



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 29, 2020 – 07:04 am BST

PDB ID : 5C3E  
Title : Crystal structure of a transcribing RNA Polymerase II complex reveals a complete transcription bubble  
Authors : Barnes, C.O.; Calero, M.; Malik, I.; Spahr, H.; Zhang, Q.; Pullara, F.; Kaplan, C.D.; Calero, G.  
Deposited on : 2015-06-17  
Resolution : 3.70 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](mailto: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.

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

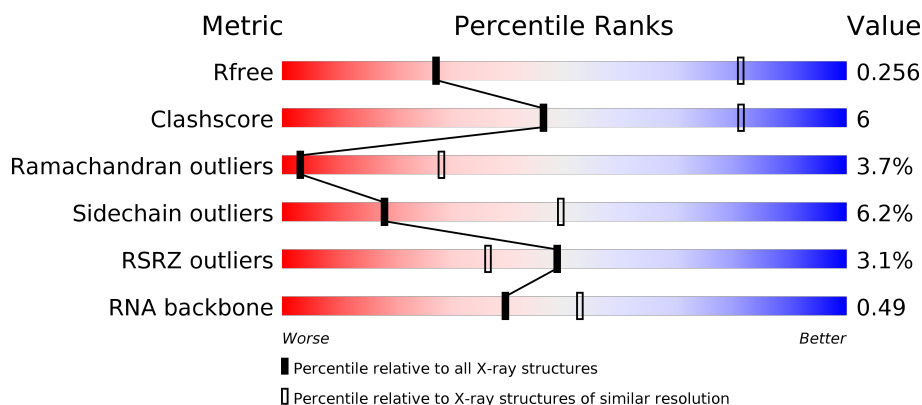
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.70 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	1049 (3.88-3.52)
Clashscore	141614	1027 (3.86-3.54)
Ramachandran outliers	138981	1069 (3.88-3.52)
Sidechain outliers	138945	1065 (3.88-3.52)
RSRZ outliers	127900	1578 (3.90-3.50)
RNA backbone	3102	1027 (4.40-3.00)

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  $\geq 3$ , 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	<div> <div>62%</div> <div>18%</div> <div>•</div> <div>17%</div> </div>
2	B	1224	<div> <div>4%</div> <div>71%</div> <div>22%</div> <div>•</div> <div>5%</div> </div>
3	C	318	<div> <div>64%</div> <div>17%</div> <div>•</div> <div>17%</div> </div>
4	D	221	<div> <div>67%</div> <div>13%</div> <div>19%</div> </div>

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Mol	Chain	Length	Quality of chain
5	E	215	
6	F	155	
7	G	179	
8	H	146	
9	I	122	
10	J	70	
11	K	120	
12	L	70	
13	R	9	
14	S	45	
15	U	45	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
16	ZN	C	401	-	-	-	X
17	MG	A	1804	-	-	-	X

## 2 Entry composition [i](#)

There are 17 unique types of molecules in this entry. The entry contains 32515 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	1430	Total	C	N	O	S	0	0	0
			11227	7069	1962	2134	62			

- Molecule 2 is a protein called DNA-directed RNA polymerase II subunit RPB2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	1157	Total	C	N	O	S	0	0	0
			9130	5767	1599	1708	56			

- Molecule 3 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	265	Total	C	N	O	S	0	0	0
			2086	1312	347	414	13			

- Molecule 4 is a protein called DNA-directed RNA polymerase II subunit RPB4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	178	Total	C	N	O	S	0	0	0
			1417	875	254	286	2			

- Molecule 5 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

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 RPABC2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	87	Total	C	N	O	S	0	0	0
			705	451	119	132	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
			1339	861	222	248	8			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	172	LEU	-	expression tag	UNP P34087
G	173	GLU	-	expression tag	UNP P34087
G	174	HIS	-	expression tag	UNP P34087
G	175	HIS	-	expression tag	UNP P34087
G	176	HIS	-	expression tag	UNP P34087
G	177	HIS	-	expression tag	UNP P34087
G	178	HIS	-	expression tag	UNP P34087
G	179	HIS	-	expression tag	UNP P34087

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	135	Total	C	N	O	S	0	0	0
			1080	679	182	214	5			

- Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	114	Total	C	N	O	S	0	0	0
			927	571	168	178	10			

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	66	Total	C	N	O	S	0	0	0
			540	345	94	95	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	0
			924	593	157	172	2			

- Molecule 12 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	43	Total	C	N	O	S	0	0	0
			344	211	69	60	4			

- Molecule 13 is a RNA chain called Synthetic RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	R	9	Total	C	N	O	P	0	0	0
			197	88	40	60	9			

- Molecule 14 is a DNA chain called Synthetic DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	S	14	Total	C	N	O	P	0	0	0
			286	137	49	86	14			

- Molecule 15 is a DNA chain called Synthetic DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	U	27	Total	C	N	O	P	0	0	0
			550	262	101	160	27			

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

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

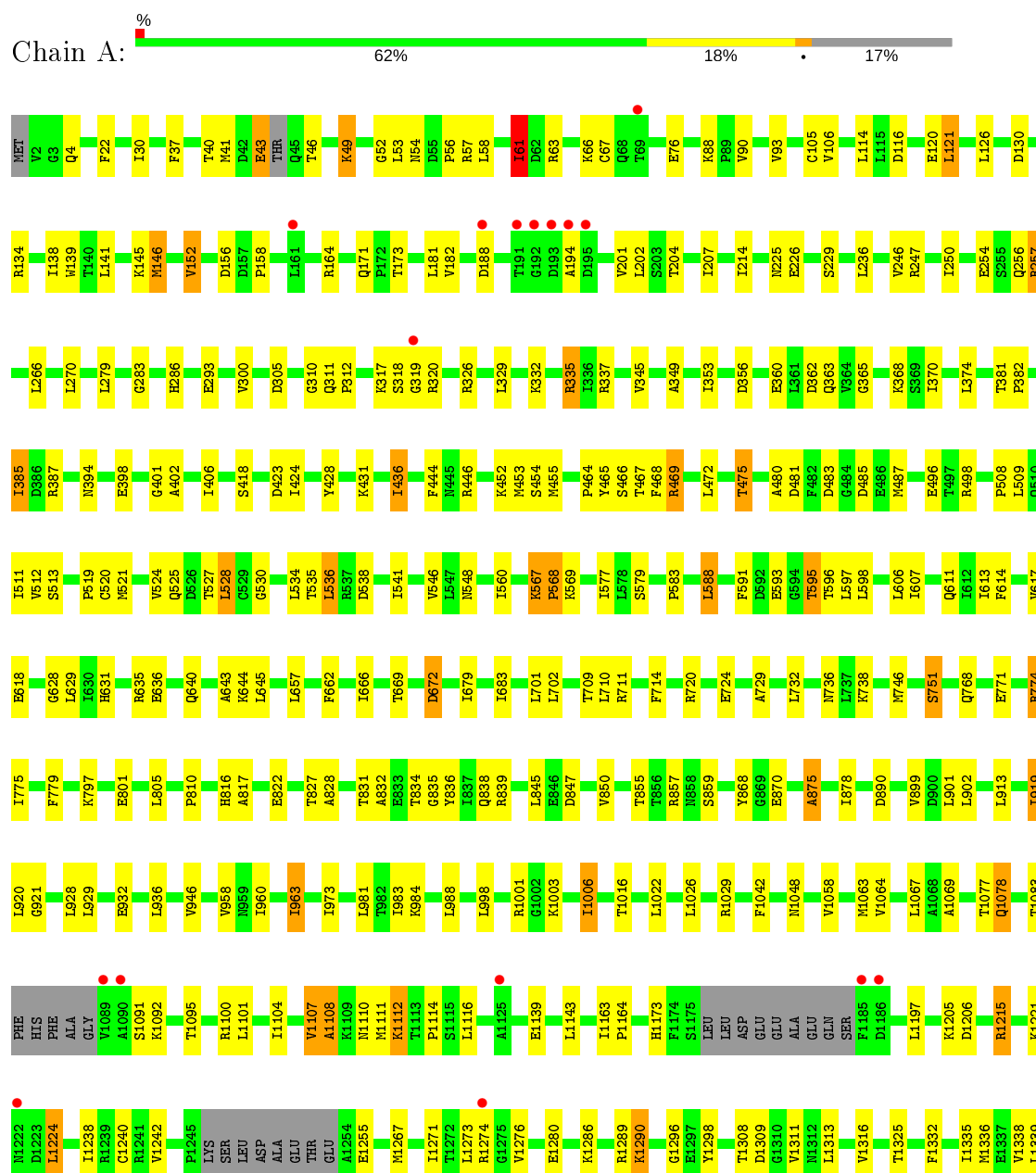
- Molecule 17 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	A	2	Total	Mg	0	0
			2	2		

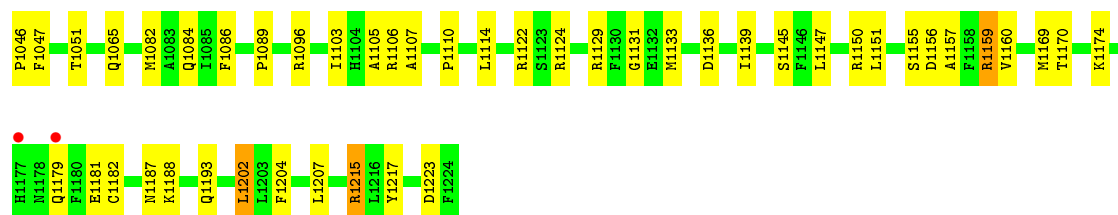
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry 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.

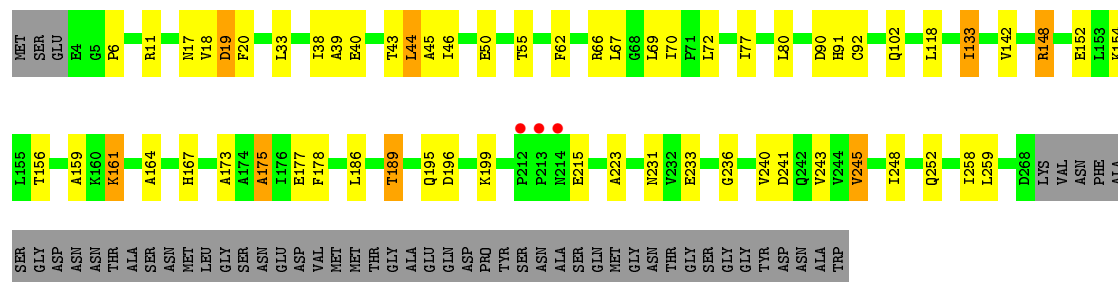
- Molecule 1: DNA-directed RNA polymerase II subunit RPB1



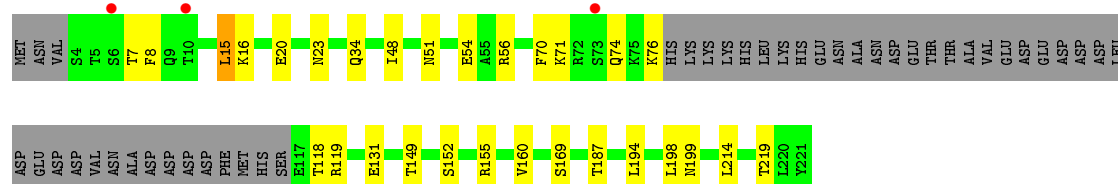




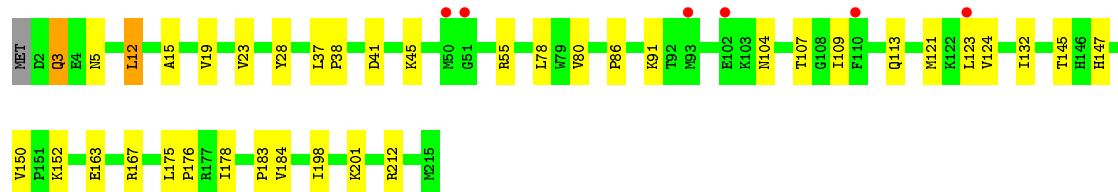
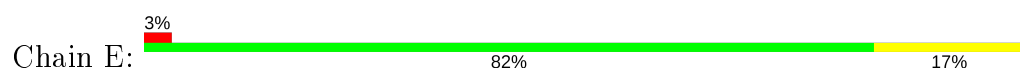
• Molecule 3: DNA-directed RNA polymerase II subunit RPB3



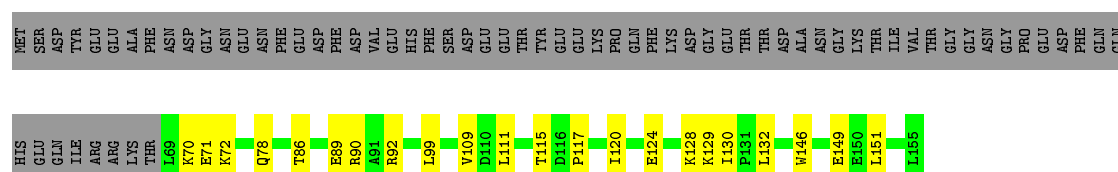
• Molecule 4: DNA-directed RNA polymerase II subunit RPB4



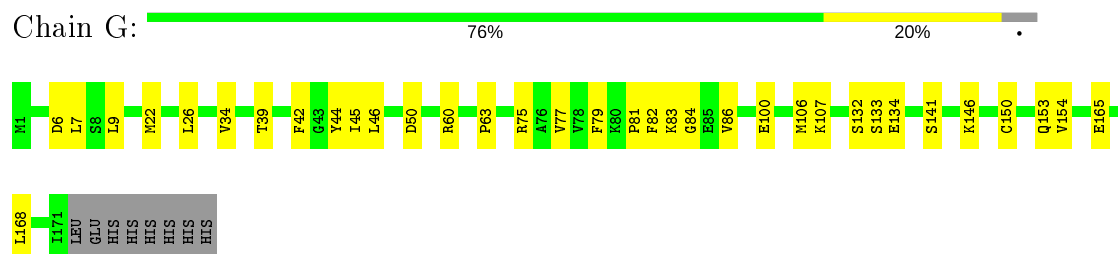
• Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1



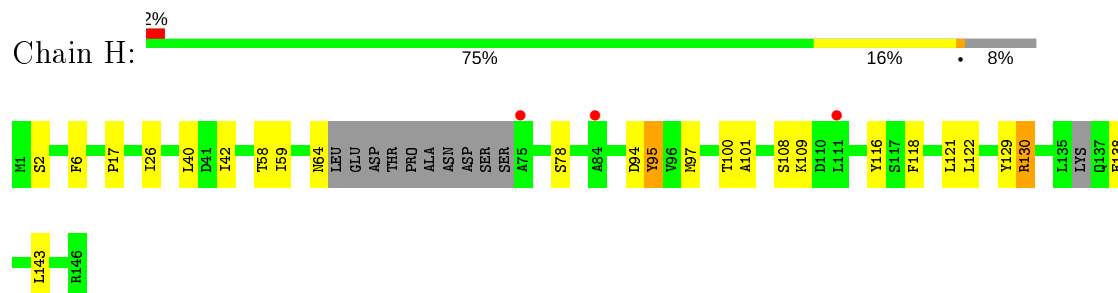
• Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2



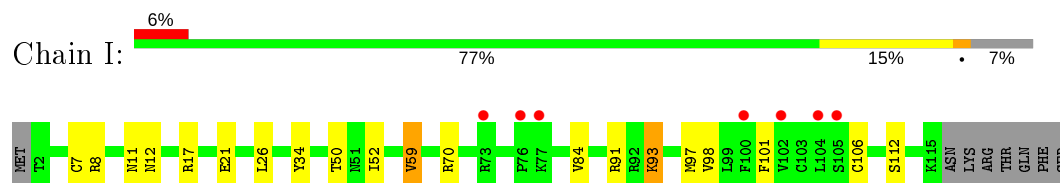
- Molecule 7: DNA-directed RNA polymerase II subunit RPB7



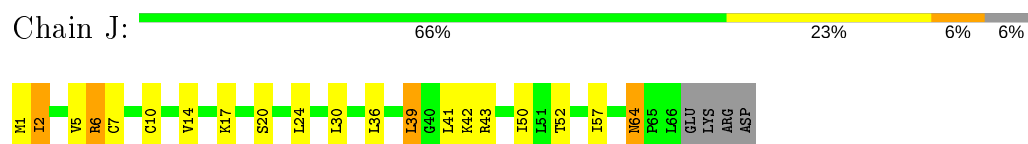
- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3



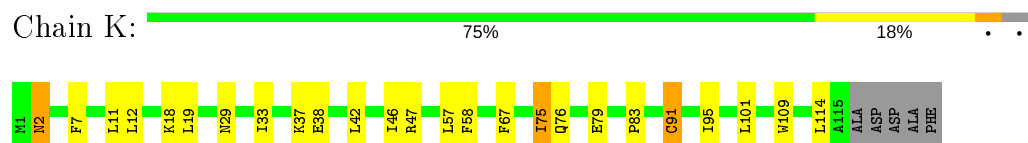
- Molecule 9: DNA-directed RNA polymerase II subunit RPB9



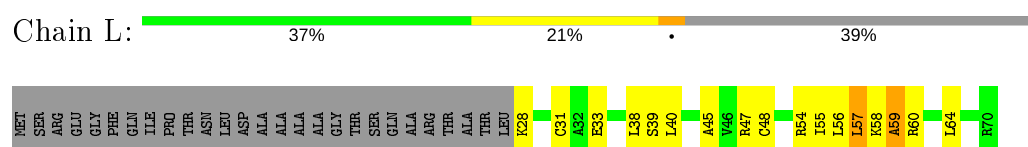
- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5



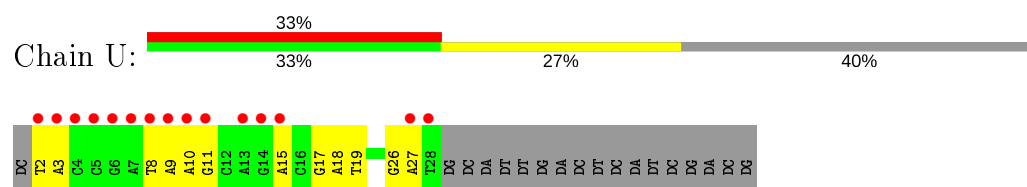
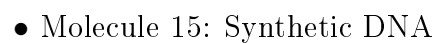
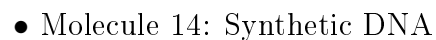
- Molecule 11: DNA-directed RNA polymerase II subunit RPB11



- Molecule 12: DNA-directed RNA polymerases I, II, and III subunit RPABC4



- Molecule 13: Synthetic RNA



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	219.05Å 390.94Å 278.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 3.70 39.98 – 3.70	Depositor EDS
% Data completeness (in resolution range)	96.4 (40.00-3.70) 96.4 (39.98-3.70)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.32	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.69 (at 3.66Å)	Xtriage
Refinement program	BUSTER-TNT BUSTER 2.10.2	Depositor
R, $R_{free}$	0.201 , 0.220 0.233 , 0.256	Depositor DCC
$R_{free}$ test set	3691 reflections (3.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	92.7	Xtriage
Anisotropy	0.383	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 100.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.37$ , $\langle L^2 \rangle = 0.19$	Xtriage
Estimated twinning fraction	0.108 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.125 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	32515	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	131.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.79% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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, 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	A	0.40	0/11427	0.66	0/15457
2	B	0.39	0/9302	0.64	2/12542 (0.0%)
3	C	0.38	0/2124	0.62	0/2879
4	D	0.38	0/1427	0.62	0/1911
5	E	0.38	0/1788	0.58	0/2406
6	F	0.40	0/717	0.64	0/967
7	G	0.38	0/1367	0.65	0/1844
8	H	0.38	0/1097	0.61	0/1484
9	I	0.38	0/945	0.63	0/1273
10	J	0.39	0/549	0.65	0/738
11	K	0.37	0/942	0.58	0/1272
12	L	0.41	0/346	0.68	0/457
13	R	0.88	0/221	0.87	1/343 (0.3%)
14	S	1.04	0/319	0.97	0/490
15	U	1.19	2/616 (0.3%)	0.96	0/947
All	All	0.43	2/33187 (0.0%)	0.65	3/45010 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	U	15	DA	O3'-P	-6.68	1.53	1.61
15	U	15	DA	N9-C8	-5.06	1.33	1.37

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	136	THR	C-N-CA	5.30	134.95	121.70
2	B	145	ARG	C-N-CA	5.14	134.54	121.70
13	R	2	U	C1'-O4'-C4'	-5.07	105.85	109.90

There are no chirality outliers.

There are no planarity outliers.

## 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	11227	0	11270	167	0
2	B	9130	0	9099	143	0
3	C	2086	0	2045	34	0
4	D	1417	0	1428	7	0
5	E	1752	0	1776	21	0
6	F	705	0	731	10	0
7	G	1339	0	1357	16	0
8	H	1080	0	1049	14	0
9	I	927	0	883	11	0
10	J	540	0	554	16	0
11	K	924	0	934	17	0
12	L	344	0	365	7	0
13	R	197	0	96	1	0
14	S	286	0	160	3	0
15	U	550	0	304	11	0
16	A	2	0	0	0	0
16	B	1	0	0	0	0
16	C	2	0	0	0	0
16	I	2	0	0	0	0
16	J	1	0	0	0	0
16	L	1	0	0	0	0
17	A	2	0	0	0	0
All	All	32515	0	32051	406	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 6.

The worst 5 of 406 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)
10:J:36:LEU:HD21	10:J:50:ILE:HD11	1.38	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:446:ARG:HD2	1:A:480:ALA:HB2	1.49	0.91
1:A:1107:VAL:HA	1:A:1108:ALA:HB2	1.54	0.88
2:B:120:ARG:HG2	2:B:955:THR:HG21	1.61	0.83
2:B:145:ARG:HA	2:B:146:GLU:HB2	1.62	0.81

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	1420/1733 (82%)	1220 (86%)	141 (10%)	59 (4%)	3	25
2	B	1139/1224 (93%)	973 (85%)	123 (11%)	43 (4%)	3	27
3	C	263/318 (83%)	230 (88%)	26 (10%)	7 (3%)	5	33
4	D	174/221 (79%)	154 (88%)	11 (6%)	9 (5%)	2	21
5	E	212/215 (99%)	194 (92%)	14 (7%)	4 (2%)	8	40
6	F	85/155 (55%)	76 (89%)	6 (7%)	3 (4%)	3	30
7	G	169/179 (94%)	143 (85%)	19 (11%)	7 (4%)	3	26
8	H	129/146 (88%)	105 (81%)	20 (16%)	4 (3%)	4	32
9	I	112/122 (92%)	96 (86%)	13 (12%)	3 (3%)	5	33
10	J	64/70 (91%)	57 (89%)	5 (8%)	2 (3%)	4	32
11	K	113/120 (94%)	109 (96%)	4 (4%)	0	100	100
12	L	41/70 (59%)	31 (76%)	6 (15%)	4 (10%)	0	8
All	All	3921/4573 (86%)	3388 (86%)	388 (10%)	145 (4%)	3	28

5 of 145 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	49	LYS

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Mol	Chain	Res	Type
1	A	66	LYS
1	A	67	CYS
1	A	76	GLU
1	A	158	PRO

### 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	1245/1520 (82%)	1150 (92%)	95 (8%)	13	43
2	B	986/1061 (93%)	924 (94%)	62 (6%)	18	49
3	C	233/274 (85%)	218 (94%)	15 (6%)	17	48
4	D	156/200 (78%)	146 (94%)	10 (6%)	17	48
5	E	196/197 (100%)	190 (97%)	6 (3%)	40	65
6	F	77/137 (56%)	74 (96%)	3 (4%)	32	60
7	G	152/160 (95%)	151 (99%)	1 (1%)	84	91
8	H	118/128 (92%)	115 (98%)	3 (2%)	47	70
9	I	108/116 (93%)	102 (94%)	6 (6%)	21	53
10	J	61/65 (94%)	55 (90%)	6 (10%)	8	33
11	K	99/102 (97%)	94 (95%)	5 (5%)	24	55
12	L	38/57 (67%)	34 (90%)	4 (10%)	7	30
All	All	3469/4017 (86%)	3253 (94%)	216 (6%)	18	49

5 of 216 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	106	ASP
2	B	612	GLU
9	I	59	VAL
2	B	175	ARG
2	B	396	ASP

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

Mol	Chain	Res	Type
1	A	1082	ASN
2	B	363	HIS
5	E	61	GLN
1	A	717	ASN
2	B	1178	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
13	R	8/9 (88%)	0	1 (12%)

There are no RNA backbone outliers to report.

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
13	R	2	U

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 11 ligands modelled in this entry, 11 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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	1430/1733 (82%)	-0.18	16 (1%) 80 71	47, 113, 205, 298	0
2	B	1157/1224 (94%)	0.02	54 (4%) 31 23	47, 128, 231, 294	0
3	C	265/318 (83%)	-0.19	3 (1%) 80 71	57, 113, 177, 299	0
4	D	178/221 (80%)	-0.16	3 (1%) 70 59	60, 118, 193, 250	0
5	E	214/215 (99%)	0.02	6 (2%) 53 40	63, 159, 239, 274	0
6	F	87/155 (56%)	-0.40	0 100 100	46, 78, 133, 162	0
7	G	171/179 (95%)	-0.28	0 100 100	59, 98, 151, 229	0
8	H	135/146 (92%)	0.13	3 (2%) 62 50	99, 162, 231, 247	0
9	I	114/122 (93%)	0.17	7 (6%) 21 14	70, 160, 237, 280	0
10	J	66/70 (94%)	-0.21	0 100 100	53, 103, 177, 216	0
11	K	115/120 (95%)	-0.23	0 100 100	56, 105, 158, 176	0
12	L	43/70 (61%)	-0.16	0 100 100	75, 141, 215, 234	0
13	R	9/9 (100%)	1.23	2 (22%) 0 0	143, 199, 257, 275	0
14	S	14/45 (31%)	3.46	14 (100%) 0 0	261, 296, 300, 300	0
15	U	27/45 (60%)	1.94	15 (55%) 0 0	136, 253, 300, 300	0
All	All	4025/4672 (86%)	-0.07	123 (3%) 49 36	46, 121, 222, 300	0

The worst 5 of 123 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1090	ALA	6.6
5	E	51	GLY	6.0
2	B	71	LEU	5.4
15	U	6	DG	5.3
1	A	69	THR	5.2

## 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 carbohydrates 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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
17	MG	A	1804	1/1	0.49	0.60	63,63,63,63	0
16	ZN	C	401	1/1	0.69	0.72	193,193,193,193	0
17	MG	A	1803	1/1	0.91	0.12	82,82,82,82	0
16	ZN	I	202	1/1	0.98	0.06	183,183,183,183	0
16	ZN	A	1801	1/1	0.98	0.07	90,90,90,90	0
16	ZN	J	101	1/1	0.99	0.18	93,93,93,93	0
16	ZN	A	1802	1/1	0.99	0.14	67,67,67,67	0
16	ZN	B	1301	1/1	0.99	0.14	72,72,72,72	0
16	ZN	I	201	1/1	0.99	0.07	113,113,113,113	0
16	ZN	L	101	1/1	0.99	0.06	93,93,93,93	0
16	ZN	C	402	1/1	0.99	0.08	74,74,74,74	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.