The Subunit Arrangement of the Type I Restriction Modification Enzyme M.AhdI

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Type I restriction-modification (R-M) systems encode multisubunit/multidomain enzymes. Two genes (M & S) are required to form the trimeric 160kDa methyltransferase that methylates a specific base within the recognition sequence and protects DNA from cleavage by the endonuclease. SAXS revealed an unusually large structural change in the methyltransferase following DNA binding; this involves a major repositioning of the subunits of the enzyme, resulting in a 60Å reduction in the dimensions of the enzyme on forming a complex with DNA.

The type I R-M enzyme M.AhdI has been prepared in two protonated/deuterated states (S and M subunits protonated, S deuterated and M protonated) for which SANS data has been collected in a number of H:D solvent contrasts in the presence and absence of DNA. *Ab initio* shape determination of this contrast matched data has allowed us to determine the change in subunit positioning that occurs on DNA binding and how this results in the 60Å reduction in the dimensions of the enzyme.

Keywords: SANS, restriction-modification, contrast