

## Crystal Structure of Yeast Hypothetical Protein, YLR351C

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Yeast proteins in sequence families for which no structural information is known, and having sequence similarity to human proteins, are being cloned, expressed, and purified for structure determination by x-ray crystallography <http://www.proteome.bnl.gov/>. The structure of yeast hypothetical protein YLR351C has been determined. This protein is a member of the Pfam CN hydrolase family, proteins that break carbon-nitrogen bonds.

Selenomethionine protein was crystallized in the pH range 5.0 to 7.0. There is a general tendency for these crystals to be twinned. However, good quality crystals diffracting to 2.5 Å were obtained at pH 6.5 with 15% PEG monomethyl ether as precipitant. Crystals belong to the monoclinic space group  $P2_1$  with cell dimensions  $a = 73.056$ ,  $b = 54.139$ ,  $c = 80.643$  Å and  $\beta = 111.97^\circ$ . The Matthews coefficient is  $2.5 \text{ \AA}^3 \text{ Da}^{-1}$  assuming two molecules per asymmetric unit. Data have been collected at three different wavelengths near the selenium absorption edge. The crystal structure has been solved by the MAD (Multiple Anomalous Dispersion) procedure using the programs SOLVE, PHASES and CCP4. The model has been built with "O" and refined by CNS. Quaternary structure of the protein shows dimeric association of monomers related by a non-crystallographic two-fold. The architecture of each monomer is a novel four-layer  $\alpha/\beta$  sandwich fold. Each  $\alpha$  layer consists of two helices and the  $\beta$  layer consists of six strands.