ESRF	**Experiment title:** Structure determination of the bipartite DNA binding domain of Tc3 transposase	**Experiment number:** LS1348
Beamline: ID14-4	Date of experiment: ID14-4 27-2-99 – 1-3-99 from: 7 am to: 7am	**Date of report:**
Shifts: group	**Local contact(s):**Anastassis Perrakis	*Received at ESRF:* - 1 SEP. 1999

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Report:
The time mentioned above has been shared with projects LS1351 (=LS1495)/LS1494 (=LS1348)/LS1492/LS1491/

Transposable elements, or transposons, are small stretches of DNA that can move from one position in the genome to another. Such elements have been identified in all organisms that have been studied in detail, where they show the capability to spread and multiply faster than the genome. The transposition process involves reactions similar to those important in the transmission of drug resistance between bacteria, antibody recombination and the spread of retroviral viruses in hosts. Transposons can cause human genetic disease and they are important as tools in genetic engineering and gene therapy.

Caenorhabditis elegans Tc transposons express a single transposase protein, called TcA, which is capable of performing the entire transposition process in vitro. Recognition of the transposon DNA is the first step in transposition. This occurs by a bi-partite DNA binding domain of which the N-terminal region (1-65) is required for specific binding and the C-terminal part for actual cleavage. We have solved the crystal structure of the N-terminal region of this DNA-binding domain of Tc3A in complex with its specific DNA. In this project we study the structure and function of the complete bi-partite DNA binding domain of Tc3A. This region has higher specificity than the shorter DNA binding region and binding of this longer region has a profound effect on the DNA conformation. Native data have been collected of the bipartite domain but because it is difficult to resolve the second

protein domain we wanted to a) collect higher resolution native and b) collect a good derivative data set.

One data set of a potential derivative was collected. However no sites could be detected in the difference fourier, using the molecular replacement solution. Further data need to be collected to find better derivatives.

Data statistics

	cell	mosaicity	compl	I/sigI last shell	Rmerge (last shell)	Reso
pt4	61.1 269.6 37.1	0.496	79.9	2.8	4.1 (29.1)	2.7