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 feature enhanced map (http://www.phenix-online.org/presentations/fem.pdf), a kind of 2Fo-Fc map calculated by PHENIX at contour of σ=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.