ESRF	**Experiment title:** *trp* RNA-binding attenuation protein (TRAP) in complex with single-stranded RNA molecules	**Experiment number:** LS1383
Beamline: ID14-4	**Date of experiment:** from: 22/02/99 to: 25/02/99	**Date of report:** 20.02.00
Shifts: BAG	**Local contact(s):** Julien Lescar	*Received at ESRF:*

Names and affiliations of applicants (* indicates experimentalists):

Fred Antson *
Guy Dodson

York Structural Biology Laboratory, Chemistry Department, University of York, Heslington, York, YO10 5DD, UK

Report:

In *B.subtilis* and several other Bacilli, attenuation of the tryptophan biosynthetic genes is controlled by the *trp* RNA-binding attenuation protein (TRAP), which senses the intracellular levels of L-tryptophan. TRAP, when activated by bound L-tryptophan, binds a specific RNA sequence in the leader segment of the nascent RNA transcript. The RNA target for TRAP contains eleven GAG or UAG trinucleotide repeats separated by two or three variable "spacer" nucleotides. By binding to this RNA, TRAP disrupts or prevents the formation of an "antiterminator" stem-loop structure allowing formation of an alternative "terminator" hairpin that leads to transcription termination.

The initial structure of TRAP in complex with RNA (53-mer with GAG triplets separated by AU dinucleotides) was determined to 1.9 Å resolution using X-ray data collected at Hamburg/EMBL BW7B beam line.

In february 1999, data sets were collected at the ESRF ID14-4 beam line from four different complexes of TRAP with RNA molecules. The use of the ID14-4 beam line resulted in an increase of the resolution of collected data (to 1.7 Å) and to a reduction in the time of each experiment by a factor of ~20, as compared to Hamburg/EMBL BW7B beam line. Three data sets were obtained from complexes of TRAP with RNA 53-mers containing GAG triplets separated by AU, UU and CC dinucleotides. The fourth data set was collected from a complex of TRAP with chimeric RNA-DNA containing deoxyribonucleotides in all positions but the third nucleotide of the TAG triplet. The refinement of all four structures is nearly

completed. Structural comparisons will aid in the understanding the specificity of TRAP/RNA interactions. All findings will be publised in due course.