ESRF	**Experiment title:** Crystal structure of bovine rhodopsin	**Experiment number:** **LS-830**
Beamline: ID13	**Date of experiment:** from: 12/10/97 to: 13/10/97	**Date of report:** 18/8/98
Shifts: 3	**Local contact(s):** C. Riekel and M. Burghammer	*Received at ESRF:* 2 8 AOUT 1998

Names and affiliations of applicants (* indicates experimentalists):

Gebhard Schertler, MRC Laboratory of Molecular Biology, Cambridge, UK
Pat Edwards, MRC Laboratory of Molecular Biology, Cambridge, UK
Paul Hargraves, Dept. of Ophtalmology, University of Florida, Gainesville, USA

Report:

Receptors for many different neurotransmitters and hormones produce their intracellular signaling response through the mediation of guanine-nucleotide binding proteins. The best characterised G-protein coupled receptor is the visual pigment rhodopsin. We have been able to obtain diffraction to better than 9A resolution either with wet mounted crystals or with crystals flash frozen in a cryoloop. In the experiment on the microfocus beamline ID13 we intended to compare the diffraction of rhodopsin crystals larger than 50μm to crystals smaller than 10μm.

We x-rayed and obtained diffraction patterns from two types of rhodopsin crystals and found the resolution improved by around 1A compared to our previous measurements. However a comparison of larger crystals with microcrystals was not yet possible because alignment of the smaller crystals was difficult.

Detailed Report:

1. We demonstrated that we could transfer the rhodopsin crystals, frozen in our dark lab under infra red light, to the microfocus diffractometer using a modified Oxford Systems extended arc and we were able to take diffraction patterns from rhodopsin crystals.

2. We compared rhodopsin crystals with crystals of a truncated form of the protein and obtained sharper diffraction spots from the truncated form. However the number of measurements made was not sufficient to reach a certain conclusion.

3. A comparison of larger crystals with microcrystals was not possible as the alignment and centring of the smaller ones was very difficult. However w e think we will be able to measure the microcrystals if the alignment procedure is improved or if we will be able to scan the cryoloop with a 50μm grid.

Perspectives

1. We need to improve the crystallization of the rhodopsin and the freezing strategy which may also be limiting resolution.

2. A better alignment procedure for microcrystals in the beam and a dev ice that can scan the loop will much improve our chances for data collection.

3. The use of a fast readout detector such as the proposed CCD camera increases our chances to measure rhodopsin microcrystals.

We would like to thank all the people from ESRF and EMBL for their help and enthusiasm in getting this experiment up and running.