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Supporting information for article:

**X-ray structures of eIF5B and the eIF5B-eIF1A complex:
conformational flexibility of eIF5B restricted on the ribosome by
interaction with eIF1A**

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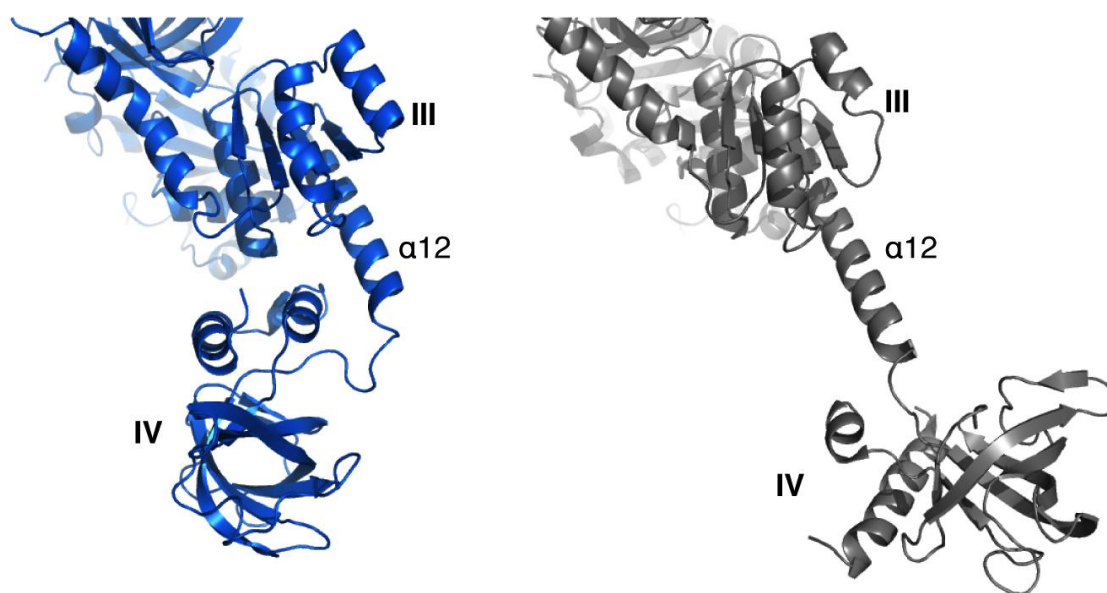


Figure S1 Comparison of domain IV position in eIF5B-1 and aIF5B by superposition of helix 12.

Unlike the “chalice-shaped” structure of archaeal aIF5B, domain IV in eIF5B-1 packs against domain III. eIF5B-1 is shown in blue and aIF5B is shown in grey.

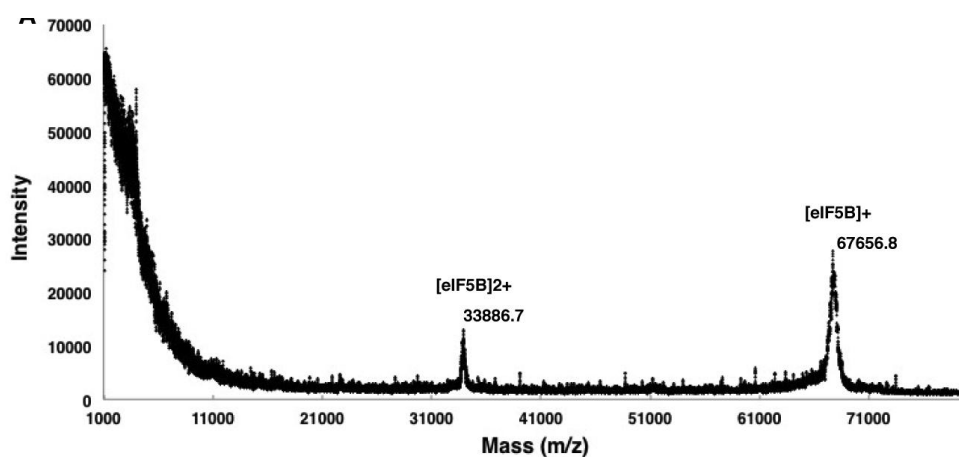


Figure S2 . The Mass spectrum of eIF5B-2 crystal. The TOF-MS map of eIF5B-2 crystal, which was washed and redissolved in MilliQ, shows the peaks of single and double charged eIF5B, confirms that domain IV of eIF5B-2 is not proteolytically degraded.

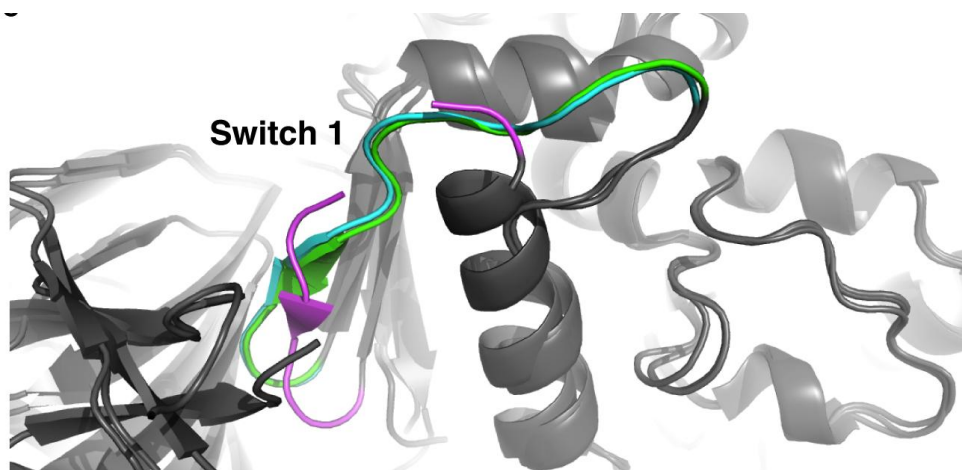


Figure S3 . The conformations of switch 1 of eIF5B. Comparison of switch 1 conformation in eIF5B-1, eIF5B-2 and aIF5B-GTP. eIF5B-1, eIF5B-2, aIF5B-GTP are shown in green, cyan, and pink, respectively. aIF5B-GTP switch 1 region is partial invisible.

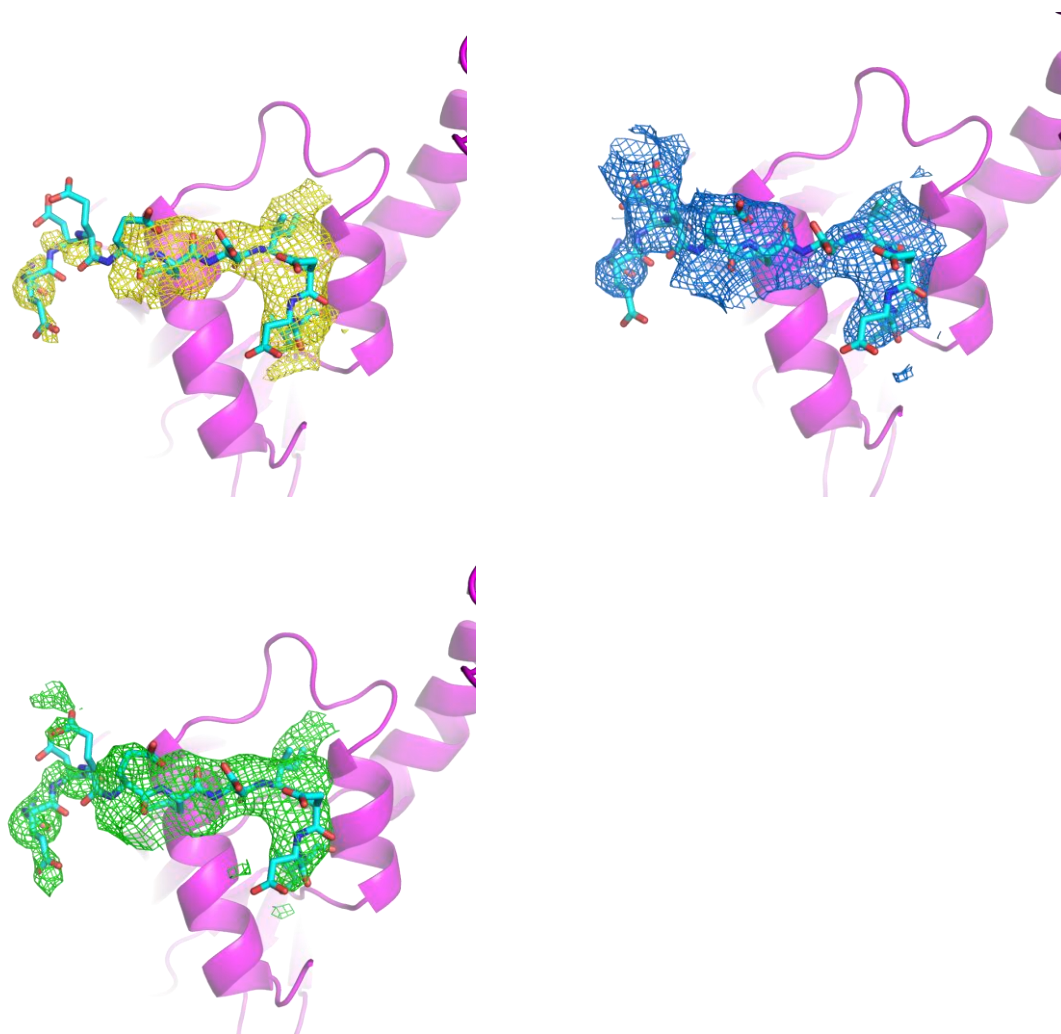


Figure S4 Omitted maps around the C-terminus of eIF1A. The C-terminus of eIF1A is shown as sticks, while magnet ribbon shows eIF5B. Omitted map in (A), (B), and (C) were calculated with contour of $\sigma = 1.8$, 1.6 and 2.0 by *PHENIX_refine*, *autoBUSTER*, and *REFMAC5*, respectively.

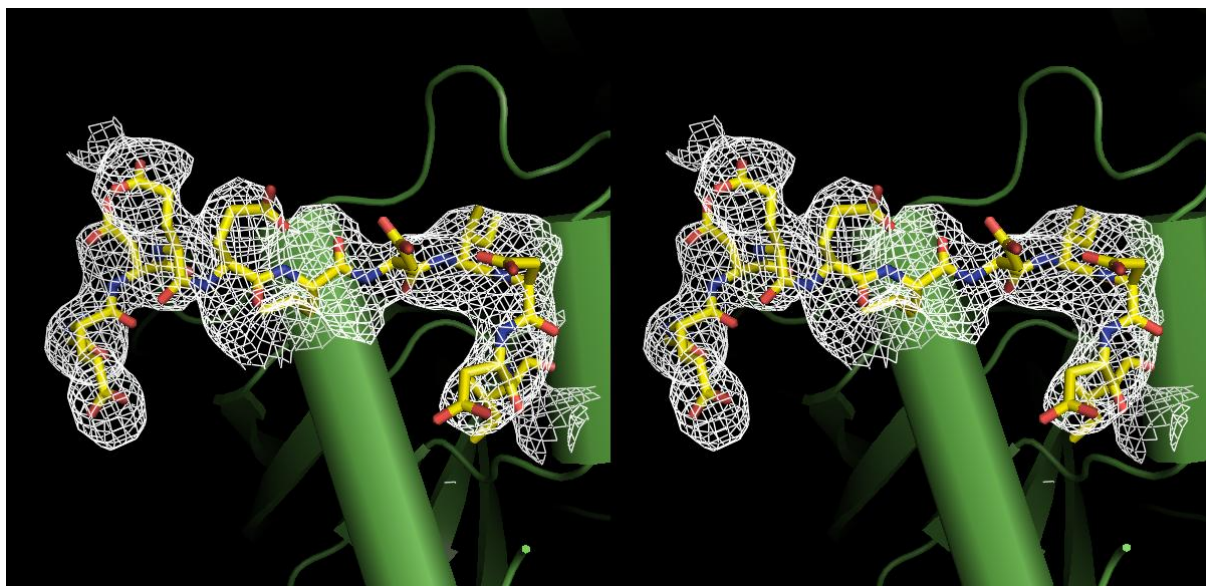


Figure S5 Stereo view of eIF5B and eIF1A interaction site. eIF5B molA is shown in green. The C-terminus of eIF1A is shown as sticks. The electron density map around residue 143-153 of eIF1A is a feature enhanced map (<http://www.phenix-online.org/presentations/fem.pdf>), a kind of 2Fo-Fc map calculated by *PHENIX* at contour of $\sigma=1.0$.

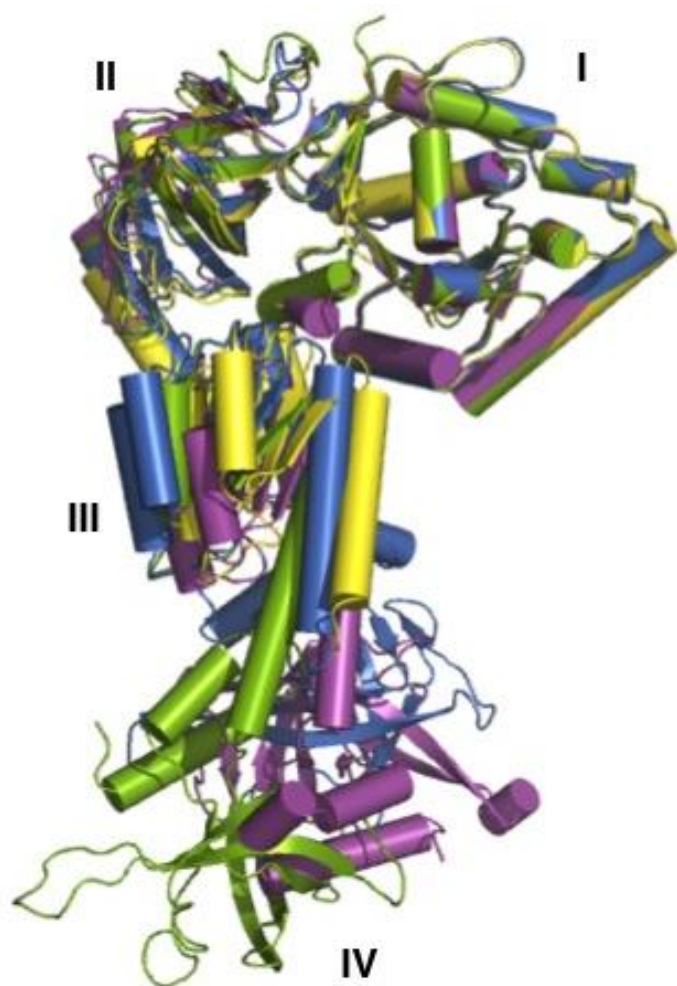


Figure S6 Comparison of eIF5B structures. The structures are superposed by domain I. eIF5B-1, eIF5B-2, molA, molB are shown in blue, yellow, green and magnet, respectively.