



	Experiment title: Cytochrome bc_1 -complex from <i>S. cerevisiae</i>	Experiment number: LS-1930
Beamline: ID14EH1	Date of experiment: from: 10.9.01 to: 11.9.01	Date of report: 18.02.02
Shifts: 3	Local contact(s): Dr. Cecile JAMIN	<i>Received at ESRF:</i>
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We determined the structure of the cytochrome bc_1 -complex (QCR) from *S. cerevisiae* bound to an antibody Fv fragment [1]. This mitochondrial multisubunit membrane protein is one of the fundamental components of the respiratory chain. It catalyzes electron transfer from ubiquinol to cytochrome c , while the process is coupled to electrogenic translocation of protons across the inner mitochondrial membrane. Tightly bound phospholipid molecules appear to have an important role for the structural as well as the functional integrity of the complex [2]. Recently, we crystallized QCR with the bound substrate cytochrome c and the structure of the complex critical for electron transfer was determined at 2.97 Å [3].

For further analysis of the molecular processes during quinone reduction, we were aiming to collect a data set with a Qi site specific inhibitor bound. Data collection was performed at 4 °C, we were only able to obtain a 75 % complete data set at 2.9 Å. We are currently enforcing our efforts to establish cryo-conditions for QCR measurements. We tried several crystals of promising pre-tested cryo-conditions for data collection, but no satisfying data could be obtained.

QCR is crystallized with the help of antibody fragments. Since the preparation of QCR crystals had been hampered by production problems of the recombinant antibody fragments – the problem has now been solved - a backup project was included in this beamtime.

Jörg Standfuß of Werner Kühlbrandts department of the Max-Planck-Institute of Biophysics was trying to collect a data set of recombinant light-harvesting complex. However, no full data set of sufficient resolution could be obtained.

[1] C. Hunte, T., J. Koepke, C. Lange, T. Rossmann and H. Michel (2000) Structure at 2.3 Å resolution of the cytochrome *bc*₁ complex from the yeast *Saccharomyces cerevisiae* co-crystallized with an antibody Fv-fragment. *Structure* 8, 669-684.

[2] Lange, C., Nett, J.H, Trumppower, B.L. and Hunte, C. Specific roles of tightly bound phospholipids in the yeast cytochrome *bc*₁ complex structure. *EMBO J.* 20, 6591-6600.

[2] Lange, C. and Hunte, C. (2002) Crystal structure of the yeast cytochrome *bc*₁ complex with its bound substrate cytochrome *c*. *PNAS*, in press

