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Crystal Structure of the Catalytic Domain of Intron Endonuclease I-TevI

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Beamline(s): X12C

Introduction: I-TevI is a member of the GIY-YIG family of homing endonucleases. Homing endonucleases catalyze site-specific double-strand cleavage of DNA to initiate a process called homing: the insertion of an intron into an intron-less copy of the intron's host gene. I-TevI consists of a N-terminal catalytic domain and a C-terminal DNA-binding domain, connected by a long flexible linker. Here we report the crystal structures of the catalytic domain.

Methods and Materials: The structure of the domain (catalytic mutant R27A) was determined by SIRAS methods, using mercury as the derivative. All data were measured at a wavelength of 1.00 Å.

Results: The structure was determined at 2.0 Å resolution and refined to R- and R_{free} -values of 0.202 and 0.255 respectively. The domain has a novel fold, consisting of a three-stranded antiparallel β -sheet flanked by two helices on one side and a third at the other side. All catalytically important residues are located on one, slightly concave, face of the molecule.

Conclusions: Determination of the structure of the catalytic domain of I-TevI has led to a hypothesis for the catalytic mechanism of GIY-YIG endonucleases [1].

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References:

[1] P. Van Roey, L. Meehan, J.C. Kowalski, M. Belfort, and V. Derbyshire, "Catalytic domain structure and hypothesis for function of GIY-YIG intron endonuclease I-TevI", *Nature Struct. Biol.*, **9**, 806-811 (2002).