar)			-0.76	0.04	
Atu0484	-	two component response regulator			-0.77	0.02	
Atu4443	-	hypothetical protein	-0.76	0.02			*
Atu3114	-	ABC transporter, substrate binding protein (sugar)	-0.76	0.02	-1.49	0.03	
Atu1339	<i>rne</i>	ribonuclease E			-0.75	0.04	
Atu2422	-	ABC transporter, substrate binding protein (amino acid)			-0.75	0.03	
Atu1691	-	GGDEF family protein	-0.75	0.02			
Atu1182	-	hypothetical protein	-0.74	0.02	-0.75	0.03	
Atu0836	<i>gst</i>	glutathione-S-transferase	-0.74	0.02			
Atu1786	<i>glmS</i>	glucosamine--fructose-6-phosphate aminotransferase	-0.74	0.03			
Atu0256	<i>rplT</i>	50S ribosomal protein L20	-0.73	0.03			
Atu3239	-	ABC transporter, substrate binding protein (sugar)	-0.73	0.02	-1.11	0.03	
Atu2371	<i>xynA</i>	endo-1,4-beta-xylanase	-0.73	0.04			
Atu4706	<i>nuoE</i>	formate dehydrogenase subunit gamma			-0.72	0.04	
Atu4707	<i>nuoF</i>	NADH ubiquinone oxidoreductase chain F			-0.74	0.04	
Atu4029	-	gluconolactonase precursor			-0.72	0.03	
Atu4113	<i>dppA</i>	ABC transporter, substrate binding protein (dipeptide)			-0.71	0.04	
Atu3118	-	hypothetical protein	-0.71	0.03			
Atu1060	-	two component response regulator	-0.71	0.05			
Atu3502	-	ABC transporter, membrane spanning protein	-0.70	0.03			
Atu0215	-	hypothetical protein			-0.73	0.04	
Atu0268	-	hypothetical protein			-0.67	0.03	
Atu0772	-	hypothetical protein	-0.70	0.03	-0.83	0.02	

Atu0204	-	hypothetical protein	-0.69	0.05			
Atu3206	-	hypothetical protein	-0.69	< 0.01			
Atu1757	-	hypothetical protein	-0.68	0.03	-1.00	0.02	
Atu3783	<i>gltD</i>	glutamate synthase subunit beta	-0.68	0.03			
Atu3330	<i>mclA</i>	methyl-accepting chemotaxis protein	-0.68	0.03	-0.76	0.03	
Atu2276	<i>braC</i>	ABC transporter, substrate binding protein (branched chain amino acid)			-0.68	0.03	
Atu2503	<i>dapA</i>	dihydrodipicolinate synthase	-0.68	0.02			
Atu1297	<i>pleD</i>	response regulator PleD	-0.68	0.03			
Atu4061	<i>exoX</i>	exopolysaccharide production repressor protein			-0.67	0.04	
Atu4062	-	hypothetical protein	-0.67	0.03			
Atu5120	-	hypothetical protein	-0.67	0.04			
Atu2336	-	hypothetical protein	-0.67	0.02	-0.72	0.04	
Atu0203	-	hypothetical protein	-0.66	0.03			
Atu3501	-	ABC transporter, nucleotide binding/ATPase protein	-0.66	0.04			
Atu1661	<i>sthA</i>	soluble pyridine nucleotide transhydrogenase	-0.66	0.03			
Atu4727	-	hypothetical protein			-0.66	0.04	
Atu2579	-	metal dependant beta lactamase protein	-0.65	0.03	-0.84	0.02	
Atu4668	-	ABC transporter, membrane spanning protein	-0.65	0.05			
Atu0669	-	hypothetical protein	-0.65	0.03			
Atu4525	-	ABC transporter, substrate binding protein (oligopeptide)	-0.65	0.01	-0.84	0.05	
Atu2726	<i>pycA</i>	pyruvate carboxylase	-0.65	0.03			
Atu5032	-	hypothetical protein			-0.65	0.03	
Atu2449	-	hypothetical protein			-0.64	0.04	
Atu3033	-	hypothetical protein	-0.64	0.03	-1.09	0.01	
Atu3784	<i>gltB</i>	glutamate synthase large subunit	-0.64	0.04			
Atu2642	<i>sdhB</i>	succinate dehydrogenase iron-sulfur subunit	-0.63	0.05			
Atu1454	<i>cysG</i>	siroheme synthase	-0.63	0.04			
Atu2644	<i>sdhD</i>	succinate dehydrogenase hydrophobic membrane anchor	-0.62	0.04			
Atu3772	-	hypothetical protein	-0.62	0.03	-0.94	0.02	
Atu3455	-	ABC transporter, substrate binding protein (oligopeptide)	-0.62	0.04	-1.13	0.02	
Atu1602	<i>fmrN</i>	Crp family transcriptional regulator			-0.62	0.05	

Atu1399	-	ABC transporter, substrate binding protein (amino acid)			-0.62	0.04	
Atu3272	<i>pssN</i>	exopolysaccharide export protein	-0.61	0.05			
Atu3462	-	AraC family transcriptional regulator	-0.61	0.05			
Atu3137	-	C4-dicarboxylate-binding protein	-0.61	0.05	-1.11	0.05	
Atu0581	<i>flhA</i>	flagellar biosynthesis protein FlhA	-0.61	0.05	-0.83	0.02	
Atu0758	<i>dnaJ</i>	DnaJ family molecular chaperone	-0.60	0.04			
Atu6132	<i>mcpA</i>	methyl-accepting chemotaxis protein	-0.60	0.05			*
Atu0458	-	hypothetical protein			-0.61	0.05	
Atu3635	-	amidohydrolase	-0.59	0.05			
Atu3253	-	ABC transporter, substrate binding protein	-0.59	0.04	-1.83	0.01	*
Atu4824	-	IclR family transcriptional regulator	-0.59	0.04			
Atu5030	-	hypothetical protein	-0.58	0.04			
Atu4476	-	hypothetical protein	-0.57	0.05			
Atu0883	-	hypothetical protein	-0.57	0.05			
Atu0148	-	hypothetical protein	-0.55	0.05			
Atu2440	-	hypothetical protein	0.56	0.05			
Atu1290	<i>lolD</i>	ABC transporter, nucleotide binding/ATPase protein (lipoprotein)			0.58	0.04	
Atu2188	-	oxidoreductase			0.57	0.05	
Atu2675	-	hypothetical protein			0.58	0.05	
Atu5431	-	hypothetical protein			0.59	0.05	
Atu2790	<i>leuD</i>	isopropylmalate isomerase small subunit	0.58	0.05			
Atu3580	<i>mutA</i>	methylmalonyl-CoA mutase	0.59	0.04			
Atu3712	-	hypothetical protein	0.59	0.04			
Atu0364	<i>rbsK</i>	ribokinase	0.59	0.05			
Atu0827	-	hypothetical protein	0.59	0.04			
Atu0169	<i>phnM</i>	hypothetical protein	0.59	0.04			
Atu0696	-	phosphatase			0.60	0.05	
Atu4642	<i>katA</i>	catalase	0.60	0.04			
Atu0803	<i>ppdK</i>	pyruvate phosphate dikinase	0.60	0.05			
Atu1499	<i>dac</i>	penicillin binding protein			0.61	0.05	
Atu3539	-	hypothetical protein	0.61	0.04			
Atu3749	<i>enhC</i>	enhanced entry protein	0.61	0.04	0.67	0.03	
Atu3274	-	AcrB/AcrD/AcrF family protein	0.61	0.04	0.70	0.03	*

Atu4068	<i>soxD</i>	sarcosine oxidase delta subunit	0.61	0.04		
Atu4230	<i>glnA</i>	glutamine synthetase III	0.62	0.04		
Atu1022	-	soluble lytic transglycosylase	0.62	0.03		
Atu4750	<i>dpe</i>	D-psicose 3-epimerase	0.62	0.05		
Atu3603	-	two component response regulator	0.63	0.04		
Atu1448	<i>ntrX</i>	two component response regulator	0.63	0.03	0.59	0.04
Atu6164	<i>tzs</i>	trans-zeatin secretion protein	0.63	0.04		
Atu3329	<i>bioA</i>	beta alanine--pyruvate transaminase	0.63	0.03		
Atu1915	-	htrA family protein			0.64	0.04
Atu2043	-	htrA family protein			0.63	0.04
Atu1104	<i>pdxA</i>	4-hydroxythreonine-4-phosphate dehydrogenase	0.64	< 0.01		
Atu2273	-	7-cyano-7-deazaguanine reductase	0.64	0.04		
Atu2123	<i>metF</i>	methylenetetrahydrofolate reductase	0.64	0.04		
Atu0454	-	hypothetical protein	0.65	0.04		
Atu3419	-	hippurate hydrolase	0.65	0.04		
Atu2415	-	glutamine synthetase translation inhibitor	0.65	0.02		
Atu2678	<i>ligT</i>	2'-5' RNA ligase	0.66	0.03		
Atu2054	-	AcrB/AcrD/AcrF family protein	0.66	0.02		
Atu2084	-	hypothetical protein	0.66	0.03		
Atu2159	<i>omp</i>	outer membrane protein			0.66	0.04
Atu2286	-	hypothetical protein			0.66	0.04
Atu2710	-	hypothetical protein			0.67	0.03
Atu3638	-	hypothetical protein			0.67	0.04
Atu3706	<i>serA</i>	D-3-phosphoglycerate dehydrogenase			0.67	0.04
Atu1144	<i>ppk</i>	polyphosphate kinase	0.67	0.02		
Atu0785	<i>rimJ</i>	ribosomal-protein (S5)-alanine N-acetyltransferase	0.67	0.02	1.06	0.02
Atu1879	-	ABC transporter, substrate binding protein (amino acid)	0.68	0.05		
Atu0691	-	hypothetical protein	0.68	0.02		
Atu1867	<i>murl</i>	glutamate racemase			0.68	0.03
Atu5137	<i>blcA</i>	NAD-dependent succinyl-semialdehyde dehydrogenase			0.69	0.03
Atu1175	-	hypothetical protein	0.68	0.02	0.70	0.04
Atu2399	-	hypothetical protein			0.70	0.05
Atu2610	-	hypothetical protein	0.70	0.02		

Atu5090	<i>rcdA</i>	Curdlan synthase	0.70	0.02			
Atu2097	<i>mraY</i>	phospho-N-acetylmuramoyl-pentapeptide-transferase			0.71	0.04	
Atu2029	-	hypothetical protein	0.71	0.02			
Atu2692	<i>ispZ</i>	intracellular septation protein A	0.71	0.02	0.83	0.02	
Atu1328	-	hypothetical protein	0.71	0.02	0.84	0.03	
Atu4352	-	hypothetical protein	0.72	0.04			
Atu2005	-	hypothetical protein	0.72	0.03	0.79	0.03	
Atu2485	-	hypothetical protein	0.72	0.02			
Atu4787	-	inositol monophosphatase family protein	0.72	0.02			
Atu1232	-	hypothetical protein	0.72	0.04			
Atu3758	-	hypothetical protein			0.60	0.05	
Atu3759	-	hypothetical protein			0.79	0.03	
Atu0007	<i>fxsA</i>	FxsA	0.72	0.02			
Atu0298	<i>pyrF</i>	orotidine 5'-phosphate decarboxylase			0.70	0.03	
Atu0349	<i>trpS</i>	tryptophanyl-tRNA synthetase			0.66	0.05	
Atu0356	<i>miaB</i>	(dimethylallyl)adenosine tRNA methylthiotransferase			0.87	0.02	
Atu1102	-	hypothetical protein			0.72	0.03	
Atu0444	-	hypothetical protein	0.72	0.02			
Atu2679	-	esterase	0.72	0.02	0.82	0.04	
Atu0032	-	hypothetical protein	0.72	0.03			
Atu3017	-	phosphoglyceromutase	0.72	0.03			
Atu1177	-	hypothetical protein			0.73	0.04	
Atu3425	-	hypothetical protein			0.73	0.05	
Atu4780	-	hypothetical protein	0.73	0.05			
Atu1219	-	hypothetical protein	0.73	0.02	1.65	0.01	*
Atu8161	-	hypothetical protein	0.73	0.02			
Atu8029	-	hypothetical protein	0.74	0.01			
Atu2193	-	hypothetical protein	0.74	0.01			
Atu6035	<i>trbL</i>	conjugal transfer protein TrbL	0.74	0.04			
Atu2098	<i>murF</i>	UDP-MurNAc-pentapeptide synthetase	0.74	0.02			
Atu3015	-	hypothetical protein	0.75	0.03			
Atu2133	-	hypothetical protein	0.75	0.02			
Atu1554	-	hypothetical protein			0.75	0.05	
Atu2638	<i>sucC</i>	succinyl-CoA synthetase subunit beta			0.76	0.05	

Atu4325	<i>cbr</i>	short chain dehydrogenase	0.76	0.02	0.75	0.03	
Atu3616	-	hypothetical protein	0.77	0.03	0.97	0.04	
Atu1099	-	hypothetical protein	0.77	0.01	1.04	0.02	
Atu3715	<i>tolA</i>	hypothetical protein	0.77	0.02			
Atu3332	-	hypothetical protein	0.78	0.01	0.92	0.04	
Atu4745	-	ABC transporter, nucleotide binding/ATPase protein (sugar)	0.78	0.01			
Atu0448	-	hypothetical protein	0.78	0.01			
Atu1105	-	hypothetical protein	0.78	0.01	0.78	0.03	
Atu4318	-	xylitol dehydrogenase	0.78	0.01			
Atu4324	-	ribitol kinase			0.78	0.02	
Atu1447	<i>ntrY</i>	two component sensor kinase			0.79	0.03	
Atu1018	-	hypothetical protein			0.79	0.03	
Atu2447	<i>purA</i>	adenylosuccinate synthetase			0.79	0.02	
Atu4486	-	nitroreductase			0.79	0.04	
Atu0633	-	hypothetical protein	0.79	0.01	0.55	0.05	
Atu0800	-	hypothetical protein	0.79	0.01	0.92	0.02	
Atu2428	<i>pssB</i>	exopolysaccharide production protein PssB	0.80	0.04	0.65	0.05	
Atu3602	-	hypothetical protein	0.80	0.01			
Atu0461	-	hypothetical protein	0.80	0.01			
Atu4037	<i>gcd</i>	glucose dehydrogenase			0.80	0.03	
Atu1299	<i>rpmG</i>	50S ribosomal protein L33			0.81	0.02	
Atu2262	-	hypothetical protein	0.81	0.02			
Atu1225	-	hypothetical protein	0.82	0.01			
Atu5091	<i>rcdB</i>	Curdlan synthesis protein	0.82	0.01			
Atu1222	-	hypothetical protein	0.82	0.02			
Atu8183	-	hypothetical protein	0.83	0.02			
Atu4351	-	hypothetical protein	0.83	0.02			
Atu3493	-	non-heme haloperoxidase	0.83	0.01	0.63	0.04	
Atu0538	-	hypothetical protein	0.83	0.01	0.79	0.02	
Atu2249	-	hypothetical protein	0.83	0.02			*
Atu2522	<i>acvB</i>	chromosomal virulence protein B	0.83	0.01	0.74	0.03	
Atu3973	-	hypothetical protein	0.83	0.03			
Atu1227	-	hypothetical protein	0.83	0.03	1.11	0.02	

Atu0766	<i>ialB</i>	invasion associated locus B	0.84	0.01	0.83	0.02	
Atu3196	<i>speF</i>	ornithine decarboxylase			0.85	0.02	
Atu0870	<i>tam</i>	trans-aconitate 2-methyltransferase	0.85	0.01			
Atu2439	-	hypothetical protein	0.85	0.02	0.87	0.03	
Atu1919	-	putative sulfite oxidase subunit YedY	0.86	0.02			
Atu3741	-	MFS permease	0.86	0.02			
Atu2099	<i>murE</i>	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	0.86	0.01	0.85	0.03	
Atu4059	<i>exoV</i>	succinoglycan biosynthesis protein	0.87	0.02	0.84	0.04	*
Atu3642	<i>vgrG</i>	vgrG protein	0.87	0.02	1.06	0.01	
Atu1373	-	hypothetical protein			0.89	0.04	
Atu1377	<i>frr</i>	ribosome recycling factor			0.85	0.02	
Atu1658	<i>cgmA</i>	cyclic glucan phosphoglycerol modification protein	0.87	0.03			
Atu0628	-	two component sensor kinase	0.87	0.05			
Atu3713	<i>palA</i>	omp16 protein	0.88	0.01			
Atu6151	<i>virH2</i>	P-450 monooxygenase	0.90	0.01			*
Atu8182	-	hypothetical protein			0.88	0.03	
Atu4014	<i>exsI</i>	transcriptional regulator	0.90	0.01	1.41	0.01	*
Atu0297	-	hypothetical protein	0.90	0.01	0.81	0.04	
Atu0811	<i>mgo</i>	malate:quinone oxidoreductase			0.90	0.04	*
Atu0064	<i>frcC</i>	ABC transporter, membrane spanning protein (sugar)	0.90	0.02			
Atu4321	<i>rbsA</i>	ABC transporter, nucleotide binding/ATPase protein (ribose)	0.90	0.01	1.01	0.01	
Atu3704	-	hypothetical protein	0.91	0.01	0.86	0.02	
Atu4744	-	ABC transporter, substrate binding protein (sugar)	0.92	0.01			
Atu3608	-	hypothetical protein	0.93	0.01			
Atu3716	<i>tolR</i>	tolR protein	0.93	0.01	0.95	0.02	
Atu0065	<i>frcA</i>	ABC transporter, nucleotide binding/ATPase protein (sugar)	0.93	0.01			
Atu4785	<i>afuB</i>	ABC transporter, membrane spanning protein (iron)	0.93	0.01			
Atu2722	<i>ompA</i>	porin	0.94	0.01	0.92	0.02	
Atu0044	<i>hslV</i>	ATP-dependent protease peptidase subunit			0.95	0.03	
Atu0045	<i>hslU</i>	ATP-dependent protease ATP-binding subunit HslU			0.84	0.03	
Atu0046	-	hypothetical protein			0.61	0.04	
Atu2445	<i>rpoH</i>	RNA polymerase factor sigma-32			0.95	0.02	

Atu2521	<i>lpiA</i>	protein regulated by acid pH	0.95	0.01			
Atu5490	<i>ecfR</i>	ECF family RNA polymerase sigma factor	0.95	0.01			
Atu0457	-	hypothetical protein	0.95	0.01			
Atu1164	-	hypothetical protein	0.96	0.01	1.05	0.03	
Atu4498	-	hypothetical protein	0.96	0.01			
Atu1333	-	outer membrane protein	0.96	0.01	1.16	0.02	
Atu3639	-	hypothetical protein	0.97	0.01			
Atu3606	<i>ftsE</i>	cell division ATP-binding protein	0.97	0.01			
Atu4349	-	acyl carrier protein	0.98	0.01	1.05	0.04	
Atu1633	<i>kefA</i>	potassium efflux system KEFA	0.98	< 0.01	1.08	0.02	
Atu4038	-	hypothetical protein	0.99	0.01			
Atu3717	<i>tolQ</i>	tolQ protein	1.00	< 0.01	0.92	0.02	
Atu3643	-	hypothetical protein	1.02	0.03			
Atu8200	-	hypothetical protein	1.02	< 0.01			
Atu0906	-	hemolysin III	1.02	0.01			
Atu2774	-	carboxy-terminal protease	1.03	< 0.01	0.86	0.02	
Atu0186	<i>mepA</i>	penicillin-insensitive murein endopeptidase	1.03	< 0.01			
Atu3016	<i>gpmB</i>	phosphoglyceromutase	1.03	0.01			
Atu3126	-	hypothetical protein	1.04	0.02			
Atu8176	-	hypothetical protein	1.05	0.01			
Atu0361	-	transcriptional regulator	1.06	0.01	1.14	0.01	
Atu3538	-	hypothetical protein	1.07	< 0.01	1.04	0.01	
Atu1621	-	hypothetical protein	1.07	< 0.01	1.00	0.01	
Atu6150	<i>virH1</i>	P-450 monooxygenase	1.07	< 0.01			*
Atu4177	<i>clpB</i>	ATP-dependent Clp protease, ATP-binding subunit			1.07	0.01	
Atu4322	<i>rbsC</i>	ABC transporter, membrane spanning protein (ribose)	1.07	0.01	1.06	0.01	*
Atu4348	<i>vgrG</i>	VgrG protein	1.07	< 0.01	0.99	0.05	
Atu3641	-	hypothetical protein	1.08	0.01	1.12	0.01	
Atu1500	<i>rlpA</i>	rare lipoprotein A	1.08	< 0.01	1.05	0.02	
Atu2122	<i>mltB</i>	lytic murein transglycosylase	1.09	< 0.01	1.23	0.02	
Atu4319	-	AraC family transcriptional regulator			1.09	0.01	*
Atu0033	<i>chvG</i>	two component sensor kinase	1.11	< 0.01	1.17	0.02	*
Atu2272	-	hypothetical protein	1.11	< 0.01	0.94	0.03	*
Atu0299	-	hypothetical protein	1.13	0.01	1.20	0.02	

Atu1545	-	hypothetical protein	1.14	< 0.01	1.17	0.02	
Atu0998	<i>bacA</i>	undecaprenyl pyrophosphate phosphatase	1.14	< 0.01	1.32	0.03	
Atu0539	<i>murA</i>	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	1.15	< 0.01			
Atu2064	-	hypothetical protein	1.16	0.01	1.32	0.02	
Atu1852	-	hypothetical protein	1.16	< 0.01	1.08	0.01	
Atu2711	-	hypothetical protein	1.16	0.01	1.27	0.02	*
Atu8017	-	hypothetical protein	1.16	< 0.01			
Atu2557	-	hypothetical protein	1.17	0.01			
Atu4784	<i>afuA</i>	ABC transporter, substrate binding protein (iron)	1.17	< 0.01			
Atu8171	-	hypothetical protein	1.18	0.04			
Atu3519	<i>ppiD</i>	peptidyl-prolyl cis-trans isomerase	1.18	< 0.01	1.13	0.01	
Atu5545	-	hypothetical protein	1.18	< 0.01			
Atu0900	-	hypothetical protein	1.19	< 0.01	0.98	0.01	
Atu3610	-	transporter	1.19	0.01	0.84	0.02	
Atu2823	<i>purH</i>	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	1.19	< 0.01	0.78	0.03	
Atu4323	<i>rdh</i>	ribitol 2-dehydrogenase	1.19	< 0.01	1.40	0.03	
Atu1724	-	hypothetical protein	1.19	0.01			
Atu3634	<i>dacF</i>	penicillin-binding protein dacF precursor	1.20	< 0.01	0.87	2.00	
Atu1741	-	hypothetical protein	1.21	0.02	0.96	0.02	
Atu3778	<i>galU</i>	UTP-glucose-1-phosphate uridylyltransferase	1.21	< 0.01	0.77	0.02	
Atu4344	<i>clpB</i>	ATP-dependent Clp protease, ATP-binding subunit	1.23	< 0.01	1.35	0.02	
Atu1341	<i>mrcA</i>	penicillin-binding protein 1a			1.21	0.01	
Atu5489	-	hypothetical protein	1.23	< 0.01			
Atu2257	-	hypothetical protein			1.24	0.01	*
Atu3081	-	hypothetical protein	1.26	< 0.01			
Atu4330	<i>impN</i>	serine/threonine protein kinase	1.27	< 0.01	1.10	0.02	
Atu5484	-	hypothetical protein	1.28	< 0.01			
Atu0488	-	hypothetical protein	1.30	< 0.01	0.95	0.02	
Atu2303	-	hypothetical protein	1.34	< 0.01	1.02	0.02	
Atu1969	-	hypothetical protein	1.34	< 0.01			
Atu4175	<i>hemK</i>	protoporphyrinogen oxidase	1.35	< 0.01	1.47	0.01	
Atu2444	-	hypothetical protein	1.35	0.01			
Atu2254	-	hypothetical protein	1.35	< 0.01	1.40	0.01	

Atu1877	-	OmpA family protein	1.36	< 0.01	0.79	0.03	
Atu0881	-	cytochrome C-556	1.39	< 0.01			*
Atu1666	-	hypothetical protein	1.39	0.01			
Atu1762	-	hypothetical protein	1.40	0.01	1.34	0.01	
Atu4638	-	two component response regulator	1.41	< 0.01			
Atu2611	-	hypothetical protein	1.41	0.01	0.80	0.02	*
Atu3714	<i>tolB</i>	translocation protein TolB	1.42	< 0.01	1.18	0.03	
Atu0063	<i>frcB</i>	ABC transporter, substrate binding protein (sugar)	1.43	< 0.01			
Atu2789	-	hypothetical protein	1.45	< 0.01	0.79	0.02	
Atu1805	-	hypothetical protein	1.47	< 0.01			*
Atu2421	-	chitooligosaccharide deacetylase	1.48	< 0.01			
Atu2760	-	hypothetical protein	1.48	< 0.01	1.07	0.01	
Atu1773	-	hypothetical protein	1.49	< 0.01	1.16	0.02	
Atu1716	-	hypothetical protein	1.50	< 0.01	1.68	0.01	
Atu0755	-	hypothetical protein	1.50	0.01	1.04	0.02	
Atu0898	-	hypothetical protein	1.52	0.01	1.71	0.01	
Atu0824	-	hypothetical protein	1.57	< 0.01			
Atu1667	-	hypothetical protein	1.59	< 0.01			*
Atu1155	-	hypothetical protein			1.65	0.01	
Atu5449	<i>hspAT2</i>	heat-shock protein			1.88	0.05	*
Atu5450	-	hypothetical protein			1.34	0.01	
Atu0875	-	hypothetical protein	1.65	< 0.01	1.11	0.02	
Atu4058	<i>exoW</i>	succinoglycan biosynthesis protein	1.66	< 0.02	1.75	0.01	*
Atu2253	<i>moxR</i>	MoxR family protein	1.66	< 0.01	0.98	0.02	
Atu1061	-	hypothetical protein	1.66	0.02			
Atu2157	-	tyrosine/serine protein phosphatase	1.67	< 0.01	1.71	0.01	
Atu1745	-	hypothetical protein	1.68	< 0.01	0.83	0.02	
Atu4640	-	hypothetical protein	1.69	0.01			
Atu4347	-	hypothetical protein	1.69	< 0.01	1.33	0.01	
Atu6162	-	hypothetical protein	1.71	0.01	1.09	0.02	
Atu0300	-	methyltransferase	1.71	< 0.01	1.16	0.03	
Atu4499	-	hypothetical protein	1.72	< 0.01	1.59	0.01	*
Atu5052	<i>hspAT1</i>	small heat shock protein			1.72	0.01	*
Atu4053	<i>exoA</i>	succinoglycan biosynthesis protein	1.73	< 0.01			

Atu0381	-	hypothetical protein	1.73	0.01	1.76	0.04	
Atu4057	<i>exoT</i>	succinoglycan biosynthesis transport protein	1.74	< 0.01	1.74	0.01	*
Atu4346	-	hypothetical protein	1.76	< 0.01	1.51	0.02	
Atu4060	<i>exoU</i>	succinoglycan biosynthesis glycosyltransferase	1.77	< 0.01	1.82	0.01	*
Atu4051	<i>exoO</i>	succinoglycan biosynthesis glycosyltransferase	1.79	< 0.01	0.90	0.03	
Atu1031	-	hypothetical protein	1.82	0.02			*
Atu4332	<i>impL</i>	IcmF family protein	1.88	< 0.01	1.53	0.03	
Atu0933	-	beta-lactamase class D	1.89	< 0.01	1.48	0.01	
Atu0943	-	hypothetical protein	1.90	0.02	1.43	0.04	
Atu4345	-	hypothetical protein	1.91	< 0.01			
Atu4055	<i>exoK</i>	endo-1,3-1,4-beta-glycanase	1.93	< 0.01	2.21	0.01	*
Atu4333	<i>impK</i>	OmpA-like porin	1.93	< 0.01	1.45	0.01	
Atu4331	<i>impM</i>	serine/threonine phosphoprotein phosphatase	1.93	< 0.01	1.49	0.01	
Atu4054	<i>exoL</i>	succinoglycan biosynthesis protein	1.93	< 0.01	1.98	0.01	*
Atu4056	<i>exoH</i>	succinoglycan biosynthesis protein	1.97	< 0.01	2.36	0.01	*
Atu0034	<i>chvI</i>	two component response regulator	1.97	< 0.01	1.84	0.01	*
Atu4049	<i>exoP</i>	exopolysaccharide polymerization/transport protein	2.01	< 0.01	1.38	0.01	*
Atu4335	<i>impl</i>	putative forkhead-type phosphopeptide-binding protein	2.01	< 0.01	1.75	0.01	*
Atu3325	<i>exoQ</i>	exopolysaccharide production protein	2.03	< 0.01	1.70	0.01	*
Atu4166	<i>galE/exoB</i>	UDP-glucose 4-epimerase	2.04	< 0.01	1.77	0.01	
Atu3991	<i>copA</i>	multicopper oxidase	2.05	0.03			
Atu2775	-	hypothetical protein	2.06	< 0.01	1.90	0.01	
Atu4052	<i>exoM</i>	UDP-hexose transferase	2.11	< 0.01	1.58	0.01	*
Atu1150	-	hypothetical protein	2.13	< 0.01	1.36	0.02	*
Atu4336	<i>impH</i>	hypothetical protein	2.14	< 0.01	1.00	0.01	
Atu3738	-	potassium/proton antiporter	2.14	< 0.01	1.19	0.04	
Atu4334	<i>impJ</i>	hypothetical protein	2.17	< 0.01	1.66	< 0.01	*
Atu4338	<i>impF</i>	hypothetical protein	2.19	< 0.01	1.96	0.01	*
Atu3540	-	hypothetical protein	2.20	0.01	1.56	0.05	
Atu2160	-	hypothetical protein	2.24	< 0.01	1.90	0.01	*
Atu4339	<i>impE</i>	hypothetical protein	2.28	< 0.01	1.83	0.01	
Atu2162	<i>pp26</i>	periplasmic immunogenic protein	2.30	< 0.01	2.06	0.01	
Atu0365	<i>rmuC</i>	RmuC domain protein	2.30	< 0.01	1.87	0.02	*
Atu4337	<i>impG</i>	hypothetical protein	2.30	< 0.01	1.89	0.01	*

Atu0841	-	amino peptidase family protein	2.38	< 0.01	1.96	0.00	*
Atu4343	<i>impA</i>	hypothetical protein	2.38	< 0.01	2.23	0.01	*
Atu0290	-	rare lipoprotein A	2.44	< 0.01	2.34	0.01	*
Atu4342	<i>impB</i>	hypothetical protein	2.49	< 0.01	2.01	0.03	*
Atu3326	<i>exoF</i>	exopolysaccharide production protein	2.65	< 0.01	2.40	0.03	
Atu4340	<i>impD</i>	hypothetical protein	2.66	< 0.01	2.06	0.01	*
Atu4341	<i>impC</i>	hypothetical protein	2.67	< 0.01	2.21	0.01	*
Atu4026	-	hypothetical protein	2.81	< 0.01	2.53	0.01	
Atu2112	<i>slt</i>	soluble lytic transglycosylase	2.87	< 0.01	1.49	0.03	
Atu3752	-	hypothetical protein	2.88	< 0.01	1.85	0.02	
Atu0944	<i>cscA</i>	sucrose hydrolase	2.90	< 0.01	2.37	0.03	*
Atu4050	<i>exoN</i>	UTP-glucose-1-phosphate uridylyltransferase	2.91	< 0.01	2.14	0.01	*
Atu6178	<i>virG</i>	two-component response regulator VirG	3.35	< 0.01	3.12	0.01	*
Atu3327	<i>exoY</i>	succinoglycan exopolysaccharide synthesis protein	3.80	< 0.01	3.32	0.03	*
Atu2198	-	hypothetical protein	3.82	< 0.01	2.37	0.01	*
Atu1131	<i>aopB</i>	outer membrane protein	4.99	< 0.01	4.66	0.03	*
Atu1221	-	hypothetical protein	5.25	< 0.01	4.85	0.01	*

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