



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 4, 2025 – 10:13 AM EDT

PDB ID : 9N5F / pdb_00009n5f
Title : RNA polymerase II elongation complex with 8-oxoG in syn-conformation with added AMP
Authors : Oh, J.; Wang, D.
Deposited on : 2025-02-04
Resolution : 3.60 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0rc1
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.45.1

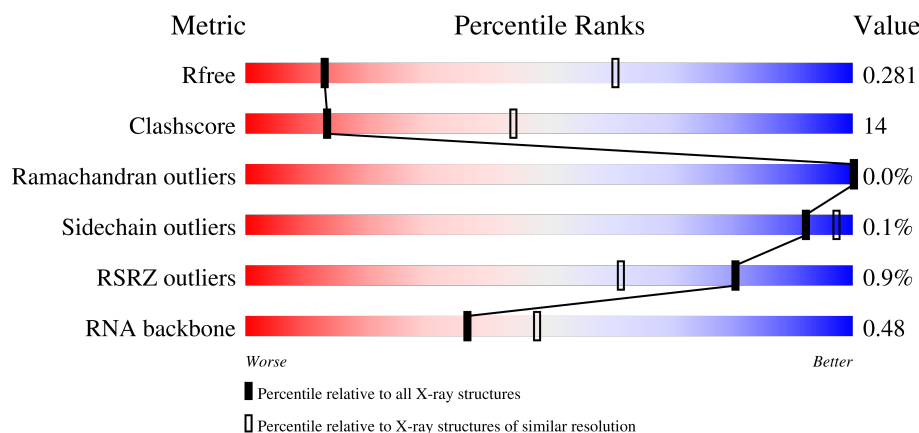
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.60 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}	164625	1563 (3.70-3.50)
Clashscore	180529	1665 (3.70-3.50)
Ramachandran outliers	177936	1641 (3.70-3.50)
Sidechain outliers	177891	1640 (3.70-3.50)
RSRZ outliers	164620	1562 (3.70-3.50)
RNA backbone	3690	1108 (4.20-3.00)

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 of 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	 60% 10% 30%
2	T	29	 17% 69% 10%
3	N	18	 17% 67% 17%
4	A	1733	 55% 24% 20%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	B	1224	<div><div><div></div><div></div><div></div></div><div>%64%27%8%</div></div>
6	C	318	<div><div><div></div><div></div><div></div></div><div>56%28%16%</div></div>
7	E	215	<div><div><div></div><div></div><div></div></div><div>2%66%33%. </div></div>
8	F	155	<div><div><div></div><div></div><div></div></div><div>41%14%45%</div></div>
9	H	146	<div><div><div></div><div></div><div></div></div><div>%63%28%9%</div></div>
10	I	122	<div><div><div></div><div></div><div></div></div><div>66%30%. </div></div>
11	J	70	<div><div><div></div><div></div><div></div></div><div>%41%51%7%</div></div>
12	K	120	<div><div><div></div><div></div><div></div></div><div>72%23%5%</div></div>
13	L	70	<div><div><div></div><div></div><div></div></div><div>%49%13%39%</div></div>

2 Entry composition

There are 15 unique types of molecules in this entry. The entry contains 29055 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	10	Total	C	N	O	P	0	0	0
			221	98	45	68	10			

- 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
			521	250	80	165	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
			317	148	71	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
			10825	6830	1892	2043	60			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	B	1120	Total	C	N	O	S	0	0	0
			8839	5596	1546	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
			1734	1102	304	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	86	Total	C	N	O	S	0	0	0
			684	437	115	129	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 (CCD ID: ZN) (formula: Zn).

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

- Molecule 15 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 1: RNA

DC	DC	T3	T4	C5	T6	C7	T8	C9	T10	C11	T12	C13	G14	C15	T16	G17	A18	G19	C20	C21	T22	C23		A27	T28	DG
----	----	----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--	-----	-----	----

DT	C2	A3	G4		A7	G8	A9	G10	A11	G12	A13	G14	A15	A16	DG	DG
----	----	----	----	--	----	----	----	-----	-----	-----	-----	-----	-----	-----	----	----

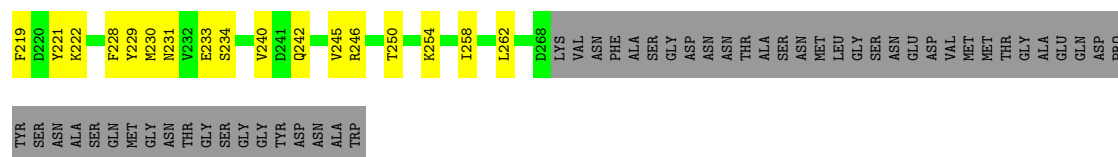
NET	VAL	GAL
Q4		
S7		
S8		
A9		
P10		
L11		
R12		
T13		
V14		
K15		
E16		
F19		
G20		
L21		
F22		
S23		
E26		
I30		
K34		
F37		
D42		
T46		
L50		
G51		
G52		
D55		
L58		
F61		
C67		
O68		
T69		
C70		
Q71		
E72		
E76		
H80		
F81		
G82		
H83		
L86		

F91	H92	V93	I96	I99	V102	V106	C107	M108	C109	C110	G111	K112	L113	L114	L115	L121	M122	A125	L126	S131	K132	I138	L141	V147	D151	V152	P153	SER	GLU	ASP	ASP	PR0	THR	GLN	L161	V162	S163	T170	Q171	P172	T173	L174	R175	K176	L179
-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------

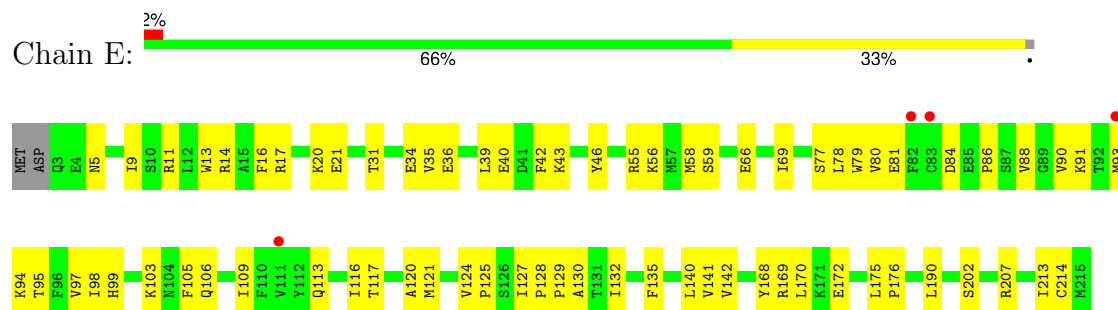
L181	L182	G183	S184	W185	K186	LYS	ASP	ARG	ALA	THR	GLY	ASP	ASP	GLU	PRO	GLU	L199	R200	V201	L202	L208	N209	L210	V216	F219	G223	F224	N225	F226	V227	F228	S229	R230	P231	F232	W233	M234	L235	P240	V241	P242	P243	P244	P245	V246	R247	P248	S249	ILE	SER	PHG	ASN
------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----

[illegible]

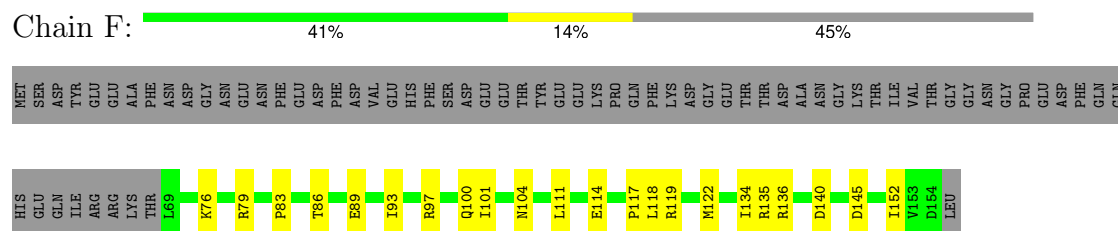




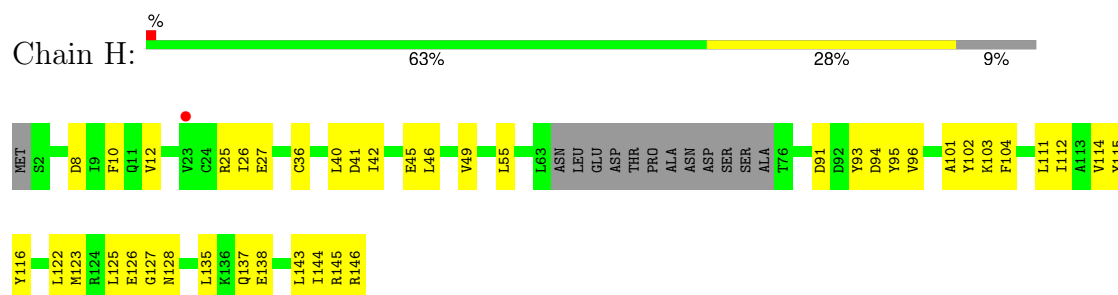
- Molecule 7: DNA-directed RNA polymerases I, II, and III subunit RPABC1



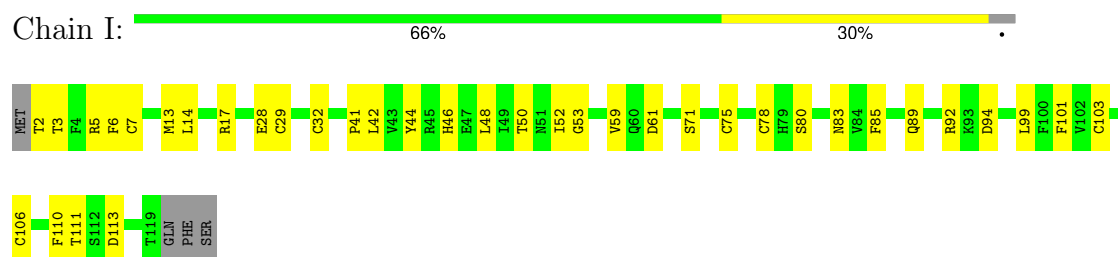
- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC2



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



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

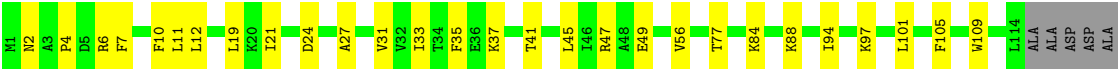


- Molecule 11: DNA-directed RNA polymerases I, II, and III subunit RPABC5

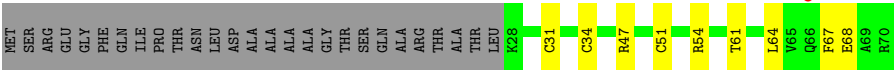




● Molecule 12: DNA-directed RNA polymerase II subunit RPB11



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



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	167.54Å 223.10Å 195.00Å 90.00° 100.38° 90.00°	Depositor
Resolution (Å)	49.22 – 3.60 49.22 – 3.60	Depositor EDS
% Data completeness (in resolution range)	97.6 (49.22-3.60) 97.5 (49.22-3.60)	Depositor EDS
R_{merge}	0.56	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.04 (at 3.57Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, R_{free}	0.248 , 0.281 0.249 , 0.281	Depositor DCC
R_{free} test set	2000 reflections (2.46%)	wwPDB-VP
Wilson B-factor (Å ²)	107.6	Xtriage
Anisotropy	0.476	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 138.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	29055	wwPDB-VP
Average B, all atoms (Å ²)	141.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.19% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 8OG, 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	0.17	0/248	0.43	0/384
2	T	0.22	0/551	0.50	0/843
3	N	0.22	0/359	0.45	0/553
4	A	0.15	0/11017	0.36	0/14905
5	B	0.14	0/9010	0.34	0/12160
6	C	0.15	0/2139	0.33	0/2899
7	E	0.14	0/1770	0.35	0/2383
8	F	0.15	0/696	0.37	0/943
9	H	0.17	0/1082	0.42	0/1466
10	I	0.14	0/970	0.38	0/1308
11	J	0.18	0/541	0.38	0/727
12	K	0.13	0/937	0.34	0/1265
13	L	0.14	0/339	0.36	0/450
All	All	0.15	0/29659	0.36	0/40286

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
4	A	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	A	55	ASP	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	221	0	110	2	0
2	T	521	0	297	25	0
3	N	317	0	166	11	0
4	A	10825	0	10863	347	0
5	B	8839	0	8795	265	0
6	C	2101	0	2057	81	0
7	E	1734	0	1755	52	0
8	F	684	0	692	18	0
9	H	1064	0	1029	42	0
10	I	952	0	898	29	0
11	J	532	0	544	34	0
12	K	919	0	929	27	0
13	L	337	0	353	14	0
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	29055	0	28488	833	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 14.

The worst 5 of 833 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)
7:E:168:TYR:HB3	7:E:170:LEU:HD23	1.20	1.15
4:A:956:LEU:HD11	4:A:1017:LEU:CD2	1.76	1.14
4:A:956:LEU:HD11	4:A:1017:LEU:HD22	1.29	1.11

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:221:TYR:CZ	9:H:46:LEU:HA	2.03	0.94
7:E:168:TYR:HB3	7:E:170:LEU:CD2	2.01	0.88

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	
4	A	1371/1733 (79%)	1321 (96%)	49 (4%)	1 (0%)	48	79
5	B	1100/1224 (90%)	1077 (98%)	23 (2%)	0	100	100
6	C	265/318 (83%)	259 (98%)	6 (2%)	0	100	100
7	E	211/215 (98%)	209 (99%)	2 (1%)	0	100	100
8	F	84/155 (54%)	83 (99%)	1 (1%)	0	100	100
9	H	129/146 (88%)	123 (95%)	6 (5%)	0	100	100
10	I	116/122 (95%)	109 (94%)	7 (6%)	0	100	100
11	J	63/70 (90%)	62 (98%)	1 (2%)	0	100	100
12	K	112/120 (93%)	110 (98%)	2 (2%)	0	100	100
13	L	41/70 (59%)	41 (100%)	0	0	100	100
All	All	3492/4173 (84%)	3394 (97%)	97 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	958	VAL

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	1193/1520 (78%)	1193 (100%)	0	100	100
5	B	954/1061 (90%)	952 (100%)	2 (0%)	92	96
6	C	235/274 (86%)	234 (100%)	1 (0%)	89	95
7	E	193/197 (98%)	193 (100%)	0	100	100
8	F	73/137 (53%)	73 (100%)	0	100	100
9	H	116/128 (91%)	116 (100%)	0	100	100
10	I	110/116 (95%)	109 (99%)	1 (1%)	75	87
11	J	60/65 (92%)	60 (100%)	0	100	100
12	K	99/102 (97%)	99 (100%)	0	100	100
13	L	37/57 (65%)	37 (100%)	0	100	100
All	All	3070/3657 (84%)	3066 (100%)	4 (0%)	92	97

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	B	1163	CYS
5	B	1166	CYS
6	C	95	CYS
10	I	7	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
5	B	494	HIS
5	B	763	GLN
7	E	174	GLN
5	B	657	HIS
5	B	835	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	R	9/10 (90%)	3 (33%)	0

All (3) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	R	2	U
1	R	9	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	8OG	T	19	1,2	22,25,26	4.11	18 (81%)	26,37,40	1.76	7 (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
2	8OG	T	19	1,2	-	5/7/21/22	0/3/3/3

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	T	19	8OG	C8-N7	7.33	1.51	1.38
2	T	19	8OG	C8-N9	6.17	1.51	1.40

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	T	19	8OG	C2-N3	6.11	1.48	1.33
2	T	19	8OG	C4-N3	5.83	1.47	1.34
2	T	19	8OG	C2-N2	4.89	1.45	1.34

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	T	19	8OG	C2-N3-C4	4.83	120.62	112.30
2	T	19	8OG	C2-N1-C6	-3.17	119.36	125.11
2	T	19	8OG	N9-C4-N3	3.14	130.05	126.13
2	T	19	8OG	C5-C6-N1	2.92	120.15	112.13
2	T	19	8OG	O6-C6-C5	-2.74	120.65	127.26

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	T	19	8OG	O4'-C4'-C5'-O5'
2	T	19	8OG	C3'-C4'-C5'-O5'
2	T	19	8OG	C4'-C5'-O5'-P
2	T	19	8OG	C2'-C1'-N9-C4
2	T	19	8OG	O4'-C1'-N9-C4

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	T	19	8OG	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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

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	R	10/10 (100%)	0.01	0 100 100	106, 130, 206, 240	0
2	T	25/29 (86%)	-0.07	0 100 100	141, 236, 282, 295	0
3	N	15/18 (83%)	0.02	0 100 100	199, 253, 307, 316	0
4	A	1385/1733 (79%)	-0.17	10 (0%) 84 67	73, 138, 224, 330	0
5	B	1120/1224 (91%)	-0.11	14 (1%) 74 53	54, 116, 194, 287	0
6	C	267/318 (83%)	-0.18	0 100 100	65, 120, 174, 212	0
7	E	213/215 (99%)	-0.16	4 (1%) 66 45	117, 186, 258, 329	0
8	F	86/155 (55%)	-0.36	0 100 100	82, 130, 203, 251	0
9	H	133/146 (91%)	-0.21	1 (0%) 82 64	112, 159, 217, 291	0
10	I	118/122 (96%)	-0.23	0 100 100	107, 146, 214, 286	0
11	J	65/70 (92%)	-0.05	1 (1%) 71 51	72, 108, 160, 219	0
12	K	114/120 (95%)	-0.34	0 100 100	68, 115, 156, 182	0
13	L	43/70 (61%)	0.04	1 (2%) 61 41	86, 180, 245, 267	0
All	All	3594/4230 (84%)	-0.16	31 (0%) 81 62	54, 132, 224, 330	0

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	B	775	LYS	4.3
5	B	819	ALA	3.6
5	B	779	GLY	3.5
4	A	776	ALA	3.0
4	A	1328	TYR	3.0

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(Å ²)	Q<0.9
2	8OG	T	19	23/24	0.90	0.10	142,155,171,184	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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(Å ²)	Q<0.9
14	ZN	A	1801	1/1	0.87	0.07	321,321,321,321	0
14	ZN	I	202	1/1	0.95	0.05	146,146,146,146	0
14	ZN	J	101	1/1	0.95	0.17	365,365,365,365	0
14	ZN	L	101	1/1	0.95	0.06	212,212,212,212	0
15	MG	A	1803	1/1	0.95	0.10	128,128,128,128	0
14	ZN	A	1802	1/1	0.96	0.05	217,217,217,217	0
14	ZN	C	401	1/1	0.96	0.06	117,117,117,117	0
14	ZN	B	1301	1/1	0.98	0.03	245,245,245,245	0
14	ZN	I	201	1/1	0.98	0.04	132,132,132,132	0

6.5 Other polymers [i](#)

There are no such residues in this entry.