Structural Studies on MsmE, a Sugar Binding Lipoprotein from S. Pneumoniae

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Streptococcal organisms share a well-conserved, binding protein dependent, Multiple Sugar Metabolism (msm) system which is responsible for the transportation and metabolism of multiple sugars. This system is comprised of 8 proteins including 2 membrane proteins (MsmF and MsmG), an ATP-binding protein (MsmK) and the 45KDa sugar-binding lipoprotein MsmE [1].

Both native and selenomethionine derivatised MsmE were crystallised in space group P6₁22. Selenomethionine derivative crystals showed diffraction to 2.5Å and 3-wavelength MAD data were collected at SRS, Daresbury. Selenium sites (19/22) were found using SnB [2] with peak data and site refinement and phasing using Sharp/AutoSharp [3] using MAD data along with a 3Å native dataset.

The initial model shows a two domain periplasmic binding protein-like fold and model-building and refinement is continuing.

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