

Supporting Information

for

**Crystal structure and specific binding mode of sisomicin to the
bacterial ribosomal decoding site**

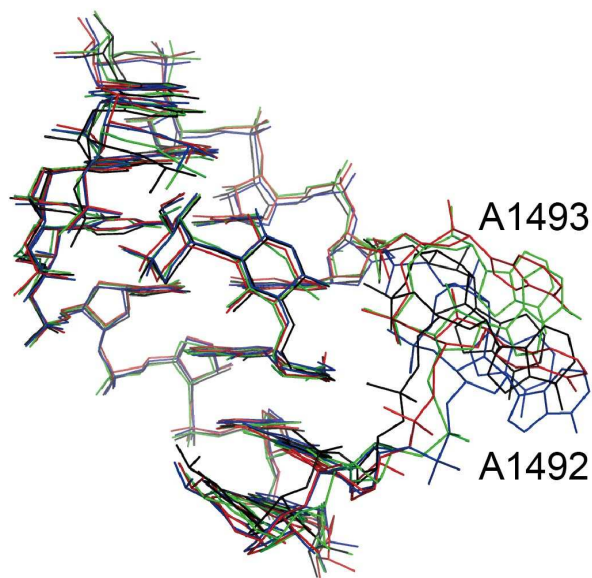
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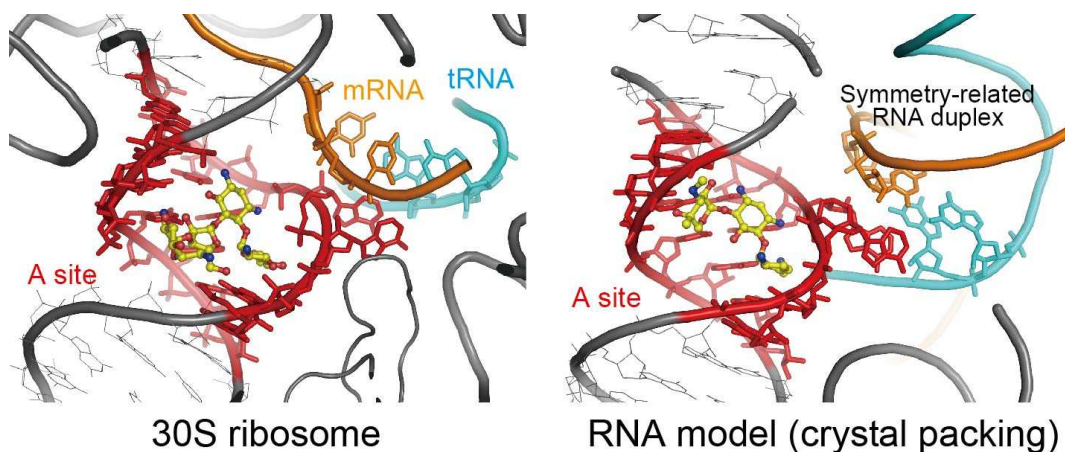
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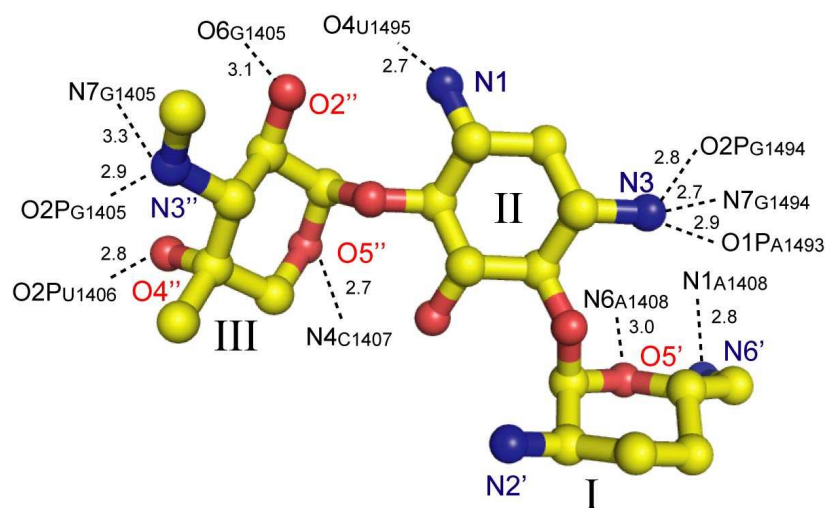
Supplementary Table 1. Crystallization conditions

Crystal code	Siso-NH ₄ ⁺	Siso-Na ⁺
Temperature	20°C	30°C
<u>RNA solution (1 μl)</u>		
RNA	1 mM	1 mM
Sisomicin sulfate	2 mM	2 mM
Sodium cacodylate (pH = 7.0)	50 mM	50 mM
<u>Crystallization solution (1 μl)</u>		
Sodium cacodylate (pH = 7.0)	50 mM	50 mM
Spermine tetrahydrochloride	1 mM	1 mM
Ammonium chloride	750 mM	-
Sodium chloride	-	100 mM
2-Methyl-2,4-pentanediol	1%	1%
<u>Reservoir solution (500 μl)</u>		
2-Methyl-2,4-pentanediol	40%	40%

**Supplementary Figure 1.** Superimposed tertiary structures of the four independent copies (black, red, blue and green) of the bacterial A site complexed with sisomicin obtained in the present study.



Supplementary Figure 2. The A-minor recognition between the bulged-out A1492 and A1493 residues from the A site and the codon-anticodon stem of the tRNA-mRNA complex observed in the 30S ribosomal particles (PDB code: 2J00, left). Crystal packing interactions observed in the present crystal structures mimic the A-minor recognition (right).



Supplementary Figure 3. Detailed interactions of gentamicin C1a with the bacterial A site (PDB code: 2ET3). Hydrogen bonds are represented by dashed lines with distances in Å.