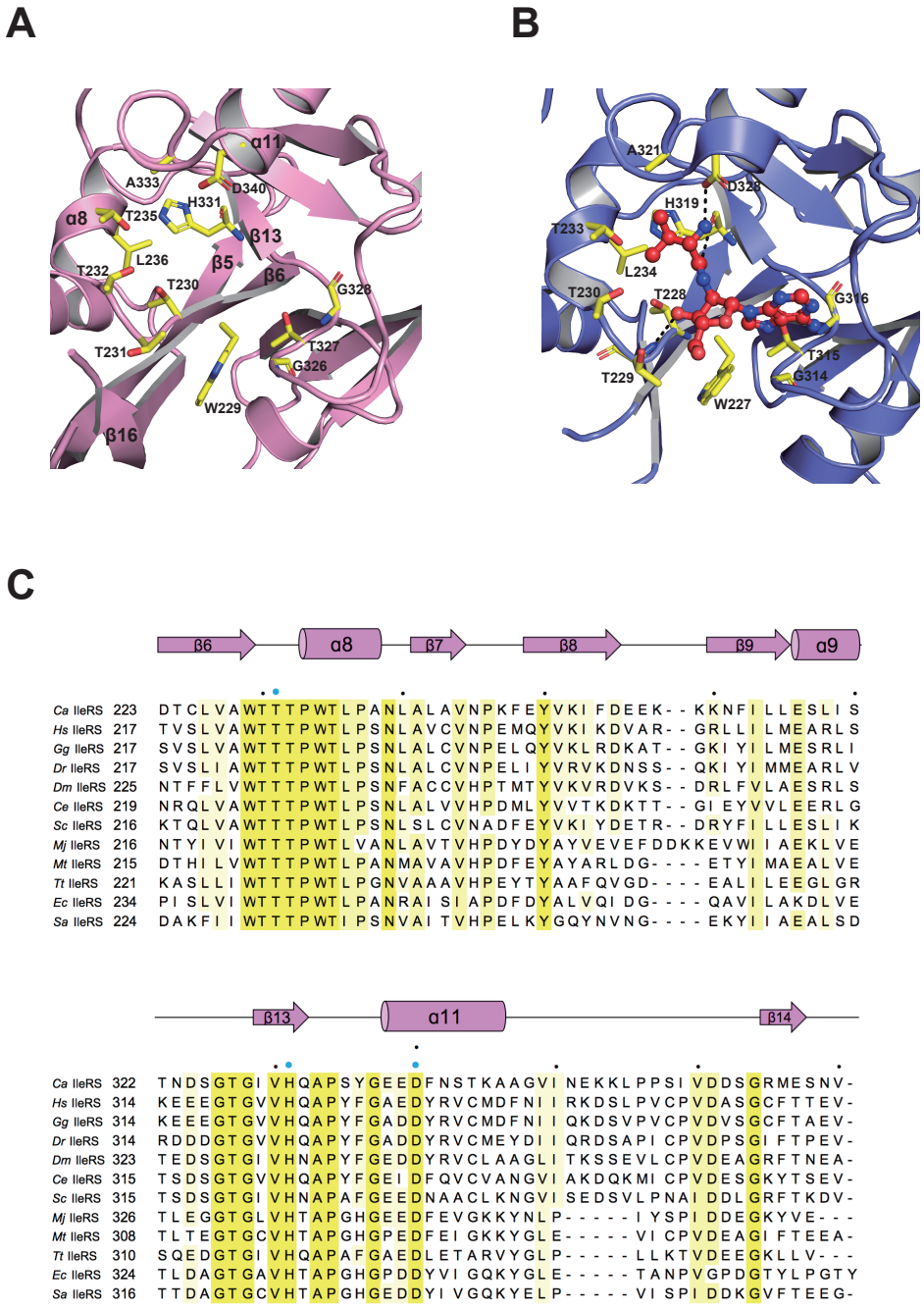
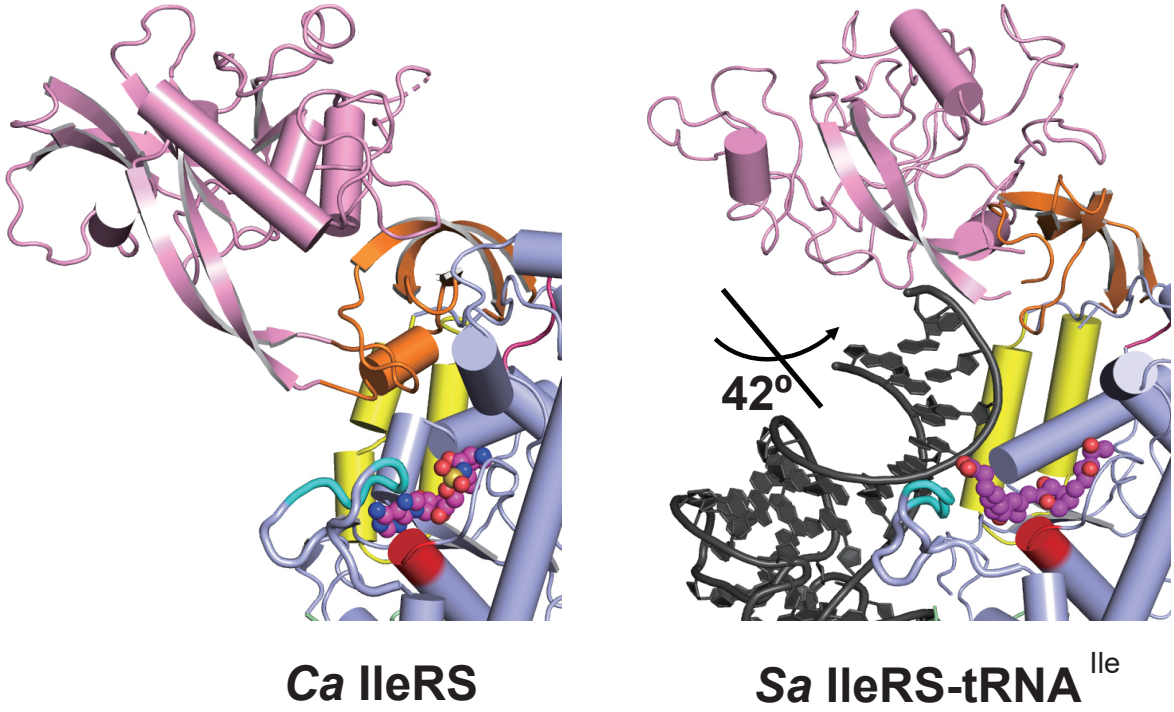


Supplementary Fig. S1. Comparison between the editing active site of *Ca*- and *Tt* IleRSs. (A) Close-up view of the editing active site of *Ca* IleRS. The binding site for Val is surrounded by the β6 strand, the α8 helix, the β13 strand, and the α11 helix. Residues predicted to interact with 2'-(L-Valyl)amino-2'-deoxyadenosine (Val-2AA) are shown. (B) Close-up view of the interactions between Val-2AA (red color) and the editing active site residues (yellow) of *Tt* IleRS (1WNZ, Fukunaga and Yokoyama, 2006). The figures are in the same orientation as in (A). (C) Structure-based sequence alignment of the editing domain of IleRS orthologues. Strictly and highly conserved residues are highlighted in yellow and pale yellow, respectively. The active site residues are indicated by blue circles.



Supplementary Fig. S2. Comparison of the structures between *Ca* IleRS and *Sa* IleRS bound to tRNA. Aligning the catalytic domain of *Ca* IleRS (left) onto *Sa* IleRS-tRNA^{Ile} (right, PDB 1FFY) provides insights how tRNA binding induced the rearrangement of the editing domain orientation relative to catalytic domain. The editing domain of *Sa* IleRS in the presence of tRNA^{Ile} undergoes a 42° rotation relative to the catalytic domain of *Ca* IleRS and open the active site. Each domains of IleRSs are colored as in Figure 3.