



	<b>Experiment title:</b> 3D structure of an amidase from <i>Sulpholobus solfataricus</i>	<b>Experiment number:</b> TC103
<b>Beamline:</b> ID14-1	<b>Date of experiment:</b> from: 10-12-2000 to: 10-12-2000	<b>Date of report:</b> 28/2/2001
<b>Shifts:</b> 1	<b>Local contact(s):</b> Dr. Ed Mitchell	<i>Received at ESRF:</i>
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## Report:

During the test time allocated for this experiment we managed to collect three data sets which have advanced considerably the progress of our project, since we had previously managed to collect only one frame that allowed us to determine the space group and cell dimension of our crystals:

### Results:

1. Two complete native data sets extending to 2.55 Å resolution, the starting resolution was 2.3 Å but the crystals showed marked decay under the beam even under cryocooling, and after 50 frames the resolution was no better than 3.0 Å.
2. One complete data set of a mercury (p-hydroxymercurybenzoate, pHMB) derivative, complete to 2.2 Å resolution, interestingly, the derivative crystals showed better diffraction quality and longer life under the beam than the native ones.

Moreover we have defined the conditions for crystal freezing, since the previous data had been collected at room temperature.

The results are the subject of a paper which we have submitted to *Acta Crystallographica D*, which acknowledges the ESRF facility. We would like to thank our local contact (Dr. Ed Mitchell) for support during data collection and recovery of our data.