



Experiment title: Crystal structure of bovine rhodopsin	Experiment number: LS-1193	
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Report:

Introduction

Receptors for many different neurotransmitters and hormones produce their intracellular signalling response through the mediation of guanine-nucleotide binding proteins. The best characterised G-protein coupled receptor is the visual pigment rhodopsin. During our previous experiment on the microfocus beamline we obtained sharper diffraction patterns but were unable to screen for crystals under 50 μ m. Our aim this time was to test diffraction from microcrystals and to try new cryo conditions.

Report

We tried different cryo conditions with crystals frozen either in liquid nitrogen or liquid ethane. In two of these conditions we obtained much improved diffraction, to better than 4\AA in one case. We were also able, for the first time, to compare diffraction patterns using both a $10\mu\text{m}$ and $30\mu\text{m}$ beam and to compare crystals from $50\mu\text{m}$ to $10\mu\text{m}$ in width. The smaller crystals with the $10\mu\text{m}$ beam gave the best diffraction patterns. The crystal shown in our figure is approximately $10\mu\text{m}$ wide and the resulting diffraction pattern was taken using a $10\mu\text{m}$ beamsize. The scanning movement along the y direction was essential in aligning these smaller microcrystals.

We were able to collect data sets from some of the crystals, however, after a short time beam damage was visible in the higher resolution range. Data analysis of these images indicates a primitive hexagonal lattice with the approximate unit cell constants of $a=b=104$ $c=77\text{\AA}$.

Summary

We were able to check improved cryo conditions, to collect data from crystals down to $10\mu\text{m}$ in size and obtain partial data sets from these, some diffracting to 4\AA resolution. The microfocus beamline was essential in these experiments. Our figure summarises our best findings.

Perspectives

1. Our aim is to repeat these conditions, collect complete data sets and to screen for heavy atom derivatives. In addition to this we have crystals of truncated rhodopsins which might diffract to higher resolution.
2. A device that can scan the cryo-loops in both x and y will improve our chances for data collection.
3. A faster computer at the beamline with MOSFLM installed for data processing would help in assessing diffraction data immediately and for selecting optimal data collection strategy. We will need to check unit cells to make sure we have isomorphous crystals and to monitor beam damage during data collection. More memory available to store data before tape backup would be helpful because last time data collection had to be interrupted to generate storage space.

