Experimental report, MX-425
29.9-30.9 2005

1. Structure of an endonuclease:DNA complex

We tried to collect data for series of crystals with an endonuclease complexed with DNA. Since we have no in-house diffractometer, assessment of crystal quality prior to visits to ESRF is currently not possible. The crystals turn out to be highly disordered (layer disorder?) causing nice spot profiles in one direction and elongated streaks and overlapping spots in the other direction. Finally, we were able to collect a low-resolution data set of a relatively large wedge in reciprocal space for one of the samples. The completeness is unfortunately only about 30%. Crystal data 52Å, 59Å, 65Å, 109, 94, 90. P1. Statistics:

Resolution	3.0Å
I/sI	13
R(sym)	5%
Completeness	Only 30%

2. MAD data collection of an endonuclease:DNA-complex

The intention was to collected full MAD datasets of a protein:DNA complex, using 5-bromourasil labelled DNA. However E-scan around the bromine edge shows that the crystals are hampered by low anomalous signal. Instead we collected two native datasets. Crystal data 53.7Å, 132.3Å, 190.7Å, 90, 90, 90. Space group I222. Statistics for best data sets:

	Xtal #1 (best)
Resolution	2.8Å
I/sI	13.7
R(sym)	6.5%
Completeness	90.2%

3. Structure of a protein:nucleotide complex

We collected a dataset of S. pombe Mag2 crystals co-crystallized with urasil in order to capture the protein_nucleotide complex. Analysis of the difference electron density maps after refinement shows no sign of a bound substrate. Crystal data 71.2Å, 84.6Å, 124.7Å, 90, 90, 90. Space group $P2_12_12$. Statistics for best data sets:

	Urasil co-crystal
Resolution	2.3Å
I/sI	13.7
R(sym)	9.8%
Completeness	99.7%