The structures of the anti-tuberculosis antibiotics viomycin and capreomycin bound to the 70S ribosome

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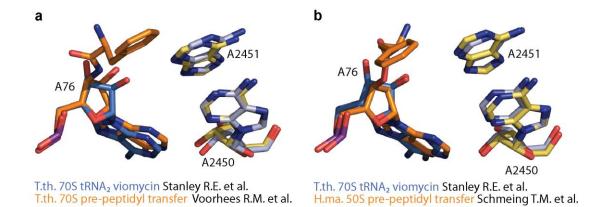
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 R_2 H N H N R 3 ΓR₁ `N´ H || 0 ŅН 0⁷ H ΗŅ H N H_2N ∥ 0 || 0 ΗŅ HN R₄ 'N' H

| Antibiotic | R ₁ | R_2 | R ₃ | R ₄ |
|--------------------|--|-------|---|----------------|
| Viomycin | NH2 NH2 | -OH | -OH | -OH |
| Tuberactinomycin A | | -OH | -OH | -OH |
| Tuberactinomycin B | •••••••••••••••••••••••••••••••••••••• | -OH | -OH | -OH |
| Tuberactinomycin N | NH2 NH2 NH2 NH2 | -OH | -OH | -H |
| Tuberactinomycin O | NH2 NH2 | -OH | -OH | -H |
| Tuberactinamine | -H | -OH | -OH | -H |
| Capreomycin IA | -H | -OH | H ₂ N H ₂ N H | -H |
| Capreomycin IB | -H | -H | H ₂ N H ₂ N H ₂ N H | -H |
| Capreomycin IIA | -H | -OH | -NH2 | -H |
| Capreomycin IIB | -H | -H | -NH2 | -H |

Supplemental figure 1: chemical structure of naturally occurring tuberactinomycins.



Supplemental figure 2: Comparison of the relative positions of A2450 and A2451 of the 23S rRNA to the A76 of a P-site substrate from structures of different ribosomal complexes. All structures were superimposed on the peptidyl transferase centre as defined by residues 2049-2074, 2244-2261, 2435-2466, 2484-2520, and 2545-2619 of 23S rRNA. (a) Comparison between *T.th.* 70S complex of a pre-peptidyl transfer reaction from the structure of Ramakrishnan and co-workers (2WDL and 2WDK) ¹² and the viomycin structure reported here. Residues of 23S rRNA are in gold and gray, the terminal residue of the P-site tRNA is in orange and blue, for the complex of the pre-peptidyl transfer reaction and for the viomycin complex, respectively.

(b) Comparison between the structure of a *H.ma*. 50S complex of a pre-peptidyl transfer reaction (1VQN) ¹¹ and the viomycin structure reported here. Residues of 23S rRNA are in gold and gray, the terminal residue of the P-site tRNA is in orange and blue, for the complex of the pre-peptidyl transfer reaction and for the viomycin complex, respectively.