

MAD SeMet Data Collection of HI1679 from H. Influenzae

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Beamline(s): **X12C**

Introduction: Many of the proteins that emerge from the genome-sequencing project have no known function. The structures of these so-called 'hypothetical proteins' may be used to leverage function when the fold has been seen previously, and if it is associated with one or a few known functions. HI1679 from H. influenzae is such an example.

Methods and Materials: HI1679 has been cloned and expressed in *E. coli*, and purified both in native form and as a seleno-methionine protein. Crystals have been obtained and characterized on the home x-ray facility, and conditions to flash-cool them established. MAD data have been collected on beamline X12C and processed with the HKL package.

Results: The MAD data extended to 2.5Å resolution. The data quality enabled the identification of most Se sites, and the phase determination resulted in an interpretable electron density map. 25% of the polypeptide chain of the tetramer present in the asymmetric unit has been traced automatically, using ARP/warp. The remaining chain was traced manually. Refinement of the structure is in progress.

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