



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 1, 2026 – 10:18 PM UTC

PDB ID : 5OT2 / pdb_00005ot2
Title : RNA polymerase II elongation complex in the presence of 3d-Napht-A
Authors : Malvezzi, S.; Farnung, L.; Aloisi, C.; Angelov, T.; Cramer, P.; Sturla, S.J.
Deposited on : 2017-08-19
Resolution : 3.20 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

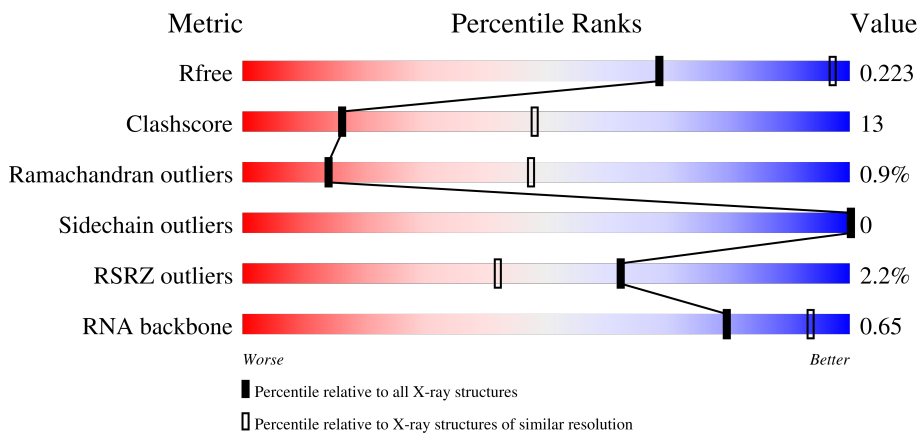
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)
RNA backbone	3983	1222 (3.50-2.90)

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	 59% 23% 19%
2	B	1224	 61% 28% 10%
3	C	318	 59% 24% 17%
4	D	221	 62% 17% 21%

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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	T	26	
14	N	14	
15	P	11	

2 Entry composition [i](#)

There are 18 unique types of molecules in this entry. The entry contains 31711 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	1412	11110	6998	1943	2107	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	1104	8769	5551	1537	1626	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	265	2087	1313	347	414	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	175	1393	863	243	285	2	0	0	0

- Molecule 5 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	E	212	1735	1102	306	316	11	0	0	0

- Molecule 6 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
6	F	87	705	451	119	132	3	0	0	0

- Molecule 7 is a protein called 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 RPABC3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
8	H	134	1076	677	182	213	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	114	927	571	168	178	10	0	0	0

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

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	114	919	590	156	171	2	0	0	0

- Molecule 12 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
12	L	44	351	217	70	60	4	0	0	0

- Molecule 13 is a DNA chain called DNA template strand.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	Br	C	N	O				P
13	T	19	378	1	182	60	116	19	0	0	0

- Molecule 14 is a DNA chain called DNA non-template strand.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
			Total	C	N	O				P
14	N	7	144	70	29	39	6	0	0	0

- Molecule 15 is a RNA chain called RNA product strand.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
			Total	C	N	O				P
15	P	10	222	98	45	69	10	0	0	0

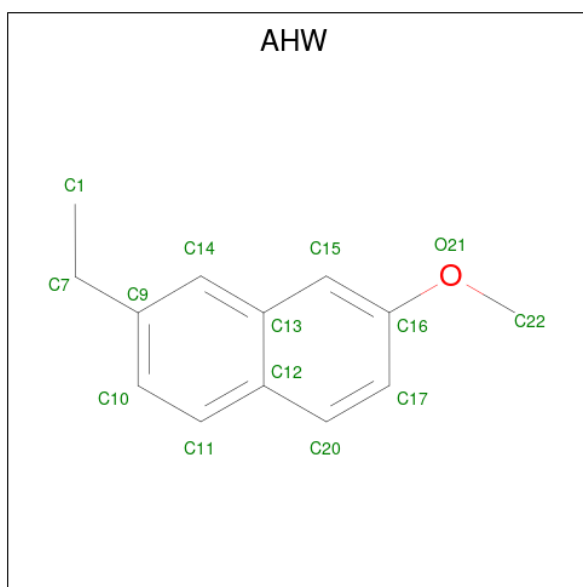
- Molecule 16 is ZINC ION (CCD ID: ZN) (formula: Zn).

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 18 is 2-ethyl-7-methoxy-naphthalene (CCD ID: AHW) (formula: C₁₃H₁₄O).

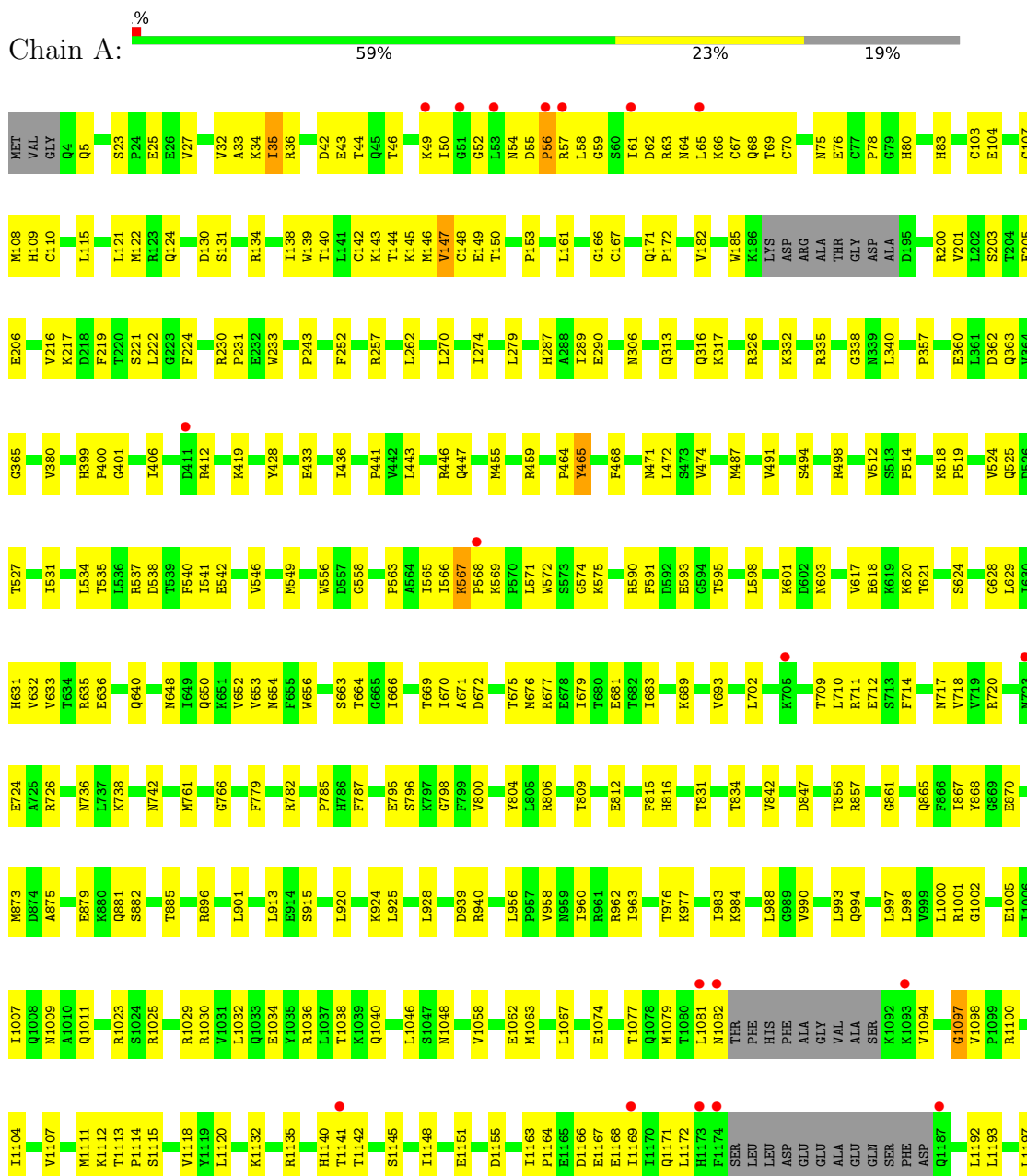


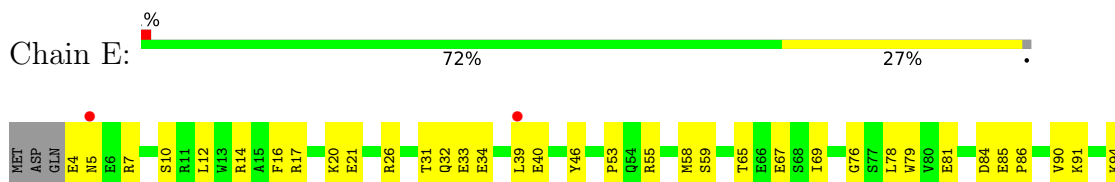
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
18	T	1	Total	C	O	0	0
			14	13	1		

3 Residue-property plots

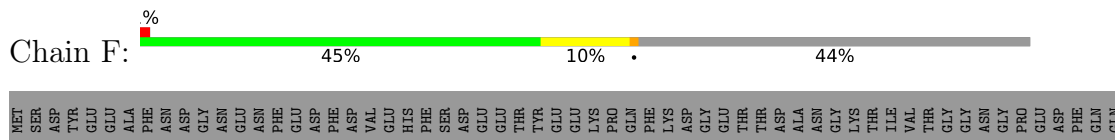
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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 subunit RPB1

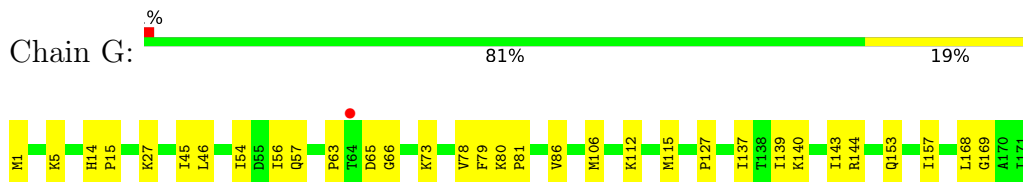




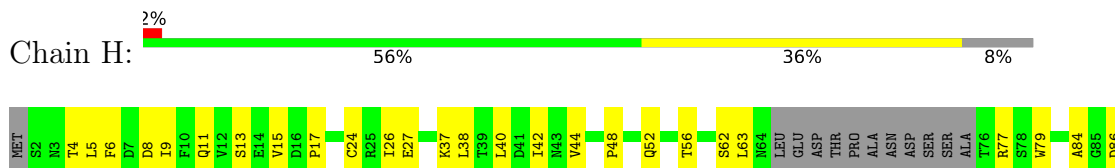
- Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2



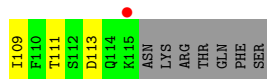
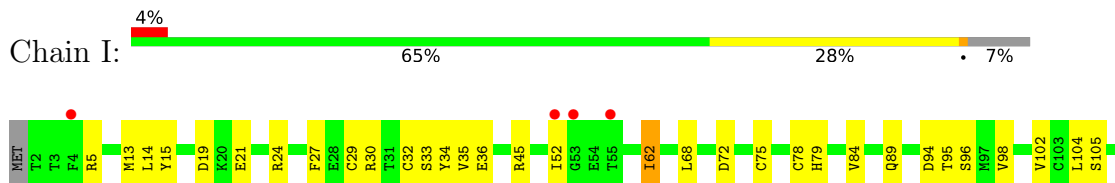
- Molecule 7: DNA-directed RNA polymerase II subunit RPB7



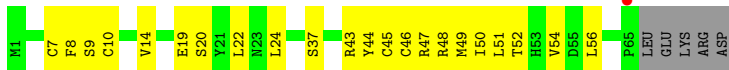
- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3



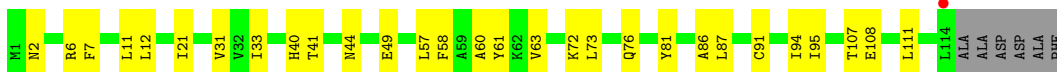
- Molecule 9: DNA-directed RNA polymerase II subunit RPB9



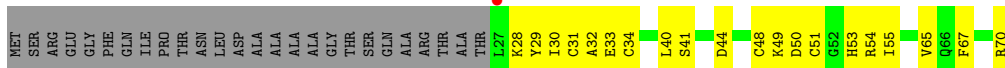
- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5



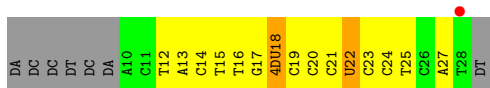
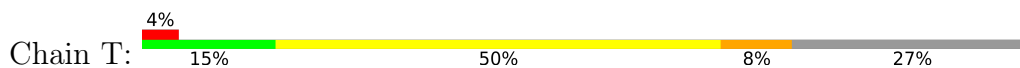
- Molecule 11: DNA-directed RNA polymerase II subunit RPB11



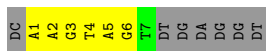
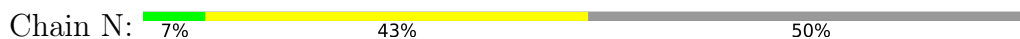
- Molecule 12: DNA-directed RNA polymerases I, II, and III subunit RPABC4



- Molecule 13: DNA template strand



- Molecule 14: DNA non-template strand



- Molecule 15: RNA product strand



4 Data and refinement statistics i

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	221.35Å 394.93Å 283.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.88 – 3.20 49.88 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.88-3.20) 99.9 (49.88-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.12 (at 3.19Å)	Xtrriage
Refinement program	PHENIX (1.11.1_2575: ???)	Depositor
R, R_{free}	0.178 , 0.222 0.183 , 0.223	Depositor DCC
R_{free} test set	1679 reflections (0.69%)	wwPDB-VP
Wilson B-factor (Å ²)	123.1	Xtrriage
Anisotropy	0.261	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 106.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	0.008 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.013 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	31711	wwPDB-VP
Average B, all atoms (Å ²)	138.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.88% 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: BRU, 4DU, MG, ZN, AHW

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	0.32	0/11308	0.57	0/15294
2	B	0.31	2/8938 (0.0%)	0.55	2/12050 (0.0%)
3	C	0.37	1/2125 (0.0%)	0.59	3/2880 (0.1%)
4	D	0.28	0/1403	0.52	0/1885
5	E	0.26	0/1771	0.51	0/2383
6	F	0.34	0/717	0.57	0/967
7	G	0.30	1/1368 (0.1%)	0.53	0/1844
8	H	0.25	0/1094	0.57	0/1481
9	I	0.38	0/945	0.64	0/1273
10	J	0.34	0/541	0.63	0/727
11	K	0.28	0/937	0.51	0/1265
12	L	0.33	0/353	0.82	0/468
13	T	0.41	0/372	0.60	0/564
14	N	0.29	0/162	0.81	0/249
15	P	0.35	0/249	0.48	0/388
All	All	0.31	4/32283 (0.0%)	0.57	5/43718 (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
4	D	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	92	CYS	CB-SG	-7.29	1.57	1.81
2	B	758	PHE	C-O	7.05	1.27	1.23
2	B	361	LEU	C-O	-5.60	1.21	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	G	169	GLY	C-O	-5.16	1.21	1.24

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	92	CYS	N-CA-CB	-7.36	98.69	110.39
3	C	86	CYS	CA-CB-SG	-6.78	98.80	114.40
3	C	87	PHE	N-CA-C	5.73	123.00	110.80
2	B	509	ALA	CA-C-N	-5.08	109.39	121.80
2	B	509	ALA	C-N-CA	-5.08	109.39	121.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	D	25	ALA	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	11110	0	11161	296	1
2	B	8769	0	8799	273	0
3	C	2087	0	2047	55	1
4	D	1393	0	1399	21	0
5	E	1735	0	1764	45	0
6	F	705	0	731	13	0
7	G	1340	0	1357	21	0
8	H	1076	0	1046	50	0
9	I	927	0	880	27	0
10	J	532	0	542	21	0
11	K	919	0	929	25	0
12	L	351	0	374	21	0
13	T	378	0	213	21	0
14	N	144	0	81	6	0
15	P	222	0	109	12	0
16	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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
18	T	14	0	0	1	0
All	All	31711	0	31432	820	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 13.

The worst 5 of 820 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)
10:J:10:CYS:SG	10:J:43:ARG:NH1	2.29	1.05
1:A:252:PHE:HA	15:P:1:U:H3	1.31	0.94
12:L:34:CYS:SG	12:L:48:CYS:HB2	2.10	0.92
9:I:78:CYS:SG	9:I:105:SER:OG	2.29	0.91
1:A:1385:THR:HG22	1:A:1387:HIS:H	1.36	0.91

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)
1:A:419:LYS:NZ	3:C:83:SER:O[4_555]	2.14	0.06

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	1402/1733 (81%)	1302 (93%)	89 (6%)	11 (1%)	16	50
2	B	1084/1224 (89%)	990 (91%)	80 (7%)	14 (1%)	9	40
3	C	263/318 (83%)	244 (93%)	19 (7%)	0	100	100
4	D	171/221 (77%)	156 (91%)	13 (8%)	2 (1%)	10	42
5	E	210/215 (98%)	199 (95%)	11 (5%)	0	100	100
6	F	85/155 (55%)	77 (91%)	6 (7%)	2 (2%)	4	28
7	G	169/171 (99%)	156 (92%)	12 (7%)	1 (1%)	21	56
8	H	130/146 (89%)	113 (87%)	15 (12%)	2 (2%)	8	37
9	I	112/122 (92%)	99 (88%)	12 (11%)	1 (1%)	14	47
10	J	63/70 (90%)	57 (90%)	6 (10%)	0	100	100
11	K	112/120 (93%)	109 (97%)	3 (3%)	0	100	100
12	L	42/70 (60%)	36 (86%)	6 (14%)	0	100	100
All	All	3843/4565 (84%)	3538 (92%)	272 (7%)	33 (1%)	14	47

5 of 33 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	65	LEU
1	A	567	LYS
2	B	502	ILE
2	B	507	LYS
1	A	68	GLN

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	1234/1520 (81%)	1234 (100%)	0	100	100
2	B	956/1061 (90%)	956 (100%)	0	100	100
3	C	233/274 (85%)	233 (100%)	0	100	100
4	D	155/200 (78%)	155 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	194/197 (98%)	194 (100%)	0	100	100
6	F	77/137 (56%)	77 (100%)	0	100	100
7	G	152/152 (100%)	152 (100%)	0	100	100
8	H	118/128 (92%)	118 (100%)	0	100	100
9	I	108/116 (93%)	108 (100%)	0	100	100
10	J	60/65 (92%)	60 (100%)	0	100	100
11	K	99/102 (97%)	99 (100%)	0	100	100
12	L	39/57 (68%)	39 (100%)	0	100	100
All	All	3425/4009 (85%)	3425 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
9	I	60	GLN
9	I	83	ASN
2	B	951	GLN
2	B	843	GLN
10	J	64	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
15	P	9/11 (81%)	1 (11%)	0

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
15	P	3	G

There are no RNA pucker outliers to report.

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

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
13	4DU	T	18	13,18	20,23,24	2.38	7 (35%)	27,33,36	2.31	7 (25%)
13	BRU	T	22	15,13	18,21,22	4.89	13 (72%)	25,30,33	2.30	6 (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
13	4DU	T	18	13,18	-	4/7/21/22	0/3/3/3
13	BRU	T	22	15,13	-	0/7/21/22	0/2/2/2

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	T	22	BRU	C2'-C3'	-7.44	1.34	1.52
13	T	22	BRU	O4'-C1'	7.36	1.58	1.42
13	T	22	BRU	C6-C5	7.15	1.48	1.34
13	T	22	BRU	C2-N1	6.99	1.49	1.38
13	T	22	BRU	O4'-C4'	-6.90	1.29	1.45

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	T	18	4DU	C4-N9-C8	7.92	113.44	106.26
13	T	22	BRU	C5-C4-N3	6.13	120.39	113.34
13	T	22	BRU	O4-C4-C5	-5.28	119.07	125.80
13	T	22	BRU	C4-N3-C2	-5.23	120.48	127.34
13	T	18	4DU	C5-C4-N9	-4.63	103.48	105.24

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
13	T	18	4DU	C3'-C4'-C5'-O5'
13	T	18	4DU	O4'-C4'-C5'-O5'
13	T	18	4DU	C2'-C1'-N9-C4
13	T	18	4DU	O4'-C1'-N9-C4

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
13	T	18	4DU	2	0
13	T	22	BRU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 9 are monoatomic - leaving 1 for Mogul analysis.

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
18	AHW	T	101	13	15,15,15	1.90	7 (46%)	20,20,20	0.78	1 (5%)

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
18	AHW	T	101	13	-	2/4/4/4	0/2/2/2

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	T	101	AHW	C14-C13	2.81	1.48	1.42
18	T	101	AHW	C20-C17	2.38	1.41	1.36
18	T	101	AHW	C13-C12	-2.37	1.37	1.42
18	T	101	AHW	C15-C13	2.33	1.47	1.42
18	T	101	AHW	C17-C16	2.20	1.42	1.38

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	T	101	AHW	C17-C16-C15	-2.09	118.11	120.83

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
18	T	101	AHW	C17-C16-O21-C22
18	T	101	AHW	C15-C16-O21-C22

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
18	T	101	AHW	1	0

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

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	1412/1733 (81%)	-0.14	21 (1%) 72 52	79, 121, 194, 258	0
2	B	1104/1224 (90%)	0.03	37 (3%) 48 30	81, 134, 209, 272	0
3	C	265/318 (83%)	-0.31	0 100 100	91, 124, 162, 219	0
4	D	175/221 (79%)	0.01	9 (5%) 33 21	101, 135, 197, 249	0
5	E	212/215 (98%)	-0.09	3 (1%) 73 54	100, 156, 215, 235	0
6	F	87/155 (56%)	-0.46	2 (2%) 61 41	81, 100, 142, 173	0
7	G	171/171 (100%)	-0.17	1 (0%) 85 73	99, 120, 162, 184	0
8	H	134/146 (91%)	0.28	3 (2%) 62 42	130, 174, 226, 245	0
9	I	114/122 (93%)	0.14	5 (4%) 39 24	123, 164, 220, 276	0
10	J	65/70 (92%)	-0.29	1 (1%) 72 52	102, 127, 175, 199	0
11	K	114/120 (95%)	-0.31	1 (0%) 81 64	87, 125, 168, 190	0
12	L	44/70 (62%)	0.47	1 (2%) 61 41	106, 156, 213, 311	0
13	T	17/26 (65%)	0.52	1 (5%) 28 18	119, 170, 287, 305	0
14	N	7/14 (50%)	0.87	0 100 100	254, 258, 314, 338	0
15	P	10/11 (90%)	0.32	1 (10%) 12 8	112, 136, 200, 205	0
All	All	3931/4616 (85%)	-0.08	86 (2%) 62 42	79, 129, 204, 338	0

The worst 5 of 86 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	65	LEU	7.6
2	B	918	ILE	6.3
9	I	52	ILE	5.9
2	B	733	HIS	5.4
1	A	1173	HIS	5.0

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(Å ²)	Q<0.9
13	4DU	T	18	21/22	0.94	0.12	124,132,154,195	0
13	BRU	T	22	20/21	0.95	0.09	112,119,157,249	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(Å ²)	Q<0.9
16	ZN	L	101	1/1	0.90	0.14	553,553,553,553	0
16	ZN	A	1802	1/1	0.93	0.12	255,255,255,255	0
18	AHW	T	101	14/14	0.94	0.25	124,149,195,201	0
16	ZN	I	202	1/1	0.98	0.04	284,284,284,284	0
16	ZN	I	201	1/1	0.99	0.04	147,147,147,147	0
16	ZN	A	1801	1/1	0.99	0.04	204,204,204,204	0
16	ZN	J	101	1/1	0.99	0.04	138,138,138,138	0
16	ZN	B	1301	1/1	0.99	0.03	111,111,111,111	0
17	MG	A	1803	1/1	0.99	0.04	97,97,97,97	0
16	ZN	C	401	1/1	0.99	0.03	106,106,106,106	0

6.5 Other polymers [i](#)

There are no such residues in this entry.