Supplementary Data

Distinct GDP/GTP Bound States of the Tandem G-Domains of EngA Regulate Ribosome Binding

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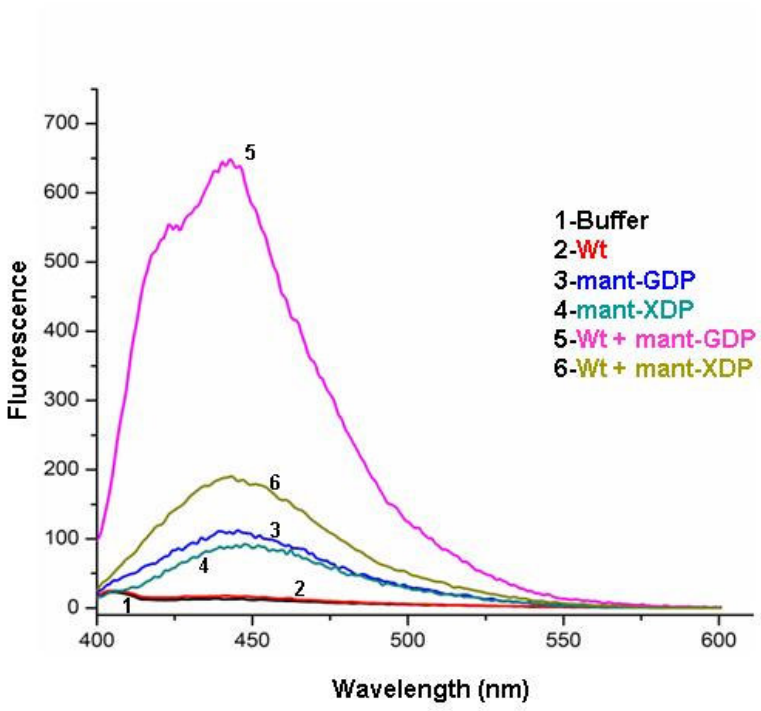

Fig.S1. **Nucleotide binding to wt EngA (*E.coli*).** Nucleotide binding was assayed by recording emission spectra (λ_{ex} 355 nm) upon incubating 8 µM of *E.coli* EngA with 0.4 µM fluorescent mant-nucleotides (mant-GDP or mant-XDP). Spectra corresponding to various nucleotide bound forms of the protein are indicated in different colors and numbers, Emission spectra indicate that wt EngA binds preferentially to mant-GDP.

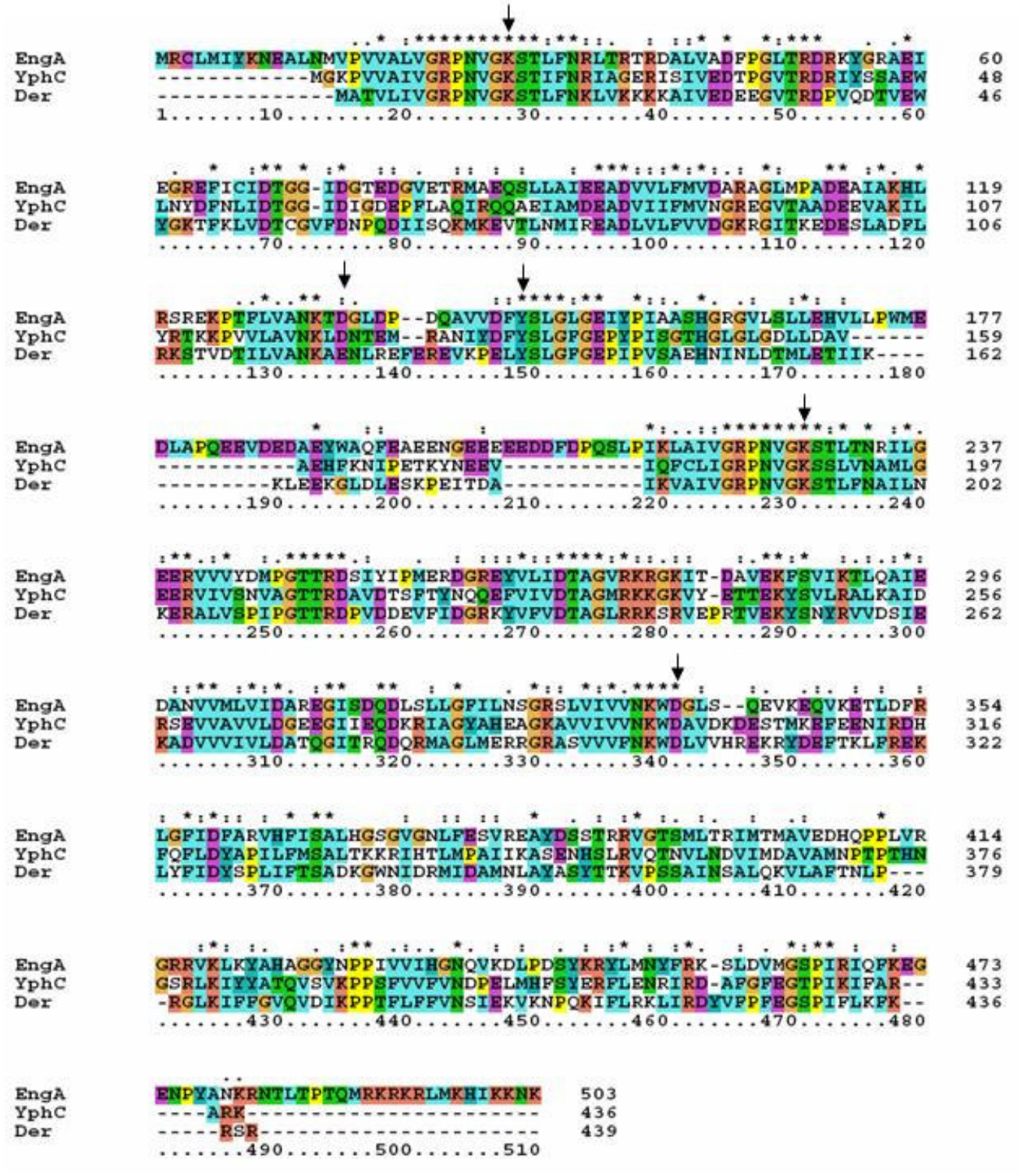

Fig.S2. **Multiple sequence alignment of EngA (*E. coli*), YphC (*B. subtilis)* and Der (*T. maritima)*.** Sequences were aligned using Clustalx (1). The residues mutatated in this study are indicated by arrows. Residues are 1 – 207 and 217 – 385 constitute the domains GD1 and GD2 of EngA.

References:

1. Thompson, J. D., Gibson, T. J., Plewniak, F., Jeanmougin, F. and Higgins, D.G. (1997) The CLUSTAL_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucl. Acids Res.*, **25**, 4876-4882.