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|    | <b>Experiment title:</b><br>BAG CBS Montpellier | <b>Experiment number:</b><br>MX-330                                |
|   | <b>Beamline:</b><br>ID29                        | <b>Date of experiment:</b><br>from: 3 december to: 4 december 2004 |
| <b>Shifts:</b><br>3   | <b>Local contact(s):</b><br>Xavier Thibault     | <i>Received at ESRF:</i>   |
| <b>Names and affiliations of applicants</b> (* indicates experimentalists):<br>François Hoh and Christian Dumas, CBS, 34060 Montpellier, France |   |  |

#### 1/. **Protegrin-Apamin peptides:**

Six crystals were tested, two data sets collected, high (up to 1.1 Å) and low resolution (total 400 frames) . Final dataset to 1.6 Å with 93% completeness and  $R_{\text{sym}}$  of 0.12.  
Tried MR (versus NMR model) and direct method (SnB), no results

#### 2/. **Retinoic acid receptor beta (RARbeta) homodimer**

Three crystals tested.

The best dataset collected at 2.3 Å resolution (200 images,  $R_{\text{sym}}=0.068$ , completeness 96.8%).

The structure was solved by molecular replacement and is under refinement.

#### 3/. **PLCR native and SeMet labelled crystals**

One native dataset collected at 3Å (high and low resolution ,350 frames). One SAD dataset at 3Å (200 frames). One MAD dataset at 3Å (total of 450 frames for pk, ip and rm). Resolution was 3 Å at the beginning of the MAD collection and drop to 3.8Å to the end. Phasing power no strong enough (ShelX or Solve). Trying to get better crystals with higher resolution.

#### 5/ **SeCys labelled protegrin-3 precursor**

**Background:** Stability of diselenide bridges under X-ray irradiation and application for RIPAS phasing

A total of 5 data sets were collected at the same wavelength (0.97914 Å).  $R_{\text{merge}}=0.07, 0.07, 0.08, 0.08$  and 0.09 for dataset 1 to 5, respectively; completeness 98%. The anomalous and isomorphous signals of the two diselenide bridges were sufficient to solve the structure by RIPAS method. A manuscript is in preparation.

#### 6/ **MOMP-Porin:**

Five crystals tested. One diffracts at  $d_{\text{max}}$  3.2 Å but is highly sensitive to x-ray exposure. A partial dataset collected (completeness 68 %,  $R_{\text{merge}}=0.086$ ).

#### 7/ **P3 protein, aphid transmission factor**

Height crystals were tested. Only one crystal gave some diffraction at around 12Å, no indexation

#### 8/ **Erythrocrucorine**

Ten crystals were tested, diffraction about 15 Å, no indexation

#### 9/ **Akt-PH/p14 complex**

Height crystals tested, one data set collected at 3Å ( 80 images,  $R_{\text{sym}}=0.16$ , completeness 97.2%).  
RM in progress

#### 10/ **TPO**

Three crystals tested, no diffraction

## **11/ CaMV**

several crystals tested, no diffraction