ESRF	**Experiment title:** Sso10 – an archaeal DNA-binding protein + DNA	**Experiment number**: LS-1951
Beamline: ID14-2	**Date of experiment**: from: 02/06/01 to: 03/06/01	**Date of report**:
Shifts: 3	**Local contact(s)**: Sigrid Kozielski	*Received at ESRF:*

Names and affiliations of applicants (* indicates experimentalists):

***Professor Garry Taylor**

***Dr Rupert Russell**

Centre for Biomolecular Sciences

University of St Andrews

St Andrews

Fife KY16 9ST

Report:

Sso10b is a 10.5kDa DNA binding protein found in abundance in archaea. The protein forms a dimer, and is highly basic. There is evidence that the protein is involved in the compaction of DNA, and may represent some kind of early histone. The protein has homologues in bacteria and some eukarya.

In Jan 2001, we solved the structure of sso10 from MAD data collected on ID14-4. This time we had grown what we thought were co-crystals with DNA. The crystals were R32 symmetry, compared to P6(5)22 for the previously solved apo structure.

Two crystal data sets were collected to 2.9Å max , 100% complete with Rmerge around 5%. We solved the structure using Amore on the fly, but difference maps showed no DNA! The data were useful in resolving which dimer is the biological dimer.

ESRF	**Experiment title:** Newcastel disease virus hemagglutinin-neuraminidase	**Experiment number**: LS-1951
Beamline: ID14-2	**Date of experiment**: from: 02/06/01 to: 03/06/01	**Date of report**:
Shifts: 3	**Local contact(s)**: Sigrid Kozielski	*Received at ESRF:*

Names and affiliations of applicants (* indicates experimentalists):

***Professor Garry Taylor**

***Dr Rupert Russell**

Centre for Biomolecular Sciences

University of St Andrews

St Andrews

Fife KY16 9ST

Report:

Several datasets were collected from HN co-crystallised with substrate and non-hydrolyseable substrates. Data from 2.4 – 2.9Å were collected – typically 90% complete with Rmerge = 7%.

Difference maps later showed poor density – the non-hydrolyseable substrate with its octyl group present for purificaiton purposes is a poor substrate – this was useful in planning other ligands.

ESRF	**Experiment title:** KDG aldolase from a hyperthermophile	**Experiment number**: LS-1951
Beamline: ID14-2	**Date of experiment**: from: 02/06/01 to: 03/06/01	**Date of report**:
Shifts: 3	**Local contact(s)**: Sigrid Kozielski	*Received at ESRF:*

Names and affiliations of applicants (* indicates experimentalists):

***Professor Garry Taylor**

***Dr Rupert Russell**

Centre for Biomolecular Sciences

University of St Andrews

St Andrews

Fife KY16 9ST

Report:

KDG aldolase catalyses the reversible aldol cleavage of 2-keto-3-deoxygluconate to pyruvate and glyceraldehyde in a non-phosphorylated pathway of glucose oxidation in the hyperthermophilic archaeon, *Sulfolobus solfataricus*. The enzyme is of biotechnological importance.

We had previously solved the structure with MAD data from ESRF in Jan 2001. These datasets were an attempt to trap the Schiff's base between the enzyme and pyruvate.

We collected data from 4 crystals – two from crystals formed from co-crystallisation with pyruvate, and two from cocrystallisation with pyruvate and BH. Data were collected to 1.9 – 2.1 Å with Rmerge of around 6%.