



	<b>Experiment title:</b> BAG-Frankfurt	<b>Experiment number:</b> MX336
<b>Beamline:</b> ID23EH1	<b>Date of experiment:</b> from: 3.12. to: 4.12. 2004	<b>Date of report:</b> 1.2.05
<b>Shifts:</b> 2	<b>Local contact(s):</b> Dr. Laurent Terradot	<i>Received at ESRF:</i>
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## Report:

In respiration, the mobile electron carrier cytochrome *c* shuttles electrons from the cytochrome *bc*<sub>1</sub> complex (QCR) to cytochrome *c* oxidase. We determined the first structure of a respiratory membrane protein complex (yeast QCR) with the mobile electron carrier cytochrome *c* (Lange et Hunte 2002) at 3Å resolution. During our previous visit we obtained a complete dataset of 1.9Å resolution for the first time, allowing a more detailed description of the complex interface and the analysis of water-mediated interactions. For the high resolution data collection, the Marmosaic CCD detector 225 of ID23EH1 is necessary for spot separation and the high intensity beam is required. Since the completeness of the high resolution dataset was only 92.3% and to improve  $I/\sigma I$  of the high resolution shells, another dataset was collected from the crystal which gave the high resolution dataset (Resolution 2.07Å,  $R_{\text{sym}}$  13.1%,  $I/\sigma I$  4.3, Completeness 76.2 %, Spacegroup  $P2_1$ , Unit cell dimensions (Å) 145.2 165.1 194.1 90 104.2 90) in order to combine it with the previous one (Resolution 1.9Å,  $R_{\text{sym}}$  8.1%,  $I/\sigma I$  8.15, Completeness 92.2%, Spacegroup  $P2_1$ , Unit cell dimensions (Å) 145.2 165.1 194.5 90 104.1 90). Another goal of the project is to analyse redox dependent

conformational changes of the electron transfer complex. To supplement the analysis, a dataset of a crystal cocrystallized with the oxidizing reagent ferricyanide has been collected (Resolution 2.56Å (crystal was initially diffracting to 2.1 Å),  $R_{\text{sym}}$  14.2%,  $I/\sigma I$  6.6, Completeness 91.3%, Spacegroup  $P2_1$ , Unit cell dimensions 143.8 164.2 194.3 90 104.4 90), the refinement of the structure is in progress ( $R_{\text{free}}$  23.9%,  $R_{\text{cryst}}$  27.4%).

### **The Mo storage protein (MOSTO)**

MOSTO from *Azotobacter vinelandii* guarantees Mo-dependent nitrogen fixation even under growth conditions of extreme Mo starvation. The protein and also the Se-methionine labeled variant could be crystallized under diverse condition. Data were collected with native MOSTO which diffracted to about 2.7 Å resolution. However, the high radiation damage does not allow to measure a complete data set. A peak data set at 3.0 Å were also collected from a Se-methionine labelled protein. The resulting  $R_{\text{sym}}$  was 7.6 % and the completeness 98.6 %. The Se-positions could, however, not be detected but it was shown that the crystals are useful for X-ray structure determination.

### **Cytochrome *bd*-type quinol oxidase**

The cytochrome *bd*-type quinol oxidase from *B.stearothermophilus* was purified from natural source and crystallised. The initial measurements was done on ESRF ID23 1 to check the quality of the crystal. The crystal was about 0.05mmx0.1mm and there was no diffraction. Experiments to improve the quality of the crystal is in progress.