Topoisomerase IV belongs to the type II class of DNA topoisomerasers, which are responsible for changing and stabilizing DNA supercoiling and are also involved in chromosome segregation in prokaryotes. Topo IIIs are essential enzymes for bacterial replication and are targeted by antibacterial drugs such as quinolones or diones. They change enzymes for bacterial replication and are targeted by antibacterial drugs such as quinolones or diones. They change DNA topology by forming a transient covalent cleavage intermediate of a type II topoisomerase. They indicate how a type II enzyme reseals DNA during its normal reaction cycle as well as how the complex is stabilized by active-site tyrosines. These are the first structures solved for putative reactive site tyrosines. The modified nucleoside 4-thiouridine (s4U) is ubiquitously contributed to the structural stability of the tRNA molecule. The modified nucleoside 4-thiouridine (s4U) is ubiquitously contributed to the structural stability of the tRNA molecule.

Keywords: Topoisomerases, breakage-reunion, Protein-DNA complexes

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Crystal structure of a homodimeric 4-thiouridine synthetase - RNA complex. Piotr Neumann*, Kristina Lakomek, Peter-Thomas Naumann, Achim Dickmanns, Charles T. Lauhoff, Ralf Ficner,
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The maturation of all types of RNA in all domains of life includes the posttranscriptional modification of nucleosides. A wide variety of rare nucleosides has been identified, among them there are 16 different thio-nucleotides including the 4-thiouridine, the 2-thiouridine and several alkylated derivatives of 2-thiouridine. Modified nucleotides have been reported to influence vastly different cellular processes. Thiouridines are prerequisites to a correct and efficient translation process and contribute to the structural stability of the tRNA molecule. The modified nucleoside 4-thiouridine (s4U) is ubiquitously located at position eight (U8) of eubacterial and archaeal tRNAs in the loop region between the acceptor and the D stem. s4U does not only stabilize the fold of the tRNA, but also plays a central role in bacterial UV protection acting as a sensor for near-UV radiation. U8 is post-transcriptionally modified by a set of enzymes including the 4-thiouridine synthetase Thil.

Here we report the crystal structure of Thil from T. maritima in complex with a truncated substrate tRNA. The structure demonstrates that Thil functions only as homo-dimer, since the tRNA acceptor stem including the 3′-recognition element ACCA is bound by the N-terminal ferredoxin-like and THUMP domains of one monomer thereby correctly positioning U8 close to the active site in the pyrophosphatase domain of the other monomer. The structure also indicates that full-length substrate tRNA has to adopt a non-canonical conformation upon binding to Thil.

Keywords: protein-RNA complexes, RNA-binding proteins, RNA structure

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Combined biophysical techniques used to derive a model for alpha crustacyanin. John R Helliwell*, Ming-chuan Wang, Natasha Rhys, Clair Baldock and J Günter Grossmann,* School of Chemistry, University of Manchester M13 9PL, UK, Faculty of Life Sciences, University of Manchester M13 9PL, UK, STFC Daresbury Laboratory, Warrington WA4 4AD, UK.
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