



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 11, 2023 – 04:16 PM EDT

PDB ID : 7RIP
Title : RNA polymerase II elongation complex with hairpin polyamide Py-Im 1, scaffold 1 soaked with CTP
Authors : Oh, J.; Dervan, P.B.; Wang, D.
Deposited on : 2021-07-20
Resolution : 3.30 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35.1
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) : 2.35.1

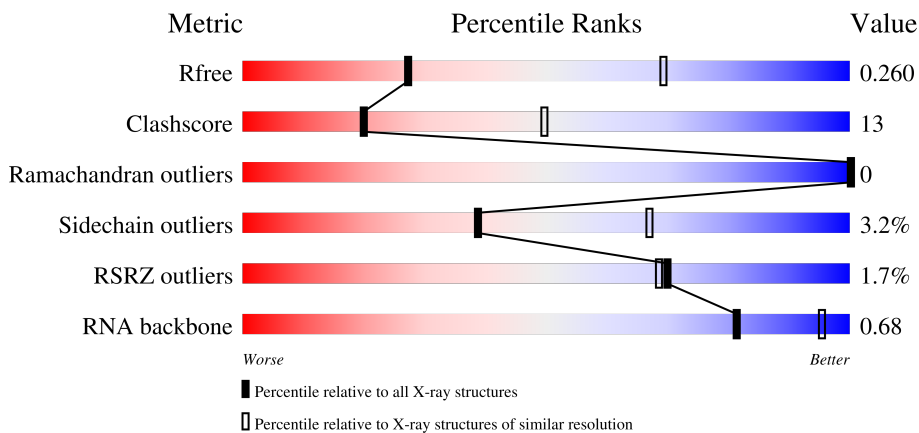
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)
RNA backbone	3102	1117 (3.70-2.90)

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	
2	T	30	
3	N	20	
4	A	1733	

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Mol	Chain	Length	Quality of chain
5	B	1224	<p>%</p> <p>64% 27% 8%</p>
6	C	318	<p>60% 23% 16%</p>
7	E	215	<p>6% 70% 29%</p>
8	F	155	<p>45% 10% 45%</p>
9	H	146	<p>3% 60% 29% 9%</p>
10	I	122	<p>76% 20%</p>
11	J	70	<p>56% 36% 7%</p>
12	K	120	<p>68% 26% 5%</p>
13	L	70	<p>4% 41% 19% 39%</p>

2 Entry composition [i](#)

There are 17 unique types of molecules in this entry. The entry contains 29193 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
			Total	C	N	O	P			
1	R	10	215	97	43	66	9	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	T	26	525	252	84	163	26	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	N	14	293	138	63	78	14	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	A	1384	10824	6829	1895	2040	60	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	B	1129	8899	5630	1561	1655	53	0	0	0

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
7	E	212	1731	1100	305	315	11	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
8	F	86	684	437	115	129	3	0	0	0

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

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

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

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

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

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

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

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

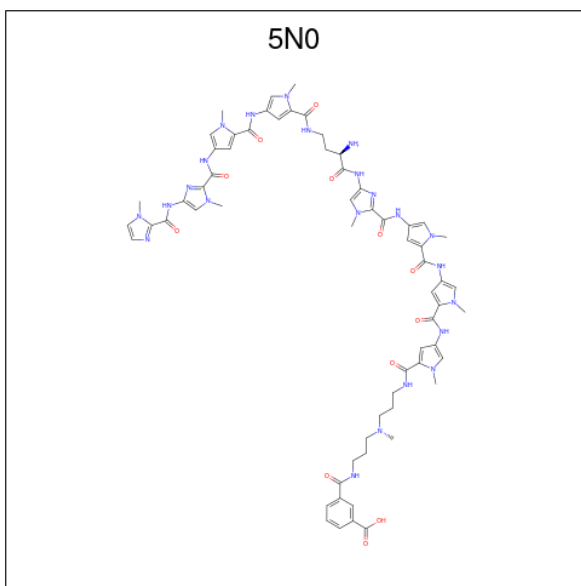
- Molecule 13 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

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

- Molecule 14 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
14	R	1	Total Mg 1 1	0	0

- Molecule 15 is 3-({3-[(3-[(4-({4-[(4-({(2R)-2-amino-4-[(1-methyl-4-{{1-methyl-4-{{1-methyl-4-[(1-methyl-1H-imidazole-2-carbonyl)amino]-1H-imidazole-2-carbonyl}amino)-1H-pyrrole-2-carbonyl]amino}-1H-pyrrole-2-carbonyl)amino]butanoyl}amino)-1-methyl-1H-imidazole-2-carbonyl]amino}-1-methyl-1H-pyrrole-2-carbonyl)amino]-1-methyl-1H-pyrrole-2-carbonyl]amino}propyl)(methylamino)propyl}carbamoyl)benzoic acid (three-letter code: 5N0) (formula: C₆₄H₇₅N₂₃O₁₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
15	T	1	Total C N O 99 64 23 12	0	0

- Molecule 16 is ZINC ION (three-letter code: ZN) (formula: Zn).

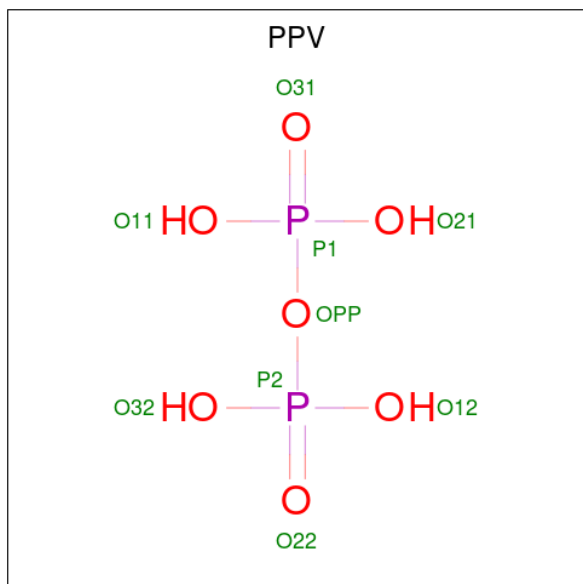
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
16	A	2	Total Zn 2 2	0	0
16	B	1	Total Zn 1 1	0	0
16	C	1	Total Zn 1 1	0	0
16	I	2	Total Zn 2 2	0	0
16	J	1	Total Zn 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	L	1	Total	Zn	0	0
			1	1		

- Molecule 17 is PYROPHOSPHATE (three-letter code: PPV) (formula: $H_4O_7P_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
17	B	1	Total	O	P	0	0
			9	7	2		

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.

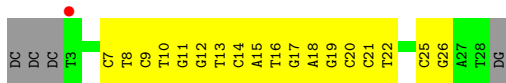
- Molecule 1: RNA

Chain R: 



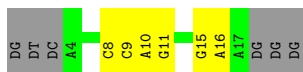
- Molecule 2: Template strand DNA

Chain T: 



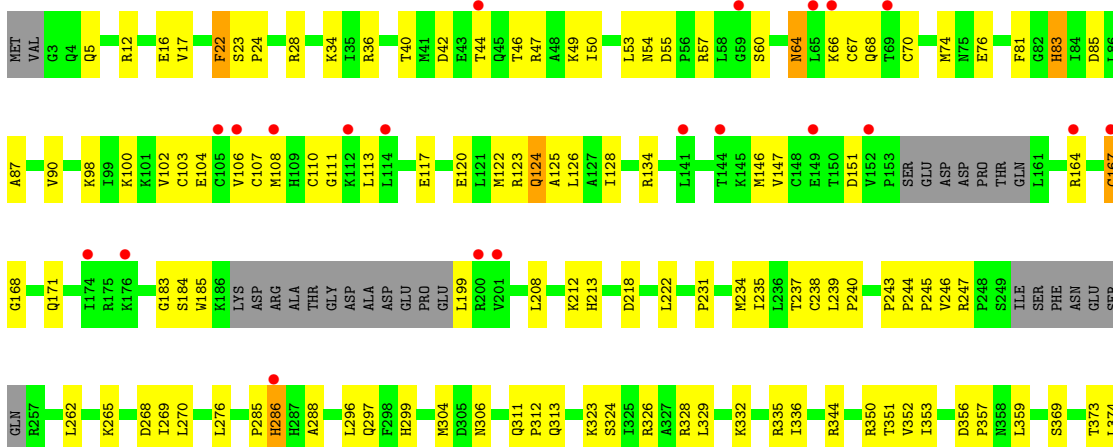
- Molecule 3: Non-template strand DNA

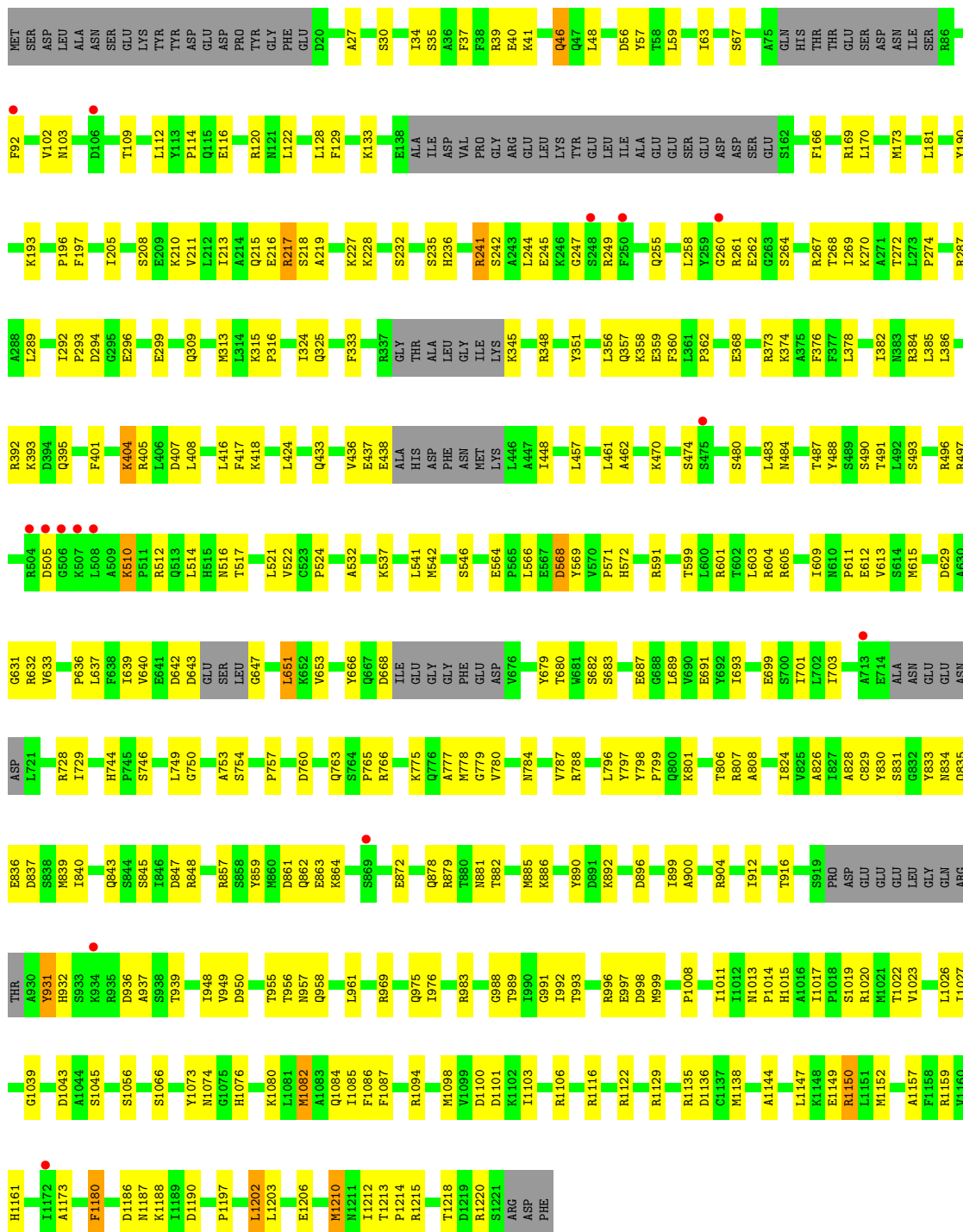
Chain N: 



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

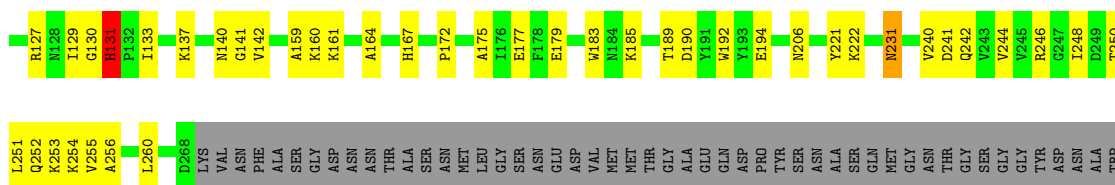
Chain A: 



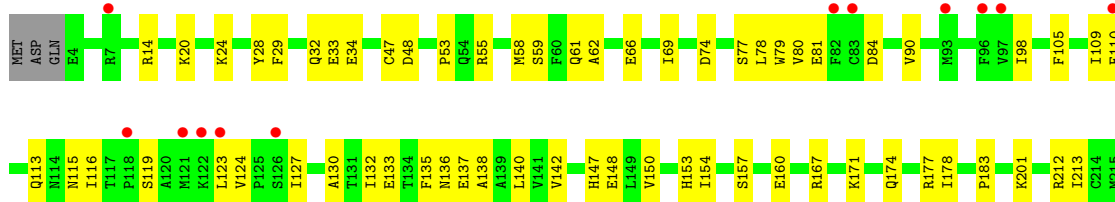


• Molecule 6: DNA-directed RNA polymerase II subunit RPB3

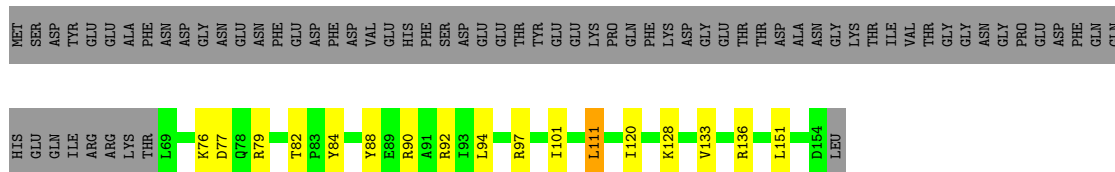




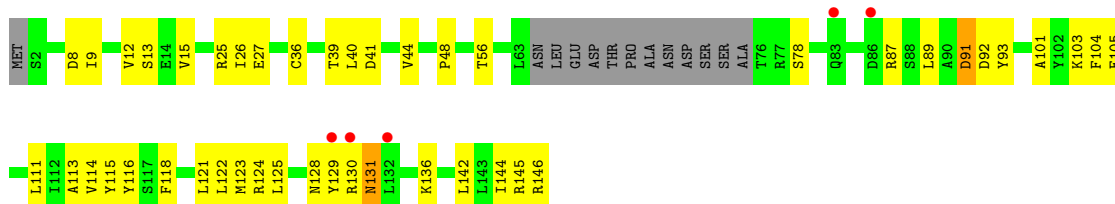
- Molecule 7: DNA-directed RNA polymerases I, II, and III subunit RPABC1



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



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

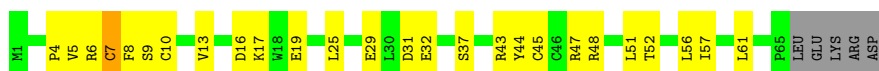


- Molecule 10: DNA-directed RNA polymerase II subunit RPB9



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





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

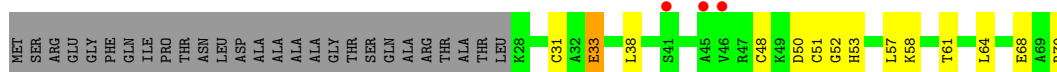
Chain K: 68% 26% 5%



ALA
PHE

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

Chain L: 41% 19% 4% 39%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	168.16Å 223.04Å 193.46Å 90.00° 100.67° 90.00°	Depositor
Resolution (Å)	49.23 – 3.30 49.22 – 3.30	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.23-3.30) 99.9 (49.22-3.30)	Depositor EDS
R_{merge}	0.38	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.18 (at 3.33Å)	Xtrriage
Refinement program	PHENIX 1.13	Depositor
R, R_{free}	0.219 , 0.261 0.219 , 0.260	Depositor DCC
R_{free} test set	1942 reflections (1.85%)	wwPDB-VP
Wilson B-factor (Å ²)	91.0	Xtrriage
Anisotropy	0.357	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 58.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	29193	wwPDB-VP
Average B, all atoms (Å ²)	111.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.70% 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: 5N0, MG, PPV, 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	0.34	0/241	0.82	0/375
2	T	0.70	0/584	1.09	0/898
3	N	0.54	0/331	0.81	0/509
4	A	0.31	0/11016	0.60	11/14902 (0.1%)
5	B	0.29	0/9071	0.50	0/12242
6	C	0.34	0/2139	0.66	4/2899 (0.1%)
7	E	0.29	0/1767	0.46	0/2378
8	F	0.27	0/696	0.46	0/943
9	H	0.28	0/1082	0.52	0/1466
10	I	0.30	0/970	0.50	0/1308
11	J	0.29	0/541	0.52	0/727
12	K	0.31	0/937	0.55	0/1265
13	L	0.31	0/339	0.55	0/450
All	All	0.32	0/29714	0.58	15/40362 (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
4	A	0	2
6	C	0	2
All	All	0	4

There are no bond length outliers.

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	64	ASN	CB-CG-OD1	29.19	179.97	121.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	64	ASN	CB-CG-ND2	-15.53	79.42	116.70
6	C	131	HIS	N-CA-CB	-14.04	85.34	110.60
4	A	1004	ASN	N-CA-CB	-13.60	86.12	110.60
6	C	131	HIS	CB-CG-CD2	-10.83	97.24	130.80

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	A	1004	ASN	Sidechain
4	A	124	GLN	Sidechain
6	C	130	GLY	Peptide
6	C	131	HIS	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	215	0	111	2	0
2	T	525	0	297	22	0
3	N	293	0	156	5	0
4	A	10824	0	10869	317	0
5	B	8899	0	8854	251	0
6	C	2101	0	2056	62	0
7	E	1731	0	1758	35	0
8	F	684	0	692	14	0
9	H	1064	0	1029	34	0
10	I	952	0	897	17	0
11	J	532	0	542	21	0
12	K	919	0	929	34	0
13	L	337	0	352	8	0
14	R	1	0	0	0	0
15	T	99	0	0	2	0
16	A	2	0	0	0	0
16	B	1	0	0	0	0
16	C	1	0	0	0	0
16	I	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	J	1	0	0	0	0
16	L	1	0	0	0	0
17	B	9	0	0	0	0
All	All	29193	0	28542	725	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 13.

The worst 5 of 725 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:1329:THR:HG22	4:A:1331:SER:H	1.09	1.14
4:A:446:ARG:NH1	4:A:447:GLN:O	1.88	1.06
4:A:1003:LYS:C	4:A:1004:ASN:HD22	1.58	1.05
5:B:218:SER:OG	5:B:241:ARG:NH2	1.94	1.00
5:B:345:LYS:HG2	5:B:348:ARG:HH12	1.27	1.00

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	1370/1733 (79%)	1290 (94%)	80 (6%)	0	100	100
5	B	1111/1224 (91%)	1057 (95%)	54 (5%)	0	100	100
6	C	265/318 (83%)	253 (96%)	12 (4%)	0	100	100
7	E	210/215 (98%)	198 (94%)	12 (6%)	0	100	100
8	F	84/155 (54%)	81 (96%)	3 (4%)	0	100	100
9	H	129/146 (88%)	119 (92%)	10 (8%)	0	100	100
10	I	116/122 (95%)	112 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	J	63/70 (90%)	62 (98%)	1 (2%)	0	100	100
12	K	112/120 (93%)	107 (96%)	5 (4%)	0	100	100
13	L	41/70 (59%)	41 (100%)	0	0	100	100
All	All	3501/4173 (84%)	3320 (95%)	181 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	
4	A	1193/1520 (78%)	1149 (96%)	44 (4%)	34	63
5	B	958/1061 (90%)	933 (97%)	25 (3%)	46	71
6	C	235/274 (86%)	231 (98%)	4 (2%)	60	78
7	E	193/197 (98%)	187 (97%)	6 (3%)	40	67
8	F	73/137 (53%)	72 (99%)	1 (1%)	67	82
9	H	116/128 (91%)	110 (95%)	6 (5%)	23	54
10	I	110/116 (95%)	108 (98%)	2 (2%)	59	78
11	J	60/65 (92%)	58 (97%)	2 (3%)	38	66
12	K	99/102 (97%)	96 (97%)	3 (3%)	41	68
13	L	37/57 (65%)	33 (89%)	4 (11%)	6	24
All	All	3074/3657 (84%)	2977 (97%)	97 (3%)	39	67

5 of 97 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	B	728	ARG
6	C	137	LYS
5	B	931	TYR
5	B	1180	PHE
7	E	48	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
5	B	103	ASN
5	B	835	GLN
12	K	2	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	R	9/10 (90%)	1 (11%)	0

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	R	10	C

There are no RNA pucker outliers to report.

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 9 are monoatomic - leaving 2 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
17	PPV	B	1301	-	6,8,8	0.75	0	13,13,13	1.09	0
15	5N0	T	101	-	93,107,107	2.34	32 (34%)	94,153,153	1.37	8 (8%)

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
17	PPV	B	1301	-	-	0/6/6/6	-
15	5N0	T	101	-	-	14/51/92/92	0/9/9/9

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	T	101	5N0	C49-N23	6.42	1.47	1.33
15	T	101	5N0	C22-N10	6.22	1.47	1.33
15	T	101	5N0	C56-N25	6.16	1.47	1.33
15	T	101	5N0	C26-N14	5.33	1.47	1.35
15	T	101	5N0	C5-N3	4.67	1.48	1.35

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	T	101	5N0	C6-C10-N6	5.84	120.03	113.69
15	T	101	5N0	C4-C5-N3	4.55	118.63	113.69
15	T	101	5N0	C24-C25-C26	-3.62	103.02	110.85
15	T	101	5N0	C30-C31-N17	2.94	116.88	113.69
15	T	101	5N0	C19-N9-C17	2.68	111.50	108.65

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

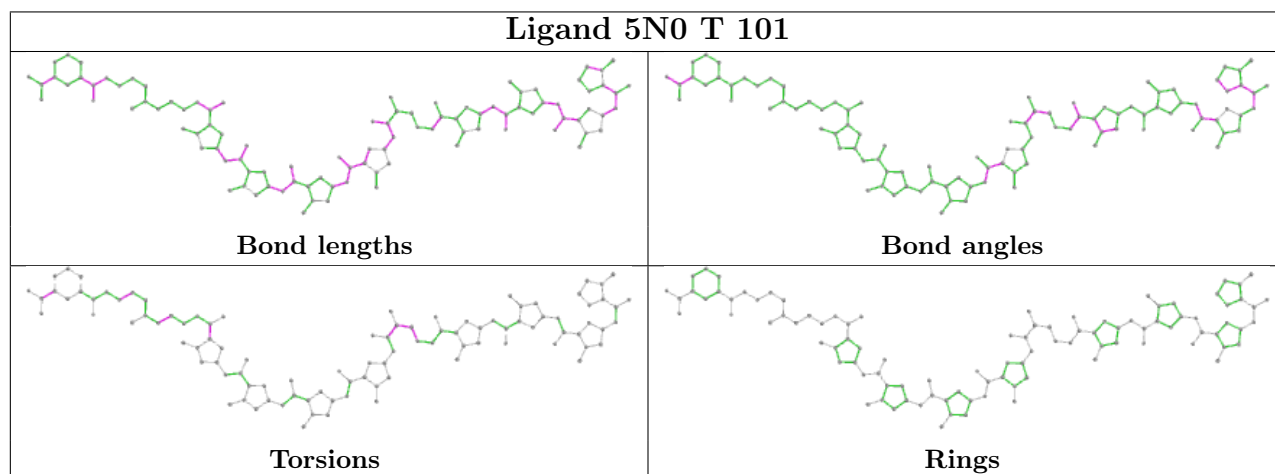
Mol	Chain	Res	Type	Atoms
15	T	101	5N0	C23-C24-C25-C26
15	T	101	5N0	C24-C25-C26-N14
15	T	101	5N0	C47-C44-C49-O9
15	T	101	5N0	C58-C59-C63-O12
15	T	101	5N0	C60-C59-C63-O11

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	T	101	5N0	2	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](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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%)	-0.41	0 100 100	87, 103, 157, 163	0
2	T	26/30 (86%)	-0.10	1 (3%) 40 37	89, 211, 242, 259	0
3	N	14/20 (70%)	0.13	0 100 100	213, 220, 241, 246	0
4	A	1384/1733 (79%)	-0.10	25 (1%) 68 67	51, 105, 187, 235	0
5	B	1129/1224 (92%)	-0.07	15 (1%) 77 77	50, 88, 153, 189	0
6	C	267/318 (83%)	-0.31	0 100 100	59, 88, 128, 156	0
7	E	212/215 (98%)	0.04	12 (5%) 23 23	81, 149, 216, 230	0
8	F	86/155 (55%)	-0.29	0 100 100	74, 107, 153, 189	0
9	H	133/146 (91%)	0.19	5 (3%) 40 37	97, 138, 173, 195	0
10	I	118/122 (96%)	-0.29	0 100 100	71, 109, 146, 171	0
11	J	65/70 (92%)	-0.36	0 100 100	55, 81, 123, 141	0
12	K	114/120 (95%)	-0.27	0 100 100	67, 96, 128, 146	0
13	L	43/70 (61%)	0.20	3 (6%) 16 16	67, 143, 191, 209	0
All	All	3601/4233 (85%)	-0.10	61 (1%) 70 68	50, 101, 182, 259	0

The worst 5 of 61 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	B	106	ASP	4.9
7	E	93	MET	4.9
5	B	507	LYS	4.4
4	A	1387	HIS	4.3
5	B	869	SER	4.2

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

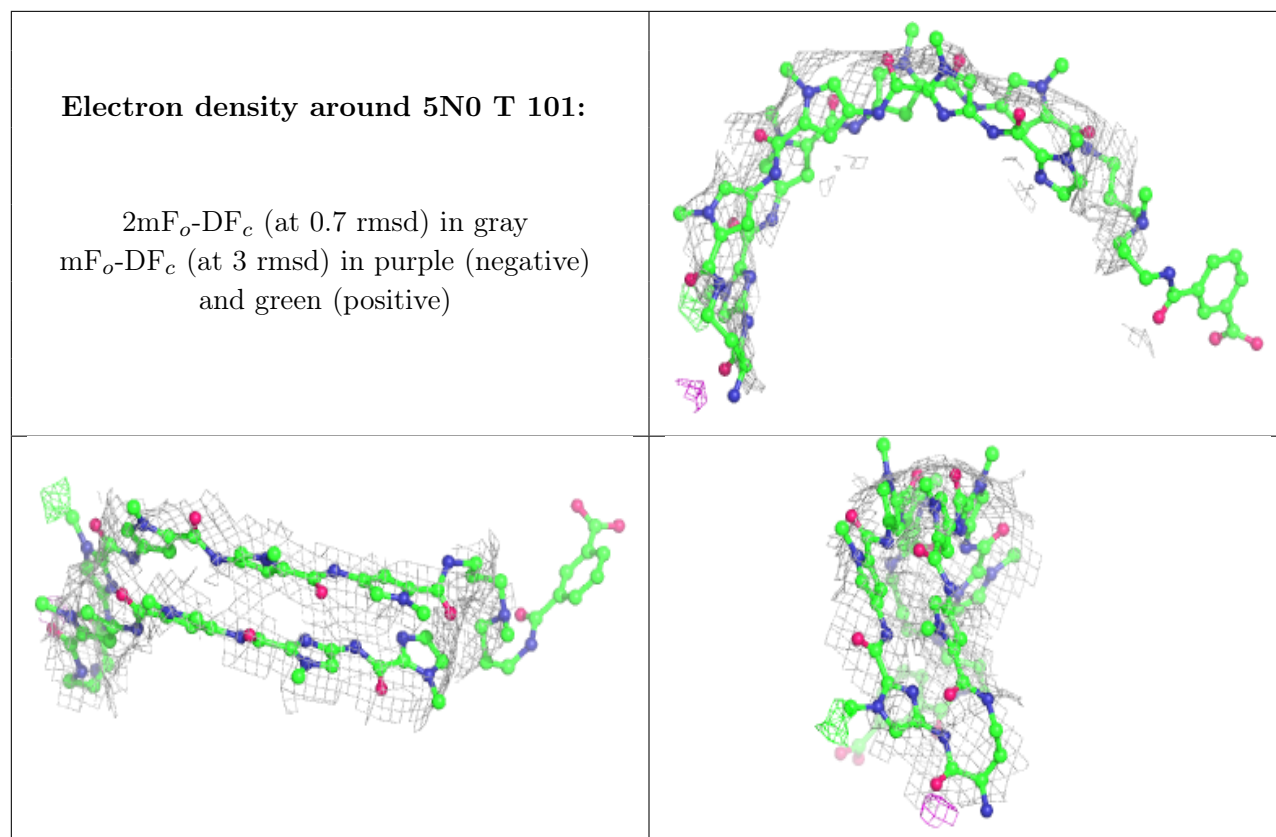
There are no monosaccharides in this entry.

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(Å ²)	Q<0.9
17	PPV	B	1301	9/9	0.73	0.33	175,175,175,175	0
15	5N0	T	101	99/99	0.80	0.36	184,225,251,258	0
16	ZN	A	1801	1/1	0.86	0.13	246,246,246,246	0
14	MG	R	2001	1/1	0.92	0.13	106,106,106,106	0
16	ZN	B	1302	1/1	0.94	0.09	184,184,184,184	0
16	ZN	L	101	1/1	0.96	0.04	164,164,164,164	0
16	ZN	C	401	1/1	0.97	0.13	82,82,82,82	0
16	ZN	J	101	1/1	0.97	0.21	77,77,77,77	0
16	ZN	I	201	1/1	0.98	0.14	97,97,97,97	0
16	ZN	I	202	1/1	0.99	0.15	93,93,93,93	0
16	ZN	A	1802	1/1	0.99	0.11	153,153,153,153	0

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 [i](#)

There are no such residues in this entry.