



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 18, 2026 – 11:05 AM UTC

PDB ID : 1K83 / pdb_00001k83
Title : Crystal Structure of Yeast RNA Polymerase II Complexed with the Inhibitor Alpha Amanitin
Authors : Bushnell, D.A.; Cramer, P.; Kornberg, R.D.
Deposited on : 2001-10-22
Resolution : 2.80 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
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

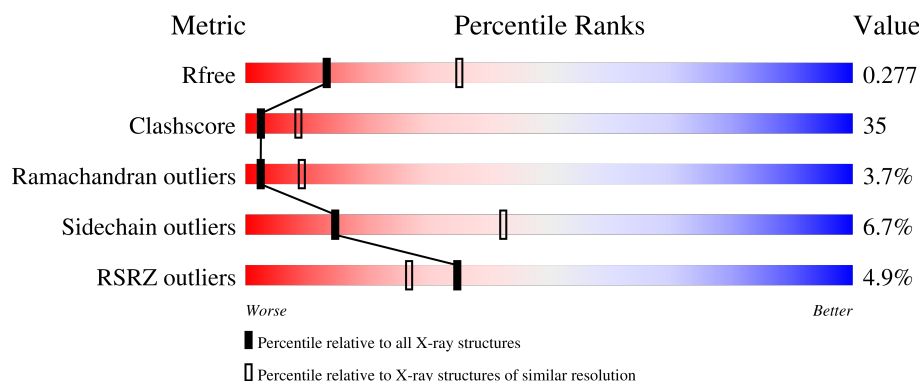
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	3% 37% 34% 7% 21%
2	B	1224	4% 45% 38% 5% 12%
3	C	318	0% 34% 42% 7% 16%
4	E	215	2% 52% 41% 6%
5	F	155	0% 23% 28% 46%

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Mol	Chain	Length	Quality of chain
6	H	146	18%27%49%13%•9%
7	I	122	5%42%51%7%
8	J	70	%46%43%••7%
9	K	120	%42%44%8%•5%
10	L	70	17%13%37%14%36%
11	M	8	25%12%50%38%

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 27902 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 SUB-UNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1366	Total	C	N	O	S	0	0	0
			10751	6785	1871	2036	59			

- Molecule 2 is a protein called DNA-DIRECTED RNA POLYMERASE II 140KD POLYPEPTIDE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	1082	Total	C	N	O	S	0	0	0
			8616	5467	1503	1594	52			

- Molecule 3 is a protein called DNA-DIRECTED RNA POLYMERASE II 45KD POLYPEPTIDE.

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 27KD POLYPEPTIDE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	213	Total	C	N	O	S	0	0	0
			1744	1107	308	318	11			

- Molecule 5 is a protein called DNA-DIRECTED RNA POLYMERASE II 23KD POLYPEPTIDE.

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

- Molecule 6 is a protein called DNA-DIRECTED RNA POLYMERASE II 14.5KD POLYPEPTIDE.

TIDE.

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

- Molecule 7 is a protein called DNA-DIRECTED RNA POLYMERASE II 14.2KD POLYPEPTIDE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	I	122	Total	C	N	O	S	0	0	0
			997	613	182	191	11			

- Molecule 8 is a protein called DNA-DIRECTED RNA POLYMERASE II 8.3KD POLYPEPTIDE.

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

- Molecule 9 is a protein called DNA-DIRECTED RNA POLYMERASE II 13.6KD POLYPEPTIDE.

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

- Molecule 10 is a protein called DNA-DIRECTED RNA POLYMERASE II 7.7KD POLYPEPTIDE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	L	45	Total	C	N	O	S	0	0	0
			359	221	71	63	4			

- Molecule 11 is a protein called ALPHA AMANITIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	M	8	Total	C	N	O	S	0	0	0
			64	39	10	14	1			

- Molecule 12 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 13 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

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

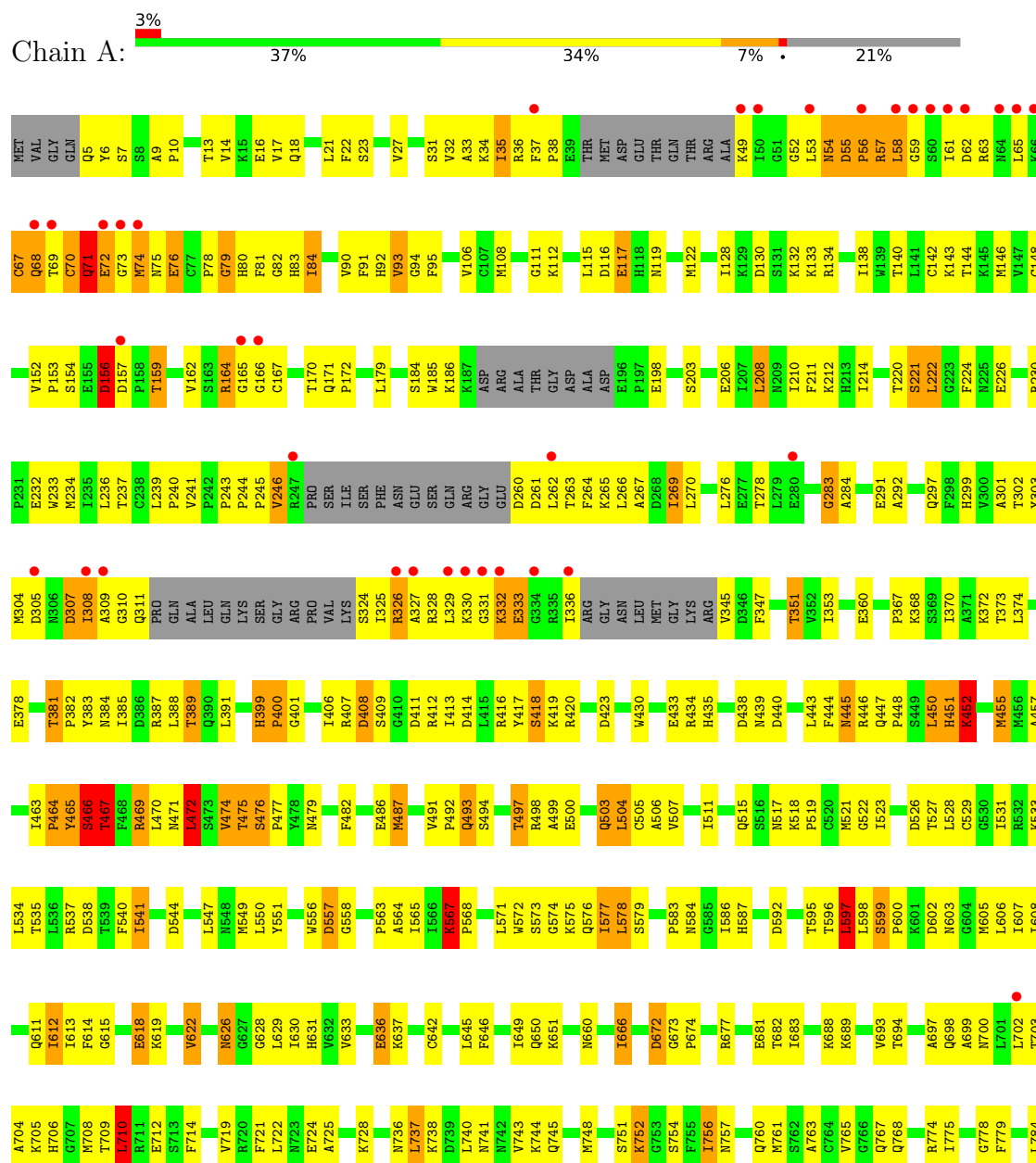
- Molecule 14 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	A	31	Total 31	O 31	0	0
14	B	23	Total 23	O 23	0	0
14	C	3	Total 3	O 3	0	0
14	E	6	Total 6	O 6	0	0
14	F	4	Total 4	O 4	0	0
14	J	1	Total 1	O 1	0	0
14	M	1	Total 1	O 1	0	0

3 Residue-property plots

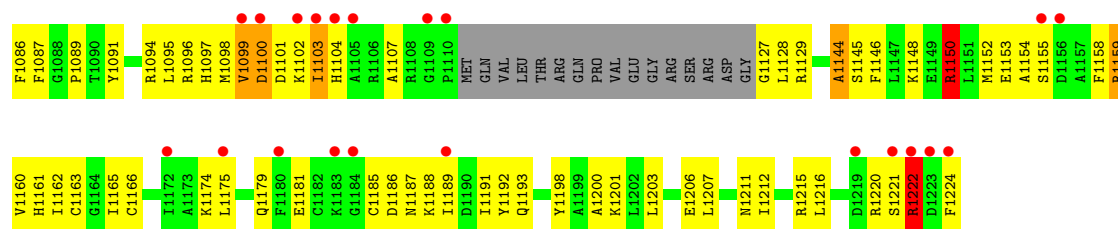
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

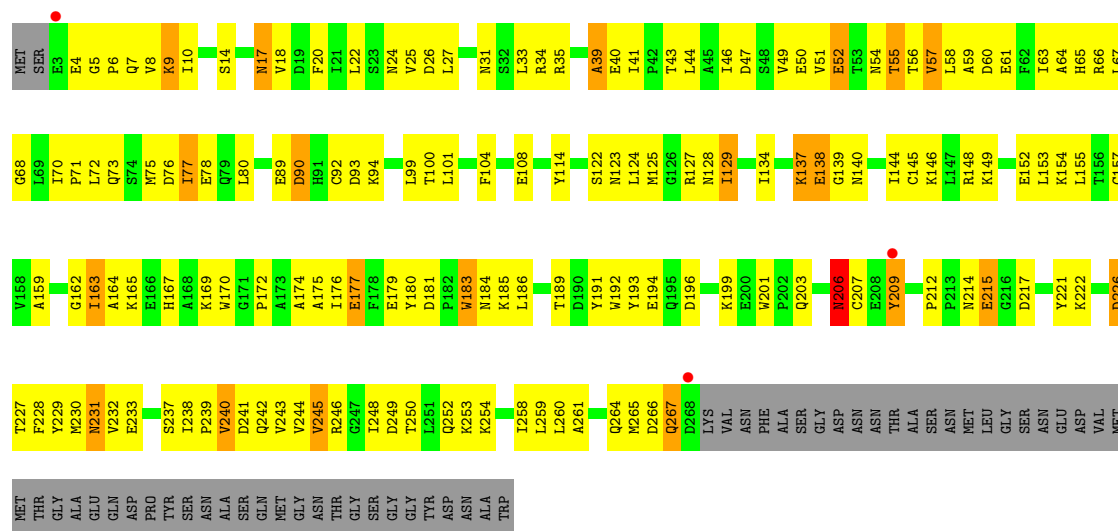




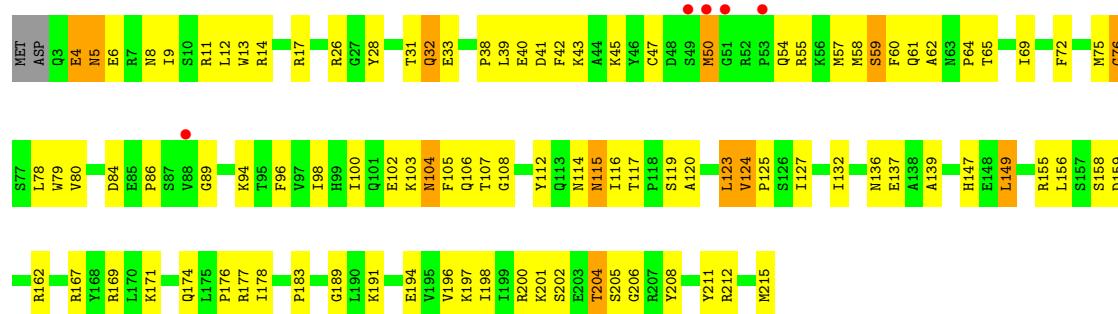




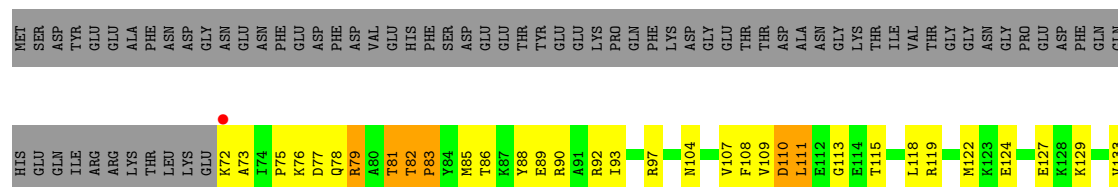
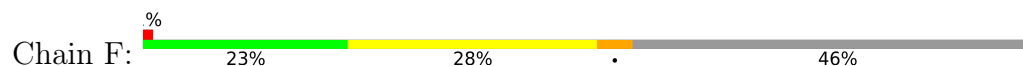
● Molecule 3: DNA-DIRECTED RNA POLYMERASE II 45KD POLYPEPTIDE

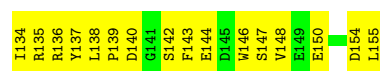


● Molecule 4: DNA-DIRECTED RNA POLYMERASE II 27KD POLYPEPTIDE

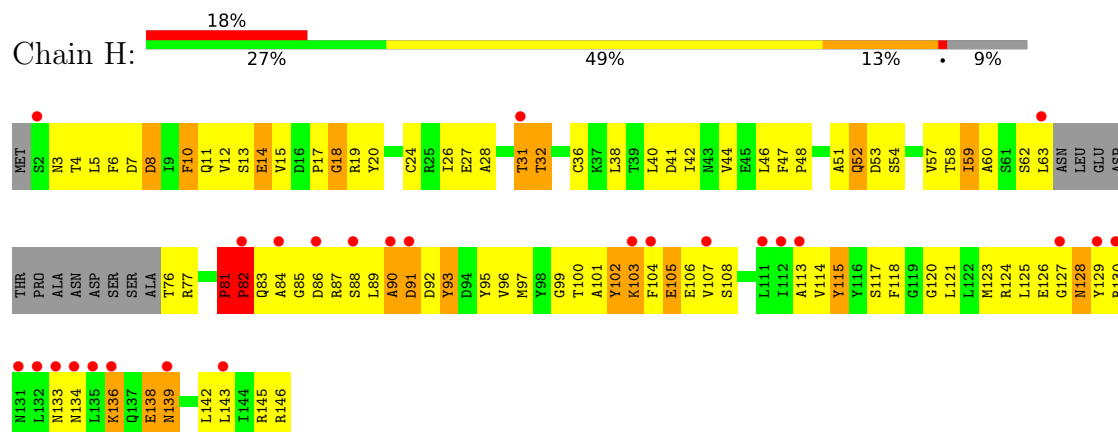


● Molecule 5: DNA-DIRECTED RNA POLYMERASE II 23KD POLYPEPTIDE

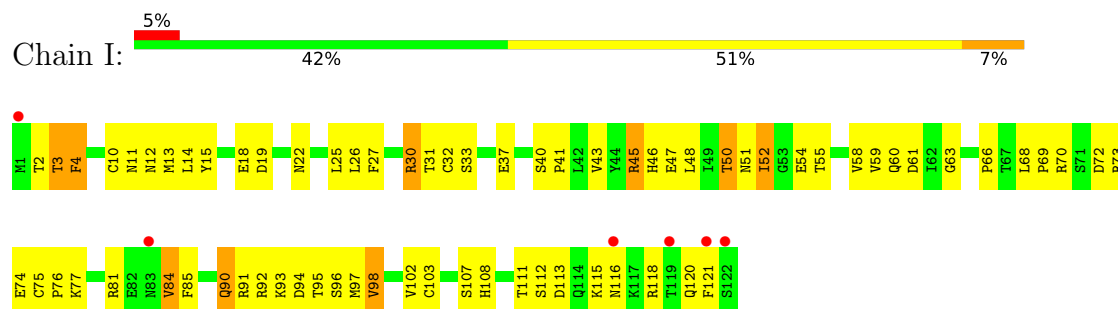




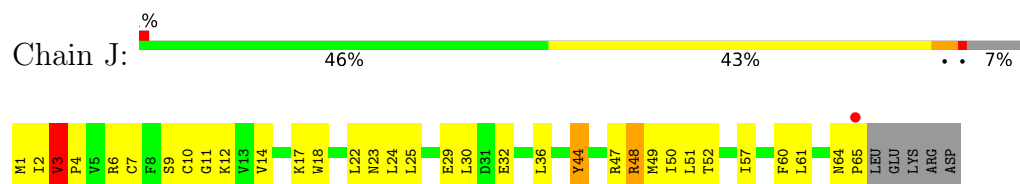
● Molecule 6: DNA-DIRECTED RNA POLYMERASE II 14.5KD POLYPEPTIDE



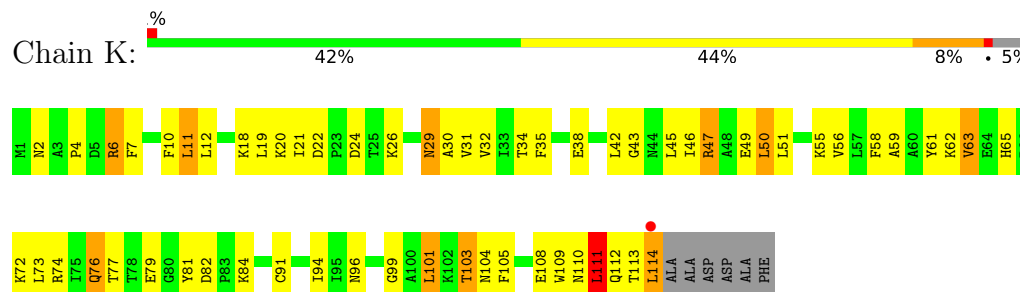
● Molecule 7: DNA-DIRECTED RNA POLYMERASE II 14.2KD POLYPEPTIDE



● Molecule 8: DNA-DIRECTED RNA POLYMERASE II 8.3KD POLYPEPTIDE

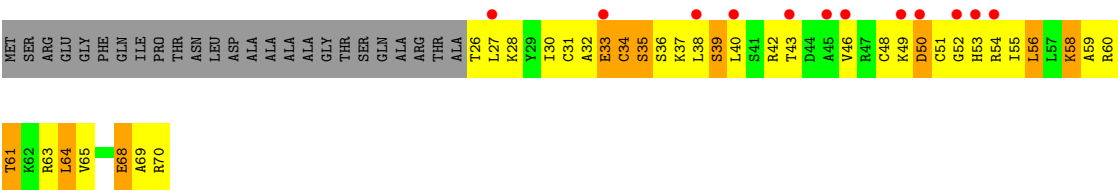


● Molecule 9: DNA-DIRECTED RNA POLYMERASE II 13.6KD POLYPEPTIDE

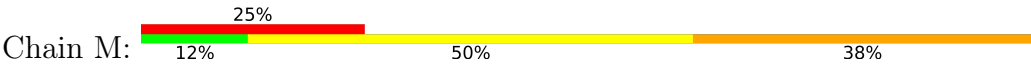


● Molecule 10: DNA-DIRECTED RNA POLYMERASE II 7.7KD POLYPEPTIDE





● Molecule 11: ALPHA AMANITIN



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	122.51Å 222.48Å 374.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.80 20.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-2.80) 92.7 (20.00-2.80)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.42 (at 2.79Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.229 , 0.280 0.227 , 0.277	Depositor DCC
R_{free} test set	3507 reflections (2.80%)	wwPDB-VP
Wilson B-factor (Å ²)	50.5	Xtriage
Anisotropy	0.352	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 41.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	27902	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.93% 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: TRX, MN, ZN, HYP, ILX, CSX

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	0.54	1/10940 (0.0%)	1.05	57/14792 (0.4%)
2	B	0.53	0/8786	1.02	47/11847 (0.4%)
3	C	0.50	0/2133	1.03	7/2891 (0.2%)
4	E	0.49	0/1780	1.00	5/2395 (0.2%)
5	F	0.56	0/691	1.05	1/933 (0.1%)
6	H	0.42	0/1086	1.04	11/1470 (0.7%)
7	I	0.52	0/1016	1.03	5/1365 (0.4%)
8	J	0.51	0/541	1.05	4/727 (0.6%)
9	K	0.45	0/937	0.88	0/1265
10	L	0.49	0/361	0.99	2/478 (0.4%)
11	M	3.44	3/22 (13.6%)	2.31	1/26 (3.8%)
All	All	0.53	4/28293 (0.0%)	1.03	140/38189 (0.4%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	M	4	ILE	CA-C	9.28	1.62	1.52
11	M	7	ASN	CA-C	6.51	1.66	1.52
1	A	487	MET	SD-CE	-6.30	1.63	1.79
11	M	4	ILE	C-O	6.20	1.31	1.24

The worst 5 of 140 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	333	GLU	N-CA-C	-10.85	100.59	114.04
1	A	827	THR	N-CA-C	-10.25	99.31	112.23
1	A	1155	ASP	CA-C-N	9.81	129.17	118.97
1	A	1155	ASP	C-N-CA	9.81	129.17	118.97
6	H	31	THR	N-CA-C	-8.92	98.75	110.53

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	10751	0	10819	796	0
2	B	8616	0	8645	605	0
3	C	2095	0	2051	178	0
4	E	1744	0	1772	96	0
5	F	679	0	701	60	0
6	H	1068	0	1040	119	0
7	I	997	0	953	83	0
8	J	532	0	542	60	0
9	K	919	0	929	70	0
10	L	359	0	382	65	1
11	M	64	0	51	7	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	0	0
12	J	1	0	0	0	0
12	L	1	0	0	0	0
13	A	1	0	0	0	0
14	A	31	0	0	1	0
14	B	23	0	0	5	0
14	C	3	0	0	0	0
14	E	6	0	0	1	0
14	F	4	0	0	0	0
14	J	1	0	0	0	0
14	M	1	0	0	0	0
All	All	27902	0	27885	1926	1

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 35.

The worst 5 of 1926 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:1161:THR:HG22	1:A:1163:ILE:H	1.09	1.15
1:A:974:ASP:HB2	6:H:136:LYS:HZ3	1.15	1.12
1:A:470:LEU:HD11	1:A:487:MET:HE1	1.21	1.10
2:B:1051:THR:HG22	2:B:1053:GLU:H	1.17	1.09
2:B:871:THR:HG22	2:B:872:GLU:H	1.09	1.09

All (1) 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)
10:L:28:LYS:NZ	10:L:28:LYS:NZ[3_655]	2.05	0.15

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	1348/1733 (78%)	1160 (86%)	134 (10%)	54 (4%)	2	8
2	B	1062/1224 (87%)	931 (88%)	107 (10%)	24 (2%)	5	18
3	C	264/318 (83%)	223 (84%)	30 (11%)	11 (4%)	2	7
4	E	211/215 (98%)	180 (85%)	23 (11%)	8 (4%)	2	9
5	F	82/155 (53%)	71 (87%)	10 (12%)	1 (1%)	10	34
6	H	129/146 (88%)	88 (68%)	23 (18%)	18 (14%)	0	0
7	I	120/122 (98%)	102 (85%)	16 (13%)	2 (2%)	7	25
8	J	63/70 (90%)	58 (92%)	5 (8%)	0	100	100
9	K	112/120 (93%)	98 (88%)	13 (12%)	1 (1%)	14	41
10	L	43/70 (61%)	23 (54%)	13 (30%)	7 (16%)	0	0
11	M	4/8 (50%)	4 (100%)	0	0	100	100
All	All	3438/4181 (82%)	2938 (86%)	374 (11%)	126 (4%)	2	9

5 of 126 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	55	ASP
1	A	56	PRO
1	A	399	HIS
1	A	464	PRO
1	A	465	TYR

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	1196/1520 (79%)	1100 (92%)	96 (8%)	11	34
2	B	940/1061 (89%)	885 (94%)	55 (6%)	18	48
3	C	234/274 (85%)	220 (94%)	14 (6%)	17	47
4	E	195/197 (99%)	190 (97%)	5 (3%)	40	75
5	F	74/137 (54%)	68 (92%)	6 (8%)	11	33
6	H	117/128 (91%)	114 (97%)	3 (3%)	40	75
7	I	116/116 (100%)	110 (95%)	6 (5%)	21	53
8	J	60/65 (92%)	57 (95%)	3 (5%)	22	54
9	K	99/102 (97%)	86 (87%)	13 (13%)	4	14
10	L	40/57 (70%)	35 (88%)	5 (12%)	4	15
11	M	2/2 (100%)	2 (100%)	0	100	100
All	All	3073/3659 (84%)	2867 (93%)	206 (7%)	15	42

5 of 206 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	408	LEU
2	B	1007	VAL
9	K	111	LEU
2	B	487	THR
2	B	648	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 98 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	1025	HIS
3	C	123	ASN
2	B	1065	GLN
2	B	1193	GLN
3	C	203	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues are 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
11	CSX	M	6	11	3,6,7	2.95	2 (66%)	1,6,8	0.39	0
11	ILX	M	1	11	8,9,10	2.47	3 (37%)	8,11,13	2.10	3 (37%)
11	TRX	M	2	11	15,16,17	3.22	10 (66%)	17,22,24	1.41	4 (23%)
11	HYP	M	8	11	7,8,9	2.73	1 (14%)	5,10,12	1.63	1 (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
11	CSX	M	6	11	-	2/2/5/7	-
11	ILX	M	1	11	-	1/11/12/14	-
11	TRX	M	2	11	-	2/5/6/8	0/2/2/2
11	HYP	M	8	11	-	0/0/11/13	0/1/1/1

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	M	8	HYP	CA-N	6.82	1.60	1.48
11	M	2	TRX	CZ2-CE2	6.13	1.49	1.39
11	M	2	TRX	CZ2-CH2	5.65	1.47	1.39
11	M	1	ILX	CB-CA	5.08	1.60	1.54
11	M	2	TRX	CD1-CG	4.36	1.43	1.36

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	M	1	ILX	CB-CA-C	-3.55	108.02	112.87
11	M	1	ILX	CG2-CB-CG1	-3.37	105.72	111.09
11	M	2	TRX	OH2-CH2-CZ3	-2.94	111.82	120.00
11	M	8	HYP	CG-CB-CA	2.82	107.01	103.75
11	M	2	TRX	OH2-CH2-CZ2	2.79	127.15	119.85

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	M	6	CSX	N-CA-CB-SG
11	M	6	CSX	C-CA-CB-SG
11	M	2	TRX	CA-CB-CG-CD2
11	M	1	ILX	C-CA-CB-CG2
11	M	2	TRX	CA-CB-CG-CD1

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	M	1	ILX	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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.

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	1366/1733 (78%)	0.04	59 (4%) 40 31	18, 48, 107, 137	0
2	B	1082/1224 (88%)	0.03	54 (4%) 34 26	20, 46, 105, 128	0
3	C	266/318 (83%)	0.11	3 (1%) 78 70	30, 53, 83, 124	0
4	E	213/215 (99%)	0.15	5 (2%) 61 51	22, 59, 99, 109	0
5	F	84/155 (54%)	-0.25	1 (1%) 76 68	24, 44, 67, 82	0
6	H	133/146 (91%)	1.29	26 (19%) 3 2	64, 94, 122, 125	0
7	I	122/122 (100%)	0.15	6 (4%) 35 27	30, 51, 89, 106	0
8	J	65/70 (92%)	-0.19	1 (1%) 72 63	26, 47, 76, 85	0
9	K	114/120 (95%)	0.08	1 (0%) 81 74	31, 60, 79, 97	0
10	L	45/70 (64%)	1.21	12 (26%) 1 1	49, 86, 108, 110	0
11	M	4/8 (50%)	1.58	2 (50%) 0 0	73, 80, 83, 84	0
All	All	3494/4181 (83%)	0.11	170 (4%) 35 27	18, 50, 105, 137	0

The worst 5 of 170 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
6	H	104	PHE	6.0
1	A	69	THR	5.8
1	A	61	ILE	5.6
1	A	68	GLN	5.3
2	B	882	THR	5.1

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($\text{\AA}^2$)	Q<0.9
11	CSX	M	6	7/8	0.71	0.15	80,82,84,86	0
11	ILX	M	1	10/11	0.82	0.23	72,74,79,80	0
11	TRX	M	2	15/16	0.90	0.15	75,77,79,80	0
11	HYP	M	8	8/9	0.91	0.12	70,72,72,73	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($\text{\AA}^2$)	Q<0.9
13	MN	A	3009	1/1	0.87	0.14	149,149,149,149	0
12	ZN	L	3005	1/1	0.96	0.04	86,86,86,86	0
12	ZN	A	3008	1/1	0.97	0.04	81,81,81,81	0
12	ZN	I	3004	1/1	0.97	0.04	62,62,62,62	0
12	ZN	B	3007	1/1	0.98	0.04	64,64,64,64	0
12	ZN	J	3001	1/1	0.99	0.03	46,46,46,46	0
12	ZN	C	3002	1/1	0.99	0.02	49,49,49,49	0
12	ZN	A	3006	1/1	0.99	0.04	64,64,64,64	0
12	ZN	I	3003	1/1	1.00	0.03	45,45,45,45	0

6.5 Other polymers [i](#)

There are no such residues in this entry.