



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 01:55 PM GMT

PDB ID : 2B51
Title : Structural Basis for UTP Specificity of RNA Editing TUTases from Trypanosoma Brucei
Authors : Deng, J.; Ernst, N.L.; Turley, S.; Stuart, K.D.; Hol, W.G.
Deposited on : 2005-09-27
Resolution : 2.05 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

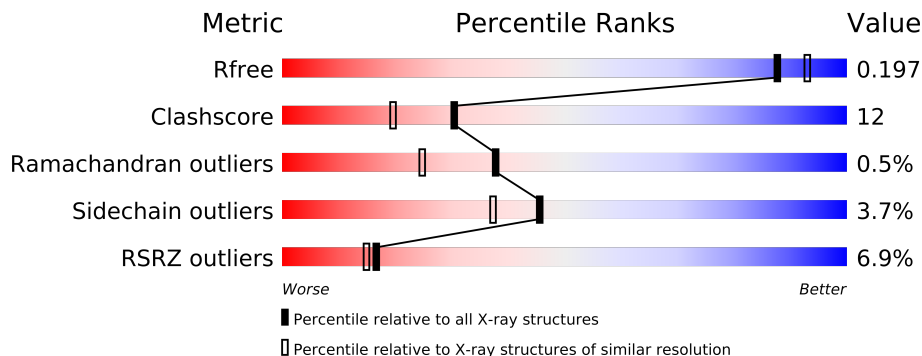
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.05 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}	66092	1380 (2.06-2.02)
Clashscore	79885	1577 (2.06-2.02)
Ramachandran outliers	78287	1565 (2.06-2.02)
Sidechain outliers	78261	1565 (2.06-2.02)
RSRZ outliers	66119	1381 (2.06-2.02)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	468	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	UTP	A	503	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4000 atoms, of which 0 are hydrogen and 0 are deuterium.

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 RNA editing complex protein MP57.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	444	Total	C	N	O	S	11	1	0
			3587	2277	642	644	24			

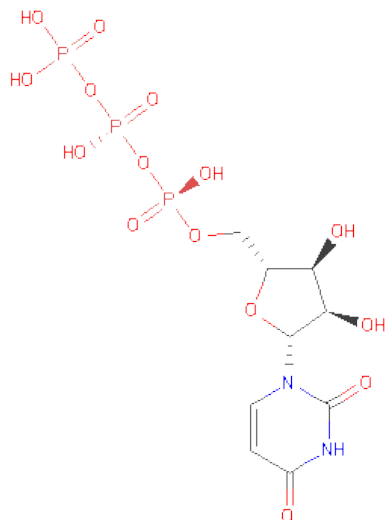
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	94	ARG	TRP	ENGINEERED	UNP Q86MV5
A	122	ARG	TRP	ENGINEERED	UNP Q86MV5
A	207	ARG	TRP	ENGINEERED	UNP Q86MV5

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mn	0	0
			1	1		

- Molecule 3 is URIDINE 5'-TRIPHOSPHATE (three-letter code: UTP) (formula: C₉H₁₅N₂O₁₅P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			29	9	2	15	3		
3	A	1	Total	C	N	O	P	0	0
			29	9	2	15	3		
3	A	1	Total	C	N	O	P	0	0
			29	9	2	15	3		

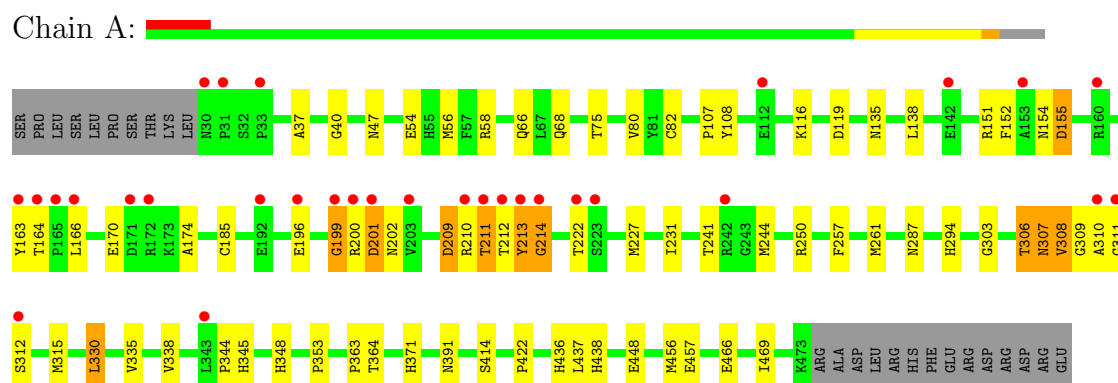
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	325	Total	O	0	0
			325	325		

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: RNA editing complex protein MP57



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	91.01Å 91.01Å 162.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.05 43.81 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.9 (50.00-2.05) 99.9 (43.81-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.187 , 0.227 0.194 , 0.197	Depositor DCC
R_{free} test set	2313 reflections (5.25%)	DCC
Wilson B-factor (Å ²)	30.3	Xtriage
Anisotropy	0.255	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 57.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 46405 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4000	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.75% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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

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	0.54	0/3685	0.63	1/4993 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	5

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	155	ASP	CB-CG-OD2	5.23	123.01	118.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	199	GLY	Peptide
1	A	213	TYR	Peptide
1	A	214	GLY	Peptide
1	A	307	ASN	Peptide
1	A	308	VAL	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3587	0	3487	84	0
2	A	1	0	0	0	0
3	A	87	0	33	4	0
4	A	325	0	0	2	0
All	All	4000	0	3520	85	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 12.

All (85) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:213:TYR:CD2	1:A:214:GLY:HA2	1.96	1.00
1:A:308:VAL:N	1:A:309:GLY:HA3	1.85	0.92
1:A:211:THR:HG21	1:A:213:TYR:CE1	2.05	0.91
1:A:306:THR:CG2	1:A:307:ASN:N	2.41	0.83
1:A:306:THR:HG23	1:A:307:ASN:H	1.44	0.83
1:A:303:GLY:O	1:A:309:GLY:HA2	1.78	0.82
1:A:211:THR:OG1	1:A:213:TYR:CZ	2.34	0.80
1:A:211:THR:CB	1:A:213:TYR:CE1	2.64	0.80
1:A:211:THR:OG1	1:A:214:GLY:HA3	1.85	0.76
1:A:68:GLN:HE22	1:A:80:VAL:H	1.35	0.75
1:A:47:ASN:HD22	1:A:294:HIS:HD2	1.34	0.73
1:A:306:THR:CG2	1:A:307:ASN:H	1.99	0.73
1:A:211:THR:CG2	1:A:213:TYR:CE1	2.71	0.72
1:A:391:ASN:HD21	1:A:422:PRO:HA	1.55	0.70
1:A:201:ASP:O	1:A:222:THR:HG21	1.91	0.69
1:A:414:SER:OG	1:A:438:HIS:HD2	1.75	0.69
1:A:306:THR:HG22	1:A:307:ASN:N	2.08	0.69
1:A:306:THR:HG22	1:A:308:VAL:HG23	1.73	0.69
1:A:47:ASN:HD22	1:A:294:HIS:CD2	2.13	0.65
1:A:308:VAL:N	1:A:309:GLY:CA	2.58	0.65
1:A:211:THR:HG21	1:A:213:TYR:CZ	2.32	0.65
1:A:211:THR:OG1	1:A:214:GLY:CA	2.45	0.64
1:A:371:HIS:HD2	4:A:581:HOH:O	1.81	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:68:GLN:NE2	1:A:80:VAL:H	1.98	0.61
1:A:306:THR:CG2	1:A:308:VAL:HG23	2.31	0.61
1:A:211:THR:OG1	1:A:213:TYR:CE2	2.49	0.61
1:A:196:GLU:OE1	1:A:200:ARG:HD2	2.00	0.60
1:A:199:GLY:HA2	1:A:200:ARG:CG	2.32	0.60
1:A:199:GLY:O	1:A:202:ASN:HB2	2.02	0.59
1:A:211:THR:HB	1:A:213:TYR:CD1	2.37	0.59
1:A:371:HIS:HE1	1:A:457:GLU:OE2	1.87	0.58
1:A:241:THR:HG23	1:A:244:MET:HE2	1.86	0.56
1:A:211:THR:OG1	1:A:213:TYR:CE1	2.57	0.55
1:A:211:THR:HB	1:A:213:TYR:CE1	2.42	0.55
1:A:391:ASN:ND2	4:A:517:HOH:O	2.40	0.55
1:A:312:SER:O	3:A:502:UTP:H1'	2.06	0.55
1:A:241:THR:HG23	1:A:244:MET:CE	2.37	0.55
1:A:306:THR:HG23	1:A:448:GLU:CD	2.28	0.54
1:A:199:GLY:HA2	1:A:200:ARG:HG2	1.88	0.54
1:A:211:THR:HG21	1:A:213:TYR:HE1	1.68	0.54
1:A:56:MET:HE3	1:A:163:TYR:CD2	2.43	0.53
1:A:330:LEU:HD13	1:A:335:VAL:HG13	1.90	0.53
1:A:456:MET:HG3	1:A:469:ILE:HD13	1.92	0.52
1:A:213:TYR:CE2	1:A:214:GLY:HA2	2.42	0.52
1:A:308:VAL:H	1:A:309:GLY:HA3	1.68	0.51
1:A:345:HIS:HB3	1:A:348:HIS:HD2	1.75	0.51
1:A:213:TYR:CD2	1:A:214:GLY:CA	2.84	0.51
1:A:82:CYS:HB3	1:A:353:PRO:HD3	1.91	0.51
1:A:54:GLU:OE2	1:A:58:ARG:NH2	2.34	0.50
1:A:211:THR:CB	1:A:213:TYR:CD1	2.95	0.50
1:A:166:LEU:HB3	1:A:170:GLU:HB2	1.92	0.49
1:A:306:THR:HG23	1:A:448:GLU:OE2	2.12	0.49
1:A:199:GLY:HA2	1:A:200:ARG:CB	2.42	0.49
1:A:344:PRO:HB2	1:A:348:HIS:HB2	1.95	0.49
1:A:56:MET:HE3	1:A:163:TYR:HD2	1.78	0.48
1:A:66:GLN:NE2	1:A:261:MET:H	2.10	0.48
1:A:231:ILE:HG23	1:A:250:ARG:HB3	1.95	0.48
1:A:56:MET:CE	1:A:163:TYR:CD2	2.96	0.47
1:A:287:ASN:ND2	3:A:503:UTP:O1G	2.45	0.47
1:A:185:CYS:SG	1:A:210:ARG:HG2	2.55	0.46
1:A:56:MET:CE	1:A:163:TYR:HD2	2.30	0.45
1:A:152:PHE:CZ	1:A:154:ASN:HA	2.52	0.44
1:A:107:PRO:HG3	1:A:345:HIS:CE1	2.53	0.44
1:A:54:GLU:O	1:A:58:ARG:HG2	2.17	0.44
1:A:199:GLY:HA2	1:A:200:ARG:HB2	2.00	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:212:THR:O	1:A:212:THR:HG22	2.18	0.43
1:A:211:THR:CG2	1:A:213:TYR:CZ	2.98	0.43
1:A:436:HIS:CE1	3:A:502:UTP:H3'	2.54	0.43
1:A:209:ASP:N	1:A:209:ASP:OD1	2.52	0.42
1:A:138:LEU:HD11	1:A:151:ARG:HD3	2.02	0.42
1:A:116:LYS:HE2	1:A:116:LYS:HB2	1.58	0.42
1:A:345:HIS:HB3	1:A:348:HIS:CD2	2.55	0.42
1:A:37:ALA:HB2	1:A:364:THR:OG1	2.20	0.42
1:A:306:THR:C	1:A:308:VAL:H	2.24	0.41
1:A:456:MET:CG	1:A:469:ILE:HD13	2.50	0.41
1:A:199:GLY:CA	1:A:200:ARG:HB2	2.50	0.41
1:A:66:GLN:HE22	1:A:261:MET:H	1.69	0.41
1:A:311:GLY:HA3	1:A:312:SER:HA	1.77	0.40
3:A:502:UTP:O5'	3:A:502:UTP:H6	2.04	0.40
1:A:107:PRO:HG2	1:A:108:TYR:CE2	2.56	0.40
1:A:174:ALA:HA	1:A:257:PHE:O	2.21	0.40
1:A:414:SER:OG	1:A:438:HIS:CD2	2.64	0.40
1:A:241:THR:H	1:A:244:MET:CE	2.34	0.40
1:A:308:VAL:H	1:A:309:GLY:CA	2.29	0.40
1:A:40:GLY:HA3	1:A:363:PRO:O	2.20	0.40

There are no symmetry-related clashes.

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	443/468 (95%)	427 (96%)	14 (3%)	2 (0%)	38	25

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	201	ASP
1	A	310	ALA

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	378/405 (93%)	363 (96%)	15 (4%)	42 33

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	75	THR
1	A	119[A]	ASP
1	A	119[B]	ASP
1	A	135	ASN
1	A	155	ASP
1	A	164	THR
1	A	209	ASP
1	A	211	THR
1	A	227	MET
1	A	306	THR
1	A	315	MET
1	A	330	LEU
1	A	338	VAL
1	A	437	LEU
1	A	466	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	35	HIS
1	A	66	GLN
1	A	68	GLN
1	A	91	GLN
1	A	283	HIS
1	A	294	HIS
1	A	334	GLN
1	A	348	HIS
1	A	371	HIS
1	A	391	ASN
1	A	416	ASN

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Mol	Chain	Res	Type
1	A	438	HIS

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 for Mogul analysis.

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	$\# Z > 2$
3	UTP	A	501	2	30,30,30	1.58	3 (10%)	43,47,47	1.59	6 (13%)
3	UTP	A	502	-	30,30,30	1.35	3 (10%)	43,47,47	1.50	5 (11%)
3	UTP	A	503	-	30,30,30	1.50	3 (10%)	43,47,47	1.25	3 (6%)

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
3	UTP	A	501	2	-	0/20/38/38	0/2/2/2
3	UTP	A	502	-	-	0/20/38/38	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	UTP	A	503	-	-	0/20/38/38	0/2/2/2

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	503	UTP	O4-C4	5.94	1.36	1.24
3	A	501	UTP	O4-C4	5.78	1.35	1.24
3	A	502	UTP	O4-C4	5.18	1.34	1.24
3	A	501	UTP	C2-N1	-4.06	1.34	1.38
3	A	503	UTP	C2-N1	-3.26	1.34	1.38
3	A	501	UTP	C6-C5	2.92	1.40	1.36
3	A	502	UTP	C6-C5	2.52	1.40	1.36
3	A	502	UTP	C2-N1	-2.43	1.35	1.38
3	A	503	UTP	C6-C5	2.32	1.39	1.36

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	UTP	N3-C2-N1	7.45	122.19	115.97
3	A	502	UTP	N3-C2-N1	5.54	120.60	115.97
3	A	503	UTP	N3-C2-N1	4.89	120.06	115.97
3	A	502	UTP	C2-N1-C1'	4.26	120.88	118.21
3	A	503	UTP	PB-O3A-PA	-2.79	123.49	131.68
3	A	502	UTP	PB-O3B-PG	-2.59	124.08	131.68
3	A	501	UTP	C3'-C2'-C1'	2.36	104.59	100.91
3	A	502	UTP	C5-C4-N3	2.13	120.72	116.70
3	A	503	UTP	C5-C4-N3	2.12	120.69	116.70
3	A	502	UTP	C3'-C2'-C1'	2.12	104.22	100.91
3	A	501	UTP	C5-C6-N1	-2.11	118.83	121.21
3	A	501	UTP	C2-N1-C1'	-2.10	116.89	118.21
3	A	501	UTP	O2'-C2'-C1'	-2.09	104.89	111.23
3	A	501	UTP	C5-C4-N3	2.05	120.57	116.70

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 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	444/468 (94%)	0.28	31 (6%) 16 15	21, 31, 49, 59	3 (0%)

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	213	TYR	6.1
1	A	200	ARG	4.8
1	A	312	SER	4.4
1	A	201	ASP	4.2
1	A	212	THR	4.1
1	A	199	GLY	4.1
1	A	163	TYR	4.0
1	A	222	THR	3.8
1	A	196	GLU	3.3
1	A	203	VAL	3.1
1	A	166	LEU	3.0
1	A	311	GLY	2.9
1	A	30	ASN	2.9
1	A	310	ALA	2.7
1	A	343	LEU	2.7
1	A	160	ARG	2.6
1	A	172	ARG	2.6
1	A	112	GLU	2.6
1	A	164	THR	2.4
1	A	165	PRO	2.4
1	A	242	ARG	2.3
1	A	153	ALA	2.3
1	A	211	THR	2.3
1	A	142	GLU	2.2
1	A	171	ASP	2.2
1	A	31	PRO	2.2
1	A	33	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	210	ARG	2.1
1	A	214	GLY	2.1
1	A	192	GLU	2.0
1	A	223	SER	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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, 95th 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	UTP	A	503	29/29	0.24	2.14	43,48,57,58	12
3	UTP	A	501	29/29	0.17	1.08	26,29,32,33	0
3	UTP	A	502	29/29	0.14	-0.16	44,47,50,51	4
2	MN	A	488	1/1	0.07	-4.42	21,21,21,21	0

6.5 Other polymers ⓘ

There are no such residues in this entry.