ESRF	**Experiment title:** Human p53 micro-crystal trail 1	**Experiment number**: TC-206
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Report:

This experiment involves determining the structure of a thermostable mutant form of the human transcription factor p53. 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. Currently we are attempting to crystallize both the dna-bound and dna-free forms of this transcription factor. The crystals that were brought to the ESRF for this visit were small, on the order of 50-100 microns, and consisted only of the transcription factor wihtout DNA.

From the time spent on the microfocus beam ID23 2, we were able to capture fairly clean diffraction patterns from two small crystals. During the following months, we were

able to index the patterns and determine a unit cell size and space group. We are currently refining the data and using molecular replacement to solve the structure of this mutant.

Currently we have reached a resolution of 2.0 angstroms, and after simulated annealing refinement steps the final r-factor is 0.3013 and the r-free is 0.3267. The unit cell size of this hp53 mutant dimer is 69.678 73.817 106.685, 90.00 90.00 90.00, with a space group of P212121. We hope that with the current data set, we will be able to refine this structure enough to have publication quality resolution and statistics. Attempts to crystallize the DNA-bound form of this mutant have been unsuccessful thus far.

Figure 1 is an image of the hp53 mutant homo-dimer alpha-carbon backbone trace. The DNA interface is positioned at the bottom of the image, and the oligomerization domain can be seen as an alpha-helix interface at the top of the image.

Figure 1. Alpha-carbon trace of the hp53 DNA-binding and oligomerization domains.