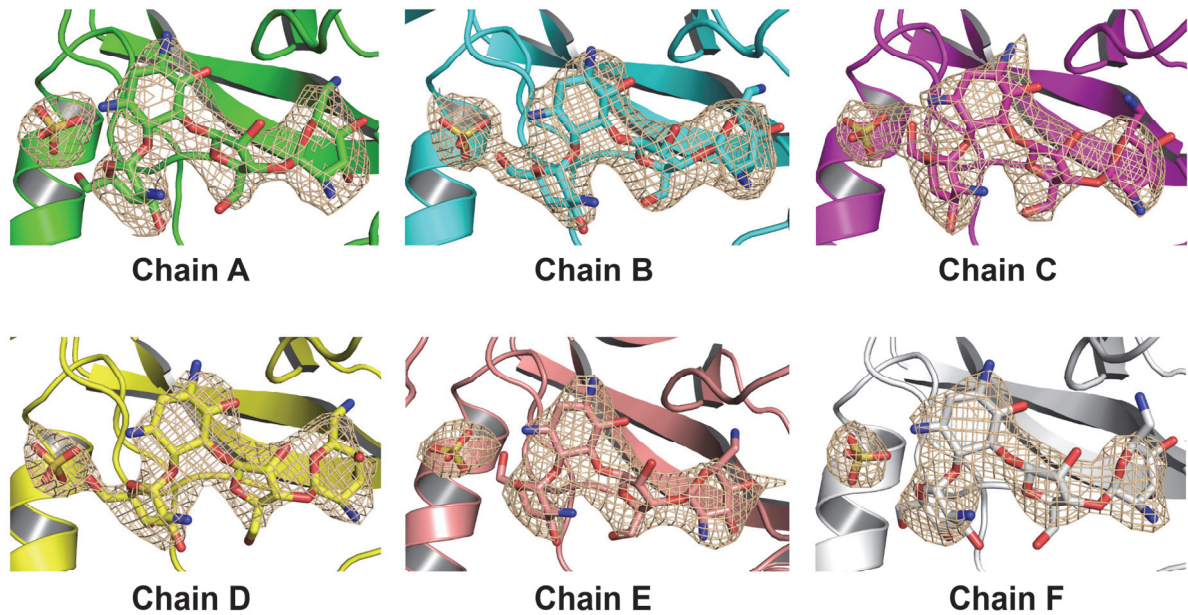
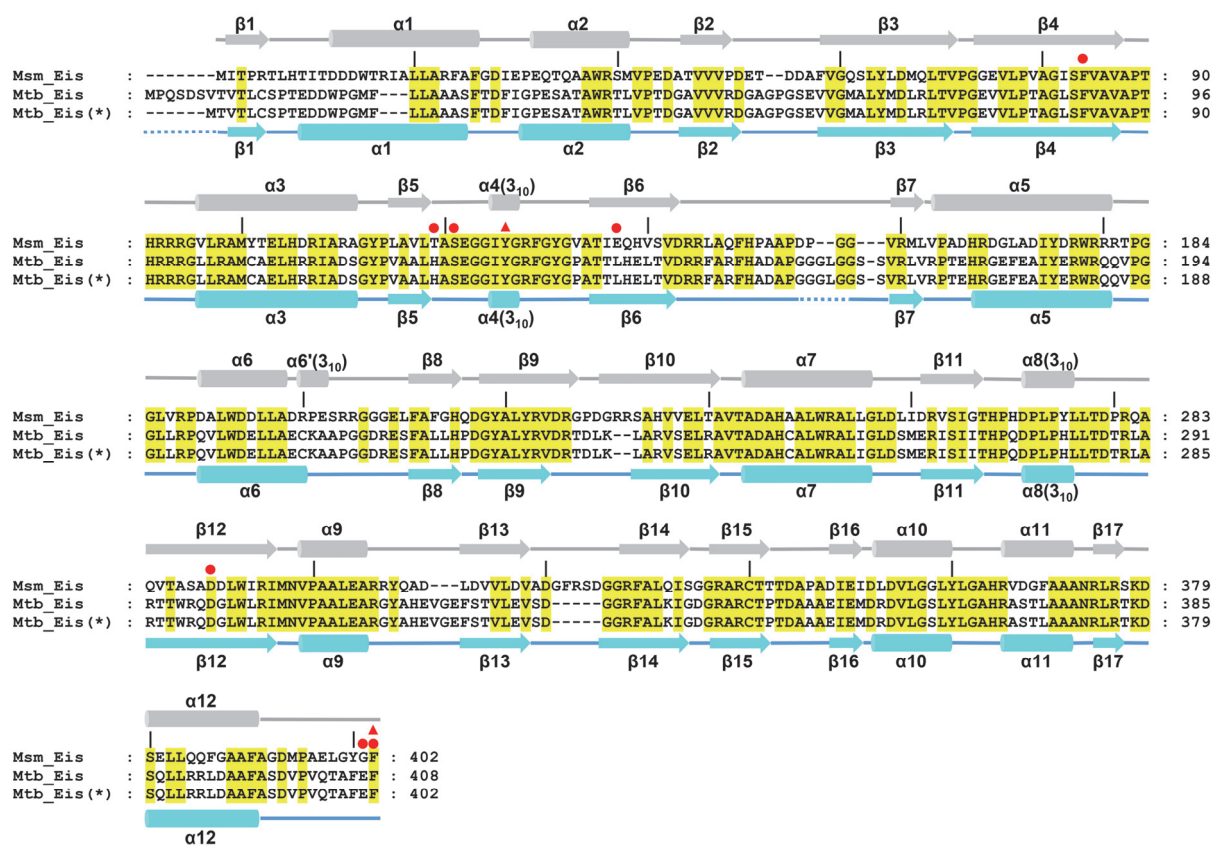


## Supplementary Figures



**Figure S1.** Simulated annealing omit *Fo-Fc* electron density maps for paromomycin and a sulfate ion bound to each subunit of the *Msm* Eis hexamer in the asymmetric unit. The electron density map was contoured at the  $3.0\sigma$  level.



**Figure S2.** Sequence alignment of *Msm* Eis and *Mtb* Eis. Conserved residues are shaded in yellow. Cylinders denote  $\alpha$ - and  $3_{10}$ -helices and arrows denote  $\beta$ -strands, respectively. Red triangles above the sequences indicate the catalytic residues (Tyr126 and Phe402 in *Msm* Eis). Red dots above the sequences indicate the residues (Thr119, Ser121, Glu137, Asp290, Gly401 and Phe402 in *Msm* Eis) interacting with paromomycin. Every 20th residue is marked with a vertical bar above the *Msm* Eis sequence. The construct of tobramycin-bound *Mtb* Eis (Houghton *et al.*, 2013) differs from the full-length *Mtb* Eis in the SWISS-PROT. Therefore, its sequence numbering, marked as Mtb\_Eis (\*), differs from that of the full-length *Mtb* Eis in the SWISS-PROT (Mtb\_Eis). This figure was drawn with *ClustalX* (Thompson *et al.*, 1997) and *GeneDoc* (<http://www.psc.edu/biomed/genedoc>).