

Biochemical and biophysical characterisation of the domain structure of the HsdS subunit of EcoR124I

University of Portsmouth, Institute of Biomedical and Biomolecular Sciences - Structure and operation of the DNA



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Structure and operation of the DNA

DNA-induced dimerization of EcoKI prior to translocation has been observed using atomic force microscopy.,

Expression and Characterisation of the N

Funding for open access charge: Rural Development Administration, Republic of Korea. The dashed line shows how the end of the endonuclease domain could join with the N terminus of HsdM to form a structure similar to the type IIG structures shown on the right. EcoKI-M 2S 1 fits a closed state type I methyltransferase, but does not provide clear information about the open state.

Structural and Functional Analysis of the Symmetrical Type I Restriction Endonuclease R.EcoR124INT

The model of the M. If so, the helical domain itself could have a previously undescribed role in the translocation cycle beyond its presumed role in interacting with methyltransferase.

structure of M.EcoKI Type I DNA methyltransferase with a DNA mimic antirestriction protein

In TTE-HsdS, the CRs were found to be composed of two long antiparallel α -helices, forming a coiled coils motif. It is possible that the carbon film affects the unbound open state and that it has a more variable conformation in solution.

fragment structure of a putative HsdR subunit of a type I restriction enzyme from *Vibrio vulnificus* YJ016: implications for DNA restriction and translocation activity

Alternatively or additionally, the different temperatures for the translocation and ATPase assays might be related to the inability to translocate efficiently despite ATPase activity.

RecB

The motor subunit HsdR is composed of four distinct structural and functional domains: an endonuclease domain at the N-terminus with characteristic motifs of the RecB nuclease superfamily ; ; ; a C-terminal α -helical domain proposed to contact methyltransferase ; and two RecA-like helicase domains situated between the endonuclease and C-terminal domains ;. A predicted model of the active form of EcoR124I MTase, HsdM-AdoMet 2 —HsdS—DNA complex The close structural similarity and evident homology between both the TRDs and the catalytic domains of Type I MTases and the Type II MTase M. MATERIALS AND METHODS Protein samples M.

Biochemical and biophysical characterisation of the genetically engineered Type I restriction

These thin linkers are likely pivot points for flexing to allow the enzyme to close up.

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