



Experiment title: Structural investigation of the transcriptional regulator LrpA

Experiment number:
1636

Beamline:

Date of experiment:

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Date of report:

28 Feb 2001

Shifts:

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Received at ESRF:

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Report:

In the intervening period between the application for beam time and the date of the experiment, the structure of *Pyrococcus furiosus* LrpA was determined by MIR methods. A manuscript describing this work will be published in EMBO J. and the coordinates have been deposited in the PDB.

Abstract

The LrpA protein from the hyperthermophilic archaeon Pyrococcus furiosus belongs to the Lrp/AsnC family of transcriptional regulatory proteins, of which the E. coli leucine-responsive regulatory protein is the archetype. Its crystal structure has been determined at 2.9 Å resolution and is the first for a member of the Lrp/AsnC family as well as one of the first for a transcriptional regulator from a hyperthermophile. The structure consists of an N-terminal domain containing a helix-turn-helix (HtH) DNA-binding motif, and a C-terminal domain of mixed α/β character reminiscent of a number of RNA- and DNA-binding domains. The P. furiosus LrpA forms a homodimer mainly through interactions between the antiparallel β -sheets of the C-terminal domain and further interactions lead to octamer formation. The LrpA structure suggests how the protein might bind and possibly distort its DNA substrate through use of its HtH motifs and control gene expression. A possible location for an effector binding site is proposed by using sequence comparisons with other members of the family coupled to mutational analysis.