



## wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Oct 28, 2019 – 03:21 PM EDT

PDB ID : 6A5R  
EMDB ID: : EMD-6983  
Title : RNA polymerase II elongation complex stalled at SHL(-2) of the nucleosome  
Authors : Kujirai, T.; Ehara, H.; Fujino, Y.; Shirouzu, M.; Sekine, S.; Kurumizaka, H.  
Deposited on : 2018-06-25  
Resolution : 8.70 Å(reported)

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report  
for a publicly released PDB/EMDB 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/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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MolProbity : 4.02b-467  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.4

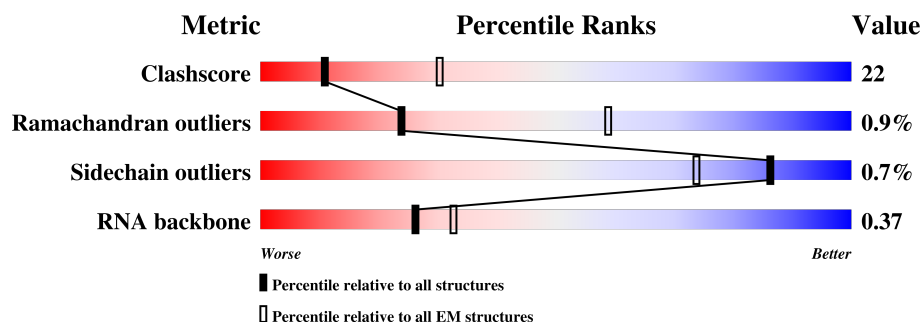
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 8.70 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)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531
RNA backbone	3747	458

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	1743	44% 35% . 19%
2	B	1227	50% 43% . 5%
3	C	304	42% 44% 13%
4	D	186	52% 32% 16%
5	E	214	54% 43% .
6	F	155	32% 21% . 46%
7	G	171	54% 44% .
8	H	145	48% 44% 8%

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Mol	Chain	Length	Quality of chain
9	I	115	
10	J	72	
11	K	118	
12	L	72	
13	P	11	
14	T	198	
15	N	198	
16	a	139	
16	e	139	
17	b	106	
17	f	106	
18	c	133	
18	g	133	
19	d	129	
19	h	129	

## 2 Entry composition

There are 21 unique types of molecules in this entry. The entry contains 42725 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1408	Total	C	N	O	S	0	0
			11095	6997	1935	2093	70		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1161	Total	C	N	O	S	0	0
			9261	5835	1636	1732	58		

- Molecule 3 is a protein called RNA polymerase II third largest subunit B44, part of central core.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	263	Total	C	N	O	S	0	0
			2098	1319	354	413	12		

- Molecule 4 is a protein called RNA polymerase II subunit B32.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	156	Total	C	N	O	S	0	0
			1210	753	210	245	2		

- Molecule 5 is a protein called RNA polymerase subunit ABC27, common to RNA polymerases I, II, and III.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	213	Total	C	N	O	S	0	0
			1740	1094	312	324	10		

- Molecule 6 is a protein called RNA polymerase subunit ABC23, common to RNA polymerases I, II, and III.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	84	Total	C	N	O	S	0	0
			677	429	114	131	3		

- Molecule 7 is a protein called RNA polymerase II subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	171	Total	C	N	O	S	0	0
			1324	858	214	247	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	133	Total	C	N	O	S	0	0
			1052	671	169	208	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	111	Total	C	N	O	S	0	0
			917	565	161	180	11		

- Molecule 10 is a protein called RNA polymerase subunit ABC10-beta, common to RNA polymerases I, II, and III.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	66	Total	C	N	O	S	0	0
			545	349	95	95	6		

- Molecule 11 is a protein called RNA polymerase II subunit B12.5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	113	Total	C	N	O	S	0	0
			932	599	160	169	4		

- Molecule 12 is a protein called RNA polymerase subunit ABC10-alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	45	Total	C	N	O	S	0	0
			359	221	72	61	5		

- Molecule 13 is a RNA chain called RNA (5'-R(P\*UP\*CP\*UP\*CP\*GP\*UP\*GP\*CP\*CP\*UP\*G)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
13	P	11	Total	C	N	O	P	0	0
			229	102	35	81	11		

- Molecule 14 is a DNA chain called DNA (198-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
14	T	136	Total	C	N	O	P	0	0
			2777	1316	529	797	135		

- Molecule 15 is a DNA chain called DNA (198-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	127	Total	C	N	O	P	0	0
			2612	1239	471	775	127		

- Molecule 16 is a protein called Histone H3.3.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	a	97	Total	C	N	O	S	0	0
			797	503	155	137	2		
16	e	97	Total	C	N	O	S	0	0
			796	501	155	138	2		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	-3	GLY	-	expression tag	UNP P84243
a	-2	SER	-	expression tag	UNP P84243
a	-1	HIS	-	expression tag	UNP P84243
e	-3	GLY	-	expression tag	UNP P84243
e	-2	SER	-	expression tag	UNP P84243
e	-1	HIS	-	expression tag	UNP P84243

- Molecule 17 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	b	80	Total	C	N	O	S	0	0
			638	401	125	111	1		
17	f	78	Total	C	N	O	S	0	0
			619	391	120	107	1		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	-3	GLY	-	expression tag	UNP P62805
b	-2	SER	-	expression tag	UNP P62805
b	-1	HIS	-	expression tag	UNP P62805
f	-3	GLY	-	expression tag	UNP P62805
f	-2	SER	-	expression tag	UNP P62805
f	-1	HIS	-	expression tag	UNP P62805

- Molecule 18 is a protein called Histone H2A type 1-B/E.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	c	103	Total	C	N	O	0	0
			796	502	155	139		
18	g	102	Total	C	N	O	0	0
			789	498	154	137		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
c	-3	GLY	-	expression tag	UNP P04908
c	-2	SER	-	expression tag	UNP P04908
c	-1	HIS	-	expression tag	UNP P04908
g	-3	GLY	-	expression tag	UNP P04908
g	-2	SER	-	expression tag	UNP P04908
g	-1	HIS	-	expression tag	UNP P04908

- Molecule 19 is a protein called Histone H2B type 1-J.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	d	95	Total	C	N	O	S	0
			746	468	136	140	2	0
19	h	90	Total	C	N	O	S	0
			707	446	127	132	2	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
d	-6	GLY	-	expression tag	UNP P06899
d	-5	SER	-	expression tag	UNP P06899
d	-4	HIS	-	expression tag	UNP P06899
h	-6	GLY	-	expression tag	UNP P06899
h	-5	SER	-	expression tag	UNP P06899
h	-4	HIS	-	expression tag	UNP P06899

- Molecule 20 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 21 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

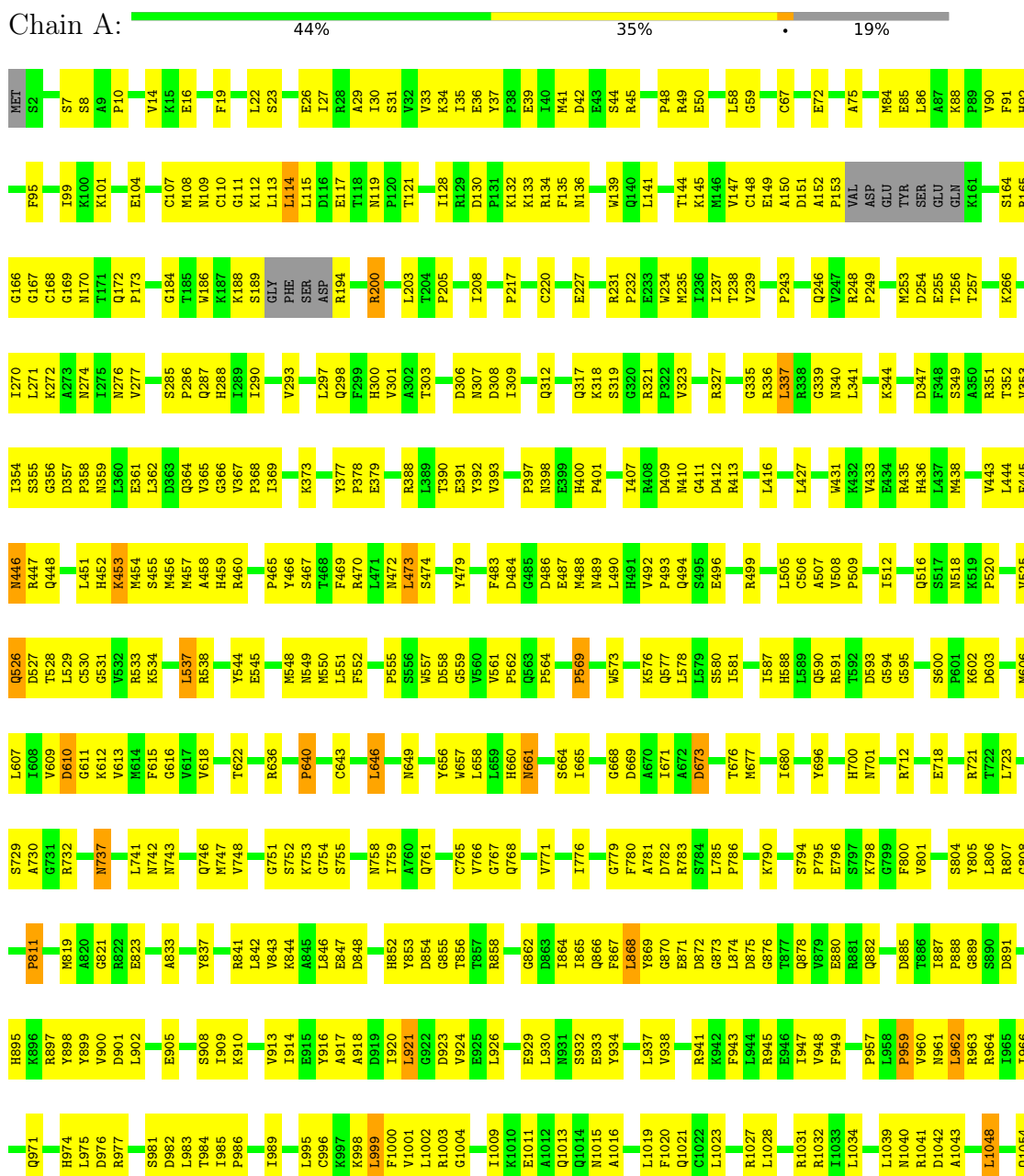
Mol	Chain	Residues	Atoms		AltConf
21	A	1	Total 1	Mg 1	0

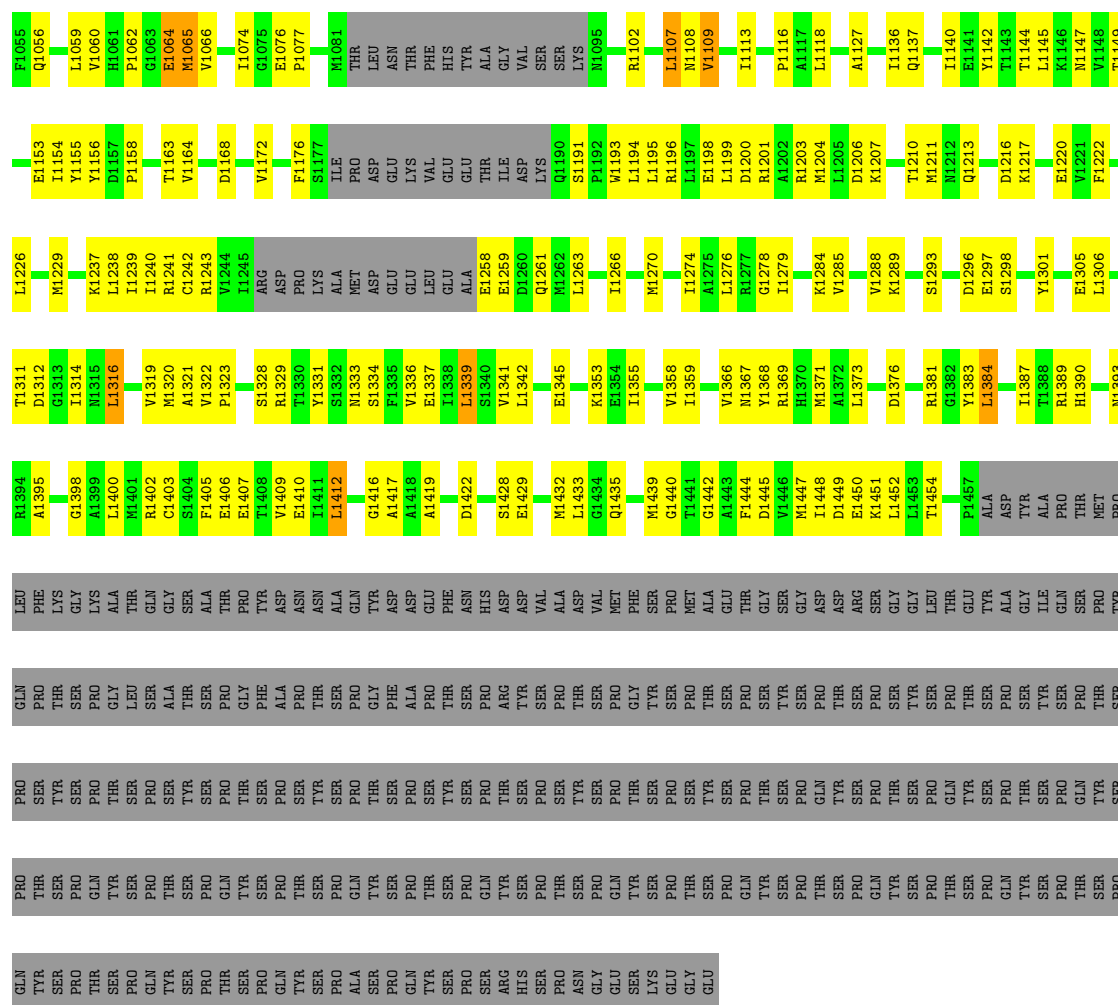


### 3 Residue-property plots

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. 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. 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.

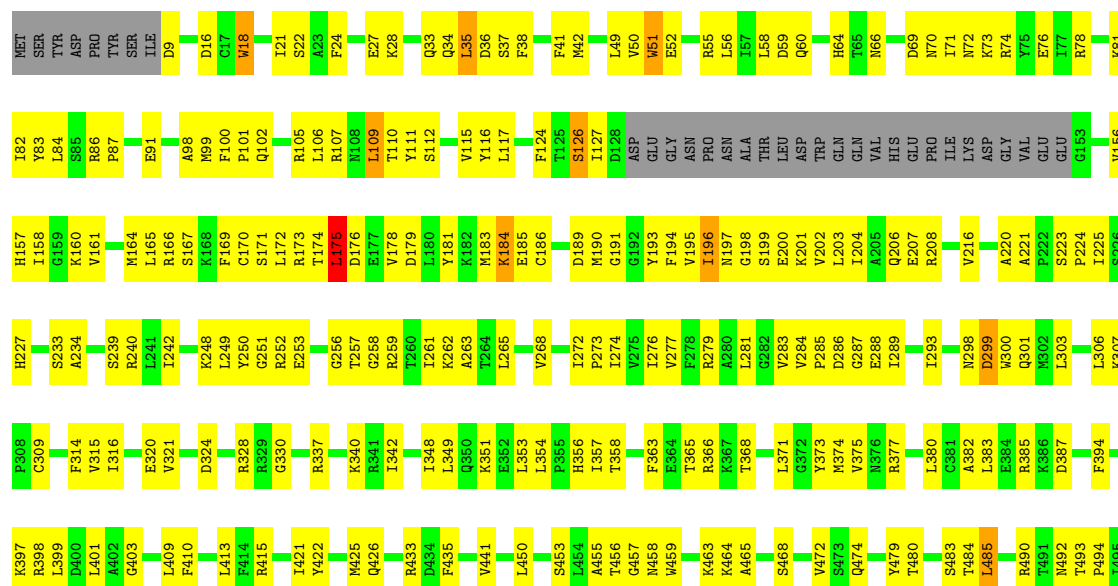
- Molecule 1: DNA-directed RNA polymerase subunit



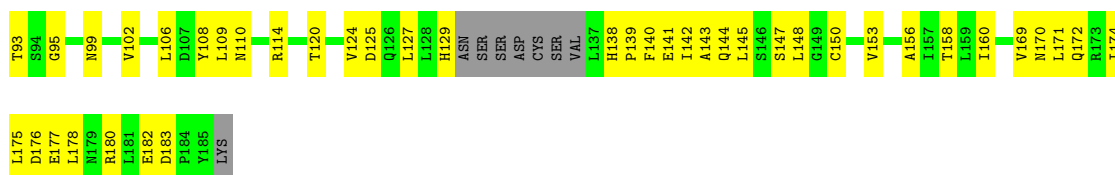


## • Molecule 2: DNA-directed RNA polymerase subunit beta

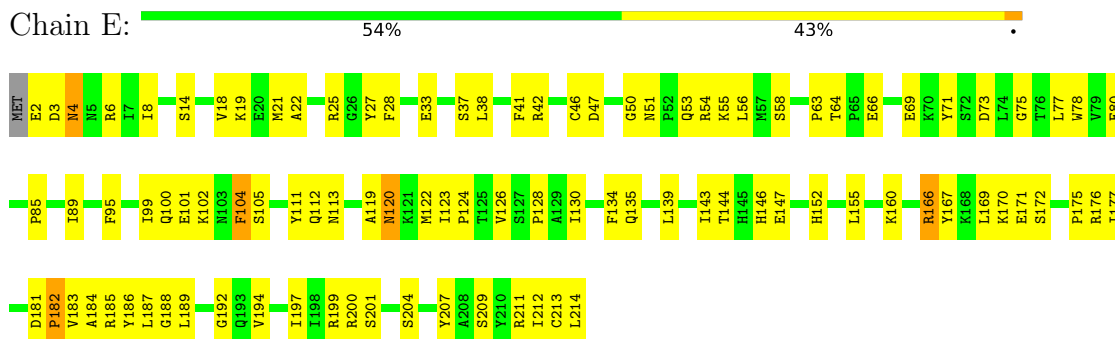
Chain B: 50% 43% 5%



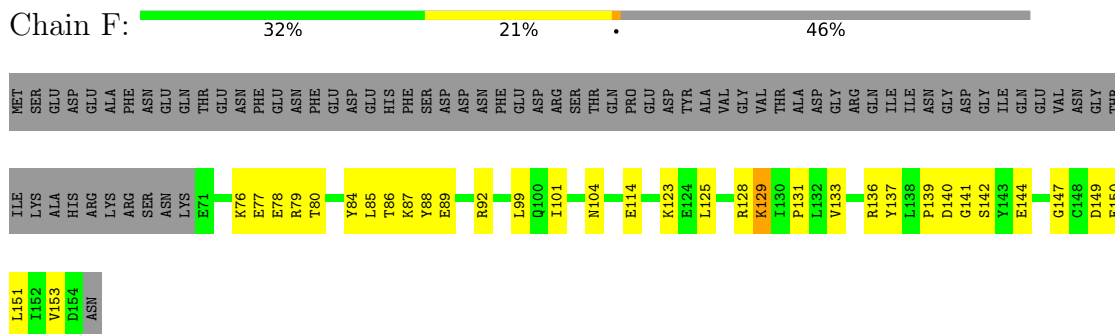




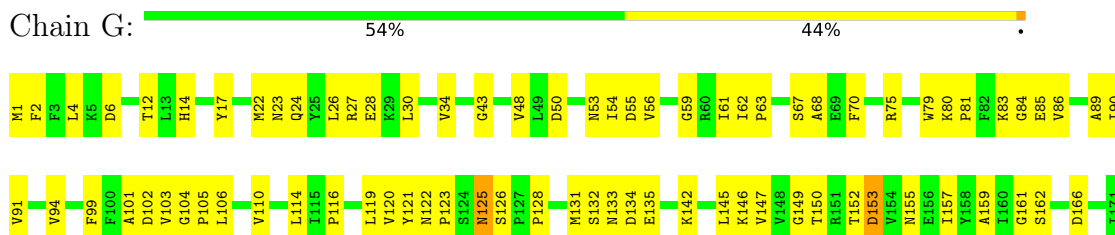
- Molecule 5: RNA polymerase subunit ABC27, common to RNA polymerases I, II, and III



- Molecule 6: RNA polymerase subunit ABC23, common to RNA polymerases I, II, and III



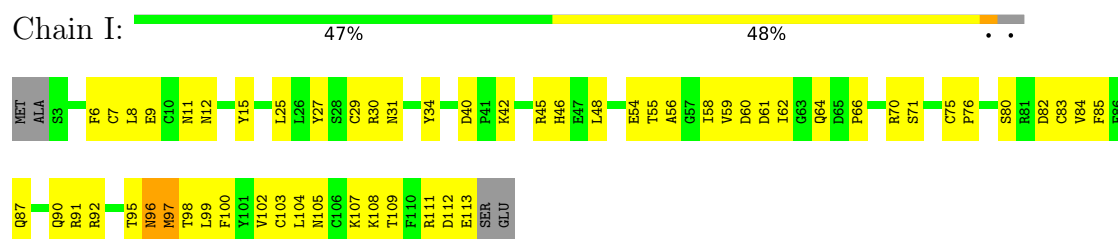
- Molecule 7: RNA polymerase II subunit



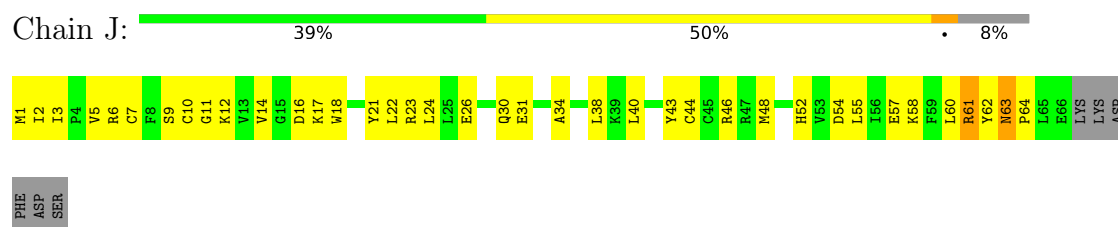
- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3



- Molecule 9: DNA-directed RNA polymerase subunit



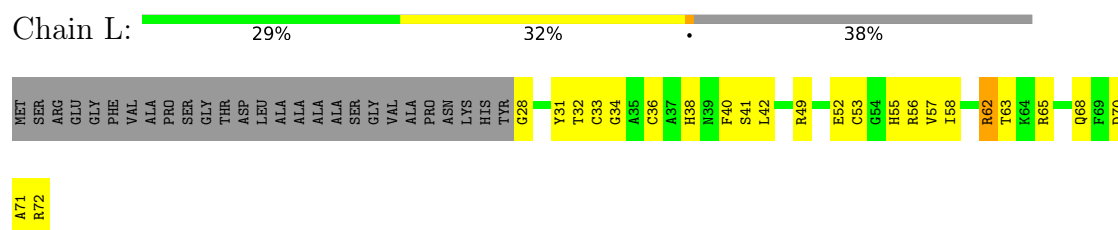
- Molecule 10: RNA polymerase subunit ABC10-beta, common to RNA polymerases I, II, and III



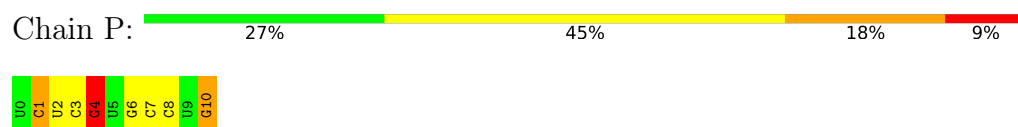
- Molecule 11: RNA polymerase II subunit B12.5



- Molecule 12: RNA polymerase subunit ABC10-alpha

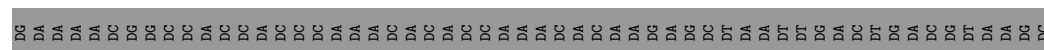
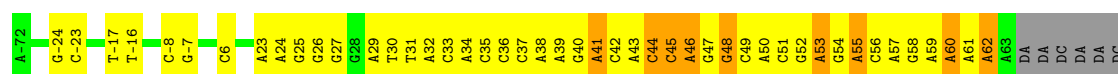


- Molecule 13: RNA (5'-R(P\*UP\*CP\*UP\*CP\*GP\*UP\*GP\*CP\*CP\*UP\*G)-3')

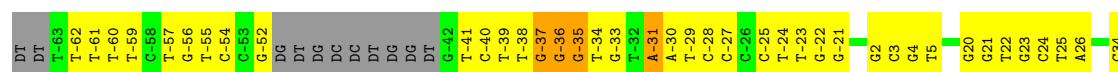
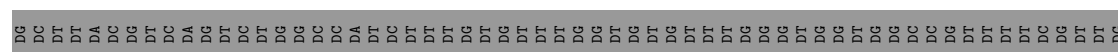


- Molecule 14: DNA (198-MER)

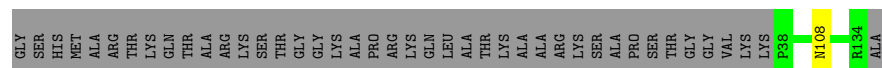




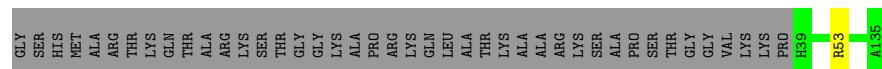
- Molecule 15: DNA (198-MER)



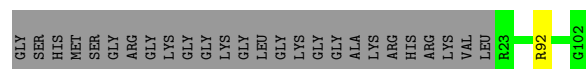
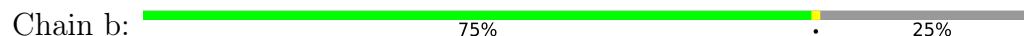
- Molecule 16: Histone H3.3



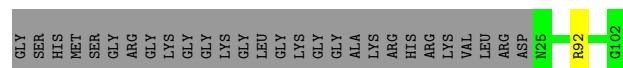
- Molecule 16: Histone H3.3



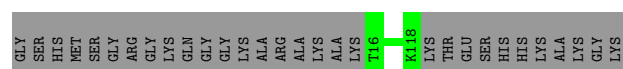
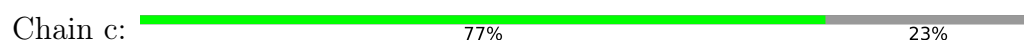
- Molecule 17: Histone H4



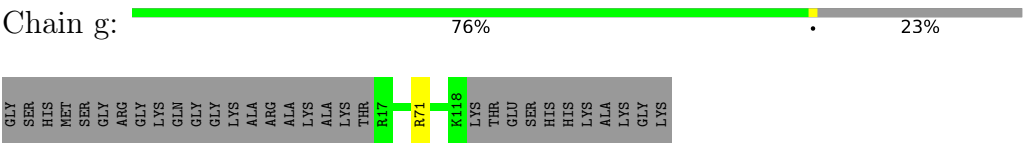
- Molecule 17: Histone H4



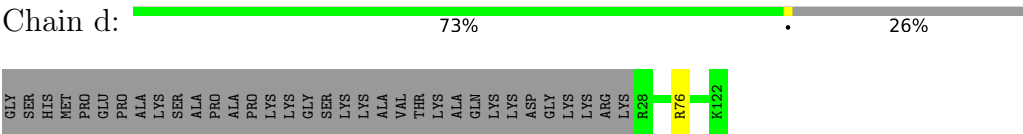
- Molecule 18: Histone H2A type 1-B/E



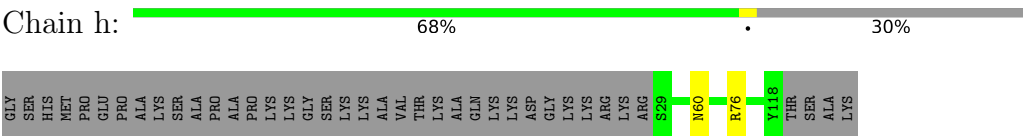
● Molecule 18: Histone H2A type 1-B/E



● Molecule 19: Histone H2B type 1-J



● Molecule 19: Histone H2B type 1-J



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	8798	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor



## 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: 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	$\# Z  > 2$	RMSZ	$\# Z  > 2$
1	A	0.68	0/11299	0.72	13/15266 (0.1%)
10	J	0.90	0/554	0.80	0/742
11	K	0.68	0/953	0.68	1/1291 (0.1%)
12	L	0.62	0/365	0.66	0/484
13	P	1.25	3/253 (1.2%)	1.15	0/391
14	T	1.03	10/3119 (0.3%)	1.00	1/4807 (0.0%)
15	N	0.91	5/2926 (0.2%)	0.97	0/4516
16	a	0.34	0/809	0.54	0/1085
16	e	0.38	0/807	0.52	0/1081
17	b	0.38	0/645	0.57	0/862
17	f	0.40	0/626	0.56	0/837
18	c	0.35	0/806	0.52	0/1089
18	g	0.35	0/799	0.52	0/1079
19	d	0.38	0/757	0.54	0/1015
19	h	0.38	0/718	0.56	0/965
2	B	0.75	1/9441 (0.0%)	0.75	9/12732 (0.1%)
3	C	0.72	0/2139	0.73	1/2895 (0.0%)
4	D	0.31	0/1221	0.53	0/1648
5	E	0.69	0/1772	0.69	0/2385
6	F	0.66	0/687	0.65	0/931
7	G	0.34	0/1353	0.59	1/1837 (0.1%)
8	H	0.77	0/1069	0.69	0/1444
9	I	0.43	0/934	0.58	0/1257
All	All	0.70	19/44052 (0.0%)	0.74	26/60639 (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
1	A	0	1
10	J	0	1
2	B	0	2
3	C	0	1
4	D	0	1
7	G	0	1
All	All	0	7

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	T	47	DG	C1'-N9	-10.07	1.33	1.47
13	P	6	G	C1'-N9	-9.39	1.33	1.46
14	T	48	DG	C1'-N9	-8.96	1.34	1.47
15	N	-35	DG	C1'-N9	-8.39	1.35	1.47
14	T	53	DA	C1'-N9	-8.13	1.35	1.47

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	473	LEU	CA-CB-CG	-9.82	92.71	115.30
2	B	556	MET	C-N-CA	-8.40	100.71	121.70
2	B	485	LEU	CA-CB-CG	-7.84	97.28	115.30
7	G	106	LEU	CA-CB-CG	6.74	130.80	115.30
1	A	1316	LEU	CA-CB-CG	-6.38	100.64	115.30

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	525	VAL	Peptide
2	B	126	SER	Peptide
2	B	175	LEU	Peptide
3	C	89	ASP	Peptide
4	D	27	LEU	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	A	11095	0	11134	592	0
2	B	9261	0	9266	513	0
3	C	2098	0	2059	118	0
4	D	1210	0	1205	54	0
5	E	1740	0	1754	78	0
6	F	677	0	693	41	0
7	G	1324	0	1342	56	0
8	H	1052	0	1050	53	0
9	I	917	0	868	64	0
10	J	545	0	560	38	0
11	K	932	0	944	52	0
12	L	359	0	360	26	0
13	P	229	0	117	22	0
14	T	2777	0	1519	132	0
15	N	2612	0	1433	137	0
16	a	797	0	835	0	0
16	e	796	0	832	0	0
17	b	638	0	676	0	0
17	f	619	0	659	0	0
18	c	796	0	848	0	0
18	g	789	0	841	0	0
19	d	746	0	771	0	0
19	h	707	0	728	0	0
20	A	2	0	0	0	0
20	B	1	0	0	0	0
20	C	1	0	0	0	0
20	I	2	0	0	0	0
20	J	1	0	0	0	0
20	L	1	0	0	0	0
21	A	1	0	0	0	0
All	All	42725	0	40494	1751	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 22.

The worst 5 of 1751 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)
15:N:-25:DC:H2''	15:N:-24:DT:C7	1.22	1.58
15:N:-25:DC:H1'	15:N:-24:DT:C4	1.46	1.49
15:N:-25:DC:C2'	15:N:-24:DT:C7	2.14	1.22
15:N:-25:DC:H1'	15:N:-24:DT:C5	1.72	1.22

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:N:-25:DC:C2'	15:N:-24:DT:H73	1.70	1.20

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 PDB entries followed by that with respect to all EM entries.

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	1396/1743 (80%)	1140 (82%)	235 (17%)	21 (2%)	11	51
2	B	1151/1227 (94%)	924 (80%)	217 (19%)	10 (1%)	19	61
3	C	261/304 (86%)	207 (79%)	51 (20%)	3 (1%)	16	58
4	D	148/186 (80%)	136 (92%)	12 (8%)	0	100	100
5	E	211/214 (99%)	175 (83%)	32 (15%)	4 (2%)	9	45
6	F	82/155 (53%)	73 (89%)	9 (11%)	0	100	100
7	G	169/171 (99%)	154 (91%)	15 (9%)	0	100	100
8	H	129/145 (89%)	104 (81%)	24 (19%)	1 (1%)	21	65
9	I	109/115 (95%)	88 (81%)	19 (17%)	2 (2%)	9	47
10	J	64/72 (89%)	53 (83%)	10 (16%)	1 (2%)	11	50
11	K	111/118 (94%)	101 (91%)	9 (8%)	1 (1%)	19	61
12	L	43/72 (60%)	31 (72%)	12 (28%)	0	100	100
16	a	95/139 (68%)	92 (97%)	3 (3%)	0	100	100
16	e	95/139 (68%)	90 (95%)	5 (5%)	0	100	100
17	b	78/106 (74%)	75 (96%)	3 (4%)	0	100	100
17	f	76/106 (72%)	72 (95%)	4 (5%)	0	100	100
18	c	101/133 (76%)	95 (94%)	6 (6%)	0	100	100
18	g	100/133 (75%)	94 (94%)	6 (6%)	0	100	100
19	d	93/129 (72%)	90 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	h	88/129 (68%)	85 (97%)	3 (3%)	0	100	100
All	All	4600/5536 (83%)	3879 (84%)	678 (15%)	43 (1%)	24	61

5 of 43 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	255	GLU
1	A	453	LYS
1	A	537	LEU
2	B	257	THR
2	B	1015	HIS

### 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 PDB entries followed by that with respect to all EM entries.

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	1223/1528 (80%)	1219 (100%)	4 (0%)	93	96
2	B	1016/1077 (94%)	1009 (99%)	7 (1%)	85	93
3	C	236/264 (89%)	235 (100%)	1 (0%)	92	95
4	D	133/160 (83%)	133 (100%)	0	100	100
5	E	196/197 (100%)	193 (98%)	3 (2%)	67	85
6	F	75/137 (55%)	74 (99%)	1 (1%)	71	86
7	G	148/148 (100%)	147 (99%)	1 (1%)	85	93
8	H	120/130 (92%)	120 (100%)	0	100	100
9	I	106/109 (97%)	105 (99%)	1 (1%)	81	90
10	J	60/66 (91%)	60 (100%)	0	100	100
11	K	104/109 (95%)	104 (100%)	0	100	100
12	L	38/56 (68%)	37 (97%)	1 (3%)	49	73
16	a	83/112 (74%)	82 (99%)	1 (1%)	74	87
16	e	82/112 (73%)	81 (99%)	1 (1%)	74	87
17	b	65/81 (80%)	64 (98%)	1 (2%)	67	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	f	63/81 (78%)	62 (98%)	1 (2%)	65	84
18	c	82/102 (80%)	82 (100%)	0	100	100
18	g	81/102 (79%)	80 (99%)	1 (1%)	74	87
19	d	81/107 (76%)	80 (99%)	1 (1%)	74	87
19	h	77/107 (72%)	75 (97%)	2 (3%)	49	73
All	All	4069/4785 (85%)	4042 (99%)	27 (1%)	86	93

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	E	4	ASN
6	F	129	LYS
18	g	71	ARG
5	E	120	ASN
2	B	184	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 46 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	108	ASN
2	B	736	HIS
11	K	44	ASN
2	B	206	GLN
2	B	524	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
13	P	10/11 (90%)	2 (20%)	0

All (2) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
13	P	1	C
13	P	4	G

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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.