Structure of the Q237W mutant of *HhaI* DNA methyltransferase: an insight into protein-protein interactions

Aiping Dong^{1,a}, Lan Zhou^{1,b}, Xing Zhang¹,
Shawn Stickel², Richard J. Roberts² and
Xiaodong Cheng^{1,*}

¹Department of Biochemistry, Emory University School of Medicine, 1510 Clifton Road, Atlanta, GA 30322, USA

²New England Biolabs, 32 Tozer Road, Beverly, MA 01915, USA

*Corresponding author
e-mail: xcheng@emory.edu

Abstract

We have determined the structure of a mutant (Q237W) of *HhaI* DNA methyltransferase, complexed with the methyl-donor product AdoHcy. The Q237W mutant proteins were crystallized in the monoclinic space group C2 with two molecules in the crystallographic asymmetric unit. Protein-protein interface calculations in the crystal lattices suggest that the dimer interface has the specific characteristics for homodimer protein-protein interactions, while the two active sites are spatially independent on the outer surface of the dimer. The solution behavior suggests the formation of *HhaI* dimers as well. The same *HhaI* dimer interface is also observed in the previously characterized binary (*M.HhaI*-AdoMet) and ternary (*M.HhaI*-DNA-AdoHcy) complex structures, crystallized in different space groups. The dimer is characterized either by a non-crystallographic two-fold symmetry or a crystallographic symmetry. The dimer interface involves three segments: the amino-terminal residues 2–8, the carboxy-terminal residues 313–327, and the linker (amino acids 179–184) between the two functional domains – the catalytic methylation domain and the DNA target recognition domain. Both the amino- and carboxy-terminal segments are part of the methylation domain. We also examined protein-protein interactions of other structurally characterized DNA MTases, which are often found as a 2-fold related ‘dimer’ with the largest dimer interface area for the group-β MTases. A possible evolutionary link between the Type I and Type II restriction-modification systems is discussed.

Keywords: DNA methyltransferase; evolutionary link; protein-protein interactions; Type I and II restriction-modification systems.

Introduction

The DNA cytosine methyltransferase (MTase) *M.HhaI* recognizes the sequence 5'-GCGC-3' and methylates the internal cytosine by flipping the target cytosine completely out of the DNA duplex (Klimašauskas et al., 1994). The remainder of the duplex is left as nearly intact B-form and the DNA gap created by base flipping is filled by insertion of the side chain of Gln237. No covalent bonds are broken to carry out the base flipping (Roberts and Cheng, 1998) – only the base-pairing hydrogen bonds are broken and the π -stacking interactions between adjacent base pairs are lost. Insertion of Gln237 into the π -gap restores the hydrogen-bonding network to the orphan guanine but interrupts the aromatic manifold by which charge migration through the DNA can occur. However, a mutant of *M.HhaI* in which Gln237 is replaced with tryptophan (G237W), an aromatic heterocyclic amino acid, appeared to restore charge migration through the DNA duplex, implying that the tryptophan insertion into the DNA gap maintains the π -stacked array (Rajski et al., 1999).

In an effort to study the nature of tryptophan insertion into the DNA gap, we attempted to crystallize the ternary complex containing the Q237W mutant, the methyl-donor product AdoHcy, and a short oligonucleotide containing the *HhaI* recognition sequence. Although no DNA is incorporated in the crystal, the mutant enzyme was crystallized in a new space group with two molecules per asymmetric unit. This observation prompted us to examine the protein-protein interactions in different crystal lattices as well as in solution.

Early solution studies suggested that some DNA MTases exist predominantly as dimers: *M.RsrI* shows partial dimerization in solution (Kaszukska et al., 1989), two *DpnI* MTases appear to exist as dimers (de la Campa et al., 1987), and *M.MspI* dimerizes in solution at high concentration (>3 mg/ml; Dubey et al., 1992), while some MTases remain monomeric in solution (*M.BamHI*, Nardone et al., 1984; *M.EcoRI*, Rubin and Modrich, 1977). In experiments involving crosslinking of the *BamHI* MTase subunits, it was shown that the enzyme in a free state exists as a dimer (Malygin et al., 2001). A similar behavior was observed for adenine *M.CcrM* from *C. crescentus* dimerized at physiological concentrations, and the dimerization does not affect DNA methylation (Shier et al., 2001).

In the absence of DNA substrate, *M.HhaI*, *M.TaqI*, *M.PvuII*, and *M.MboIIA* were crystallized with two molecules per asymmetric unit (Cheng et al., 1993; Labahn et al., 1994; Gong et al., 1997; Osipiuk et al., 2003), while *M.DpnII*, *M.RsrI*, and *M.EcoT4Dam* with one molecule (Tran et al., 1998; Scavetta et al., 2000; Yang et al., 2003). In the presence of DNA substrate, *M.HhaI*-DNA existed as one protomer and a single copy of double-stranded DNA (Klimašauskas et al., 1994), while *M.HaeIII*-DNA and

^aPresent address: Department of Biochemistry, University of Toronto, Toronto, Ontario M5S1A8, Canada

^bPresent address: Office of Information Technology, Georgia Institute of Technology, Atlanta, GA 30332, USA

Figure 1 The *M.HhaI* dimer in the crystal lattices and solution.

(A) Two views of the dimer of the *M.HhaI* mutant Q237W. The insert shows the side chains from one protomer in yellow and from the other in black.

(B) *HhaI* MTase dimer in the presence of DNA. A schematic drawing shows the MTase domain in green, the TRD domain is indicated in red, and the dimer interface in yellow.

(C) Elution profile of *M.HhaI* on a Superdex 2000HR column.

(D) Cross-linking of *M.HhaI* with disuccinimidyl suberate (DSS). The concentration of protein and cross-linker and the size of the molecular mass marker are indicated. The amount of protein (5 μg) loaded onto the gel was the same in all five slots.

M.TaqI-DNA complexes contained two such complexes in the asymmetric unit (Reinisch et al., 1995; Goedecke et al., 2001).

For non-DNA AdoMet-dependent MTases, many enzymes are monomeric, while some exhibit features of dimerization and/or oligomerization. For example, small molecule glycine N-MTase is a tetrameric enzyme (Takata et al., 2003), guanidinoacetate MTase forms a dimer (Komoto et al., 2002), RNA MTases of the SPOUT family are dimers with their active sites constructed as a topological knot (Michel et al., 2002; Nureki et al., 2002), and protein arginine MTases (PRMTs) form ring-like dimers that can be further oligomerized in some cases (Weiss et al., 2000; Zhang et al., 2000; Zhang and Cheng, 2003). Here we examined the protein-protein interactions of *M.HhaI* in three different crystal lattices. The dimerization behavior of *M.HhaI* in solution and its potential link to other types of restriction-modification systems are also discussed.

Results

Structure of the Q237W mutant

Although a short DNA duplex containing a *HhaI* recognition site was used for crystallization, the cognate oli-

gonucleotide was missing from the new crystal structure. There are two possible reasons. First, although the mutant methylates DNA *in vivo* and *in vitro*, the specific activity is only about 2% of the wild-type enzyme (Mi et al., 1995). Second, Trp237 radical formation would be thermodynamically feasible but appears not to yield significant amounts of kinetically trapped products (Rajski et al., 1999). However, the bound AdoHcy indicates that cofactor binding is not affected by the mutation.

Q237W mutant proteins were crystallized in the C-centered monoclinic space group C2 with two molecules in the crystallographic asymmetric unit. The two protomers present in the asymmetric unit are very similar: least squares superposition of the two molecules gave a root-mean-square-deviation of 0.647 Å for 307 pairs of Cα atoms. The overall structure of Q237W is shown in Figure 1A. The structure contains two parts: a catalytic methylation domain (green) and a DNA binding domain (red). The methylation domain is formed by a mixed seven-stranded β-sheet (green), a characteristic feature of the class-I AdoMet-dependent MTases (Schubert et al., 2003). While a contiguous region forms the DNA binding domain (red), the catalytic domain consists of two non-contiguous regions: the N-terminal region (green) and a carboxy-terminal helix αZ (yellow) located on one side of the β-sheet.

Table 1 Protein interface parameters.

Parameter	M.Hhal	32 homodimers examined (Jones and Thornton, 1996)
ΔASA ($\text{\AA}^2$)	652.5	1685 $\pm$ 1101 (range 584–2786)
Planarity ^a	1.9	3.5 $\pm$ 1.7
Interface residue segments ^b	3	5 $\pm$ 2.6
Hydrogen bonds	4	0.7 $\pm$ 0.5 per 100 $\text{\AA}^2$

^aFor definitions, see Jones and Thornton (1996).^bInterface residues separated by more than five residues were allocated to different segments.**Table 2** Summary of the dynamic light scattering experiments.

[c] (mg/ml)	D_T^a	R_H (nm)	MW (kDa)	Polydispersity (%)
0.87	382	4.04	85	40
2.32	385	4.01	84	30
7.94	383	4.03	85	28

^aDiffusion constant, expressed in units of 10^{-9} cm²/s; $D_T = K_B T / 6\pi\eta R_H$ where K_B is the Boltzmann constant, T is the absolute temperature in Kelvin, η is the solvent viscosity (10% glycerol used in the experiment), and R_H is the hydrodynamic radius of the average scattering particle.

While the mutant Q237W-AdoHcy was crystallized in the C-centered monoclinic space group C2, the M.Hhal-AdoMet complex was previously crystallized in the monoclinic space group P2₁ (Cheng et al., 1993; O'Gara et al., 1999). The crystallization conditions (polyethylene glycol 4000 vs. ammonium sulfate) and crystal properties such as space groups (P2₁ vs. C2) and unit cell dimensions ($a=55.3$ $\text{\AA}$, $b=74.68$ $\text{\AA}$, $c=90.96$ $\text{\AA}$, and $\beta=103^\circ$ vs. $a=155.0$ $\text{\AA}$, $b=47.0$ $\text{\AA}$, $c=122.7$ $\text{\AA}$, and $\beta=121^\circ$) are completely different in these two cases. One common feature is that both crystals contain two molecules per asymmetric unit and the loop containing the residue 237 is not involved in any crystal packing contacts. Furthermore, in both monoclinic lattices, a pair of the protomers is related through the carboxy-terminal helix α_Z (yellow) by a two-fold non-crystallographic rotation. A more intriguing finding is that the same dimer interface also exists in the M.Hhal-DNA-AdoHcy complexes (Klimasauskas et al., 1994; Vilkaitis et al., 2000); in the ternary complexes, the dimer is characterized by a 2-fold crystallographic symmetry in the rhombohedral space group R32 (Figure 1B).

The two DNA substrates, and hence the active sites, are located on the outer surface of the dimer. These observations prompted us to examine the protein-protein interactions in different crystal lattices.

Hhal dimer formation in crystal lattices

We calculated all possible protein-protein interfaces in the lattices of P2₁, C2, and R32 based on the change in solvent accessible surface area (ΔASA) when going from a monomeric to a dimeric state (<http://www.biochem.ucl.ac.uk/bsm/PP/server>; Jones and Thornton, 1996). The largest change in ΔASA was found for a pair of the protomers related through the carboxy-terminal helix by a two-fold rotation in all three lattices (Figure 1A, B). There are several indications (Table 1) that this interface has the characteristics specific for dimer protein-protein interactions (Jones and Thornton, 1995): (i) the 652 $\text{\AA}^2$ of ΔASA is within the limits, though in the lower end, of the 32 homodimers examined (Jones and Thornton, 1996); (ii) the interface is mainly hydrophobic

Table 3 Summary of DNA MTase interface surface area related by 2-fold NCS or CS.

Enzyme	PDB	Space group	Molecule or complex per asymmetric unit	Molecule related by 2-fold symmetry	ΔASA ($\text{\AA}^2$)
5 mC MTases					
M.Hhal	1SVU (Q237W)	C2	2	+ (NCS)	699
	2HMY	P2 ₁	2	+ (NCS)	761
	1MHT	R32	1 (protein/DNA)	+ (CS)	725
M.HaelIII	1DCT	P2 ₁ ,2 ₁	2 (protein/DNA)	+ (NCS)	607
DNMT2	1G55	I4 ₁	1	+ (CS)	782
Group α amino-MTases					
M.DpnII	2DPM	P2 ₁ ,2 ₁	1	-	-
T4DAM	1Q0T	P2 ₁	2 (protein/DNA)	+ (NCS)	404
	1Q0S	P2 ₁ ,2 ₁	1	-	-
Group β amino-MTases					
M.PvuII	1BOO	P2 ₁	2	+ (NCS)	2317
M.RsrI	1EG2	C222 ₁	1	+ (CS)	1706
M.MboII	1G60	P2 ₁	2	+ (NCS)	1966
Group γ amino-MTases					
M.TaqI	2ADM	P2 ₁ ,2 ₁	2	+ (NCS)	164
	1G38	P2 ₁	2 (protein/DNA)	-	-

Figure 2 The 2-fold related DNA MTase structures.

One protomer is shown in yellow and the other in green. The dimer is related by a 2-fold non-crystallographic symmetry (NCS) or crystallographic symmetry (NC). The dimer interface area (ΔASA) was calculated using AREAIMOL of CCP4.

formed by Tyr313, Tyr316, Phe324, Pro326, and Tyr327 (Figure 1A) and 62.5% of the atoms in the interface are non-polar; (iii) the interface also involves two hydrogen bonds – the side chain of Asn323 to the side chain of Gln8 and the side chain of Asn317 to the main chain of Tyr327; (iv) three segments (amino acids 2–8, 179–184, 313–327) of the polypeptide chain are involved in the interface. The amino-terminal segment and the carboxy-terminal segment are part of the methylation domain (colored green in Figure 1A and B), while the residues 179–184 are part of the linker between the methylation and DNA-binding domains.

***HhaI* dimer formation in solution**

There are several indications that this structural dimer may also exist in solution: (i) gel filtration results suggest that *M.HhaI* has an apparent molecular mass of a dimer. On a Superdex 200 column (Pharmacia), *M.HhaI* eluted as a 60 kDa globular protein (Figure 1C), larger than the calculated molecular mass (37 kDa). (ii) Dynamic light scattering measurement at a range of protein concentrations suggested that the hydrodynamic radius of *M.HhaI* is 4 nm and would correspond to an 85 kDa globular protein (Table 2). This dimension ($2 \times 4 = 8$ nm) is between

the shorter (4.7 nm) and the longer (12 nm) dimensions of the dimer (Figure 1A). (iii) A portion of *M.HhaI* formed a covalent dimer after cross-linking by glutaraldehyde or disuccinimidyl suberate (Figure 1D). These data suggest that the dimers seen in the crystal structures of *M.HhaI* could also exist in solution.

Comparison with other structurally characterized DNA MTases

At this time, the structural characterization of nine DNA MTases has been reported (Table 3). These include three generating 5mC (*M.HhaI*, *M.HaeIII*, and human Dnmt2), one generating N4mC (*M.PvuII*), and five generating N6mA (*M.TaqI*, *M.DpnII*, *M.RsrI*, *M.MboIIA*, and *M.EcoT4Dam*). We examined the protein-protein interactions in the crystal lattices to search for a pair of protomers related by a 2-fold rotation, either through non-crystallographic symmetry (NCS) if two proteins or protein-DNA complexes existed in the asymmetric unit or through crystallographic symmetry (CS) if only one protein or protein-DNA complex was present in each asymmetric unit.

With the exception of *M.DpnII*, all other structurally characterized MTases can be found as a 2-fold related

'dimer' (Figure 2). The dimer interface does not block the active site or the DNA binding cleft. The Δ ASA values are distributive: (i) the largest Δ ASA values are from *M.MboIIA* (1966 Å²), *M.RsrI* (1706 Å²), and *M.PvuII* (2317 Å²) (Figure 2D–F). These values are at the high end of the homodimers examined by Jones and Thornton (1996). All three are β -group DNA MTases (Malone et al., 1995) and show, interestingly, a similar protomer interface between two molecules (Osipiuk et al., 2003). Most likely, these β -group DNA MTases are dimeric in solution (Kaszukska et al., 1989; Osipiuk et al., 2003). (ii) For the 5mC MTases examined (Figure 2A–C), the Δ ASA values, being at the low end but within the limit of Jones and Thornton (1996), are approximately 3 times less than that of β -group enzymes. As demonstrated by *M.MspI* (Dubey et al., 1992), these enzymes could dimerize in solution in a concentration-dependent fashion. (iii) The smallest Δ ASA value is from *M.TaqI* in the absence of DNA (164 Å²); this value is outside of the lower limit of Jones and Thornton (1996). This may explain that the *M.TaqI* interface shown in Figure 2G is not observed for the *M.TaqI*-DNA complex, even though two such complexes existed in the asymmetric unit. (iv) Similarly, the *M.EcoT4Dam* interface (Figure 2H) observed in the presence of DNA (404 Å²) does neither exist in the substrate-free T4Dam nor in a GATC-related orthologous *M.DpnII* structure, although both α -group MTases were previously suggested to dimerize in solution (de la Campa et al., 1987; Evdokimov et al., 2002).

Discussion

The type II restriction-modification systems consist of two independent components that, respectively, restrict and modify DNA (Roberts and Halford, 1993). Restriction involves a homodimeric endonuclease (ENase) cleaving DNA by hydrolyzing the phosphodiester backbone on both strands, while modification involves a MTase adding a methyl group to a DNA base on one strand at a time. Both the restriction and the modification activities recognize the same DNA sequence. The cleavage occurs at fixed positions that are symmetrically-disposed relative to the symmetrical recognition sequence, and within or adjacent to that sequence. The methylation occurs at a position within the palindromic recognition sequence that blocks the paired restriction activity.

Most of the structurally characterized Type II ENase-DNA complexes comprise a protein dimer and a single copy of a double-stranded oligonucleotide in the crystallographic asymmetric unit, the smallest repeating unit within a crystal. However, for the *R.BglI*-DNA complex, there was only one protein subunit and one DNA strand in the asymmetric unit, and thus the biologically active homodimer was generated by a two-fold axis of crystallographic symmetry (Newman et al., 1998).

Although the functional significance, if any, of the Type II MTase dimer is unclear, one possibility is that the dimeric form of *HhaI* MTase allows formation of a large enzyme-substrate network with high molecular weight DNA, as demonstrated for *Serratia* nuclease (Franke et al., 1999). Although the two subunits of *Serratia* nuclease

Table 4 Summary of crystallographic data.

Space group	C2	
Unit cell dimensions	a=155.0 Å b=47.0 Å c=122.7 Å $\beta=121^\circ$	
Resolution range (Å)	24.54–2.66	2.75–2.66
Completeness (%)	91.6	89.1
$R_{\text{merge}} = \sum I - \langle I \rangle / \sum I$	0.082	0.231
$\langle I/\sigma \rangle$	16.8	3.0
Observed reflections	69 737	-
Unique reflections	19 780	1916
Refinement		
Number of atoms		
Protein	2432 (molecule A) 2446 (molecule B)	
AdoHcy	26×2	
SO ₄	5×2	
Water	43	
$R_{\text{factor}} = \sum F_o - F_c / \sum F_o $	0.189	0.267
R_{free} (5% of the data)	0.266	0.337
Rms deviation from ideal		
Bond lengths (Å)	0.009	
Bond angles (°)	1.4	
Dihedrals (°)	27.8	
Improper (°)	0.68	
Estimated coordinate error		
Luzzati plot (Å)	0.29	
Mean B value (Å ²)	37.7	

function independently of each other, they bind simultaneously to one macromolecular DNA, forming a large network between the enzyme and the substrate. Homodimeric DNA MTases may serve the same function. At present, we do not have any evidence against the notion that two monomers act independently from each other in the *HhaI* homodimer.

Type II MTase dimers might also provide an evolutionarily link to other types of restriction-modification systems. Type II MTases are bilobal molecules with a catalytic methylation domain (shown in green in Figure 1A and B), responsible for AdoMet binding and the methyl transfer reaction, and a target recognition domain (TRD) responsible for DNA binding. In some cases, MTases are expressed as two polypeptides that associate to form the active enzymes (Karreman and de Waard, 1990; Lee et al., 1996). In addition, the Type IIS systems consist of two MTases (sometimes expressed as a single fusion protein) that individually modify the two asymmetric strands of the recognition sequences.

The Type I systems are heteropentamers with two modification (M) subunits, one DNA specificity (S) subunit, and two restriction (R) subunits (Rao et al., 2000). With respect to the Type II systems, the Type I S subunit contains two TRDs (Sturrock and Dryden, 1997) and the M₂S complex is active as a MTase (see Dryden, 1999).

Interestingly, the Type IIH systems have Type II ENases and Type I-like MTases (G.G. Wilson, personal communication). The *XcmI* MTase likely is a dimer because the gene for the methylation domain (M) is fused to that for a single TRD (in effect one half of an S subunit). The *AhdI* MTase is active as a tetramer (two M subunits and two single TRDs) that is very similar to the artificial Type I systems (Marks et al., 2003). The Type IIH MTases form

a clear link between Type I and Type II restriction-modification systems by utilizing gene fusions and the shuffling of structural and functional domains (Dryden, 1999). The *M.HhaI* dimer, mediated mainly by the catalytic domain (or M subunit) and the linker, but not the DNA binding domain (or S subunit), may simply reflect such an evolutionary relationship.

Materials and methods

The mutant protein Q237W was engineered, expressed, and purified as described previously (Kumar et al., 1992; Mi et al., 1995). For recording the elution profile of *M.HhaI* on a Superdex 2000HR column (Pharmacia, Piscataway, USA), the protein was loaded onto the column at a concentration of 5 mg/ml. The column buffer was 20 mM HEPES pH 7.0, 50 mM NaCl, 0.1 mM Na₂EDTA, 5% glycerol and 0.1% 2-mercaptoethanol. Cross-linking of *M.HhaI* with disuccinimidyl suberate (DSS) was performed at room temperature for 30 min in buffer containing 20 mM HEPES pH 7.0, 0.2 M NaCl, 0.1 mM EDTA, 5% glycerol and 0.1% 2-mercaptoethanol. Total protein (5 µg) was loaded on a 10% SDS polyacrylamide gel. The dynamic light scattering experiments were performed at 16 °C using a DynaPro Molecular Sizing Instrument (Protein Solutions, High Wycombe, UK). Because polydispersity is greater than 25%, a multiple-exponential algorithm (regularization analysis) was employed.

The cofactor-free Q237W protein in 20 mM Tris-HCl, 100 mM NaCl, 5% glycerol, 1 mM EDTA, 1 mM DTT was concentrated to 25 mg/ml (0.68 mM) and incubated with AdoHcy and DNA (5'-TGATAGCGCTATC-3') in an equal molar ratio. Crystals were grown under the conditions of 2.2 M ammonium sulfate, 50 mM sodium citrate, pH 5.8. The X-ray diffraction intensities were measured from a single crystal frozen under a cryogenic temperature at beam-line X12C of the National Synchrotron Light Source, Brookhaven National Laboratory. The crystal diffracted to 2.66 Å resolution (Table 4).

The structure was solved by the molecular replacement program AmoRe (Navaza, 2001) using the refined protomer T250G structure (Vilkaitis et al., 2000) as the search model by deleting the side chain of residue 237; two solutions were found indicating each asymmetric unit contains two molecules. The solution was confirmed by the appearance of the electron densities corresponding to the side chains of Thr250 and Trp237. Numerous cycles of model refinement using XPLOR (Brunger et al., 1998) and manual rebuilding using O (Jones and Kjeldgaard, 1997) were conducted. A series of simulated annealing omit maps were used to correct the model. The non-crystallographic restraints were imposed on the two protein molecules throughout the refinement and were only released from protein side chains at the last cycle to account for a different packing environment with each molecule. The final model consists of 307 out of 328 amino acids in protein chain A, 314 amino acids in protein chain B, and two AdoHcy molecules. The missing residues, amino acid residues 80–99 in protomer A and residues 84–96 in protomer B that could not be modeled due to the poor quality of the electron density, are part of the active-site loop that undergoes large conformational changes upon DNA binding (Cheng et al., 1993; Klimašauskas et al., 1994).

Acknowledgments

We thank Susan Sunay (Emory University, Atlanta, USA) for dynamic light scattering measurement and gel filtration experiments and G.G. Wilson (New England Biolabs, Beverly, USA) for sharing his unpublished data. This work was supported in part

by National Institutes of Health grants GM46127 to R.J.R. and GM49245 to X.C.

References

- Brunger, A.T., Adams, P.D., Clore, G.M., DeLano, W.L., Gros, P., Grosse-Kunstleve, R.W., Jiang, J.S., Kuszewski, J., Nilges, M., Pannu, N.S. et al. (1998). Crystallography & NMR system: a new software suite for macromolecular structure determination. *Acta Crystallogr. D Biol. Crystallogr.* 54, 905–921.
- Cheng, X., Kumar, S., Posfai, J., Pflugrath, J.W., and Roberts, R.J. (1993). Crystal structure of the *HhaI* DNA methyltransferase complexed with S-adenosyl-L-methionine. *Cell* 74, 299–307.
- de la Campa, A.G., Kale, P., Springhorn, S.S., and Lacks, S.A. (1987). Proteins encoded by the *DpnII* restriction gene cassette: two methylases and an endonuclease. *J. Mol. Biol.* 196, 457–469.
- Dryden, D.T.F. (1999). Bacterial DNA methyltransferases. In: *S-adenosylmethionine-Dependent Methyltransferases: Structures and Functions*, X. Cheng and R.M. Blumenthal, eds. (Singapore: World Scientific Publishing), pp. 283–340.
- Dubey, A.K., Mollet, B., and Roberts, R.J. (1992). Purification and characterization of the *MspI* DNA methyltransferase cloned and overexpressed in *E. coli*. *Nucleic Acids Res.* 20, 1579–1585.
- Evdokimov, A.A., Zinoviev, V.V., Malygin, E.G., Schlagman, S.L., and Hattman, S. (2002). Bacteriophage T4 Dam DNA-(N6-adenine)-methyltransferase. Processivity and orientation to the methylation target. *J. Biol. Chem.* 278, 7829–7833.
- Franke, I., Meiss, G., and Pingoud, A. (1999). On the advantage of being a dimer, a case study using the dimeric *Serratia* nuclease and the monomeric nuclease from *Anabaena* sp. strain PCC 7120. *J. Biol. Chem.* 274, 825–832.
- Goedecke, K., Pignot, M., Goody, R.S., Scheidig, A.J., and Weinhold, E. (2001). Structure of the N6-adenine DNA methyltransferase *M.TaqI* in complex with DNA and a cofactor analog. *Nature Struct. Biol.* 8, 121–125.
- Gong, W., O'Gara, M., Blumenthal, R.M., and Cheng, X. (1997). Structure of *PvuII* DNA-(cytosine N4) methyltransferase, an example of domain permutation and protein fold assignment. *Nucleic Acids Res.* 25, 2702–2715.
- Jones, S., and Thornton J.M. (1995). Protein-protein interactions: a review of protein dimer structures. *Prog. Biophys. Mol. Biol.* 63, 31–65.
- Jones, S., and Thornton J.M. (1996). Principles of protein-protein interactions. *Proc. Natl. Acad. Sci. USA* 93, 13–20.
- Jones, T.A., and Kjeldgaard, M. (1997). Electron-density map interpretation. *Methods Enzymol.* 277, 173–208.
- Karremans, C., and de Waard, A. (1990). *Agmenellum quadruplicatum* *M.AqI*, a novel modification methylase. *J. Bacteriol.* 172, 266–272.
- Kaszubski, W., Aiken, C., O'Connor, C.D., and Gumpert, R.I. (1989). Purification, cloning and sequence analysis of *RsrI* DNA methyltransferase: lack of homology between two enzymes, *RsrI* and *EcoRI*, that methylate the same nucleotide in identical recognition sequences. *Nucleic Acids Res.* 17, 10403–10425.
- Klimašauskas, S., Kumar, S., Roberts, R.J., and Cheng, X. (1994). *HhaI* methyltransferase flips its target base out of the DNA helix. *Cell* 76, 357–369.
- Komoto, J., Huang, Y., Takata, Y., Yamada, T., Konishi, K., Oga, H., Gomi, T., Fujioka, M., and Takusagawa, F. (2002). Crystal structure of guanidinoacetate methyltransferase from rat liver: a model structure of protein arginine methyltransferase. *J. Mol. Biol.* 320, 223–235.
- Kumar, S., Cheng, X., Pflugrath, J.W., and Roberts, R.J. (1992). Purification, crystallization, and preliminary X-ray diffraction analysis of an *M.HhaI*-AdoMet complex. *Biochemistry* 31, 8648–8653.

- Labahn, J., Granzin, J., Schluckebier, G., Robinson, D.P., Jack, W.E., Schildkraut, I., and Saenger, W. (1994). Three-dimensional structure of the adenine-specific DNA methyltransferase *M.Taq* I in complex with the cofactor S-adenosylmethionine. *Proc. Natl. Acad. Sci. USA* 91, 10957–10961.
- Lee, K.-F., Liaw, Y.-C., and Shaw, P.-C. (1996). Overproduction, purification and characterization of *M.EcoHK31*, a bacterial methyltransferase with two polypeptides. *Biochem. J.* 314, 321–326.
- Malone, T., Blumenthal, R.M., and Cheng X. (1995). Structure-guided analysis reveals nine sequence motifs conserved among DNA amino-methyltransferases, and suggests a catalytic mechanism for these enzymes. *J. Mol. Biol.* 253, 618–632.
- Malygin, E.G., Ovechkina, L.G., Zinovev, V.V., Lindstrom, U.M., and Reich, N.O. (2001). DNA-(N4-cytosine)-methyltransferase from *Bacillus amyloliquefaciens*: kinetic and substrate binding properties. *Mol. Biol. (Moscow)* 35, 42–51.
- Marks, P., McGeehan, J., Wilson, G., Errington, N., and Kneale, G. (2003). Purification and characterisation of a novel DNA methyltransferase, *M.AhdI*. *Nucleic Acids Res.* 31, 2803–2810.
- Mi, S., Alonso, D., and Roberts, R.J. (1995). Functional analysis of Gln-237 mutants of *HhaI* methyltransferase. *Nucleic Acids Res.* 23, 620–627.
- Michel, G., Sauve, V., Larocque, R., Li, Y., Matte, A., and Cygler, M. (2002). The structure of the RlmB 23S rRNA methyltransferase reveals a new methyltransferase fold with a unique knot. *Structure* 10, 1303–1315.
- Navaza, J. (2001). Implementation of molecular replacement in AMoRe. *Acta Crystallogr. D Biol. Crystallogr.* 57, 1367–1372.
- Newman, M., Lunnen, K., Wilson, G., Greci, J., Schildkraut, I., and Phillips, S.E. (1998). Crystal structure of restriction endonuclease *BglI* bound to its interrupted DNA recognition sequence. *EMBO J.* 17, 5466–5476.
- Nardone, G., George, J., and Chirikjian, J.G. (1984). Sequence-specific *BamHI* methylase: purification and characterization. *J. Biol. Chem.* 259, 10357–10362.
- Nureki, O., Shirouzu, M., Hashimoto, K., Ishitani, R., Terada, T., Tamakoshi, M., Oshima, T., Chijimatsu, M., Takio, K., Vas-silyev, D.G. et al. (2002). An enzyme with a deep trefoil knot for the active-site architecture. *Acta Crystallogr. D Biol. Crystallogr.* 58, 1129–1137.
- O'Gara, M., Zhang, X., Roberts, R.J., and Cheng, X. (1999). Structure of a binary complex of *HhaI* methyltransferase with S-adenosyl-L-methionine formed in the presence of a short non-specific DNA oligonucleotide. *J. Mol. Biol.* 287, 201–209.
- Osipiuk, J., Walsh, M.A., and Joachimiak, A. (2003). Crystal structure of *MbolIA* methyltransferase. *Nucleic Acids Res.* 31, 5440–5448.
- Rajski, S. R., Kumar, S., Roberts, R.J., and Barton, J.K. (1999). Protein-mediated DNA electron transfer. *J. Am. Chem. Soc.* 121, 5615–5616.
- Rao, D.N., Saha, S., and Krishnamurthy, V. (2000). ATP-dependent restriction enzymes. *Prog. Nucleic Acid Res. Mol. Biol.* 64, 1–63.
- Reinisch, K.M., Chen, L., Verdine, G.L., and Lipscomb, W.N. (1995). The crystal structure of *HaeIII* methyltransferase covalently complexed to DNA: an extrahelical cytosine and rearranged base pairing. *Cell* 82, 143–153.
- Roberts, R.J., and Halford, S.E. (1993). Type II restriction endonucleases. In: *Nucleases*, S.M. Linn, R.S. Lloyd, and R.J. Roberts, eds. (Cold Spring Harbor, NY, USA: Cold Spring Harbor Laboratory Press), pp. 35–88.
- Roberts, R.J., and Cheng, X. (1998). Base flipping. *Annu. Rev. Biochem.* 67, 181–198.
- Rubin, R.A., and Modrich, P. (1977). *EcoRI* methylase: physical and catalytic properties of the homogeneous enzyme. *J. Biol. Chem.* 252, 7265–7272.
- Scavetta, R.D., Thomas, C.B., Walsh, M.A., Szegedi, S., Joachimiak, A., Gumpert, R.I., and Churchill, M.E.A. (2000). Structure of *RsrI* methyltransferase, a member of the N6-adenine β class of DNA methyltransferases. *Nucleic Acids Res.* 28, 3950–3961.
- Schubert, H.L., Blumenthal, R.M., and Cheng, X. (2003). Many paths to methyltransfer: a chronicle of convergence. *Trends Biochem. Sci.* 28, 329–335.
- Shier, V.K., Hancey, C.J., and Benkovic, S.J. (2001). Identification of the active oligomeric state of an essential adenine DNA methyltransferase from *Caulobacter crescentus*. *J. Biol. Chem.* 276, 14744–14751.
- Sturrock, S.S., and Dryden, D.T. (1997). A prediction of the amino acids and structures involved in DNA recognition by type I DNA restriction and modification enzymes. *Nucleic Acids Res.* 25, 3408–3414.
- Takata, Y., Huang, Y., Komoto, J., Yamada, T., Konishi, K., Oga-wa, H., Gomi, T., Fujioka, M., and Takusagawa, F. (2003). Catalytic mechanism of glycine N-methyltransferase. *Biochemistry* 42, 8394–8402. [Erratum published in *Biochemistry* 42 (2003), p. 10874.]
- Tran, P.H., Korszun, Z.R., Cerrirelli, S., Springhorn, S.S., and Lacks, S.A. (1998). Crystal structure of the *DpnI* DNA adenine methyltransferase from the *DpnII* restriction system of *Streptococcus pneumoniae* bound to S-adenosylmethionine. *Structure* 6, 1563–1575.
- Vilkaitis, G., Dong, A., Weinhold, E., Cheng, X., and Klimasauskas, S. (2000). Functional roles of the conserved threonine 250 in the target recognition domain of *HhaI* DNA methyltransferase. *J. Mol. Chem.* 275, 38722–38730.
- Weiss, V.H., McBride, A.E., Soriano, M.A., Filman, D.J., Silver, P.A., and Hogle, J.M. (2000). The structure and oligomerization of the yeast arginine methyltransferase, Hmt1. *Nat. Struct. Biol.* 7, 1165–1171.
- Yang, Z., Horton, J.R., Zhou, L., Zhang, X.J., Dong, A., Zhang, X., Schlagman, S.L., Kossykh, V., Hattman, S., and Cheng, X. (2003). Structure of the bacteriophage T4 DNA adenine methyltransferase. *Nat. Struct. Biol.* 10, 849–855.
- Zhang, X., and Cheng, X. (2003). Structure of the predominant protein arginine methyltransferase PRMT1 and analysis of its binding to substrate peptides. *Structure* 11, 509–520.
- Zhang, X., Zhou, L., and Cheng, X. (2000). Crystal structure of the conserved core of protein arginine methyltransferase PRMT3. *EMBO J.* 19, 3509–3519.

Received January 9, 2004; accepted February 9, 2004