

Report of MX497 at the beamline ID14-3 (22/07/2006)

We had many difficulties during the 3 shifts assigned at ID14-3 beamline. We started our data collection at ID14-3, but unfortunately after collecting the first data set a problem occurred in the alignment of the beam that could not be solved so that we had to switch to ID14-2 beamline. This beamline is efficient and user friendly, the system of automatic centring of the crystal is very efficient and the access to the goniometer head is good, making mounting frozen crystals very easy. During data acquisition we experienced a problem with the beam stopper alignment which probably was caused by a crash with some other component of the beamline. We lost quite a lot of time since the realignment of the beam stopper proved to be not trivial; finally it was necessary to replace the beam stopper. However, we had the opportunity to recover the beamtime we lost and we could finish our experiments.

We tested several crystals of *Xenopus laevis* Glutathione S-transferase, grown at different pH, but despite their dimensions they diffracted poorly (>3.5 Å), finally we collected a crystal at 2.8 Å resolution using an oscillation range of 0.5 degrees because of a long axis. Data processing is still in progress.

We then tested several tiny crystals (average size 20µm) of murine neuroglobin, soaked with Xenon in order to identify the protein cavities, but none of them diffracted at a reasonable resolution.

After that we tested several crystals of Laminarinase endo-β-glucanase (LamA) from *Pyrococcus furiosus*, an enzyme which displays its main hydrolytic activity on the β-1,3-glucose polymer laminarin. Only one of the crystals we tested diffracted at reasonable resolution and we collected a dataset at 2.6 Å resolution. A summary of data collection is reported in table below:

| LamA | |
|------------------|---|
| Space group | C2 |
| Unit cell | a=120.9 Å, b=72.8 Å, c=91.5 Å $\alpha=90.00^\circ$, $\beta=100.54^\circ$, $\gamma=90.00^\circ$ |
| Wavelength (Å) | 0.931 |
| Resolution (Å) | 60.00 – 2.60 |
| Completeness (%) | 98.4 |
| Rmerge (%) | 6.8 |