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Double-stranded DNA translocation: structure and function of hexameric FtsK

Jan Löwe[a], Thomas H. Massey[b], Christopher P. Sherratt[b]

[a]MRC Laboratory of Molecular Biology, Cambridge, UK. [b]Department of Biochemistry, University of Oxford, UK. E-mail: jyl@mrc-lmb.cam.ac.uk

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FtsK is a DNA translocase that coordinates chromosome segregation and cell division in bacteria. In addition to its role as activator of XerCD site-specific recombination, FtsK can translocate double-stranded DNA rapidly and directionally, and reverse direction. We present crystal structures of the FtsK motor domain monomer, showing it has a RecA-like core, and the Ftsk hexamer, showing it is a ring with a large central annulus. Electron microscopy demonstrates the DNA-dependent existence of hexamers in solution and shows that duplex DNA passes through the middle of each ring. Comparison of FtsK monomer structures from two different crystal forms highlights a conformational change that we propose is the structural basis for a rotary inchworm mechanism of DNA translocation. We also show that two hexamers of FtsK can form a head-to-head double-ring, which suggests a model for bidirectional DNA translocation by this protein.

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Structures of viral receptor-binding fibres

Mark J. van Raaij[a]

Departamento de Bioquímica y Biología Molecular, Facultad de Farmacia, Universidad de Santiago de Compostela, Campus Sur, E-15782 Santiago de Compostela, Spain. E-mail: vanraaij@usc.es

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A distinctive family of beta-structured folds has recently been described for fibrous proteins from viruses. Virus fibers are usually involved in specific host-cell recognition. They are asymmetric homo-trimeric proteins consisting of an amino-terminal virus binding tail, a central shaft or stalk domain and a carboxy-terminal globular receptor-binding domain. Often they are entirely or nearly entirely composed of beta-structure. Apart from their biological relevance and possible gene therapy applications, their shape, stability and rigidity suggest they may be useful as blueprints for biomechanical design. Folding and unfolding studies suggest their globular carboxy-terminal domain may fold first, followed by a ″zipping-up″ of the shaft domains. The carboxy-terminal domains appear to be important for registration, because peptides corresponding to shaft domains alone aggregate into non-native fibers and/or amyloid structures. Carboxy-terminal domains can be exchanged between different fibers and the resulting chimeric proteins are useful as a way to solve structures of unknown parts of the shaft domains. The following natural triple beta-stranded fibrous folds will be discussed: the triple beta-spiral, first discovered for adenovirus fibre [1] and later found in reovirus fibre [2,3] and the bacteriophage PRD1 spike [4], triple beta-helix and T4 short tail fiber fold, both discovered in the bacteriophage T4 short tail fibre structure [5,6]. All have a central longitudinal hydrophobic core and extensive inter-monomer polar and non-polar interactions. Now a reasonable body of structural and folding knowledge has been assembled about these fibrous proteins, the next challenge and opportunity is to start to use this information in veterinary, medical and industrial applications, such as vaccination, gene therapy and nano-technology.

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