

Crystal structure of NAD⁺-dependent DNA ligase: modular architecture and functional implications

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DNA ligases catalyze the crucial step of joining the breaks in duplex DNA during DNA replication, repair and recombination, utilizing either ATP or NAD⁺ as a cofactor. Despite the difference in cofactor specificity and limited overall sequence similarity, the two classes of DNA ligase share basically the same catalytic mechanism. In this study, the crystal structure of an NAD⁺-dependent DNA ligase from *Thermus filiformis*, a 667 residue multidomain protein, has been determined by the multiwavelength anomalous diffraction (MAD) method. It reveals highly modular architecture and a unique circular arrangement of its four distinct domains. It also provides clues for protein flexibility and DNA-binding sites. A model for the multidomain ligase action involving large conformational changes is proposed.

Keywords: DNA ligase/helix–hairpin–helix motif/
nucleotidyl transferase/oligomer-binding fold/zinc finger
motif

Introduction

All life forms on earth depend on DNA ligases for joining the breaks in double-stranded DNA, which is a crucial step in replication and repair of DNA and in genetic recombination (Lehman, 1974; Lindahl and Barnes, 1992; Tomkinson and Levin, 1997). They catalyze the formation of phosphodiester bonds at single-stranded or double-stranded breaks between adjacent 3'-hydroxyl and 5'-phosphate termini (Lehman, 1974; Tomkinson and Levin, 1997). DNA ligases fall into two classes depending on the cofactor specificity. ATP-dependent ligases are ubiquitous in eukaryotes and they are also encoded by eukaryotic DNA viruses, bacteriophages of the T series and archaeobacteria. In contrast, NAD⁺-dependent ligases are found exclusively in eubacteria. This makes NAD⁺-dependent DNA ligases a potential target for developing novel antibiotics. Thermostable bacterial DNA ligases with high fidelity have applications in detecting disease-associated mutations by ligase chain reaction (Barany, 1991). The sequence similarity between these two classes is not detected readily except for the Lys-Xaa-Asp-Gly

(KXDG) sequence motif, which is one of the six conserved sequence elements (I, III, IIIa, IV, V and VI) present among members of the covalent nucleotidyl transferase superfamily including ATP-dependent DNA ligases, RNA and tRNA ligases, and the eukaryotic mRNA guanylyl transferases (capping enzymes) (Shuman and Schwer, 1995). The recently developed iterative sequence database search method, however, allowed the detection of five of the conserved sequence motifs, with the exception being VI (Aravind and Koonin, 1999).

Apart from the difference in cofactor requirement, the reactions catalyzed by the two classes of DNA ligase are identical. In the first step, an AMP group derived from either cofactor is covalently attached to the conserved lysine residue within the KXDG motif. The AMP moiety is then transferred from the adenylated enzyme intermediate to the free 5'-phosphoryl group at a nicked site of duplex DNA. Finally, the AMP group is released from the adenylated DNA intermediate as the phosphodiester bond is formed (Lehman, 1974; Tomkinson and Levin, 1997). Several structures of nucleotidyl transferases including the 41 kDa ATP-dependent DNA ligase from bacteriophage T7 (Subramanya *et al.*, 1996), a GTP-dependent mRNA guanylyl transferase (Håkansson *et al.*, 1997; Håkansson and Wigley, 1998) and the N-terminal fragment ('adenylation' domain) of an NAD⁺-dependent DNA ligase from *Bacillus stearothermophilus* (*Bst* ligase) (Singleton *et al.*, 1999) provided the details on the cofactor binding site and adenylation/guanylation step of the reaction. However, our understanding of the architecture of multidomain DNA ligases of more typical size, the DNA-binding mode and possible domain rearrangements during catalytic steps is very limited. To gain insight into such questions, we solved the crystal structure of the entire NAD⁺-dependent DNA ligase from *Thermus filiformis* (*Tfi* ligase), a monomeric protein of 667 amino acid residues (M_r 75 936 Da). This study provides the first view of the full-length NAD⁺-dependent DNA ligase, including the C-terminal half, which was reported to play an important role in DNA binding (Timson and Wigley, 1999). It reveals highly modular architecture suited for the possible large conformational changes that seem to be necessary for its action.

Results and discussion

Structure determination

Recombinant *Tfi* DNA ligase, in both native and selenomethionine (SeMet)-substituted forms, was expressed, purified and crystallized as described in Materials and methods. Due to the severe non-isomorphism of heavy atom derivative crystals, initial trials with the multiple isomorphous replacement method were not successful and the structure had to be determined using three-wavelength

Table I. Crystallographic data, phasing and refinement statistics

Data set	Radiation	Resolution (Å)	Total/unique reflections	Completeness (%) ^a $I/\sigma(I)$	R_{sym} (%) ^b	Phasing power ^c acentric/centric
Native	1.009 Å, X8-C	30–2.8 (2.9–2.8)	142 175/43 634	97.9 (95.3)	11.5 (5.7)	6.4 (45.6)
SeMet-1 (remote)	0.9400 Å, X12-C	30–2.9 (3.0–2.9)	215 788/40 641	97.9 (79.2)	9.8 (4.0)	7.0 (46.3)
SeMet-2 (inflection)	0.9788 Å, X12-C	30–2.9 (3.0–2.9)	311 355/40 546	98.1 (80.8)	11.8 (5.4)	5.9 (34.1)
SeMet-3 (peak)	0.9784 Å, X12-C	30–2.9 (3.0–2.9)	315 581/40 572	98.2 (81.9)	12.0 (5.5)	6.4 (32.1)
Figure of merit ^d for MAD phasing using SeMet-1–3 data (calculated for 30–2.9 Å)				0.52 (before DM)/0.80 (after DM)		
Data set	Resolution (Å)	No. of reflections ^e	Total no. of atoms ^f	R -factor/ R_{free} (%) ^g	R.m.s. deviations ^h	
					bond lengths (Å)	bond angles (°)
Native	8.0–2.8	38 138 (90.7%)	10 080 (264)	25.1/31.6	0.012	1.91
SeMet-1	20–2.9	36 053 (89.5%)	9674 (242)	22.8/29.8	0.007	1.52

^aCompleteness for $I/\sigma(I) > 1.0$, high-resolution shell in parentheses.

^b $R_{\text{sym}} = \sum_h \sum_i |I(h)_i - \langle I(h) \rangle| / \sum_h \sum_i I(h)_i$, where $I(h)$ is the intensity of reflection h , \sum_h is the sum over all reflections and \sum_i is the sum over i measurements of reflection h . Numbers in parentheses reflect statistics for the last shell.

^cPhasing power is the mean value of the heavy atom structure factor amplitude divided by the residual lack of closure error for both acentric and centric reflections.

^dFigure of merit = $\langle |\sum P(\alpha) e^{i\alpha} / \sum P(\alpha)| \rangle$, where α is the phase and $P(\alpha)$ is the phase probability distribution.

^eNumbers reflect the reflections with $F/\sigma(F) > 2.0$, overall completeness in parentheses.

^fNumbers in parentheses are water molecules.

^g $R = \sum |F_{\text{obs}}| - |F_{\text{calc}}| / \sum |F_{\text{obs}}|$, where R_{free} (Brünger, 1992b) is calculated for a randomly chosen 10% of reflections [$F/\sigma(F) > 2.0$] that were not used for structure refinement, and the R -factor is calculated for the remaining reflections.

^hDeviations from ideal bond lengths and angles.

multiwavelength anomalous diffraction (MAD) data collected from a crystal of the SeMet-substituted enzyme (see Table I). Subsequently, the structure of the native enzyme was also refined. Two molecules of *Tfi* ligase in the asymmetric unit of the crystal take somewhat different conformations. The conformational difference between the two copies is more pronounced in the crystal of the native enzyme than in the crystal of the SeMet-substituted enzyme. Root-mean-square (r.m.s.) deviations are 2.1 and 1.1 Å for 581 C_{α} atom pairs, respectively. The electron density for residues beyond 581 is missing for all but one molecule of the native enzyme in the most closed conformation. Since the electron density for this part was rather poor, only a polyalanine model was built for most of the residues 582–660 in this molecule.

Modular architecture of *Tfi* ligase

Tfi ligase is toroidal with approximate dimensions of $95 \times 75 \times 55$ Å, displaying highly modular architecture (Figure 1A and B). The polypeptide chain is folded into four discrete domains. Domain 1 (residues 1–317) consists of two subdomains. Subdomain 1a (residues 1–73) is mainly α -helical. The ‘adenylation’ subdomain 1b (residues 74–317) comprises two mainly antiparallel β -sheets flanked by α -helices and contains the adenylation site (Lys116) within the KXDG motif. Domain 2 (residues 318–403) contains a five-stranded antiparallel β -barrel of the oligomer-binding (OB) fold (Murzin, 1993), which is formed by β -strands 12–16 and α -helix M. The latter helix, located between strands 14 and 15, covers one end of the β -barrel. Domain 3 (residues 404–581) consists of two subdomains. Subdomain 3a (residues 404–429) is a Cys₄-type zinc finger (Schmiedeskamp and Klevit, 1994; Klug and Schwabe, 1995; Mackay and Crossley, 1998), which includes a β -hairpin formed by strands 17 and 18. Subdomain 3b (residues 430–581) comprises four helix–hairpin–helix (HhH) motifs (helix

pairs O–P, R–S, U–V and X–Y) (Thayer *et al.*, 1995; Doherty *et al.*, 1996). Domain 4 (residues 582–660) is a distinct member of the BRCT (BRCA1 C-terminus) domain superfamily (Bork *et al.*, 1997; Callebaut and Mornon, 1997). All adjacent (sub-) domains are linked by a single chain. A circular arrangement of the four domains leads to a hole large enough to hold a double-stranded DNA with average side chain–side chain distances of 15 Å (height) \times 25 Å (width) \times 25–50 Å (depth).

The C-terminal BRCT domain was invisible in the MAD-phased electron density map of the SeMet-substituted enzyme, probably because it is disordered in the crystal. However, one of the two ligase molecules in the asymmetric unit of the native enzyme crystal, which adopted the most closed conformation, showed a weak and discontinuous electron density for the BRCT domain. This indicates that the BRCT domain of *Tfi* ligase is rather mobile as a whole in the open conformation but its mobility is somewhat restricted in the closed conformation. Compared with the most open conformation, domain 3 in the most closed conformation is shifted by ~ 6.4 Å toward domain 1, by a rigid-body rotation around the hinge in the loop between domains 2 and 3 (Figure 2A). As a consequence, the BRCT domain nearly contacts the conserved segment around the N-terminus of helix B. The orientation of subdomain 1a relative to subdomain 1b in the N-terminal fragment of *Bst* ligase is significantly different from that of *Tfi* ligase (Singleton *et al.*, 1999). Subdomain 1a of *Bst* ligase is rotated by $\sim 90^\circ$ around Pro68, which is also conserved in *Tfi* ligase (Figure 2B). If subdomain 1a of *Tfi* ligase takes the orientation of *Bst* ligase, its interaction with the BRCT domain is more extensive. It is not clear whether this discrepancy is related to the adenylation state of domain 1b. However, it suggests that subdomain 1a can make a large domain movement relative to subdomain 1b.

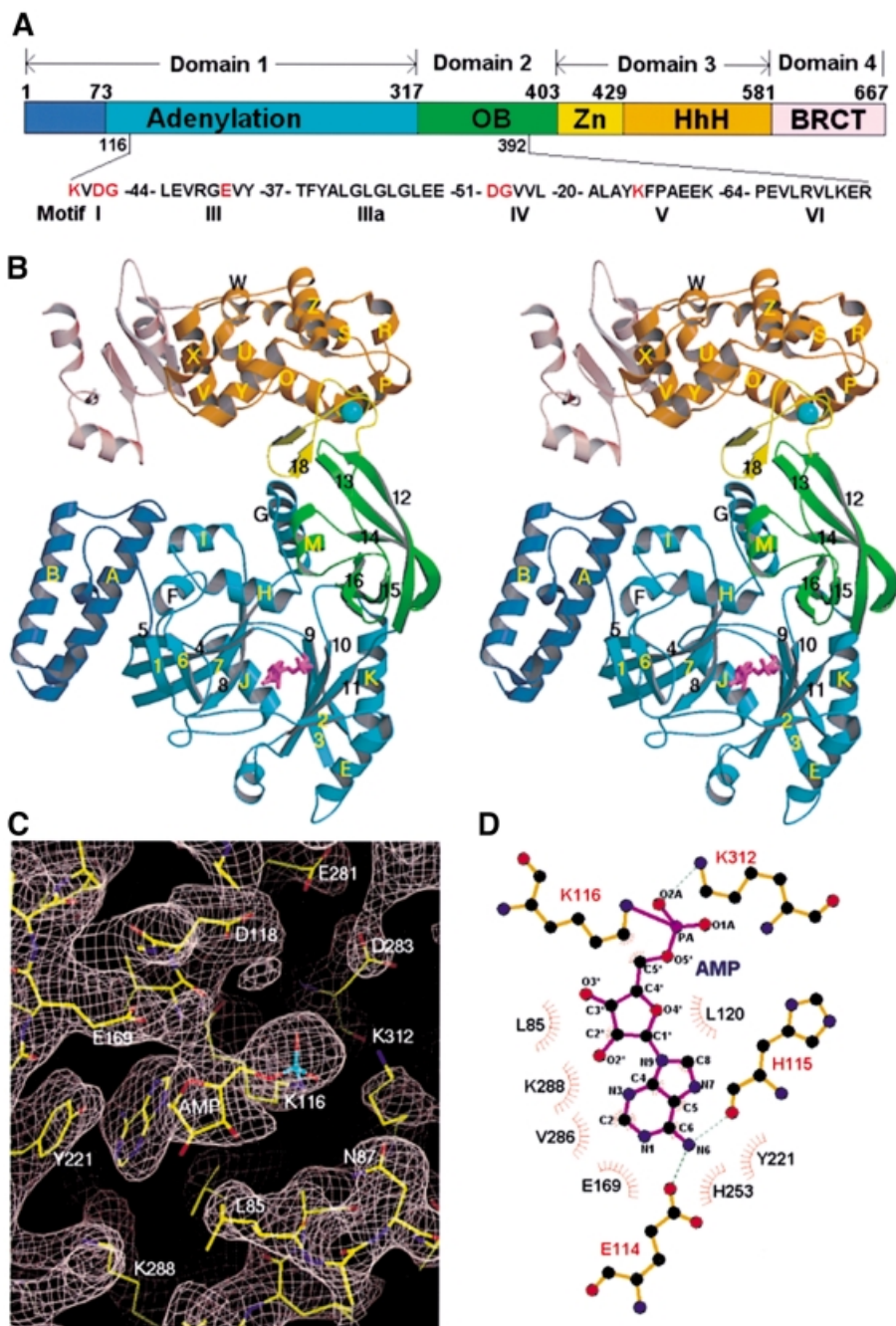


Fig. 1. The structure of *Tfi* DNA ligase. **(A)** Domains and conserved sequence motifs of *Tfi* DNA ligase. Domains are in different colors: subdomain 1a, blue; subdomain 1b, cyan; domain 2, green; subdomain 3a, yellow; subdomain 3b, orange; domain 4, light pink. Residues in red are more strongly conserved than others. **(B)** Stereo ribbon diagram of *Tfi* DNA ligase. Drawn with MOLSCRIPT (Kraulis, 1991) and RASTER3D (Merritt and Bacon, 1997). Domain colors are the same as in (A). The covalently bound AMP moiety (stick model in purple) and a zinc ion (a cyan ball) are shown. Secondary structures were defined by PROCHECK (Laskowski *et al.*, 1993). **(C)** Electron density map calculated using MAD solvent-flattened phases around the covalently bound AMP group. Atoms are yellow for carbon, red for oxygen, blue for nitrogen and cyan for phosphorus. **(D)** Residues around the AMP moiety. Atom colors are the same as above except black for carbon. Hydrogen bonds between the AMP and protein residues are represented by green dotted lines. Drawn with LIGPLOT (Wallace *et al.*, 1995).

Adenylation domain

Although the cofactor NAD⁺ was not added deliberately during protein purification and crystallization, an AMP moiety was covalently attached to Lys116 within the KXDG motif, as indicated by the initial MAD-phased, solvent-flattened electron density map (Figure 1C). Thus, the present structure provides a direct view of the covalent enzyme–adenylate intermediate of the proposed catalytic mechanism. The AMP-binding pocket is located between the two β -sheets of subdomain 1b (Figure 1B). The

interactions between the covalently bound AMP and the enzyme are depicted in Figure 1D. The negative charge of α -phosphate is compensated for by the positive charge on Lys312 (distance 3.1 Å). The adenine ring is stacked against the side chain of Tyr221 in a deep pocket, which is lined with Leu85, Leu120, Val286 and the aliphatic portions of Glu169, Tyr221, His253 and Lys288. The 6-amino group of the adenine ring makes hydrogen bonds with the main chain carbonyl of His115 and the side chain of Glu114. Lys288 and Glu114 form an ion pair at the

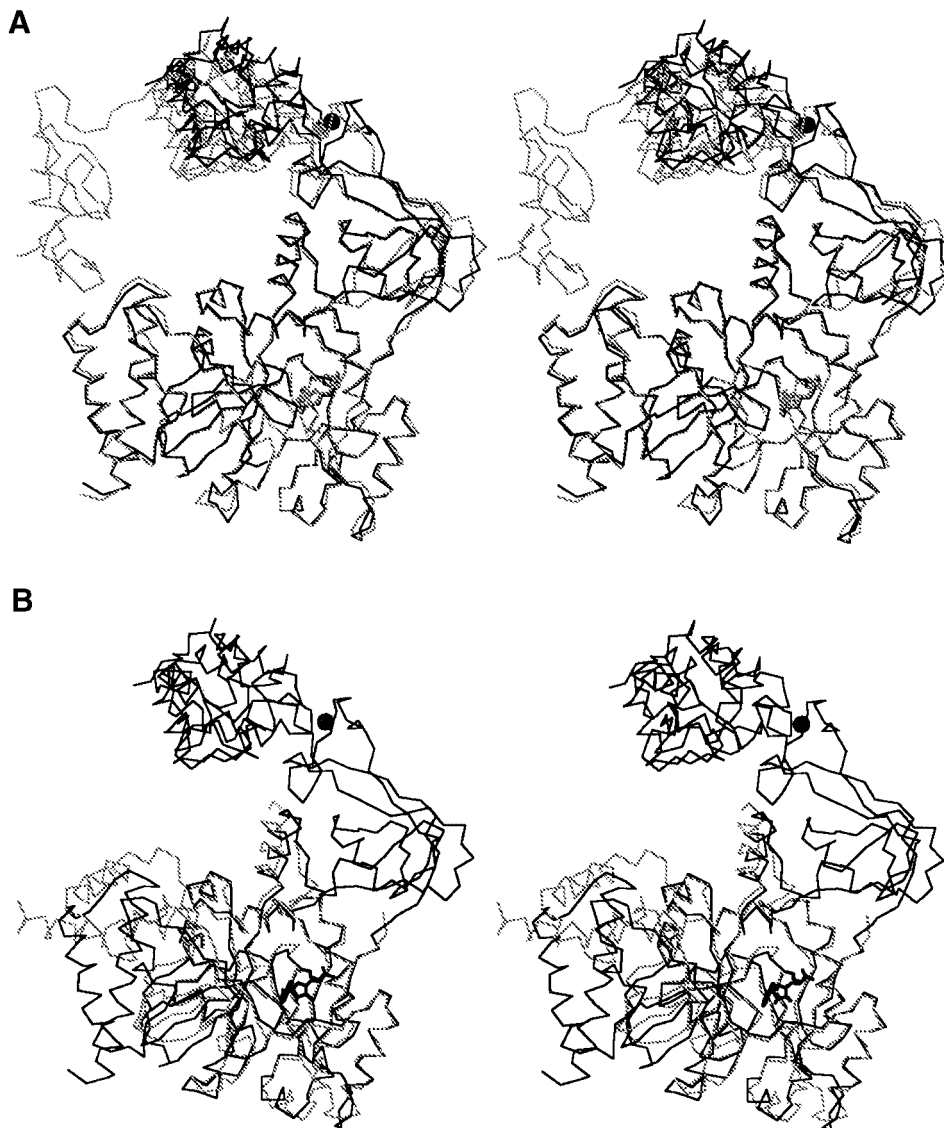


Fig. 2. Stereo C_{α} superposition of *Tfi* DNA ligase. (A) One of the two crystallographically independent ligase molecules in the native structure takes a more closed conformation (gray) than the other (black), and its BRCT domain is visible in the electron density map. Superposition is made for domain 1. (B) Subdomain 1a of *Bst* ligase (gray) takes a very different orientation from that of *Tfi* ligase (black). Superposition is made for subdomain 1b.

base of the AMP-binding pocket. A similar ion pair is also present in the ATP-dependent DNA ligase from bacteriophage T7 (Lys222 and Glu32) (Subramanya *et al.*, 1996). Many of the residues that line the AMP-binding pocket of *Tfi* ligase belong to five (motifs I, III, IIIa, IV and V) of the six sequence elements conserved among covalent nucleotidyl transferases (Shuman and Schwer, 1995). The observed binding mode is conserved in other non-covalent or covalent complexes of T7 DNA ligase (Subramanya *et al.*, 1996) and *Chlorella* virus mRNA guanylyl transferase (Håkansson *et al.*, 1997; Håkansson and Wigley, 1998). Motif VI encompasses the last strand of the 'OB-fold' domain 2 (strand 16). It was proposed that the corresponding motif in the mRNA guanylyl transferase binds and positions the triphosphate tail of GTP (Håkansson *et al.*, 1997). Site-directed mutagenesis studies on human DNA ligase III also implicated this motif in the interaction with nicked DNA (Mackey *et al.*, 1999). The location of this motif in the *Tfi* ligase structure

does not seem to rule out the possibility of its involvement in interactions with both the cofactor NAD^{+} and DNA.

OB-fold domain

Domain 2 of *Tfi* ligase contains all of the three structural determinants of the OB-fold as defined previously (Bycroft *et al.*, 1997). This fold is common among RNA or single-stranded DNA-binding (SSB) proteins (Murzin, 1993; Draper and Reynaldo, 1999), including the bacterial ribosomal proteins S1 (Bycroft *et al.*, 1997) and S17 (Jaishree *et al.*, 1996), the subunits of replication protein A (the eukaryotic SSB protein) (Bochkarev *et al.*, 1997, 1999), the *Oxytricha nova* telomere end-binding protein (Horvath *et al.*, 1998), bacterial cold-shock proteins CspA and CspB (Schindler *et al.*, 1998), *Pyrobaculum aerophilum* translation initiation factor (IF) 5A (Peat *et al.*, 1998), *Escherichia coli* translation IF 1 (Sette *et al.*, 1997), *E. coli* SSB protein (Raghunathan *et al.*, 1997), *E. coli* RuvA DNA recombination protein (Roe *et al.*, 1998), staphylococcal

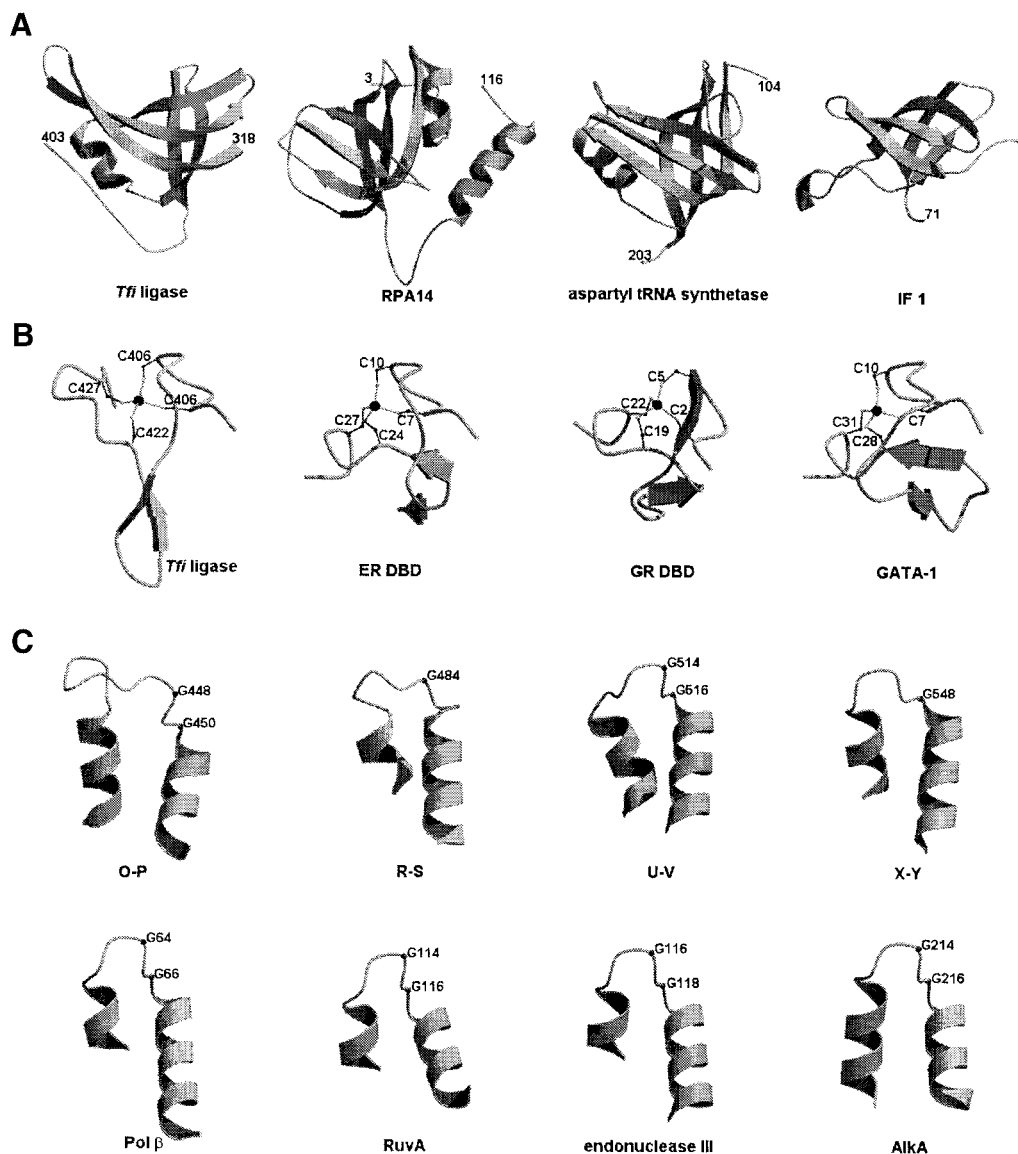


Fig. 3. Comparison of OB-fold domains, zinc fingers and HhH motifs. (A) OB-fold domains of *Tfi* ligase, human replication protein A subunit (RPA14), yeast aspartyl tRNA synthetase and *E.coli* translation initiation factor 1 (IF 1) are shown in similar orientations. (B) Cys₄-type zinc fingers of *Tfi* ligase, human estrogen receptor DNA-binding domain (ER DBD), rat glucocorticoid receptor DBD (GR DBD) and chicken erythroid transcription factor (GATA-1) are shown in similar orientations. Cysteines that coordinate the zinc ion are labeled. (C) HhH motifs of *Tfi* ligase (top row), human DNA polymerase β, *Mycobacterium leprae* RuvA, *E.coli* endonuclease III and *E.coli* AlkA (bottom row) are shown in similar orientations. Conserved glycine residues are indicated.

nuclease (Murzin, 1993) and several tRNA synthetases (Murzin, 1993). A structural comparison is shown in Figure 3A. Many of the OB-fold proteins bind their ligands on the side surface of the β-barrel distant from the middle of the first strand (strand 12 in *Tfi* ligase). The equivalent domain in T7 DNA ligase is a much shortened version of the OB-fold. Also, compared with *Tfi* ligase, its orientation in the non-covalent ATP complex is rotated around the loop just before the first strand of the OB-fold domain so that its expected DNA-binding surface is not exactly facing the active site (Subramanya *et al.*, 1996). This may be understandable, because the adenylation site should not be blocked by binding the DNA until the conserved lysine at the active site is adenylated. This orientation may change upon self-adenylation so that the putative DNA-binding groove will be completed. Since T7 DNA ligase with a more compact OB-fold domain is

fully functional, we suggest that domain 1 together with the OB-fold domain is the minimal unit for the bacterial DNA ligases and that this minimal ligase should have the nick sensing as well as the ligation activities. Our suggestion is supported further by the recent finding that the 298 residue ATP-dependent DNA ligase of *Chlorella* virus, the smallest eukaryotic DNA ligase known, has intrinsic specificity for binding to nicked duplex DNA (Odell and Shuman, 1999).

Zinc finger motif

A very strong peak of electron density tetrahedrally liganded by the four conserved cysteine residues (Cys406, Cys409, Cys422 and Cys427) was interpreted as a zinc ion. The presence of zinc ions in stoichiometric amounts (one Zn²⁺ ion per *Tfi* ligase molecule) was confirmed by inductively coupled plasma atomic emission spectrometry.

Since the four cysteine residues that coordinate the zinc ion are strictly conserved among bacterial DNA ligases, it is expected that other ligases have a similar zinc finger. The overall fold of this zinc finger is similar to other Cys₄-type zinc fingers (Figure 3B), including the first of the two zinc fingers in the DNA-binding domain (DBD) of steroid/nuclear hormone receptors such as estrogen receptor (ER) (Schmiedeskamp and Klevit, 1994; Klug and Schwabe, 1995; Mackay and Crossley, 1998). The two zinc-binding motifs of the ER DBD are folded to form a single structural unit in each monomer, and two such monomers form a symmetrical dimer when bound to the cognate DNA. Similar DBDs of receptor proteins can also bind to cognate or non-cognate DNA targets as a monomer (Gewirth and Sigler, 1995; Meinke and Sigler, 1999). In all these cases, the phosphate backbone of DNA interacts with the residues on the β -hairpin and the α -helix of the first zinc finger, with the latter helix sitting in the major groove of double-stranded DNA. Conceivable roles for the *Tfi* ligase zinc finger motif (subdomain 3a) may include a direct interaction with the nicked DNA as well as a structural support for subdomain 3b and domain 4. This suggestion is largely consistent with the results of mutagenesis of the zinc-coordinating cysteines, which abolished the DNA-binding activity of *Thermus thermophilus* DNA ligase (*Tth* ligase) (Luo and Barany, 1996). It is also interesting to note that human DNA ligase III possesses a Cys-Cys/His-Cys-type zinc finger motif that is homologous to the two zinc fingers present in human poly(ADP-ribose) polymerase (PARP) (Taylor *et al.*, 1998; Mackey *et al.*, 1999), the second of which is involved in the specific recognition of a DNA strand break (Gradwohl *et al.*, 1990). It has been demonstrated that the human DNA ligase III zinc finger forms a specific complex with a nick in duplex DNA (Mackey *et al.*, 1999). The possibility that the zinc finger in *Tfi* ligase may be involved in recognizing the nick in duplex DNA deserves further study.

HhH motif domain

Tfi ligase provides a unique example in which the four clustered HhH motifs form a single compact structure (subdomain 3b). They are helix pairs O-P, R-S, U-V and X-Y with the intervening hairpins (residues 430–460, 474–498, 502–528 and 537–560, respectively) (Figure 1B). Interestingly, all the hairpins are located in a linear chain at the bottom of this subdomain. This surface is also rich in positively charged residues. Similar HhH motifs are present in a number of DNA repair enzymes (Doherty *et al.*, 1996; Aravind *et al.*, 1999), including *E.coli* endonuclease III (Thayer *et al.*, 1995), *E.coli* AlkA (Labahn *et al.*, 1996), *E.coli* MutY (Guan *et al.*, 1998) and human DNA polymerase β (Pol β) (Mullen and Wilson, 1997). A structural comparison is shown in Figure 3C. Compared with the two HhH motifs of Pol β , the second and third HhH motifs of *Tfi* ligase show r.m.s. deviations of 0.8–1.5 Å for 18 C $_{\alpha}$ atoms. The first and last HhH motifs are more divergent (1.9–2.7 Å r.m.s. deviations for 18 C $_{\alpha}$ atoms). The sequence of the third HhH motif of *Tfi* ligase, Leu-Pro-Gly-Val-Gly-(Xaa)₃-Ala, is conserved in endonuclease III, MutY and Pol β . The HhH motif has been implicated in non-sequence-specific DNA binding

(Thayer *et al.*, 1995; Doherty *et al.*, 1996). This HhH motif subdomain is suggested to provide one of the two DNA-binding sites in *Tfi* ligase, as discussed below.

BRCT domain

Our structure of *Tfi* ligase is the first case in which the BRCT domain is seen as part of a multidomain protein. It consists of a four-stranded parallel β -sheet flanked by three α -helices. Its overall fold is grossly similar to that of the C-terminal BRCT domain of the human DNA repair protein, X-ray cross-complementing group I (XRCC1) (Zhang *et al.*, 1998). At present, a quantitative comparison is not possible, because the coordinates of the XRCC1 BRCT domain are not yet available. The most significant characteristic of the *Tfi* ligase BRCT domain is its high mobility as a whole. As a consequence, it is completely disordered in the open conformation and exhibits a high average *B*-factor in the closed conformation. For the ligase molecule in the most closed conformation, the average *B*-factors and the real space correlation coefficients of domains 1–4 are 56/72/55/84 Å² and 0.69/0.62/0.67/0.53, respectively, for the main chain atoms only.

The BRCT domain present in NAD⁺-dependent DNA ligases is a distinct version of its kind and is shared by the large subunits of eukaryotic replication factor C and PARP (Bork *et al.*, 1997). Evolutionarily, it must be the ancestor of eukaryotic BRCT domains. It was suggested that BRCT domains are likely to perform critical functions in the cell cycle control of organisms from bacteria to humans (Bork *et al.*, 1997; Callebaut and Mornon, 1997). They may act as a signal transducer that transmits the signal from DNA damage sensors such as, for example, the central region (301–402) of PARP, to other components of the DNA damage-responsive checkpoint machinery via specific protein–protein interactions (Bork *et al.*, 1997). Mammalian XRCC1, a multidomain protein functioning in the repair of single strand breaks in DNA, forms repair complexes with DNA ligase III, PARP and Pol β . The two BRCT domains of XRCC1 interact with PARP and DNA ligase III, while the N-terminal domain (NTD) of XRCC1 interacts with Pol β (Marintchev *et al.*, 1999). The XRCC1 C-terminal BRCT domain forms a specific heterodimer *in vitro* with the BRCT domain of mammalian DNA ligase III α (Nash *et al.*, 1997). A recent solution structure of XRCC1 NTD showed that it binds a gapped DNA–Pol β complex (Marintchev *et al.*, 1999). All these available data suggest a plausible scenario for *Tfi* ligase function: after other DNA repair proteins/enzymes recognize and repair the damaged DNA, it is recruited to the nick site for ligation through protein–protein interactions with its BRCT domain. However, the possibility of the BRCT domain being involved in other uncharacterized functions should not be ruled out.

Two distinct DNA-binding sites

The present structure of *Tfi* ligase in the covalently adenylated state is likely to represent the enzyme conformation that is ready to bind the nicked duplex DNA so that the ligation reaction continues after self-adenylation. The electrostatic potential at the molecular surface and shape complementarity (Figure 4), together with the nucleic acid-binding properties of protein modules related to domains 2 and 3, suggest that two distinct putative

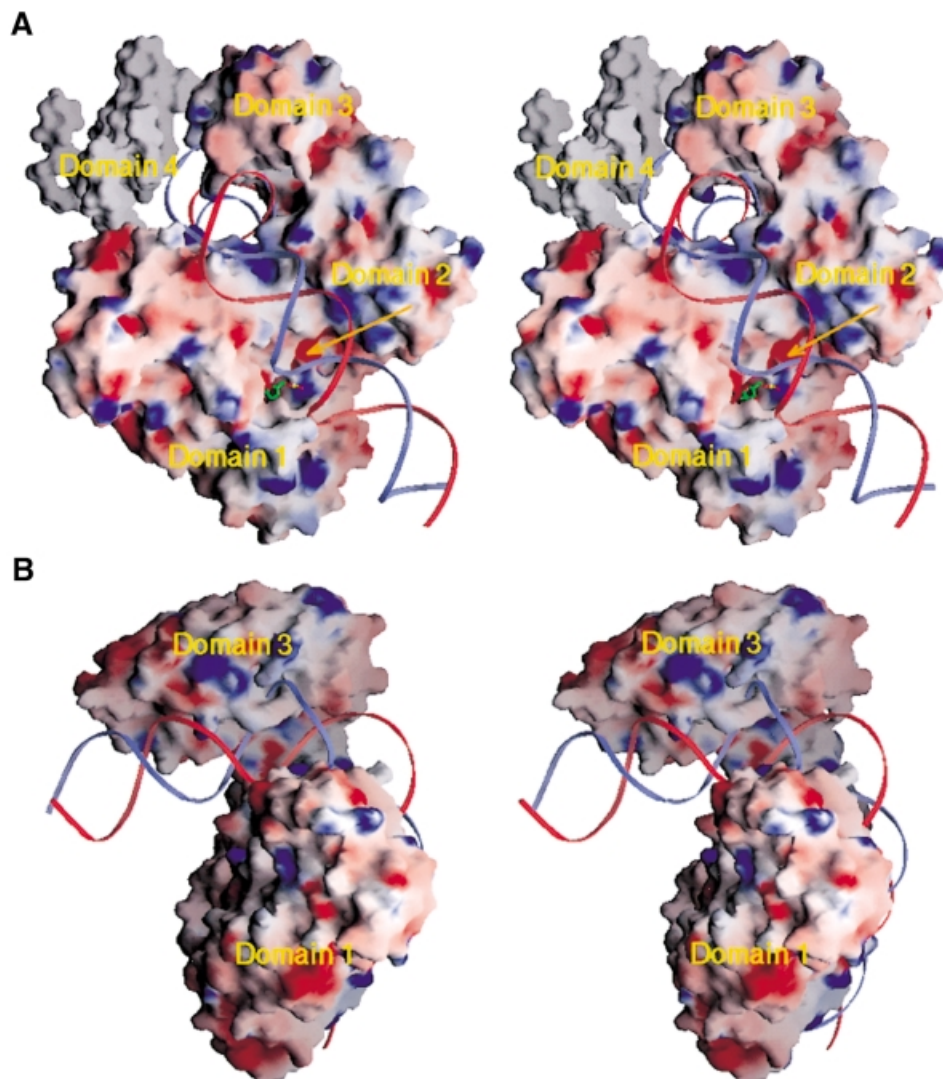


Fig. 4. Possible interactions between a duplex DNA and *Tfi* ligase in the observed adenylated structure. (A) Stereo view of the electrostatic potential surface (Nicholls *et al.*, 1991) of *Tfi* ligase with a duplex DNA interacting with the two putative binding sites. The surface is color-coded according to the potential: red, -15 kT; white, 0 kT; blue, +10 kT. The covalently bound AMP is indicated in a ball-and-stick model. The BRCT domain is in gray because its model lacks side chains. The arrow indicates the highly negatively charged site near Lys116 that is formed by Asp118, Glu281 and Asp283. This view shows the 'catalytic' DNA-binding site between domains 1 and 2. (B) This was obtained by rotating the view in (A) by 90° around the vertical axis. In order to show the 'non-catalytic' DNA-binding site, the BRCT domain has been omitted from this figure.

DNA-binding sites exist in *Tfi* ligase. One is a positively charged groove at the interface between domains 1 and 2. This is called the 'catalytic' DNA-binding site, because it encompasses the active site. One side of this site is lined by residues from the conserved sequence motif VI (a blue surface around the arrow in Figure 4A). The 'catalytic' DNA-binding site of *Tfi* ligase is not symmetrical about Lys116, with the lower half a little shorter than the upper half (Figure 4A). Therefore, the nicked duplex DNA protected by binding to the 'catalytic' DNA-binding site is expected to be asymmetrical in length about the nick. This is supported by the footprinting study on 298 residue *Chlorella* virus DNA ligase bound to a nick in duplex DNA, which showed that the footprint is asymmetric, extending 8 or 9 nucleotides on the 3'-hydroxyl side of the nick and 11 or 12 nucleotides on the 5'-phosphate side (Odell and Shuman, 1999). This small ligase is roughly equivalent to a more compact version of subdomain 1b and domain 2 of *Tfi* ligase. The

'catalytic' DNA-binding site is connected to the positively charged surface at the tip between strands 12 and 13 of the OB-fold domain (around the conserved Arg331) and continues to the bottom of the HhH motif subdomain 3b (Figure 1B). All four HhH motifs seem to be involved in DNA binding, as suggested by the observation that their hairpins are all located at the bottom of subdomain 3b. We propose that this is the second DNA-binding site; it is called the 'non-catalytic' DNA-binding site because it is well separated from the adenylation site.

Our proposal is largely consistent with the result of a limited proteolysis study on homologous *Bst* ligase (Timson and Wigley, 1999). It was shown that the DNA-binding activity of the C-terminal fragment of *Bst* ligase (residues 397–670), corresponding to domains 3 and 4 of *Tfi* ligase, is comparable to the full-length protein, and the activity of this fragment is independent of the N-terminal fragment (residues 1–318), which is responsible for self-adenylation (Timson and Wigley, 1999). The N-terminal

fragment itself, corresponding to domain 1 of *Tfi* ligase, showed minimal DNA-binding activity. This suggests that the C-terminal domains 3 and 4 play an important role in DNA binding and that domain 1 alone is not sufficient for high-affinity DNA binding. Our structure of *Tfi* ligase suggests that the inability of the N-terminal fragment of *Bst* ligase to bind strongly to duplex DNA may be due to the loss of the OB-fold domain 2 that occurred during limited proteolysis, because this domain provides one side of the 'catalytic' DNA-binding site. In the case of human DNA ligase III, two functionally distinct DNA-binding regions have been identified (Mackey *et al.*, 1999).

Figure 4 shows one possible mode of DNA binding to *Tfi* ligase, in which the duplex DNA is bound to both the 'catalytic' and 'non-catalytic' DNA-binding sites without causing any change in the ligase structure, as modeled

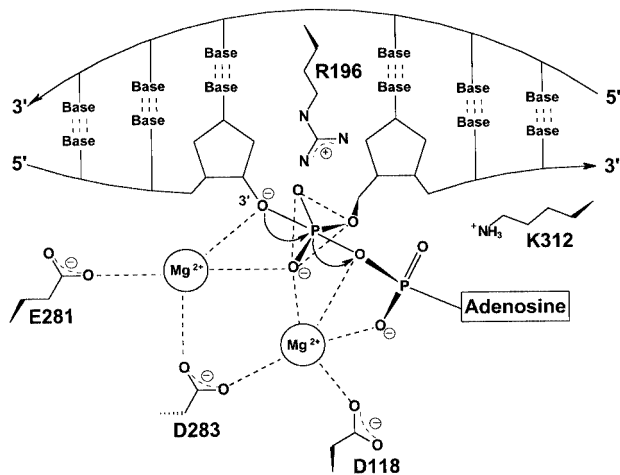


Fig. 5. Schematic model proposed for the *Tfi* ligase active site. Residues that are likely to participate in binding metal ions and the 5'-phosphate end of the nick are indicated.

using the graphics program O (Jones *et al.*, 1991). In this hypothetical model, DNA is kinked by $\sim 110^\circ$ around the β -hairpin of the zinc finger motif, with the kink occurring at the nick site of duplex DNA; the active site lies ~ 11 bp away from the kinked site. This implies that a major rearrangement of domains in *Tfi* ligase is very likely to be required for the nick to be placed near the active site.

A model for the active site

The final step of ligation reaction, deadenylation of the adenylated DNA intermediate and phosphodiester bond formation, is analogous to the polymerizing step by DNA polymerases, for which a divalent metal ion mechanism was proposed (Steitz *et al.*, 1994). The adenylated DNA intermediate in ligation corresponds to deoxyribonucleoside 5'-triphosphate in polymerization. Therefore, it is reasonable to expect a fundamentally related active site configuration of divalent metal ions, their ligands and the adenylated DNA intermediate in DNA ligases. A homologous *Thermus* DNA ligase demonstrated a divalent metal ion-dependent activity, showing the maximum activity with magnesium or manganese ions and approximately half the maximum activity with calcium ions (Tong *et al.*, 1999). The last step of the ligation reaction by human DNA ligase I was shown to require magnesium ions and it was inhibited by ATP and pyridoxal phosphate, indicating that the availability of the AMP-binding pocket in the enzyme is essential for completion of the reaction (Yang and Chan, 1992).

Some of the highly conserved residues Asp118, Glu169, Glu281, Asp283 and Glu317 are likely to participate in magnesium ion binding. This is supported by the identification of a putative metal ion-binding site by the program package SPASM (Kleywegt, 1999). It was found that the side chain configuration of Asp118, Glu281 and Asp283 in *Tfi* ligase matches well with that of Asp97,

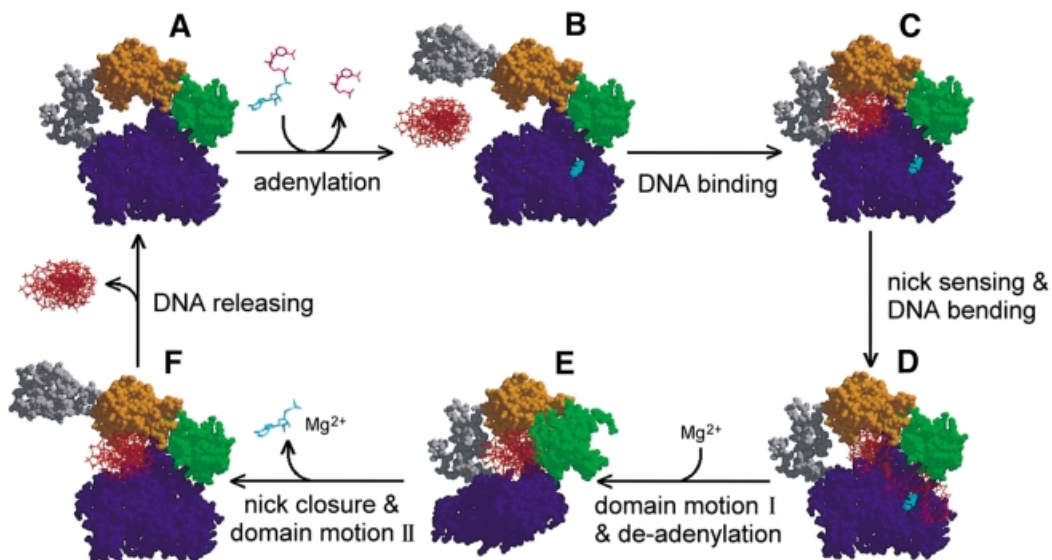


Fig. 6. Model for *Tfi* ligase action. Domains are color-coded: domain 1, blue; domain 2, green; domain 3, orange; domain 4, gray. DNA is in red and the bound AMP is in cyan. Apo enzyme (A) is self-adenylated (B) and a duplex DNA is bound to the 'non-catalytic' DNA-binding site (C). *Tfi* ligase slides along DNA and recognizes a nick (D). The duplex DNA is kinked at the nick (D) and the kinked DNA is bound to both the 'catalytic' and 'non-catalytic' DNA-binding sites, triggering a major domain rearrangement (E). The AMP is de-adenylated from Lys116 and is transferred to the 5'-phosphate of the nicked site, and magnesium ions are bound (E). Nick closure occurs and the ligated duplex DNA is now detached from the 'catalytic' DNA-binding site, and the second domain movement restores the ligase conformation (F). The duplex DNA is released to continue another reaction cycle.

Glu235 and Asp108 in *E. coli* methionine aminopeptidase, which form the binding site for two cobalt ions. The former three residues form a highly negatively charged pocket near Lys116 (Figure 4A). The strictly conserved Arg196 is likely to interact with the 5'-phosphate end of the nicked strand, while the strictly conserved Phe192, exposed to the solvent, seems to be involved in stacking with DNA bases. A highly schematic model proposed for the *Tfi* ligase active site is shown in Figure 5. The crystal structure of *Chlorella* virus mRNA guanylyl transferase in complex with a cap analog revealed that the 5' RNA base is stacked against the hydrophobic Ile86, the fourth residue from the adenylated Lys82 toward the C-terminus (Håkansson and Wigley, 1998). By analogy, the base at the 5' end is likely to be in contact with Leu120 in *Tfi* ligase. High fidelity of homologous *Tth* ligase against the mismatch at the 3' side of the nick was found to be influenced by mutation of Lys294 (Luo *et al.*, 1996). This residue corresponds to Lys288 of *Tfi* ligase, which forms a conserved ion pair with Glu114. These findings are all consistent with the 5' side of the nick lying above the AMP-linked Lys116 in Figure 1B.

Possible conformational changes: a model for the multidomain DNA ligase action

A model for *Tfi* ligase action involving conformational changes is described in Figure 6. The proposed DNA-binding sites and the toroidal architecture of *Tfi* ligase suggest that its BRCT domain may act as a gate for DNA binding and release. Analogous opening and closing of the DNA-binding hole was suggested for *E. coli* DNA topoisomerase I (Lima *et al.*, 1994). This suggests that *Tfi* ligase may also clamp around and slide along the DNA until it encounters the nick site or interacting partners bound to the damaged site. A precedent for this type of mechanism is provided by mammalian DNA ligase I, which interacts with the sliding clamp, proliferating cell nuclear antigen, through its N-terminal domain (Levin *et al.*, 1997). When the nick is recognized, perhaps by the zinc finger motif, the duplex DNA may be kinked at the nick so that it contacts the 'catalytic' DNA-binding site. This may trigger a major rearrangement of domains and in this process the nick would get close enough to the active site for ligation to take place. Modeling studies indicate that such a domain rearrangement is possible by simple concerted hinge motions of domain 2 around Pro314 and of domain 3 around Pro403. This domain movement would allow a tighter binding of duplex DNA to *Tfi* ligase without imposing substantial bending or kinking on DNA. An alternative model of the duplex DNA remaining unchanged during the domain rearrangement is also feasible. It is interesting to note that the two prolines are located at the interdomain regions and are strongly conserved. It is also worth mentioning that Pro314 is strategically located next to the strictly conserved Lys312, which interacts with the α -phosphate group of the covalently bound AMP (Figure 1C and D). Although no suitable methods are available to observe the proposed conformational changes directly, it may be possible to obtain evidence for this speculative model through structure determination of the DNA complex of *Tfi* ligase. However, we have not yet been able to grow crystals of the enzyme in complex with DNA.

The modular architecture of *Tfi* ligase seems to be highly suited for the proposed large-scale domain movements. The presence of two conformers within the same crystal lattice and the positional variability of the BRCT domain provide additional support for domain motions. Proposed domain rearrangements are also hinted at by the significantly different orientations of the OB-fold domain in *Tfi* ligase and T7 ligase and the very different orientations of the N-terminal subdomain 1a in *Tfi* ligase and *Bst* ligase. There are numerous examples in which a large movement of domains was actually observed (Gerstein *et al.*, 1994). For example, GTP binding by *Thermus aquaticus* elongation factor EF-Tu leads to dramatic conformational changes that expose the tRNA-binding site (Kjeldgaard *et al.*, 1993). In the case of PcrA DNA helicase from *E. coli*, large and distinct conformational changes occur on binding DNA and the nucleotide cofactor (Velankar *et al.*, 1999). The *E. coli* Rep helicase bound to single-stranded DNA undergoes a large reorientation of one of the domains upon binding ADP (Korolev *et al.*, 1997).

Conclusions

The present structure of *Tfi* ligase reveals an interesting organization of the OB-fold domain (domain 2), the zinc finger motif (subdomain 3a) and the HhH motif domain (subdomain 3b), representing a unique combination and spatial arrangement of these protein modules, which are all known to bind to nucleic acids. These modules, along with the BRCT domain, may have fused with domain 1 during evolution to yield a multidomain protein of highly specific function. As a member of a large superfamily of covalent nucleotidyl transferases that includes mammalian DNA ligases, the structure of *Tfi* ligase should provide a framework for understanding the domain organization, catalytic function and evolution of this important class of enzymes. It should also serve as a useful model for other enzymes that share the protein modules such as the OB-fold, the zinc finger, the HhH motif and the BRCT domain. For example, human DNA ligase III α possesses one BRCT domain at the C-terminus and a zinc finger at the N-terminus, while human DNA ligase IV possesses two BRCT domains at the C-terminus (Chen *et al.*, 1995; Wei *et al.*, 1995; Tomkinson and Levin, 1997; Tomkinson and Mackey, 1998). Terminal nucleotidyl transferase, involved in immunoglobulin gene somatic recombination, also has both a BRCT domain and two HhH motifs at the N-terminus (Bork *et al.*, 1997). *Tfi* ligase now joins a large group of structures available for DNA polymerases, an ATP-dependent DNA ligase and DNA repair enzymes. This study helps to secure a more comprehensive picture of the machinery for preserving the intact structure of DNA at the atomic level and enhances our understanding of one of the most fundamental processes of biological systems. The proposed model for *Tfi* ligase action may be generally applicable to eukaryotic multidomain DNA ligases. It would not be surprising if the structural principles related to that observed in this study are found to work in other functionally related enzymes such as the eukaryotic multidomain DNA ligases.

Materials and methods

Purification, crystallization and data collection

Recombinant *Tfi* ligase was expressed and purified as described previously (Kim and Kwon, 1998). Crystallization of the native enzyme

will be described elsewhere (Lee *et al.*, 2000). Neither NAD⁺ nor zinc ions were added deliberately during purification and crystallization. The reservoir solution for the vapor diffusion crystallization consisted of 100 mM sodium citrate pH 5.6, 5% methoxyPEG 5000 and 5 mM calcium chloride. The native enzyme crystallized into the *P*₂₁ space group with unit cell parameters of *a* = 89.51, *b* = 115.63, *c* = 97.17 Å and β = 115.73°. The asymmetric unit contains two molecules of monomeric enzyme. SeMet-substituted *Tfi* ligase was produced in *E. coli* B834(DE3) cells by growth in minimal media supplemented with SeMet. Its purification procedure was identical to that of the native protein except that buffers contained 5 mM dithiothreitol to prevent selenium oxidation. The crystals of SeMet-substituted enzyme were isomorphous to the native crystals, with slightly different unit cell parameters of *a* = 89.21, *b* = 117.33, *c* = 97.48 Å and β = 115.09°. For the cryo-cooling, a crystal of *Tfi* DNA ligase was transferred initially to a solution of 100 mM sodium citrate pH 5.6 containing 10% methoxyPEG 5000 and 5 mM calcium chloride. The glycerol concentration was increased stepwise from 0 to 25% (v/v) over a period of 2 h before the crystal was flash-frozen in a cold nitrogen stream at 100 K. Data were collected on beamlines X12-C and X8-C at the National Synchrotron Light Source, Brookhaven National Laboratory. An ADSC Quantum 4R charge-coupled device (CCD) detector or a Brandeis CCD detector was used. Diffraction data were processed and scaled using the HKL software package (Otwinowski and Minor, 1997).

Structure determination and refinement

Twelve of 14 possible selenium sites in the asymmetric unit were located with SOLVE (Terwilliger and Berendzen, 1999). The phases were calculated with SHARP (de la Fortelle and Bricogne, 1997) and were improved by the 2-fold non-crystallographic symmetry (NCS) averaging, solvent flattening and histogram matching with DM (CCP4, 1994). Two zinc sites were also located by SOLVE but were omitted from the phase calculation. The model was built with O (Jones *et al.*, 1991). The protein model was refined with X-PLOR (Brünger, 1992a) and CNS (Brünger *et al.*, 1998), including the bulk solvent correction. The 2-fold NCS was tightly maintained for the SeMet-substituted model, whereas it had to be relaxed for the native model. The model of the SeMet-substituted enzyme accounts for 1162 residues in two molecules of *Tfi* ligase (residues 1–581) in the crystallographic asymmetric unit, two AMP moieties covalently bound to Lys116, two zinc ions and 242 water molecules. No electron density was observed for the C-terminal residues 582–667. Subsequently, the crystal structure of the native enzyme was also refined. The model of the native enzyme accounts for 1162 residues in two molecules of *Tfi* ligase (residues 1–581) in the asymmetric unit, two AMP moieties, two zinc ions and 264 water molecules. In addition, it includes a polyalanine model of the C-terminal residues 582–660 in one of the two ligase molecules. The occupancy of all atoms including those in the AMP moieties was assumed to be 1.0. An average *B*-factor for the AMP moiety in the closed conformation is higher than that for the other AMP in the open conformation (76 versus 45 Å² for the SeMet-substituted enzyme and 72 versus 41 Å² for the native enzyme). Coordinates for the SeMet-substituted enzyme and the native enzyme have been deposited in the Protein Data Bank under ID codes 1DGS and 1DGT, respectively.

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