



wwPDB X-ray Structure Validation Summary Report ⓘ

May 12, 2020 – 11:25 pm BST

PDB ID : 2ZJT
Title : Crystal structure of dna gyrase B' domain sheds lights on the mechanism for T-segment navigation
Authors : Fu, G.S.; Zhu, D.Y.; Hu, Y.L.; Wang, D.C.
Deposited on : 2008-03-10
Resolution : 2.80 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

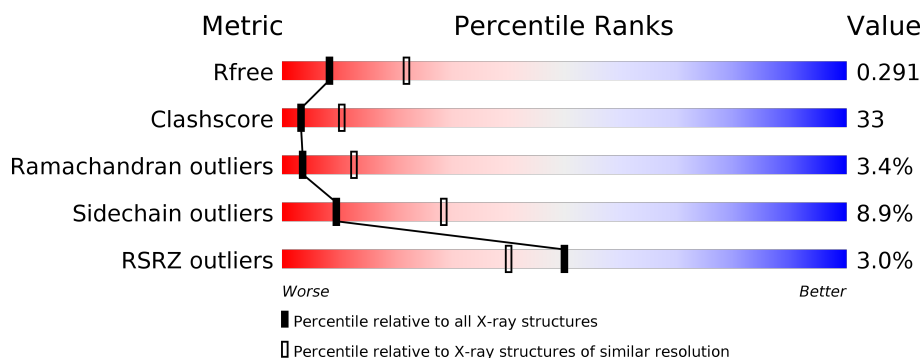
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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 $\leq 5\%$. 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
1	A	247	<div> <div>2%</div> <div> <div></div> <div>40%</div> <div>28%</div> <div>6%</div> <div>25%</div> </div> </div>
1	B	247	<div> <div>2%</div> <div> <div></div> <div>40%</div> <div>29%</div> <div>5%</div> <div>25%</div> </div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2962 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 DNA gyrase subunit B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	185	Total	C	N	O	S	0	0	0
			1481	946	254	275	6			
1	B	185	Total	C	N	O	S	0	0	0
			1481	946	254	275	6			

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	481	MET	-	EXPRESSION TAG	UNP P0C5C5
A	482	THR	-	EXPRESSION TAG	UNP P0C5C5
A	483	PRO	-	EXPRESSION TAG	UNP P0C5C5
A	484	TYR	-	EXPRESSION TAG	UNP P0C5C5
A	485	ALA	-	EXPRESSION TAG	UNP P0C5C5
A	486	PHE	-	EXPRESSION TAG	UNP P0C5C5
A	715	LYS	-	EXPRESSION TAG	UNP P0C5C5
A	716	LEU	-	EXPRESSION TAG	UNP P0C5C5
A	717	ALA	-	EXPRESSION TAG	UNP P0C5C5
A	718	ALA	-	EXPRESSION TAG	UNP P0C5C5
A	719	ALA	-	EXPRESSION TAG	UNP P0C5C5
A	720	LEU	-	EXPRESSION TAG	UNP P0C5C5
A	721	GLU	-	EXPRESSION TAG	UNP P0C5C5
A	722	HIS	-	EXPRESSION TAG	UNP P0C5C5
A	723	HIS	-	EXPRESSION TAG	UNP P0C5C5
A	724	HIS	-	EXPRESSION TAG	UNP P0C5C5
A	725	HIS	-	EXPRESSION TAG	UNP P0C5C5
A	726	HIS	-	EXPRESSION TAG	UNP P0C5C5
A	727	HIS	-	EXPRESSION TAG	UNP P0C5C5
B	481	MET	-	EXPRESSION TAG	UNP P0C5C5
B	482	THR	-	EXPRESSION TAG	UNP P0C5C5
B	483	PRO	-	EXPRESSION TAG	UNP P0C5C5
B	484	TYR	-	EXPRESSION TAG	UNP P0C5C5
B	485	ALA	-	EXPRESSION TAG	UNP P0C5C5
B	486	PHE	-	EXPRESSION TAG	UNP P0C5C5

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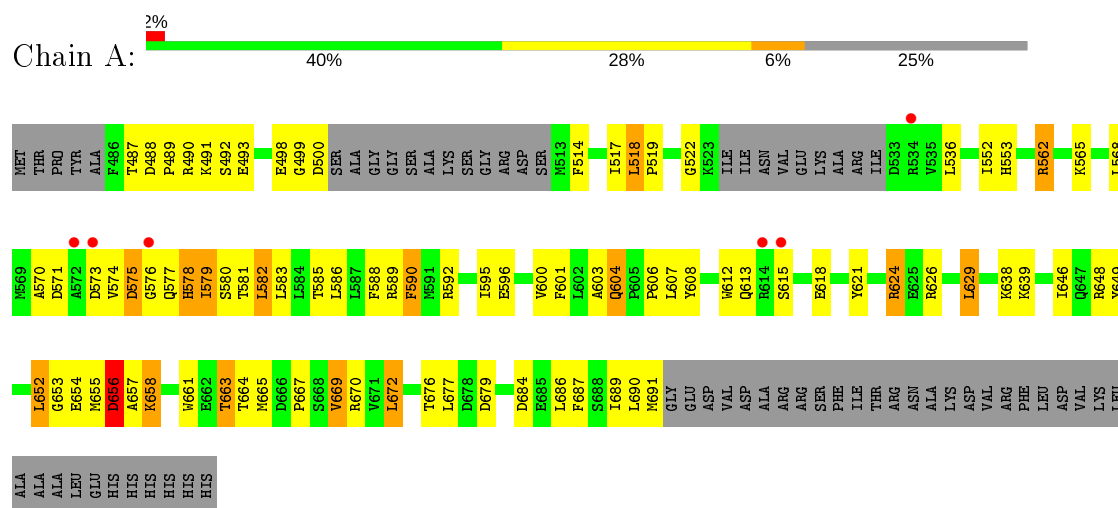
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Chain	Residue	Modelled	Actual	Comment	Reference
B	715	LYS	-	EXPRESSION TAG	UNP P0C5C5
B	716	LEU	-	EXPRESSION TAG	UNP P0C5C5
B	717	ALA	-	EXPRESSION TAG	UNP P0C5C5
B	718	ALA	-	EXPRESSION TAG	UNP P0C5C5
B	719	ALA	-	EXPRESSION TAG	UNP P0C5C5
B	720	LEU	-	EXPRESSION TAG	UNP P0C5C5
B	721	GLU	-	EXPRESSION TAG	UNP P0C5C5
B	722	HIS	-	EXPRESSION TAG	UNP P0C5C5
B	723	HIS	-	EXPRESSION TAG	UNP P0C5C5
B	724	HIS	-	EXPRESSION TAG	UNP P0C5C5
B	725	HIS	-	EXPRESSION TAG	UNP P0C5C5
B	726	HIS	-	EXPRESSION TAG	UNP P0C5C5
B	727	HIS	-	EXPRESSION TAG	UNP P0C5C5

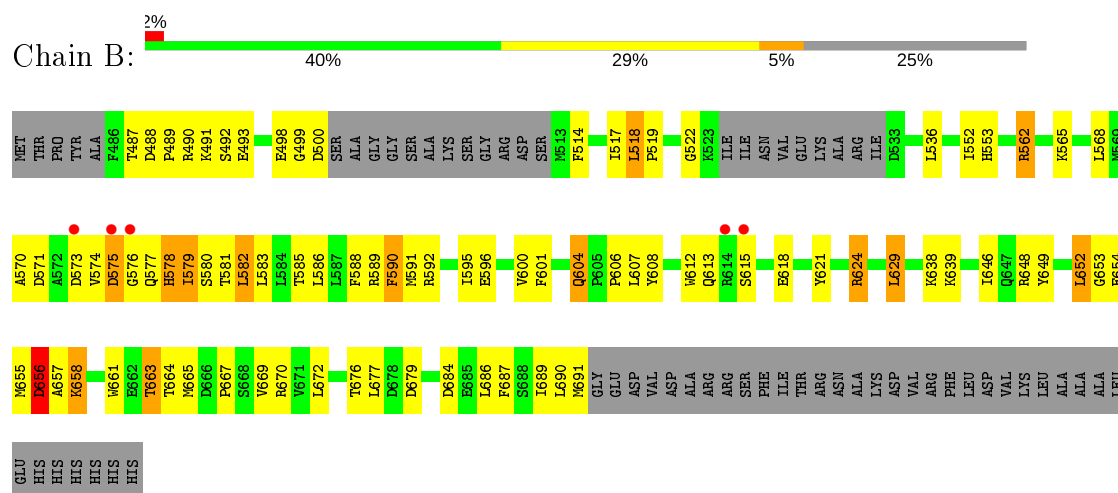
3 Residue-property plots [i](#)

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: DNA gyrase subunit B



• Molecule 1: DNA gyrase subunit B



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	52.83Å 52.76Å 192.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.03 – 2.80 23.44 – 2.80	Depositor EDS
% Data completeness (in resolution range)	91.8 (19.03-2.80) 95.9 (23.44-2.80)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.36 (at 2.80Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.244 , 0.280 0.255 , 0.291	Depositor DCC
R_{free} test set	679 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	61.8	Xtriage
Anisotropy	0.059	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 31.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.480 for k,h,-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	2962	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.86% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.43	0/1506	0.70	0/2027
1	B	0.42	0/1506	0.70	0/2027
All	All	0.42	0/3012	0.70	0/4054

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	1481	0	1498	102	0
1	B	1481	0	1498	101	0
All	All	2962	0	2996	195	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 33.

The worst 5 of 195 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:577:GLN:HB3	1:B:580:SER:HB3	1.37	1.04
1:B:657:ALA:O	1:B:658:LYS:HB3	1.59	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:577:GLN:HB3	1:A:580:SER:HB3	1.39	1.01
1:A:657:ALA:O	1:A:658:LYS:HB3	1.59	0.99
1:A:686:LEU:O	1:A:690:LEU:HG	1.73	0.88

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	179/247 (72%)	154 (86%)	19 (11%)	6 (3%)	3	13
1	B	179/247 (72%)	154 (86%)	19 (11%)	6 (3%)	3	13
All	All	358/494 (72%)	308 (86%)	38 (11%)	12 (3%)	3	13

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	575	ASP
1	A	656	ASP
1	B	575	ASP
1	B	656	ASP
1	A	576	GLY

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	158/207 (76%)	144 (91%)	14 (9%)	9	28
1	B	158/207 (76%)	144 (91%)	14 (9%)	9	28
All	All	316/414 (76%)	288 (91%)	28 (9%)	9	28

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	669	VAL
1	B	518	LEU
1	B	663	THR
1	A	672	LEU
1	B	489	PRO

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	604	GLN
1	A	674	GLN
1	B	604	GLN
1	B	674	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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, 95th 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	185/247 (74%)	0.08	6 (3%)	47 37	30, 56, 87, 96	0
1	B	185/247 (74%)	0.05	5 (2%)	54 44	31, 56, 87, 96	0
All	All	370/494 (74%)	0.06	11 (2%)	50 40	30, 57, 88, 96	0

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	615	SER	4.9
1	A	573	ASP	3.7
1	A	615	SER	3.4
1	A	614	ARG	3.3
1	B	614	ARG	3.2

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.