



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 14, 2018 – 09:46 am GMT

PDB ID : 4ZC0  
Title : Structure of a dodecameric bacterial helicase  
Authors : Bazin, A.; Cherrier, M.V.; Gutsche, I.; Timmins, J.; Terradot, L.  
Deposited on : 2015-04-15  
Resolution : 6.70 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.7.3 (157068), CSD as539be (2018)  
Xtriage (Phenix) : 1.13  
EDS : trunk31020  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk31020

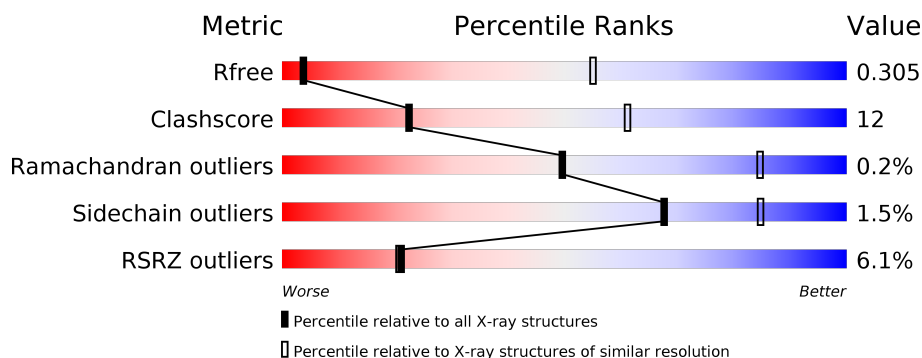
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 6.70 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))
$R_{free}$	111664	1066 (9.50-3.80)
Clashscore	122126	1144 (9.50-3.80)
Ramachandran outliers	120053	1070 (9.50-3.80)
Sidechain outliers	120020	1037 (9.50-3.80)
RSRZ outliers	108989	1012 (9.50-3.70)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	521	<div> <div>3%</div> <div>60%</div> <div>25%</div> <div>15%</div> </div>
1	B	521	<div> <div>9%</div> <div>59%</div> <div>23%</div> <div>17%</div> </div>
1	C	521	<div> <div>2%</div> <div>20%</div> <div>8%</div> <div>72%</div> </div>
1	D	521	<div> <div>19%</div> <div>8%</div> <div>72%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	TBR	B	501	-	-	X	-

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9140 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 Replicative DNA helicase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	445	Total	C	N	O	S	0	0	0
			3491	2199	611	667	14			
1	B	434	Total	C	N	O	S	0	0	0
			3397	2141	595	647	14			
1	C	148	Total	C	N	O	S	0	0	0
			1122	714	193	212	3			
1	D	146	Total	C	N	O	S	0	0	0
			1112	708	191	210	3			

There are 132 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-32	MET	-	initiating methionine	UNP O25916
A	-31	HIS	-	expression tag	UNP O25916
A	-30	HIS	-	expression tag	UNP O25916
A	-29	HIS	-	expression tag	UNP O25916
A	-28	HIS	-	expression tag	UNP O25916
A	-27	HIS	-	expression tag	UNP O25916
A	-26	HIS	-	expression tag	UNP O25916
A	-25	GLY	-	expression tag	UNP O25916
A	-24	LYS	-	expression tag	UNP O25916
A	-23	PRO	-	expression tag	UNP O25916
A	-22	ILE	-	expression tag	UNP O25916
A	-21	PRO	-	expression tag	UNP O25916
A	-20	ASN	-	expression tag	UNP O25916
A	-19	PRO	-	expression tag	UNP O25916
A	-18	LEU	-	expression tag	UNP O25916
A	-17	LEU	-	expression tag	UNP O25916
A	-16	GLY	-	expression tag	UNP O25916
A	-15	LEU	-	expression tag	UNP O25916
A	-14	ASP	-	expression tag	UNP O25916
A	-13	SER	-	expression tag	UNP O25916
A	-12	THR	-	expression tag	UNP O25916

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	GLU	-	expression tag	UNP O25916
A	-10	ASN	-	expression tag	UNP O25916
A	-9	LEU	-	expression tag	UNP O25916
A	-8	TYR	-	expression tag	UNP O25916
A	-7	PHE	-	expression tag	UNP O25916
A	-6	GLN	-	expression tag	UNP O25916
A	-5	GLY	-	expression tag	UNP O25916
A	-4	ILE	-	expression tag	UNP O25916
A	-3	ASP	-	expression tag	UNP O25916
A	-2	PRO	-	expression tag	UNP O25916
A	-1	PHE	-	expression tag	UNP O25916
A	0	THR	-	expression tag	UNP O25916
B	-32	MET	-	initiating methionine	UNP O25916
B	-31	HIS	-	expression tag	UNP O25916
B	-30	HIS	-	expression tag	UNP O25916
B	-29	HIS	-	expression tag	UNP O25916
B	-28	HIS	-	expression tag	UNP O25916
B	-27	HIS	-	expression tag	UNP O25916
B	-26	HIS	-	expression tag	UNP O25916
B	-25	GLY	-	expression tag	UNP O25916
B	-24	LYS	-	expression tag	UNP O25916
B	-23	PRO	-	expression tag	UNP O25916
B	-22	ILE	-	expression tag	UNP O25916
B	-21	PRO	-	expression tag	UNP O25916
B	-20	ASN	-	expression tag	UNP O25916
B	-19	PRO	-	expression tag	UNP O25916
B	-18	LEU	-	expression tag	UNP O25916
B	-17	LEU	-	expression tag	UNP O25916
B	-16	GLY	-	expression tag	UNP O25916
B	-15	LEU	-	expression tag	UNP O25916
B	-14	ASP	-	expression tag	UNP O25916
B	-13	SER	-	expression tag	UNP O25916
B	-12	THR	-	expression tag	UNP O25916
B	-11	GLU	-	expression tag	UNP O25916
B	-10	ASN	-	expression tag	UNP O25916
B	-9	LEU	-	expression tag	UNP O25916
B	-8	TYR	-	expression tag	UNP O25916
B	-7	PHE	-	expression tag	UNP O25916
B	-6	GLN	-	expression tag	UNP O25916
B	-5	GLY	-	expression tag	UNP O25916
B	-4	ILE	-	expression tag	UNP O25916
B	-3	ASP	-	expression tag	UNP O25916

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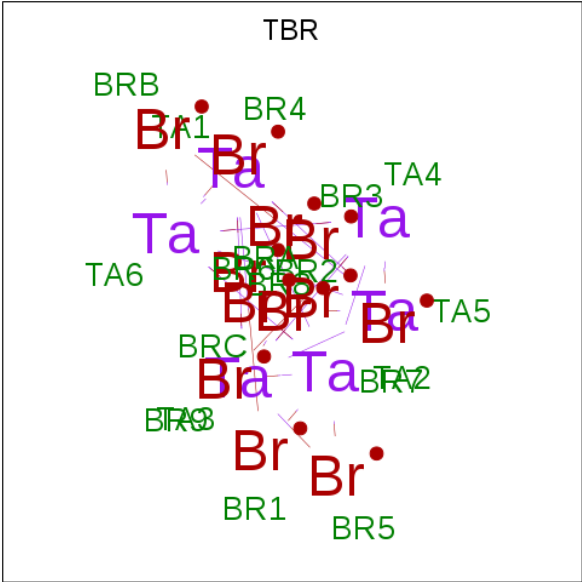
Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	PRO	-	expression tag	UNP O25916
B	-1	PHE	-	expression tag	UNP O25916
B	0	THR	-	expression tag	UNP O25916
C	-32	MET	-	initiating methionine	UNP O25916
C	-31	HIS	-	expression tag	UNP O25916
C	-30	HIS	-	expression tag	UNP O25916
C	-29	HIS	-	expression tag	UNP O25916
C	-28	HIS	-	expression tag	UNP O25916
C	-27	HIS	-	expression tag	UNP O25916
C	-26	HIS	-	expression tag	UNP O25916
C	-25	GLY	-	expression tag	UNP O25916
C	-24	LYS	-	expression tag	UNP O25916
C	-23	PRO	-	expression tag	UNP O25916
C	-22	ILE	-	expression tag	UNP O25916
C	-21	PRO	-	expression tag	UNP O25916
C	-20	ASN	-	expression tag	UNP O25916
C	-19	PRO	-	expression tag	UNP O25916
C	-18	LEU	-	expression tag	UNP O25916
C	-17	LEU	-	expression tag	UNP O25916
C	-16	GLY	-	expression tag	UNP O25916
C	-15	LEU	-	expression tag	UNP O25916
C	-14	ASP	-	expression tag	UNP O25916
C	-13	SER	-	expression tag	UNP O25916
C	-12	THR	-	expression tag	UNP O25916
C	-11	GLU	-	expression tag	UNP O25916
C	-10	ASN	-	expression tag	UNP O25916
C	-9	LEU	-	expression tag	UNP O25916
C	-8	TYR	-	expression tag	UNP O25916
C	-7	PHE	-	expression tag	UNP O25916
C	-6	GLN	-	expression tag	UNP O25916
C	-5	GLY	-	expression tag	UNP O25916
C	-4	ILE	-	expression tag	UNP O25916
C	-3	ASP	-	expression tag	UNP O25916
C	-2	PRO	-	expression tag	UNP O25916
C	-1	PHE	-	expression tag	UNP O25916
C	0	THR	-	expression tag	UNP O25916
D	-32	MET	-	initiating methionine	UNP O25916
D	-31	HIS	-	expression tag	UNP O25916
D	-30	HIS	-	expression tag	UNP O25916
D	-29	HIS	-	expression tag	UNP O25916
D	-28	HIS	-	expression tag	UNP O25916
D	-27	HIS	-	expression tag	UNP O25916

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-26	HIS	-	expression tag	UNP O25916
D	-25	GLY	-	expression tag	UNP O25916
D	-24	LYS	-	expression tag	UNP O25916
D	-23	PRO	-	expression tag	UNP O25916
D	-22	ILE	-	expression tag	UNP O25916
D	-21	PRO	-	expression tag	UNP O25916
D	-20	ASN	-	expression tag	UNP O25916
D	-19	PRO	-	expression tag	UNP O25916
D	-18	LEU	-	expression tag	UNP O25916
D	-17	LEU	-	expression tag	UNP O25916
D	-16	GLY	-	expression tag	UNP O25916
D	-15	LEU	-	expression tag	UNP O25916
D	-14	ASP	-	expression tag	UNP O25916
D	-13	SER	-	expression tag	UNP O25916
D	-12	THR	-	expression tag	UNP O25916
D	-11	GLU	-	expression tag	UNP O25916
D	-10	ASN	-	expression tag	UNP O25916
D	-9	LEU	-	expression tag	UNP O25916
D	-8	TYR	-	expression tag	UNP O25916
D	-7	PHE	-	expression tag	UNP O25916
D	-6	GLN	-	expression tag	UNP O25916
D	-5	GLY	-	expression tag	UNP O25916
D	-4	ILE	-	expression tag	UNP O25916
D	-3	ASP	-	expression tag	UNP O25916
D	-2	PRO	-	expression tag	UNP O25916
D	-1	PHE	-	expression tag	UNP O25916
D	0	THR	-	expression tag	UNP O25916

- Molecule 2 is HEXATANTALUM DODECABROMIDE (three-letter code: TBR) (formula: Br<sub>12</sub>Ta<sub>6</sub>).



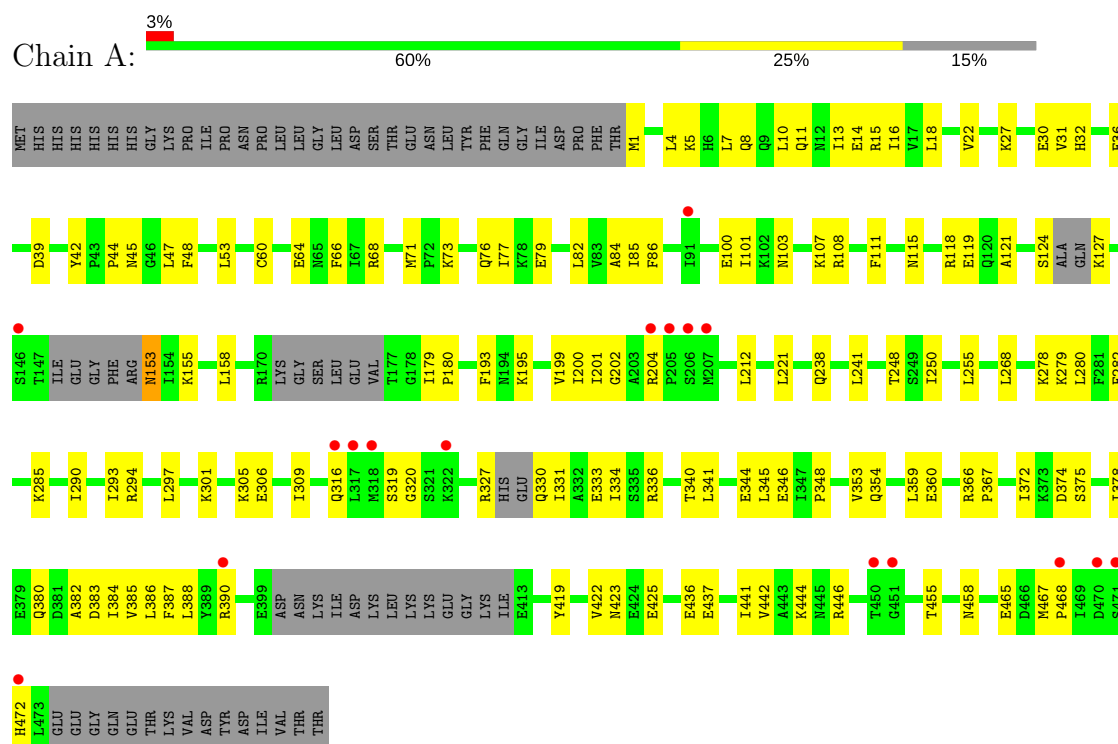
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	Br	Ta	0	0
			18	12	6		



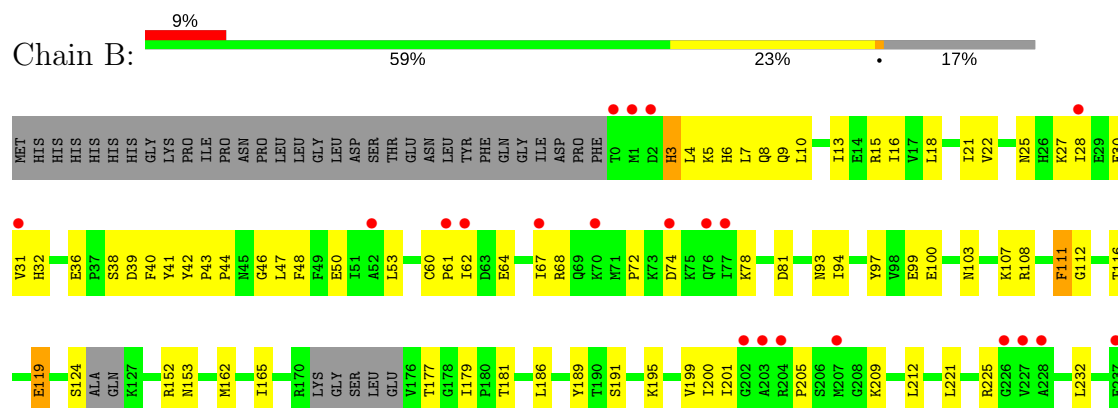
### 3 Residue-property plots

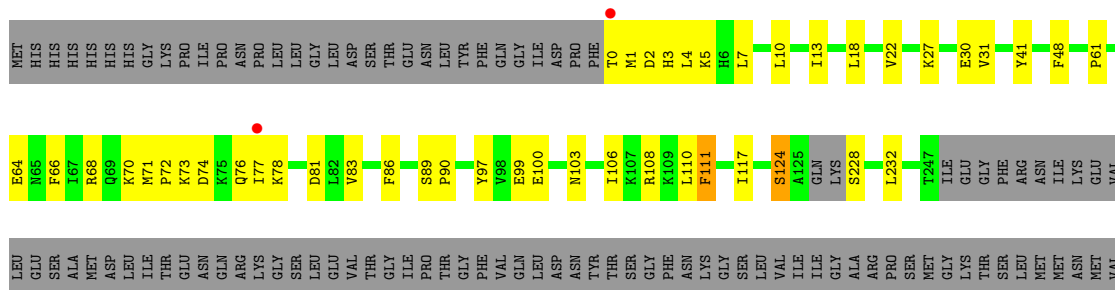
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: Replicative DNA helicase



#### • Molecule 1: Replicative DNA helicase





ASN	ALA	LEU	LYS	LYS	LEU
ALA	GLU	LYS	LYS	LYS	SER
PRO	ASP	THR	THR	LEU	ALA
PHE	ASN	LEU	PHE	PHE	LEU
THR	LYS	ALA	ASP	TYR	ASN
ARG	ILE	ARG	GLU	ASP	ASP
TYR	ASP	GLU	LEU	LYS	ARG
GLU	LYS	LEU	GLU	GLY	ASP
ASP	LEU	ILE	ILE	TYR	GLY
PRO	LYS	PRO	VAL	VAL	ALA
ILE	GLU	ILE	ILE	ARG	VAL
ASP	GLY	ILE	ILE	ILE	PHE
SER	LYS	ALA	GLU	GLU	SER
HIS	ILE	LEU	LEU	GLN	LEU
LEU	GLU	VAL	VAL	ILE	GLU
GLU	GLU	GLN	ASN	ARG	NET
GLY	ALA	LEU	LEU	LEU	SER
GLN	GLN	ASN	GLN	GLN	ALA
GLU	GLU	ARG	LEU	LEU	GLU
THR	TYR	SER	SER	LYS	GLN
THR	TYR	LEU	ARG	ARG	LEU
LYS	LEU	GLU	GLU	LEU	ALA
VAL	LYS	ASN	ASN	LYS	LEU
ASP	VAL	ARG	ARG	SER	LEU
TYR	ASN	ASP	ASP	GLN	ARG
ASP	GLU	ASP	ASP	ASN	ALA
ILE	GLU	LYS	LYS	HIS	LEU
VAL	ARG	ARG	GLU	SER	SER
THR	ARG	PRO	LEU	ASP	ASP
THR	ILE	ILE	GLY	LEU	LEU
	HIS	LEU	ILE	ILE	THR
	LYS	SER	LEU	ILE	SER
	GLN	ASN	ASP	PHE	ASN
	ASN	ILE	ILE	ILE	ILE
	GLY	LYS	ASP	ASP	GLY
	SER	ASP	TYR	ASP	ARG
	ILE	GLU	SER	TYR	GLY
	GLU	GLY	GLY	LEU	GLY
	GLU	ILE	ILE	GLN	GLY
	VAL	ALA	ALA	LYS	ARG
	LYS	ASP	ASP	ALA	ASP
	ASN	ILE	THR	THR	GLN
	ARG	VAL	LYS	GLN	LYS
	ASN	LEU	GLY	ARG	CYS
	ASN	PHE	ARG	GLU	LYS
	GLY	LEU	ILE	ILE	ALA
	ALA	THR	ALA	GLU	PHE
	THR	GLY	GLY	GLU	ASP
	THR	GLY	THR	ILE	HIS
	THR	THR	GLN	SER	LEU
	ARG	MET	ARG	ARG	GLN
	PHE	ARG	GLU	GLY	GLN

## 4 Data and refinement statistics

Property	Value	Source
Space group	I 21 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	283.47Å 283.47Å 283.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.24 – 6.70 47.24 – 6.70	Depositor EDS
% Data completeness (in resolution range)	99.8 (47.24-6.70) 99.9 (47.24-6.70)	Depositor EDS
$R_{merge}$	0.18	Depositor
$R_{sym}$	0.18	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.43 (at 6.67Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, $R_{free}$	0.258 , 0.299 0.266 , 0.305	Depositor DCC
$R_{free}$ test set	355 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	579.5	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 363.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.037 for -l,-k,-h	Xtriage
$F_o, F_c$ correlation	0.84	EDS
Total number of atoms	9140	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	315.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.04% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: TBR

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	0.25	0/3536	0.46	0/4757
1	B	0.25	0/3439	0.45	0/4624
1	C	0.28	0/1140	0.50	1/1542 (0.1%)
1	D	0.28	0/1130	0.47	0/1528
All	All	0.26	0/9245	0.46	1/12451 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	-2	PRO	N-CA-CB	5.69	110.13	103.30

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	3491	0	3456	93	2
1	B	3397	0	3357	80	2
1	C	1122	0	1062	29	0
1	D	1112	0	1062	35	0
2	B	18	0	0	6	0
All	All	9140	0	8937	226	2

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 12.

The worst 5 of 226 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:47:LEU:HG	2:B:501:TBR:BR9	2.15	1.01
1:B:301:LYS:NZ	1:B:305:LYS:O	2.07	0.86
1:A:301:LYS:NZ	1:A:305:LYS:O	2.08	0.84
1:C:99:GLU:O	1:C:103:ASN:ND2	2.13	0.81
1:B:39:ASP:O	1:B:108:ARG:NH2	2.14	0.80

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:121:ALA:O	1:B:107:LYS:NZ[9_555]	1.94	0.26
1:A:107:LYS:NZ	1:B:124:SER:O[9_555]	2.02	0.18

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	433/521 (83%)	423 (98%)	10 (2%)	0	100	100
1	B	422/521 (81%)	409 (97%)	13 (3%)	0	100	100
1	C	144/521 (28%)	138 (96%)	5 (4%)	1 (1%)	24	67
1	D	142/521 (27%)	136 (96%)	5 (4%)	1 (1%)	24	67
All	All	1141/2084 (55%)	1106 (97%)	33 (3%)	2 (0%)	49	84

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	124	SER
1	C	73	LYS

### 5.3.2 Protein sidechains ⓘ

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	369/461 (80%)	365 (99%)	4 (1%)	76	88
1	B	356/461 (77%)	348 (98%)	8 (2%)	55	77
1	C	110/461 (24%)	109 (99%)	1 (1%)	81	90
1	D	110/461 (24%)	109 (99%)	1 (1%)	81	90
All	All	945/1844 (51%)	931 (98%)	14 (2%)	67	85

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	111	PHE
1	B	119	GLU
1	B	458	ASN
1	B	93	ASN
1	B	434	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	76	GLN
1	A	472	HIS

### 5.3.3 RNA ⓘ

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](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	TBR	B	501	-	0,36,36	0.00	-	0,180,180	0.00	-

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	TBR	B	501	-	-	0/0/696/696	0/0/19/19

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	501	TBR	6	0



## 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	445/521 (85%)	0.18	17 (3%) 40 35	58, 291, 466, 550	0
1	B	434/521 (83%)	0.55	45 (10%) 6 8	75, 341, 550, 550	0
1	C	148/521 (28%)	0.29	8 (5%) 26 25	118, 270, 425, 539	0
1	D	146/521 (28%)	-0.03	2 (1%) 75 67	114, 260, 386, 539	0
All	All	1173/2084 (56%)	0.30	72 (6%) 21 21	58, 301, 502, 550	0

The worst 5 of 72 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	388	LEU	6.7
1	B	467	MET	6.4
1	B	203	ALA	5.6
1	B	466	ASP	4.7
1	B	318	MET	4.7

### 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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	TBR	B	501	18/18	0.90	0.18	550,550,550,550	18

## 6.5 Other polymers [i](#)

There are no such residues in this entry.