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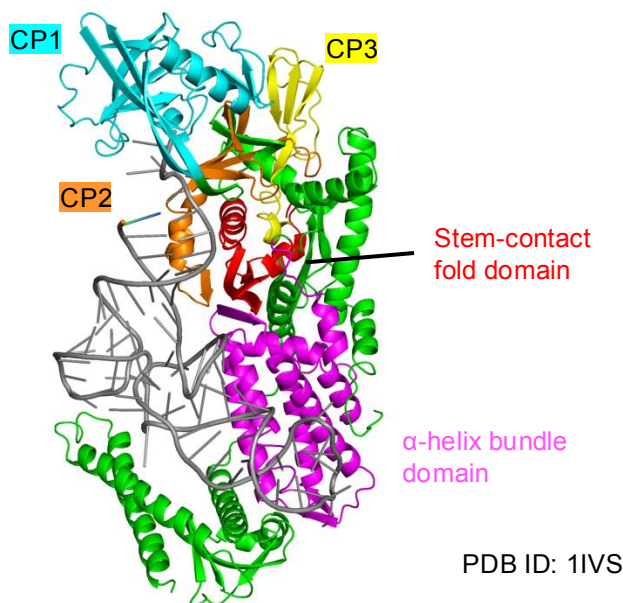


Fig. S2. Comparison of ValRS. (A) Sequence alignment of ValRS from *E. coli*, *L. casei*, and *T. thermophilus*. Organism names are abbreviated as follows: Ec, *E. coli*; Lc, *L. casei*; Tt, *T. thermophilus*. The numbering of amino acids residues is based on *E. coli* ValRS. Inserted regions of *E. coli* ValRS are surrounded by blue squares. The bars below the alignment indicate domains. The alignment was generated using ESPrpt 3.0. (B) Crystal structure of *Thermus thermophilus* ValRS complexed with tRNA^{Val} (Protein Data Bank ID 1HVS). The complex structure is shown in cartoon model using PYMOL 3.0 (Schrödinger, Inc.). The domains of ValRS are colored as follows: CP1 domain, Cyan; CP2 domain, orange; CP3 domain, yellow; stem-contact fold, red; α -helix bundle domain, magenta.