



wwPDB EM Validation Summary Report ⓘ

Mar 30, 2026 – 04:40 AM UTC

PDB ID : 7Z1N / pdb_00007z1n
EMDB ID : EMD-14449
Title : Structure of yeast RNA Polymerase III Delta C53-C37-C11
Authors : Girbig, M.; Mueller, C.W.
Deposited on : 2022-02-24
Resolution : 3.90 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

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A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

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:

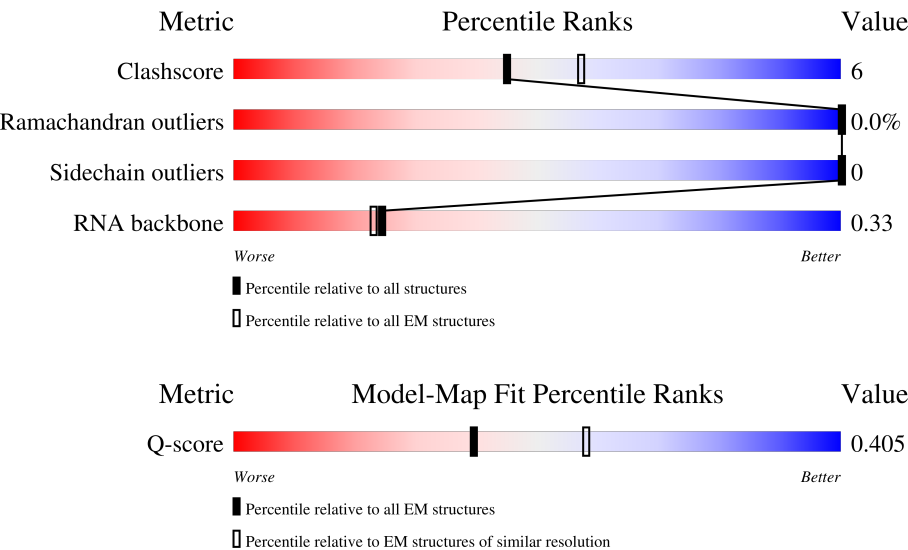
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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.



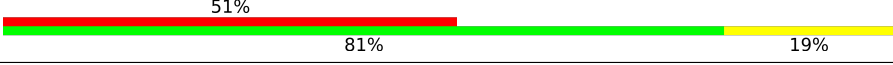
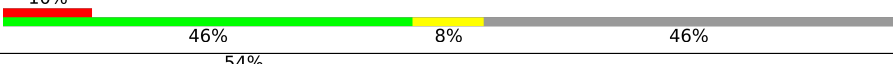
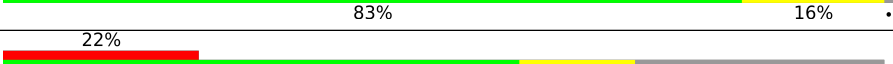
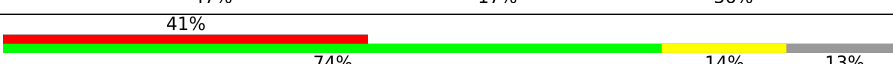
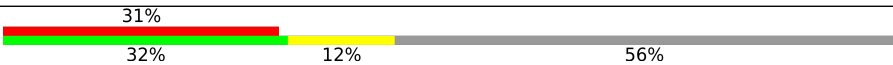
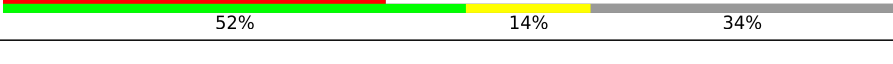
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8855 (3.40 - 4.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1460	29% 83% 15% .
2	B	1149	37% 79% 18% .
3	C	335	35% 83% 16%

Continued on next page...

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Mol	Chain	Length	Quality of chain
4	D	161	
5	E	215	
6	F	155	
7	G	212	
8	H	146	
9	J	70	
10	K	142	
11	L	70	
12	O	654	
13	P	317	
14	Q	251	
15	R	24	
16	S	44	
17	T	44	

2 Entry composition

There are 20 unique types of molecules in this entry. The entry contains 38601 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 III subunit RPC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1433	Total	C	N	O	S	0	0
			11209	7067	1977	2104	61		

- Molecule 2 is a protein called DNA-directed RNA polymerase III subunit RPC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1112	Total	C	N	O	S	0	0
			8771	5549	1514	1648	60		

- Molecule 3 is a protein called DNA-directed RNA polymerases I and III subunit RPAC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	334	Total	C	N	O	S	0	0
			2647	1676	453	510	8		

- Molecule 4 is a protein called DNA-directed RNA polymerase III subunit RPC9.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	145	Total	C	N	O	S	0	0
			1185	755	200	224	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	215	Total	C	N	O	S	0	0
			1759	1116	310	321	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	83	Total	C	N	O	S	0	0
			671	429	114	125	3		

- Molecule 7 is a protein called DNA-directed RNA polymerase III subunit RPC8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	199	Total	C	N	O	S	0	0
			1610	1046	258	298	8		

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	135	Total	C	N	O	S	0	0
			1083	683	183	213	4		

- Molecule 9 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	69	Total	C	N	O	S	0	0
			569	362	101	100	6		

- Molecule 10 is a protein called DNA-directed RNA polymerases I and III subunit RPAC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	102	Total	C	N	O	S	0	0
			801	501	131	164	5		

- Molecule 11 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	45	Total	C	N	O	S	0	0
			358	221	71	62	4		

- Molecule 12 is a protein called DNA-directed RNA polymerase III subunit RPC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	O	570	Total	C	N	O	S	0	0
			4577	2908	787	863	19		

- Molecule 13 is a protein called DNA-directed RNA polymerase III subunit RPC6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	P	140	Total	C	N	O	S	0	0
			1162	757	180	221	4		

- Molecule 14 is a protein called DNA-directed RNA polymerase III subunit RPC7.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Q	123	Total	C	N	O	S	0	0
			981	633	163	182	3		

- Molecule 15 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	R	9	Total	C	N	O	P	0	0
			195	87	39	60	9		

- Molecule 16 is a DNA chain called NT-DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	S	18	Total	C	N	O	P	0	0
			366	176	61	111	18		

- Molecule 17 is a DNA chain called T-DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	T	29	Total	C	N	O	P	0	0
			597	284	109	175	29		

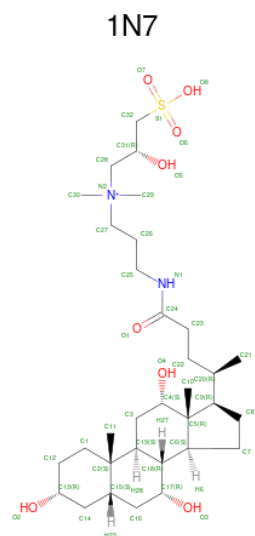
- Molecule 18 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
18	A	2	Total	Zn	0
			2	2	
18	B	1	Total	Zn	0
			1	1	
18	J	1	Total	Zn	0
			1	1	
18	L	1	Total	Zn	0
			1	1	

- Molecule 19 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
19	A	1	Total	Mg	0
			1	1	

- Molecule 20 is CHAPSO (CCD ID: 1N7) (formula: C₃₂H₅₉N₂O₈S).

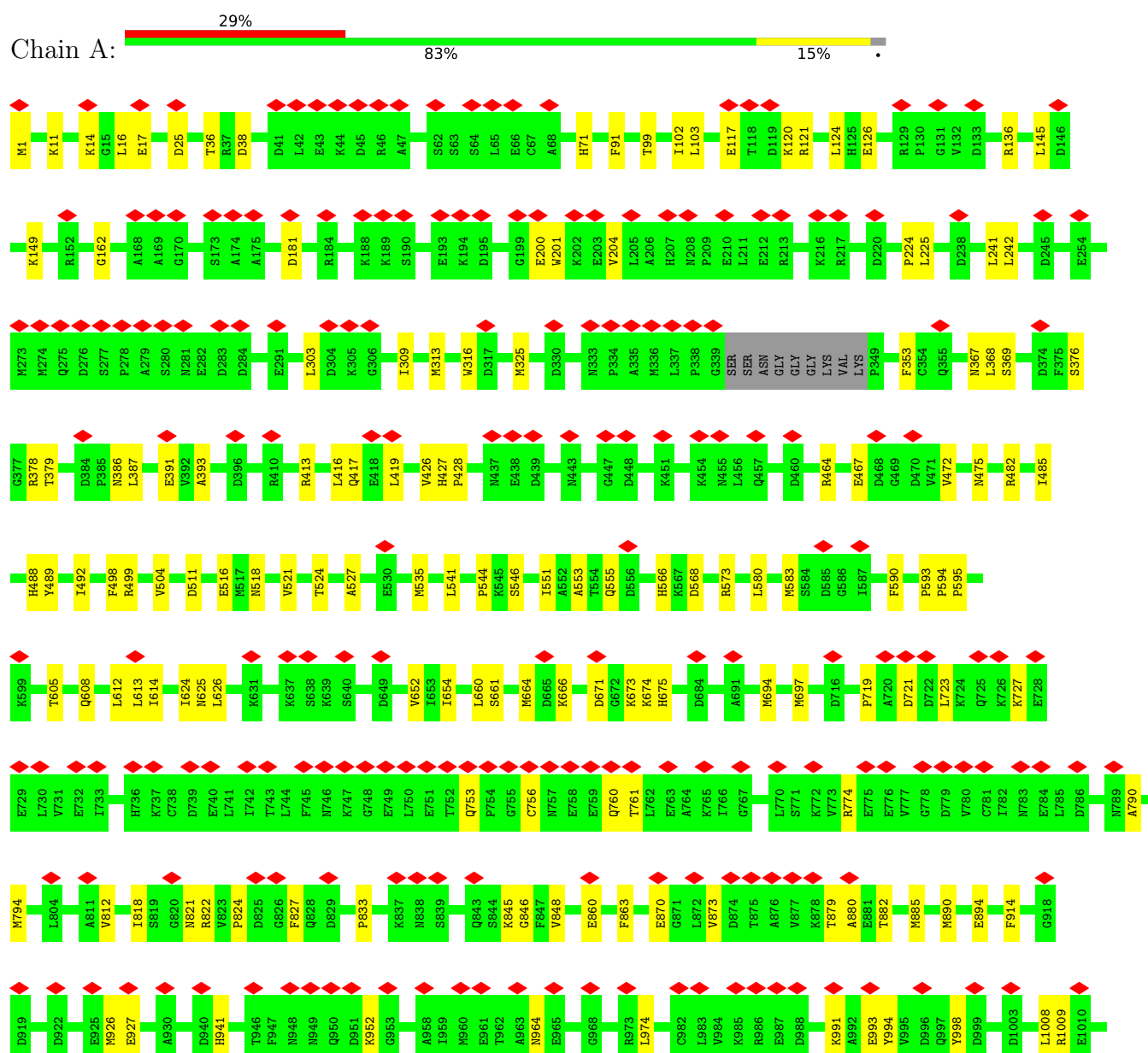


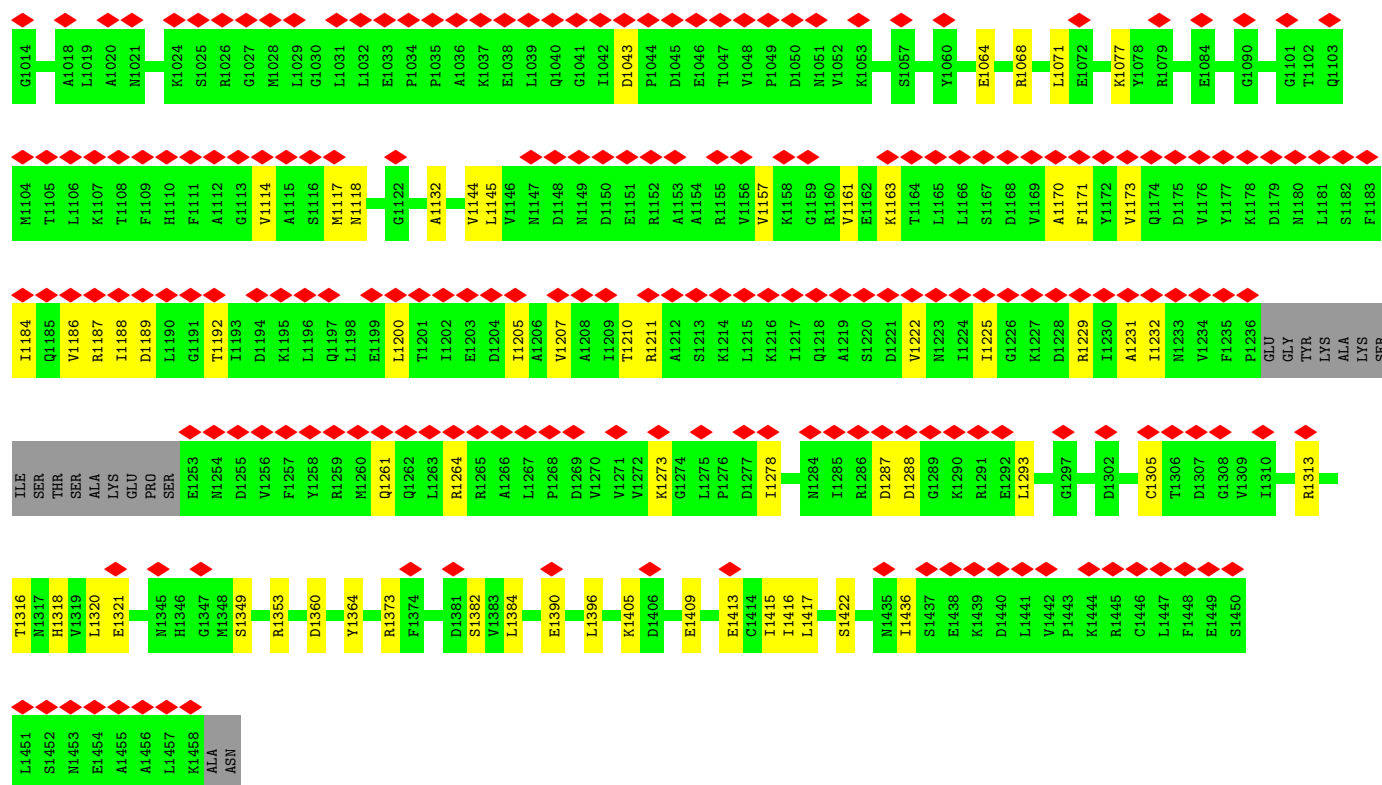
Mol	Chain	Residues	Atoms			AltConf
20	A	1	Total 27	C 24	O 3	0
20	K	1	Total 27	C 24	O 3	0

3 Residue-property plots [i](#)

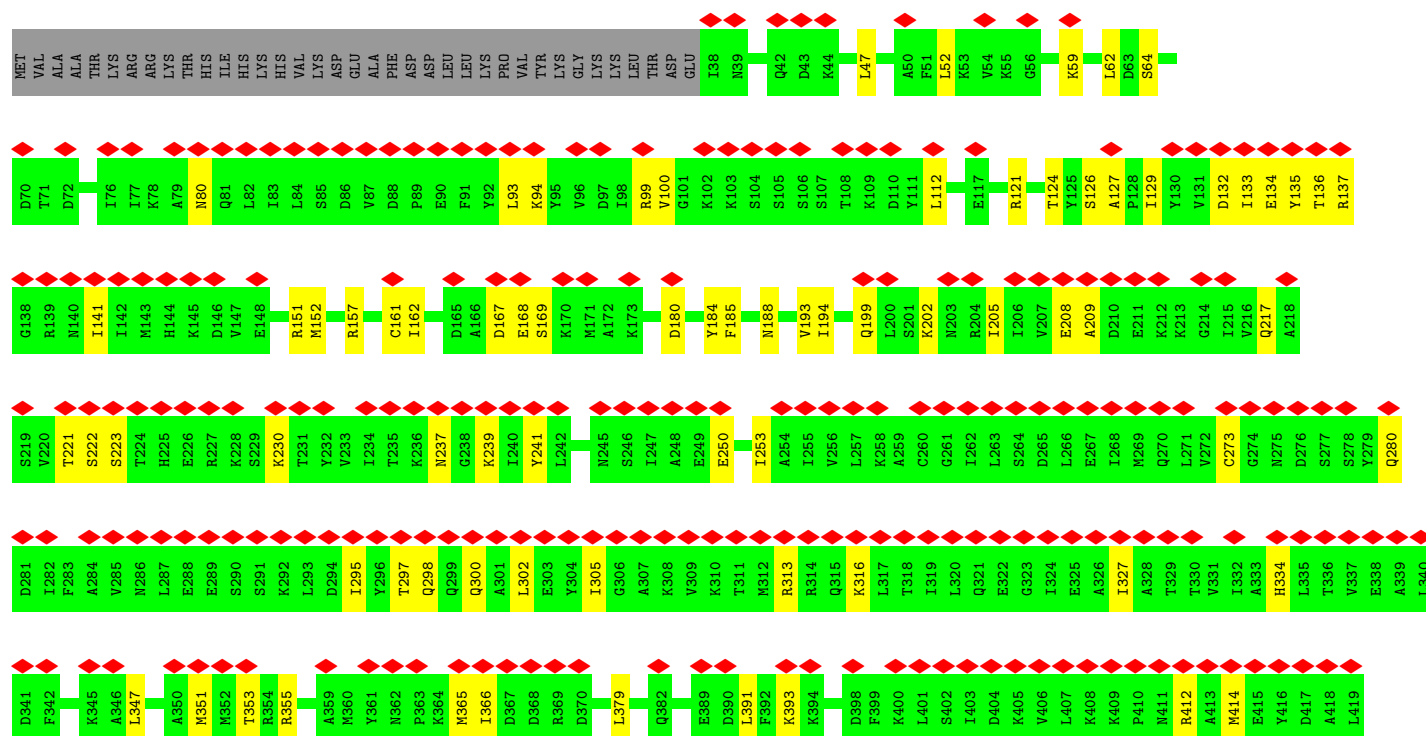
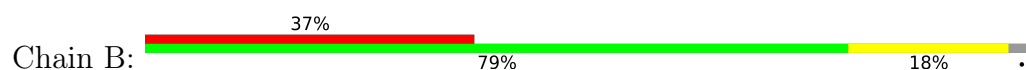
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

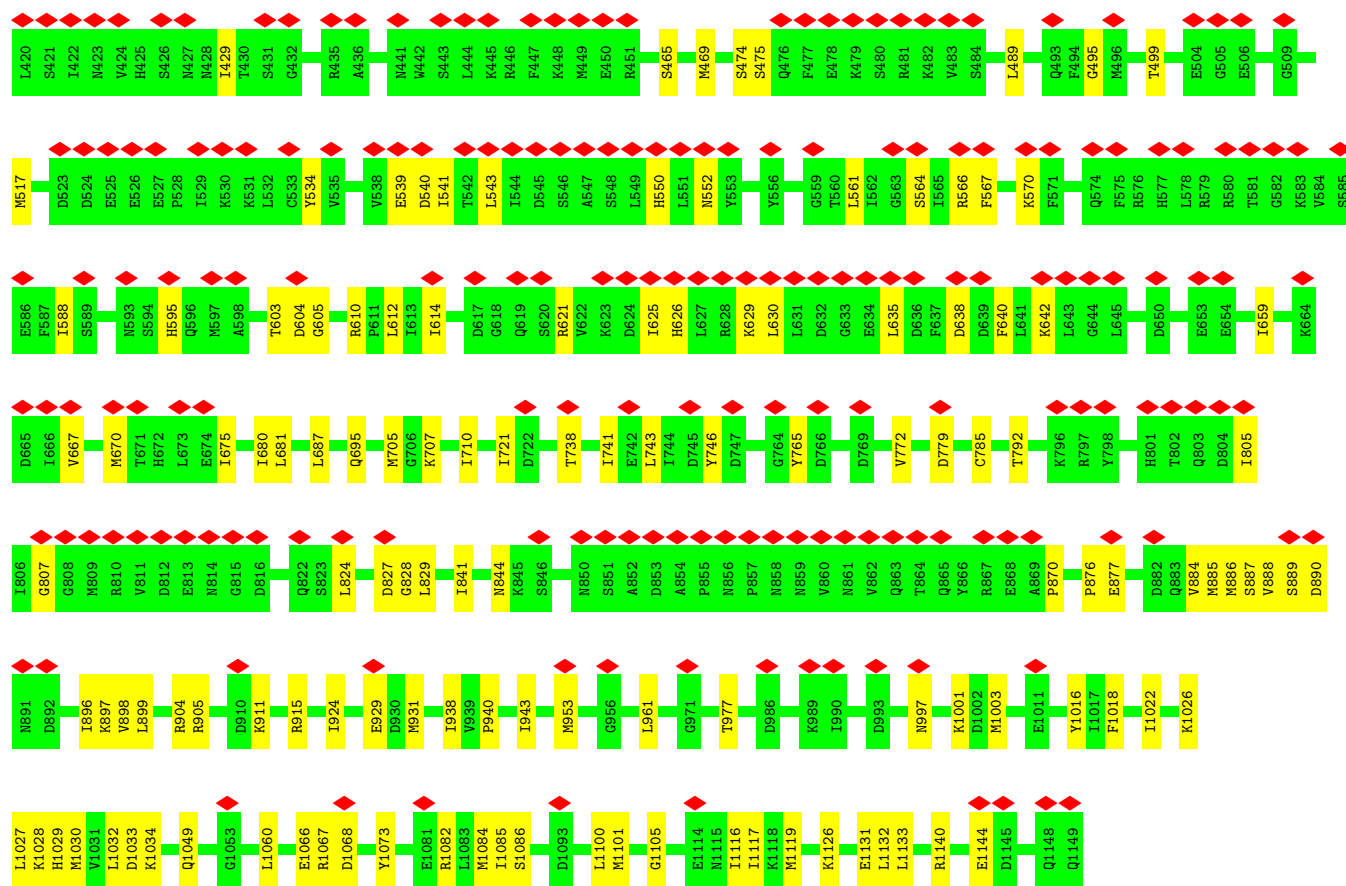
- Molecule 1: DNA-directed RNA polymerase III subunit RPC1



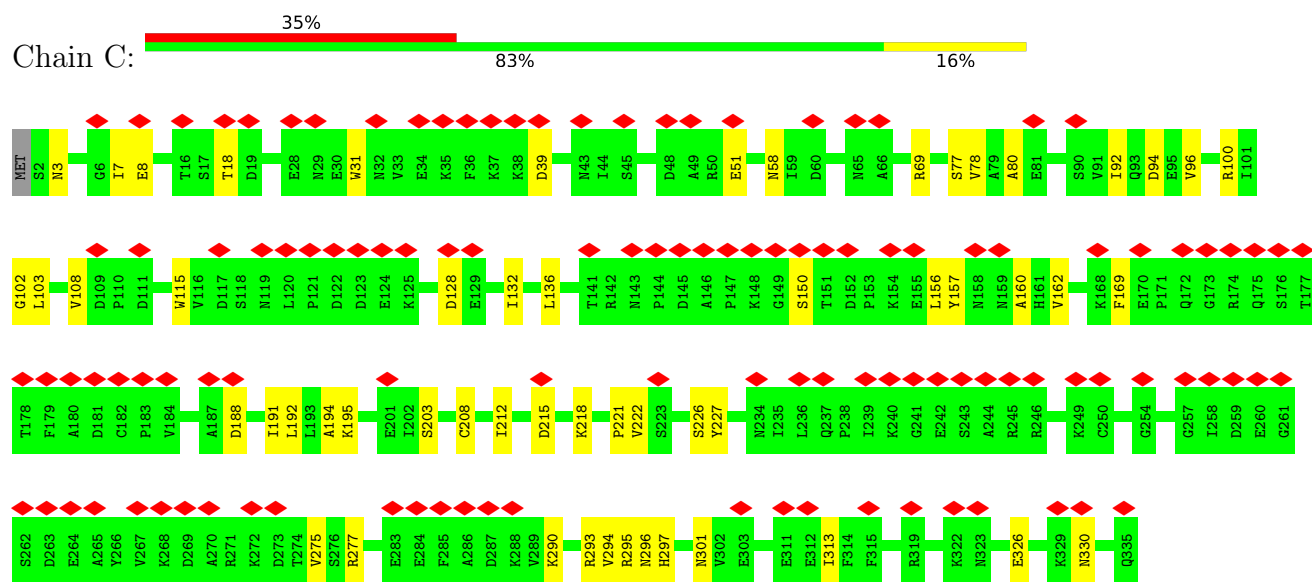


• Molecule 2: DNA-directed RNA polymerase III subunit RPC2

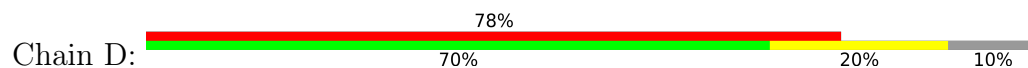




- Molecule 3: DNA-directed RNA polymerases I and III subunit RPAC1

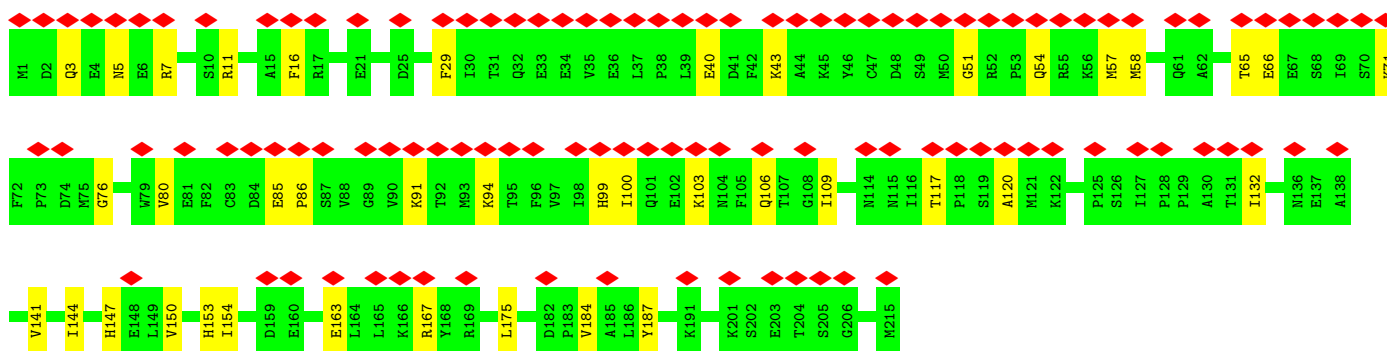
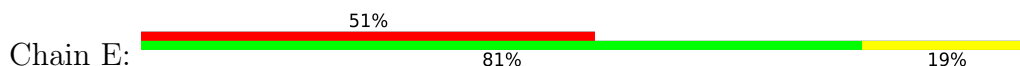


- Molecule 4: DNA-directed RNA polymerase III subunit RPC9

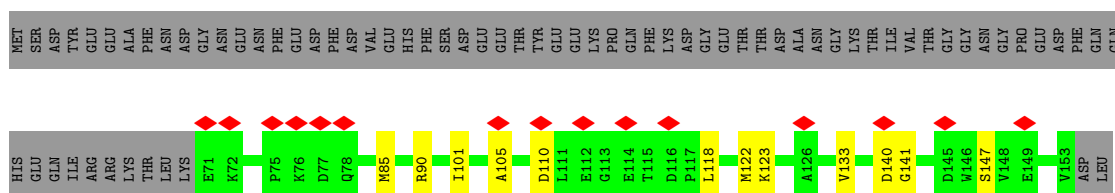




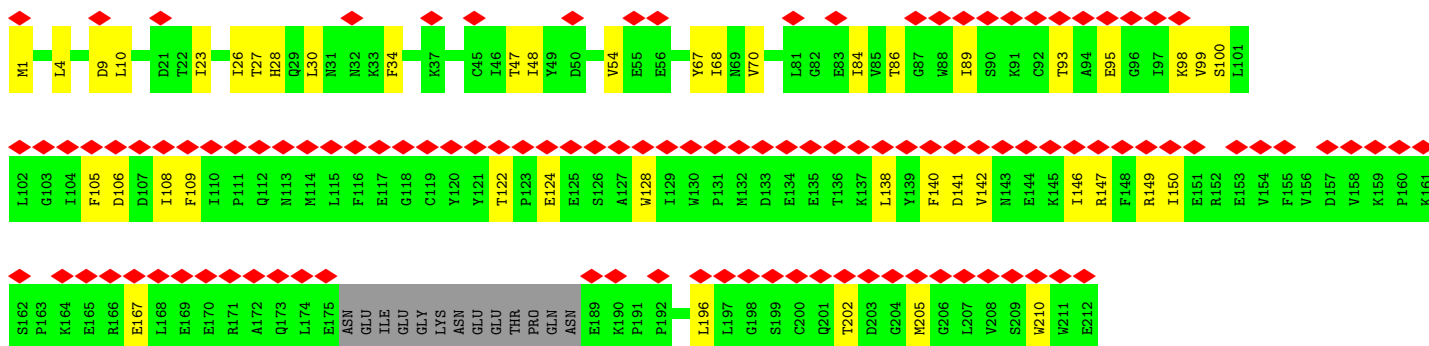
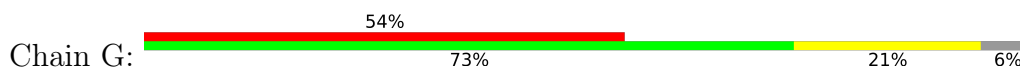
- Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1



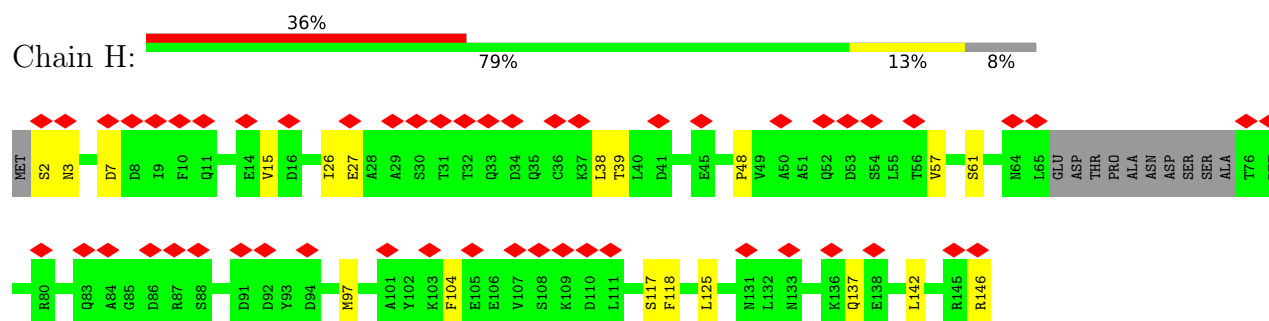
- Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2



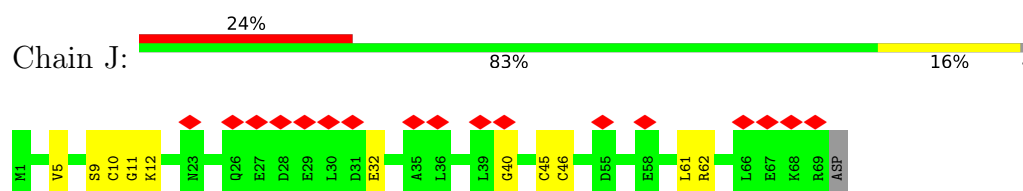
- Molecule 7: DNA-directed RNA polymerase III subunit RPC8



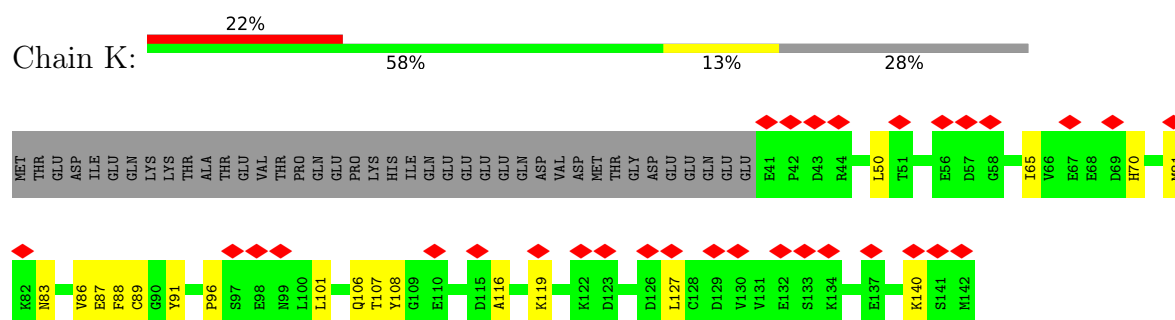
- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3



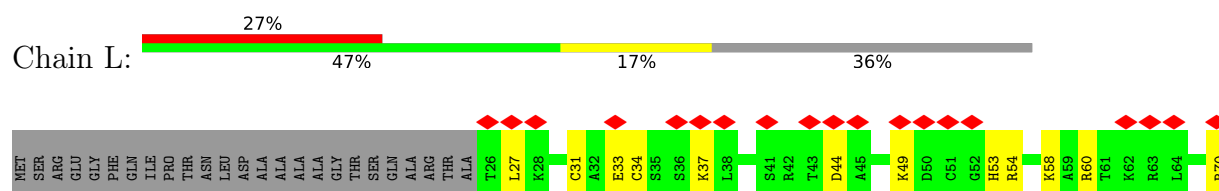
- Molecule 9: DNA-directed RNA polymerases I, II, and III subunit RPABC5



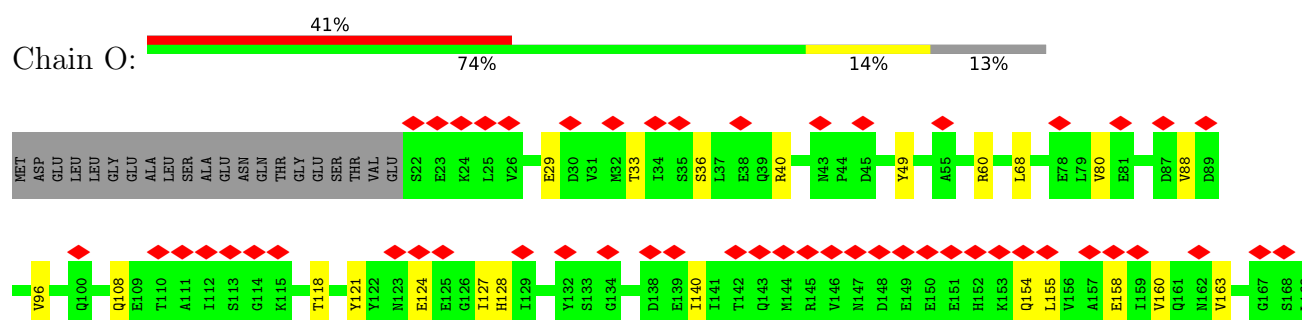
- Molecule 10: DNA-directed RNA polymerases I and III subunit RPAC2

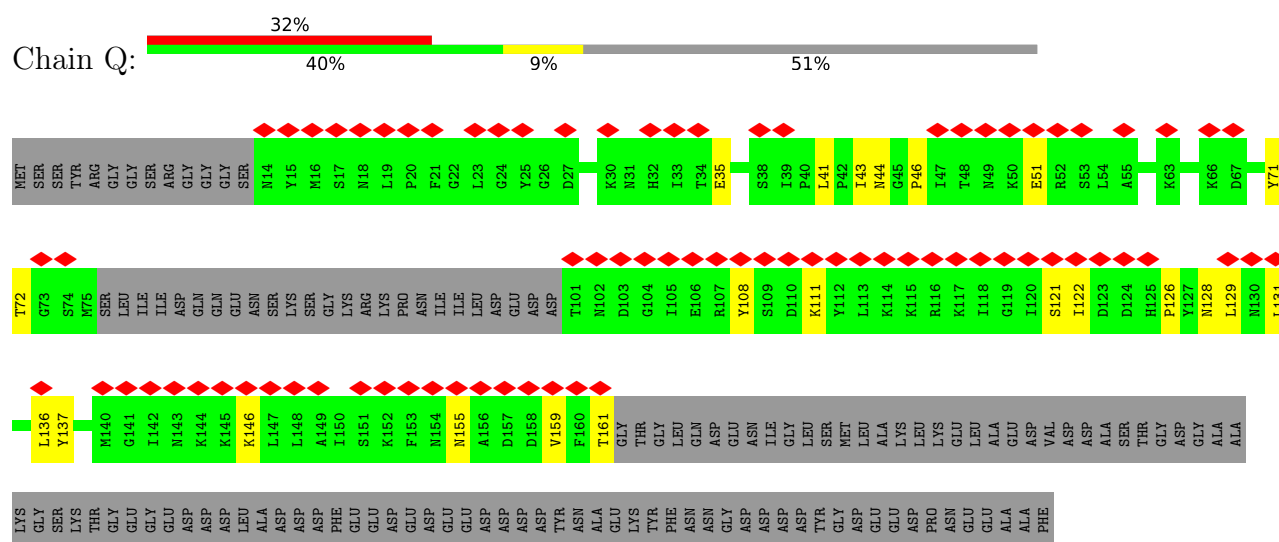


- Molecule 11: DNA-directed RNA polymerases I, II, and III subunit RPABC4

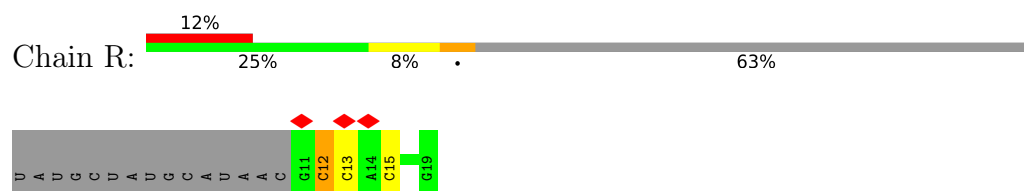


- Molecule 12: DNA-directed RNA polymerase III subunit RPC3

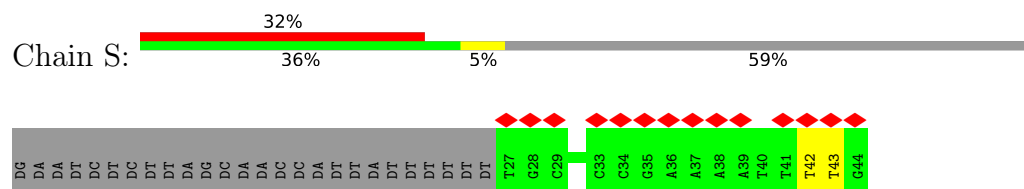




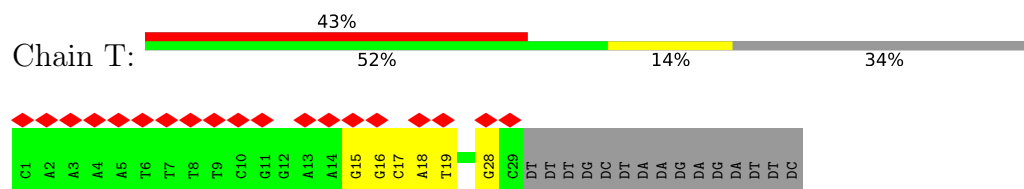
- Molecule 15: RNA



- Molecule 16: NT-DNA



- Molecule 17: T-DNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	18530	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	39.6	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.362	Depositor
Minimum map value	-0.030	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	364.33798, 364.33798, 364.33798	wwPDB
Map dimensions	346, 346, 346	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.053, 1.053, 1.053	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 1N7, MG, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.22	0/11411	0.44	3/15417 (0.0%)
2	B	0.21	0/8926	0.43	0/12045
3	C	0.20	0/2703	0.44	0/3666
4	D	0.18	0/1203	0.50	0/1610
5	E	0.22	0/1795	0.48	0/2416
6	F	0.20	0/683	0.36	0/923
7	G	0.18	0/1650	0.41	0/2237
8	H	0.19	0/1101	0.45	0/1492
9	J	0.22	0/578	0.46	0/775
10	K	0.20	0/812	0.38	0/1096
11	L	0.20	0/360	0.39	0/478
12	O	0.19	0/4646	0.40	0/6267
13	P	0.19	0/1193	0.54	3/1620 (0.2%)
14	Q	0.18	0/1004	0.46	0/1354
15	R	0.14	0/218	0.19	0/338
16	S	0.23	0/408	0.40	0/627
17	T	0.24	0/669	0.40	0/1031
All	All	0.21	0/39360	0.44	6/53392 (0.0%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	P	230	VAL	N-CA-C	-7.49	105.83	113.10
13	P	231	ALA	CA-C-N	7.00	134.91	121.54
13	P	231	ALA	C-N-CA	7.00	134.91	121.54
1	A	1409	GLU	N-CA-C	-5.66	107.37	114.56
1	A	555	GLN	CA-C-N	5.07	131.23	121.54

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	11209	0	11339	146	0
2	B	8771	0	8891	128	0
3	C	2647	0	2616	37	0
4	D	1185	0	1206	23	0
5	E	1759	0	1788	25	0
6	F	671	0	692	6	0
7	G	1610	0	1602	31	0
8	H	1083	0	1057	12	0
9	J	569	0	585	9	0
10	K	801	0	795	16	0
11	L	358	0	381	8	0
12	O	4577	0	4754	65	0
13	P	1162	0	1113	24	0
14	Q	981	0	979	17	0
15	R	195	0	99	1	0
16	S	366	0	206	1	0
17	T	597	0	328	4	0
18	A	2	0	0	0	0
18	B	1	0	0	0	0
18	J	1	0	0	0	0
18	L	1	0	0	0	0
19	A	1	0	0	0	0
20	A	27	0	39	3	0
20	K	27	0	39	3	0
All	All	38601	0	38509	485	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 6.

The worst 5 of 485 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:827:PHE:HE2	1:A:833:PRO:HG3	1.47	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:J:10:CYS:SG	9:J:11:GLY:N	2.58	0.77
5:E:54:GLN:NE2	5:E:57:MET:SD	2.59	0.76
1:A:378:ARG:NE	1:A:516:GLU:OE1	2.22	0.72
1:A:890:MET:HE3	2:B:1068:ASP:HB3	1.70	0.72

There are no symmetry-related clashes.

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 PDB entries followed by that with respect to all EM entries.

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	1427/1460 (98%)	1351 (95%)	75 (5%)	1 (0%)	48	80
2	B	1110/1149 (97%)	1058 (95%)	52 (5%)	0	100	100
3	C	332/335 (99%)	320 (96%)	12 (4%)	0	100	100
4	D	141/161 (88%)	132 (94%)	8 (6%)	1 (1%)	18	53
5	E	213/215 (99%)	202 (95%)	11 (5%)	0	100	100
6	F	81/155 (52%)	78 (96%)	3 (4%)	0	100	100
7	G	195/212 (92%)	184 (94%)	11 (6%)	0	100	100
8	H	131/146 (90%)	123 (94%)	8 (6%)	0	100	100
9	J	67/70 (96%)	65 (97%)	2 (3%)	0	100	100
10	K	100/142 (70%)	99 (99%)	1 (1%)	0	100	100
11	L	43/70 (61%)	39 (91%)	4 (9%)	0	100	100
12	O	566/654 (86%)	544 (96%)	22 (4%)	0	100	100
13	P	136/317 (43%)	127 (93%)	9 (7%)	0	100	100
14	Q	119/251 (47%)	112 (94%)	7 (6%)	0	100	100
All	All	4661/5337 (87%)	4434 (95%)	225 (5%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1114	VAL
4	D	132	VAL

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 PDB entries followed by that with respect to all EM entries.

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	1237/1257 (98%)	1237 (100%)	0	100	100
2	B	973/1006 (97%)	973 (100%)	0	100	100
3	C	295/296 (100%)	295 (100%)	0	100	100
4	D	133/145 (92%)	133 (100%)	0	100	100
5	E	197/197 (100%)	197 (100%)	0	100	100
6	F	73/137 (53%)	73 (100%)	0	100	100
7	G	178/190 (94%)	178 (100%)	0	100	100
8	H	119/128 (93%)	119 (100%)	0	100	100
9	J	64/65 (98%)	64 (100%)	0	100	100
10	K	92/130 (71%)	92 (100%)	0	100	100
11	L	40/57 (70%)	40 (100%)	0	100	100
12	O	524/593 (88%)	524 (100%)	0	100	100
13	P	131/285 (46%)	131 (100%)	0	100	100
14	Q	109/212 (51%)	109 (100%)	0	100	100
All	All	4165/4698 (89%)	4165 (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 39 such sidechains are listed below:

Mol	Chain	Res	Type
5	E	114	ASN
12	O	616	ASN
5	E	153	HIS
10	K	106	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
13	P	193	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
15	R	8/24 (33%)	3 (37%)	0

All (3) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
15	R	12	C
15	R	13	C
15	R	15	C

There are no RNA pucker outliers to report.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 6 are monoatomic - leaving 2 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$
20	1N7	K	401	-	30,30,46	1.83	11 (36%)	47,48,72	3.46	26 (55%)
20	1N7	A	2003	-	30,30,46	1.94	11 (36%)	47,48,72	3.59	26 (55%)

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
20	1N7	K	401	-	-	1/7/72/92	0/4/4/4
20	1N7	A	2003	-	-	0/7/72/92	0/4/4/4

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
20	A	2003	1N7	C16-C15	4.24	1.60	1.53
20	K	401	1N7	C16-C15	3.72	1.59	1.53
20	A	2003	1N7	C7-C6	-3.36	1.47	1.54
20	A	2003	1N7	C5-C6	-3.27	1.50	1.55
20	A	2003	1N7	C16-C17	3.26	1.58	1.52

The worst 5 of 52 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	A	2003	1N7	C10-C5-C4	9.27	118.34	109.06
20	K	401	1N7	C10-C5-C4	8.45	117.51	109.06
20	A	2003	1N7	C1-C2-C15	6.85	117.57	107.75
20	K	401	1N7	C10-C5-C6	-6.41	101.15	111.20
20	A	2003	1N7	C11-C2-C1	-6.40	98.13	108.31

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
20	K	401	1N7	C22-C20-C9-C5

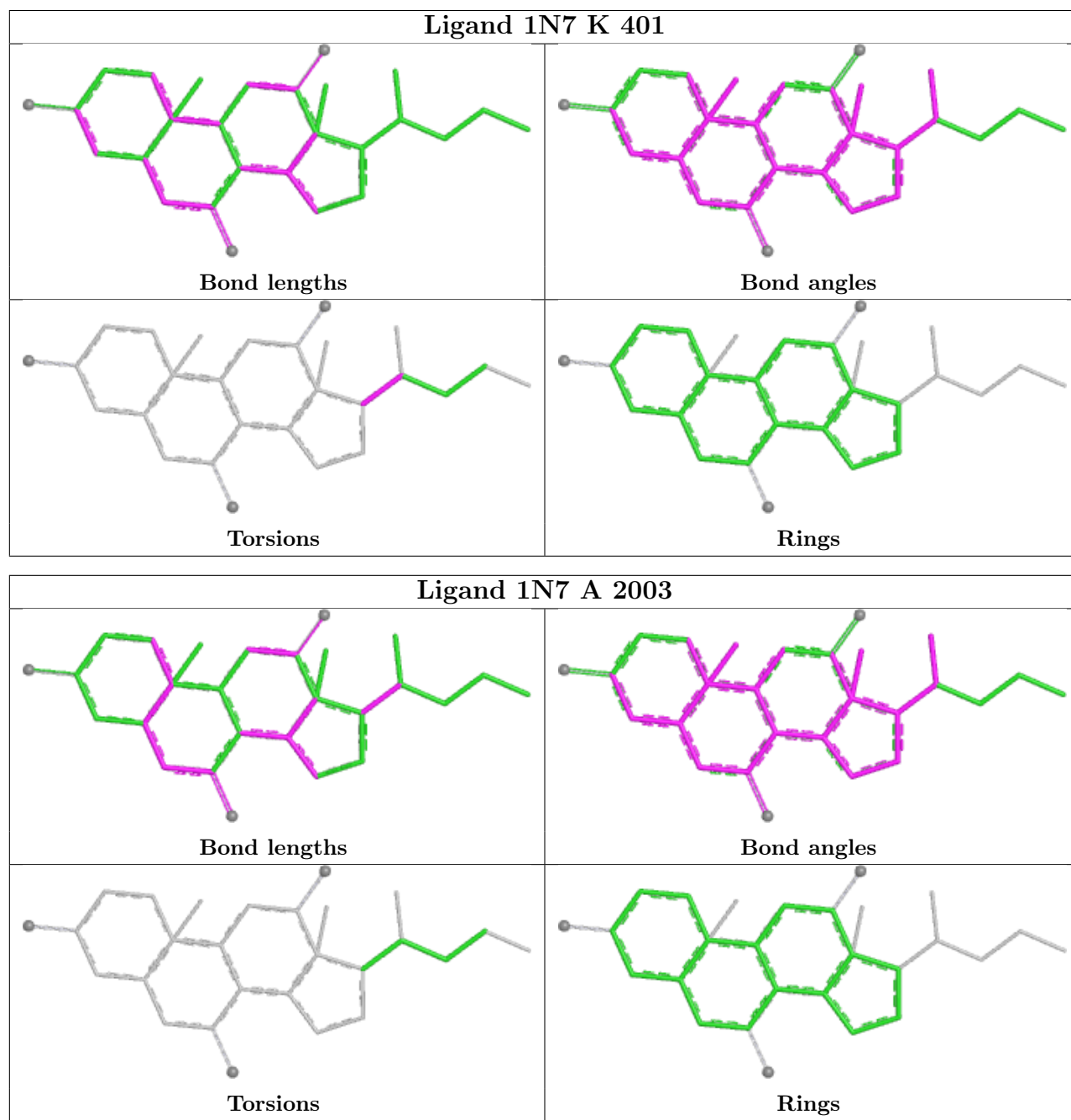
There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
20	K	401	1N7	3	0
20	A	2003	1N7	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

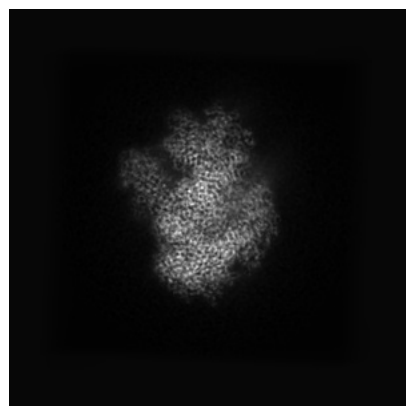
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14449. These allow visual inspection of the internal detail of the map and identification of artifacts.

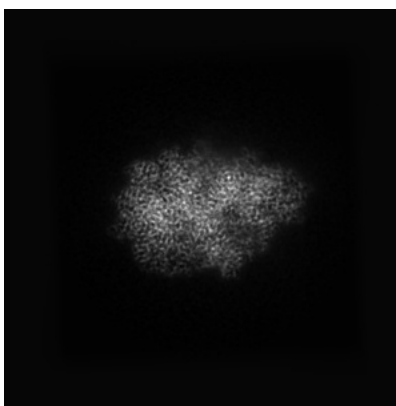
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

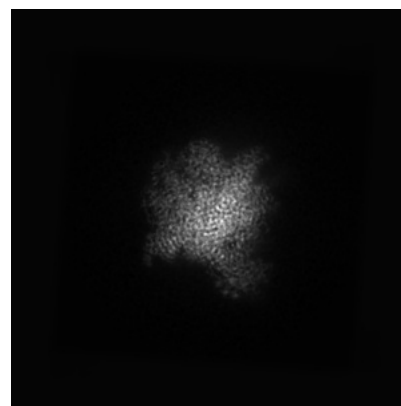
6.1.1 Primary map



X

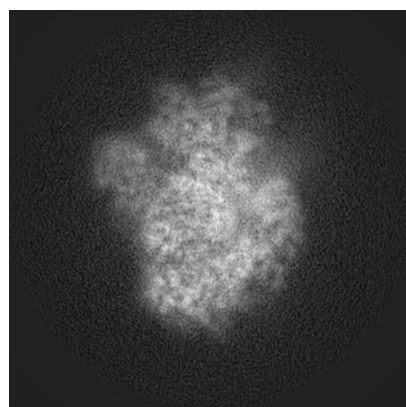


Y

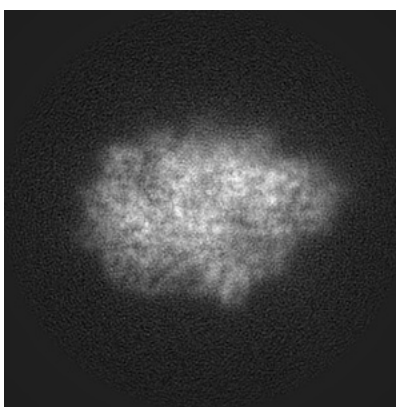


Z

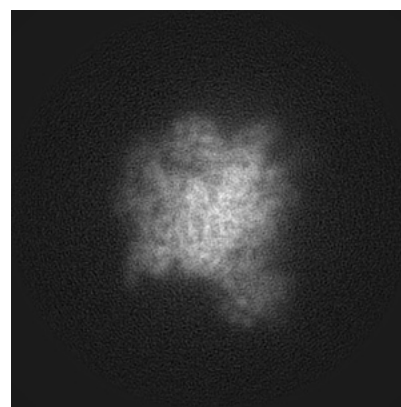
6.1.2 Raw map



X



Y

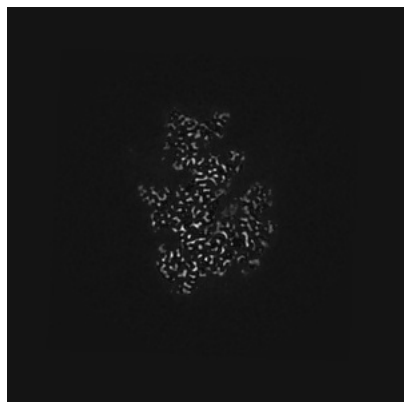


Z

The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 173

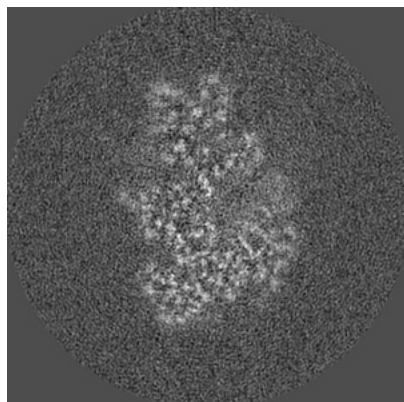


Y Index: 173

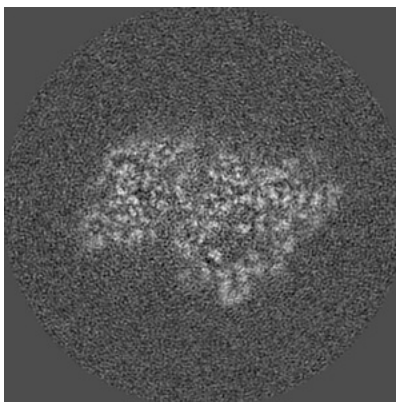


Z Index: 173

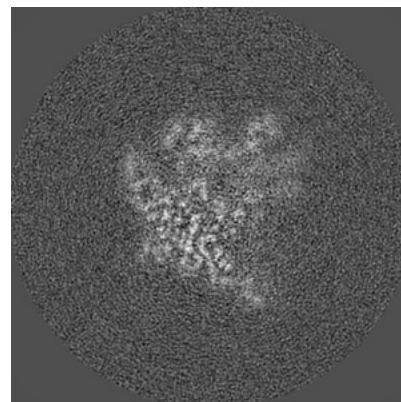
6.2.2 Raw map



X Index: 130



Y Index: 130

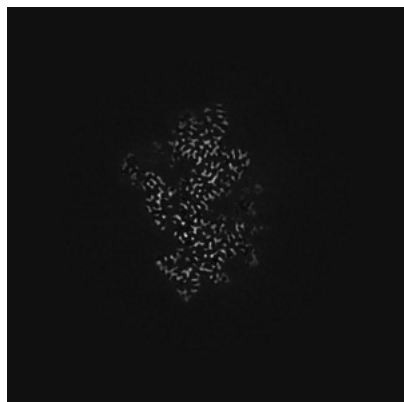


Z Index: 130

The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 182

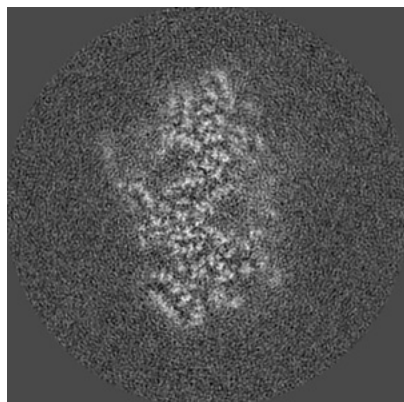


Y Index: 161

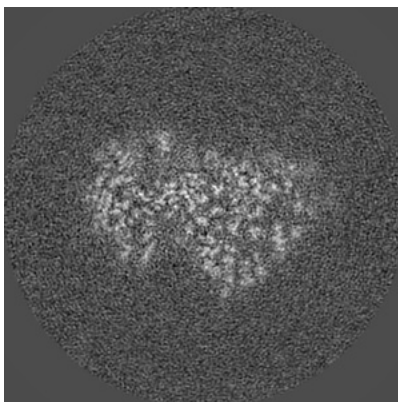


Z Index: 145

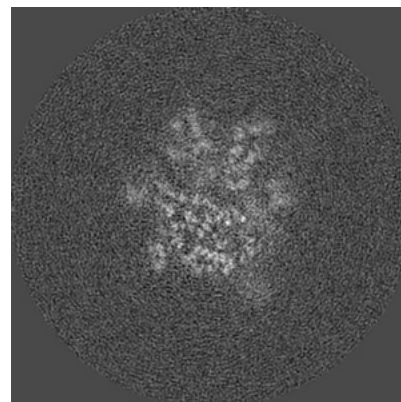
6.3.2 Raw map



X Index: 136



Y Index: 123

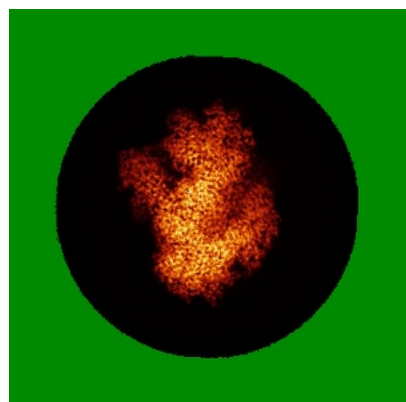


Z Index: 120

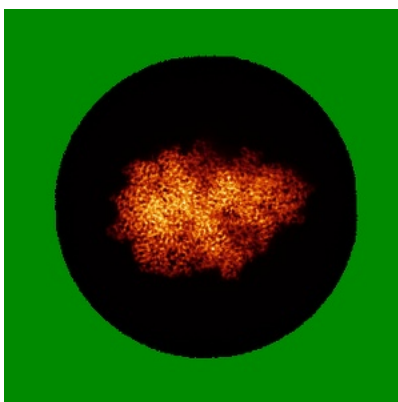
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

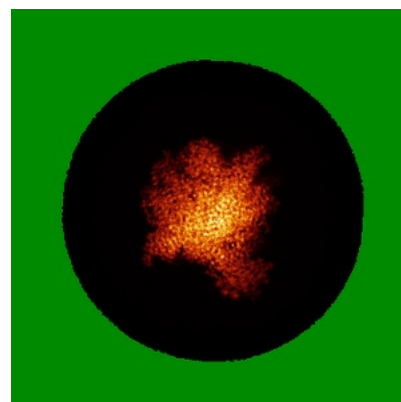
6.4.1 Primary map



X

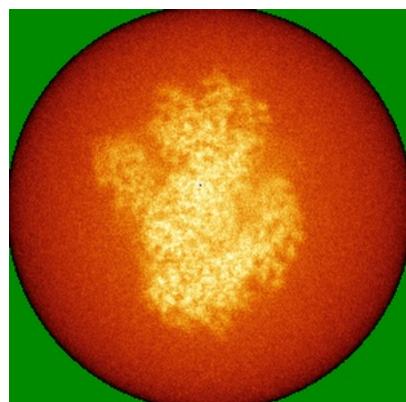


Y

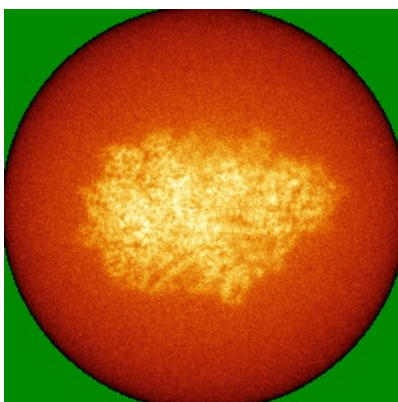


Z

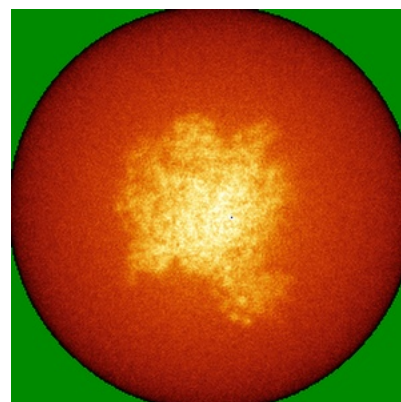
6.4.2 Raw map



X



Y

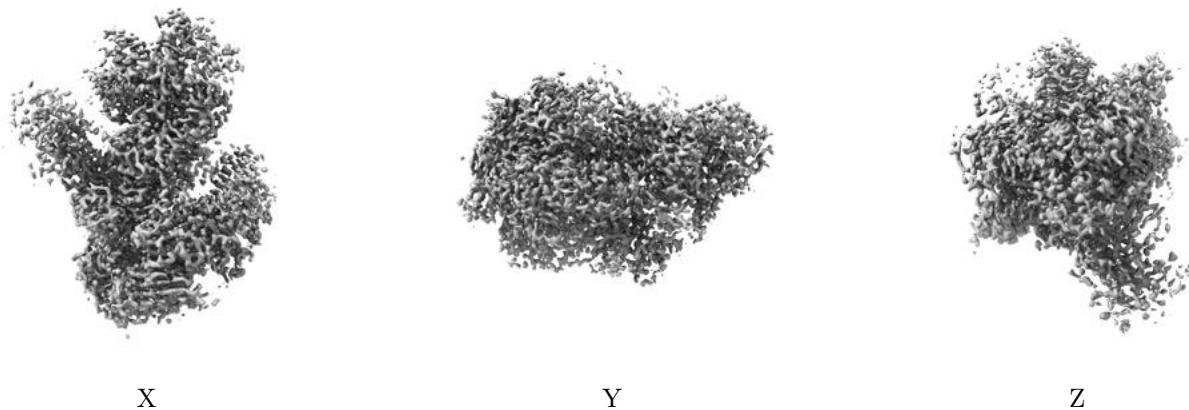


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

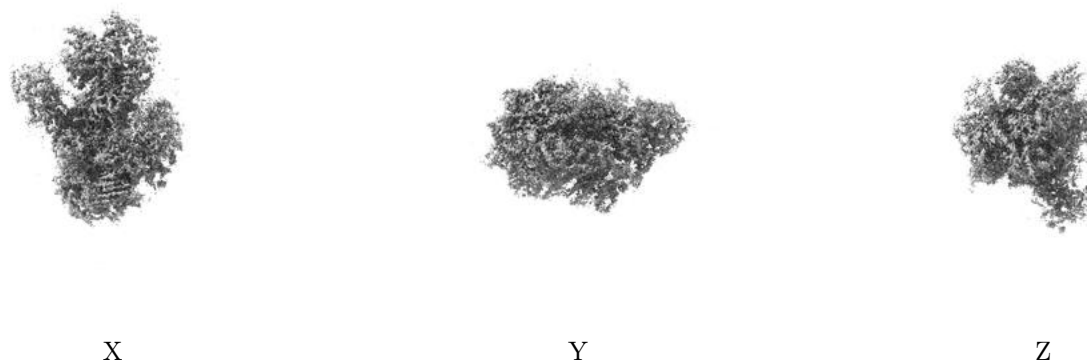
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

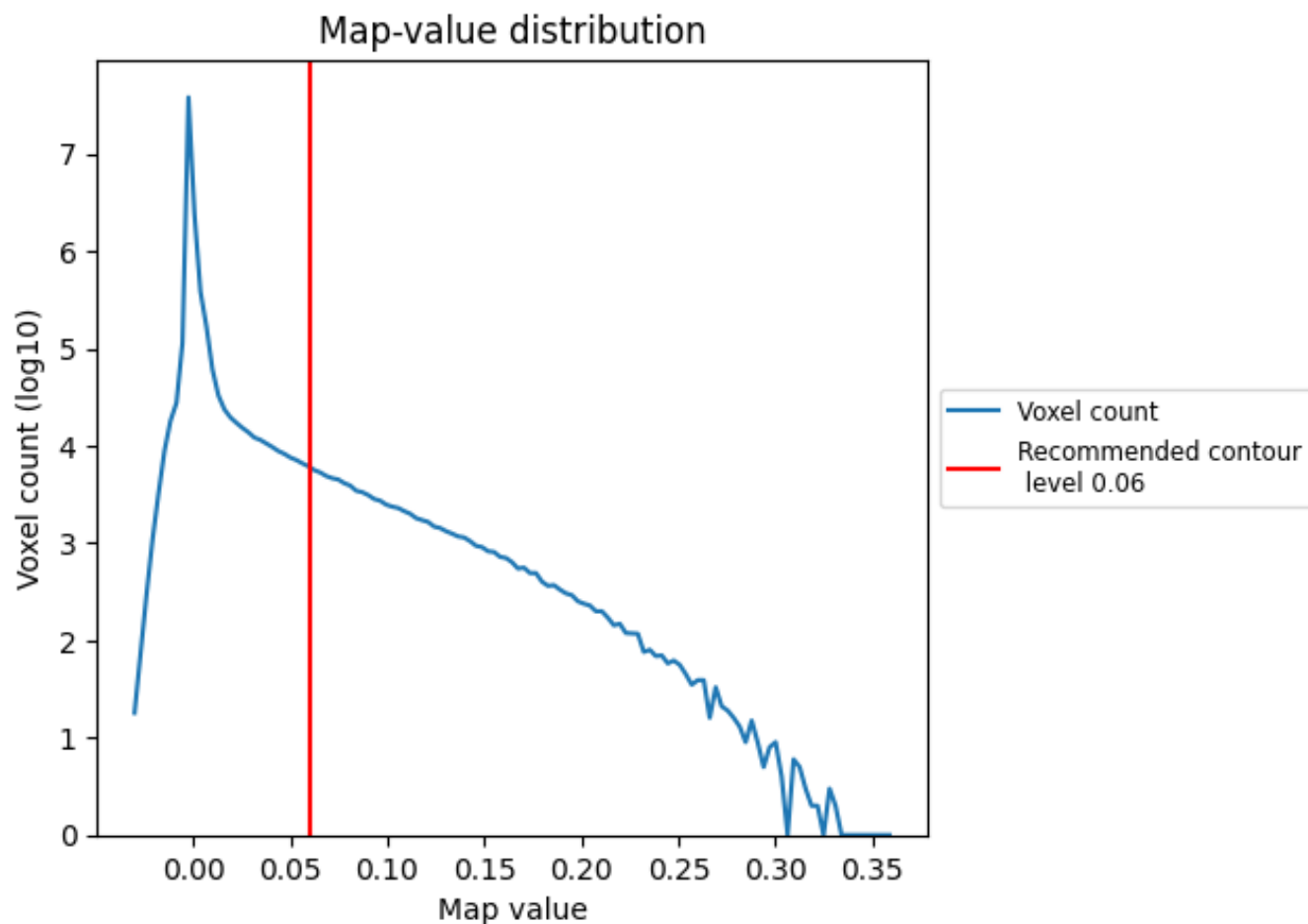
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

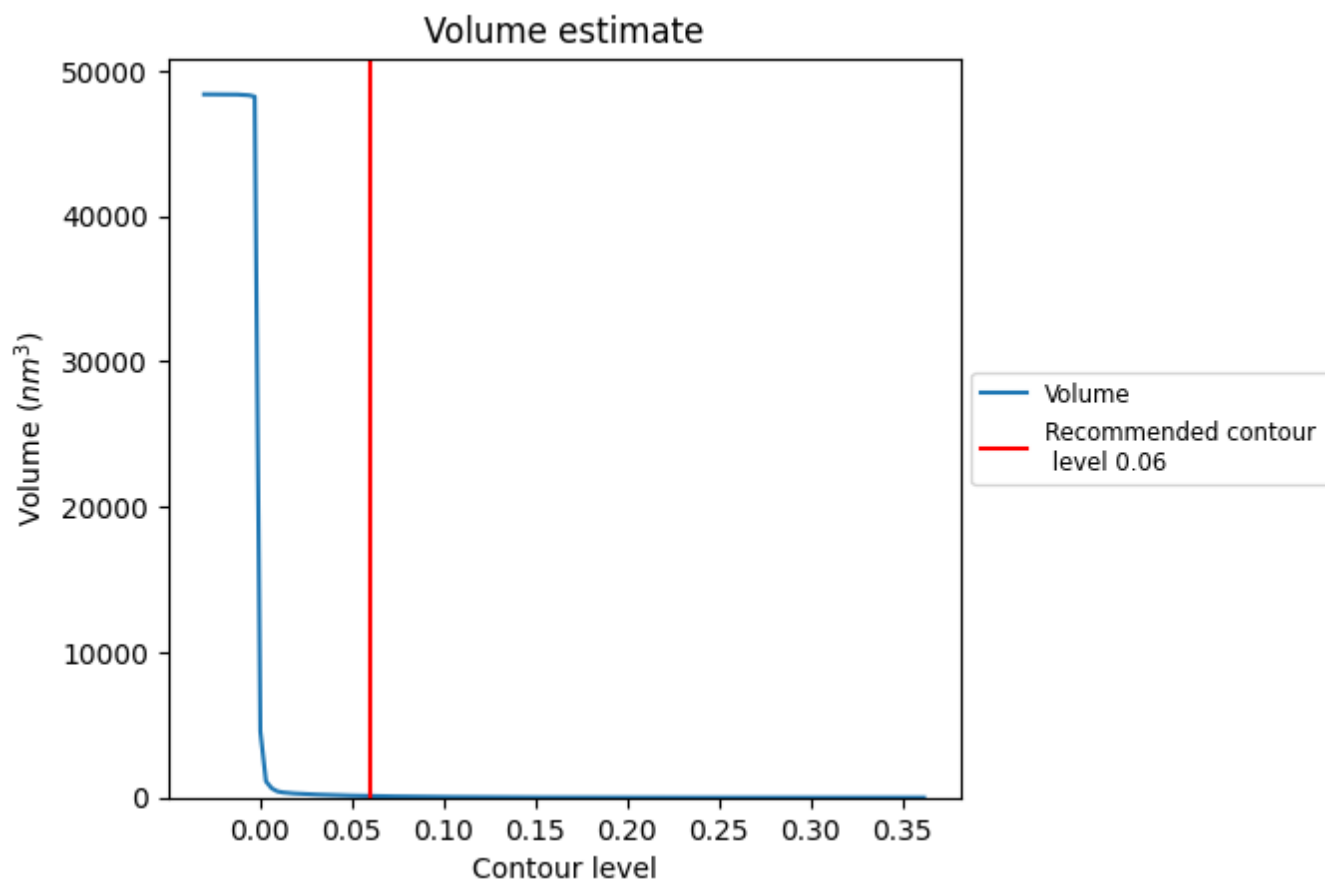
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

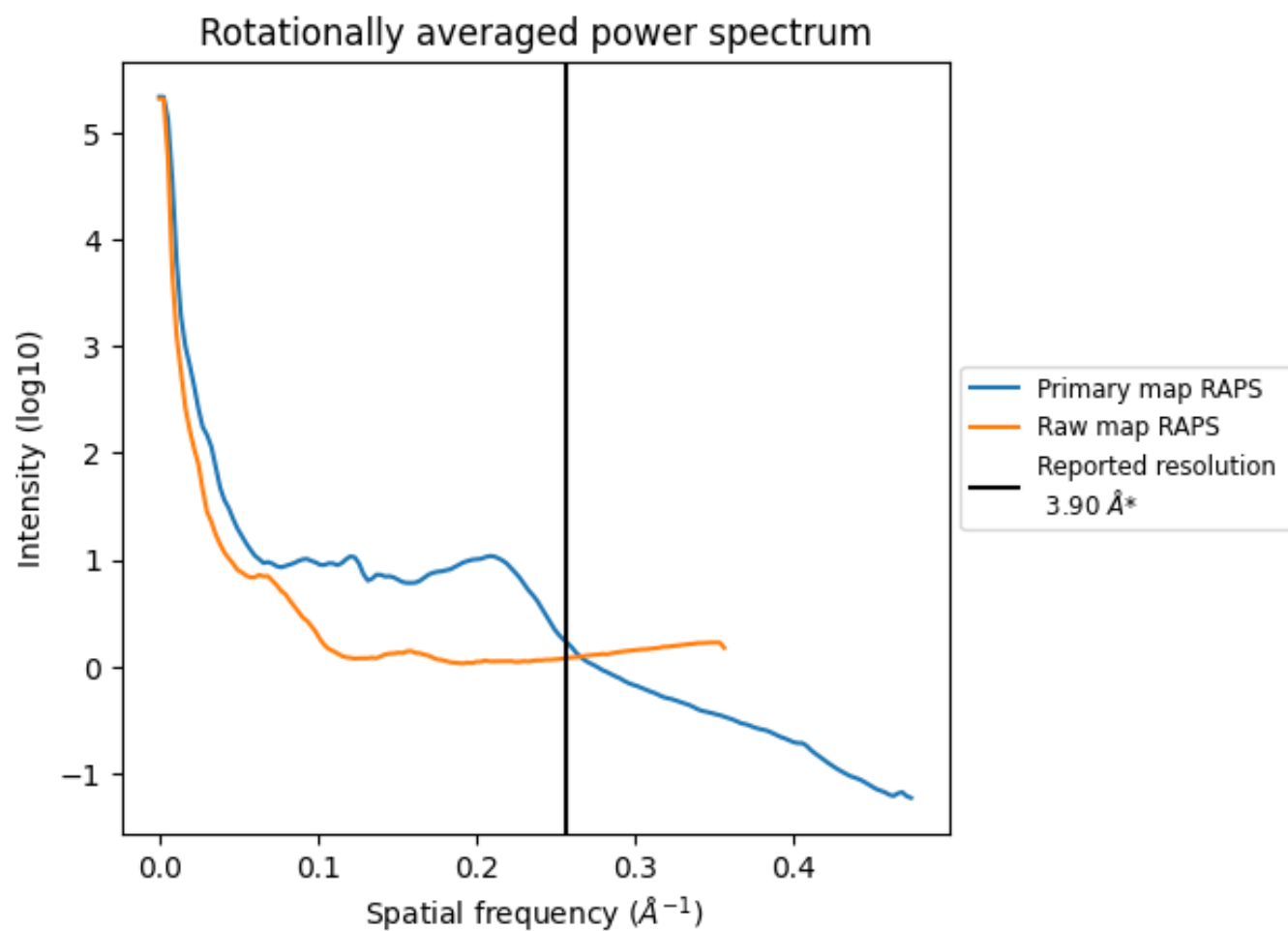
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 106 nm^3 ; this corresponds to an approximate mass of 96 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

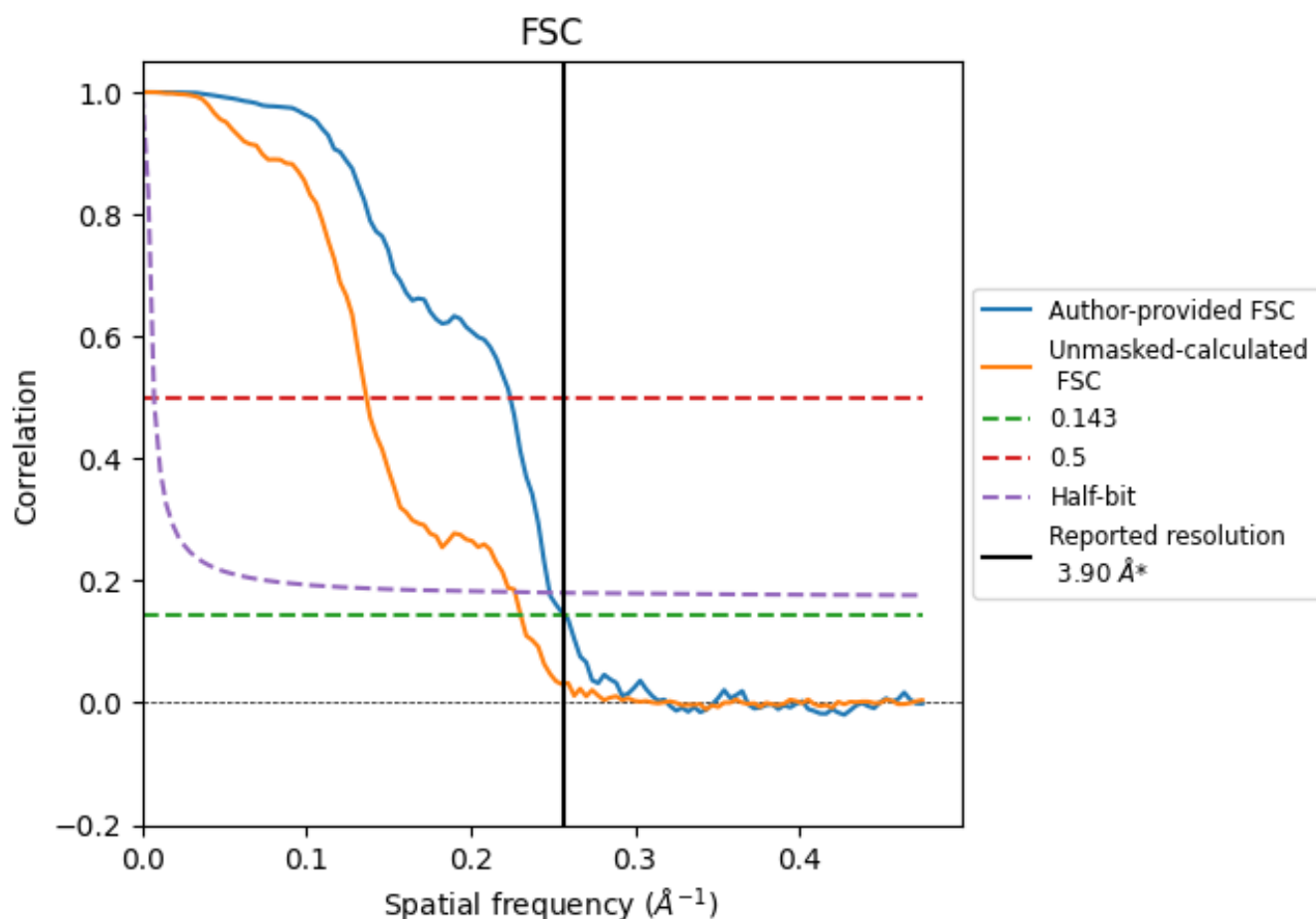


*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.256 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

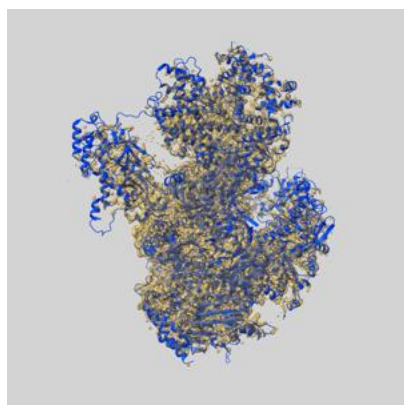
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.89	4.46	4.03
Unmasked-calculated*	4.34	7.33	4.41

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.34 differs from the reported value 3.9 by more than 10 %

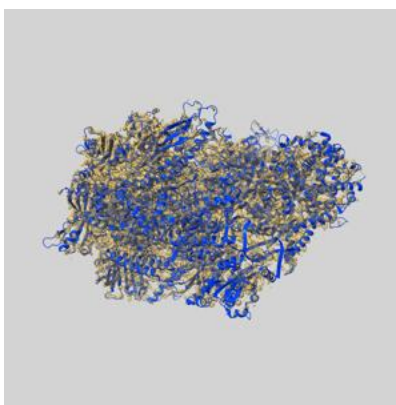
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14449 and PDB model 7Z1N. Per-residue inclusion information can be found in section [3](#) on page [8](#).

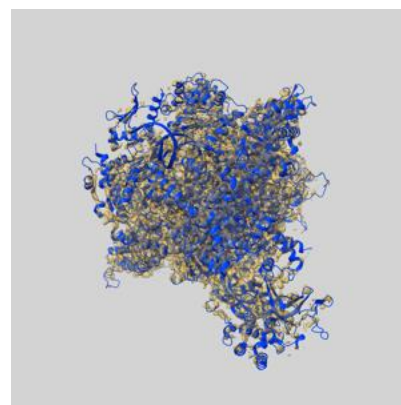
9.1 Map-model overlay [i](#)



X



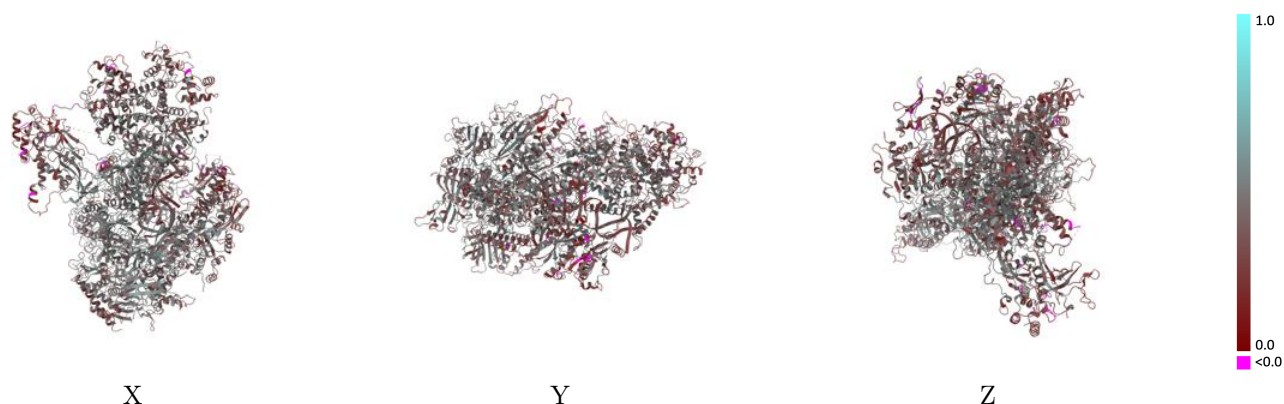
Y



Z

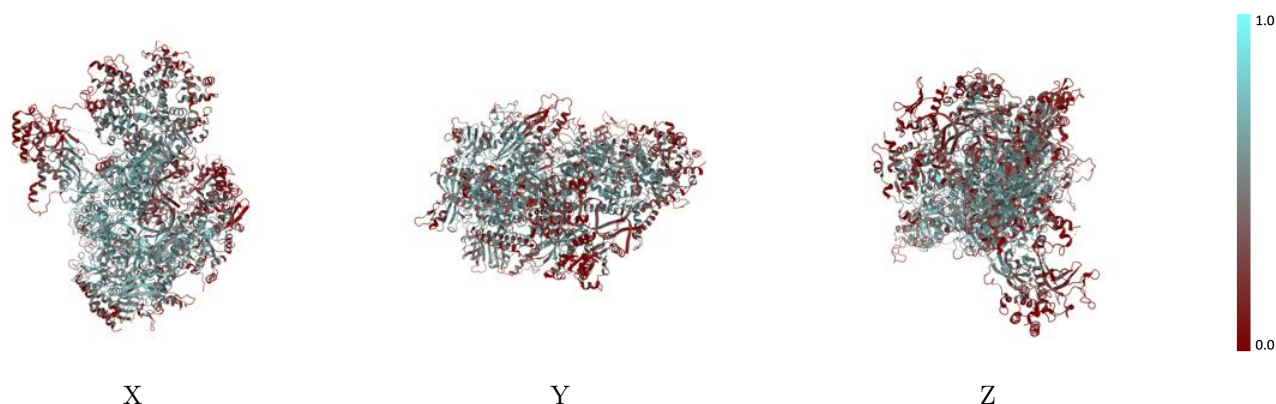
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



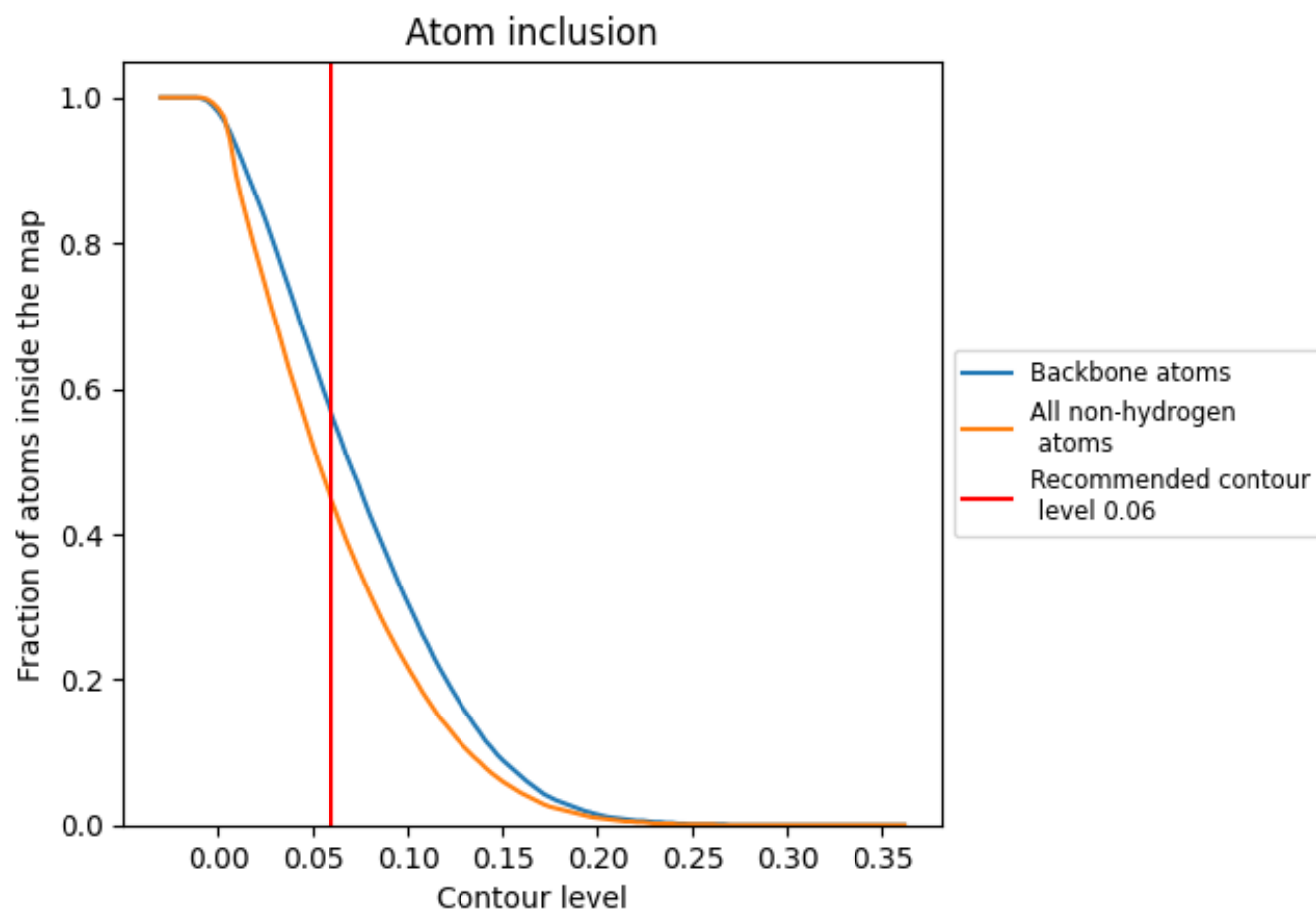
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.06).

9.4 Atom inclusion [i](#)



At the recommended contour level, 56% of all backbone atoms, 45% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4460	0.4050
A	0.5120	0.4250
B	0.4570	0.4160
C	0.4720	0.4240
D	0.1780	0.2920
E	0.4040	0.3980
F	0.5850	0.4620
G	0.3420	0.3750
H	0.4720	0.4280
J	0.5360	0.4330
K	0.4800	0.4080
L	0.4450	0.4480
O	0.4220	0.3920
P	0.2880	0.3500
Q	0.3060	0.3490
R	0.5180	0.4060
S	0.2730	0.2880
T	0.3670	0.3320

1.0

0.0

<0.0