

**Experiment title:**

Crystallographic Investigation of Structure and Function of Photosystems I and II

**Experiment****number:**

LS-2188

<b>Beamline:</b> ID14 2	<b>Date of experiment:</b> from: 22.02.2003 to: 24.02.2003	<b>Date of report:</b> 10.01.2004
<b>Shifts:</b> 6	<b>Local contact(s):</b> Dr Elena Micossi	<i>Received at ESRF:</i>

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**Report:**

During beamtime allocation LS-2188, we collected a full data set at ID14-2. Data statistics are summarized in following table:

<b>Data set</b>	<b>native</b>
X-ray source	ESRF (Grenoble), ID14-2
Wavelength (Å)	0.933
Resolution* (Å)	50 - 3.3
Unique reflections	122,001
$R_{\text{sym}}^*$	0.106 (0.681)
Completeness* (%)	91.3 (56.1)
$I/\sigma(I)^*$	12.8 (2.0)
Redundancy	3.6

\*Values in parentheses apply to highest resolution shell.

These was the data set with the highest resolution, collected by our BAG in Grenoble. The model of PSII contains 38,000 atoms corresponding to nearly 70% of the expected total number of atoms. Refinement of coordinates with CNS converged at  $R/R_{\text{free}}$  of 0.36/0.42. Despite relatively good quality of electron density maps, reliable sequence assignment was only possible in regions with specific sequence landmarks. Therefore, amino acid side chains

of fragments of the structure where sequence assignment was ambiguous were truncated and modeled as poly-Ala or C $\alpha$ -trace, resulting in a final structure containing 24,180 atoms. The refinement of these data set, reached an intermediate state, where we could assign the amino acid sequence of most of the subunits. Furthermore we identified cofactors in the electron density, which have not seen before.