Crystal Structure of Glutaredoxin of CxxC1 Type from Poplar

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Glutaredoxins are small ubiquitous oxidoreductases of the thioredoxin family. The major function of glutaredoxin and thioredoxin is to selectively reduce disulfide bridges of target proteins. One of the major differences between glutaredoxin and thioredoxin is that the latter is reduced by various thioredoxin reductases whereas the former requires glutathione. The functions of plant glutaredoxins are not well understood compared to those of *E. coli* and animals. Nineteen poplar glutaredoxins have been annotated based on its genome information and they are classified into three classes [1]. We started crystal structure analysis of poplar glutaredoxin of CxxC1 type belonging to one of the three classes for deepening our understanding of plant glutaredoxins.

The glutaredoxin was overexpressed in *E.coli* cells and crystals were obtained by the hanging drop vapor diffusion method. X-ray diffraction data with three wavelengths were collected at 100K on beam line BL5A of the Photon factory, Tsukuba up to 2.3 Å resolution. The crystals belonged to space group P6₁ with unit cell dimensions a=b=97.5 Å and c=91.7 Å. The structure has been determined by the multiple-wavelength anomalous dispersion method. The polypeptide chain was traced in the electron density map and is now being refined. The molecule has a structure typical of the glutaredoxin fold but contains several new features.

[1] Rouhier N., Gelhaye E., Jacquot J.P., *Cell Mol Life Sci*, 2004, **61**, 1. **Keywords: redox enzyme, protein structure determination, MAD**