

CORRECTION

# Correction: Unusually Situated Binding Sites for Bacterial Transcription Factors Can Have Hidden Functionality

PLOS ONE staff

A formatting error was introduced into Table 3 during article production. Please view the correct table here. The publisher apologizes for the error.

**Table 3. Phylogentic distribution of DUF1602-containing proteins**

Kingdom/Species	Number of DUF1602-containing proteins
<i>Archaea (all Euryarchaeota)</i>	5
<b>Bacteria:</b>	<b>146</b>
<i>Actinobacteria</i>	20
<i>Chlamydiae</i> :	2
<i>Cyanobacteria</i> :	2
<i>Firmicutes</i> :	18
<i>Proteobacteria</i> :	100
<b>Eukaryotes</b>	<b>59</b>
<i>Fungi</i> :	14
<i>Metazoa</i> :	1
<i>Chlorophyta</i> :	1
<i>Streptophyta</i> :	43
<b>Unclassified sequences</b>	<b>4</b>

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## Reference

1. Haycocks JRJ, Grainger DC (2016) Unusually Situated Binding Sites for Bacterial Transcription Factors Can Have Hidden Functionality. PLoS ONE 11(6): e0157016. doi:10.1371/journal.pone.0157016 PMID: 27258043



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