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**The Structure Determination of APC24466 from 1.4-Å SAD Data Collected at the Structural Biology Center 19BM Beamline.** R. Zhang, F.J. Rotella, R. Wu, R.W. Alkire, N.E.C. Duke, A. Joachimiak, Biosciences Div., Argonne National Laboratory, Argonne, IL 60439.

The combination of third-generation synchrotron sources, such as Argonne's Advanced Photon Source (APS), advanced computing and sophisticated software have expanded the capabilities of protein crystallography, enabling data to be collected and structures determined and refined within a day or two. The protein APC24466 was expressed, purified and crystallized as a project of the Midwest Center for Structural Genomics. The experiment facilities of the bending-magnet beamline of the Structural Biology Center (Sector 19 at the APS), which include a  $3 \times 3$ -tiled CCD detector with an active area of  $441 \text{ cm}^2$ , were used to acquire single-wavelength anomalous diffraction (SAD) data. The data were collected at the peak wavelength of the Se K-edge in approximately 30 minutes employing inverse-beam geometry for the monoclinic sample ( $P2_1$ ,  $a = 40.9 \text{ \AA}$ ,  $b = 107.8 \text{ \AA}$ ,  $c = 51.2 \text{ \AA}$ ,  $\beta = 111.49^\circ$ ,  $Z = 2$ , MW = 22 kDa). The data set covered a rotation range of  $340^\circ$  in  $1^\circ$  images with a 3-second exposure time per image. X-ray diffraction from the sample was observed to a resolution of  $1.4 \text{ \AA}$ . Images were processed using HKL2000.<sup>1</sup> Data collection, data processing, structure solution and model building were performed in 2.5 hours. Further details of data collection, structure solution and structure refinement will be presented.

<sup>1</sup>Otwinowski, Z. and Minor, W. (1997). *Methods Enzymol.* **276**, 307–326.

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