



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 9, 2020 – 12:40 PM BST

PDB ID : 6UQ0
Title : RNA polymerase II elongation complex with 5-guanidinohydantoin lesion in state 4
Authors : Oh, J.; Wang, D.
Deposited on : 2019-10-18
Resolution : 3.56 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 : 2.13.1
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) : 2.13.1

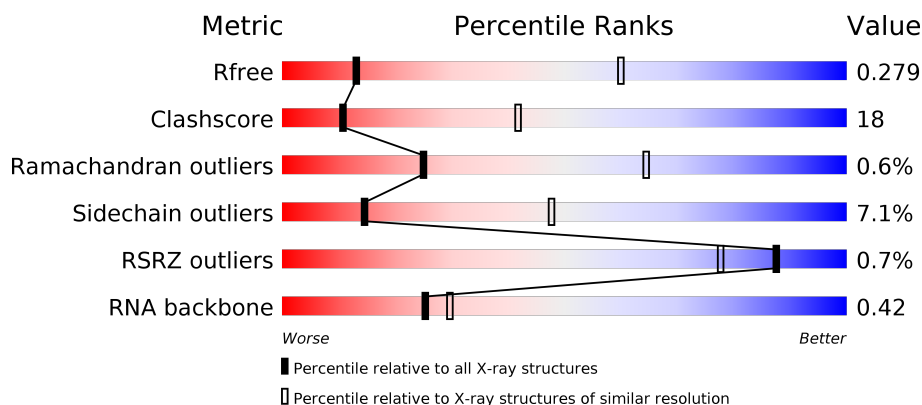
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.56 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	1020 (3.62-3.50)
Clashscore	141614	1100 (3.62-3.50)
Ramachandran outliers	138981	1065 (3.62-3.50)
Sidechain outliers	138945	1066 (3.62-3.50)
RSRZ outliers	127900	1009 (3.64-3.48)
RNA backbone	3102	1008 (4.10-3.00)

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 $\leq 5\%$. 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	R	10	
2	T	29	
3	N	18	
4	A	1733	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	B	1224	<div><div></div><div>57%32%8%</div></div>
6	C	318	<div><div></div><div>54%29%16%</div></div>
7	E	215	<div><div>3%</div><div></div><div>54%42%.</div></div>
8	F	155	<div><div></div><div>37%15%.46%</div></div>
9	H	146	<div><div></div><div>49%38%.9%</div></div>
10	I	122	<div><div></div><div>63%32%. .</div></div>
11	J	70	<div><div></div><div>44%46%.7%</div></div>
12	K	120	<div><div></div><div>64%28%.5%</div></div>
13	L	70	<div><div></div><div>29%33%39%</div></div>

2 Entry composition

There are 15 unique types of molecules in this entry. The entry contains 29050 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	R	9	Total	C	N	O	P	0	0	0
			198	88	40	61	9			

- Molecule 2 is a DNA chain called Template strand DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	T	26	Total	C	N	O	P	0	0	0
			519	248	81	164	26			

- Molecule 3 is a DNA chain called Non-template strand DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	N	15	Total	C	N	O	P	0	0	0
			320	149	73	83	15			

- Molecule 4 is a protein called DNA-directed RNA polymerase II subunit RPB1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	A	1385	Total	C	N	O	S	0	0	0
			10846	6840	1901	2045	60			

- Molecule 5 is a protein called DNA-directed RNA polymerase II subunit RPB2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	B	1121	Total	C	N	O	S	0	0	0
			8846	5599	1550	1644	53			

- Molecule 6 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	C	267	Total	C	N	O	S	0	0	0
			2101	1320	349	419	13			

- Molecule 7 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	E	213	Total	C	N	O	S	0	0	0
			1736	1102	306	317	11			

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	F	84	Total	C	N	O	S	0	0	0
			671	428	113	127	3			

- Molecule 9 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	H	133	Total	C	N	O	S	0	0	0
			1064	670	179	211	4			

- Molecule 10 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	I	118	Total	C	N	O	S	0	0	0
			952	585	173	184	10			

- Molecule 11 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

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

- Molecule 12 is a protein called DNA-directed RNA polymerase II subunit RPB11.

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

- Molecule 13 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	L	43	Total	C	N	O	S	0	0	0
			337	208	66	59	4			

- Molecule 14 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	J	1	Total 1	Zn 1	0	0
14	B	1	Total 1	Zn 1	0	0
14	I	2	Total 2	Zn 2	0	0
14	C	1	Total 1	Zn 1	0	0
14	A	2	Total 2	Zn 2	0	0
14	L	1	Total 1	Zn 1	0	0

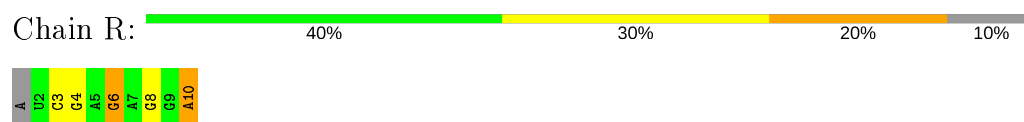
- Molecule 15 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	A	1	Total 1	Mg 1	0	0

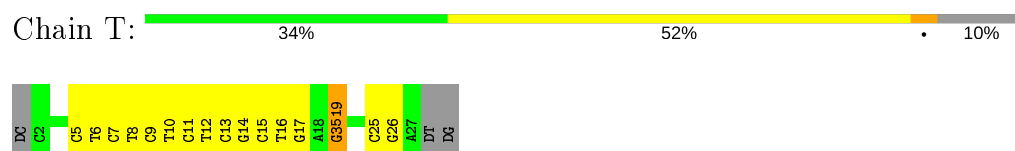
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

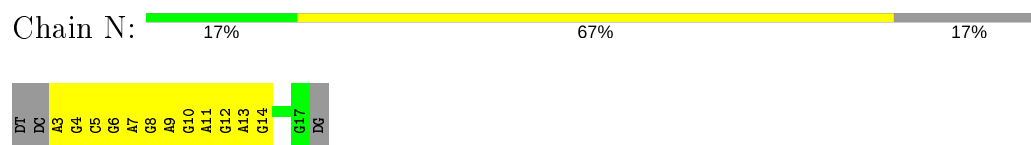
- Molecule 1: RNA



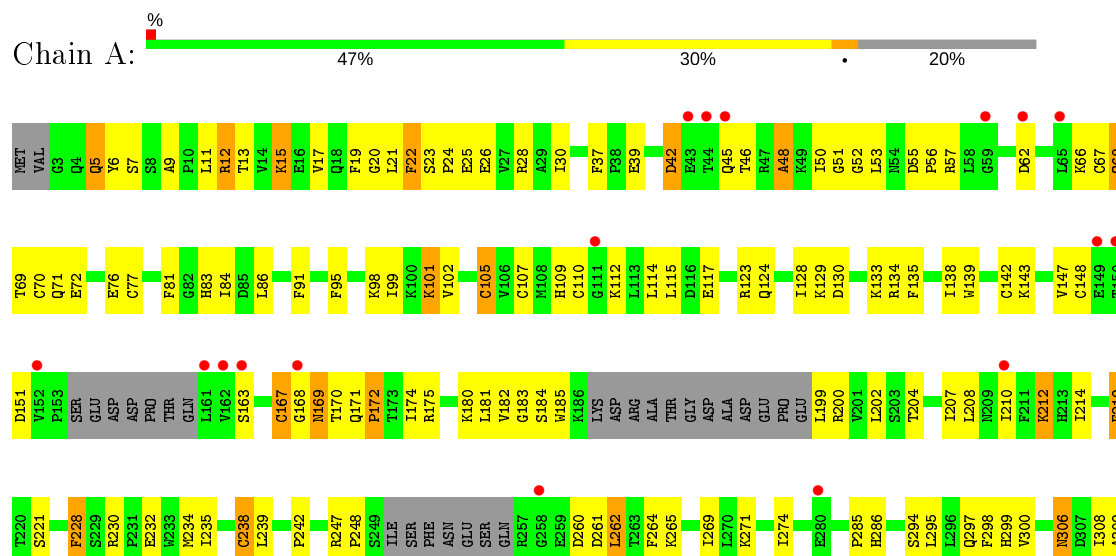
- Molecule 2: Template strand DNA



- Molecule 3: Non-template strand DNA



- Molecule 4: DNA-directed RNA polymerase II subunit RPB1



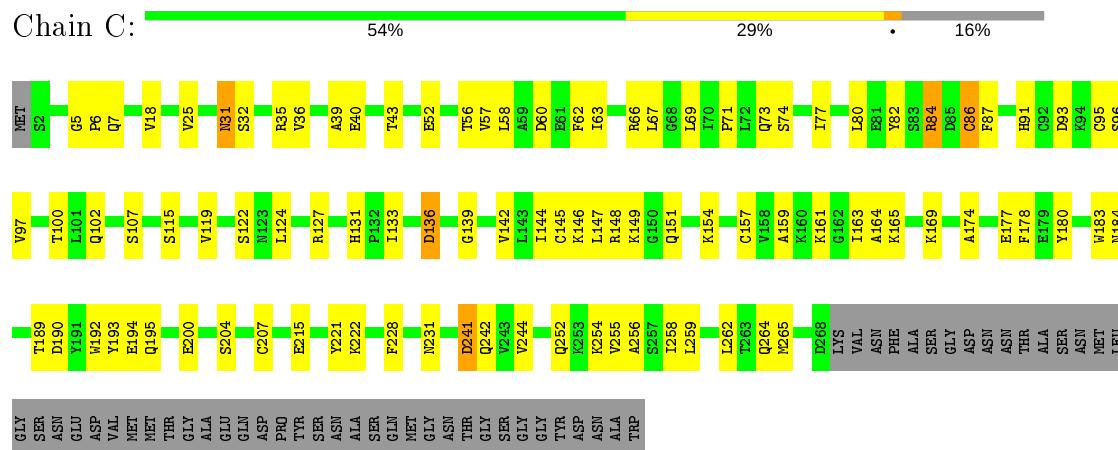


Chain B:

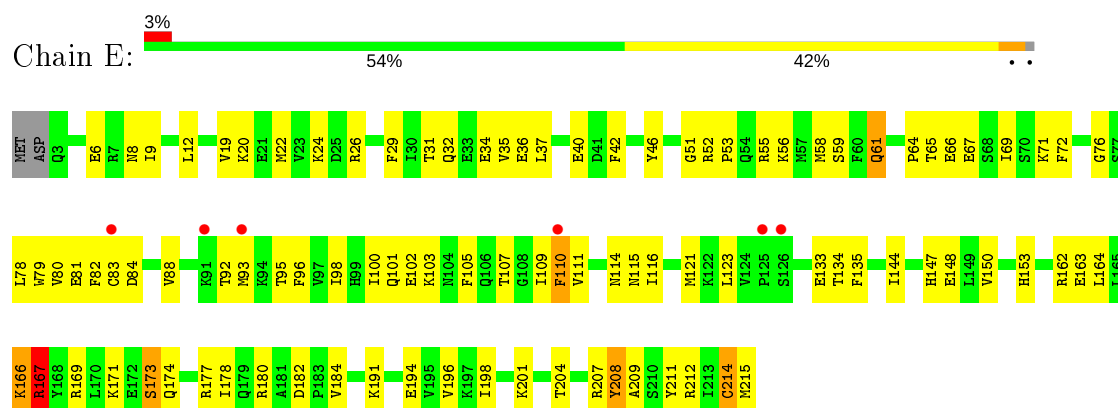




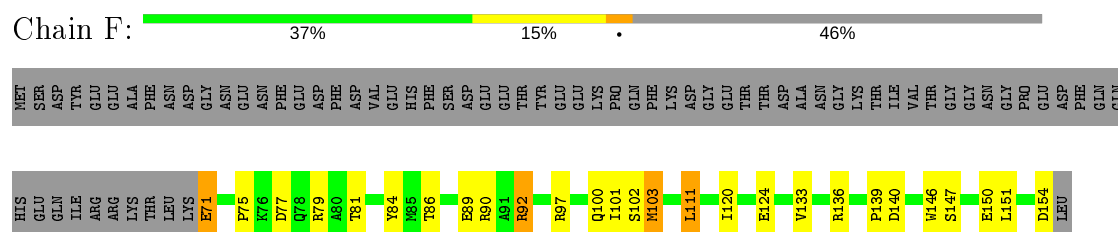
- Molecule 6: DNA-directed RNA polymerase II subunit RPB3



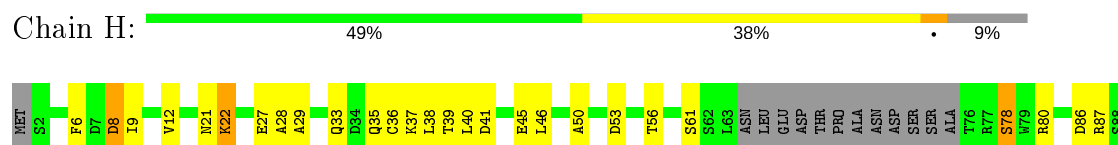
- Molecule 7: DNA-directed RNA polymerases I, II, and III subunit RPABC1



- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC2



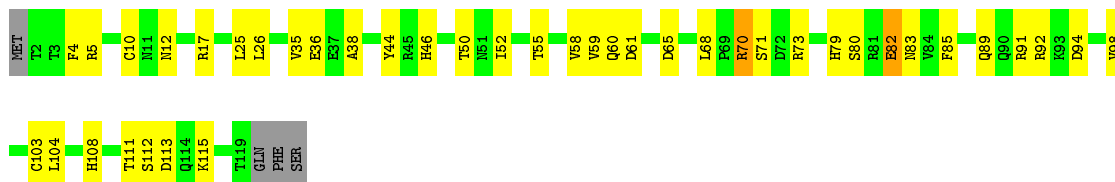
- Molecule 9: DNA-directed RNA polymerases I, II, and III subunit RPABC3





- Molecule 10: DNA-directed RNA polymerase II subunit RPB9

Chain I: 63% 32% • •



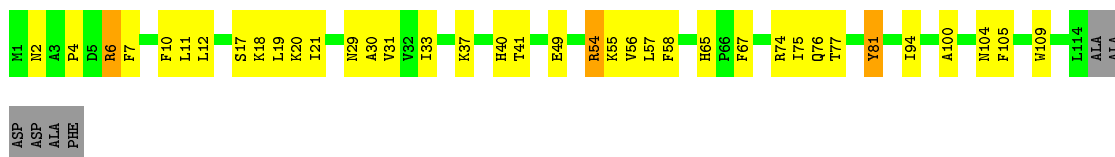
- Molecule 11: DNA-directed RNA polymerases I, II, and III subunit RPABC5

Chain J: 44% 46% • 7%



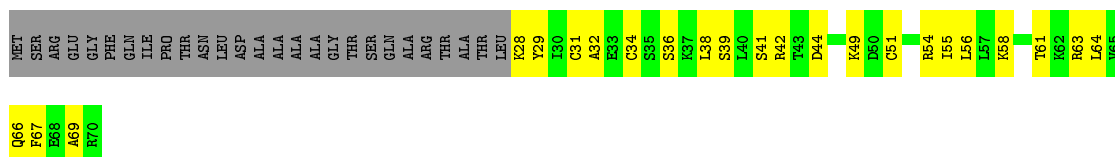
- Molecule 12: DNA-directed RNA polymerase II subunit RPB11

Chain K: 64% 28% • 5%



- Molecule 13: DNA-directed RNA polymerases I, II, and III subunit RPABC4

Chain L: 29% 33% 39%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	167.90Å 223.27Å 193.14Å 90.00° 100.94° 90.00°	Depositor
Resolution (Å)	49.70 – 3.56 49.70 – 3.56	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.70-3.56) 99.9 (49.70-3.56)	Depositor EDS
R_{merge}	0.68	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.25 (at 3.57Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.235 , 0.278 0.236 , 0.279	Depositor DCC
R_{free} test set	1996 reflections (2.39%)	wwPDB-VP
Wilson B-factor (Å ²)	75.6	Xtriage
Anisotropy	0.526	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 72.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.21$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	29050	wwPDB-VP
Average B, all atoms (Å ²)	91.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.05% 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: ZN, G35, MG

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	0.30	0/222	1.11	2/345 (0.6%)
2	T	0.69	0/550	1.08	0/841
3	N	0.59	0/363	0.87	0/560
4	A	0.30	0/11038	0.54	3/14930 (0.0%)
5	B	0.29	0/9017	0.51	0/12168
6	C	0.29	0/2139	0.52	0/2899
7	E	0.30	0/1772	0.54	0/2386
8	F	0.30	0/683	0.56	1/925 (0.1%)
9	H	0.29	0/1082	0.57	0/1466
10	I	0.31	0/970	0.56	1/1308 (0.1%)
11	J	0.28	0/541	0.53	0/727
12	K	0.32	0/937	0.57	1/1265 (0.1%)
13	L	0.29	0/339	0.57	0/450
All	All	0.31	0/29653	0.57	8/40270 (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
7	E	0	1

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	K	19	LEU	CB-CG-CD2	-8.11	97.22	111.00
4	A	1433	MET	CG-SD-CE	-7.75	87.80	100.20
4	A	325	ILE	CG1-CB-CG2	-7.12	95.75	111.40

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	472	LEU	CB-CG-CD1	-6.27	100.33	111.00
8	F	92	ARG	NE-CZ-NH2	6.19	123.39	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	E	167	ARG	Peptide

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	R	198	0	97	2	0
2	T	519	0	298	21	0
3	N	320	0	166	19	0
4	A	10846	0	10899	507	1
5	B	8846	0	8804	355	0
6	C	2101	0	2057	79	1
7	E	1736	0	1755	68	0
8	F	671	0	679	25	0
9	H	1064	0	1029	45	0
10	I	952	0	897	28	2
11	J	532	0	543	41	0
12	K	919	0	929	32	0
13	L	337	0	352	16	1
14	A	2	0	0	0	0
14	B	1	0	0	0	0
14	C	1	0	0	0	0
14	I	2	0	0	0	0
14	J	1	0	0	0	0
14	L	1	0	0	0	0
15	A	1	0	0	0	0
All	All	29050	0	28505	1049	4

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 18.

The worst 5 of 1049 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)
4:A:873:MET:HE1	4:A:957:PRO:CB	1.68	1.23
4:A:873:MET:HE1	4:A:957:PRO:HB3	1.20	1.18
4:A:873:MET:CE	4:A:957:PRO:HB3	1.80	1.12
4:A:569:LYS:HD2	6:C:221:TYR:HB2	1.39	1.04
4:A:873:MET:CE	4:A:957:PRO:CB	2.39	0.99

All (4) 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)
10:I:82:GLU:CD	10:I:82:GLU:OE1[2_556]	1.28	0.92
13:L:28:LYS:CE	13:L:28:LYS:NZ[2_555]	1.51	0.69
4:A:418:SER:OG	6:C:87:PHE:O[2_555]	2.12	0.08
10:I:82:GLU:OE1	10:I:82:GLU:OE2[2_556]	2.16	0.04

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	
4	A	1371/1733 (79%)	1279 (93%)	77 (6%)	15 (1%)	14	54
5	B	1101/1224 (90%)	1042 (95%)	55 (5%)	4 (0%)	34	71
6	C	265/318 (83%)	250 (94%)	15 (6%)	0	100	100
7	E	211/215 (98%)	197 (93%)	13 (6%)	1 (0%)	29	67
8	F	82/155 (53%)	77 (94%)	5 (6%)	0	100	100
9	H	129/146 (88%)	120 (93%)	9 (7%)	0	100	100
10	I	116/122 (95%)	106 (91%)	9 (8%)	1 (1%)	17	57
11	J	63/70 (90%)	61 (97%)	2 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	K	112/120 (93%)	106 (95%)	6 (5%)	0	100	100
13	L	41/70 (59%)	37 (90%)	3 (7%)	1 (2%)	6	37
All	All	3491/4173 (84%)	3275 (94%)	194 (6%)	22 (1%)	25	64

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	248	PRO
4	A	311	GLN
4	A	517	ASN
4	A	567	LYS
5	B	367	LEU

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	
4	A	1197/1520 (79%)	1105 (92%)	92 (8%)	13	44
5	B	953/1061 (90%)	893 (94%)	60 (6%)	18	52
6	C	235/274 (86%)	219 (93%)	16 (7%)	16	49
7	E	193/197 (98%)	179 (93%)	14 (7%)	14	46
8	F	72/137 (53%)	68 (94%)	4 (6%)	21	56
9	H	116/128 (91%)	101 (87%)	15 (13%)	4	24
10	I	110/116 (95%)	104 (94%)	6 (6%)	21	56
11	J	60/65 (92%)	58 (97%)	2 (3%)	38	69
12	K	99/102 (97%)	92 (93%)	7 (7%)	14	48
13	L	37/57 (65%)	34 (92%)	3 (8%)	11	42
All	All	3072/3657 (84%)	2853 (93%)	219 (7%)	14	48

5 of 219 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	B	252	SER
5	B	601	ARG
10	I	17	ARG
5	B	309	GLN
5	B	429	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
4	A	1070	GLN
5	B	309	GLN
5	B	1211	ASN
4	A	877	HIS
5	B	761	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	R	8/10 (80%)	3 (37%)	0

All (3) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	R	6	G
1	R	8	G
1	R	10	A

There are no RNA pucker outliers to report.

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

1 non-standard protein/DNA/RNA residue 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	G35	T	19	2	18,23,24	4.76	14 (77%)	20,33,36	1.62	1 (5%)

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	G35	T	19	2	-	4/10/41/42	0/2/2/2

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	T	19	G35	C2-N3	9.36	1.49	1.33
2	T	19	G35	O4'-C4'	7.71	1.62	1.45
2	T	19	G35	C3'-C4'	-6.89	1.34	1.53
2	T	19	G35	C8-N9	6.83	1.47	1.37
2	T	19	G35	C5-N7	5.99	1.45	1.37

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	T	19	G35	C5-C4-N9	5.80	109.98	102.28

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	T	19	G35	C3'-C4'-C5'-O5'
2	T	19	G35	O4'-C4'-C5'-O5'
2	T	19	G35	C2'-C1'-N9-C8
2	T	19	G35	C4'-C5'-O5'-P

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	T	19	G35	3	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 9 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

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, 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	R	9/10 (90%)	-0.41	0 100 100	81, 90, 129, 136	0
2	T	25/29 (86%)	-0.38	0 100 100	77, 163, 203, 216	0
3	N	15/18 (83%)	-0.21	0 100 100	125, 169, 239, 269	0
4	A	1385/1733 (79%)	-0.31	17 (1%) 79 65	33, 85, 160, 262	0
5	B	1121/1224 (91%)	-0.40	3 (0%) 94 88	28, 74, 139, 207	0
6	C	267/318 (83%)	-0.49	0 100 100	45, 76, 118, 156	0
7	E	213/215 (99%)	-0.23	6 (2%) 53 37	50, 113, 185, 243	0
8	F	84/155 (54%)	-0.52	0 100 100	59, 83, 125, 170	0
9	H	133/146 (91%)	-0.28	0 100 100	60, 95, 158, 206	0
10	I	118/122 (96%)	-0.45	0 100 100	45, 92, 125, 183	0
11	J	65/70 (92%)	-0.62	0 100 100	41, 67, 101, 139	0
12	K	114/120 (95%)	-0.45	0 100 100	43, 77, 117, 142	0
13	L	43/70 (61%)	-0.14	0 100 100	49, 118, 188, 206	0
All	All	3592/4230 (84%)	-0.36	26 (0%) 87 78	28, 83, 158, 269	0

The worst 5 of 26 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	A	59	GLY	4.1
7	E	126	SER	3.8
4	A	111	GLY	3.8
4	A	44	THR	3.7
4	A	45	GLN	3.6

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. 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	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	G35	T	19	22/23	0.93	0.22	92,107,135,138	0

6.3 Carbohydrates [i](#)

There are no monosaccharides 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, 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	RSCC	RSR	B-factors(\AA^2)	Q<0.9
14	ZN	A	1801	1/1	0.61	0.15	234,234,234,234	0
14	ZN	B	1301	1/1	0.93	0.09	191,191,191,191	0
14	ZN	J	101	1/1	0.96	0.15	74,74,74,74	0
14	ZN	L	101	1/1	0.96	0.06	142,142,142,142	0
14	ZN	I	202	1/1	0.96	0.20	135,135,135,135	0
15	MG	A	1803	1/1	0.97	0.06	84,84,84,84	0
14	ZN	A	1802	1/1	0.97	0.11	130,130,130,130	0
14	ZN	C	401	1/1	0.98	0.12	92,92,92,92	0
14	ZN	I	201	1/1	0.98	0.10	72,72,72,72	0

6.5 Other polymers [i](#)

There are no such residues in this entry.