

## Poster Presentation

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### *Crystal structure of Rv2258c, a putative SAM-dependent methyltransferase*

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The Mycobacterium tuberculosis protein Rv2258c belongs to a large family of putative S-adenosylmethionine (SAM)-dependent methyltransferases in mycobacteria. As part of a laboratory-scale structural genomics project on conserved hypothetical proteins in pathogenic bacteria, we have determined the crystal structure of Rv2258c from M. tuberculosis H37Rv at 1.8 Å resolution. The crystals of apo Rv2258c belong to space group C2, with unit cell parameters  $a = 109.2 \text{ \AA}$ ,  $b = 140.6 \text{ \AA}$ ,  $c = 97.2 \text{ \AA}$ , and  $\beta = 98.5^\circ$ . Assuming that three monomers are present in the asymmetric unit, the Matthews parameter and the solvent fraction are  $3.32 \text{ \AA}^3 \text{ Da}^{-1}$  and 63.0%, respectively. The crystal structure of Rv2258c has been solved by a combination of the molecular replacement and single wavelength anomalous diffraction technique, using platinum atoms as anomalous scattering centers and the coordinates of the RebM from Lechevalieria aerocolonigenes (PDB entry 3BUS) as the search model. In addition, two binary complex structures, Rv2258c-SAM and Rv2258c-S-adenosylhomocysteine (SAH), have been determined by molecular replacement using the model of apo Rv2258c.

**Keywords:** Mycobacterium tuberculosis, S-adenosylmethionine (SAM)-dependent methyltransferase