

# wwPDB X-ray Structure Validation Summary Report (i)

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PDB ID : 1WP5

Title: Crystal structure of the C-terminal domain of DNA topoisomerase IV

Authors: Hsieh, T.-J.; Farh, L.; Huang, W.M.; Chan, N.-L.

Deposited on : 2004-08-30

Resolution : 1.79 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at

https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity : 4.02b-467

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.11

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Refmac: 5.8.0158

 $\begin{array}{cccc} & CCP4 & : & 7.0.044 \; (Gargrove) \\ Ideal \; geometry \; (proteins) & : & Engh \; \& \; Huber \; (2001) \end{array}$ 

Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

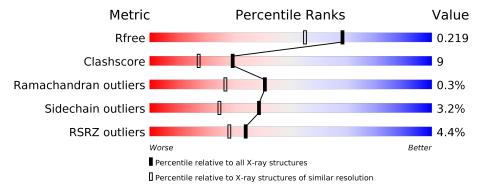
Validation Pipeline (wwPDB-VP) : 2.11

## 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 1.79 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$egin{aligned}  ext{Similar resolution} \ (\# ext{Entries},  ext{resolution range}( ext{Å})) \end{aligned}$
$R_{free}$	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain		
			4%		
1	A	323	85%	12%	•



# 2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 2952 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

• Molecule 1 is a protein called topoisomerase IV.

Mol	Chain	Residues		Atoms			ZeroOcc	AltConf	Trace		
1	А	323	Total	С	Ν	О	S	Se	0	0	0
	11	020	2575	1631	445	490	1	8			

• Molecule 2 is water.

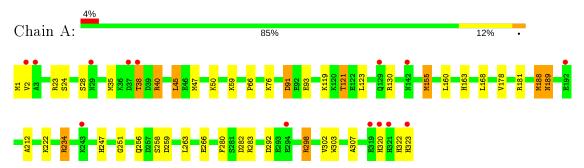
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	377	Total O 377 377	0	0



# 3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: topoisomerase IV





# 4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 32	Depositor	
Cell constants	83.21Å 83.21Å 45.00Å	D : 4	
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $120.00^{\circ}$	Depositor	
Resolution (Å)	23.00 - 1.79	Depositor	
Resolution (A)	21.19 - 1.79	EDS	
% Data completeness	93.7 (23.00-1.79)	Depositor	
(in resolution range)	93.8 (21.19-1.79)	EDS	
$R_{merge}$	(Not available)	Depositor	
$R_{sum}$	0.10	Depositor	
$< I/\sigma(I) > 1$	$3.05 \; ({\rm at} \; 1.79 {\rm \AA})$	Xtriage	
Refinement program	REFMAC 5.1.24	Depositor	
υ .	0.160 , 0.214	Depositor	
$R, R_{free}$	0.172 , $0.219$	DCC	
$R_{free}$ test set	1548 reflections $(5.05\%)$	wwPDB-VP	
Wilson B-factor (Å <sup>2</sup> )	19.6	Xtriage	
Anisotropy	0.017	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.37, 60.5	EDS	
L-test for twinning <sup>2</sup>	$< L >=0.48, < L^2>=0.31$	Xtriage	
	0.025 for -h,-k,l		
Estimated twinning fraction	0.032 for h,-h-k,-l	Xtriage	
	0.026  for -k,-h,-l		
$F_o, F_c$ correlation	0.95	EDS	
Total number of atoms	2952	wwPDB-VP	
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.93% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $< L^2>$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 5 Model quality (i)

### 5.1 Standard geometry (i)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with |Z| > 5 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Boı	nd lengths	Bo	nd angles
MIOI	Mol Chain		# Z  > 5	RMSZ	# Z >5
1	Α	0.96	3/2612~(0.1%)	1.00	$9/3513 \ (0.3\%)$

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(\operatorname{\AA})$
1	A	188	MSE	SE-CE	-7.24	1.52	1.95
1	A	121	THR	CB-CG2	-5.49	1.34	1.52
1	A	93	GLU	CD-OE2	5.31	1.31	1.25

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}(^{o})$
1	A	283	ARG	NE-CZ-NH2	-6.30	117.15	120.30
1	A	259	ASP	CB-CG-OD1	6.26	123.94	118.30
1	A	292	ASP	CB-CG-OD1	6.07	123.76	118.30
1	A	298	ARG	NE-CZ-NH2	-5.46	117.57	120.30
1	A	282	ASP	CB-CG-OD1	5.39	123.15	118.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2575	0	2590	49	0
2	A	377	0	0	18	0
All	All	2952	0	2590	49	0



The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

The worst 5 of 49 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{aligned}  ext{Interatomic} \  ext{distance} \ ( ext{Å}) \end{aligned}$	$egin{aligned}  ext{Clash} \  ext{overlap} & ( ext{Å}) \end{aligned}$
1:A:160:LEU:HB2	1:A:188:MSE:HE1	1.36	1.06
1:A:168:LEU:HB3	1:A:188:MSE:HE2	1.37	1.05
1:A:168:LEU:HB3	1:A:188:MSE:CE	2.04	0.88
1:A:1:MSE:HE3	1:A:66:PRO:CG	2.08	0.84
1:A:35:MSE:C	2:A:565:HOH:O	2.22	0.78

There are no symmetry-related clashes.

#### 5.3 Torsion angles (i)

#### 5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	321/323 (99%)	313 (98%)	7 (2%)	1 (0%)	41 27

All (1) Ramachandran outliers are listed below:

Mol	Chain	${f Res}$	Type
1	A	2	VAL

#### 5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.



Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	282/274 (103%)	273 (97%)	9 (3%)	39 25

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	123	LEU
1	A	320	HIS
1	A	189	ASN
1	A	38	THR
1	A	155	MSE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	81	HIS
1	A	163	HIS
1	A	247	HIS
1	A	321	HIS

#### 5.3.3 RNA (i)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

#### 5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

### 5.6 Ligand geometry (i)

There are no ligands in this entry.

### 5.7 Other polymers (i)

There are no such residues in this entry.



# 5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



## 6 Fit of model and data (i)

#### 6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ>2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median,  $95^{th}$  percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ $>$	#RSRZ	>2	$OWAB(Å^2)$	Q < 0.9
1	A	315/323 (97%)	0.14	14 (4%) 34	28	14, 21, 39, 65	0

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	VAL	9.1
1	A	320	HIS	6.2
1	A	323	HIS	5.9
1	A	321	HIS	4.1
1	A	3	ALA	4.0

#### 6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

#### 6.4 Ligands (i)

There are no ligands in this entry.

### 6.5 Other polymers (i)

There are no such residues in this entry.

