



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 03:59 PM GMT

PDB ID : 4E10  
Title : Protelomerase tela Y201A covalently complexed with substrate DNA  
Authors : Shi, K.; Aihara, H.  
Deposited on : 2012-03-05  
Resolution : 2.51 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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  
<http://wwpdb.org/validation/2016/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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

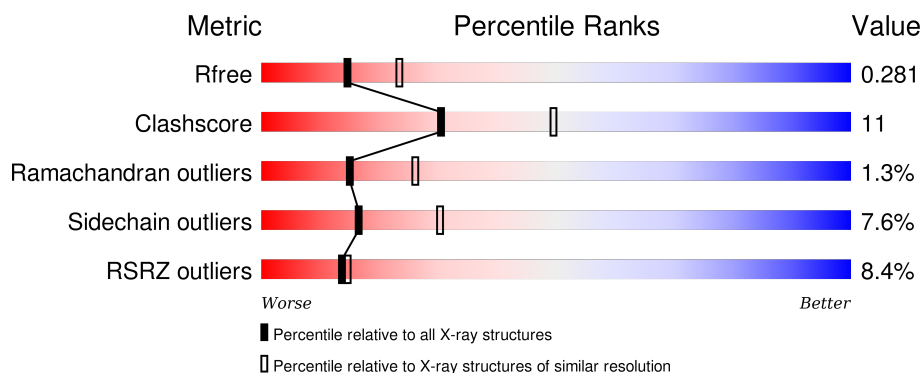
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.51 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))
$R_{free}$	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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	462	<div> <div>6%</div> <div> <div>50%</div> <div>16%</div> <div>•</div> <div>31%</div> </div> </div>
2	C	13	<div> <div>46%</div> <div>46%</div> <div>8%</div> </div>
3	D	18	<div> <div>11%</div> <div> <div>39%</div> <div>33%</div> <div>11%</div> <div>17%</div> </div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3278 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 Protelomerase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	318	2514	1594	436	470	1	13	0	0	0

There are 145 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	EXPRESSION TAG	UNP Q7CWV1
A	-18	GLY	-	EXPRESSION TAG	UNP Q7CWV1
A	-17	SER	-	EXPRESSION TAG	UNP Q7CWV1
A	-16	SER	-	EXPRESSION TAG	UNP Q7CWV1
A	-15	HIS	-	EXPRESSION TAG	UNP Q7CWV1
A	-14	HIS	-	EXPRESSION TAG	UNP Q7CWV1
A	-13	HIS	-	EXPRESSION TAG	UNP Q7CWV1
A	-12	HIS	-	EXPRESSION TAG	UNP Q7CWV1
A	-11	HIS	-	EXPRESSION TAG	UNP Q7CWV1
A	-10	HIS	-	EXPRESSION TAG	UNP Q7CWV1
A	-9	SER	-	EXPRESSION TAG	UNP Q7CWV1
A	-8	SER	-	EXPRESSION TAG	UNP Q7CWV1
A	-7	GLY	-	EXPRESSION TAG	UNP Q7CWV1
A	-6	LEU	-	EXPRESSION TAG	UNP Q7CWV1
A	-5	VAL	-	EXPRESSION TAG	UNP Q7CWV1
A	-4	PRO	-	EXPRESSION TAG	UNP Q7CWV1
A	-3	ARG	-	EXPRESSION TAG	UNP Q7CWV1
A	-2	GLY	-	EXPRESSION TAG	UNP Q7CWV1
A	-1	SER	-	EXPRESSION TAG	UNP Q7CWV1
A	0	HIS	-	EXPRESSION TAG	UNP Q7CWV1
A	1	MET	-	EXPRESSION TAG	UNP Q7CWV1
A	2	LEU	-	EXPRESSION TAG	UNP Q7CWV1
A	3	ALA	-	EXPRESSION TAG	UNP Q7CWV1
A	4	ALA	-	EXPRESSION TAG	UNP Q7CWV1
A	5	LYS	-	EXPRESSION TAG	UNP Q7CWV1
A	6	ARG	-	EXPRESSION TAG	UNP Q7CWV1
A	7	LYS	-	EXPRESSION TAG	UNP Q7CWV1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	8	THR	-	EXPRESSION TAG	UNP Q7CWV1
A	9	LYS	-	EXPRESSION TAG	UNP Q7CWV1
A	10	THR	-	EXPRESSION TAG	UNP Q7CWV1
A	11	PRO	-	EXPRESSION TAG	UNP Q7CWV1
A	12	VAL	-	EXPRESSION TAG	UNP Q7CWV1
A	13	LEU	-	EXPRESSION TAG	UNP Q7CWV1
A	14	VAL	-	EXPRESSION TAG	UNP Q7CWV1
A	15	GLU	-	EXPRESSION TAG	UNP Q7CWV1
A	16	ARG	-	EXPRESSION TAG	UNP Q7CWV1
A	17	ILE	-	EXPRESSION TAG	UNP Q7CWV1
A	18	ASP	-	EXPRESSION TAG	UNP Q7CWV1
A	19	GLN	-	EXPRESSION TAG	UNP Q7CWV1
A	20	PHE	-	EXPRESSION TAG	UNP Q7CWV1
A	21	VAL	-	EXPRESSION TAG	UNP Q7CWV1
A	22	GLY	-	EXPRESSION TAG	UNP Q7CWV1
A	23	GLN	-	EXPRESSION TAG	UNP Q7CWV1
A	24	ILE	-	EXPRESSION TAG	UNP Q7CWV1
A	25	LYS	-	EXPRESSION TAG	UNP Q7CWV1
A	26	GLU	-	EXPRESSION TAG	UNP Q7CWV1
A	27	ALA	-	EXPRESSION TAG	UNP Q7CWV1
A	28	MET	-	EXPRESSION TAG	UNP Q7CWV1
A	29	LYS	-	EXPRESSION TAG	UNP Q7CWV1
A	30	SER	-	EXPRESSION TAG	UNP Q7CWV1
A	31	ASP	-	EXPRESSION TAG	UNP Q7CWV1
A	32	ASP	-	EXPRESSION TAG	UNP Q7CWV1
A	33	ALA	-	EXPRESSION TAG	UNP Q7CWV1
A	34	SER	-	EXPRESSION TAG	UNP Q7CWV1
A	35	ARG	-	EXPRESSION TAG	UNP Q7CWV1
A	36	ASN	-	EXPRESSION TAG	UNP Q7CWV1
A	37	ARG	-	EXPRESSION TAG	UNP Q7CWV1
A	38	LYS	-	EXPRESSION TAG	UNP Q7CWV1
A	39	ILE	-	EXPRESSION TAG	UNP Q7CWV1
A	40	ARG	-	EXPRESSION TAG	UNP Q7CWV1
A	41	ASP	-	EXPRESSION TAG	UNP Q7CWV1
A	42	LEU	-	EXPRESSION TAG	UNP Q7CWV1
A	43	TRP	-	EXPRESSION TAG	UNP Q7CWV1
A	44	ASP	-	EXPRESSION TAG	UNP Q7CWV1
A	45	ALA	-	EXPRESSION TAG	UNP Q7CWV1
A	46	GLU	-	EXPRESSION TAG	UNP Q7CWV1
A	47	VAL	-	EXPRESSION TAG	UNP Q7CWV1
A	48	ARG	-	EXPRESSION TAG	UNP Q7CWV1
A	49	TYR	-	EXPRESSION TAG	UNP Q7CWV1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	50	HIS	-	EXPRESSION TAG	UNP Q7CWV1
A	51	PHE	-	EXPRESSION TAG	UNP Q7CWV1
A	52	ASP	-	EXPRESSION TAG	UNP Q7CWV1
A	53	ASN	-	EXPRESSION TAG	UNP Q7CWV1
A	54	GLY	-	EXPRESSION TAG	UNP Q7CWV1
A	55	ARG	-	EXPRESSION TAG	UNP Q7CWV1
A	56	THR	-	EXPRESSION TAG	UNP Q7CWV1
A	57	GLU	-	EXPRESSION TAG	UNP Q7CWV1
A	58	LYS	-	EXPRESSION TAG	UNP Q7CWV1
A	59	THR	-	EXPRESSION TAG	UNP Q7CWV1
A	60	LEU	-	EXPRESSION TAG	UNP Q7CWV1
A	61	GLU	-	EXPRESSION TAG	UNP Q7CWV1
A	62	LEU	-	EXPRESSION TAG	UNP Q7CWV1
A	63	TYR	-	EXPRESSION TAG	UNP Q7CWV1
A	64	ILE	-	EXPRESSION TAG	UNP Q7CWV1
A	65	MET	-	EXPRESSION TAG	UNP Q7CWV1
A	66	LYS	-	EXPRESSION TAG	UNP Q7CWV1
A	67	TYR	-	EXPRESSION TAG	UNP Q7CWV1
A	68	ARG	-	EXPRESSION TAG	UNP Q7CWV1
A	69	ASN	-	EXPRESSION TAG	UNP Q7CWV1
A	70	ALA	-	EXPRESSION TAG	UNP Q7CWV1
A	71	LEU	-	EXPRESSION TAG	UNP Q7CWV1
A	72	LYS	-	EXPRESSION TAG	UNP Q7CWV1
A	73	ALA	-	EXPRESSION TAG	UNP Q7CWV1
A	74	GLU	-	EXPRESSION TAG	UNP Q7CWV1
A	75	PHE	-	EXPRESSION TAG	UNP Q7CWV1
A	76	GLY	-	EXPRESSION TAG	UNP Q7CWV1
A	77	PRO	-	EXPRESSION TAG	UNP Q7CWV1
A	78	LYS	-	EXPRESSION TAG	UNP Q7CWV1
A	79	SER	-	EXPRESSION TAG	UNP Q7CWV1
A	80	THR	-	EXPRESSION TAG	UNP Q7CWV1
A	81	PRO	-	EXPRESSION TAG	UNP Q7CWV1
A	82	LEU	-	EXPRESSION TAG	UNP Q7CWV1
A	83	ALA	-	EXPRESSION TAG	UNP Q7CWV1
A	84	ILE	-	EXPRESSION TAG	UNP Q7CWV1
A	85	CYS	-	EXPRESSION TAG	UNP Q7CWV1
A	86	ASN	-	EXPRESSION TAG	UNP Q7CWV1
A	87	MET	-	EXPRESSION TAG	UNP Q7CWV1
A	88	LYS	-	EXPRESSION TAG	UNP Q7CWV1
A	89	LYS	-	EXPRESSION TAG	UNP Q7CWV1
A	90	LEU	-	EXPRESSION TAG	UNP Q7CWV1
A	91	ARG	-	EXPRESSION TAG	UNP Q7CWV1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	92	GLU	-	EXPRESSION TAG	UNP Q7CWV1
A	93	ARG	-	EXPRESSION TAG	UNP Q7CWV1
A	94	LEU	-	EXPRESSION TAG	UNP Q7CWV1
A	95	ASN	-	EXPRESSION TAG	UNP Q7CWV1
A	96	THR	-	EXPRESSION TAG	UNP Q7CWV1
A	97	TYR	-	EXPRESSION TAG	UNP Q7CWV1
A	98	ILE	-	EXPRESSION TAG	UNP Q7CWV1
A	99	ALA	-	EXPRESSION TAG	UNP Q7CWV1
A	100	ARG	-	EXPRESSION TAG	UNP Q7CWV1
A	101	GLY	-	EXPRESSION TAG	UNP Q7CWV1
A	102	ASP	-	EXPRESSION TAG	UNP Q7CWV1
A	201	ALA	TYR	ENGINEERED MUTATION	UNP Q7CWV1
A	421	LEU	-	EXPRESSION TAG	UNP Q7CWV1
A	422	LYS	-	EXPRESSION TAG	UNP Q7CWV1
A	423	ARG	-	EXPRESSION TAG	UNP Q7CWV1
A	424	THR	-	EXPRESSION TAG	UNP Q7CWV1
A	425	ASN	-	EXPRESSION TAG	UNP Q7CWV1
A	426	GLU	-	EXPRESSION TAG	UNP Q7CWV1
A	427	ARG	-	EXPRESSION TAG	UNP Q7CWV1
A	428	THR	-	EXPRESSION TAG	UNP Q7CWV1
A	429	LEU	-	EXPRESSION TAG	UNP Q7CWV1
A	430	GLN	-	EXPRESSION TAG	UNP Q7CWV1
A	431	GLN	-	EXPRESSION TAG	UNP Q7CWV1
A	432	MET	-	EXPRESSION TAG	UNP Q7CWV1
A	433	ALA	-	EXPRESSION TAG	UNP Q7CWV1
A	434	THR	-	EXPRESSION TAG	UNP Q7CWV1
A	435	ILE	-	EXPRESSION TAG	UNP Q7CWV1
A	436	ALA	-	EXPRESSION TAG	UNP Q7CWV1
A	437	PRO	-	EXPRESSION TAG	UNP Q7CWV1
A	438	VAL	-	EXPRESSION TAG	UNP Q7CWV1
A	439	SER	-	EXPRESSION TAG	UNP Q7CWV1
A	440	ARG	-	EXPRESSION TAG	UNP Q7CWV1
A	441	LYS	-	EXPRESSION TAG	UNP Q7CWV1
A	442	GLY	-	EXPRESSION TAG	UNP Q7CWV1

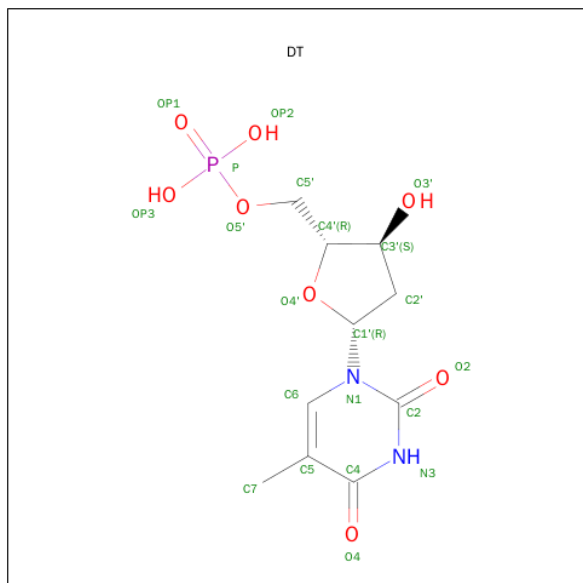
- Molecule 2 is a DNA chain called DNA (5'-D(\*CP\*AP\*TP\*AP\*AP\*(BRU)P\*AP\*AP\*CP\*AP\*AP\*(BRU)P\*AP\*T)-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	C	13	Total	Br	C	N	O	P	0	0	0
			263	3	125	52	71	12			

- Molecule 3 is a DNA chain called DNA (5'-D(\*CP\*AP\*TP\*GP\*AP\*TP\*AP\*(BRU)P\*(BRU)P\*GP\*(BRU)P\*(BRU)P\*AP\*(BRU)P\*(BRU)P\*AP\*(BRU)P\*G)-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	D	15	Total	Br	C	N	O	P	0	0	0
			307	7	143	51	92	14			

- Molecule 4 is THYMIDINE-5'-MONOPHOSPHATE (three-letter code: DT) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>2</sub>O<sub>8</sub>P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			17	10	2	5		

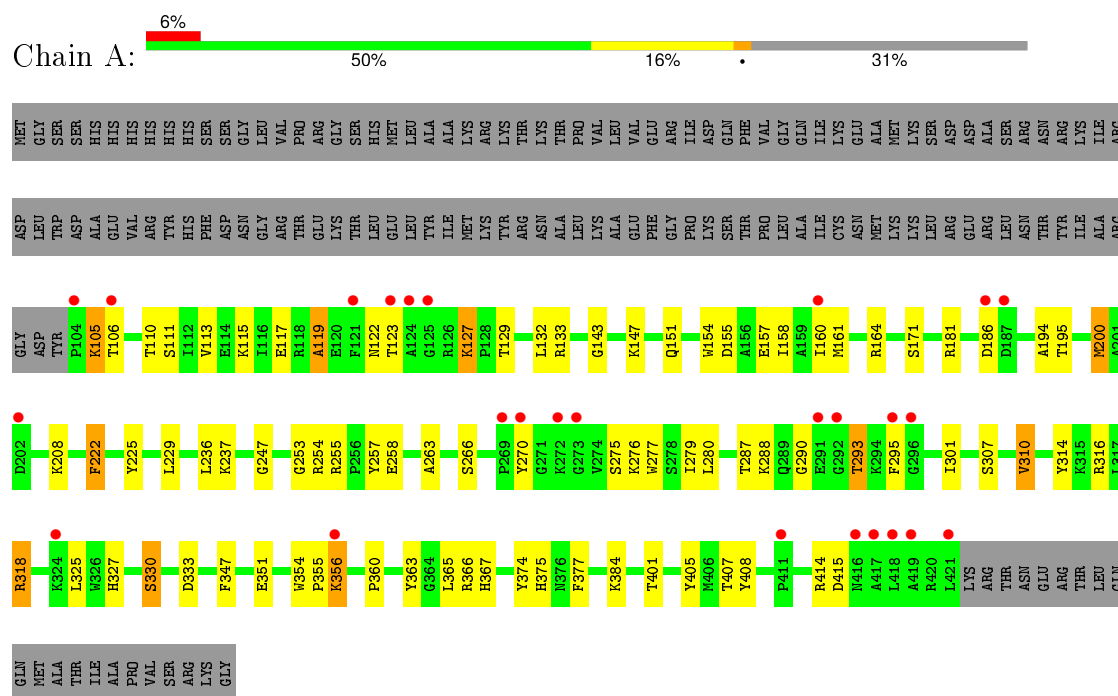
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	144	Total	O	0	0
			144	144		
5	C	15	Total	O	0	0
			15	15		
5	D	18	Total	O	0	0
			18	18		

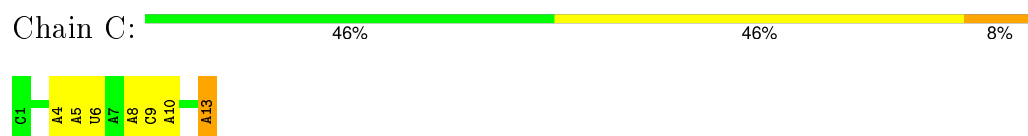
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

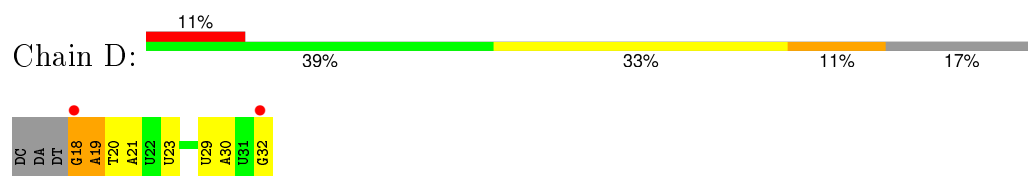
#### • Molecule 1: Protelomerase



#### • Molecule 2: DNA (5'-D(\*CP\*AP\*TP\*AP\*AP\*(BRU)P\*AP\*AP\*CP\*AP\*AP\*(BRU)P\*AP\*T)-3')



#### • Molecule 3: DNA (5'-D(\*CP\*AP\*TP\*GP\*AP\*TP\*AP\*(BRU)P\*(BRU)P\*GP\*(BRU)P\*(BRU)P\*AP\*(BRU)P\*(BRU)P\*AP\*(BRU)P\*G)-3')



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	116.34Å 119.66Å 56.63Å 90.00° 111.30° 90.00°	Depositor
Resolution (Å)	35.05 – 2.51 37.14 – 2.51	Depositor EDS
% Data completeness (in resolution range)	73.5 (35.05-2.51) 73.6 (37.14-2.51)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.06 (at 2.51Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1184)	Depositor
R, $R_{free}$	0.183 , 0.270 0.199 , 0.281	Depositor DCC
$R_{free}$ test set	956 reflections (5.52%)	DCC
Wilson B-factor (Å <sup>2</sup> )	36.5	Xtriage
Anisotropy	0.149	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 64.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 18263 reflections	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	3278	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.58% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

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

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	0.70	0/2551	0.81	0/3445
2	C	1.34	2/227 (0.9%)	1.96	9/340 (2.6%)
3	D	1.40	0/185	2.00	6/275 (2.2%)
All	All	0.82	2/2963 (0.1%)	1.07	15/4060 (0.4%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	13	DA	C3'-O3'	-6.45	1.35	1.44
2	C	13	DA	N9-C4	-5.17	1.34	1.37

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	19	DA	O4'-C4'-C3'	-9.86	100.08	106.00
3	D	21	DA	C8-N9-C4	-7.31	102.88	105.80
3	D	32	DG	O4'-C4'-C3'	-6.53	101.89	104.50
2	C	9	DC	O4'-C1'-C2'	-6.28	100.88	105.90
3	D	20	DT	O4'-C1'-N1	-6.04	103.77	108.00
2	C	8	DA	C5-C6-N1	-5.96	114.72	117.70
2	C	13	DA	C4-C5-C6	-5.94	114.03	117.00
2	C	13	DA	O4'-C1'-N9	-5.79	103.95	108.00
3	D	18	DG	N3-C4-N9	5.78	129.47	126.00
2	C	13	DA	N1-C2-N3	-5.55	126.53	129.30
2	C	10	DA	N1-C6-N6	-5.54	115.28	118.60
3	D	18	DG	N9-C4-C5	-5.48	103.21	105.40
2	C	13	DA	N3-C4-C5	5.33	130.53	126.80
2	C	13	DA	C8-N9-C4	5.18	107.87	105.80
2	C	10	DA	C5-C6-N6	5.00	127.70	123.70

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	2514	0	2498	56	0
2	C	263	0	139	7	0
3	D	307	0	154	6	0
4	A	17	0	14	3	0
5	A	144	0	0	7	0
5	C	15	0	0	1	0
5	D	18	0	0	1	0
All	All	3278	0	2805	65	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 11.

All (65) 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:A:266:SER:HB2	1:A:280:LEU:HB2	1.62	0.79
2:C:4:DA:H2'	2:C:5:DA:C8	2.17	0.79
1:A:354:TRP:CD1	1:A:355:PRO:HD2	2.27	0.70
3:D:18:DG:N7	5:D:111:HOH:O	2.25	0.69
1:A:414:ARG:NH1	1:A:415:ASP:OD1	2.27	0.67
1:A:119:ALA:HA	1:A:122:ASN:HD21	1.59	0.66
1:A:263:ALA:O	1:A:314:TYR:OH	2.04	0.63
1:A:119:ALA:HA	1:A:122:ASN:ND2	2.13	0.62
1:A:367:HIS:CD2	1:A:405:PTR:HD2	2.35	0.61
4:A:501:DT:H1'	2:C:13:DA:C4	2.36	0.61
1:A:129:THR:HA	1:A:132:LEU:HD12	1.87	0.55
1:A:157:GLU:O	1:A:160:ILE:HG22	2.05	0.55
1:A:375:HIS:HB2	5:A:679:HOH:O	2.06	0.55
1:A:181:ARG:HD3	1:A:186:ASP:OD1	2.06	0.55
1:A:222:PHE:CE1	1:A:355:PRO:HD3	2.43	0.54
1:A:318:ARG:HA	1:A:318:ARG:NE	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:367:HIS:ND1	1:A:407:THR:OG1	2.31	0.53
2:C:4:DA:H4'	2:C:5:DA:OP1	2.09	0.53
1:A:405:PTR:P	2:C:13:DA:O3'	2.67	0.52
2:C:4:DA:H2''	2:C:5:DA:O5'	2.09	0.51
1:A:316:ARG:HG3	5:A:718:HOH:O	2.10	0.51
3:D:18:DG:H2''	3:D:19:DA:O5'	2.10	0.51
1:A:354:TRP:CG	1:A:355:PRO:HD2	2.46	0.50
1:A:113:VAL:O	1:A:117:GLU:HG3	2.11	0.50
1:A:401:THR:HG23	4:A:501:DT:O3'	2.12	0.50
1:A:327:HIS:HE1	5:A:695:HOH:O	1.96	0.49
2:C:6:BRU:OP1	5:C:101:HOH:O	2.20	0.49
1:A:277:TRP:HB3	1:A:377:PHE:CE1	2.49	0.47
1:A:356:LYS:HG3	1:A:356:LYS:H	1.36	0.47
1:A:236:LEU:HD23	1:A:247:GLY:HA3	1.95	0.47
1:A:154:TRP:CE2	1:A:194:ALA:HA	2.49	0.47
1:A:257:TYR:HB2	3:D:23:BRU:OP2	2.15	0.46
1:A:347:PHE:O	1:A:351:GLU:HB2	2.16	0.45
1:A:290:GLY:O	1:A:293:THR:HB	2.16	0.45
1:A:236:LEU:O	5:A:602:HOH:O	2.21	0.45
1:A:279:ILE:HD13	1:A:310:VAL:HG11	1.99	0.45
3:D:29:BRU:H2'	3:D:30:DA:C8	2.53	0.45
1:A:354:TRP:HB2	1:A:360:PRO:HG3	1.99	0.44
1:A:327:HIS:HB2	5:A:704:HOH:O	2.17	0.44
1:A:255:ARG:NH1	1:A:258:GLU:OE2	2.47	0.44
1:A:270:TYR:HB2	1:A:275:SER:HB2	1.99	0.44
1:A:365:LEU:HD23	1:A:365:LEU:HA	1.77	0.44
1:A:288:LYS:O	1:A:293:THR:HG21	2.18	0.44
1:A:225:TYR:HD2	1:A:229:LEU:HD11	1.81	0.44
1:A:314:TYR:CZ	1:A:318:ARG:HD2	2.52	0.44
1:A:253:GLY:O	1:A:366:ARG:NH1	2.51	0.44
1:A:367:HIS:CD2	1:A:405:PTR:CD2	3.01	0.43
1:A:110:THR:HG23	5:A:720:HOH:O	2.17	0.43
1:A:111:SER:O	1:A:115:LYS:HG3	2.18	0.43
1:A:133:ARG:HD3	1:A:160:ILE:HG21	2.00	0.43
1:A:374:TYR:CD2	1:A:384:LYS:HD2	2.54	0.43
1:A:301:ILE:O	1:A:301:ILE:HG13	2.18	0.43
2:C:4:DA:H2	3:D:29:BRU:HN3	1.66	0.42
1:A:158:ILE:HA	1:A:158:ILE:HD13	1.68	0.42
1:A:254:ARG:HD3	1:A:254:ARG:HA	1.75	0.42
1:A:405:PTR:HE1	1:A:405:PTR:O2P	2.20	0.41
1:A:354:TRP:CB	1:A:360:PRO:HG3	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:195:THR:HG21	3:D:19:DA:OP2	2.20	0.41
1:A:151:GLN:HG3	1:A:155:ASP:OD2	2.21	0.41
1:A:105:LYS:HE3	1:A:143:GLY:HA2	2.02	0.41
1:A:270:TYR:O	5:A:710:HOH:O	2.22	0.41
1:A:208:LYS:NZ	4:A:501:DT:O4'	2.54	0.41
1:A:200:MET:HE3	1:A:200:MET:HB3	1.89	0.41
1:A:287:THR:HG23	1:A:295:PHE:HB2	2.03	0.40
1:A:127:LYS:HD2	1:A:127:LYS:HA	1.82	0.40

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	315/462 (68%)	283 (90%)	28 (9%)	4 (1%)	15	26

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	119	ALA
1	A	330	SER
1	A	310	VAL
1	A	333	ASP

### 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	262/388 (68%)	242 (92%)	20 (8%)	16	30

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	105	LYS
1	A	106	THR
1	A	123	THR
1	A	127	LYS
1	A	147	LYS
1	A	161	MET
1	A	164	ARG
1	A	171	SER
1	A	200	MET
1	A	222	PHE
1	A	237	LYS
1	A	276	LYS
1	A	293	THR
1	A	307	SER
1	A	318	ARG
1	A	325	LEU
1	A	330	SER
1	A	356	LYS
1	A	363	TYR
1	A	408	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	122	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

11 non-standard protein/DNA/RNA residues are 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
1	PTR	A	405	1	11,15,17	2.19	1 (9%)	13,19,24	0.75	0
2	BRU	C	12	3,2	13,21,22	1.41	2 (15%)	16,30,33	2.47	4 (25%)
2	BRU	C	3	3,2	13,21,22	1.76	3 (23%)	16,30,33	2.96	10 (62%)
2	BRU	C	6	3,2	13,21,22	1.59	4 (30%)	16,30,33	2.24	2 (12%)
3	BRU	D	22	3,2	13,21,22	1.79	6 (46%)	16,30,33	2.81	5 (31%)
3	BRU	D	23	3,2	13,21,22	1.65	5 (38%)	16,30,33	2.98	4 (25%)
3	BRU	D	25	3,2	13,21,22	1.46	2 (15%)	16,30,33	2.64	4 (25%)
3	BRU	D	26	3,2	13,21,22	1.75	6 (46%)	16,30,33	1.97	3 (18%)
3	BRU	D	28	3,2	13,21,22	1.75	4 (30%)	16,30,33	2.50	4 (25%)
3	BRU	D	29	3,2	13,21,22	1.89	5 (38%)	16,30,33	1.84	3 (18%)
3	BRU	D	31	3,2	13,21,22	1.64	5 (38%)	16,30,33	2.26	2 (12%)

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
1	PTR	A	405	1	-	0/6/10/13	0/1/1/1
2	BRU	C	12	3,2	-	0/3/21/22	0/2/2/2
2	BRU	C	3	3,2	-	0/3/21/22	0/2/2/2
2	BRU	C	6	3,2	-	0/3/21/22	0/2/2/2
3	BRU	D	22	3,2	-	0/3/21/22	0/2/2/2
3	BRU	D	23	3,2	-	0/3/21/22	0/2/2/2
3	BRU	D	25	3,2	-	0/3/21/22	0/2/2/2
3	BRU	D	26	3,2	-	0/3/21/22	0/2/2/2
3	BRU	D	28	3,2	-	0/3/21/22	0/2/2/2
3	BRU	D	29	3,2	-	0/3/21/22	0/2/2/2
3	BRU	D	31	3,2	-	0/3/21/22	0/2/2/2

All (43) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	405	PTR	OH-CZ	-7.07	1.29	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	3	BRU	C2'-C3'	-3.65	1.43	1.52
3	D	23	BRU	C2'-C3'	-3.26	1.44	1.52
3	D	29	BRU	C2'-C3'	-3.03	1.44	1.52
3	D	26	BRU	C2'-C3'	-3.00	1.44	1.52
3	D	22	BRU	C2'-C3'	-2.98	1.44	1.52
3	D	28	BRU	C2'-C3'	-2.95	1.44	1.52
3	D	29	BRU	C3'-C4'	-2.90	1.44	1.53
3	D	28	BRU	C3'-C4'	-2.74	1.45	1.53
3	D	29	BRU	C5'-C4'	-2.73	1.42	1.51
2	C	6	BRU	C2'-C3'	-2.72	1.45	1.52
3	D	28	BRU	O3'-C3'	-2.61	1.37	1.43
3	D	31	BRU	C2'-C3'	-2.61	1.45	1.52
3	D	25	BRU	C2'-C3'	-2.58	1.45	1.52
3	D	26	BRU	O3'-C3'	-2.50	1.37	1.43
2	C	12	BRU	C2'-C3'	-2.43	1.46	1.52
3	D	29	BRU	O3'-C3'	-2.43	1.37	1.43
3	D	26	BRU	C3'-C4'	-2.42	1.46	1.53
2	C	6	BRU	O3'-C3'	-2.38	1.38	1.43
3	D	23	BRU	C5'-C4'	-2.24	1.44	1.51
2	C	6	BRU	C5'-C4'	-2.24	1.44	1.51
3	D	25	BRU	C3'-C4'	-2.22	1.46	1.53
3	D	26	BRU	C5'-C4'	-2.20	1.44	1.51
3	D	31	BRU	C3'-C4'	-2.20	1.46	1.53
2	C	6	BRU	C3'-C4'	-2.19	1.46	1.53
3	D	31	BRU	C5'-C4'	-2.16	1.44	1.51
3	D	23	BRU	C3'-C4'	-2.14	1.47	1.53
3	D	26	BRU	C2'-C1'	-2.13	1.46	1.52
2	C	12	BRU	C5'-C4'	-2.12	1.44	1.51
2	C	3	BRU	O3'-C3'	-2.12	1.38	1.43
3	D	22	BRU	C3'-C4'	-2.10	1.47	1.53
3	D	23	BRU	C4-C5	-2.08	1.35	1.38
3	D	28	BRU	C5'-C4'	-2.02	1.45	1.51
3	D	23	BRU	O3'-C3'	-2.02	1.38	1.43
3	D	22	BRU	C2'-C1'	-2.01	1.46	1.52
3	D	31	BRU	C2'-C1'	-2.01	1.46	1.52
3	D	26	BRU	BR-C5	2.05	1.95	1.90
3	D	22	BRU	C4-C5	2.09	1.41	1.38
3	D	31	BRU	BR-C5	2.14	1.95	1.90
2	C	3	BRU	C4-N3	2.21	1.37	1.33
3	D	29	BRU	BR-C5	2.33	1.96	1.90
3	D	22	BRU	C4-N3	2.34	1.37	1.33
3	D	22	BRU	BR-C5	2.42	1.96	1.90

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	22	BRU	C5-C4-N3	-5.64	117.98	124.00
3	D	23	BRU	C5-C4-N3	-5.48	118.15	124.00
2	C	12	BRU	C5-C4-N3	-5.41	118.22	124.00
3	D	25	BRU	C5-C4-N3	-5.14	118.51	124.00
2	C	6	BRU	C5-C4-N3	-5.02	118.64	124.00
3	D	28	BRU	C5-C4-N3	-4.88	118.79	124.00
3	D	31	BRU	C5-C4-N3	-4.04	119.69	124.00
2	C	3	BRU	O3'-C3'-C2'	-4.01	97.46	110.74
2	C	3	BRU	C5-C4-N3	-3.73	120.02	124.00
3	D	26	BRU	C5-C4-N3	-3.60	120.15	124.00
3	D	29	BRU	C5-C4-N3	-3.19	120.59	124.00
2	C	3	BRU	C4'-O4'-C1'	-3.00	101.88	109.47
3	D	22	BRU	C4'-O4'-C1'	-2.92	102.10	109.47
2	C	3	BRU	C3'-C2'-C1'	-2.55	96.25	102.40
2	C	12	BRU	O3'-C3'-C4'	-2.12	101.46	110.05
3	D	28	BRU	O4'-C1'-C2'	-2.12	102.05	106.27
2	C	3	BRU	C2'-C3'-C4'	-2.09	98.44	102.77
2	C	3	BRU	C2'-C1'-N1	-2.08	109.11	114.16
3	D	25	BRU	O4'-C1'-N1	-2.04	104.19	107.72
3	D	29	BRU	C3'-C2'-C1'	2.23	107.77	102.40
3	D	23	BRU	O5'-C5'-C4'	2.53	118.40	109.12
2	C	12	BRU	C2'-C1'-N1	2.69	120.71	114.16
3	D	22	BRU	O5'-C5'-C4'	2.81	119.41	109.12
3	D	26	BRU	O5'-C5'-C4'	2.89	119.71	109.12
3	D	23	BRU	O4'-C1'-N1	2.96	112.83	107.72
3	D	25	BRU	O5'-C5'-C4'	2.98	120.04	109.12
3	D	22	BRU	BR-C5-C4	3.10	126.69	121.48
2	C	3	BRU	O5'-C5'-C4'	3.37	121.45	109.12
3	D	28	BRU	O5'-C5'-C4'	3.66	122.51	109.12
2	C	3	BRU	O4'-C1'-N1	3.84	114.36	107.72
2	C	3	BRU	BR-C5-C4	3.86	127.98	121.48
3	D	26	BRU	C4-N3-C2	5.44	119.95	115.25
3	D	29	BRU	C4-N3-C2	5.67	120.15	115.25
2	C	6	BRU	C4-N3-C2	6.32	120.71	115.25
2	C	3	BRU	C4-N3-C2	6.43	120.80	115.25
2	C	12	BRU	C4-N3-C2	6.97	121.28	115.25
3	D	31	BRU	C4-N3-C2	7.08	121.37	115.25
3	D	22	BRU	C4-N3-C2	7.09	121.38	115.25
3	D	28	BRU	C4-N3-C2	7.11	121.40	115.25
3	D	25	BRU	C4-N3-C2	7.73	121.93	115.25
3	D	23	BRU	C4-N3-C2	9.30	123.29	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	405	PTR	4	0
2	C	6	BRU	1	0
3	D	23	BRU	1	0
3	D	29	BRU	2	0

## 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	$\# Z  > 2$
4	DT	A	501	-	13,18,22	1.42	2 (15%)	16,26,33	5.10	5 (31%)

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
4	DT	A	501	-	-	0/2/18/22	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	501	DT	C6-C5	-2.51	1.33	1.40
4	A	501	DT	C4-N3	3.93	1.40	1.33

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	501	DT	C5-C4-N3	-11.52	112.31	125.14
4	A	501	DT	O4'-C1'-N1	-2.48	103.42	107.72
4	A	501	DT	C2'-C1'-N1	2.10	119.28	114.16
4	A	501	DT	O4'-C4'-C5'	2.48	114.53	109.17
4	A	501	DT	C4-N3-C2	16.03	129.10	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	501	DT	3	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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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	317/462 (68%)	0.48	26 (8%) 14 15	29, 63, 97, 125	0
2	C	10/13 (76%)	0.30	0 100 100	52, 69, 123, 129	0
3	D	8/18 (44%)	0.81	2 (25%) 1 1	48, 82, 113, 141	0
All	All	335/493 (67%)	0.48	28 (8%) 14 14	29, 64, 102, 141	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	419	ALA	5.9
1	A	272	LYS	5.3
1	A	417	ALA	4.8
1	A	291	GLU	4.6
1	A	121	PHE	4.5
1	A	421	LEU	3.7
1	A	418	LEU	3.3
1	A	124	ALA	3.2
1	A	125	GLY	3.1
1	A	270	TYR	3.0
1	A	296	GLY	3.0
1	A	104	PRO	2.8
1	A	292	GLY	2.7
1	A	269	PRO	2.6
3	D	32	DG	2.5
1	A	295	PHE	2.4
1	A	356	LYS	2.4
1	A	202	ASP	2.3
3	D	18	DG	2.3
1	A	324	LYS	2.3
1	A	187	ASP	2.3
1	A	106	THR	2.3
1	A	411	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	123	THR	2.2
1	A	416	ASN	2.2
1	A	186	ASP	2.1
1	A	160	ILE	2.1
1	A	273	GLY	2.1

## 6.2 Non-standard residues in protein, DNA, RNA chains [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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	BRU	D	25	20/21	0.97	0.14	-	57,63,79,92	0
3	BRU	D	22	20/21	0.97	0.14	-	46,53,67,82	0
3	BRU	D	29	20/21	0.91	0.17	-	102,108,127,138	0
3	BRU	D	26	20/21	0.96	0.15	-	66,72,82,105	0
3	BRU	D	28	20/21	0.95	0.14	-	88,95,116,120	0
2	BRU	C	12	20/21	0.97	0.12	-	44,56,79,97	0
1	PTR	A	405	15/17	0.97	0.17	-	33,41,49,50	0
2	BRU	C	3	20/21	0.88	0.24	-	128,133,149,151	0
3	BRU	D	23	20/21	0.98	0.15	-	45,50,70,74	0
2	BRU	C	6	20/21	0.96	0.14	-	74,85,92,106	0
3	BRU	D	31	20/21	0.89	0.24	-	113,120,135,170	0

## 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	DT	A	501	17/21	0.80	0.29	1.59	72,80,121,121	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.