

**Structural insights into translational recoding by frameshift
suppressor tRNA^{SufJ}**

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Footnotes:

Running title: Structure of ASL^{SufJ} bound to the ribosomal A site

PDB codes: 4TUA, 4TUB, 4TUC, 4TUD, 4TUE

Keywords: ribosome, mRNA, reading frame, anticodon stem-loop, decoding, X-ray crystal structure

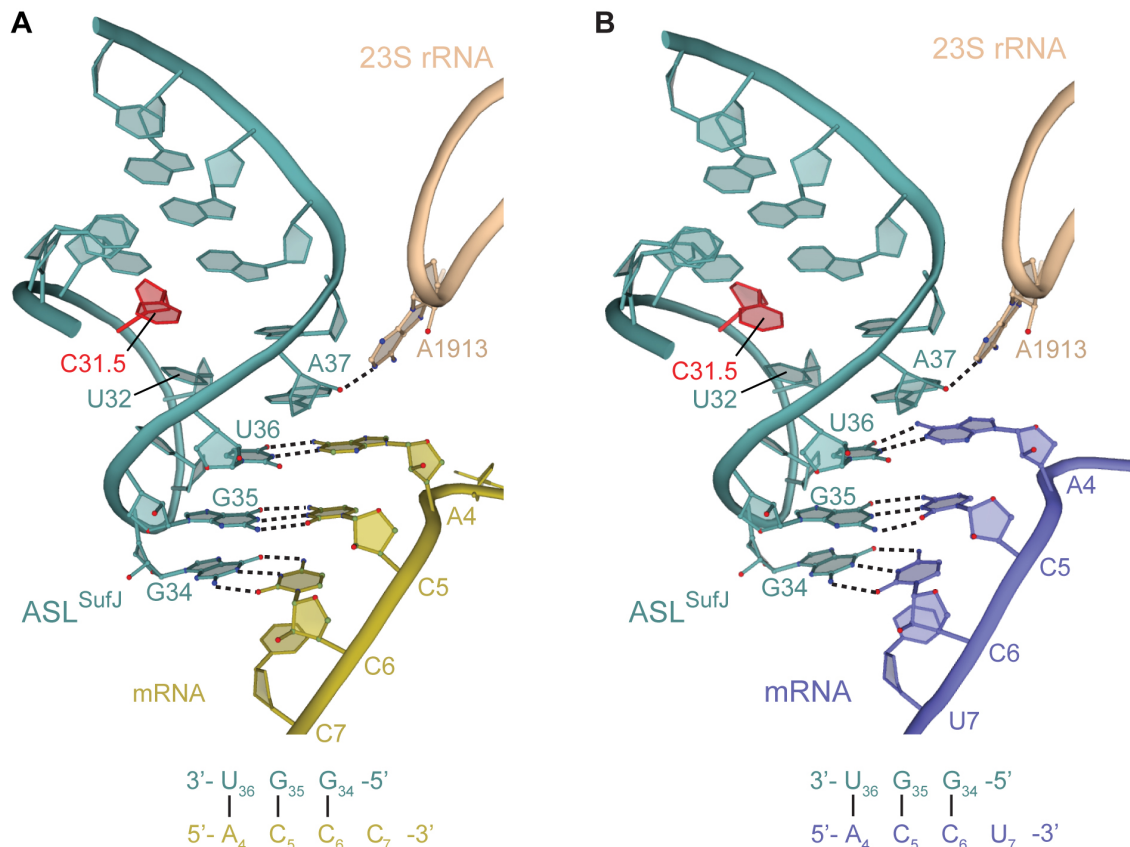


Figure S1. ASL^{SufJ} interactions with mRNA in the A site. ASL^{SufJ} (blue) forms three Watson-Crick base pairs with the first three nucleotides of the +1 suppressible codons **(A)** ACC-C (gold) and **(B)** ACC-U (dark blue) in the zero frame. These structures were solved with the antibiotic paromomycin. The C31.5 insertion (red) expands the anticodon loop to eight nucleotides. The ASL is stabilized by hydrogen bonding with 23S rRNA nucleotide A1913 (tan).

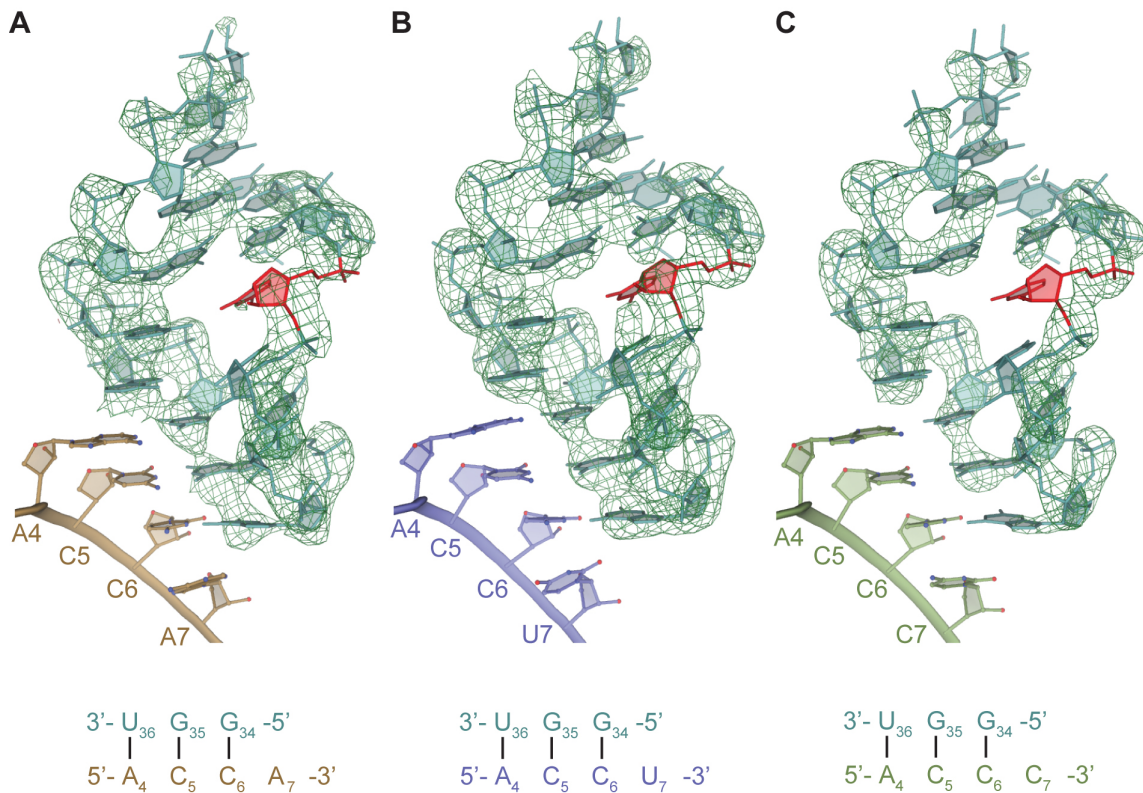


Figure S2. Electron density maps for ASL^{SufJ} bound to the A site. Unbiased F_o-F_c electron density map for ASL^{SufJ} (blue) bound to the +1 suppressible codons **(A)** ACC-A **(B)** ACC-U and **(C)** ACC-C shows strong density for nucleotides 29-42 (contoured at 3 σ). The 70S structures containing the **(B)** ACC-U and **(C)** ACC-C codons contain the antibiotic paromomycin while the 70S structure containing the **(A)** ACC-A codon is without.

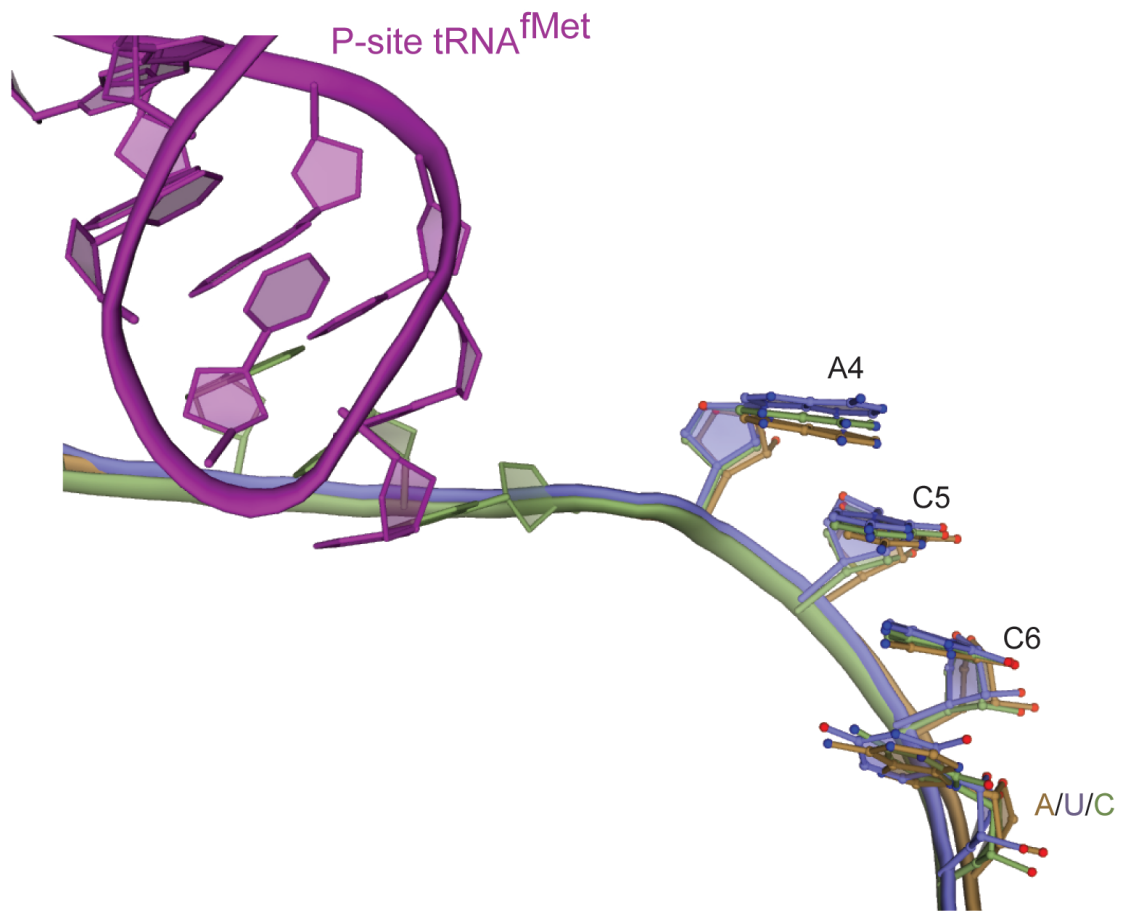


Figure S3. The mRNA path of each +1 suppressible codon is similar. The mRNA path is unaffected by the fourth nucleotide in the ACC-A (brown), ACC-U (dark blue) and ACC-C (green) codons. The P-site tRNA^{fMet} is in magenta.

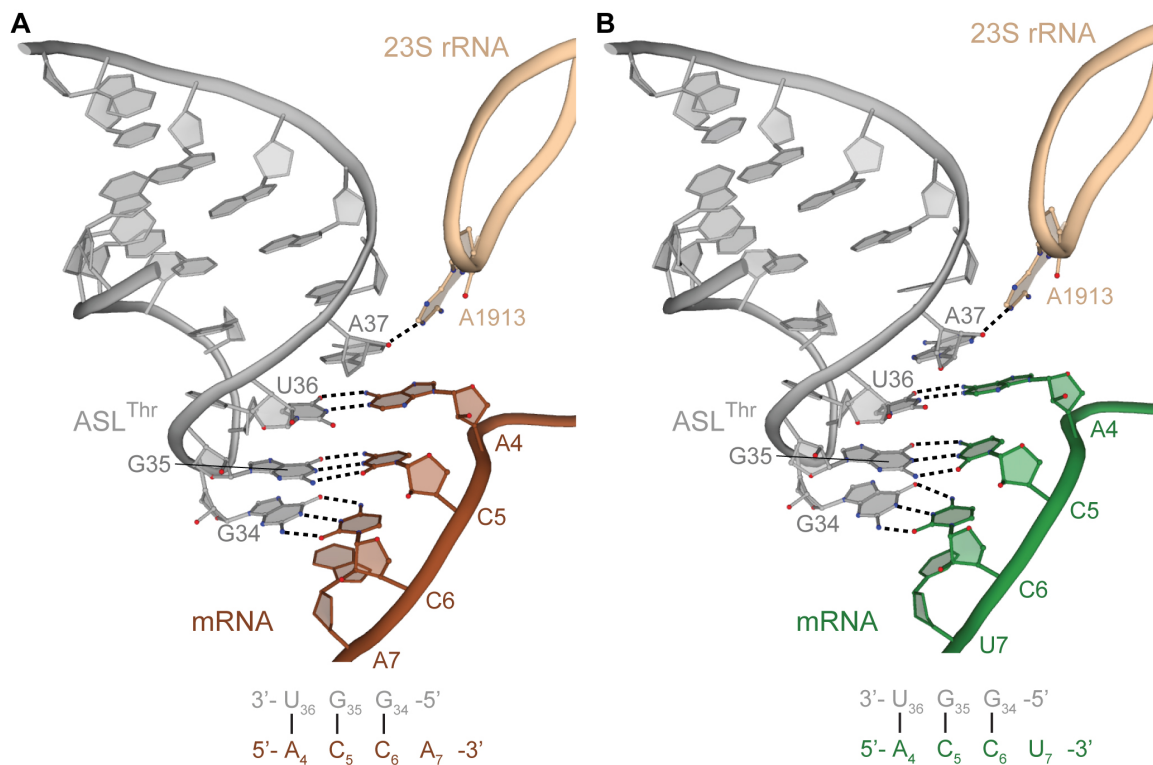


Figure S4. ASL^{Thr} interactions with mRNA in the A site. ASL^{Thr} (gray) forms three Watson-Crick base pairs with the first three nucleotides of the +1 suppressible codons **(A)** ACC-A (brown) and **(B)** ACC-C (green) in the zero frame. These structures were solved with the antibiotic paromomycin. The ASL is stabilized by a hydrogen bonding with 23S rRNA nucleotide A1913 (tan).