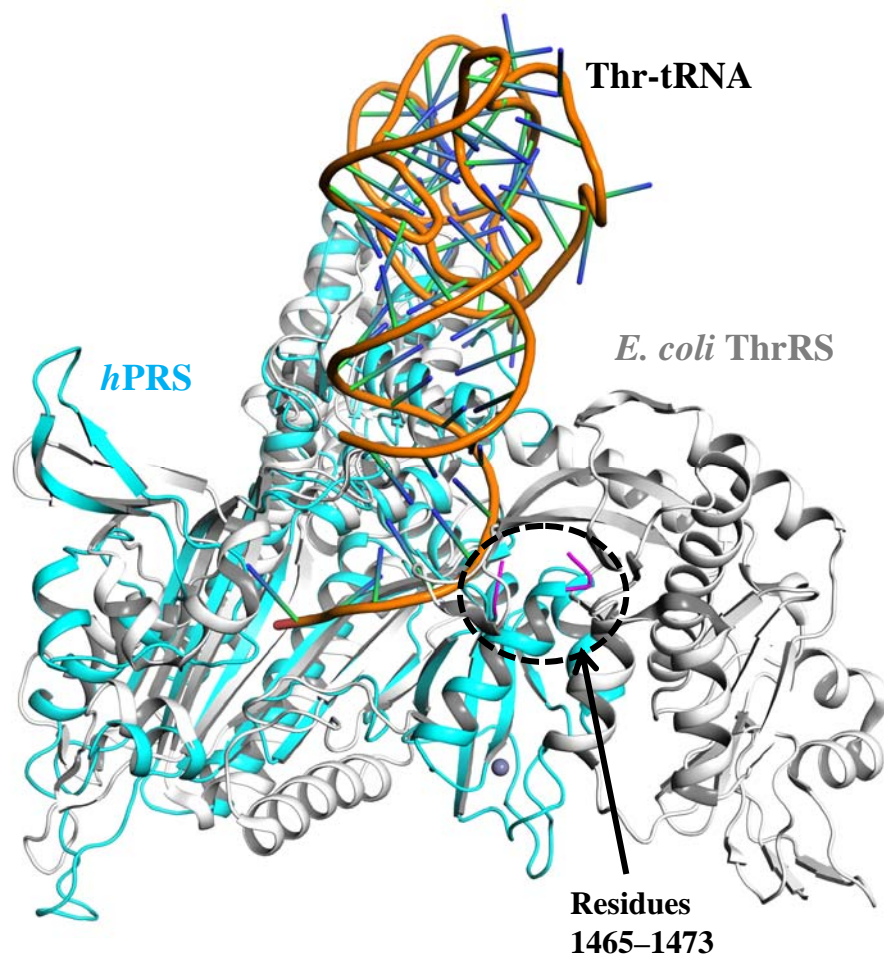
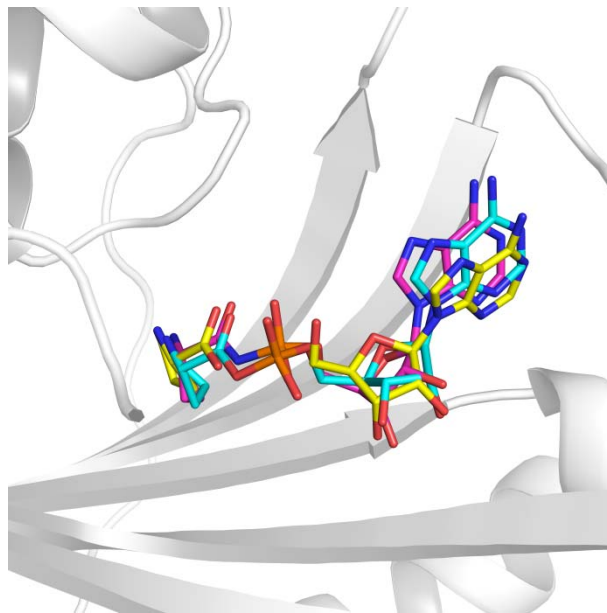


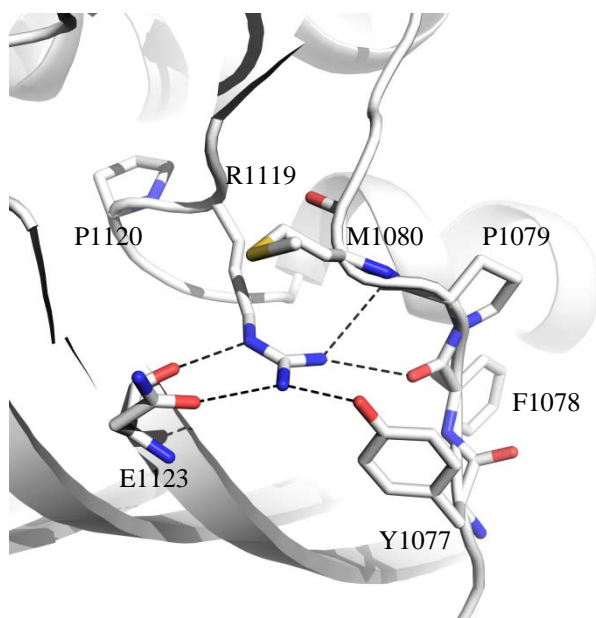
Supplementary Figure S1 The multiple sequence alignment of PRS proteins from the various source. The partial region of full sequence alignment is shown and *hPRS* has an insertion between $\alpha 13$ -helix and $\beta 22$ -strand compared to other PRS sequences. This inserted region includes residues 1465-1473 is indicated by a red square which is disordered in crystal structure shown in Supplementary Fig. S2. GlPRS, *Giardia lamblia*; MjPRS, *Methanocaldococcus jannaschii*; MtPRS, *Methanothermobacter thermautotrophicus*; ThPRS, *Thermus thermophilus*; EfPRS, *Enterococcus faecalis*; RpPRS, *Rhodopseudomonas palustris*.



Supplementary Figure S2 The *hPRS*-apo structure is superposed onto the structure of *E.coli* ThrRS (Threonyl-tRNA synthetase) complexed with Thr-tRNA. The *hPRS* (cyan) and *E.coli* ThrRS (gray) with Thr-tRNA (orange backbone) are represented by cartoon model. The disordered region of *hPRS*-apo, residues 1465-1473, is indicated by dashed lines circle.



Supplementary Figure S3 The substrates superposition of PRS proteins. Prolyl-adenylate molecules from *Giardia lamblia* (magenta) and *Thermus thermophilus* (cyan) are superposed onto *hPRS-sub* (yellow). The bound molecules are displayed by thick stick model.



Supplementary Figure S4 The R1119 interactions with neighboring residues in *hPRS*-sub. The residues Y1077, F1078, P1079 and E1123 form hydrogen bondings with R1119. They are represented by stick model and the interactions are indicated by dashed lines.