



Experiment title: Cambridge MRC Block Allocation Group
AML1/DNA complex

Experiment number:
BAG LS-1669

Beamline:
ID 14-1

Date of experiment:
from:15/5/00 to:17/5/00

Date of report:

Shifts:
3

Local contact(s):
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Report:

The AML1/CBF β heterodimeric transcription factor complex is the most common target for mutations in acute leukaemia. We have previously solved the structure of the AML1/CBF β heterodimer in the absence of DNA, and we now aim to extend the study to establish the mode of DNA binding of the heterodimeric complex by determining the structure of the ternary complex of AML1/CBF β with DNA.

The proteins are bacterially expressed, and form a 40 kDa ternary complex with DNA. The crystals are small, 150 x 20 x 20 μ m. The space group is p6222, unit cell a=b=207 \AA , c=79 \AA , with one molecule per asymmetric unit. Crystals diffract weakly to 6-7 \AA .

Data collected:

1. Native (hexagonal) resolution 7 \AA , 98% complete, 3-fold redundancy
2. Native (hexagonal) resolution 6 \AA , 98% complete, 3-fold redundancy

We are currently trying to optimise the crystallisation conditions to improve the resolution of the data. We aim to solve the structure by molecular replacement from the existing DNA-unbound structure.