



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 02:43 PM GMT

PDB ID : 4A3K
Title : RNA Polymerase II initial transcribing complex with a 7nt DNA-RNA hybrid
Authors : Cheung, A.C.M.; Sainsbury, S.; Cramer, P.
Deposited on : 2011-09-30
Resolution : 3.50 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

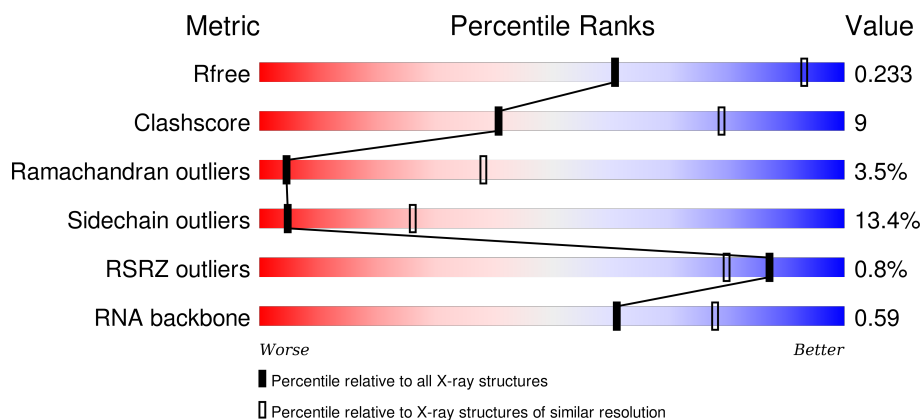
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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}	91344	1051 (3.60-3.40)
Clashscore	102246	1157 (3.60-3.40)
Ramachandran outliers	100387	1120 (3.60-3.40)
Sidechain outliers	100360	1121 (3.60-3.40)
RSRZ outliers	91569	1058 (3.60-3.40)
RNA backbone	2183	1050 (4.20-2.80)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 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 $\leq 5\%$. 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	<div> <div>%</div> <div> <div></div> <div>59%</div> <div>19%</div> <div>•</div> <div>18%</div> </div> </div>
2	B	1224	<div> <div>%</div> <div> <div></div> <div>63%</div> <div>24%</div> <div>•</div> <div>9%</div> </div> </div>
3	C	318	<div> <div></div> <div> <div>60%</div> <div>19%</div> <div>•</div> <div>16%</div> </div> </div>
4	D	221	<div> <div></div> <div> <div>54%</div> <div>21%</div> <div>5%</div> <div>19%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
5	E	215	 76% 22% •
6	F	155	 36% 14% • 46%
7	G	171	 64% 26% 10%
8	H	146	 65% 19% 7% 9%
9	I	122	 79% 17% • •
10	J	70	 53% 34% 6% 7%
11	K	120	 62% 29% 5% •
12	L	70	 7% 29% 26% 11% 34%
13	N	11	 64% 27% 9%
14	P	7	 100%
15	T	26	 54% 19% 27%

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 31940 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1422	Total	C	N	O	S	0	0	0
			11174	7037	1954	2121	62			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	1115	Total	C	N	O	S	0	0	0
			8859	5609	1554	1641	55			

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

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 SUBUNIT RPB4.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	N	10	Total	C	N	O	P	0	0	0
			207	99	39	59	10			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	P	7	Total	C	N	O	P	0	0	0
			152	68	31	46	7			

- Molecule 15 is a DNA chain called 5'-D(*AP*GP*CP*TP*CP*AP*AP*GP*TP*AP*CP*TP*TP*DTP*TP*TP*CP*CP*BRU*GP*GP*TP*CP*AP*TP*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	T	19	Total	Br	C	N	O	P	0	0
			385	1	185	60	120	19		

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

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

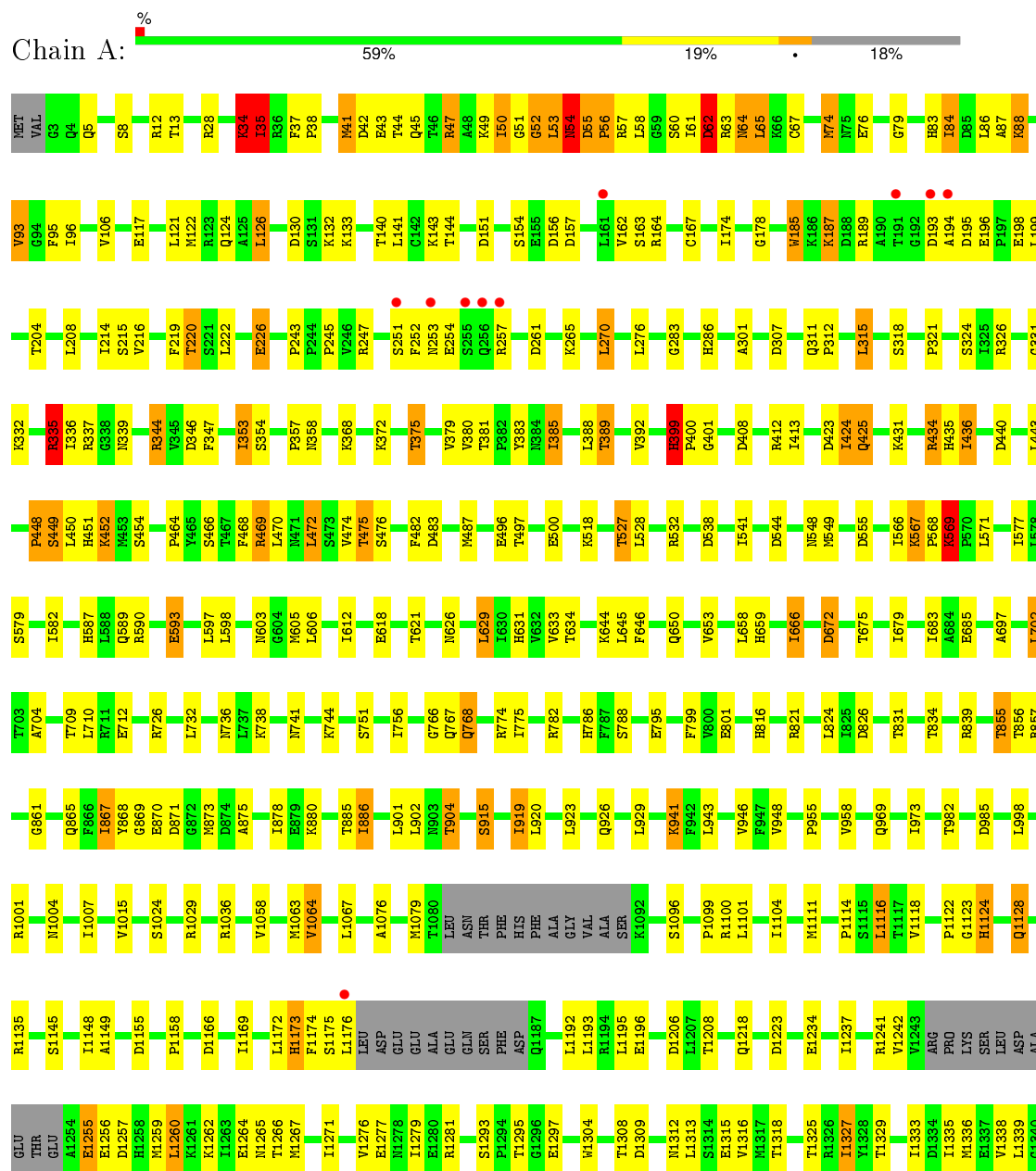
- Molecule 17 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

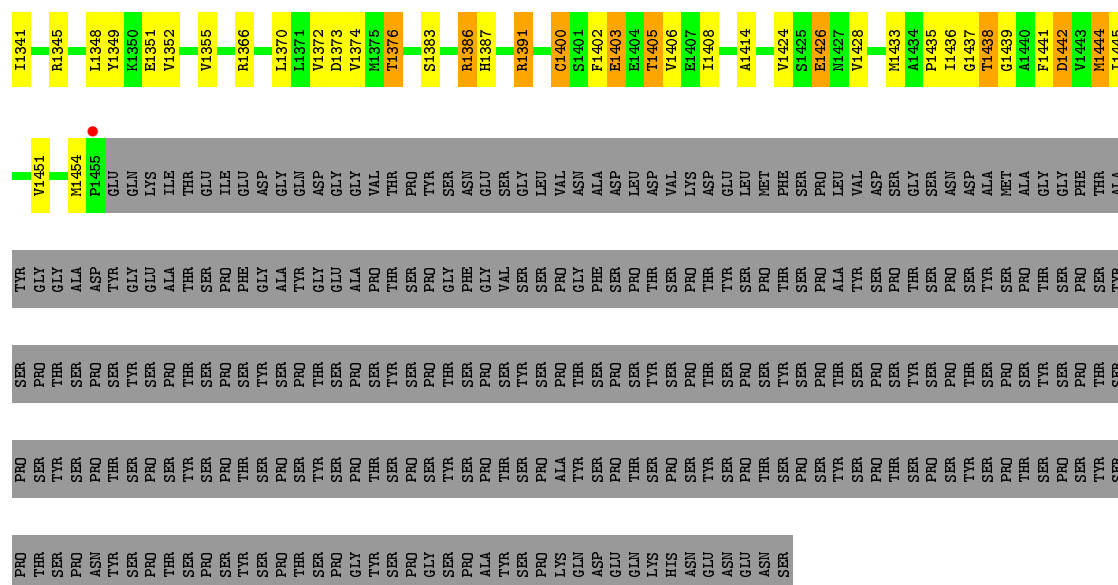
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	A	1	Total	Mg	0	0
			1	1		

3 Residue-property plots

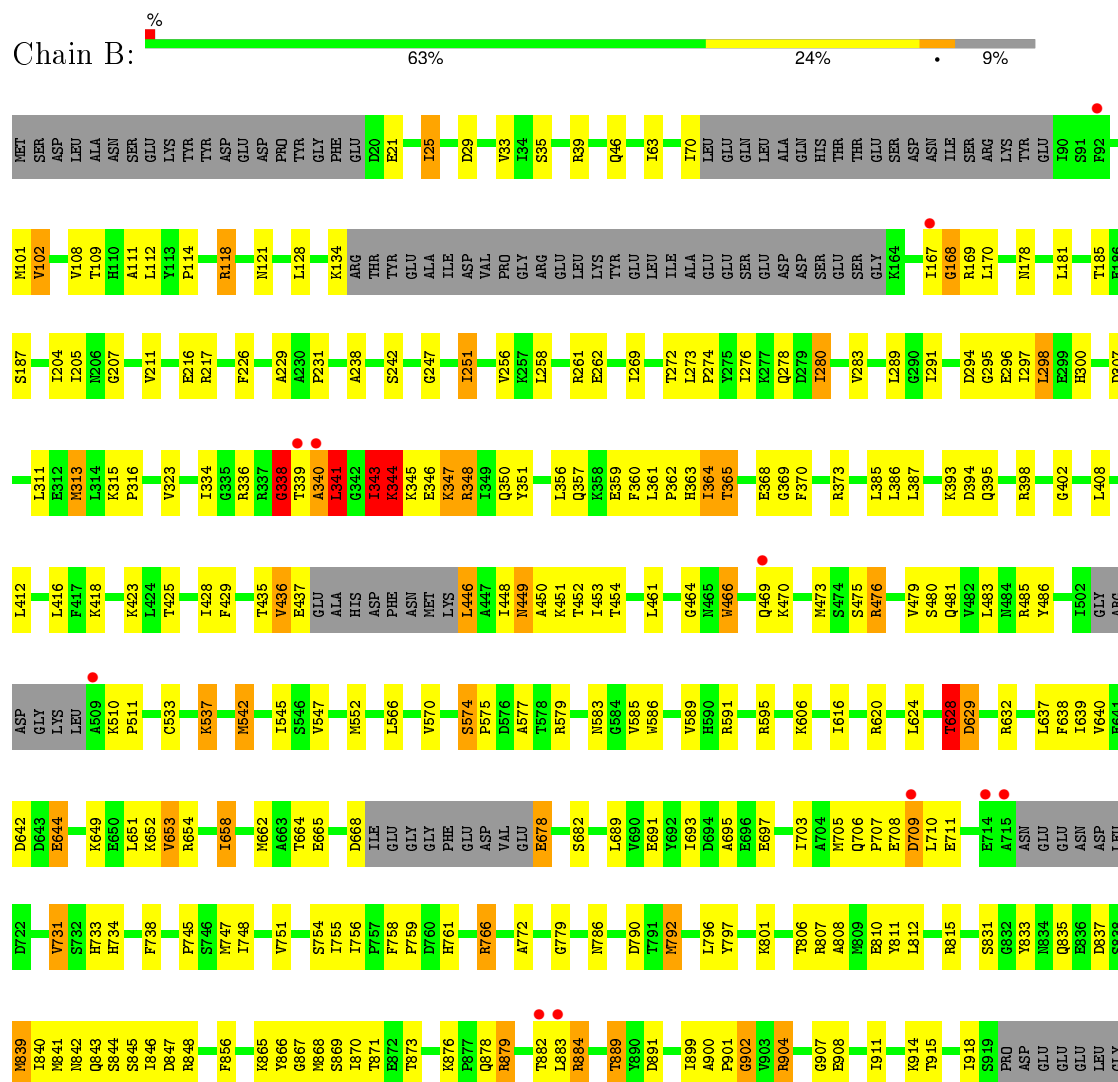
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

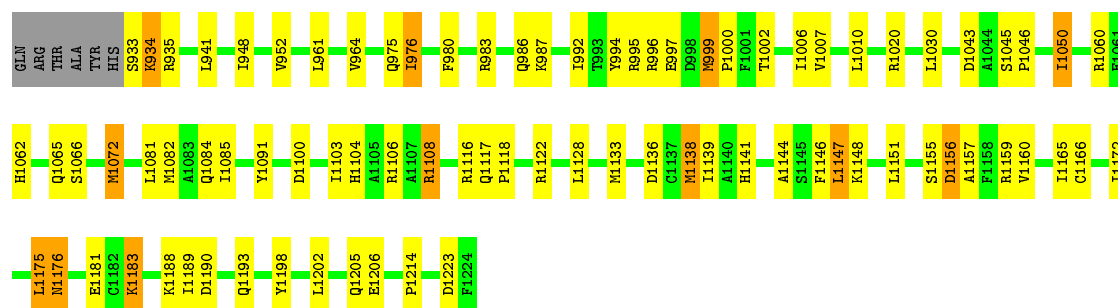
- Molecule 1: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB1



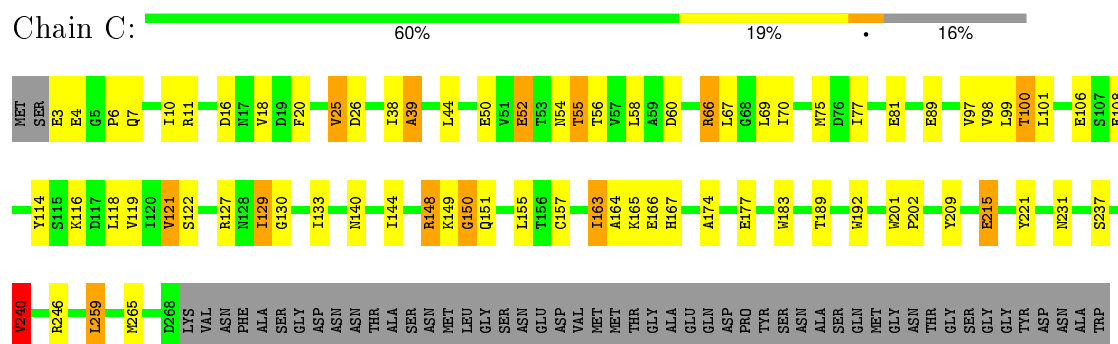


• Molecule 2: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB2

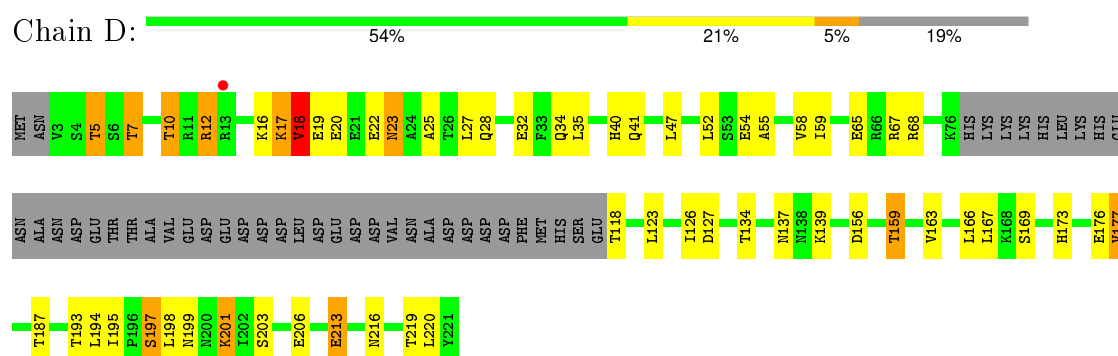




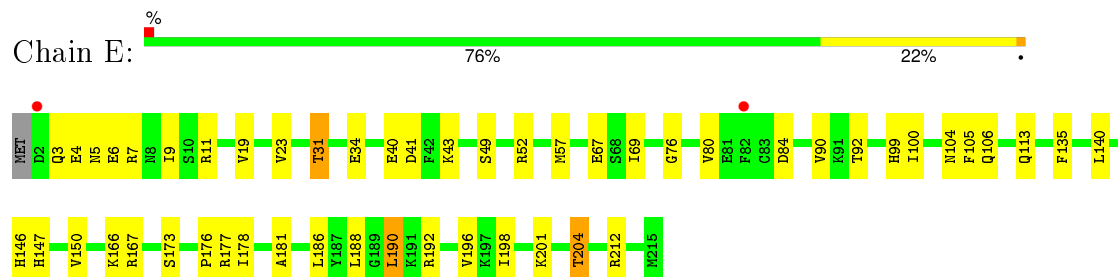
• Molecule 3: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB3



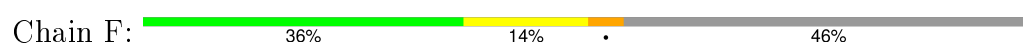
• Molecule 4: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB4



• Molecule 5: DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 1

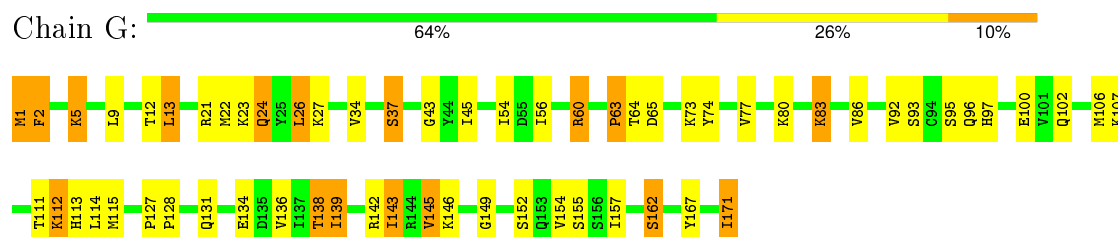


• Molecule 6: DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 2

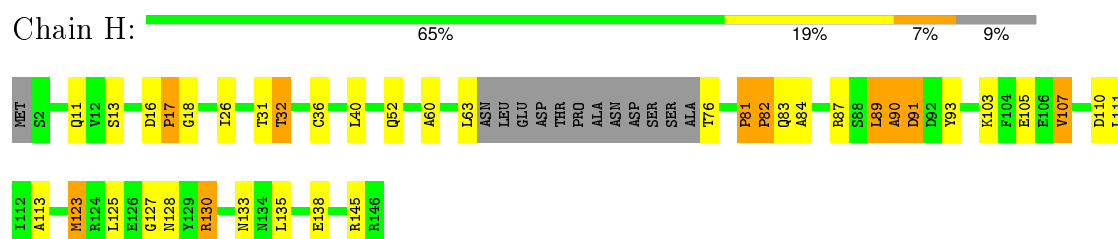




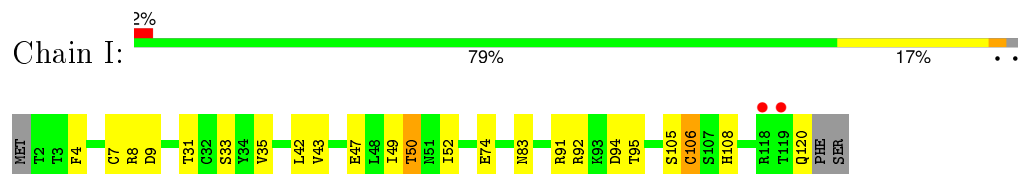
- Molecule 7: RPB7, DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB7



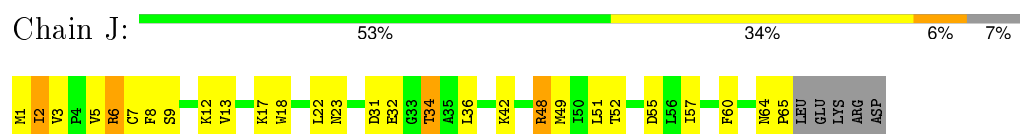
- Molecule 8: DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 3



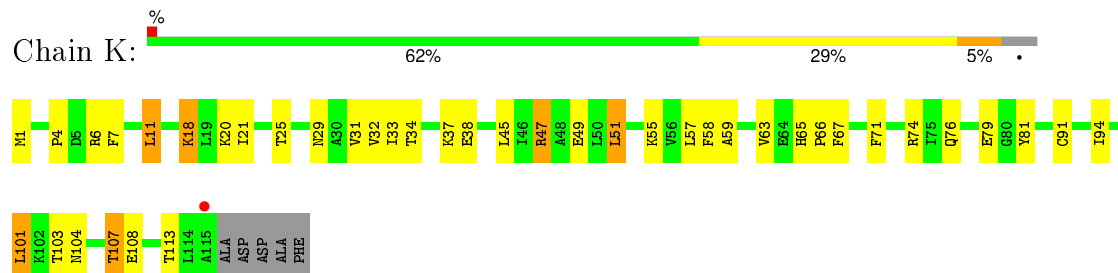
- Molecule 9: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB9



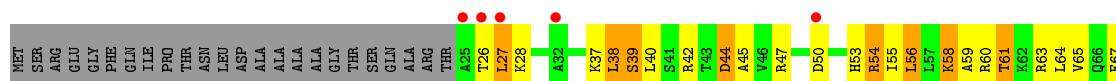
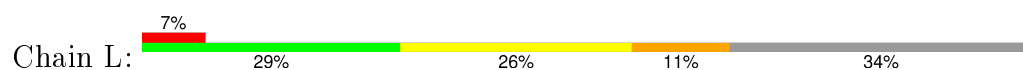
- Molecule 10: DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 5



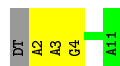
- Molecule 11: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB11



- 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)-3'



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



There are no outlier residues recorded for this chain.

- Molecule 15: 5'-D(*AP*GP*CP*TP*CP*AP*AP*GP*TP*AP*CP*TP*TP*DTP *TP*TP*CP*CP*BRU*GP*GP*TP*CP*AP*TP*T)-3'



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	221.91Å 391.36Å 283.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.95 – 3.50 49.11 – 3.37	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.95-3.50) 98.2 (49.11-3.37)	Depositor EDS
R_{merge}	1.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.49 (at 3.40Å)	Xtriage
Refinement program	BUSTER 2.11.2	Depositor
R, R_{free}	0.158 , 0.185 0.220 , 0.233	Depositor DCC
R_{free} test set	3051 reflections (2.01%)	DCC
Wilson B-factor (Å ²)	97.8	Xtriage
Anisotropy	0.391	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 91.3	EDS
Estimated twinning fraction	0.019 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.028 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	0 of 169418 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	31940	wwPDB-VP
Average B, all atoms (Å ²)	112.0	wwPDB-VP

Xtriage'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.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: MG, ZN, BRU

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	1/11374 (0.0%)	0.84	8/15383 (0.1%)
2	B	0.51	0/9029	0.80	2/12171 (0.0%)
3	C	0.50	0/2133	0.80	2/2891 (0.1%)
4	D	0.52	0/1444	0.82	1/1935 (0.1%)
5	E	0.47	0/1788	0.72	0/2406
6	F	0.61	0/691	0.80	0/933
7	G	0.50	0/1368	0.83	0/1844
8	H	0.50	0/1086	0.80	0/1470
9	I	0.46	0/989	0.80	0/1331
10	J	0.56	0/541	0.83	1/727 (0.1%)
11	K	0.48	0/938	0.73	0/1267
12	L	0.59	0/365	1.04	0/485
13	N	1.15	0/232	1.03	0/356
14	P	1.04	0/170	0.80	0/263
15	T	1.30	0/405	1.13	1/620 (0.2%)
All	All	0.55	1/32553 (0.0%)	0.82	15/44082 (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	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	867	ILE	CG1-CD1	5.19	1.86	1.50

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	34	LYS	C-N-CA	8.15	142.07	121.70
1	A	399	HIS	N-CA-CB	7.04	123.28	110.60
1	A	54	ASN	C-N-CA	6.02	136.75	121.70
1	A	35	ILE	N-CA-CB	5.82	124.19	110.80
1	A	56	PRO	C-N-CA	5.70	135.96	121.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	34	LYS	Mainchain,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	11174	0	11233	201	1
2	B	8859	0	8901	173	0
3	C	2095	0	2051	46	0
4	D	1434	0	1460	24	0
5	E	1752	0	1776	24	0
6	F	679	0	701	21	0
7	G	1340	0	1357	43	1
8	H	1068	0	1040	17	0
9	I	971	0	927	6	1
10	J	532	0	542	15	0
11	K	920	0	929	28	0
12	L	363	0	386	17	0
13	N	207	0	114	4	0
14	P	152	0	77	0	0
15	T	385	0	216	5	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	31940	0	31710	547	2

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 9.

The worst 5 of 547 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:867:ILE:CD1	1:A:867:ILE:CG1	1.86	1.53
1:A:53:LEU:HD23	1:A:54:ASN:H	0.97	1.11
4:D:40:HIS:HB3	7:G:73:LYS:HE3	1.34	1.08
7:G:1:MET:HE2	7:G:2:PHE:H	1.19	1.06
1:A:53:LEU:CD2	1:A:54:ASN:H	1.78	0.97

All (2) 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:904:THR:N	9:I:33:SER:O[8_555]	2.18	0.02
7:G:95:SER:OG	7:G:97:HIS:CD2[3_654]	2.18	0.02

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%)	1252 (88%)	112 (8%)	50 (4%)	4	38
2	B	1095/1224 (90%)	969 (88%)	82 (8%)	44 (4%)	4	33
3	C	264/318 (83%)	236 (89%)	24 (9%)	4 (2%)	13	56
4	D	174/221 (79%)	154 (88%)	14 (8%)	6 (3%)	5	39
5	E	212/215 (99%)	186 (88%)	24 (11%)	2 (1%)	21	68

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	F	82/155 (53%)	77 (94%)	4 (5%)	1 (1%)	16	61
7	G	169/171 (99%)	160 (95%)	6 (4%)	3 (2%)	11	53
8	H	129/146 (88%)	101 (78%)	19 (15%)	9 (7%)	1	18
9	I	117/122 (96%)	96 (82%)	18 (15%)	3 (3%)	7	45
10	J	63/70 (90%)	55 (87%)	4 (6%)	4 (6%)	2	21
11	K	113/120 (94%)	108 (96%)	5 (4%)	0	100	100
12	L	44/70 (63%)	27 (61%)	9 (20%)	8 (18%)	0	2
All	All	3876/4564 (85%)	3421 (88%)	321 (8%)	134 (4%)	4	38

5 of 134 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	47	ARG
1	A	57	ARG
1	A	58	LEU
1	A	74	MET
1	A	193	ASP

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	1240/1519 (82%)	1070 (86%)	170 (14%)	4	25
2	B	966/1061 (91%)	845 (88%)	121 (12%)	6	29
3	C	234/274 (85%)	207 (88%)	27 (12%)	7	33
4	D	160/200 (80%)	131 (82%)	29 (18%)	2	12
5	E	196/197 (100%)	176 (90%)	20 (10%)	9	40
6	F	74/137 (54%)	64 (86%)	10 (14%)	5	26
7	G	152/152 (100%)	128 (84%)	24 (16%)	3	19
8	H	117/128 (91%)	100 (86%)	17 (14%)	4	23
9	I	113/116 (97%)	100 (88%)	13 (12%)	7	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	J	60/65 (92%)	51 (85%)	9 (15%)	3	21
11	K	99/102 (97%)	85 (86%)	14 (14%)	4	24
12	L	40/57 (70%)	32 (80%)	8 (20%)	1	9
All	All	3451/4008 (86%)	2989 (87%)	462 (13%)	5	26

5 of 462 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	398	ARG
2	B	879	ARG
9	I	83	ASN
2	B	452	THR
2	B	628	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	465	ASN
2	B	1084	GLN
8	H	137	GLN
2	B	572	HIS
2	B	975	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
14	P	6/7 (85%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

1 non-standard protein/DNA/RNA residue is 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	15,14	13,21,22	1.48	2 (15%)	16,30,33	3.51	4 (25%)

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	15,14	-	0/3/21/22	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	T	22	BRU	C4-C5	3.18	1.42	1.38
15	T	22	BRU	C6-N1	3.77	1.40	1.35

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
15	T	22	BRU	C5-C4-N3	-5.11	118.54	124.00
15	T	22	BRU	C2'-C1'-N1	-3.84	104.82	114.16
15	T	22	BRU	O4'-C1'-N1	5.88	117.89	107.72
15	T	22	BRU	C4-N3-C2	10.97	124.73	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	1422/1732 (82%)	-0.15	11 (0%) 87 80	52, 99, 156, 225	0
2	B	1115/1224 (91%)	-0.12	11 (0%) 84 76	59, 109, 169, 210	0
3	C	266/318 (83%)	-0.21	0 100 100	71, 97, 136, 170	0
4	D	178/221 (80%)	0.04	1 (0%) 90 85	75, 111, 171, 186	0
5	E	214/215 (99%)	-0.04	2 (0%) 85 78	75, 132, 177, 194	0
6	F	84/155 (54%)	-0.29	0 100 100	58, 79, 110, 126	0
7	G	171/171 (100%)	-0.03	0 100 100	67, 98, 134, 153	0
8	H	133/146 (91%)	0.23	0 100 100	109, 140, 177, 200	0
9	I	119/122 (97%)	-0.06	2 (1%) 73 64	105, 136, 174, 191	0
10	J	65/70 (92%)	-0.29	0 100 100	79, 94, 139, 159	0
11	K	115/120 (95%)	-0.14	1 (0%) 85 78	69, 96, 132, 148	0
12	L	46/70 (65%)	0.57	5 (10%) 7 7	85, 165, 184, 194	0
13	N	10/11 (90%)	0.21	0 100 100	173, 193, 239, 248	0
14	P	7/7 (100%)	-0.16	0 100 100	101, 108, 155, 173	0
15	T	18/26 (69%)	0.13	0 100 100	125, 160, 250, 251	0
All	All	3963/4608 (86%)	-0.10	33 (0%) 87 80	52, 105, 169, 251	0

The worst 5 of 33 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	883	LEU	5.4
12	L	27	LEU	5.1
2	B	340	ALA	4.7
12	L	25	ALA	4.3
1	A	1455	PRO	4.2

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
15	BRU	T	22	20/21	0.93	0.13	-	123,129,133,134	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
16	ZN	I	1121	1/1	0.93	0.13	-0.17	125,125,125,125	0
16	ZN	B	2225	1/1	0.92	0.16	-1.04	82,82,82,82	0
16	ZN	A	2457	1/1	0.96	0.16	-1.09	72,72,72,72	0
16	ZN	C	1269	1/1	0.96	0.09	-1.63	84,84,84,84	0
16	ZN	I	1122	1/1	0.96	0.06	-1.76	175,175,175,175	0
16	ZN	A	2456	1/1	0.89	0.07	-1.77	127,127,127,127	0
16	ZN	J	1066	1/1	0.95	0.20	-1.87	82,82,82,82	0
16	ZN	L	1071	1/1	0.97	0.05	-3.52	192,192,192,192	0
17	MG	A	2458	1/1	0.94	0.13	-	78,78,78,78	0

6.5 Other polymers [i](#)

There are no such residues in this entry.