

# EUROPEAN SYNCHROTRON RADIATION FACILITY

ESRF User Office

BP 220, F-38043 GRENOBLE CEDEX, France

Delivery address: 6 rue Jules Horowitz, 38043 GRENOBLE, France

tel: +33 (0)4 7688 2552; fax: +33 (0)4 7688 2020; email: [useroff@esrf.fr](mailto:useroff@esrf.fr); web:

<http://www.esrf.fr>



	Human multidomain p53 in complex with non specific DNA	MX-1597
ID23-2	28th of November 2013	
1 shift	Local contact: PETOSA Carlo	

## Experimental Report

### Aim of the experiment and specific background :

We aim to solve the co-crystal structure of the human transcription factor containing both the p53 DNA-binding and oligomerization domains in complex with non-specific DNA. We have already determined the structure of the co-crystal structure of p53 in complex with specific consensus DNA as well as in complex with one of its natural response element (*CDKN1A* (*p21*)) (Figure 1) (1-3). Our structure shows two p53 dimers, having in total four DNA binding domains, bound to double stranded DNA. We observed that the loop L1 that interacts with DNA has two different conformations, recessed and extended. We demonstrated that the p53-DNA binding occurs via an induced fit mechanism with a switch in the conformation that involves the loop L1 (2). We solved the structure of the loop mutant p53 in its apo form and in complex with DNA (4,5,6).

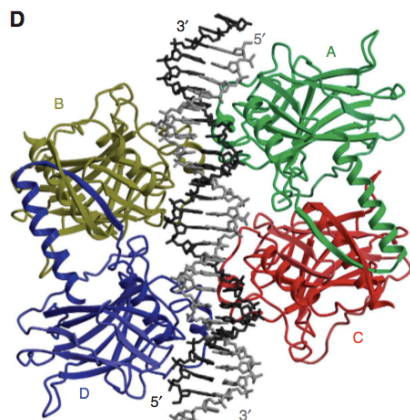


Figure 1. Structure of p53 in complex with DNA

### **Experimental method :**

We purified a stable p53 containing both the DNA-binding and oligomerization domains. We proceeded then to screen crystallographic conditions in order to obtain crystals. All experiments, from purification through crystal screening, were performed at 4 degrees Celsius to reduce precipitation and increase the chances of obtaining crystals.

We obtained p53 crystals with different sizes in a range of 30 to 50 microns (Figure 2).

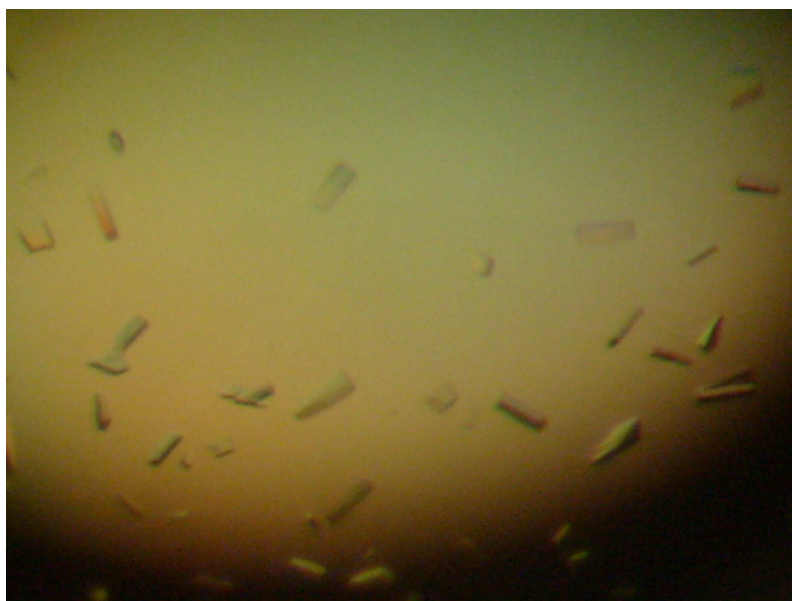


Figure 2. Crystals of p53 with non-specific DNA

### **Results:**

We were able to collect diffraction data from the four complex of p53 with non specific we had. We obtained a resolution average of about 3.5-4 Angström. However, after processing the data we were not able to determine a high resolution structure. We plan to optimize the conditions of the crystal growth in order to have better crystals.

### **References :**

1. MX-832 report
2. Petty TJ, Emamzadah S, Costantino L, Petkova I, Stavridi ES, Saven JG, Vauthey E, Halazonetis TD. *An induced fit mechanism regulates p53 DNA binding kinetics to confer sequence specificity.* EMBO J. 2011 Jun 1;30(11):2167-76
3. Emamzadah S, Tropia L, Halazonetis TD  
*Crystal structure of a multidomain human p53 tetramer bound to the natural CDKN1A (p21) p53-response element.* Mol Cancer Res. 2011 Nov; 9(11): 1493-9

4. MX-1316 report
5. MX-1506 report
6. Emamzadah S et al. *Reversal of the DNA-Binding-Induced Loop L1 Conformational Switch in an Engineered Human p53 Protein*. J Mol Biol. 2014 Feb 20; 426(4): 936-44.