

Structure of Rv2372c identifies a RsmE-like methyltransferase from *M. tuberculosis*

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Supporting Information

Figure S1: **SDS-PAGE of Rv2372c:**

SDS-PAGE of Rv2372c obtained from crystals (lane 1) or purified protein (lane 2) indicates similar sizes, suggesting that the C-terminal tail of 14-residues in Rv2372c is disordered (and not truncated in the crystals).

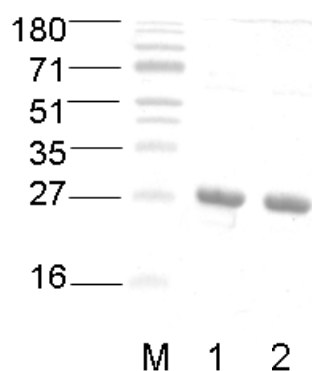


Figure S2: **Structural comparison of NTD of Rv2372c with PUA-domains on the basis of DALI search.** Superposition of NTD (cyan) with PUA domain of t RNA- Pseudouridine synthetase (PDBID: 2ANE) and 50S ribosomal protein L2 (PDBID: 2NWA) in pink and gold colours respectively reveals significant divergence between them.

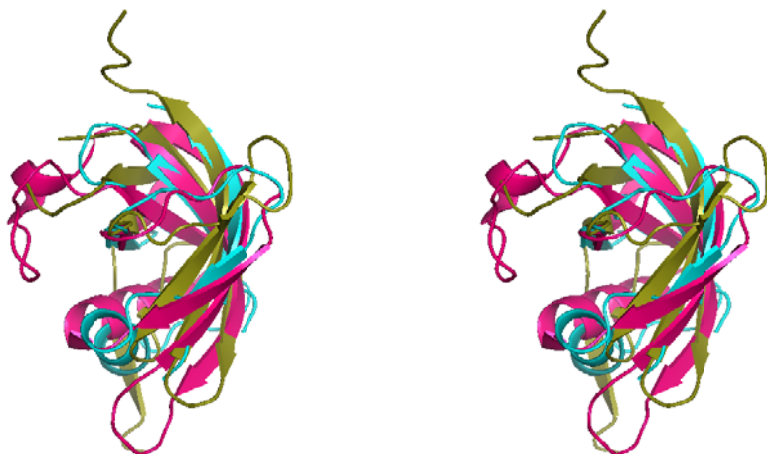


Figure S3: **Structural comparison of CTD of Rv2372c with SPOUT-domains on the basis of DALI search** Superposition of CTD (cyan) with catalytic domain (with deep trefoil knot) of 2'-O methyltransferase (PDBID: 1IPA) (yellow); tRNA methyltransferase TrmH (PDBID: 1V2X) (grey) and tRNA methyltransferase TrmD (PDBID: 1P9P) (purple) reveals overall structural similarities.

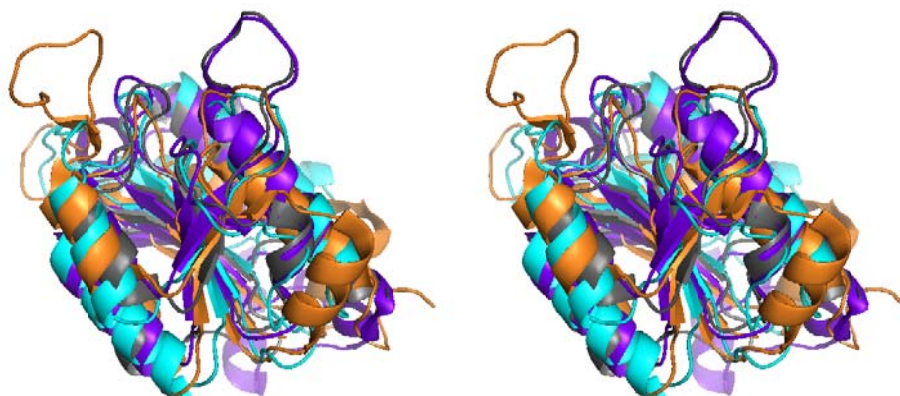


Figure S4: **Crosslinking with glutaraldehyde for analysis of the oligomeric state of protein in solution**

- A. Oligomeric state of RSM-13 (lanes 5-8) was monitored by crosslinking with increasing concentrations of glutaraldehyde (0%, 1%, 2%, 3% v/v), at room temperature. Stable oligomeric states were identified on a 12% SDS-PAGE with standard molecular weight marker (M). Rv2372c (marked RSM) as a control was similarly cross-linked with glutaraldehyde (lanes 1-4) and also forms dimers as expected.
- B. Cross-linking of RSM-16 with increasing concentrations of glutaraldehyde (0%, 1%, 2%, 3% v/v), at room temperature did not identify any stable dimers. Dimers, however, could be identified for Rv2372c (marked RSM) as a control (lanes 1-4). The expected size of the dimer is indicated.

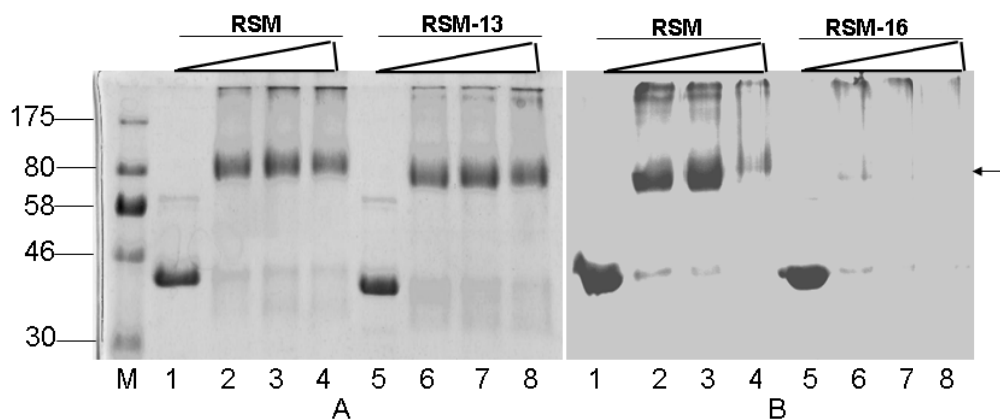
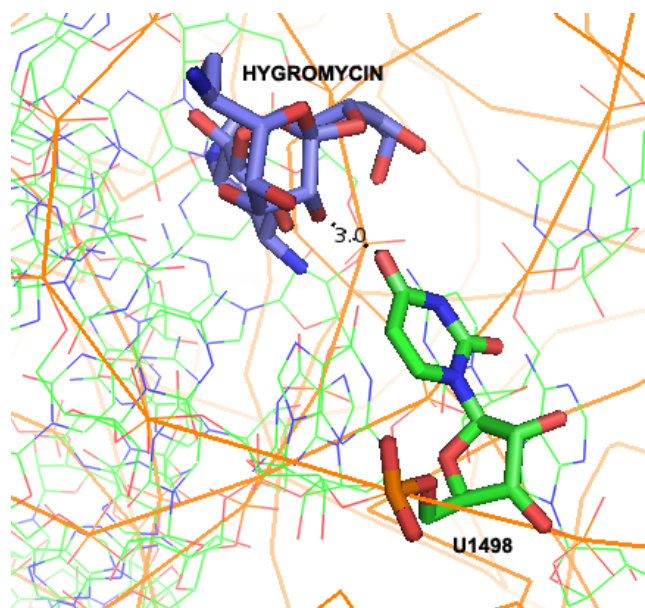
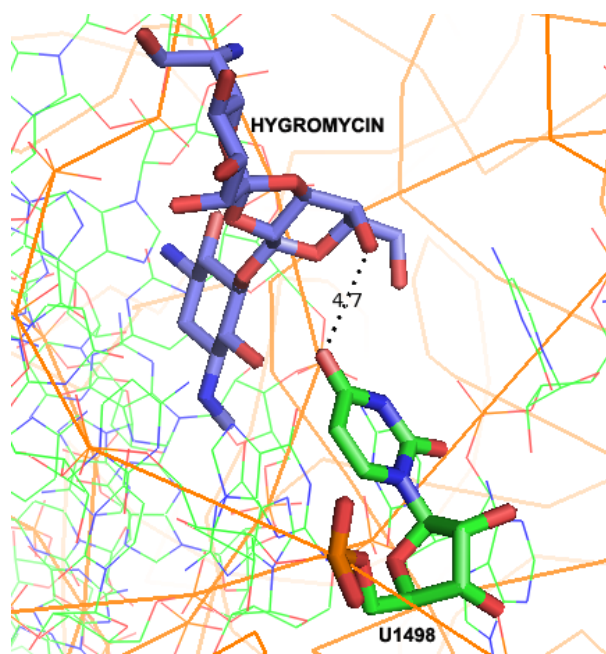


Figure S5: Interactions of antibiotics with U1498

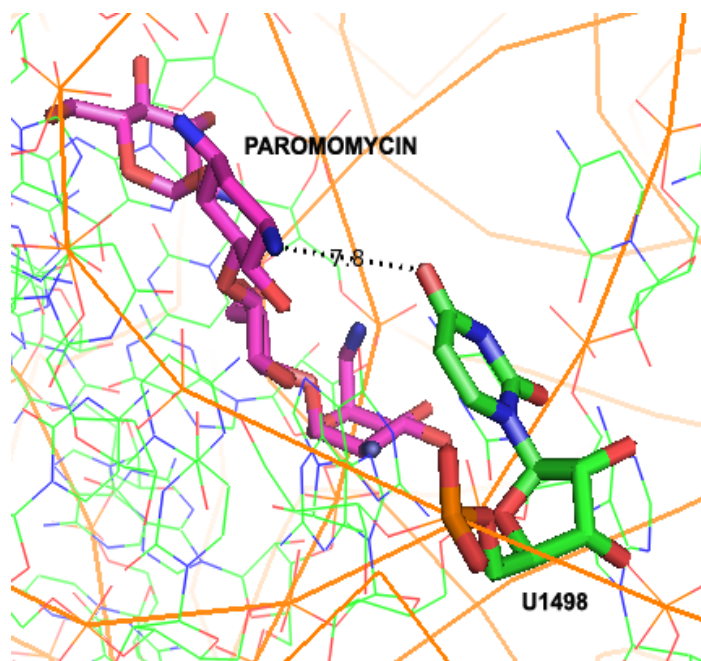
Complexes of ribosome with antibiotics showing the interaction of U1498 of 16S rRNA with (A) Hygromycin (PDBID: 1HNZ), (B) Hygromycin (PDBID: 3DF1), (C) Paromomycin (PDBID: 2WDG), (D) Viomycin (PDBID: 3KNH)



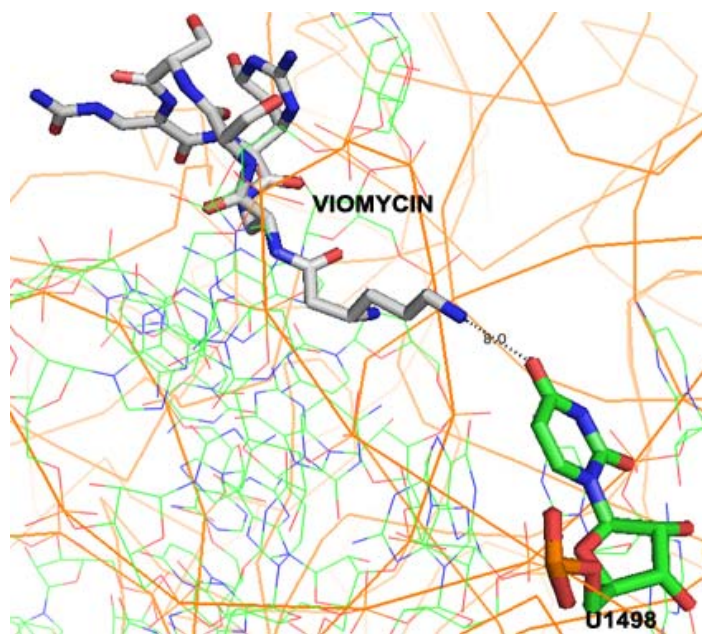
A



B



C



D

Table S1: Zone of inhibition with indicated antibiotics for *E. coli* KL16 and *E. coli* KL16 Δ RsmE cells

Name of Antibiotic	Zone of inhibition in mm (<i>E. coli</i> KL16)	Zone of inhibition in mm (<i>E. coli</i> KL16ΔRsmE)
Netilmicin (30 μ g/disc)	29 \pm 1.15	28.5 \pm 0.57
Streptomycin (25 μ g/disc)	25 \pm 0.58	26.5 \pm 0.58
Tobramycin (30 μ g/disc)	28 \pm 0.56	29 \pm 1.73
Gentamicin (30 μ g/disc)	30 \pm 0.58	29 \pm 1.00
Amikacin (30 μ g/disc)	30 \pm 1.15	31 \pm 0.58
Erythromycin (15 μ g/disc)	16.6 \pm 0.57	16.6 \pm 0.57
Tetracycline (10 μ g/disc)	22.3 \pm 0.57	24 \pm 1.00
Rifampicin (5 μ g/disc)	10.6 \pm 0.57	10 \pm 0.00