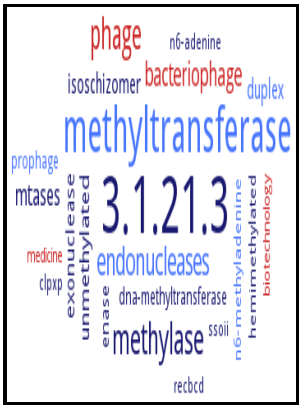
Biochemical and biophysical characterisation of the domain structure of the HsdS subunit of EcoR124I

University of Portsmouth, Institute of Biomedical and Biomolecular Sciences - Domain structure and subunit interactions in the type I DNA methyltransferase M.EcoR124I



Description: -
-Biochemical and biophysical characterisation of the domain structure of the HsdS subunit of EcoR124I
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Probing the Domain Structure of the Type IC DNA Methyltransferase M.EcoR124I by Limited Proteolysis

The Trp 212 Arg mutant of HsdS EcoR124I Mutagenesis carried out previously by Weiserova et al. Computer-aided interpretation of analytical sedimentation data for proteins. To find the best fits, normal mode analysis was performed to generate a range of conformations of HsdS and HsdM.

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

Therefore, the role of these residues must be to stabilize the position of the residues that make DNA contacts rather than stabilize the whole protein structure.

HsdR Subunit of the Type I Restriction

The HsdM in the foreground shows the N-terminal domain aa 1—153 in orange, the catalytic domain aa 154—469 in red and the C-terminal domain aa 470—529 in magenta. In addition, this region lies within the sixth beta strand of TRD2, which is also present in the crystal structure of the HsdS MjaXPI subunit and this beta strand forms the core of the TRD.

Expression and Characterisation of the N

However, this motif was disordered in the EcoR124I structure , but it is located close to the four putative nucleolytic residues in the present structure.

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