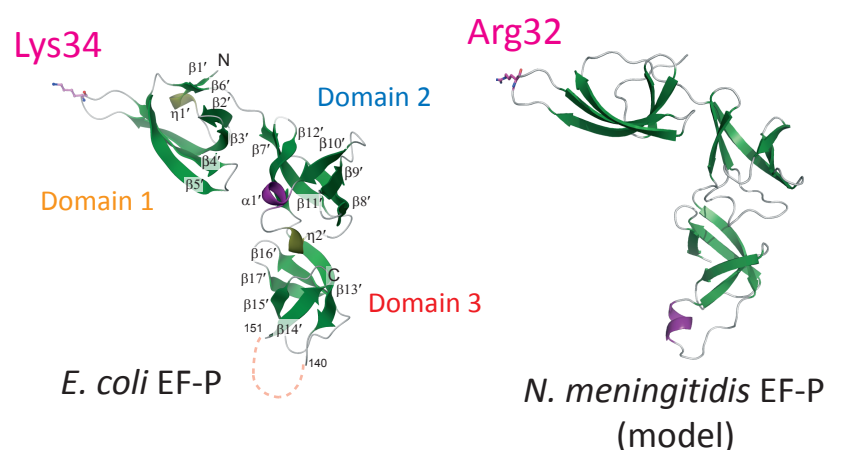
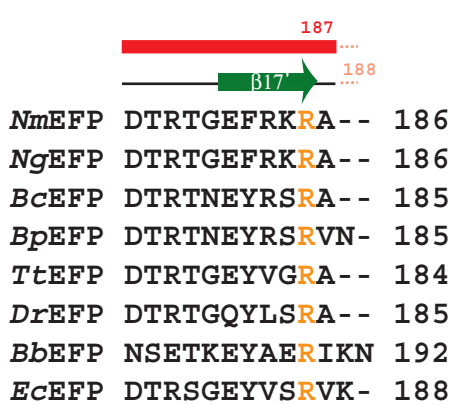
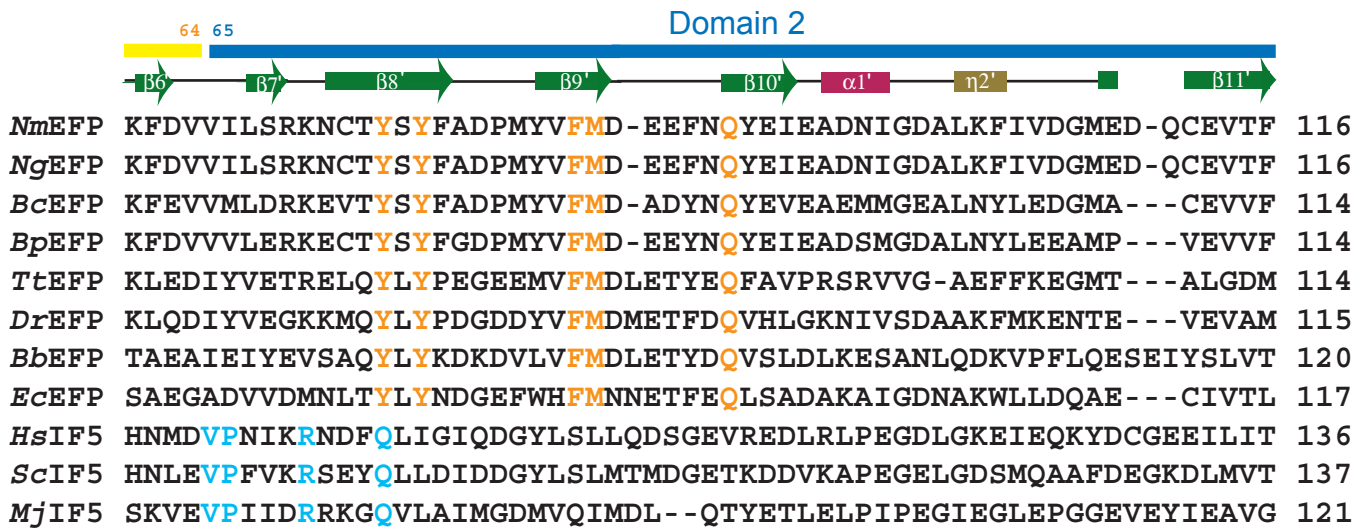
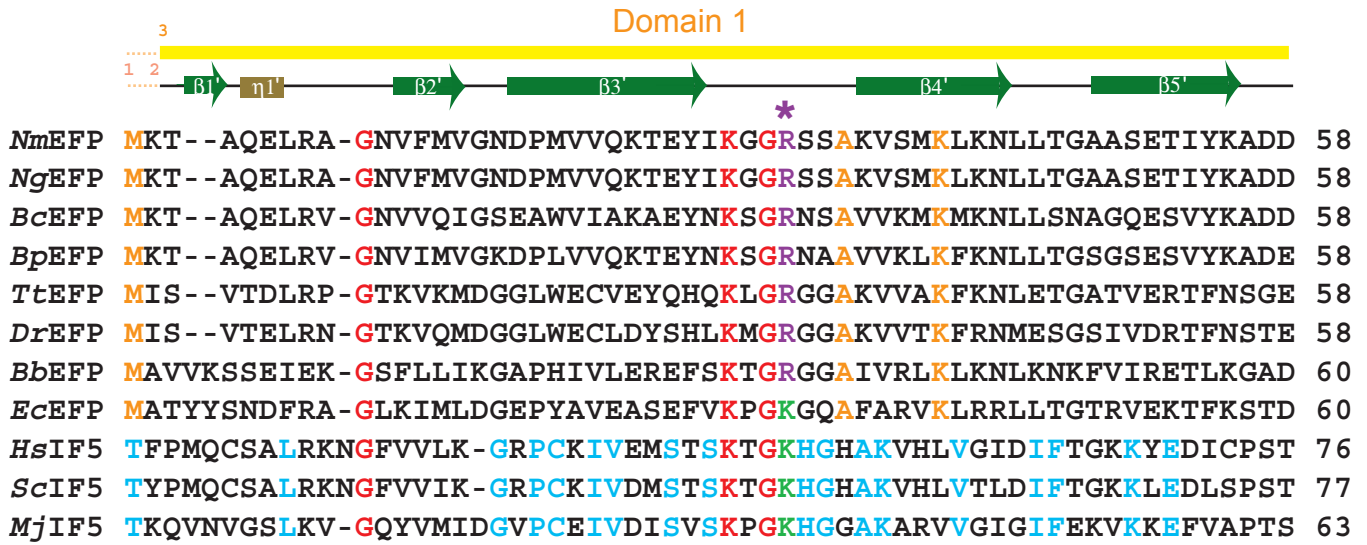


# Yanagisawa *et al.*, Fig. S2



## Fig. S2. Structure-based sequence alignment of EF-P and a/eIF5A

The amino acid sequences were aligned using the program CLUSTAL W (56), and then partly optimized and adjusted manually. Highly conserved residues between EF-P and a/eIF5A are colored red. Highly conserved residues in EF-P are colored orange, and those in a/eIF5A are colored sky blue. The rhamnosylated Arg32 of *N. meningitidis* EF-P is highlighted with a purple asterisk above the sequence alignment. Dashes represent breaks in the actual amino acid sequences of the respective proteins, to allow sequence alignment with *N. meningitidis* EF-P. *Nm*EFP, *N. meningitidis* EF-P (EFV64285); *N. Ec*EFP, *E. coli* EF-P (AAA97046); *Ng*EFP, *Neisseria gonorrhoeae* EF-P (YP\_208043); *Bp*EFP, *Bordetella pertussis* EF-P (NP\_880680); *Bc*EFP, *Burkholderia cepacia* EF-P (WP\_014897640); *Bb*EFP, *Borrelia burgdorferi* EF-P (YP\_005806412); *Tt*EFP, *Thermus thermophilus* EF-P (BAD70948); *Dr*EFP, *Deinococcus radiodurans* EF-P (AAF09709); *Hs*IF5, *Homo sapiens* eIF5A (AAH80196); *Sc*IF5, *Saccharomyces cerevisiae* eIF5A (AAA34425); *Mj*IF5, *Methanocaldococcus jannaschii* aIF5A (C64453). An overview of a ribbon diagram of the crystal structure of *E. coli* EF-P (left) and a structural model of *N. meningitidis* EF-P (right) built by the Phyre2 server (57), using *P. aeruginosa* EF-P (PDB code: 3OYY) as the template, and visualized by the PyMOL viewer (<https://www.pymol.org/>). The Lys34 residue in EF-P(*Ec*) and the corresponding residue (Arg32) in EF-P(*Nm*) are shown as stick models. Secondary structure assignments ( $\alpha$ -helices,  $3_{10}$ -helices, and  $\beta$ -sheets) in EF-P(*Ec*) are represented as  $\alpha$ ,  $\eta$ , and  $\beta$ , respectively. The  $\alpha$ -helices,  $3_{10}$ -helices, and  $\beta$ -sheets are colored deep purple, dark olive, and green, respectively.