



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 14, 2023 – 10:35 PM EDT

PDB ID : 1R5U
Title : RNA POLYMERASE II TFIIB COMPLEX
Authors : Bushnell, D.A.; Westover, K.D.; Davis, R.; Kornberg, R.D.
Deposited on : 2003-10-13
Resolution : 4.50 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
Xtriage (Phenix) : 1.13
EDS : 2.35
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

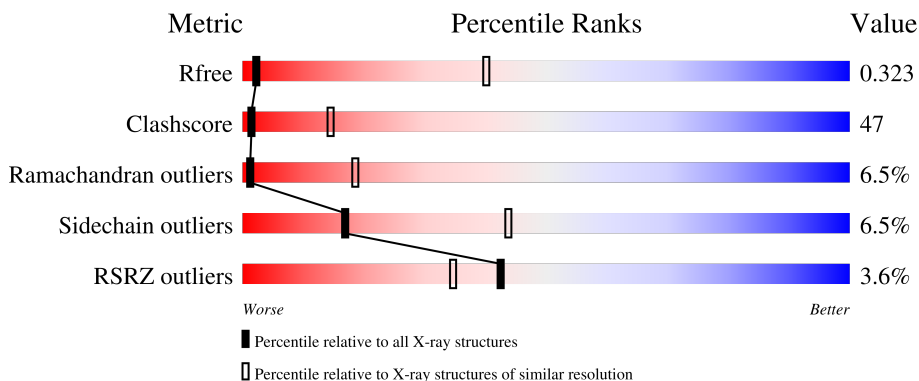
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.50 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.



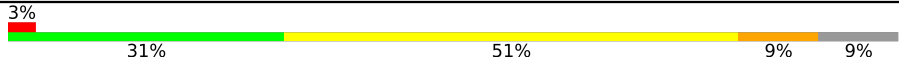

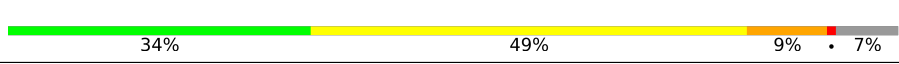
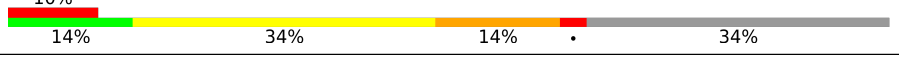
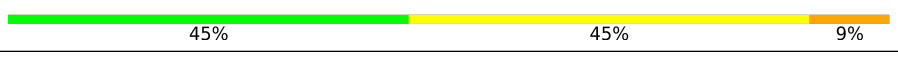
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1055 (5.20-3.80)
Clashscore	141614	1123 (5.20-3.80)
Ramachandran outliers	138981	1069 (5.20-3.80)
Sidechain outliers	138945	1050 (5.20-3.80)
RSRZ outliers	127900	1101 (5.30-3.70)

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	 2% 31% 41% 7% 20%
2	B	1224	 4% 32% 50% 7% 10%
3	C	318	 % 38% 39% 7% 16%
4	E	215	 6% 42% 54%
5	F	155	 % 17% 34% 46%

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Mol	Chain	Length	Quality of chain
6	H	146	
7	I	122	
8	J	70	
9	K	120	
10	L	70	
11	M	86	

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
12	ZN	I	203	-	-	-	X
12	ZN	I	204	-	-	X	-

2 Entry composition [i](#)

There are 13 unique types of molecules in this entry. The entry contains 28300 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 largest subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	1380	10850	6847	1898	2044	61	0	0	0

- Molecule 2 is a protein called DNA-directed RNA polymerase II 140 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	1097	8721	5526	1523	1618	54	0	0	0

- Molecule 3 is a protein called DNA-directed RNA polymerase II 45 kDa polypeptide.

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

- Molecule 4 is a protein called DNA-directed RNA polymerases I, II, and III 27 kDa polypeptide.

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

- Molecule 5 is a protein called DNA-directed RNA polymerases I, II, and III 23 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	F	84	679	434	115	127	3	0	0	0

- Molecule 6 is a protein called DNA-directed RNA polymerases I, II, and III 14.5 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
6	H	133	1068	673	180	211	4	0	0	0

- Molecule 7 is a protein called DNA-directed RNA polymerase II 14.2 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
7	I	118	967	594	178	185	10	0	0	0

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III 8.3 kDa polypeptide.

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

- Molecule 9 is a protein called DNA-directed RNA polymerase II 13.6 kDa polypeptide.

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

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III 7.7 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
10	L	46	364	224	72	64	4	0	0	0

- Molecule 11 is a protein called TRANSCRIPTION FACTOR II B (TFIIB).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
11	M	86	343	171	86	86	0	0	0

- Molecule 12 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	2	Total	Zn	0	0
			2	2		
12	B	1	Total	Zn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	C	1	Total 1	Zn 1	0	0
12	I	2	Total 2	Zn 2	0	0
12	J	1	Total 1	Zn 1	0	0
12	L	1	Total 1	Zn 1	0	0
12	M	1	Total 1	Zn 1	0	0

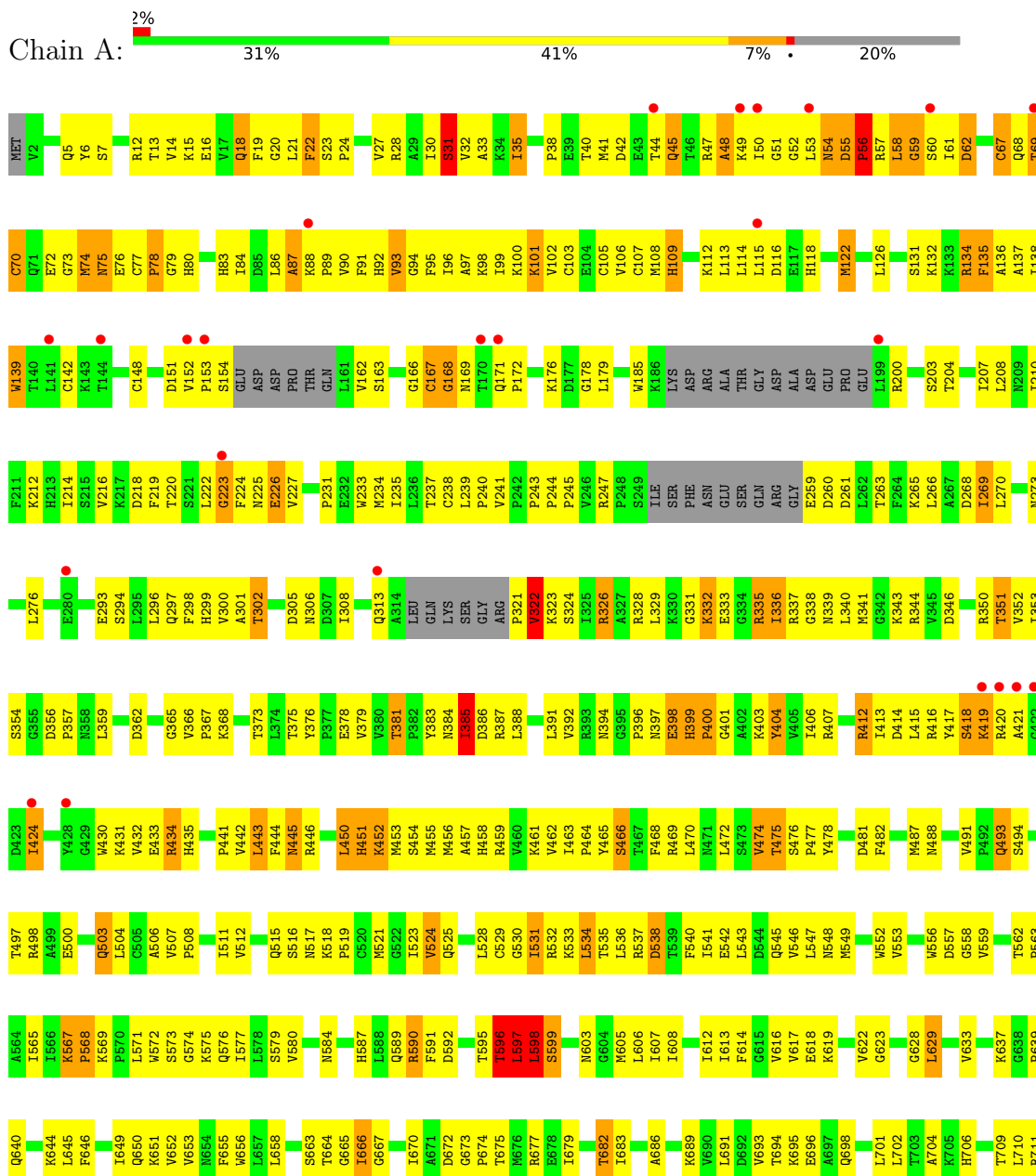
- Molecule 13 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

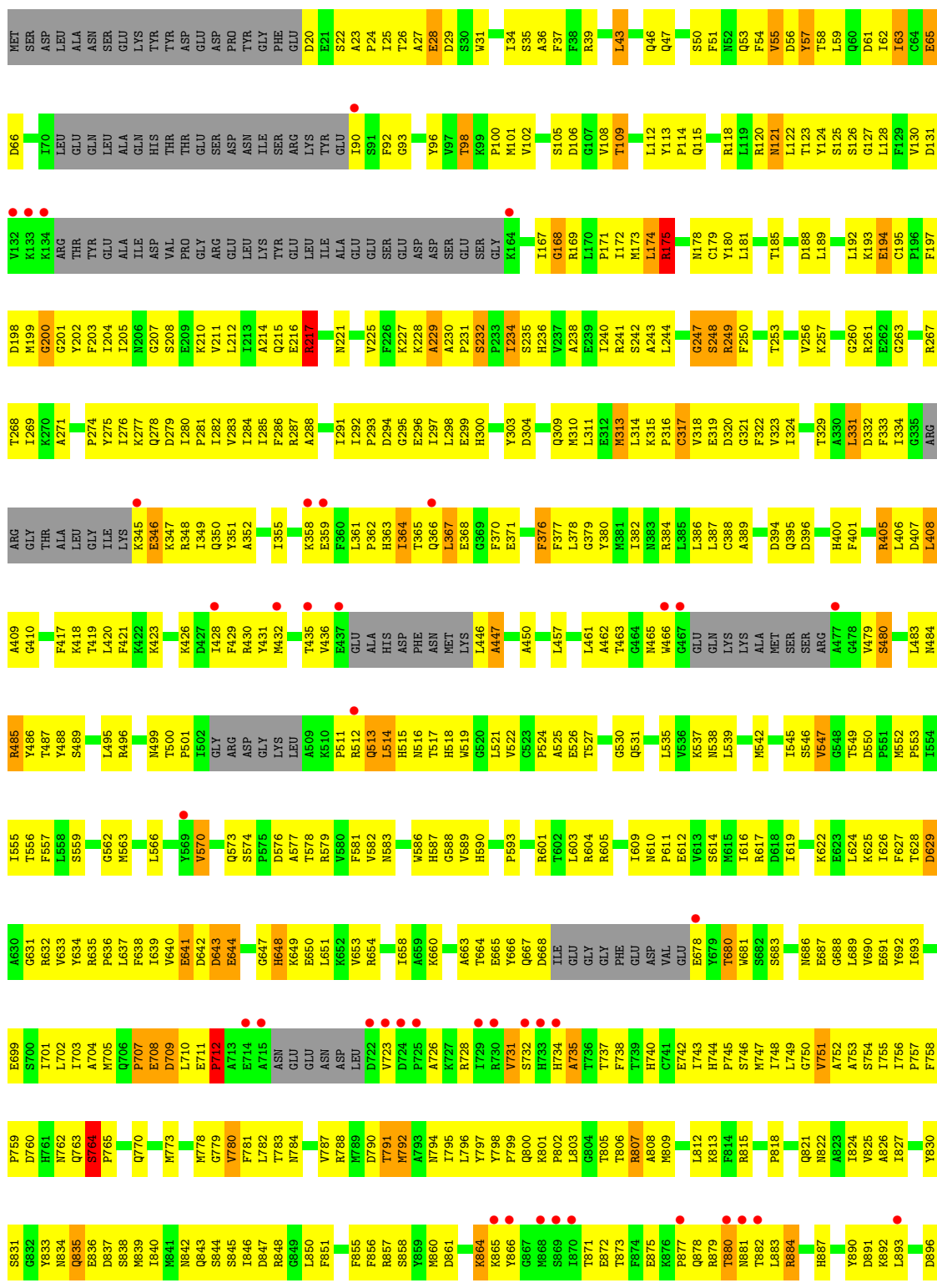
3 Residue-property plots

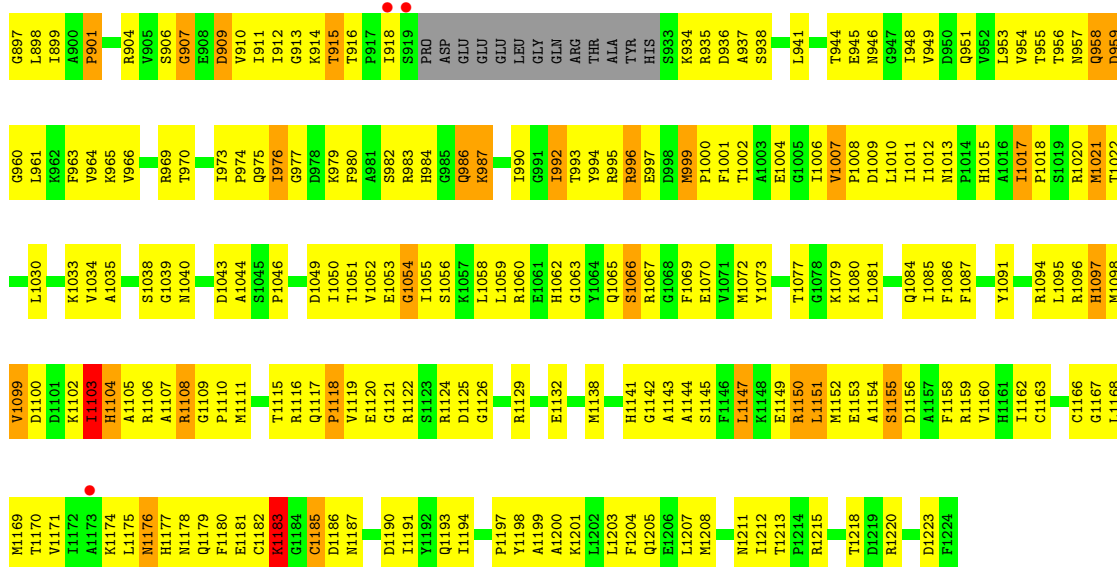
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

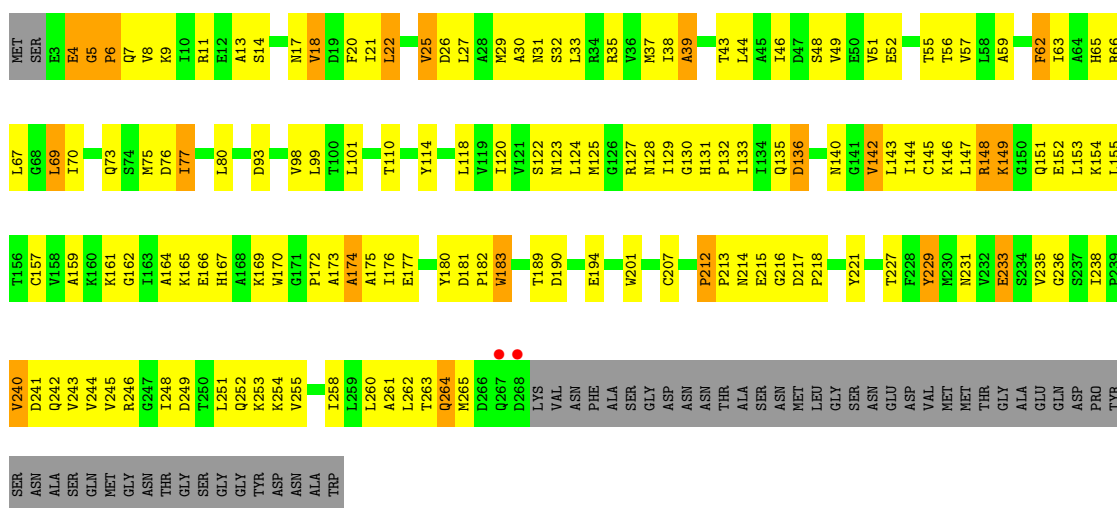


● Molecule 2: DNA-directed RNA polymerase II 140 kDa polypeptide

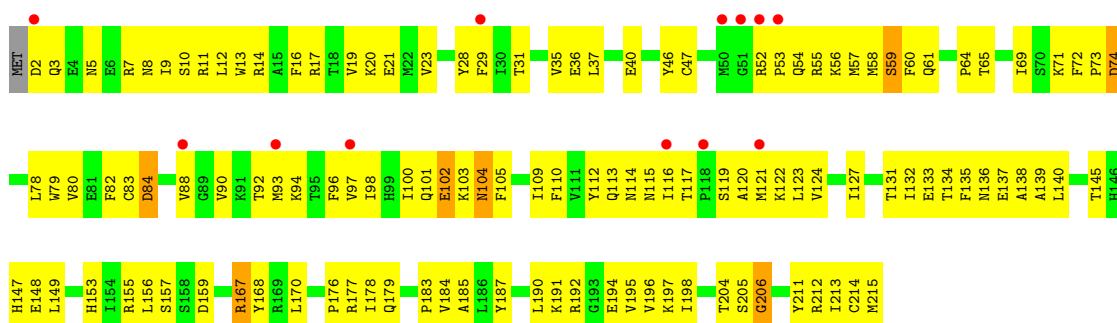




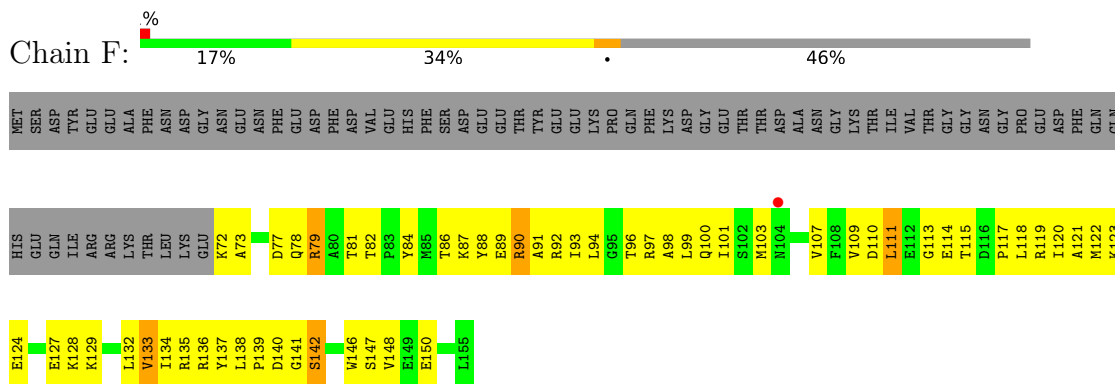
• Molecule 3: DNA-directed RNA polymerase II 45 kDa polypeptide



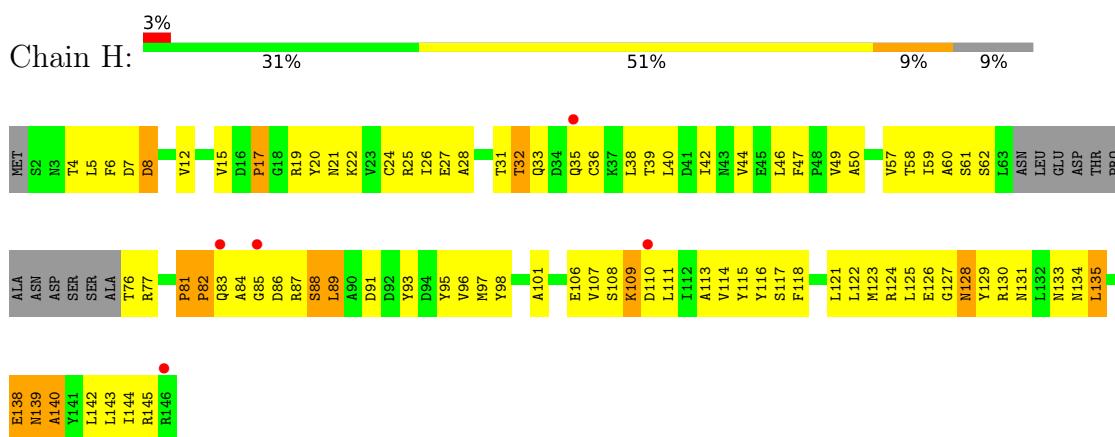
• Molecule 4: DNA-directed RNA polymerases I, II, and III 27 kDa polypeptide



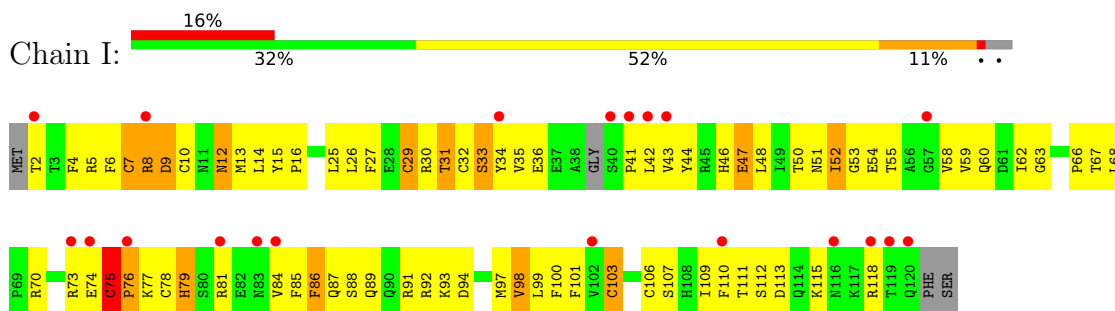
- Molecule 5: DNA-directed RNA polymerases I, II, and III 23 kDa polypeptide



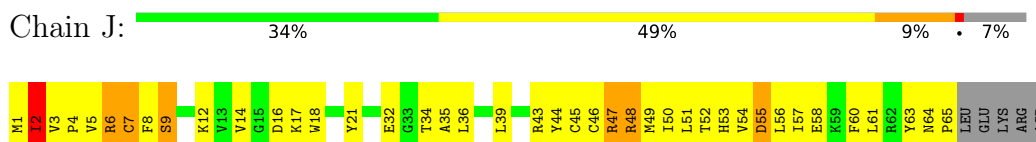
- Molecule 6: DNA-directed RNA polymerases I, II, and III 14.5 kDa polypeptide



- Molecule 7: DNA-directed RNA polymerase II 14.2 kDa polypeptide

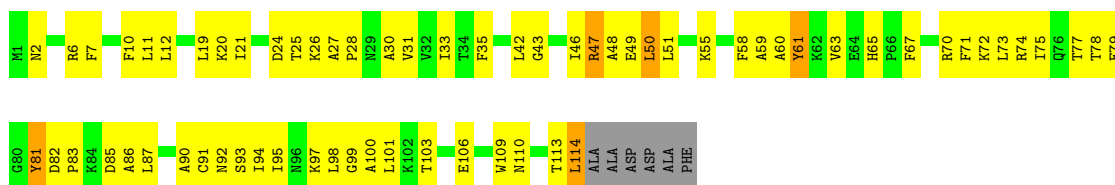


- Molecule 8: DNA-directed RNA polymerases I, II, and III 8.3 kDa polypeptide

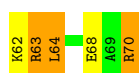
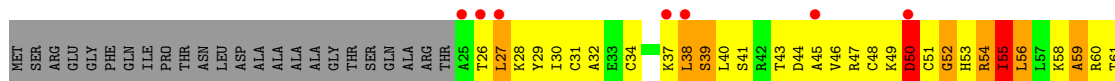


- Molecule 9: DNA-directed RNA polymerase II 13.6 kDa polypeptide

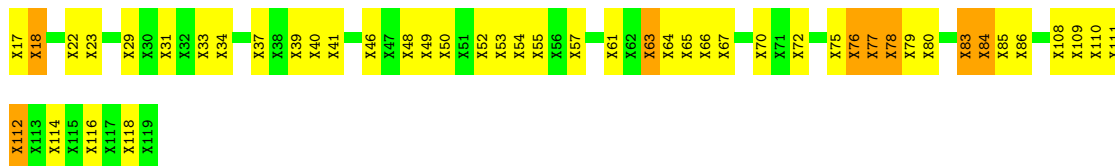




- Molecule 10: DNA-directed RNA polymerases I, II, and III 7.7 kDa polypeptide



- Molecule 11: TRANSCRIPTION FACTOR II B (TFIIB)



4 Data and refinement statistics i

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	212.44Å 217.18Å 422.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 4.50 51.23 – 4.50	Depositor EDS
% Data completeness (in resolution range)	98.6 (50.00-4.50) 99.2 (51.23-4.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.01 (at 4.46Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.345 , 0.373 0.305 , 0.323	Depositor DCC
R_{free} test set	3333 reflections (3.00%)	wwPDB-VP
Wilson B-factor (Å ²)	124.1	Xtrriage
Anisotropy	1.220	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 177.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.000 for k,h,-l	Xtrriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	28300	wwPDB-VP
Average B, all atoms (Å ²)	189.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.11% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 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	0.48	3/11040 (0.0%)	0.73	15/14922 (0.1%)
2	B	0.49	2/8891 (0.0%)	0.72	3/11990 (0.0%)
3	C	0.48	0/2133	0.76	2/2891 (0.1%)
4	E	0.36	0/1788	0.65	0/2406
5	F	0.40	0/691	0.64	0/933
6	H	0.40	0/1086	0.73	0/1470
7	I	0.48	0/984	0.76	1/1323 (0.1%)
8	J	0.53	0/541	0.78	0/727
9	K	0.46	0/937	0.68	0/1265
10	L	0.49	0/366	0.78	0/485
All	All	0.47	5/28457 (0.0%)	0.73	21/38412 (0.1%)

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
2	B	0	2
11	M	0	33
All	All	0	35

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1274	ARG	C-N	21.02	1.70	1.33
2	B	217	ARG	C-N	-14.21	1.01	1.34
1	A	1141	THR	C-N	10.82	1.58	1.34
2	B	1150	ARG	C-N	9.61	1.56	1.34
1	A	346	ASP	C-N	8.96	1.54	1.34

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1141	THR	O-C-N	-12.22	103.15	122.70
1	A	1274	ARG	O-C-N	-8.93	108.02	123.20
2	B	217	ARG	O-C-N	-8.89	108.48	122.70
1	A	1141	THR	CA-C-N	8.53	135.97	117.20
1	A	1141	THR	C-N-CA	8.49	142.94	121.70

There are no chirality outliers.

5 of 35 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	217	ARG	Mainchain
2	B	405	ARG	Mainchain
11	M	18	UNK	Peptide,Mainchain
11	M	29	UNK	Mainchain
11	M	54	UNK	Mainchain

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	A	10850	0	10952	1129	3
2	B	8721	0	8747	936	1
3	C	2095	0	2052	164	0
4	E	1752	0	1776	129	1
5	F	679	0	701	63	0
6	H	1068	0	1040	129	0
7	I	967	0	929	140	2
8	J	532	0	544	77	0
9	K	919	0	929	87	0
10	L	364	0	388	54	0
11	M	343	0	19	34	0
12	A	2	0	0	0	0
12	B	1	0	0	0	0
12	C	1	0	0	0	0
12	I	2	0	0	2	0
12	J	1	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	L	1	0	0	0	0
12	M	1	0	0	0	0
13	A	1	0	0	0	0
All	All	28300	0	28077	2624	4

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 47.

The worst 5 of 2624 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)
1:A:783:THR:HG21	1:A:815:PHE:CZ	1.39	1.57
1:A:783:THR:CG2	1:A:815:PHE:CZ	2.00	1.43
1:A:1274:ARG:C	1:A:1275:GLY:N	1.70	1.42
1:A:1147:THR:O	7:I:48:LEU:CD1	1.77	1.33
1:A:1151:GLU:CG	7:I:44:TYR:O	1.79	1.31

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:903:ASN:OD1	7:I:33:SER:OG[7_554]	1.06	1.14
2:B:1223:ASP:O	2:B:1223:ASP:CB[2_565]	1.71	0.49
1:A:903:ASN:OD1	7:I:33:SER:CB[7_554]	2.14	0.06
1:A:163:SER:OG	4:E:74:ASP:OD1[2_565]	2.19	0.01

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	1362/1733 (79%)	1020 (75%)	252 (18%)	90 (7%)	1 18

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	1077/1224 (88%)	836 (78%)	172 (16%)	69 (6%)	1	19
3	C	264/318 (83%)	208 (79%)	40 (15%)	16 (6%)	1	19
4	E	212/215 (99%)	170 (80%)	33 (16%)	9 (4%)	3	25
5	F	82/155 (53%)	64 (78%)	15 (18%)	3 (4%)	3	28
6	H	129/146 (88%)	93 (72%)	21 (16%)	15 (12%)	0	6
7	I	114/122 (93%)	90 (79%)	15 (13%)	9 (8%)	1	14
8	J	63/70 (90%)	48 (76%)	11 (18%)	4 (6%)	1	19
9	K	112/120 (93%)	96 (86%)	16 (14%)	0	100	100
10	L	44/70 (63%)	22 (50%)	12 (27%)	10 (23%)	0	1
All	All	3459/4173 (83%)	2647 (76%)	587 (17%)	225 (6%)	1	18

5 of 225 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	31	SER
1	A	48	ALA
1	A	55	ASP
1	A	56	PRO
1	A	74	MET

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	
1	A	1205/1520 (79%)	1128 (94%)	77 (6%)	17	44
2	B	952/1061 (90%)	886 (93%)	66 (7%)	15	42
3	C	234/274 (85%)	222 (95%)	12 (5%)	24	50
4	E	196/197 (100%)	189 (96%)	7 (4%)	35	60
5	F	74/137 (54%)	68 (92%)	6 (8%)	11	37
6	H	117/128 (91%)	112 (96%)	5 (4%)	29	55
7	I	113/116 (97%)	104 (92%)	9 (8%)	12	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	J	60/65 (92%)	56 (93%)	4 (7%)	16	43
9	K	99/102 (97%)	90 (91%)	9 (9%)	9	32
10	L	40/57 (70%)	35 (88%)	5 (12%)	4	21
All	All	3090/3657 (84%)	2890 (94%)	200 (6%)	17	44

5 of 200 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	762	ASN
3	C	22	LEU
10	L	70	ARG
2	B	835	GLN
2	B	999	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 75 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	112	ASN
9	K	52	ASN
3	C	167	HIS
4	E	104	ASN
1	A	969	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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 10 ligands modelled in this entry, 10 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
11	M	12
1	A	1
2	B	1

The worst 5 of 14 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	M	88:UNK	C	106:UNK	N	28.95
1	A	1274:ARG	C	1275:GLY	N	1.70
1	M	75:UNK	C	76:UNK	N	1.17
1	M	84:UNK	C	85:UNK	N	1.16
1	M	72:UNK	C	73:UNK	N	1.13

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	A	1380/1733 (79%)	0.02	36 (2%) 56 46	47, 179, 269, 300	0
2	B	1097/1224 (89%)	0.09	43 (3%) 39 31	26, 192, 280, 300	0
3	C	266/318 (83%)	-0.07	2 (0%) 86 79	45, 168, 245, 293	0
4	E	214/215 (99%)	0.12	12 (5%) 24 21	76, 206, 284, 300	0
5	F	84/155 (54%)	0.02	1 (1%) 79 70	61, 160, 231, 277	0
6	H	133/146 (91%)	0.36	5 (3%) 40 32	119, 207, 300, 300	0
7	I	118/122 (96%)	0.86	20 (16%) 1 2	133, 246, 300, 300	0
8	J	65/70 (92%)	-0.07	0 100 100	76, 169, 230, 270	0
9	K	114/120 (95%)	-0.14	0 100 100	72, 155, 241, 274	0
10	L	46/70 (65%)	0.68	7 (15%) 2 3	129, 222, 288, 300	0
11	M	0/86	-	-	-	-
All	All	3517/4259 (82%)	0.08	126 (3%) 42 35	26, 186, 278, 300	0

The worst 5 of 126 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	919	SER	8.5
10	L	26	THR	8.0
2	B	881	ASN	6.8
10	L	25	ALA	6.8
7	I	41	PRO	6.3

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
12	ZN	M	209	1/1	0.36	0.27	156,156,156,156	0
12	ZN	I	203	1/1	0.44	0.64	166,166,166,166	0
12	ZN	I	204	1/1	0.84	0.10	166,166,166,166	0
13	MG	A	1736	1/1	0.88	0.40	47,47,47,47	0
12	ZN	A	1735	1/1	0.89	0.11	166,166,166,166	0
12	ZN	A	1734	1/1	0.92	0.12	166,166,166,166	0
12	ZN	B	1307	1/1	0.93	0.14	166,166,166,166	0
12	ZN	L	105	1/1	0.95	0.11	175,175,175,175	0
12	ZN	C	319	1/1	0.97	0.15	166,166,166,166	0
12	ZN	J	101	1/1	0.99	0.13	166,166,166,166	0

6.5 Other polymers [i](#)

There are no such residues in this entry.