

CORRECTION

# Correction: Characterization of the Rel<sub>Bbu</sub> Regulon in *Borrelia burgdorferi* Reveals Modulation of Glycerol Metabolism by (p)ppGpp

The *PLOS ONE* Staff

There are formatting errors in [Table 1](#). Please see the corrected [Table 1](#) here:



## OPEN ACCESS

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**Table 1. Modulated selected genes with annotated function in *B. burgdorferi* 297  $\Delta rel_{Bbu}$  during growth in vitro at 34°C<sup>a</sup>.**

Gene	Description	Exponential phase		Stationary phase	
		Mean expression(log <sub>2</sub> [ $\Delta rel_{Bbu}$ /WT])	P	Mean expression(log <sub>2</sub> [ $\Delta rel_{Bbu}$ /WT])	P
<b>Transcriptional regulators</b>					
BB0168	<i>dnaK</i> suppressor ( <i>dksA</i> )	1.31	0.002	3.26	<0.001
BB0419	response regulatory protein ( <i>rrp-1</i> )			1.42	0.001
BB0420	sensory transduction histidine kinase/response regulator ( <i>hk1</i> )	2.65	0.001	2.39	<0.001
BB0712	RNA polymerase $\sigma^{70}$ factor ( <i>rpoD</i> )	<b>1.05</b>	<b>0.013</b>	2.19	<0.001
<b>DNA synthesis/repair</b>					
BB0022	Holliday junction DNA helicase ( <i>ruvB</i> )			2.58	<0.001
BB0344	DNA helicase ( <i>uvrD</i> )			2.79	0.006
BB0438	DNA polymerase III, $\beta$ subunit ( <i>dnaN</i> )	2.41	0.006	1.56	<0.001
BB0552	DNA ligase ( <i>lig</i> )			2.64	0.010
BB0579	DNA polymerase III, $\alpha$ subunit ( <i>dnaE</i> )			4.95	0.001
BB0710	DNA primase ( <i>dnaG</i> ), authentic frameshift	1.26	<0.001	1.33	<0.001
BB0836	excinuclease ABC, B subunit ( <i>uvrB</i> )			2.35	<0.001
BB0837	excinuclease ABC, A subunit ( <i>uvrA</i> )			1.04	0.003
<b>Cell division</b>					
BB0177	glucose inhibited division protein B ( <i>gidB</i> )			3.81	0.007
BB0178	glucose inhibited division protein A ( <i>gidA</i> )			3.07	0.005
BB0302	cell division protein ( <i>ftsW</i> )			2.96	0.001
BB0781	GTP-binding protein ( <i>obg</i> )	1.03	0.004	1.95	<0.001
BB0789	cell division protein ( <i>ftsH</i> )			1.01	<0.001
<b>Protein synthesis</b>					
BB0229	ribosomal protein L31 ( <i>rpmE</i> )			1.54	<0.001
BB0251	leucyl-tRNA synthetase ( <i>leuS</i> )			3.41	<0.001
BB0514	phenylalanyl-tRNA synthetase, $\beta$ subunit ( <i>pheT</i> )			1.63	0.009
BB0615	ribosomal protein S4 ( <i>rpsD</i> )			2.87	<0.001
BB0691	translation elongation factor G ( <i>fus-2</i> )			0.96	0.001
BB0778	ribosomal protein L21 ( <i>rpL1</i> )			1.51	0.002
BB0780	ribosomal protein L27 ( <i>rpmA</i> )			1.03	<0.001
<b>Motility/chemotaxis</b>					
BB0147	flagellar filament 41 kDa core protein ( <i>flaB</i> )			-1.31	0.001
BB0181	flagellar hook-associated protein ( <i>flgK</i> )			-1.14	0.010
BB0271	flagellar biosynthesis protein ( <i>flhA</i> )			1.95	0.002
BB0578	methyl-accepting chemotaxis protein ( <i>mcp-1</i> )			3.06	0.012
BB0668	flagellar filament outer layer protein ( <i>flaA</i> )			-1.13	<0.001
BB0670	purine-binding chemotaxis protein ( <i>cheW-3</i> )			2.03	0.011
BB0775	flagellar hook-basal body complex protein ( <i>flhO</i> )			1.03	<0.001
<b>Cell envelope</b>					
BB0382 <sup>d</sup>	basic membrane protein B ( <i>bmpB</i> )	-1.02	0.012	-1.59	<0.001
BB0383	basic membrane protein A ( <i>bmpA</i> )			-1.15	0.016
BB0385	basic membrane protein D ( <i>bmpD</i> )	-2.93	0.007		
BBA15	outer surface protein A ( <i>ospA</i> )			-1.81	0.001
BBA16	outer surface protein B ( <i>ospB</i> )			-1.54	0.002
BBA60	surface lipoprotein P27			-5.07	<0.001
BBA74	membrane-associated periplasmic protein			-2.03	<0.001

(Continued)

Table 1. (Continued)

Gene	Description	Exponential phase		Stationary phase	
		Mean expression(log <sub>2</sub> [ $\Delta$ rel <sub>Bbu</sub> /WT])	P	Mean expression(log <sub>2</sub> [ $\Delta$ rel <sub>Bbu</sub> /WT])	P
BBB07	$\alpha$ 3 $\beta$ 1 integrin-binding protein	<b>1.42</b>	<0.001		
BBJ41	antigen P35, putative			-8.62	<0.001
BBM23 <sup>b</sup>	holin ( <i>blyA</i> )	<b>1.74</b>	<0.001	1.43	<0.001
BBN24 <sup>c</sup>	holin ( <i>blyB</i> )	2.99	<0.001	1.17	<0.001
<b>Central metabolism/carbon source transporters</b>					
BB0240	glycerol uptake facilitator ( <i>glpF</i> )	-4.54	<0.001	-4.76	<0.001
BB0241	glycerol kinase ( <i>glpK</i> )	-8.27	<0.001	-5.47	<0.001
BB0243	glycerol-3-phosphate dehydrogenase ( <i>glpD</i> )	-6.52	<0.001	-3.79	<0.001
BB0328	oligopeptide ABC transporter, periplasmic oligopeptide-binding protein ( <i>oppA-1</i> )	-1.16	0.001	-2.65	0.002
BB0329	oligopeptide ABC transporter, periplasmic oligopeptide-binding protein ( <i>oppA-2</i> )			-1.33	<0.001
BB0330	oligopeptide ABC transporter, periplasmic oligopeptide-binding protein ( <i>oppA-3</i> )			-4.07	0.015
BB0334	oligopeptide ABC transporter, ATP-binding protein ( <i>oppD</i> )	-3.25	0.006	-1.21	0.002
BB0335	oligopeptide ABC transporter, ATP-binding protein ( <i>oppF</i> )			-1.51	<0.001
BBB04	chitobiose transporter protein ( <i>chbC</i> )	1.83	0.004	2.11	<0.001
BBB05	chitobiose transporter protein ( <i>chbA</i> )	4.05	0.013	5.07	<0.001
BBB06	chitobiose transporter protein ( <i>chbB</i> )			5.02	<0.001
BB0683	3-hydroxy-3-methylglutaryl-CoA synthase ( <i>hmgS</i> )	1.23	0.010	1.65	<0.001
BB0685	3-hydroxy-3-methylglutaryl-CoA reductase ( <i>mvaA</i> )	<b>1.36</b>	<0.001	4.39	<0.001

<sup>a</sup>Transcriptional analysis from microarrays (regular font) or RT-PCR (boldface). Where data from RT-PCR is shown, microarrays showed no significant difference in gene expression between *B. burgdorferi* 297  $\Delta$ rel<sub>Bbu</sub> and wild type.

<sup>b</sup>Expression values for *blyA* orthologs BBM23, BBP23, BBR23 that showed increased expression in stationary phase and BBN23, BBR23 and BBS23 that showed increased expression in exponential phase were considered as a single transcript because they are 100% identical in sequence.

<sup>c</sup>Expression values for *blyB* orthologs BBN24, BBR24, BBS24 that showed increased expression in stationary phase and BBN24, BBR24, and BBS23 that showed increased expression in exponential phase were considered as a single transcript because they are 100% identical in sequence.

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## Reference

1. Bugrysheva JV, Pappas CJ, Terekhova DA, Iyer R, Godfrey HP, Schwartz I, et al. (2015) Characterization of the Rel<sub>Bbu</sub> Regulon in *Borrelia burgdorferi* Reveals Modulation of Glycerol Metabolism by (p) ppGpp. PLoS ONE 10(2): e0118063. doi: [10.1371/journal.pone.0118063](https://doi.org/10.1371/journal.pone.0118063) PMID: [25688856](https://pubmed.ncbi.nlm.nih.gov/25688856/)