ESRF	Experiment title: Adenovirus ssDNA binding protein in complex with ssDNA	Experiment number: LS331
Beamline: BL19	Date of experiment: from:12/12/1995 to:15/12/1995	Date of report: 2/8/1996
Shifts: 1	Local contact(s): Dr. A. Thompson	*Received at ESRF:* 12 AUG 1996

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Report:

The aim of the experiment was to determine an anomalous signal derived from the zinc atoms in crystals of the adenovirus single-stranded DNA binding protein complexed with ssDNA. We hoped to thus improve the phase information and obtain a better interpretation of the (low resolution) density around the primary DNA binding site. The experiment was considered viable because we had previously determined conditions for flash cooling the crystals.

We initially determined experimentally the position of the zinc absorption edge and set the wavelength slightly shorter (1.28Å) to try to maximise f". Obtaining crystals that were flash cooled and diffracted to better than 8Å proved time consuming and difficult. Thus although data were eventually measured on one crystal to 5.0Å maximum resolution (76% complete with R_{sym}=7.3%), the data in the higher resolution shells were very poor (eg 5.0-5. 1Å, R_{sym}=62. 1%). Not surprisingly the anomalous difference Patterson was too noisy to be interpreted. Based on phasing from the previously determined molecular replacement solution, density is seen in the primary DNA binding site but is rather more noisy than that from a 5.5Å data set previously measured on BW7B at Hamburg from a larger crystal at 4°C[1]. The data sets could not be usefully

combined, probably because they were collected at different temperatures resulting in a change in cell dimensions (a=149.6Å, c=120.4Å at l00K compared with a=151.5Å, c= 124.0Å at 277 K). The problem appears to be that large crystals (>0.5mm maximum dimension) do not tolerate the flash cooling but the diffraction is weak from the smaller crystals (<0.2mm maximum dimension) that do tolerate the cooling. The brightness of the beam on this beamline was not adequate for the attempted experiment, although it should be pointed out that the ring was only working in 4-bunch mode during the experimental period. It seems therefore that the way forward on this project is to measure from very small crystals on a high brilliance beamline like BL4.

Kanellopoulos, P. N., van der Zandt, H., Tsernoglou, D., van der Vliet, P.C. and Tucker, P.A. (1995). Crystallization and preliminary X-ray crystallographic studies on the adenovirus ssDNA binding protein in complex with ssDNA. *J. Struct. Biol.* , 115, 113-116.