



wwPDB X-ray Structure Validation Summary Report ⓘ

May 22, 2020 – 02:10 pm BST

PDB ID : 1R9S
Title : RNA POLYMERASE II STRAND SEPARATED ELONGATION COM-
PLEX, MATCHED NUCLEOTIDE
Authors : Westover, K.D.; Bushnell, D.A.; Kornberg, R.D.
Deposited on : 2003-10-30
Resolution : 4.25 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
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
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

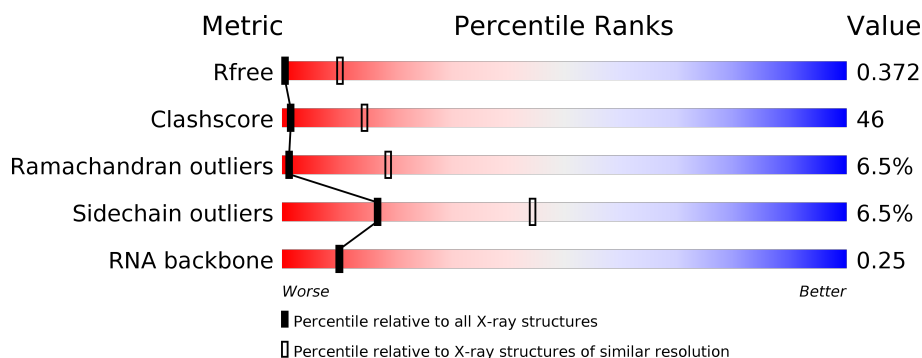
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.25 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.




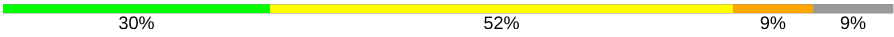
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1017 (4.72-3.78)
Clashscore	141614	1059 (4.72-3.80)
Ramachandran outliers	138981	1014 (4.72-3.80)
Sidechain outliers	138945	1018 (4.72-3.78)
RNA backbone	3102	1057 (5.50-3.00)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	R	10	50% 50%
2	T	14	21% 64% 14%
3	A	1733	31% 41% 7% 20%
4	B	1224	32% 51% 7% 10%
5	C	318	37% 40% 7% 16%
6	E	215	40% 56% .

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Mol	Chain	Length	Quality of chain
7	F	155	
8	H	146	
9	I	122	
10	J	70	
11	K	120	
12	L	70	

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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
14	UTP	R	3000	X	-	-	-
15	ZN	I	204	-	-	X	-

2 Entry composition [i](#)

There are 15 unique types of molecules in this entry. The entry contains 28491 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 RNA chain called RNA strand.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	R	10	Total	C	N	O	P	0	0	0
			217	98	45	65	9			

- Molecule 2 is a DNA chain called DNA strand.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	T	14	Total	C	N	O	P	0	0	0
			279	135	48	83	13			

- Molecule 3 is a protein called DNA-directed RNA polymerase II largest subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	1381	Total	C	N	O	S	0	0	0
			10857	6851	1899	2046	61			

- Molecule 4 is a protein called DNA-directed RNA polymerase II 140 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	B	1097	Total	C	N	O	S	0	0	0
			8720	5526	1523	1617	54			

- Molecule 5 is a protein called DNA-directed RNA polymerase II 45 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	C	266	Total	C	N	O	S	0	0	0
			2095	1317	348	417	13			

- Molecule 6 is a protein called DNA-directed RNA polymerases I, II, and III 27 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	E	214	Total	C	N	O	S	0	0	0
			1752	1111	309	321	11			

- Molecule 7 is a protein called DNA-directed RNA polymerases I, II, and III 23 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	F	84	Total	C	N	O	S	0	0	0
			679	434	115	127	3			

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III 14.5 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	133	Total	C	N	O	S	0	0	0
			1068	673	180	211	4			

- Molecule 9 is a protein called DNA-directed RNA polymerase II 14.2 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	119	Total	C	N	O	S	0	0	0
			971	596	179	186	10			

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III 8.3 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	65	Total	C	N	O	S	0	0	0
			532	339	93	94	6			

- Molecule 11 is a protein called DNA-directed RNA polymerase II 13.6 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	114	Total	C	N	O	S	0	0	0
			919	590	156	171	2			

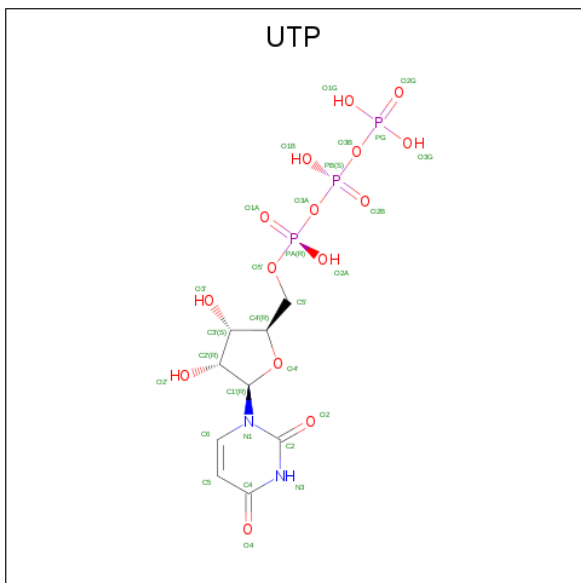
- Molecule 12 is a protein called DNA-directed RNA polymerases I, II, and III 7.7 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	46	Total	C	N	O	S	0	0	0
			363	224	72	63	4			

- Molecule 13 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	R	1	Total	Mg	0	0
			1	1		
13	A	1	Total	Mg	0	0
			1	1		

- Molecule 14 is URIDINE 5'-TRIPHOSPHATE (three-letter code: UTP) (formula: C₉H₁₅N₂O₁₅P₃).



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. 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. 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.

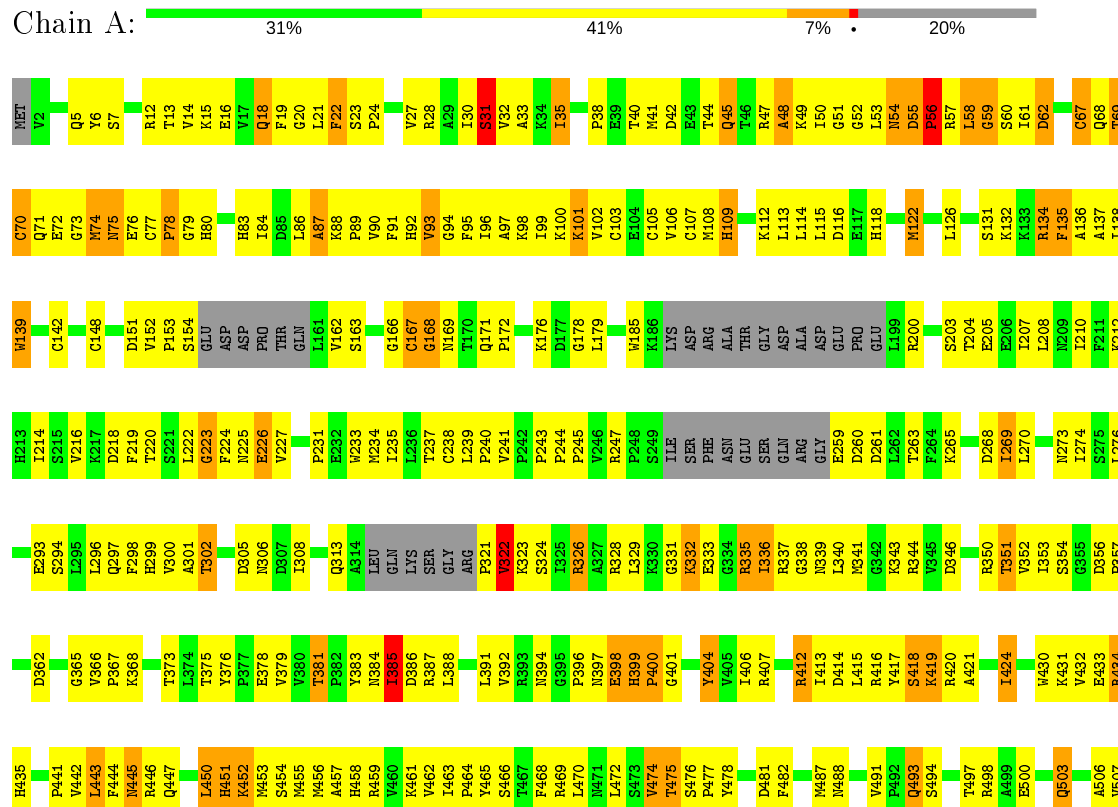
- Molecule 1: RNA strand



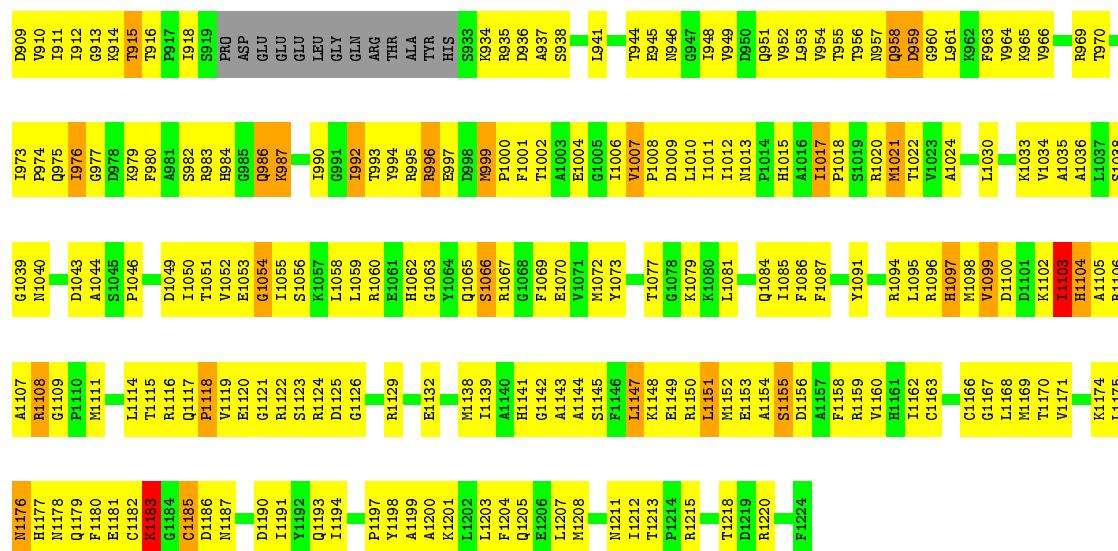
- Molecule 2: DNA strand

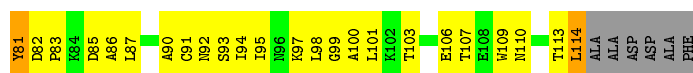


- Molecule 3: DNA-directed RNA polymerase II largest subunit

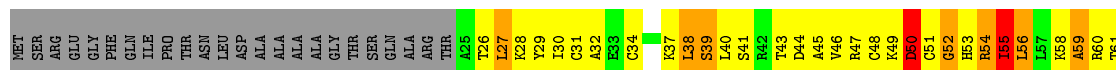








- Molecule 12: DNA-directed RNA polymerases I, II, and III 7.7 kDa polypeptide



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	169.65Å 222.34Å 194.32Å 90.00° 101.67° 90.00°	Depositor
Resolution (Å)	40.00 – 4.25 39.94 – 4.20	Depositor EDS
% Data completeness (in resolution range)	95.8 (40.00-4.25) 84.6 (39.94-4.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.00 (at 4.13Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.349 , 0.398 0.319 , 0.372	Depositor DCC
R_{free} test set	5207 reflections (10.13%)	wwPDB-VP
Wilson B-factor (Å ²)	96.8	Xtriage
Anisotropy	0.402	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 104.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.71	EDS
Total number of atoms	28491	wwPDB-VP
Average B, all atoms (Å ²)	130.0	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.*

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 ⓘ

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

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	R	3.97	33/244 (13.5%)	3.92	44/380 (11.6%)
2	T	4.38	37/311 (11.9%)	3.99	55/477 (11.5%)
3	A	0.41	0/11048	0.71	5/14936 (0.0%)
4	B	0.46	0/8890	0.72	1/11990 (0.0%)
5	C	0.48	0/2133	0.76	2/2891 (0.1%)
6	E	0.36	0/1788	0.65	0/2406
7	F	0.40	0/691	0.64	0/933
8	H	0.40	0/1086	0.73	0/1470
9	I	0.48	0/989	0.76	1/1331 (0.1%)
10	J	0.53	0/541	0.78	0/727
11	K	0.46	0/937	0.68	0/1265
12	L	0.48	0/365	0.78	0/485
All	All	0.72	70/29023 (0.2%)	0.92	108/39291 (0.3%)

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	R	0	1
2	T	1	2
All	All	1	3

The worst 5 of 70 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	T	3	DG	O3'-P	-35.59	1.18	1.61
2	T	4	DA	O3'-P	-30.26	1.24	1.61
1	R	10	A	P-OP1	-23.82	1.08	1.49
1	R	5	A	O3'-P	-22.75	1.33	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	T	3	DG	C3'-O3'	-20.45	1.17	1.44

The worst 5 of 108 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	T	3	DG	O3'-P-O5'	-28.04	50.72	104.00
1	R	9	G	P-O3'-C3'	28.01	153.31	119.70
1	R	4	G	OP2-P-O3'	-25.63	48.80	105.20
2	T	3	DG	P-O3'-C3'	-25.44	89.17	119.70
2	T	7	DC	O5'-P-OP1	25.27	141.02	110.70

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	T	7	DC	C3'

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	R	10	A	Sidechain
2	T	7	DC	Sidechain
2	T	9	DC	Sidechain

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	R	217	0	110	48	0
2	T	279	0	160	69	0
3	A	10857	0	10959	1037	18
4	B	8720	0	8746	901	13
5	C	2095	0	2052	164	0
6	E	1752	0	1776	133	0
7	F	679	0	701	67	0
8	H	1068	0	1040	134	0
9	I	971	0	933	105	59
10	J	532	0	544	77	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	K	919	0	929	85	0
12	L	363	0	388	55	0
13	A	1	0	0	0	0
13	R	1	0	0	0	0
14	R	29	0	8	8	0
15	A	2	0	0	0	0
15	B	1	0	0	0	0
15	C	1	0	0	0	0
15	I	2	0	0	2	0
15	J	1	0	0	1	0
15	L	1	0	0	0	0
All	All	28491	0	28346	2619	59

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 46.

The worst 5 of 2619 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:R:10:A:OP1	1:R:10:A:P	1.08	1.47
2:T:6:DC:H2''	2:T:7:DC:C5'	1.54	1.36
2:T:7:DC:C5'	2:T:7:DC:O5'	1.78	1.30
3:A:567:LYS:HB2	3:A:568:PRO:HD2	1.18	1.17
9:I:111:THR:HG22	9:I:113:ASP:H	1.05	1.15

The worst 5 of 59 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)
4:B:736:THR:CB	9:I:79:HIS:CD2[2_556]	0.78	1.42
4:B:736:THR:OG1	9:I:79:HIS:NE2[2_556]	0.83	1.37
9:I:81:ARG:O	9:I:81:ARG:CB[2_556]	1.01	1.19
4:B:736:THR:OG1	9:I:79:HIS:CD2[2_556]	1.02	1.18
3:A:923:LEU:CD1	9:I:35:VAL:C[4_546]	1.06	1.14

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	
3	A	1365/1733 (79%)	1023 (75%)	252 (18%)	90 (7%)	1	18
4	B	1077/1224 (88%)	839 (78%)	169 (16%)	69 (6%)	1	19
5	C	264/318 (83%)	208 (79%)	40 (15%)	16 (6%)	1	19
6	E	212/215 (99%)	170 (80%)	33 (16%)	9 (4%)	3	25
7	F	82/155 (53%)	64 (78%)	15 (18%)	3 (4%)	3	28
8	H	129/146 (88%)	93 (72%)	21 (16%)	15 (12%)	0	6
9	I	117/122 (96%)	93 (80%)	15 (13%)	9 (8%)	1	15
10	J	63/70 (90%)	48 (76%)	11 (18%)	4 (6%)	1	19
11	K	112/120 (93%)	96 (86%)	15 (13%)	1 (1%)	17	56
12	L	44/70 (63%)	22 (50%)	12 (27%)	10 (23%)	0	1
All	All	3465/4173 (83%)	2656 (77%)	583 (17%)	226 (6%)	1	19

5 of 226 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	31	SER
3	A	48	ALA
3	A	55	ASP
3	A	56	PRO
3	A	74	MET

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	
3	A	1206/1520 (79%)	1128 (94%)	78 (6%)	17	44
4	B	952/1061 (90%)	886 (93%)	66 (7%)	15	43
5	C	234/274 (85%)	222 (95%)	12 (5%)	24	51
6	E	196/197 (100%)	189 (96%)	7 (4%)	35	60
7	F	74/137 (54%)	68 (92%)	6 (8%)	11	38
8	H	117/128 (91%)	112 (96%)	5 (4%)	29	55
9	I	113/116 (97%)	104 (92%)	9 (8%)	12	38
10	J	60/65 (92%)	56 (93%)	4 (7%)	16	43
11	K	99/102 (97%)	90 (91%)	9 (9%)	9	32
12	L	40/57 (70%)	35 (88%)	5 (12%)	4	22
All	All	3091/3657 (84%)	2890 (94%)	201 (6%)	17	44

5 of 201 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	B	261	ARG
4	B	644	GLU
10	J	47	ARG
4	B	309	GLN
4	B	466	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 76 such sidechains are listed below:

Mol	Chain	Res	Type
4	B	236	HIS
4	B	518	HIS
9	I	12	ASN
4	B	325	GLN
4	B	484	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	R	10/10 (100%)	3 (30%)	3 (30%)

All (3) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	R	2	U
1	R	5	A
1	R	6	G

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	R	1	A
1	R	4	G
1	R	5	A

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](#)

Of 11 ligands modelled in this entry, 10 are monoatomic - leaving 1 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
14	UTP	R	3000	1,13	26,30,30	3.30	11 (42%)	34,47,47	3.24	9 (26%)

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
14	UTP	R	3000	1,13	1/1/7/7	4/22/38/38	0/2/2/2

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	R	3000	UTP	C1'-N1	7.74	1.61	1.46
14	R	3000	UTP	C6-C5	-6.77	1.34	1.52
14	R	3000	UTP	C3'-C4'	-5.50	1.38	1.53
14	R	3000	UTP	C5'-C4'	5.26	1.68	1.51
14	R	3000	UTP	O2'-C2'	5.17	1.55	1.43

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	R	3000	UTP	O4'-C4'-C5'	13.11	152.51	109.37
14	R	3000	UTP	O5'-C5'-C4'	6.78	132.33	108.99
14	R	3000	UTP	C5'-C4'-C3'	-6.59	90.48	115.18
14	R	3000	UTP	O3'-C3'-C2'	-4.56	97.06	111.82
14	R	3000	UTP	O4'-C4'-C3'	4.34	113.69	105.11

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
14	R	3000	UTP	C4'

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
14	R	3000	UTP	C5'-O5'-PA-O2A
14	R	3000	UTP	C5'-O5'-PA-O3A
14	R	3000	UTP	C4'-C5'-O5'-PA
14	R	3000	UTP	O4'-C4'-C5'-O5'

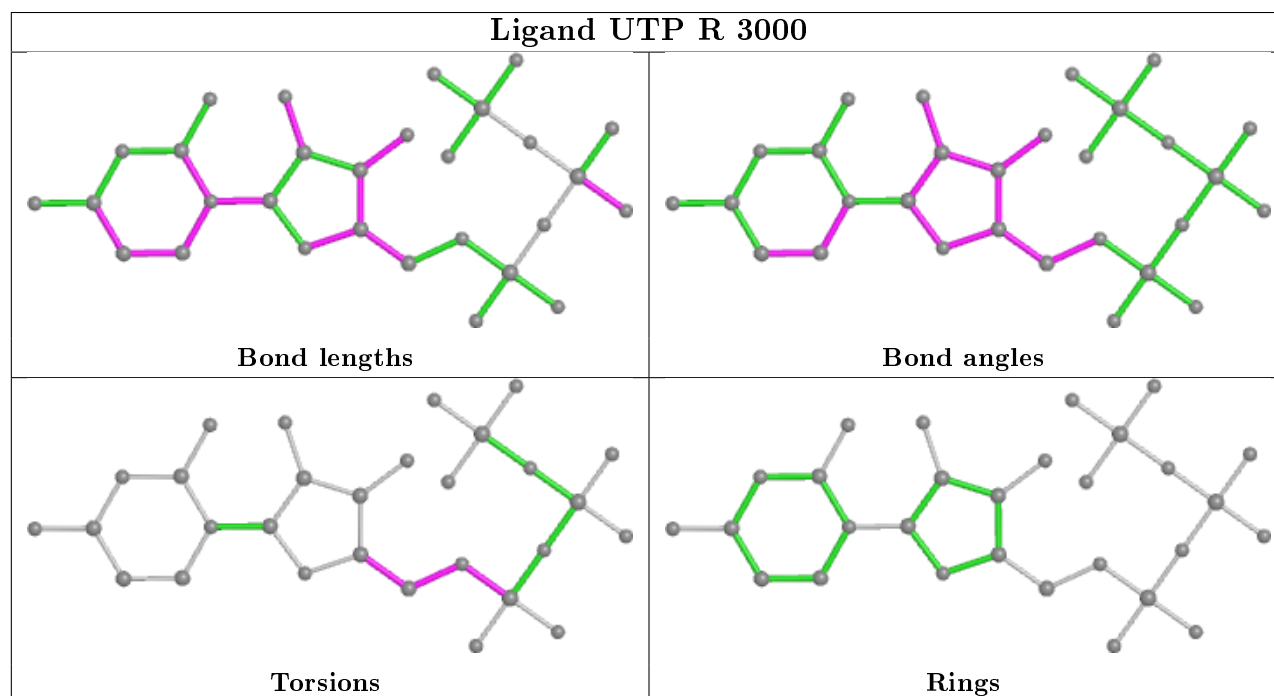
There are no ring outliers.

1 monomer is involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
14	R	3000	UTP	8	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	T	3
1	R	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	T	7:DC	O3'	8:DT	P	1.39

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	R	5:A	O3'	6:G	P	1.33
1	T	4:DA	O3'	5:DT	P	1.24
1	T	3:DG	O3'	4:DA	P	1.18

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

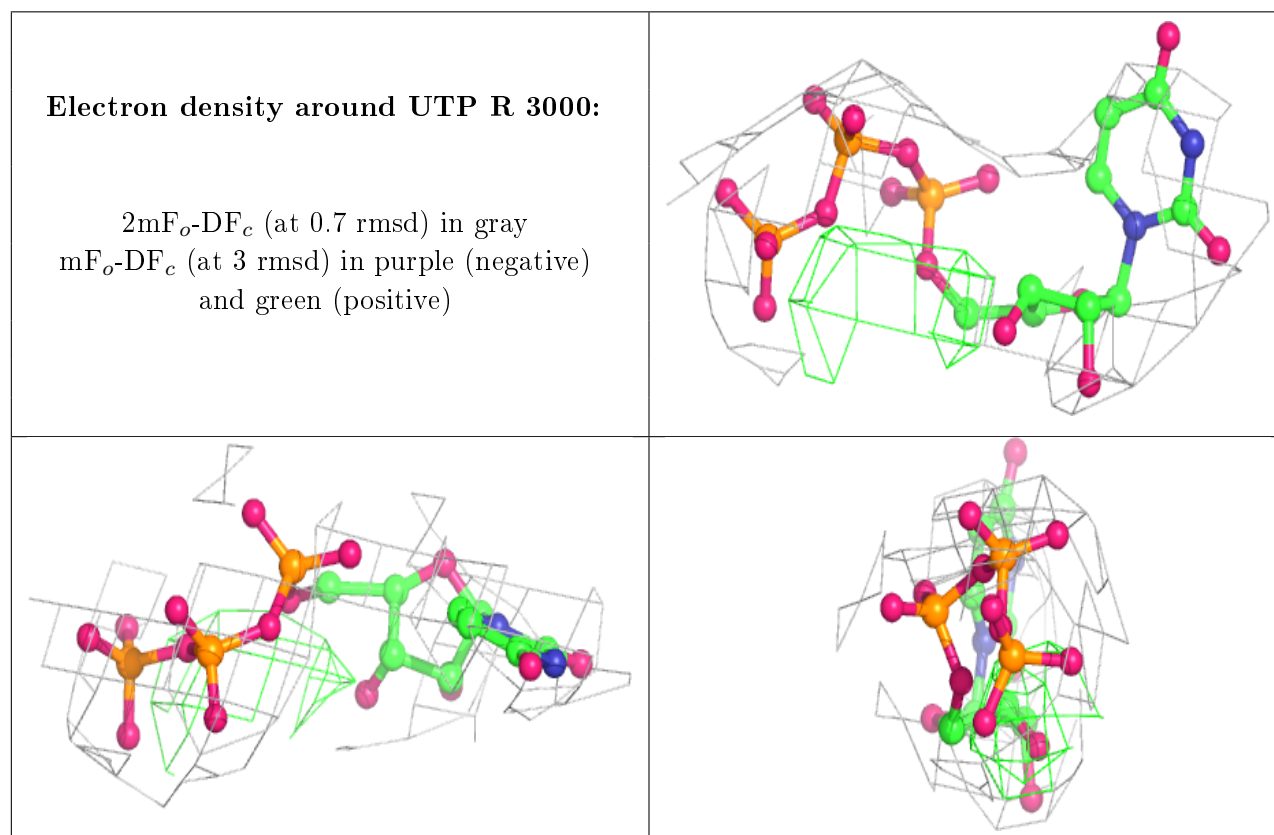
6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.