ESRF	**Experiment title:** Structure determination of the specific enhancer factor MEF2 DNA binding domain	**Experiment number:** LS 498
Beamline: BM02	**Date of Experiment:** from: 8/10/96 to: 10/10/96	**Date of Report:** 14/2/97
Shifts: 6	**Local contact(s):** Eric Fanchon	*Received at ESRF :* 24 FEV. 1997

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Report:

MEF2a is a member of the MADS box family of transcription factors, which are found in organisms ranging from plants to humans (Shore, P & Sharrocks, A. D., *Eur. J. Biochem.*, 1995; 229:l).

On the beamline BM02, several crystals of Mef were tested for diffraction quality. The obtained diffraction was not better than 4 Å and therefore no data from these crystals were collected. Further work is in progress to improve the crystals.

Collection of the DNA modification enzyme β-glucosyltransferase.

In T-even phage DNA cytosine bases are modified to 5'-hydroxymethylcytosine (HMC) and subsequently glucosylated by the enzyme P-glucosyltranferase (BGT). This modification is thought to protect the viral genome from host-specific restriction endonuclease attack. BGT does not recognise any specific nucleotide sequence except the modified base HMC. The structure of the free BGT enzyme and the UDPG complex have been solved by Vrielink et al, EMBO J., 1994; 13: 3413. The glucose and two loops of about 10 residues each are not defined in the electron density map and are thus missing.

A complete dataset of one crystal of the UDPG-BGT was collected on BM02 at 2.3 Å resolution. This crystal belongs to a new crystal form $P2_12_12_1$ with cell parameters :

a=69.4Å b=102.5Å c=59.4Å.

The structure was solved by Molecular replacement using the previous structure. We now have the whole structure including the two missing loops which are likely involved in DNA binding. However, the glucose is still not defined in the electron density map.

Further work is in progress to study BGT mechanism in this new crystal form.