a.o.Univ.Prof. Dr. Ulrike G. Wagner
Institut für Chemie
Heinrichstrasse 28
A-8010 Graz
Austria

Struktur Biologie
UNI GRAZ
Karl-Franzens-Universität Graz

Report on Activities during the beam time from Oct. 5th 2002 to Oct. 7th 2002 on proposal MX53

Che a 3
Very small rod-like crystals of the pollen protein have been obtained and showed limited diffraction at our home source. At ESRF one of the crystals diffracted to 1.6 A and yielded data with acceptable R-factors up to 1.7 A. A complete dataset was collected, processed and scaled. Structure solution by molecular replacement using the structure of the homologous Phl p 7 protein is in progress.

Phl p 7
The structure of Phl p 7 has been solved recently (Verdino et.el. EMBO J. 2002, **21**, 5007-16.) We now got crystals diffracting to substantially higher resolution and collected data to 1.25 A. The objective of this experiment was the characterization of a potential ligand in the internal cavity of the dimer. The high resolution structure of Phl p 7 has been refined, however no clear density for the putative ligand was visible.

SbsC7
SbsC7 is a surface layer protein from *B. stearothermophilus*. We crystallized the C-terminal deletion mutant SbsC7, which diffracted to 3.1 A. We collected a native and 3 putative derivative datasets. Data were processed and scaled to native and derivative data obtained from earlier Synchrotron data collections. Only 2 derivative datasets gave reasonable R-factors. A problem with all SbsC7 data sets collected during this beamtime was the rapid decay of the crystals due to radiation damage and the resulting lack of completeness.

Tel +43 316 380 5432 Fax .. 9850 Ulrike.Wagner@Uni-Graz.at http://physchem.kfunigraz.ac.at/sb/

SBM
Our goal was to collect data to a moderate resolution. The very long c-axis (550 Å) makes the data processing difficult, because very small errors in the orientation matrix result in wrong predictions. The crystal has good mosaicity and the spots are well separated but we still have some problems to get good enough data to solve the structure. It might be helpful to recollect one of our crystals with even smaller oscillation angles.

EstA
The collected data of a presumable Osmium derivative show a peak with very low occupancy and not enough phasing power to solve the structure. We would therefore like to collect some other derivative data to finally solve this protein structure.