



	Experiment title: Crystallographic Investigation of Structure and Function of Photosystems I and II	Experiment number: LS-2188
Beamline: ID14 1	Date of experiment: from: 16.02.-18.02.2002	Date of report: 28.04.02
Shifts: 6	Local contact(s): Dr. Joane McCarthey	<i>Received at ESRF:</i>
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Report:

We are elucidating the three-dimensional structure of the photosystem II (PSII) purified from the thermophilic cyanobacterium *Synechococcus elongatus*. Besides the problems with long cell axis, anisotropic diffraction; the high mosaicity – in the range of 0.8° up to 1.0° - makes data collection at cryogenic temperatures to a difficult task.

Therefore we were searching for a new cryo-protocol. Many trials were not successful, but, none of them led to a decreased mosaicity. Finally we were able to establish successfully a new freezing protocol.

We were able to collect a native data set to 3.9 \AA and a completeness of 97.9 % (97.2 %). The data set was of reasonable quality with $R_{\text{sym}} = 0.081$ and $\langle I/\sigma(I) \rangle = 17$ ($R_{\text{sym}} = 0.432$ and $\langle I/\sigma(I) \rangle = 2.4$). The most significant difference to other data sets of PSII is the low mosaicity of 0.4° . The spot separation especially along the longest axes ($c = 309.87$), was Compared to former native data set, the completeness in the higher resolution shells did not drop down so

dramatically. This is due to the observation that we had a smaller number of overlapping reflection profiles due to a lower mosaicity of the crystal.

Reference

Zouni, A., Witt, H.-T., Kern, J., Fromme, P., Krauß, N., Saenger, W., Orth, P. (2001) Crystal structure of photosystem II from *Synechococcus elongatus* at 3.8 Å resolution. *Nature* **409**, 739-743.