



	<b>Experiment title:</b> Human p53 thermostable mutant with DNA co-crystal trial 1	<b>Experiment number:</b> TC-211
<b>Beamline:</b> ID23 2	<b>Date of experiment:</b> from: 16 April 2008 to: 16 April 2008	<b>Date of report:</b> 18 April 2008
<b>Shifts:</b> 1	<b>Local contact(s):</b> Dr Didier NURIZZO (didier.nurizzo@esrf.fr)	<i>Received at ESRF:</i>

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**Report:**

This experiment involves determining the structure of a thermostable mutant form of the human transcription factor p53 bound to DNA. The molecule of interest contains both the dna-binding domain (DBD) and the oligomerization domain, and we hypothesized that it would crystallize as a homo-dimer that would bind to a double-stranded DNA oligo pair containing the consensus hp53 binding site sequence. The crystals that were brought to the ESRF for this visit were small, on the order of 50-100 microns, and consisted of the transcription factor with DNA.

From the time spent on the microfocus beam ID23 2, we were able to capture fairly clean diffraction patterns from four small crystals grown in similar conditions. Unfortunately, most of our crystals did not give usable diffraction patterns. Of the crystals that did diffract, we were only able to acquire data in the 6 angstrom range. However, this should be enough to guide future optimization experiments in attempts to create larger, better diffracting crystals.

From initial passes through indexing we have determined a space group of C2 and unit cell dimensions of approximately 62, 36, 123. We feel that this is indicative of a unit cell large enough to contain both the hp53 dimer as well as the double stranded DNA.

We hope to return to the ESRF in the near future with more crystals to test, with the goal of finding crystals that diffract to a resolution of at least 2 angstroms. After we define the conditions giving higher resolution diffraction, we will attempt to grow crystals large enough to enable us to collect a complete, high-resolution data set from this protein-DNA complex.