

W0601

The Structure Determination of a Crp/Fnr Protein from 1.9-Å SAD Data Collected at the Structural Biology Center 19ID Beamline. F.J. Rotella, R.G. Zhang, R. Mulligan, S. Moy, A. Joachimiak, Biosciences Div., Argonne National Laboratory, Argonne, IL 60439 USA.

A transcriptional regulator protein, Crp/Fnr family, from *Porphyromonas gingivalis*, was expressed, purified and crystallized as a project of the Midwest Center for Structural Genomics. The experiment facilities of the insertion-device beamline of the Structural Biology Center (Sector 19 at the Advanced Photon Source) were used to acquire single-wavelength anomalous diffraction (SAD) data. The data were collected at the peak wavelength of the Se K-edge employing inverse-beam geometry for the tetragonal sample ($P4_12_12$, $a = 76.723 \text{ \AA}$, $c = 86.320 \text{ \AA}$, $Z = 8$, MW = 26.3 kDa). X-ray diffraction from the sample was observed to a resolution of 1.9 Å. Images were processed and the structure was solved using HKL2000. The structure consists of two domains: an hTh DNA-binding domain and a cAMP domain (PDB ID: 2gau). Additional details of data collection and structure solution, refinement and analysis will be presented.

This work was supported by the National Institutes of Health Grant GM62414 and the U. S. Department of Energy, Office of Biological and Environmental Research, under Contract W-31-109-ENG-38.