



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 11:05 AM UTC

PDB ID : 4A93 / pdb\_00004a93  
Title : RNA Polymerase II elongation complex containing a CPD Lesion  
Authors : Walmacq, C.; Cheung, A.C.M.; Kireeva, M.L.; Lubkowska, L.; Ye, C.; Gotte, D.; Strathern, J.N.; Carell, T.; Cramer, P.; Kashlev, M.  
Deposited on : 2011-11-23  
Resolution : 3.40 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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

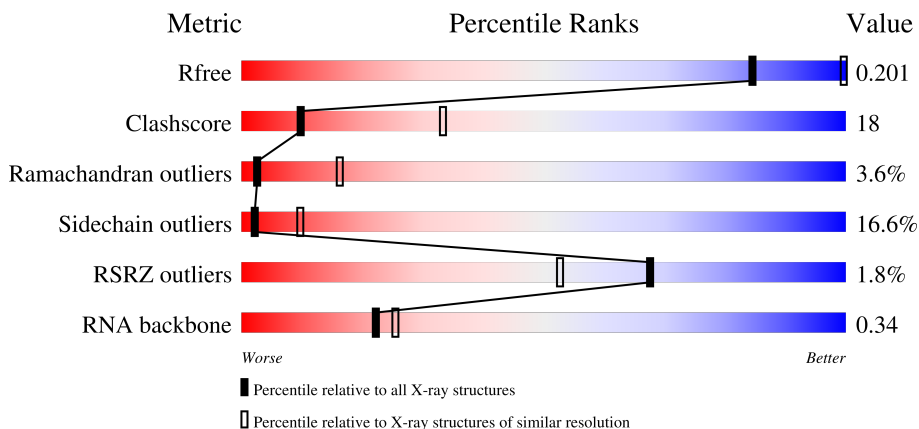
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.40 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.






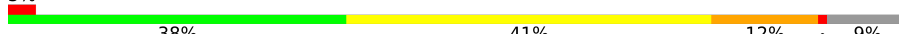

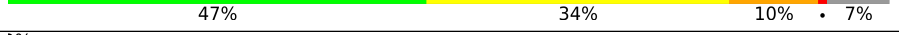
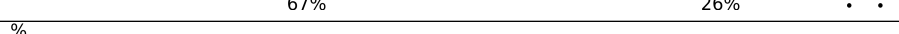
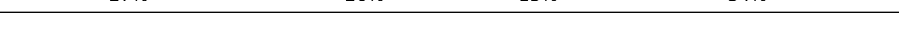

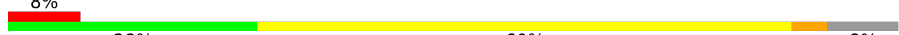

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	1001 (3.44-3.36)
Clashscore	190562	1022 (3.44-3.36)
Ramachandran outliers	187476	1012 (3.44-3.36)
Sidechain outliers	187428	1012 (3.44-3.36)
RSRZ outliers	180081	1001 (3.44-3.36)
RNA backbone	3983	1157 (3.80-3.00)

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 of 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	1732	 44% 29% 8% 18%
2	B	1224	 49% 33% 8% 9%
3	C	318	 47% 31% 6% 16%
4	D	221	 40% 27% 11% 19%

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Mol	Chain	Length	Quality of chain
5	E	215	
6	F	155	
7	G	171	
8	H	146	
9	I	122	
10	J	70	
11	K	120	
12	L	70	
13	N	14	
14	P	12	
15	T	25	

## 2 Entry composition [i](#)

There are 17 unique types of molecules in this entry. The entry contains 32105 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
			Total	C	N	O	S			
1	A	1422	11174	7037	1954	2121	62	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	1113	8839	5597	1548	1639	55	0	0	0

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

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 POLYMERASE II SUBUNIT RPB4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	178	1434	887	257	288	2	0	0	0

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

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

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

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

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

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

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

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

- Molecule 9 is a protein called DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
9	I	119	971	596	179	186	10	0	0	0

- Molecule 10 is a protein called DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 5.

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

- Molecule 11 is a protein called DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB11.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
12	L	46	363	224	72	63	4	0	0	0

- Molecule 13 is a DNA chain called 5'-D(\*TP\*AP\*AP\*GP\*TP\*AP\*CP\*TP\*TP\*GP\*AP\*GP\*CP\*TP)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
13	N	12	247	118	44	73	12	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
14	P	9	197	88	41	59	9	0	0	0

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

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	Br	C	N	O	P			
15	T	23	485	1	234	81	146	23	0	0	0

- Molecule 16 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 17 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

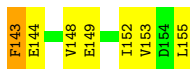
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	A	1	Total	Mg	0	0
			1	1		





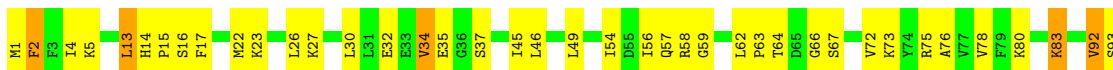






- Molecule 7: RPB7, DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB7

Chain G: 58% 36% 5%



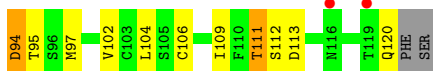
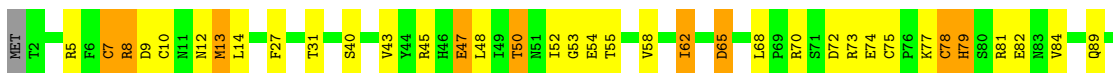
- Molecule 8: DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 3

Chain H: 3% 38% 41% 12% 9%



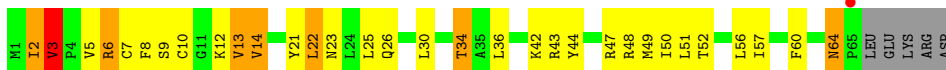
- Molecule 9: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB9

Chain I: 2% 59% 30% 9%



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

Chain J: % 47% 34% 10% 7%

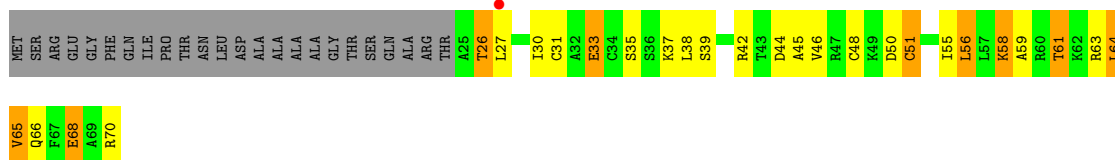
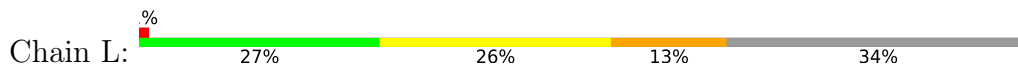


- Molecule 11: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB11

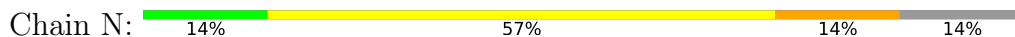
Chain K: 2% 67% 26%



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



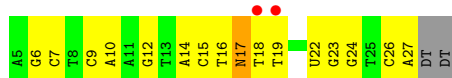
- Molecule 13: 5'-D(\*TP\*AP\*AP\*GP\*TP\*AP\*CP\*TP\*TP\*GP\*AP\*GP\*CP\*TP)-3'



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



- Molecule 15: 5'-D(\*AP\*GP\*CP\*TP\*CP\*AP\*AP\*GP\*TP\*AP\*CP\*T\*TTP\*TP\*TP\*CP\*C B RUP\*GP\*GP\*TP\*CP\*AP\*TP\*T)-3'



## 4 Data and refinement statistics i

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	221.64Å 391.52Å 281.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	54.09 – 3.40 54.09 – 3.40	Depositor EDS
% Data completeness (in resolution range)	100.0 (54.09-3.40) 99.9 (54.09-3.40)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.25 (at 3.40Å)	Xtrriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.165 , 0.199 0.172 , 0.201	Depositor DCC
$R_{free}$ test set	3298 reflections (1.97%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	103.5	Xtrriage
Anisotropy	0.405	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 109.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	0.025 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.029 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	32105	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	117.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.85% 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 i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: TT, MG, BRU, 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	0.67	1/11374 (0.0%)	1.10	42/15383 (0.3%)
2	B	0.62	0/9010	1.06	48/12149 (0.4%)
3	C	0.61	0/2133	1.03	8/2891 (0.3%)
4	D	0.79	3/1444 (0.2%)	1.11	7/1935 (0.4%)
5	E	0.51	0/1788	0.99	5/2406 (0.2%)
6	F	0.82	1/691 (0.1%)	1.28	7/933 (0.8%)
7	G	0.64	0/1368	1.08	6/1844 (0.3%)
8	H	0.47	0/1086	0.97	4/1470 (0.3%)
9	I	0.51	0/989	1.03	8/1331 (0.6%)
10	J	0.67	0/541	1.16	3/727 (0.4%)
11	K	0.63	0/938	0.96	0/1267
12	L	0.68	0/365	1.12	1/485 (0.2%)
13	N	0.38	0/276	1.17	4/424 (0.9%)
14	P	0.48	0/221	0.74	1/343 (0.3%)
15	T	0.31	0/475	0.90	0/725
All	All	0.64	5/32699 (0.0%)	1.07	144/44313 (0.3%)

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	5
4	D	0	1
All	All	0	6

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	187	THR	CA-CB	13.01	1.75	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	187	THR	CB-CG2	9.31	1.83	1.52
4	D	25	ALA	CA-C	6.19	1.60	1.53
1	A	1051	ALA	CA-CB	-5.88	1.44	1.53
6	F	82	THR	CA-C	-5.29	1.47	1.53

The worst 5 of 144 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	26	THR	N-CA-C	-11.22	99.89	112.57
7	G	62	LEU	CA-C-N	-10.22	107.07	119.84
7	G	62	LEU	C-N-CA	-10.22	107.07	119.84
10	J	5	VAL	N-CA-C	-8.96	98.02	109.58
8	H	92	ASP	N-CA-C	-8.59	102.11	112.59

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	311	GLN	Peptide
1	A	34	LYS	Peptide
1	A	399	HIS	Peptide
1	A	55	ASP	Peptide
1	A	63	ARG	Peptide

## 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	11174	0	11233	450	0
2	B	8839	0	8876	309	0
3	C	2095	0	2051	76	0
4	D	1434	0	1460	66	0
5	E	1752	0	1776	58	0
6	F	679	0	701	31	0
7	G	1340	0	1357	43	0
8	H	1068	0	1040	54	0
9	I	971	0	927	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	J	532	0	542	26	0
11	K	920	0	929	29	0
12	L	363	0	386	14	0
13	N	247	0	137	14	0
14	P	197	0	99	27	0
15	T	485	0	273	22	0
16	A	2	0	0	0	0
16	B	1	0	0	0	0
16	C	1	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	1	0	0	0	0
All	All	32105	0	31787	1120	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 18.

The worst 5 of 1120 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)
4:D:187:THR:CB	4:D:187:THR:CA	1.75	1.60
4:D:187:THR:CB	4:D:187:THR:CG2	1.83	1.55
14:P:11:A:C8	14:P:11:A:H5''	1.77	1.18
1:A:1100:ARG:HH21	1:A:1351:GLU:HG2	1.11	1.14
14:P:11:A:C8	14:P:11:A:C5'	2.30	1.13

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	1414/1732 (82%)	1209 (86%)	145 (10%)	60 (4%)	2	14
2	B	1096/1224 (90%)	945 (86%)	120 (11%)	31 (3%)	4	19
3	C	264/318 (83%)	237 (90%)	23 (9%)	4 (2%)	8	30
4	D	174/221 (79%)	146 (84%)	15 (9%)	13 (8%)	1	5
5	E	212/215 (99%)	193 (91%)	14 (7%)	5 (2%)	4	22
6	F	82/155 (53%)	74 (90%)	7 (8%)	1 (1%)	10	35
7	G	169/171 (99%)	153 (90%)	13 (8%)	3 (2%)	6	26
8	H	129/146 (88%)	102 (79%)	19 (15%)	8 (6%)	1	7
9	I	117/122 (96%)	100 (86%)	12 (10%)	5 (4%)	2	13
10	J	63/70 (90%)	56 (89%)	4 (6%)	3 (5%)	2	11
11	K	113/120 (94%)	104 (92%)	9 (8%)	0	100	100
12	L	44/70 (63%)	31 (70%)	6 (14%)	7 (16%)	0	0
All	All	3877/4564 (85%)	3350 (86%)	387 (10%)	140 (4%)	2	16

5 of 140 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	43	GLU
1	A	48	ALA
1	A	57	ARG
1	A	58	LEU
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	1240/1519 (82%)	1032 (83%)	208 (17%)	2	9
2	B	964/1061 (91%)	789 (82%)	175 (18%)	2	7
3	C	234/274 (85%)	196 (84%)	38 (16%)	2	10
4	D	160/200 (80%)	132 (82%)	28 (18%)	2	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	196/197 (100%)	172 (88%)	24 (12%)	5	19
6	F	74/137 (54%)	64 (86%)	10 (14%)	4	15
7	G	152/152 (100%)	131 (86%)	21 (14%)	3	14
8	H	117/128 (91%)	98 (84%)	19 (16%)	2	10
9	I	113/116 (97%)	97 (86%)	16 (14%)	3	13
10	J	60/65 (92%)	52 (87%)	8 (13%)	4	15
11	K	99/102 (97%)	88 (89%)	11 (11%)	6	21
12	L	40/57 (70%)	26 (65%)	14 (35%)	0	0
All	All	3449/4008 (86%)	2877 (83%)	572 (17%)	2	10

5 of 572 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	E	95	THR
6	F	109	VAL
5	E	90	VAL
8	H	114	VAL
1	A	1391	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
4	D	37	GLN
9	I	79	HIS
5	E	115	ASN
8	H	52	GLN
11	K	96	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
14	P	9/12 (75%)	2 (22%)	2 (22%)

All (2) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
14	P	4	A

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Mol	Chain	Res	Type
14	P	11	A

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
14	P	3	G
14	P	10	A

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

2 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
15	BRU	T	22	14,15	18,21,22	1.49	4 (22%)	25,30,33	2.51	9 (36%)
15	TT	T	17	15	40,43,44	1.28	5 (12%)	58,69,72	2.08	14 (24%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	BRU	T	22	14,15	-	2/7/21/22	0/2/2/2
15	TT	T	17	15	-	9/18/105/106	0/5/6/6

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	T	17	TT	C2-N3	-3.28	1.32	1.38
15	T	17	TT	C2-N1	3.04	1.42	1.36
15	T	17	TT	C1R-N1T	3.02	1.49	1.45
15	T	17	TT	C4-N3	-2.94	1.32	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	T	22	BRU	C4-N3	-2.86	1.33	1.38

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	T	17	TT	O4R-C1R-N1T	8.05	118.19	108.65
15	T	17	TT	C4-N3-C2	-6.42	116.98	126.67
15	T	22	BRU	C5-C4-N3	5.74	119.95	113.34
15	T	22	BRU	C4-N3-C2	-5.31	120.37	127.34
15	T	22	BRU	O4-C4-C5	-5.12	119.27	125.80

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
15	T	22	BRU	C3'-C4'-C5'-O5'
15	T	22	BRU	O4'-C4'-C5'-O5'
15	T	17	TT	C2R-C1R-N1T-C6T
15	T	17	TT	O3'-C7-O5R-C5R
15	T	17	TT	C3'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	T	17	TT	5	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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	1422/1732 (82%)	-0.46	15 (1%) 78 65	56, 101, 162, 298	0
2	B	1113/1224 (90%)	-0.18	34 (3%) 51 38	53, 113, 185, 237	0
3	C	266/318 (83%)	-0.65	0 100 100	72, 102, 141, 189	0
4	D	178/221 (80%)	-0.25	8 (4%) 38 28	80, 116, 180, 211	0
5	E	214/215 (99%)	-0.40	1 (0%) 87 78	77, 137, 188, 195	0
6	F	84/155 (54%)	-0.78	1 (1%) 76 63	59, 80, 109, 134	0
7	G	171/171 (100%)	-0.45	0 100 100	63, 100, 139, 166	0
8	H	133/146 (91%)	-0.00	5 (3%) 44 31	106, 151, 194, 218	0
9	I	119/122 (97%)	-0.16	2 (1%) 69 54	107, 141, 182, 219	0
10	J	65/70 (92%)	-0.54	1 (1%) 72 57	77, 106, 146, 157	0
11	K	115/120 (95%)	-0.64	2 (1%) 69 54	66, 101, 137, 163	0
12	L	46/70 (65%)	0.23	1 (2%) 62 47	91, 154, 198, 202	0
13	N	12/14 (85%)	0.32	0 100 100	164, 177, 260, 301	0
14	P	9/12 (75%)	-0.01	1 (11%) 10 11	132, 150, 197, 204	0
15	T	21/25 (84%)	0.30	2 (9%) 14 13	125, 177, 286, 307	0
All	All	3968/4615 (85%)	-0.35	73 (1%) 67 53	53, 110, 179, 307	0

The worst 5 of 73 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	502	ILE	6.5
1	A	1080	THR	6.3
2	B	1224	PHE	6.0
8	H	63	LEU	5.5
2	B	883	LEU	5.2

## 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, 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(Å <sup>2</sup> )	Q<0.9
15	TT	T	17	38/39	0.89	0.18	112,230,240,242	0
15	BRU	T	22	20/21	0.90	0.11	161,193,214,215	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, 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(Å <sup>2</sup> )	Q<0.9
17	MG	A	2458	1/1	0.94	0.14	124,124,124,124	0
16	ZN	L	1071	1/1	0.99	0.03	187,187,187,187	0
16	ZN	I	1122	1/1	0.99	0.03	196,196,196,196	0
16	ZN	C	1269	1/1	1.00	0.02	75,75,75,75	0
16	ZN	I	1121	1/1	1.00	0.03	120,120,120,120	0
16	ZN	A	2456	1/1	1.00	0.02	127,127,127,127	0
16	ZN	J	1066	1/1	1.00	0.03	90,90,90,90	0
16	ZN	A	2457	1/1	1.00	0.01	70,70,70,70	0
16	ZN	B	2225	1/1	1.00	0.01	75,75,75,75	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.