

Supporting information

Structural and Mutagenesis Studies Evince the Role of the Extended Protuberant Domain of Ribosomal Protein uL10 in Protein Translation

Kwok-Ho Andrew Choi,[†] Lei Yang,[†] Ka-Ming Lee,[†] Conny Wing-Heng Yu,[†] David K. Banfield,[‡] Kosuke Ito,[§] Toshio Uchiumi,[§] and Kam-Bo Wong ^{*,†}

[†]School of Life Sciences, Centre for Protein Science and Crystallography, State Key Laboratory of Agrobiotechnology, The Chinese University of Hong Kong, Shatin, Hong Kong, China

[‡] Division of Life Science, Hong Kong University of Science and Technology, Clear Water Bay, Hong Kong, China

[§] Department of Biology, Faculty of Science, Niigata University, Ikarashi 2-8050, Nishi-ku, Niigata 950-2191, Japan

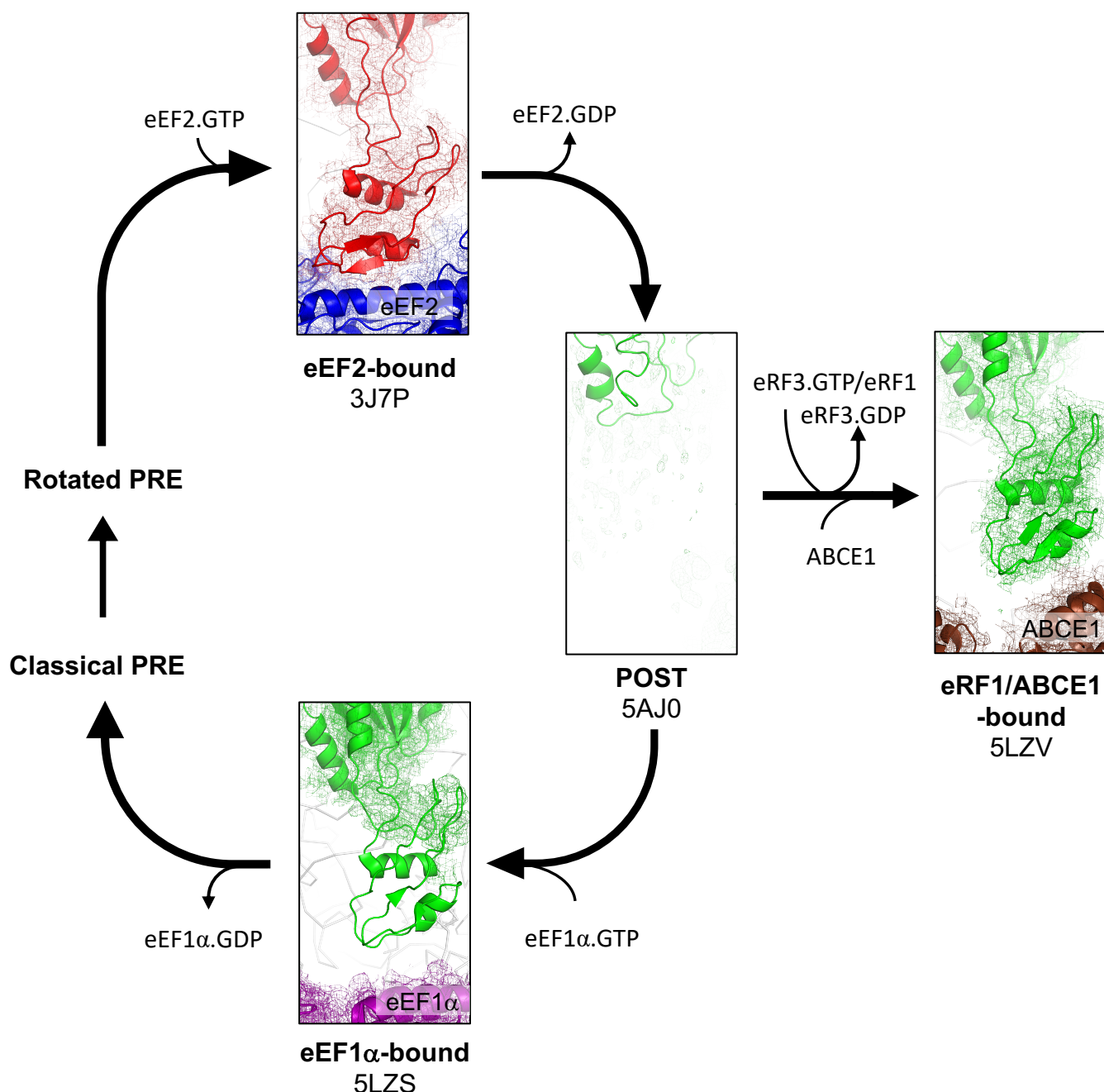


Figure S2. Structures of the uL10ext domain in various states of eukaryotic ribosomes. The classification of various states in the elongation cycle is described by Behrmann and co-workers⁷⁰. Cryo-EM densities for the uL10ext domain and the surrounding area are shown with the fitted models. Structures of the eEF2-bound (PDB accession code: 3J7P⁶⁵), eRF1/ABCE1-bound (PDB accession code: 5LZV⁶⁴), eEF1α-bound (PDB accession code: 5LZS⁶⁴) and post-translocation state (POST) (PDB accession code: 5AJ0⁷⁰) of ribosomes were shown. The uL10ext domain is defined only in the eEF2-bound and eRF1/ABCE1-bound ribosomes.

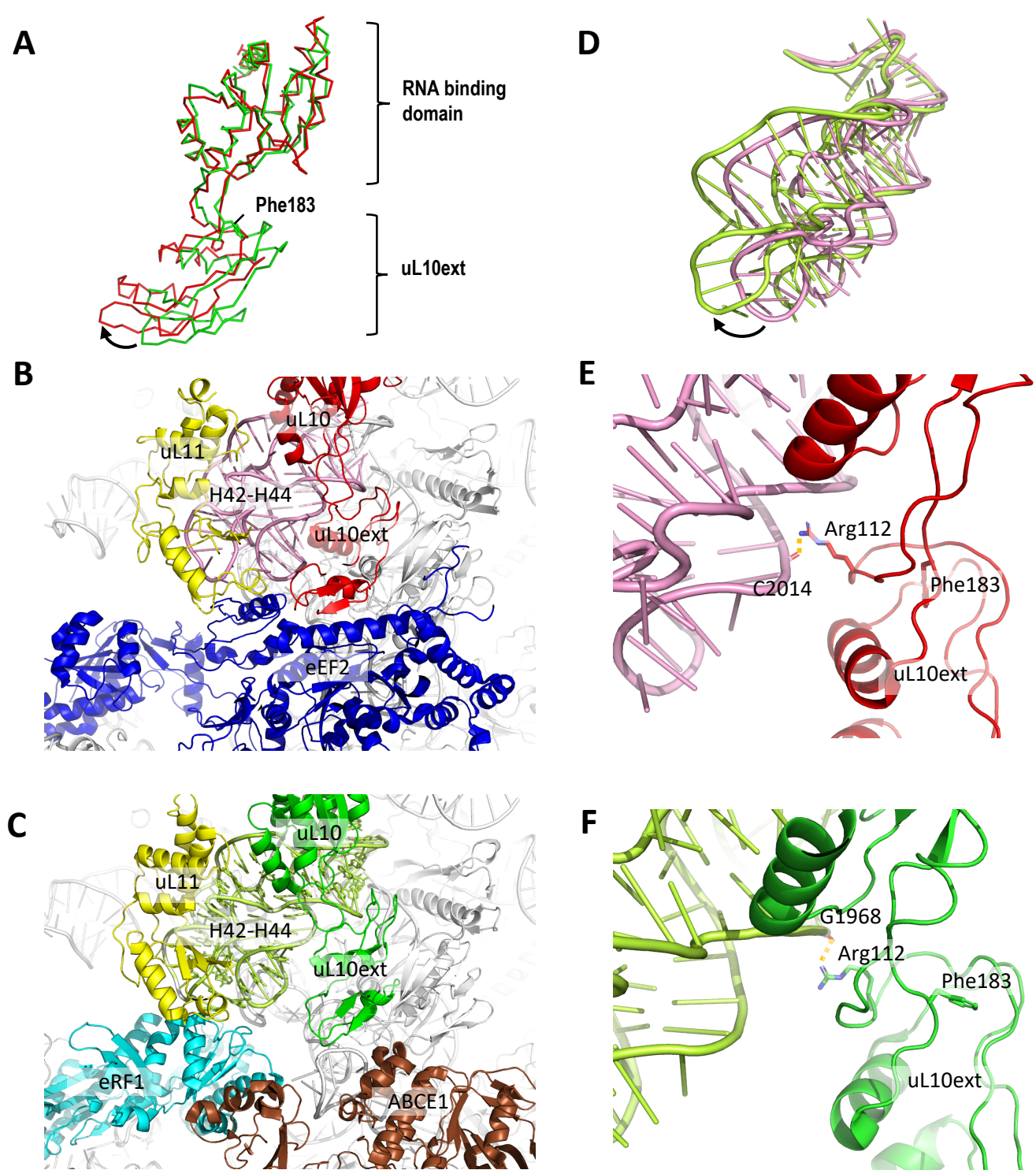
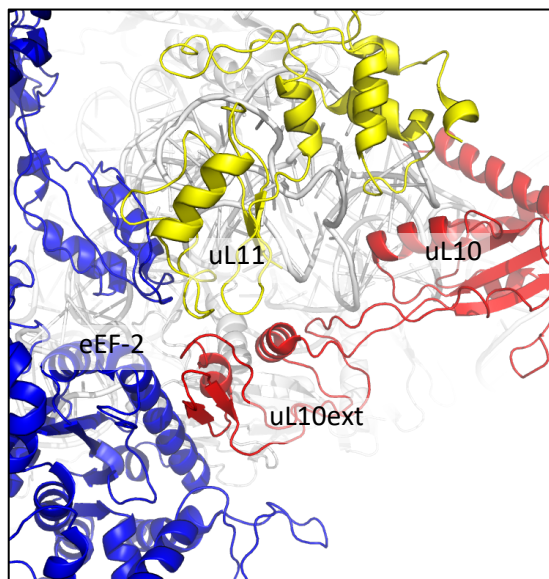


Figure S3. Structural changes in the stalk base of eukaryotic ribosomes. **(A)** The structure of uL10 from eRF1/ABCE1-bound ribosomes (green) was superimposed with that from the eEF2-bound ribosomes (red) based on residues in the RNA-binding domain. As denoted by an arrow, the uL10ext domain in the eRF1/ABCE1-bound ribosomes exhibits a rigid-body hinging motion relative to the RNA-binding domain. **(B)** The conformation of the stalk base in the eEF2-bound ribosome. Both the uL10ext domain (red) and uL11 (yellow) make extensive contacts with the bound eEF2 (blue). **(C)** The conformation of the stalk base in the eRF1/ABCE1-bound ribosomes. **(D)** Interactions between uL11 and eRF1 induce the rRNA stem loop H42-H44 move towards the eRF1 binding site in eRF1/ABCE1-bound ribosomes (light green) as compared to the eEF2-bound ribosomes (pink). **(E)** In the eEF2-bound ribosomes, Arg112 from the uL10ext domain forms a salt bridge with C2014 of rRNA. **(F)** In the eRF1/ABCE1-bound ribosomes, the conserved arginine residue moves to a new position and forms a salt bridge with G1968 of rRNA (light green), inducing the rigid-body hinging motion of the uL10ext domain (green).

Eukaryotic 80S ribosome



Bacterial 70S ribosome

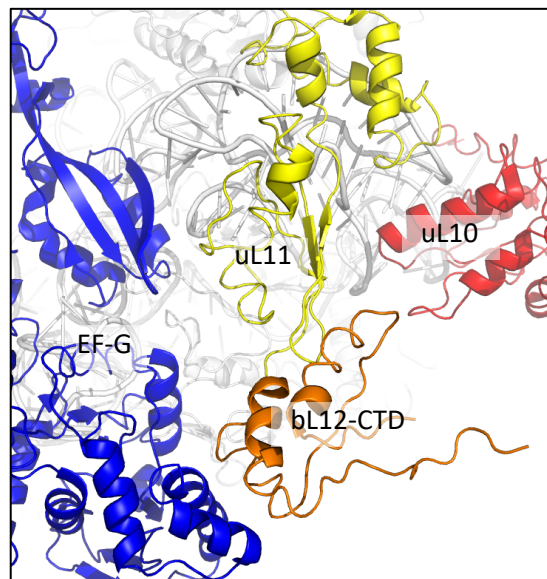


Figure S4. Structural comparison of the stalk base of the eEF2-bound eukaryotic ribosomes (PDB accession code: 3J7P ⁶⁵) and the EF-G-bound bacterial ribosomes (PDB accession code: 4V5F ⁸⁰). The uL10ext domain occupies a location that is similar to that occupied by the C-terminal domain (CTD) of bL12.