Poster Presentation

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Structure for the N-terminal domain of HCV glycoprotein E1

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Single-wavelength anomalous dispersion of sulfur atoms (S-SAD) is an elegant phasing method to determine crystal structures that does not require heavy atom incorporation or selenomethionine derivatization. Nevertheless this technique has been limited by the paucity of the signal at usual X-ray wavelengths, requiring very accurate measurement of the anomalous differences. Here we report the data collection and structure solution of the N-terminal domain of the ectodomain of Hepatitis C virus (HCV) E1, from crystals that diffracted very weakly. By combining the data from 32 crystals it was possible to solve the sulfur substructure and calculate initial maps at 7Å resolution, and after density modification and phase extension, using a higher resolution native dataset, to 3.5Å resolution, model building was achievable. The crystal structure of the N-terminal domain of reveals a complex network of covalently linked intertwined homodimers that do not harbor the expected truncated class II fusion protein fold.

Keywords: HCV E1, sulfur SAD