

BAG Beam time Progress Report

This represents a summary of the BAG progress in the reporting period, and is **in addition** to the standard ESRF report sheet for each project which will be used for the Review of the BAG.

BAG Title BARCELONA

Allocation Period Nov-99 Feb-00

List of publications resulting from ESRF beam time

Crystal structure of the human post-chaperonin b-tubulin binding cofactor.

A. Guasch., J.C. Zabala, & M. Coll (manuscript in preparation).

Global Summary

In vitro synthesis of tubulins gives rise to the formation of different multimolecular complexes (termed C900 and C300) in addition to monomers and dimmers. P14 protein is responsible for beta-tubulin monomer release from C300 complexes. We have determined the protein structure from several data sets at different wavelengths of Se.Met protein .

The connector particle from dsDNA bacteriophage phi29 has been crystallized (Guasch et al. 1998). The crystals diffracted at least 1.9 Å at beam line ID20. A native data set was collected and processed with 98% completeness to 2.8 Å. The space group is I422 and the unit cell dimensions are $a=b=155.81$ Å and $c=160.96$ Å. The cell volume corresponds to fourth part of connector particle in the asymmetric unit. Although the orientation of the particles has been determined (Guasch et al 1998) the position of the particles in the c axis of unit cell is less certain, since the translation functions calculated using a low resolution EM model did not give a clear solution. Data collection of heavy atoms derivatives have been done. A MAD data of p10 with Ta6Br14 have been collected at BM30 beam line, data have been processed but no clear peak positions were found. Other different derivatives were collected, as Pt, Au, Ag and Hg despite the high high quality of date, no clear positions were found.

Guasch, A., Pous, J., Pàrrega, A., Valpuesta, J.M., Carrascosa, J.L., & Coll, M. (1998) Purification, crystallization and preliminary X-ray diffraction studies of bacteriophage phi29 connector particle. FEBS letters 430, 238-287.

Guasch, A., Pous, J., Pàrrega, A., Valpuesta, J.M., Carrascosa, J.L., & Coll, M. (1998) Crystallographic analysis reveals the 12 fold symmetry of the bacteriophage phi29 connector particle. J. Mol. Biol. 281, 1-7.

Visits made to the ESRF

Date(s) of visits	Beamline	No. of Shifts	Short Summary of each Visit
1. 20-22 Nov	ID142	3	4 heavy atom derivatives of p10 protein were collected
2. 24-25 Nov	BM30	3	1 MAD data set at 4 wavelengths of TaBr-p10
3. 25-26 Feb	BM14	3	1 MAD data set at 4 wavelengths of p14Semet