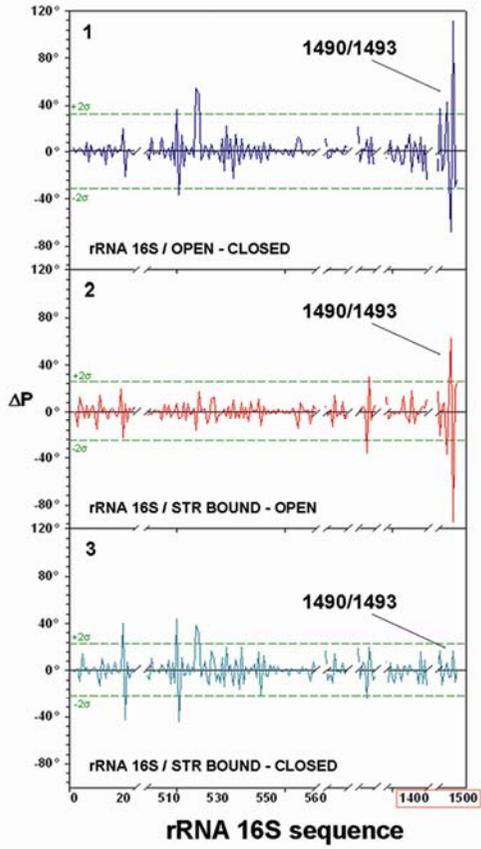
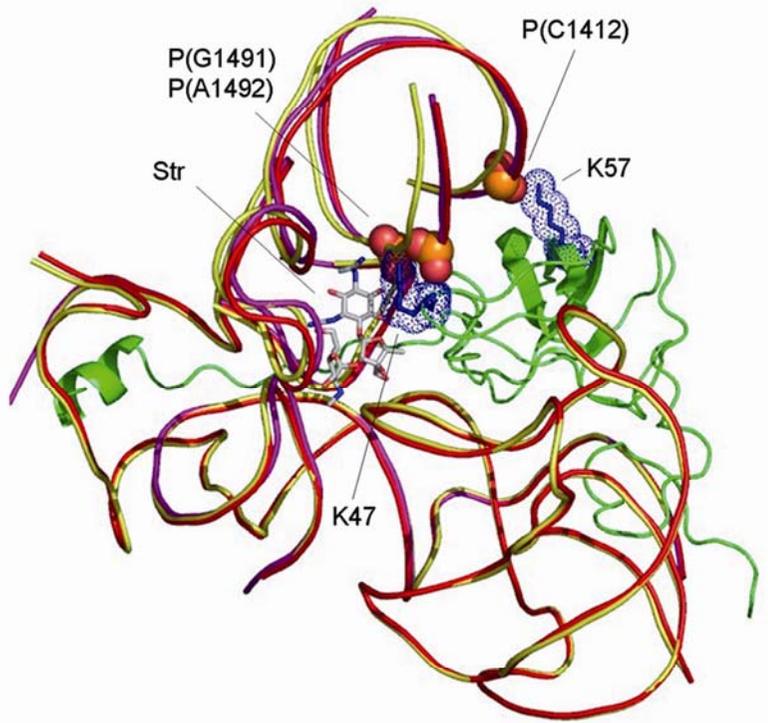
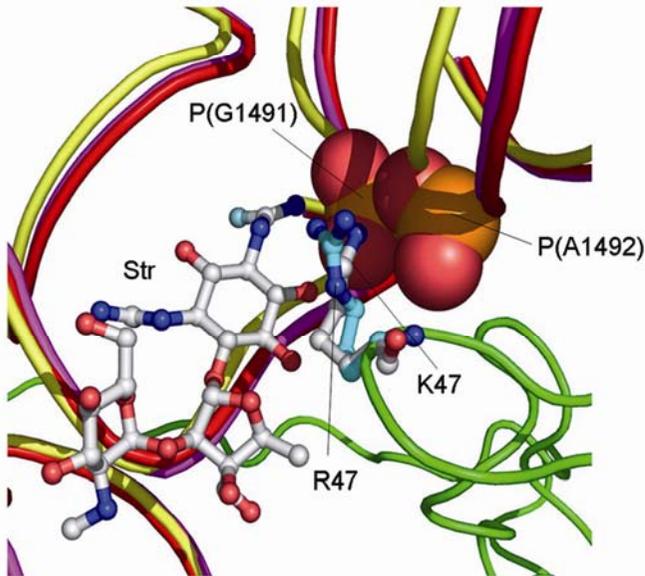
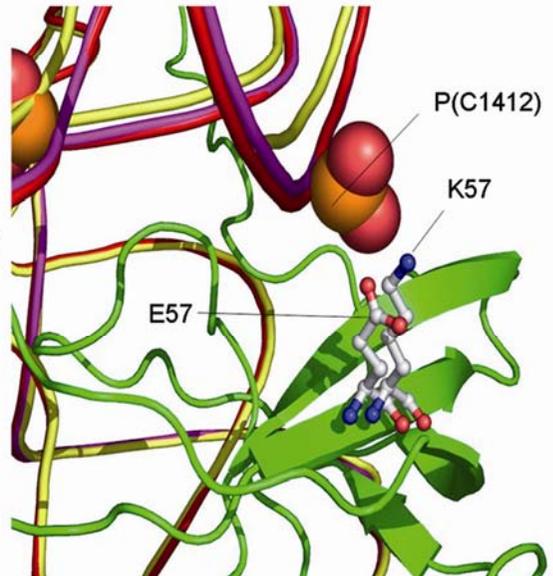


**A****B****C****D**

## Legends to supplementary figures

### **Figure S1. Comparison of rRNA 16S and S12 structures and analysis of backbone torsion angles localized in the vicinity of residues K47 and K57.**

**A)** Differences in phosphate dihedral angles ( $\Delta P$ ) along the rRNA 16S backbone chain among the open, closed and streptomycin-bound forms of the complex. Sequence numbering refers to the rRNA 16S in 1J5E, 1N32, 1FJG protein data bank files. Panel 1 shows the  $\Delta P$  values for the open vs. closed forms deviations, panel 2 the Str-bound vs. open forms, and panel 3 the Str-bound vs. closed forms. The horizontal dashed lines represent the mean of the difference for all residues  $\pm 2\sigma$ .

**B)** Structural comparison for the relative position of S12 protein (green trace) and rRNA 16S in open (yellow trace), closed (red trace) and streptomycin-bound (magenta trace) forms, showing the displacement of the trace in the vicinity of phosphates corresponding to bases G1491, A1492, as well as C1412, in contact to K47 and K57 respectively. Position of streptomycin molecule (Str) in the streptomycin-bound form of the complex is indicated.

**C)** Comparison of the contacts established by K47 and mutated R47. Note the displacement of rRNA backbones in the three states (colours as in panel C). Position of streptomycin is indicated.

**D)** Mutated E57 is located in contact to phosphate group of Cytosine 1412, an unstable position.