



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 7, 2026 – 01:49 AM UTC

PDB ID : 4BY1 / pdb_00004by1
Title : elongating RNA Polymerase II-Bye1 TLD complex soaked with AMPCPP
Authors : Kinkelin, K.; Wozniak, G.G.; Rothbart, S.B.; Lidschreiber, M.; Strahl, B.D.; Cramer, P.
Deposited on : 2013-07-17
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 Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

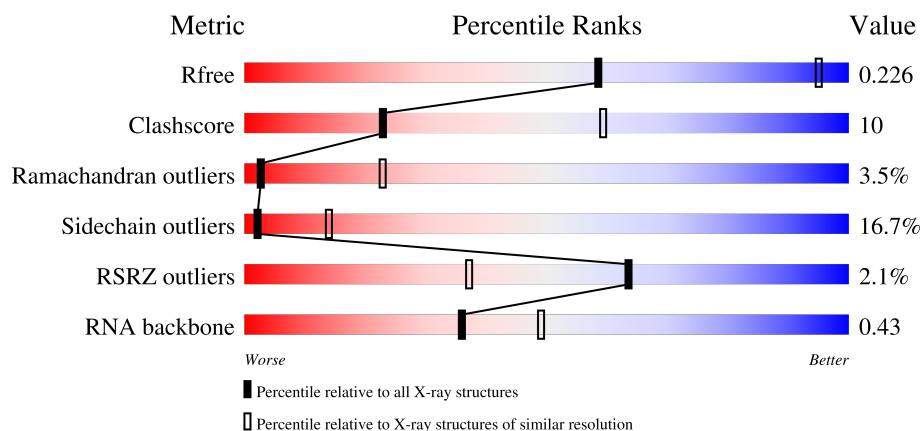
1 Overall quality at a glance

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.



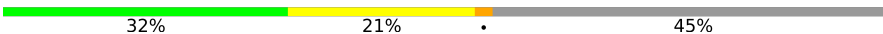
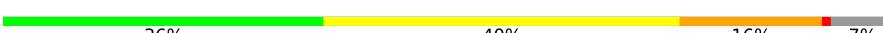
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1747 (3.70-3.50)
Clashscore	190562	1827 (3.70-3.50)
Ramachandran outliers	187476	1773 (3.70-3.50)
Sidechain outliers	187428	1772 (3.70-3.50)
RSRZ outliers	180081	1745 (3.70-3.50)
RNA backbone	3983	1014 (4.14-3.06)

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	A	1733	49% 26% 6% 18%
2	B	1224	57% 27% 6% 10%
3	C	318	52% 27% 16%
4	D	221	53% 24% 20%

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Mol	Chain	Length	Quality of chain
5	E	215	
6	F	155	
7	G	171	
8	H	146	
9	I	122	
10	J	70	
11	K	120	
12	L	70	
13	N	14	
14	P	11	
15	T	26	
16	X	146	

2 Entry composition

There are 19 unique types of molecules in this entry. The entry contains 33026 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 protein called DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1427	Total	C	N	O	S	0	0	0
			11230	7072	1960	2136	62			

- Molecule 2 is a protein called DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	1106	Total	C	N	O	S	0	0	0
			8793	5569	1538	1631	55			

- Molecule 3 is a protein called DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB3.

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

- Molecule 4 is a protein called DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	177	Total	C	N	O	S	0	0	0
			1356	840	241	273	2			

- Molecule 5 is a protein called DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 1.

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

- Molecule 6 is a protein called DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	85	Total	C	N	O	S	0	0	0
			688	439	116	130	3			

- Molecule 7 is a protein called DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	171	Total	C	N	O	S	0	0	0
			1340	861	222	249	8			

- Molecule 8 is a protein called DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 3.

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 SUBUNIT RPB9.

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 SUBUNIT RPABC 5.

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 SUBUNIT RPB11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	115	Total	C	N	O	S	0	0	1
			920	590	157	171	2			

- Molecule 12 is a protein called DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 4.

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 a DNA chain called 5'-D(*AP*AP*AP*GP*TP*AP*CP*TP*TP*GP*AP*G

P*CP*TP)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	N	11	Total	C	N	O	P	0	0	0
			229	109	44	65	11			

- Molecule 14 is a RNA chain called 5'-R(*UP*UP*CP*GP*AP*CP*CP*AP*GP*GP*AP)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	P	10	Total	C	N	O	P	0	0	0
			215	96	41	68	10			

- Molecule 15 is a DNA chain called 5'-D(*AP*GP*CP*TP*CP*AP*AP*GP*TP*AP*CP*T
P*TP*AP *TP*TP*CP*CP*BRUP*GP*GP*TP*CP*AP*AP*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	T	24	Total	Br	C	N	O	P	0	0
			481	1	230	75	151	24		

- Molecule 16 is a protein called TRANSCRIPTION FACTOR BYE1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	X	116	Total	C	N	O	S	0	0	0
			953	611	158	181	3			

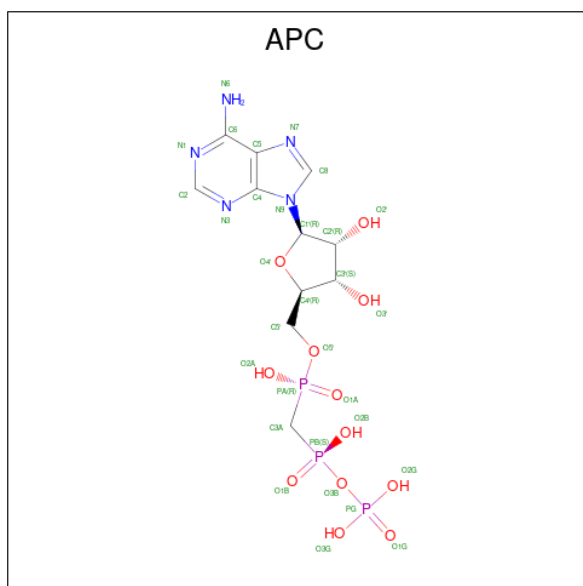
- Molecule 17 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 18 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 19 is DIPHOSPHOMETHYLPHOSPHONIC ACID ADENOSYL ESTER (CCD ID: APC) (formula: $C_{11}H_{18}N_5O_{12}P_3$).

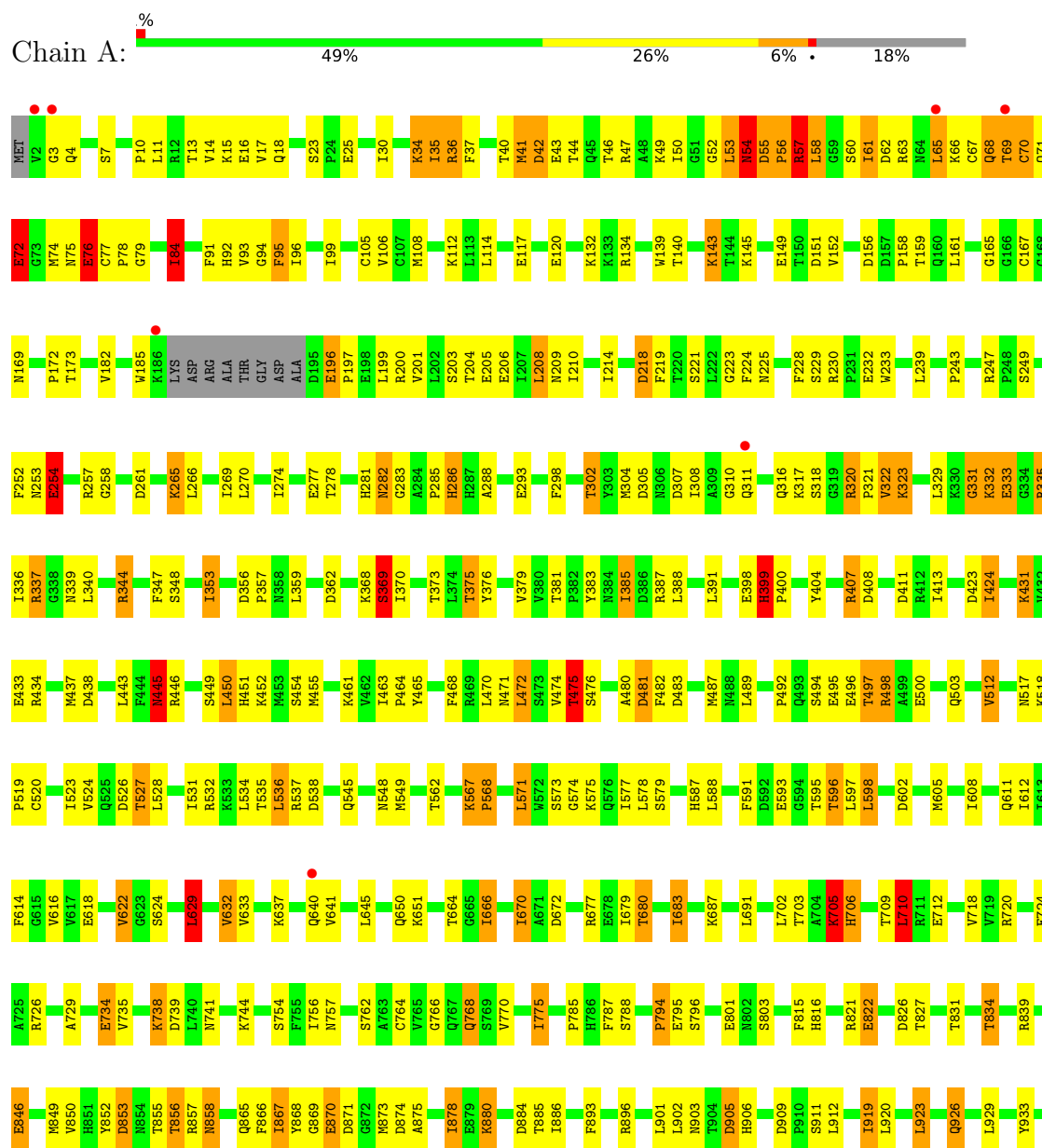


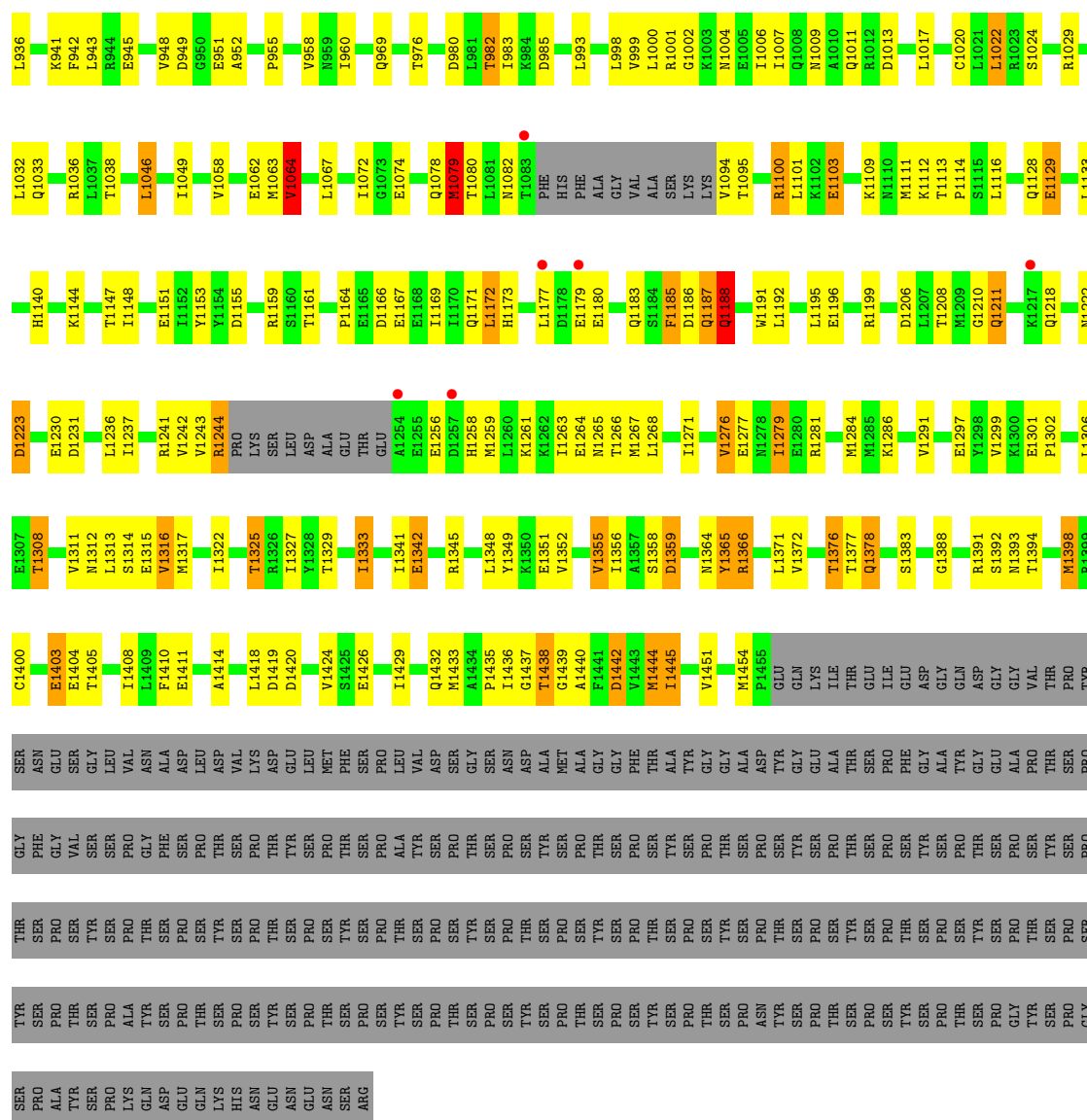
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
19	P	1	Total	C	N	O	P	0	0
			31	11	5	12	3		

3 Residue-property plots

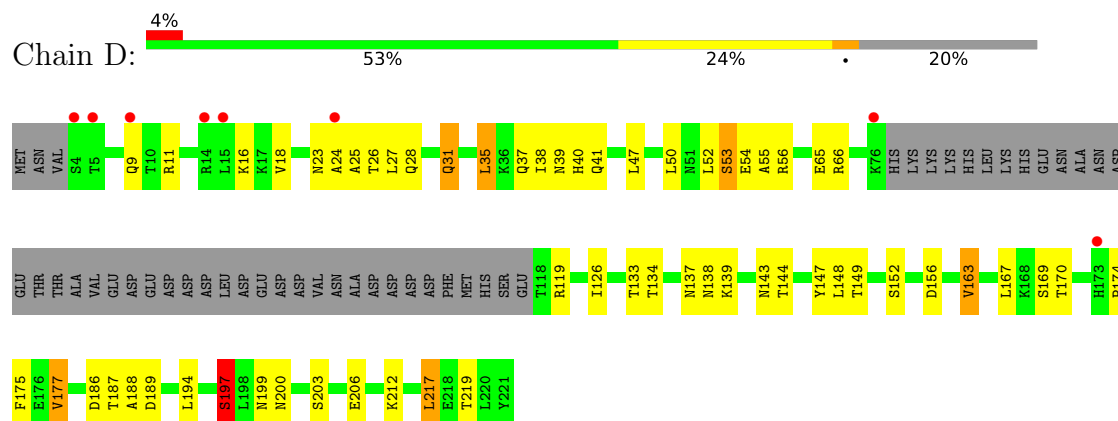
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB1

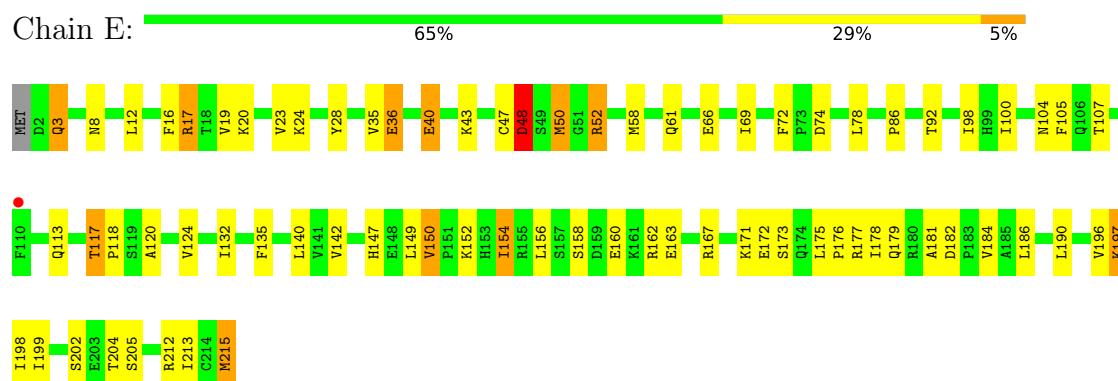




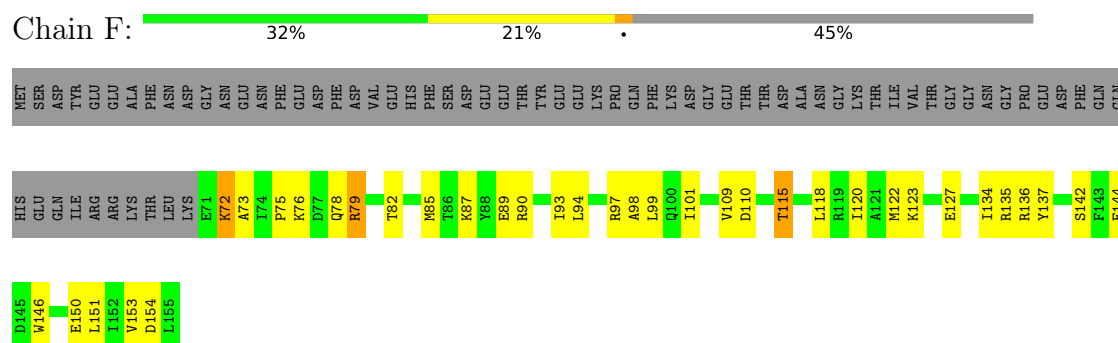
• Molecule 4: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB4



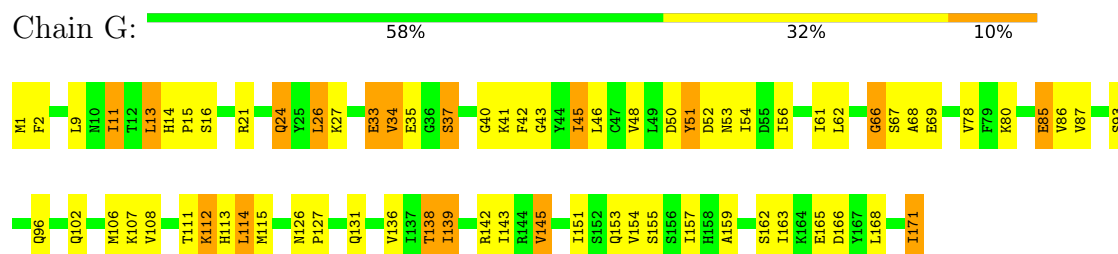
• Molecule 5: DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 1



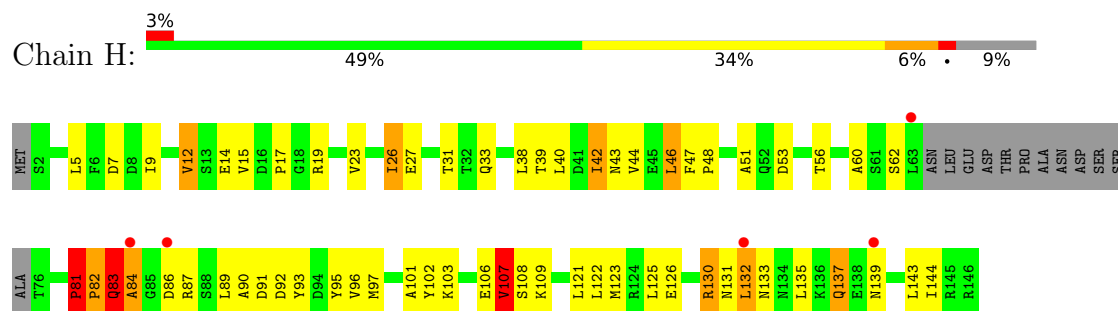
• Molecule 6: DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 2



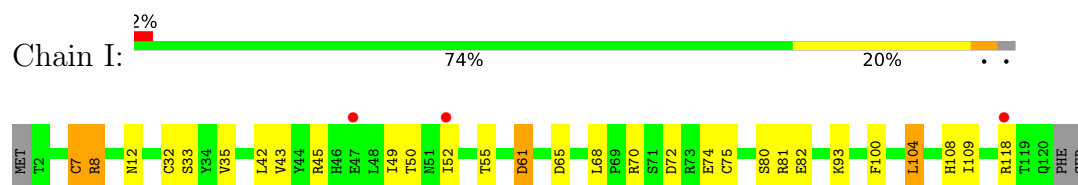
• Molecule 7: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB7



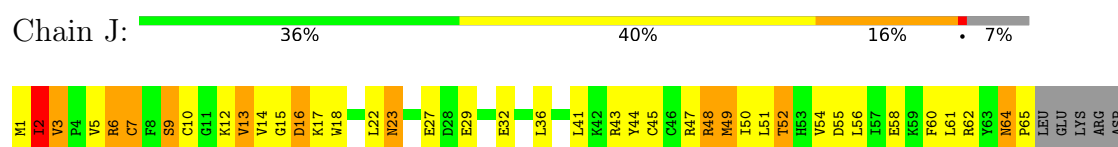
• Molecule 8: DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 3



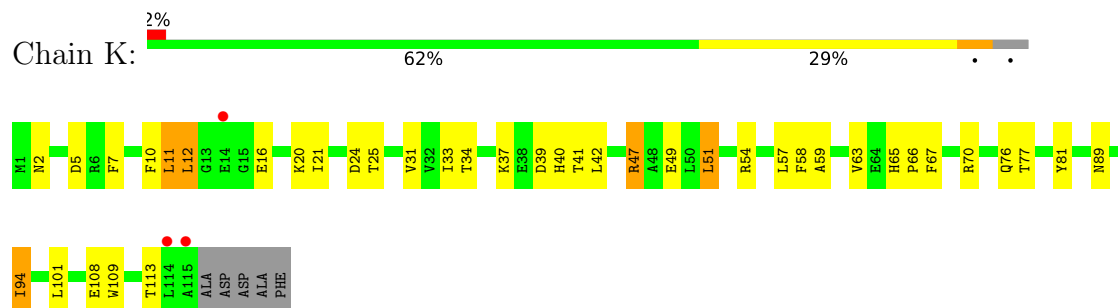
• Molecule 9: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB9



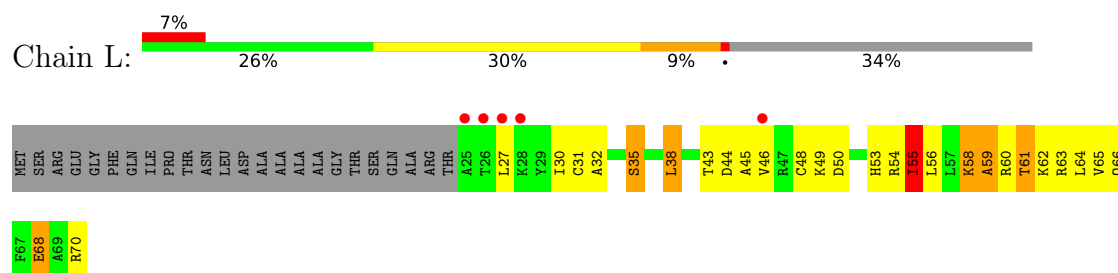
• Molecule 10: DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 5



• Molecule 11: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB11



• Molecule 12: DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 4



• Molecule 13: 5'-D(*AP*AP*AP*GP*TP*AP*CP*TP*TP*GP*AP*GP*CP*TP)-3'

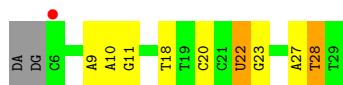




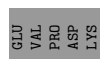
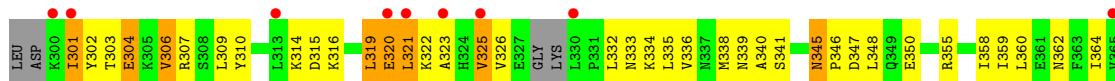
- Molecule 14: 5'-R(*UP*UP*CP*GP*AP*CP*CP*AP*GP*GP*AP)-3'



- Molecule 15: 5'-D(*AP*GP*CP*TP*CP*AP*AP*GP*TP*AP*CP*TP*TP*AP *TP*TP*CP*CP*BRUP*GP*GP*TP*CP*AP*AP*T)-3'



- Molecule 16: TRANSCRIPTION FACTOR BYE1



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	222.24Å 391.58Å 281.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.95 – 3.60 48.95 – 3.60	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.95-3.60) 99.9 (48.95-3.60)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.04 (at 3.57Å)	Xtriage
Refinement program	BUSTER 2.11.5	Depositor
R, R_{free}	0.175 , 0.206 0.195 , 0.226	Depositor DCC
R_{free} test set	2784 reflections (1.97%)	wwPDB-VP
Wilson B-factor (Å ²)	106.1	Xtriage
Anisotropy	0.211	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 141.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.019 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.027 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	33026	wwPDB-VP
Average B, all atoms (Å ²)	125.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.80% 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: MG, BRU, APC, 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	A	0.91	11/11431 (0.1%)	1.53	122/15462 (0.8%)
2	B	0.88	3/8963 (0.0%)	1.44	88/12085 (0.7%)
3	C	0.85	0/2133	1.39	16/2891 (0.6%)
4	D	0.90	0/1365	1.62	20/1837 (1.1%)
5	E	0.85	0/1788	1.44	12/2406 (0.5%)
6	F	0.94	0/700	1.43	5/945 (0.5%)
7	G	0.88	0/1368	1.40	11/1844 (0.6%)
8	H	0.83	0/1086	1.39	15/1470 (1.0%)
9	I	0.83	0/989	1.31	4/1331 (0.3%)
10	J	0.89	1/541 (0.2%)	1.53	5/727 (0.7%)
11	K	0.75	0/938	1.36	7/1267 (0.6%)
12	L	1.07	0/365	1.67	6/485 (1.2%)
13	N	0.46	0/257	0.66	0/395
14	P	1.02	2/240 (0.8%)	0.85	0/372
15	T	0.58	0/512	0.68	0/783
16	X	0.96	1/963 (0.1%)	1.61	17/1287 (1.3%)
All	All	0.88	18/33639 (0.1%)	1.46	328/45587 (0.7%)

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
14	P	0	1
15	T	0	3
All	All	0	4

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1172	ILE	CG1-CD1	6.45	1.76	1.51
16	X	254	VAL	CA-C	6.20	1.59	1.52
1	A	84	ILE	CG1-CD1	6.14	1.75	1.51
2	B	467	GLU	CA-C	6.01	1.60	1.52
1	A	56	PRO	C-N	5.92	1.42	1.33

The worst 5 of 328 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	26	THR	N-CA-C	-12.57	96.66	112.88
2	B	296	GLU	N-CA-C	-11.08	99.28	113.12
1	A	223	GLY	CA-C-N	9.88	135.35	120.82
1	A	223	GLY	C-N-CA	9.88	135.35	120.82
2	B	1016	ALA	CA-C-N	9.16	129.23	120.43

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
14	P	3	C	Sidechain
15	T	18	DT	Sidechain
15	T	23	DG	Sidechain
15	T	28	DT	Sidechain

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	A	11230	0	11280	298	0
2	B	8793	0	8824	178	0
3	C	2095	0	2051	50	0
4	D	1356	0	1319	19	0
5	E	1752	0	1776	42	0
6	F	688	0	707	21	0
7	G	1340	0	1357	37	0
8	H	1068	0	1040	39	0
9	I	971	0	927	8	0
10	J	532	0	542	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	K	920	0	929	24	0
12	L	363	0	386	9	0
13	N	229	0	125	3	0
14	P	215	0	109	5	0
15	T	481	0	264	7	0
16	X	953	0	969	24	0
17	A	2	0	0	0	0
17	B	1	0	0	0	0
17	C	1	0	0	0	0
17	I	2	0	0	0	0
17	J	1	0	0	0	0
17	L	1	0	0	0	0
18	A	1	0	0	0	0
19	P	31	0	14	0	0
All	All	33026	0	32619	685	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 10.

The worst 5 of 685 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)
2:B:1172:ILE:CD1	2:B:1172:ILE:CG1	1.76	1.58
1:A:84:ILE:CG1	1:A:84:ILE:CD1	1.75	1.56
1:A:853:ASP:OD1	1:A:855:THR:HG22	1.55	1.04
1:A:1187:GLN:HA	1:A:1188:GLN:HB2	1.42	0.98
1:A:14:VAL:H	1:A:1432:GLN:HE22	1.17	0.93

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	
1	A	1419/1733 (82%)	1223 (86%)	142 (10%)	54 (4%)	2	21
2	B	1086/1224 (89%)	949 (87%)	99 (9%)	38 (4%)	3	23
3	C	264/318 (83%)	229 (87%)	31 (12%)	4 (2%)	8	37
4	D	173/221 (78%)	155 (90%)	11 (6%)	7 (4%)	2	20
5	E	212/215 (99%)	199 (94%)	11 (5%)	2 (1%)	14	46
6	F	83/155 (54%)	75 (90%)	7 (8%)	1 (1%)	10	41
7	G	169/171 (99%)	153 (90%)	14 (8%)	2 (1%)	10	41
8	H	129/146 (88%)	102 (79%)	18 (14%)	9 (7%)	1	10
9	I	117/122 (96%)	93 (80%)	23 (20%)	1 (1%)	14	46
10	J	63/70 (90%)	51 (81%)	6 (10%)	6 (10%)	0	6
11	K	113/120 (94%)	106 (94%)	6 (5%)	1 (1%)	14	46
12	L	44/70 (63%)	33 (75%)	3 (7%)	8 (18%)	0	1
16	X	106/146 (73%)	90 (85%)	9 (8%)	7 (7%)	1	12
All	All	3978/4711 (84%)	3458 (87%)	380 (10%)	140 (4%)	3	23

5 of 140 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4	GLN
1	A	35	ILE
1	A	57	ARG
1	A	58	LEU
1	A	76	GLU

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1249/1520 (82%)	1015 (81%)	234 (19%)	1	10
2	B	960/1061 (90%)	807 (84%)	153 (16%)	2	15
3	C	234/274 (85%)	201 (86%)	33 (14%)	3	19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	D	140/200 (70%)	121 (86%)	19 (14%)	3	20
5	E	196/197 (100%)	168 (86%)	28 (14%)	3	19
6	F	75/137 (55%)	67 (89%)	8 (11%)	6	28
7	G	152/152 (100%)	128 (84%)	24 (16%)	2	15
8	H	117/128 (91%)	99 (85%)	18 (15%)	2	16
9	I	113/116 (97%)	97 (86%)	16 (14%)	3	19
10	J	60/65 (92%)	46 (77%)	14 (23%)	1	5
11	K	99/102 (97%)	87 (88%)	12 (12%)	5	23
12	L	40/57 (70%)	27 (68%)	13 (32%)	0	2
16	X	107/136 (79%)	87 (81%)	20 (19%)	1	10
All	All	3542/4145 (86%)	2950 (83%)	592 (17%)	2	14

5 of 592 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	E	197	LYS
16	X	243	LYS
7	G	13	LEU
5	E	190	LEU
9	I	33	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 116 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	573	GLN
11	K	65	HIS
2	B	1176	ASN
10	J	26	GLN
7	G	96	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
14	P	10/11 (90%)	4 (40%)	1 (10%)

All (4) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
14	P	3	C
14	P	4	G
14	P	5	A
14	P	9	G

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
14	P	2	U

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	$\# Z > 2$
15	BRU	T	22	14,15	18,21,22	1.57	4 (22%)	25,30,33	2.46	10 (40%)

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
15	BRU	T	22	14,15	-	0/7/21/22	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	T	22	BRU	C4-N3	-3.31	1.32	1.38
15	T	22	BRU	C6-N1	-3.23	1.32	1.38
15	T	22	BRU	C2-N3	-2.84	1.33	1.38
15	T	22	BRU	C2-N1	2.70	1.42	1.38

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	T	22	BRU	C5-C4-N3	4.56	118.59	113.34
15	T	22	BRU	C4-N3-C2	-4.54	121.39	127.34
15	T	22	BRU	O4-C4-C5	-4.39	120.20	125.80
15	T	22	BRU	BR-C5-C4	4.38	123.06	118.02
15	T	22	BRU	N3-C2-N1	4.27	120.45	114.89

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	T	22	BRU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 9 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	$\# Z > 2$
19	APC	P	12	18	29,33,33	1.90	8 (27%)	44,52,52	2.06	9 (20%)

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
19	APC	P	12	18	-	6/19/38/38	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	P	12	APC	C5-C4	4.90	1.47	1.39
19	P	12	APC	PA-O1A	4.46	1.62	1.51
19	P	12	APC	C5-C6	3.42	1.50	1.41
19	P	12	APC	PB-O3B	3.25	1.62	1.58
19	P	12	APC	PA-O2A	-3.16	1.48	1.56

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	P	12	APC	C5-C4-N3	-6.91	117.20	126.72
19	P	12	APC	C4-C5-N7	-4.93	104.95	110.58
19	P	12	APC	N3-C4-N9	4.61	135.00	127.17
19	P	12	APC	C2-N3-C4	4.37	122.50	111.83
19	P	12	APC	N3-C2-N1	-3.54	123.23	128.58

There are no chirality outliers.

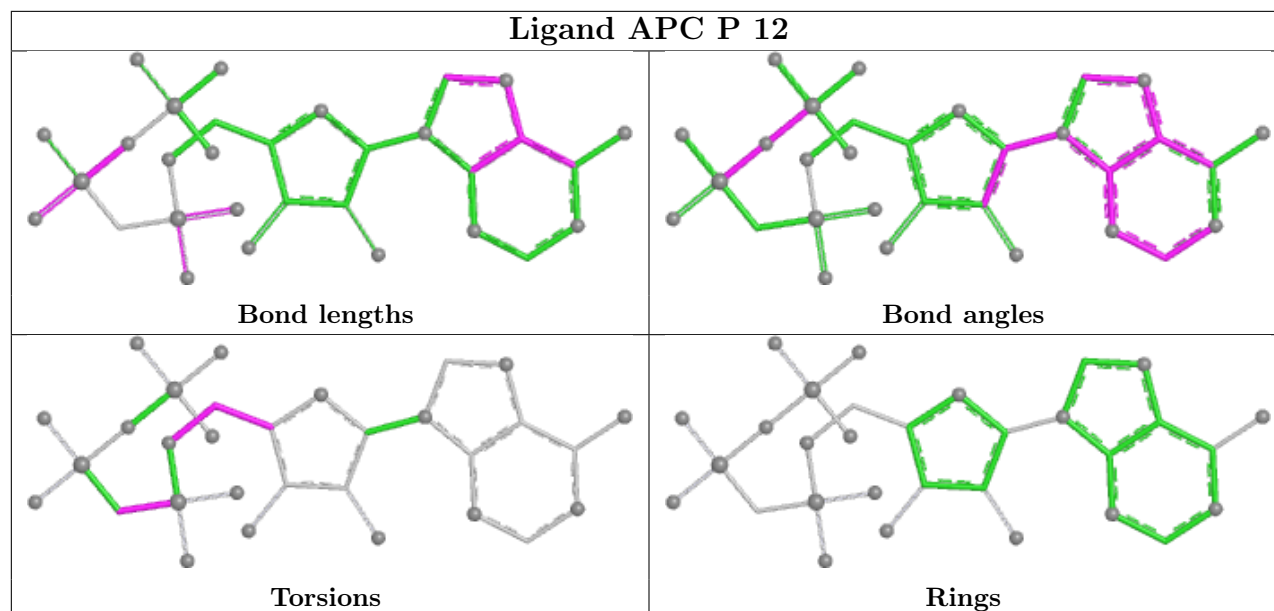
5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
19	P	12	APC	PB-C3A-PA-O1A
19	P	12	APC	PB-C3A-PA-O2A
19	P	12	APC	PB-C3A-PA-O5'
19	P	12	APC	O4'-C4'-C5'-O5'
19	P	12	APC	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

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	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	934:LYS	C	935:ARG	N	3.57

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	1427/1733 (82%)	-0.25	13 (0%) 81 56	58, 108, 175, 232	0
2	B	1106/1224 (90%)	-0.09	29 (2%) 57 33	65, 120, 181, 216	0
3	C	266/318 (83%)	-0.34	0 100 100	81, 109, 151, 180	0
4	D	177/221 (80%)	-0.04	8 (4%) 38 21	85, 123, 173, 199	0
5	E	214/215 (99%)	-0.25	1 (0%) 87 66	83, 139, 189, 210	0
6	F	85/155 (54%)	-0.47	0 100 100	68, 91, 124, 144	0
7	G	171/171 (100%)	-0.23	0 100 100	79, 108, 151, 169	0
8	H	133/146 (91%)	0.20	5 (3%) 44 25	118, 153, 189, 226	0
9	I	119/122 (97%)	0.10	3 (2%) 58 34	117, 159, 198, 220	0
10	J	65/70 (92%)	-0.33	0 100 100	88, 105, 148, 160	0
11	K	115/120 (95%)	-0.30	3 (2%) 57 33	77, 106, 155, 173	0
12	L	46/70 (65%)	0.69	5 (10%) 10 9	105, 175, 195, 205	0
13	N	11/14 (78%)	0.93	0 100 100	176, 194, 264, 267	0
14	P	10/11 (90%)	0.24	2 (20%) 3 3	85, 113, 169, 174	0
15	T	23/26 (88%)	0.37	1 (4%) 40 22	83, 148, 246, 258	0
16	X	116/146 (79%)	0.88	14 (12%) 8 7	163, 195, 212, 220	0
All	All	4084/4762 (85%)	-0.14	84 (2%) 63 37	58, 118, 189, 267	0

The worst 5 of 84 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	882	THR	8.4
2	B	335	GLY	5.2
11	K	115	ALA	4.8
1	A	1177	LEU	4.6
16	X	291	LEU	4.6

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(Å ²)	Q<0.9
15	BRU	T	22	20/21	0.97	0.07	87,97,123,144	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

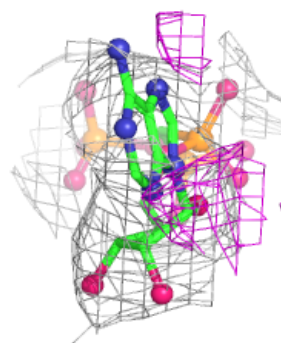
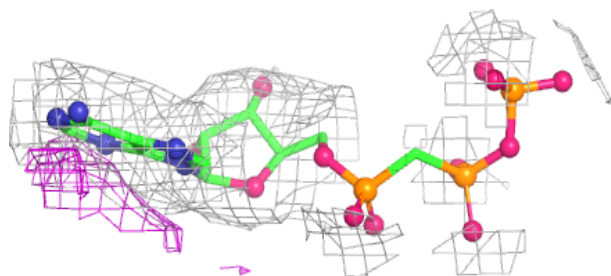
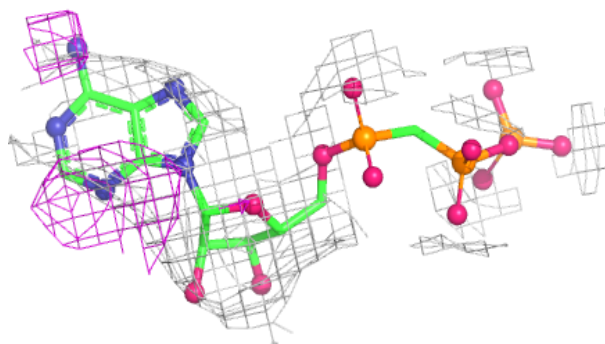
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
19	APC	P	12	31/31	0.92	0.10	102,118,169,170	0
17	ZN	I	1122	1/1	0.97	0.05	234,234,234,234	0
17	ZN	L	1071	1/1	0.99	0.03	192,192,192,192	0
17	ZN	C	1269	1/1	1.00	0.03	92,92,92,92	0
17	ZN	I	1121	1/1	1.00	0.04	129,129,129,129	0
17	ZN	A	2456	1/1	1.00	0.02	128,128,128,128	0
17	ZN	J	1066	1/1	1.00	0.01	85,85,85,85	0
17	ZN	A	2457	1/1	1.00	0.05	77,77,77,77	0
18	MG	A	2458	1/1	1.00	0.01	58,58,58,58	0
17	ZN	B	2225	1/1	1.00	0.03	92,92,92,92	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.

Electron density around APC P 12:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.