



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:58 AM UTC

PDB ID : 7AST / pdb_00007ast
EMDB ID : EMD-11904
Title : Apo Human RNA Polymerase III
Authors : Ramsay, E.P.; Abascal-Palacios, G.; Daiss, J.L.; King, H.; Gouge, J.; Pilsl, M.;
Beuron, F.; Morris, E.; Gunkel, P.; Engel, C.; Vannini, A.
Deposited on : 2020-10-28
Resolution : 4.00 Å(reported)

This is a wwPDB EM 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/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:

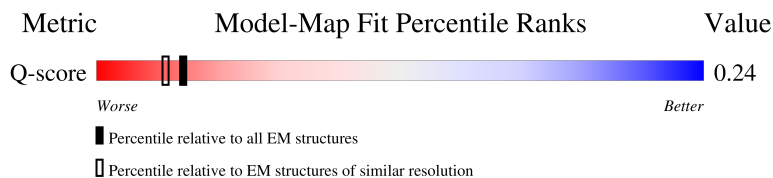
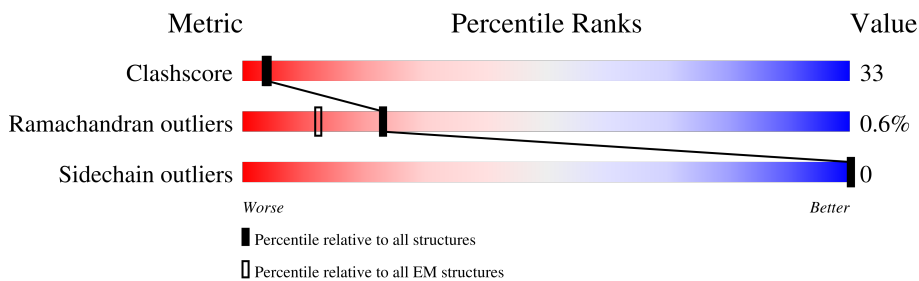
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.00 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	-
Q-score	-	25397	7587 (3.50 - 4.50)

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			
			5%	43%	45%	11%
1	N	1390	5%	43%	45%	11%
2	A	108	18%	16%	66%	
3	B	67	43%	52%		
4	C	58	28%	50%	21%	

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Mol	Chain	Length	Quality of chain
5	D	150	21% 55% 19% 6%
6	E	127	24% 39% 36% 6%
7	F	210	45% 53%
8	G	133	39% 36% 25%
9	H	346	38% 56% 5%
10	I	148	34% 50% 16% 31%
11	J	204	45% 43% 12% 19%
12	K	708	8% 11% 81%
13	L	398	7% 13% 79%
14	M	1133	42% 55%
15	Z	316	12% 8% 80% 5%
16	X	534	52% 30% 18% 30%
17	Y	36	72% 28% 47%

2 Entry composition [i](#)

There are 17 unique types of molecules in this entry. The entry contains 34518 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
			Total	C	N	O	S		
1	N	1238	9385	5928	1643	1746	68	0	0

- Molecule 2 is a protein called DNA-directed RNA polymerase III subunit RPC10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	A	37	288	179	55	49	5	0	0

- Molecule 3 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	B	64	507	328	86	87	6	0	0

- Molecule 4 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	C	46	388	241	75	66	6	0	0

- Molecule 5 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	D	121	972	627	160	179	6	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	E	81	649	414	111	119	5	0	0

- Molecule 7 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	F	209	1715	1083	300	324	8	0	0

- Molecule 8 is a protein called DNA-directed RNA polymerases I and III subunit RPAC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	G	100	794	493	142	152	7	0	0

- Molecule 9 is a protein called DNA-directed RNA polymerases I and III subunit RPAC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	H	329	2635	1663	472	489	11	0	0

- Molecule 10 is a protein called DNA-directed RNA polymerase III subunit RPC9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	I	125	1008	631	175	199	3	0	0

- Molecule 11 is a protein called DNA-directed RNA polymerase III subunit RPC8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	J	179	1442	938	226	271	7	0	0

- Molecule 12 is a protein called DNA-directed RNA polymerase III subunit RPC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	K	137	1119	718	192	204	5	0	0

- Molecule 13 is a protein called DNA-directed RNA polymerase III subunit RPC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	L	82	620	397	104	115	4	0	0

- Molecule 14 is a protein called DNA-directed RNA polymerase III subunit RPC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	M	1114	8811	5581	1540	1621	69	0	0

- Molecule 15 is a protein called DNA-directed RNA polymerase III subunit RPC6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	Z	63	518	337	78	99	4	0	0

- Molecule 16 is a protein called DNA-directed RNA polymerase III subunit RPC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	X	440	3487	2193	607	665	22	0	0

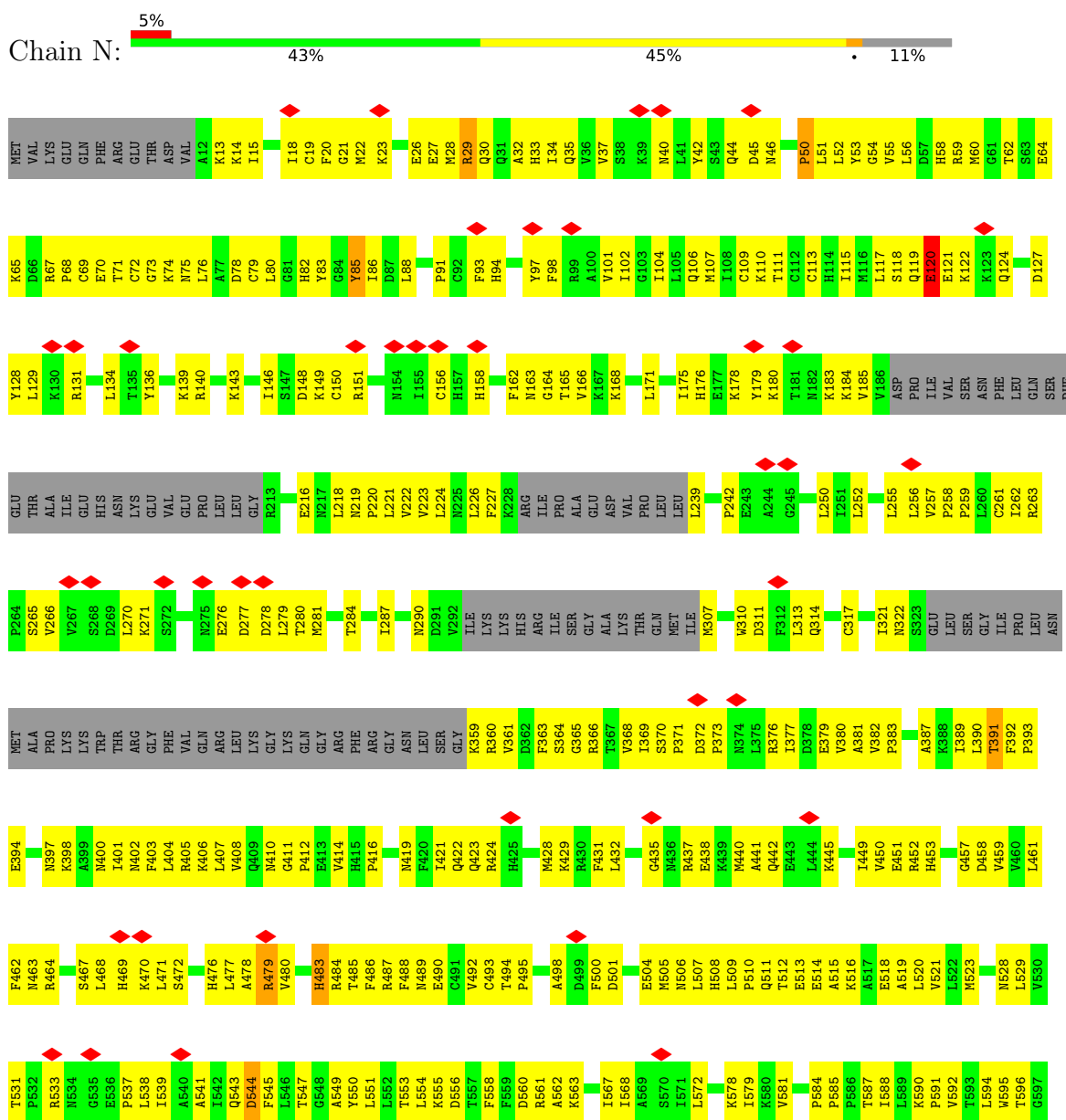
- Molecule 17 is a protein called DNA-directed RNA polymerase III subunit RPC7-beta.

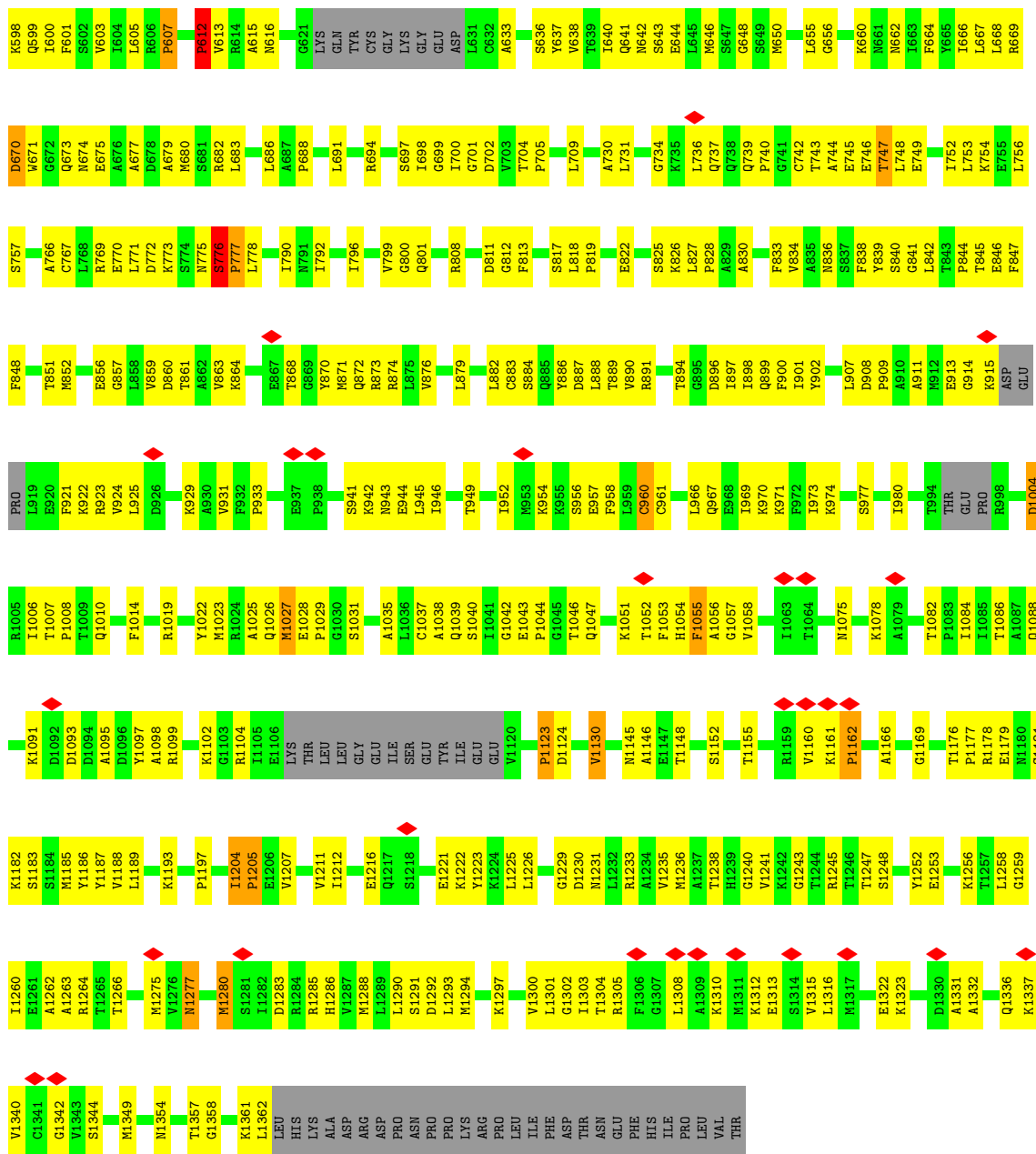
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
17	Y	36	180	108	36	36	0	0

3 Residue-property plots

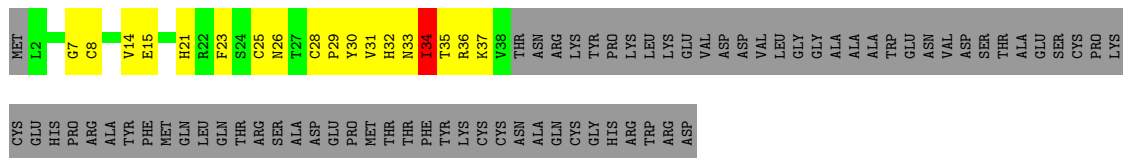
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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 bar. Residues present in the sample, but not in the model, are shown in grey.

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



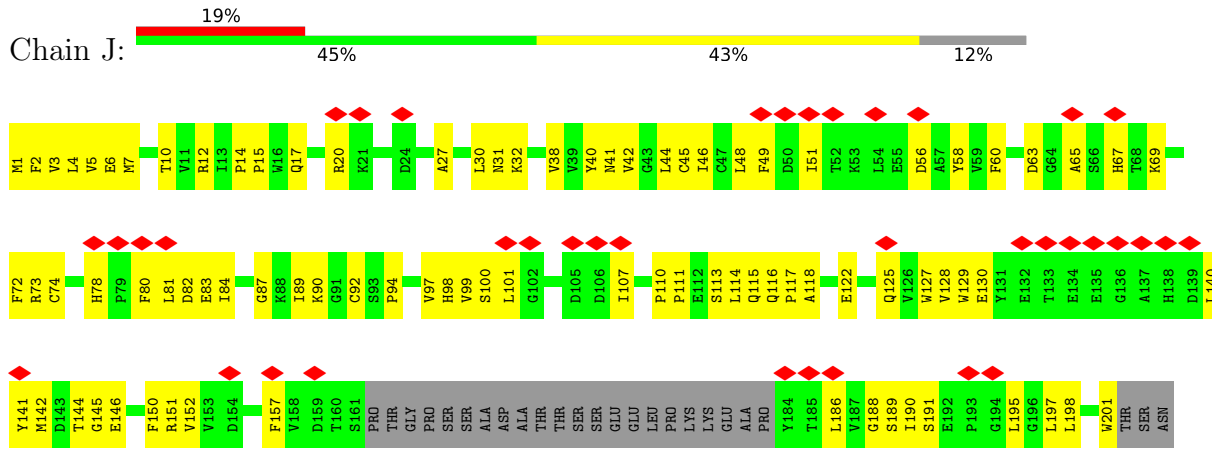


• Molecule 2: DNA-directed RNA polymerase III subunit RPC10

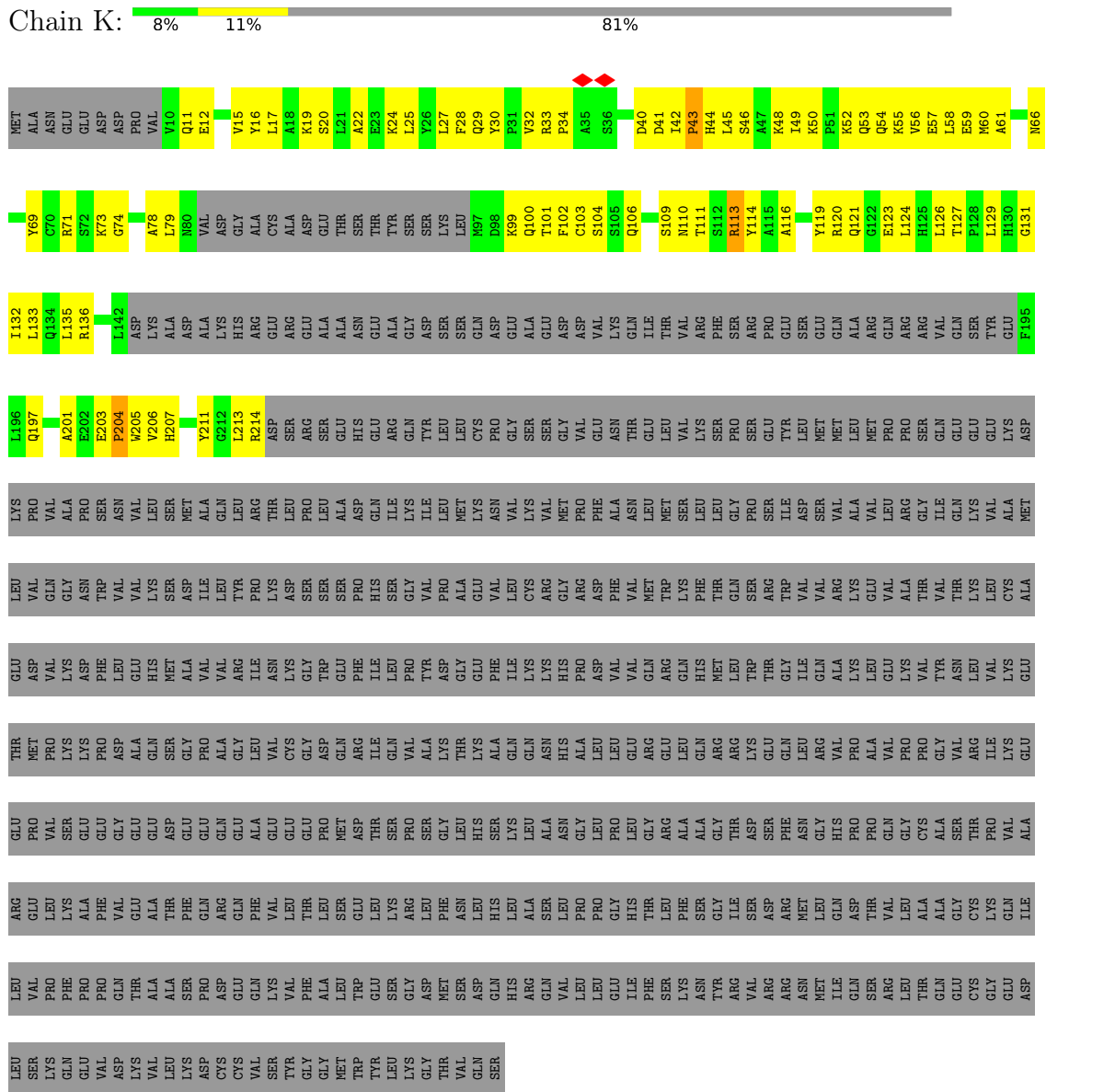


• Molecule 3: DNA-directed RNA polymerases I, II, and III subunit RPABC5

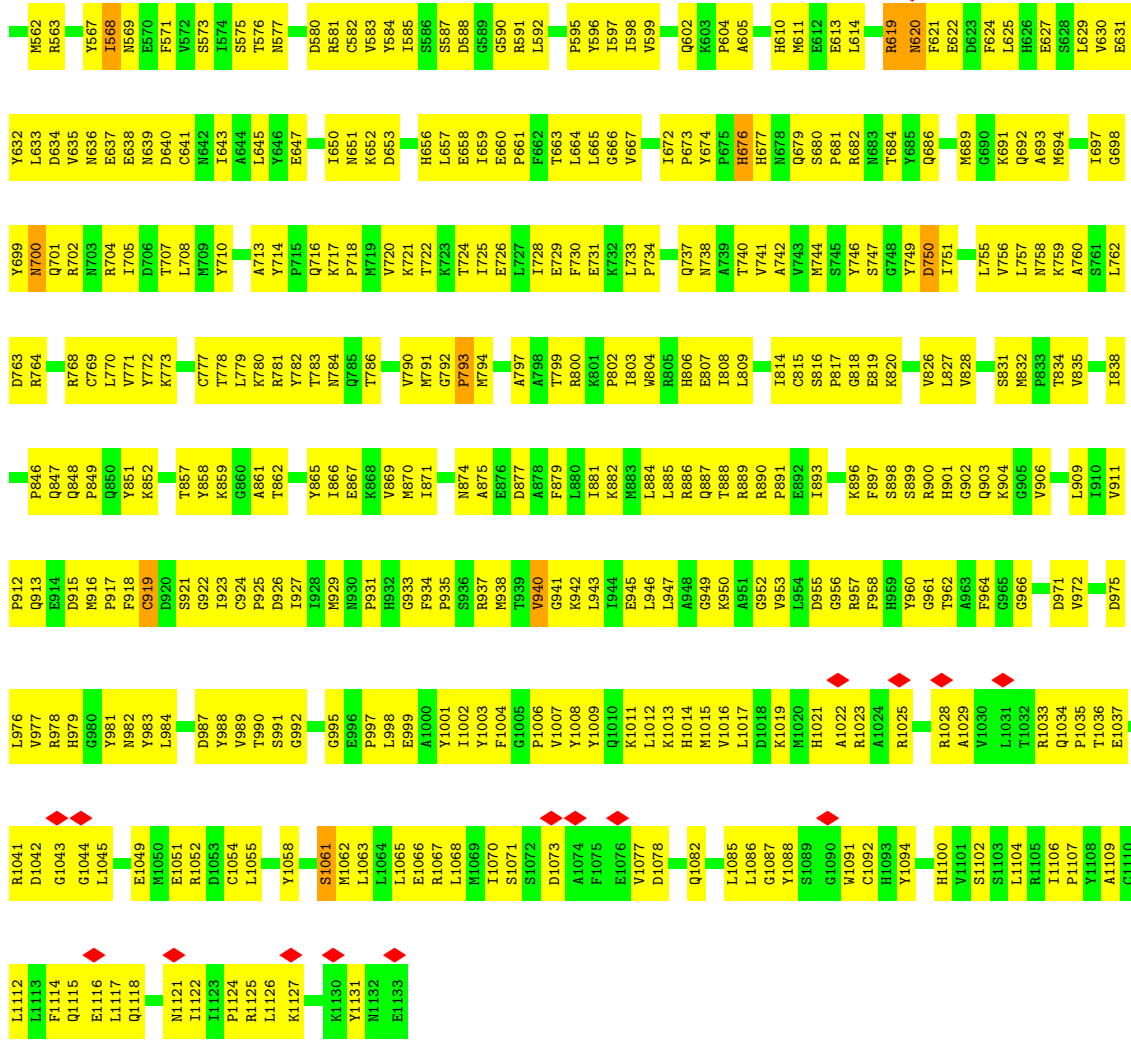




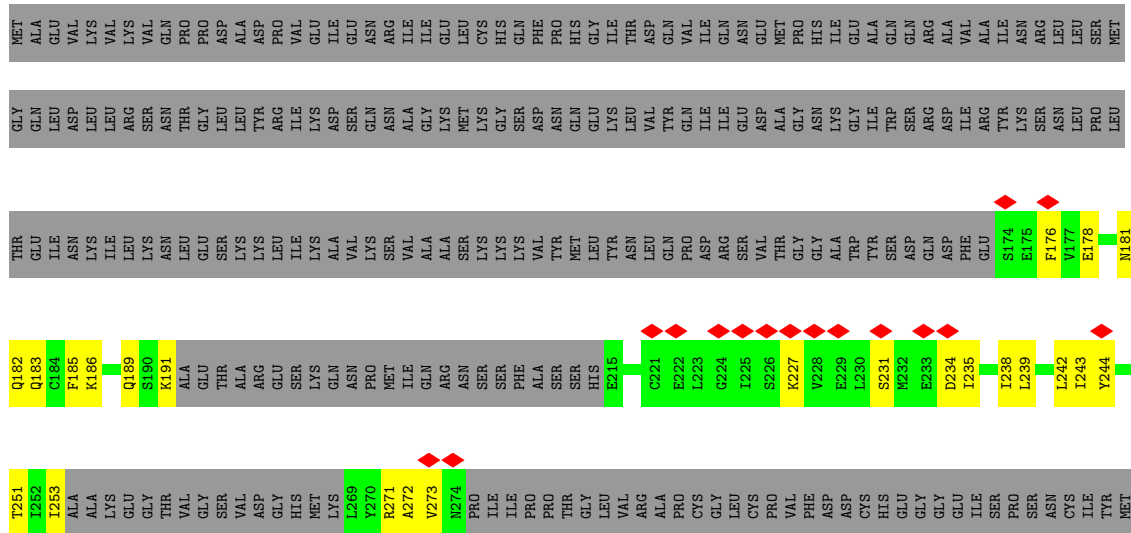
• Molecule 12: DNA-directed RNA polymerase III subunit RPC5



• Molecule 13: DNA-directed RNA polymerase III subunit RPC4

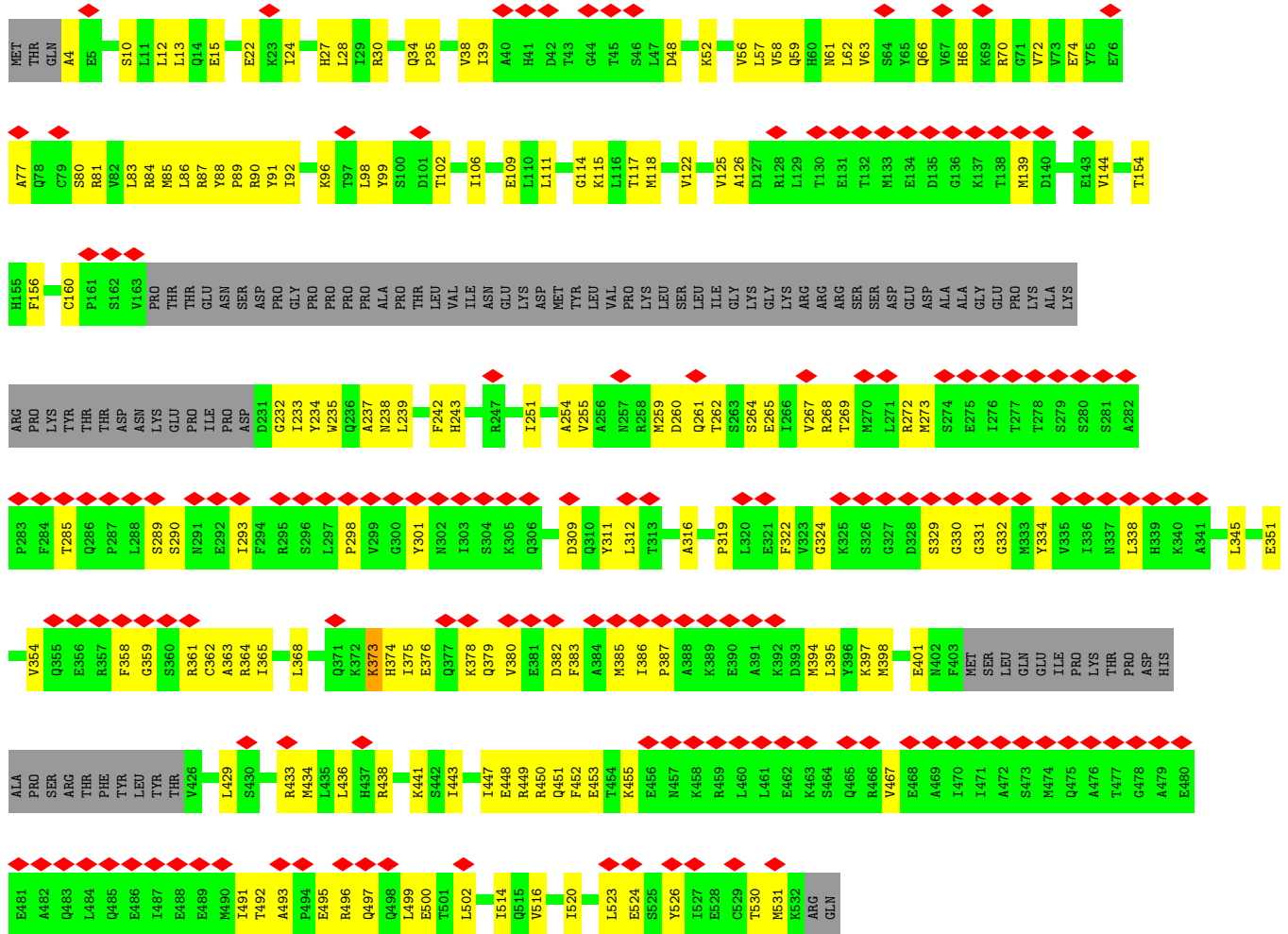


● Molecule 15: DNA-directed RNA polymerase III subunit RPC6

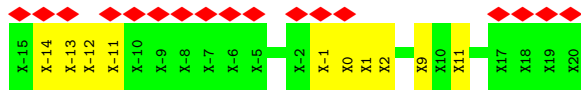
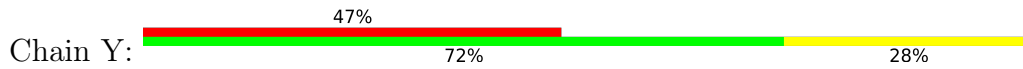


THR
GLU
TRP
LEU
GLU
PHE

• Molecule 16: DNA-directed RNA polymerase III subunit RPC3



• Molecule 17: DNA-directed RNA polymerase III subunit RPC7-beta



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	25369	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.8	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	75000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.365	Depositor
Minimum map value	-0.253	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.027	Depositor
Map size (Å)	383.40002, 383.40002, 383.40002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.065, 1.065, 1.065	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	N	0.77	8/9535 (0.1%)	0.68	16/12862 (0.1%)
2	A	0.27	0/294	0.86	2/396 (0.5%)
3	B	0.37	0/516	0.70	0/696
4	C	0.25	0/394	0.69	0/524
5	D	2.20	7/988 (0.7%)	0.97	4/1323 (0.3%)
6	E	0.21	0/659	0.63	0/891
7	F	0.18	0/1745	0.53	1/2358 (0.0%)
8	G	0.30	0/808	0.57	0/1090
9	H	0.28	0/2689	0.67	0/3644
10	I	0.17	0/1021	0.46	0/1377
11	J	0.19	0/1481	0.46	0/2013
12	K	0.20	0/1146	0.57	0/1549
13	L	0.19	0/626	0.59	0/842
14	M	0.29	0/8982	0.65	5/12118 (0.0%)
15	Z	0.17	0/523	0.53	0/701
16	X	0.14	0/3534	0.41	0/4766
All	All	0.58	15/34941 (0.0%)	0.63	28/47150 (0.1%)

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	N	0	16
2	A	0	1
3	B	0	1
4	C	0	1
5	D	0	5
6	E	0	1
7	F	0	2
9	H	0	7
12	K	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
13	L	0	4
14	M	0	16
16	X	0	1
All	All	0	58

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	N	29	ARG	CB-CG	57.79	3.25	1.52
5	D	146	LYS	CD-CE	52.46	3.09	1.52
5	D	88	PHE	CD1-CE1	20.25	1.99	1.38
5	D	88	PHE	CD2-CE2	20.19	1.99	1.38
1	N	85	TYR	CD2-CE2	20.18	1.99	1.38

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	146	LYS	CG-CD-CE	13.09	141.41	111.30
1	N	29	ARG	CA-CB-CG	10.35	134.80	114.10
1	N	29	ARG	CB-CG-CD	10.05	134.41	111.30
1	N	612	PRO	N-CA-CB	8.24	111.90	103.25
1	N	1123	PRO	N-CA-CB	7.59	110.40	103.34

There are no chirality outliers.

5 of 58 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	N	120	GLU	Peptide
1	N	480	VAL	Peptide
1	N	483	HIS	Peptide
1	N	563	LYS	Peptide
1	N	572	LEU	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	N	9385	0	9273	689	0
2	A	288	0	279	24	0
3	B	507	0	525	53	0
4	C	388	0	395	38	0
5	D	972	0	959	159	0
6	E	649	0	678	60	0
7	F	1715	0	1733	104	0
8	G	794	0	780	54	0
9	H	2635	0	2620	211	0
10	I	1008	0	1035	77	0
11	J	1442	0	1396	82	0
12	K	1119	0	1109	84	0
13	L	620	0	660	67	0
14	M	8811	0	8937	671	0
15	Z	518	0	525	26	0
16	X	3487	0	3523	139	0
17	Y	180	0	41	5	0
All	All	34518	0	34468	2263	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 33.

The worst 5 of 2263 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:N:85:TYR:CZ	1:N:85:TYR:CE2	1.75	1.70
1:N:85:TYR:CZ	1:N:85:TYR:CE1	1.75	1.60
5:D:88:PHE:CE1	5:D:88:PHE:CZ	1.95	1.54
1:N:85:TYR:CE1	1:N:85:TYR:CD1	1.96	1.53
5:D:88:PHE:CZ	5:D:88:PHE:CE2	1.95	1.53

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 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	N	1220/1390 (88%)	948 (78%)	258 (21%)	14 (1%)	11	44
2	A	35/108 (32%)	23 (66%)	11 (31%)	1 (3%)	3	26
3	B	62/67 (92%)	54 (87%)	8 (13%)	0	100	100
4	C	44/58 (76%)	32 (73%)	11 (25%)	1 (2%)	5	31
5	D	115/150 (77%)	77 (67%)	38 (33%)	0	100	100
6	E	79/127 (62%)	56 (71%)	22 (28%)	1 (1%)	9	41
7	F	207/210 (99%)	182 (88%)	24 (12%)	1 (0%)	24	60
8	G	98/133 (74%)	71 (72%)	27 (28%)	0	100	100
9	H	327/346 (94%)	246 (75%)	80 (24%)	1 (0%)	36	70
10	I	123/148 (83%)	113 (92%)	10 (8%)	0	100	100
11	J	175/204 (86%)	138 (79%)	37 (21%)	0	100	100
12	K	131/708 (18%)	92 (70%)	38 (29%)	1 (1%)	16	52
13	L	78/398 (20%)	60 (77%)	17 (22%)	1 (1%)	9	41
14	M	1112/1133 (98%)	831 (75%)	276 (25%)	5 (0%)	30	65
15	Z	57/316 (18%)	50 (88%)	7 (12%)	0	100	100
16	X	434/534 (81%)	405 (93%)	29 (7%)	0	100	100
All	All	4297/6030 (71%)	3378 (79%)	893 (21%)	26 (1%)	23	57

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	N	607	PRO
1	N	612	PRO
1	N	777	PRO
1	N	1162	PRO
1	N	1205	PRO

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 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	N	983/1212 (81%)	983 (100%)	0	100	100
2	A	33/94 (35%)	33 (100%)	0	100	100
3	B	53/56 (95%)	53 (100%)	0	100	100
4	C	43/55 (78%)	43 (100%)	0	100	100
5	D	103/131 (79%)	103 (100%)	0	100	100
6	E	70/111 (63%)	70 (100%)	0	100	100
7	F	191/192 (100%)	191 (100%)	0	100	100
8	G	89/119 (75%)	89 (100%)	0	100	100
9	H	289/302 (96%)	289 (100%)	0	100	100
10	I	117/136 (86%)	117 (100%)	0	100	100
11	J	160/181 (88%)	160 (100%)	0	100	100
12	K	122/622 (20%)	122 (100%)	0	100	100
13	L	72/347 (21%)	72 (100%)	0	100	100
14	M	973/988 (98%)	973 (100%)	0	100	100
15	Z	60/280 (21%)	60 (100%)	0	100	100
16	X	386/476 (81%)	386 (100%)	0	100	100
All	All	3744/5302 (71%)	3744 (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 58 such sidechains are listed below:

Mol	Chain	Res	Type
10	I	7	ASN
16	X	244	GLN
14	M	62	ASN
16	X	14	GLN
14	M	1034	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

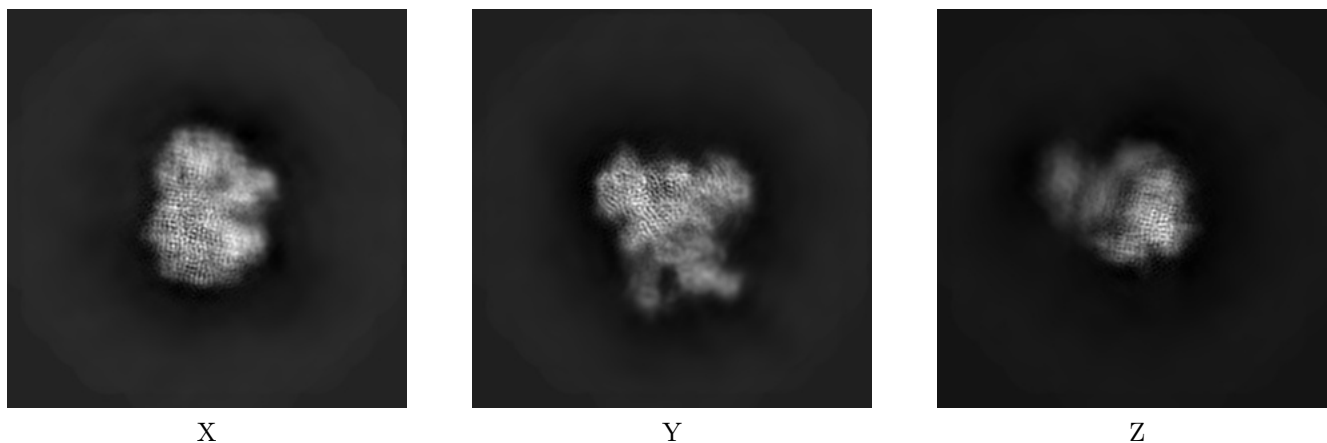
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11904. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

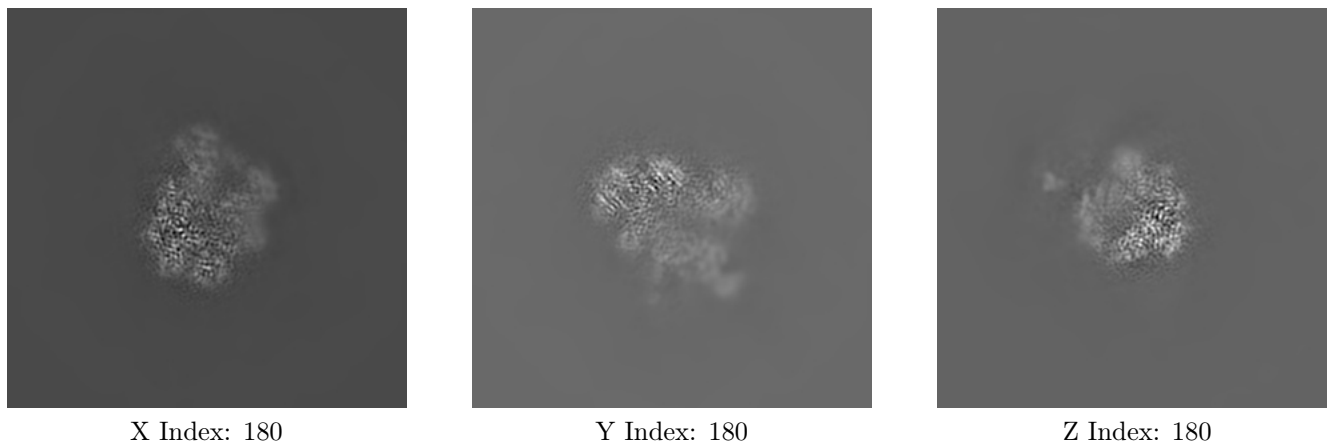
6.1.1 Primary map



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

6.2 Central slices [i](#)

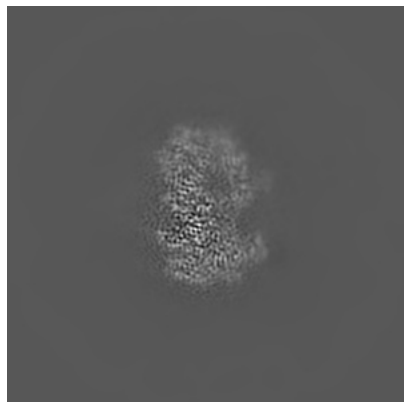
6.2.1 Primary map



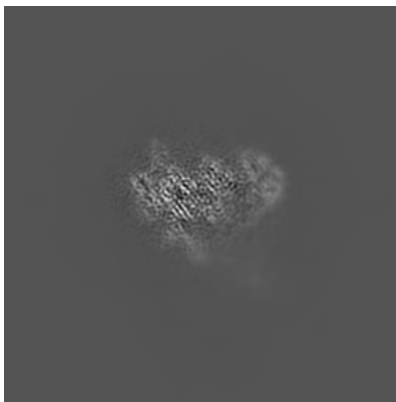
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

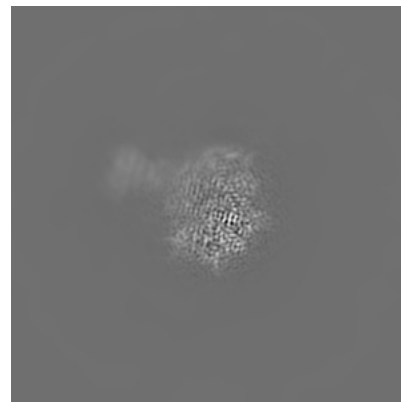
6.3.1 Primary map



X Index: 202



Y Index: 157

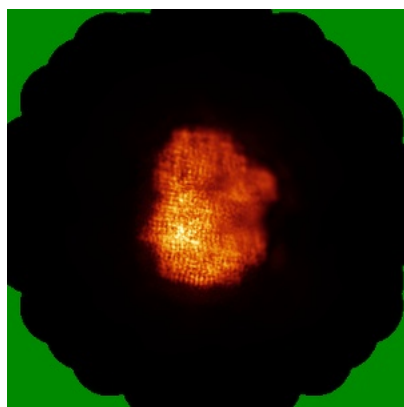


Z Index: 150

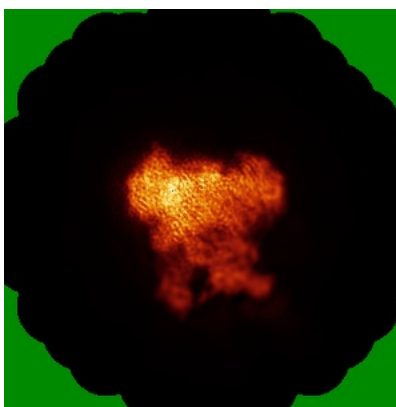
The images above show the largest variance slices of the map in three orthogonal directions.

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

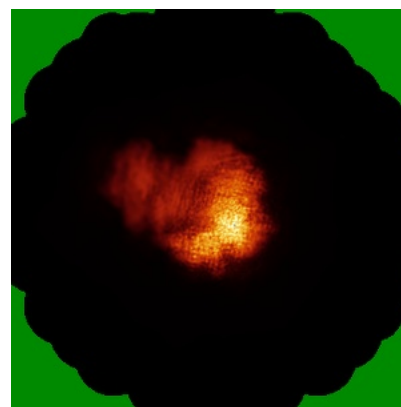
6.4.1 Primary map



X



Y



Z

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

This section was not generated.

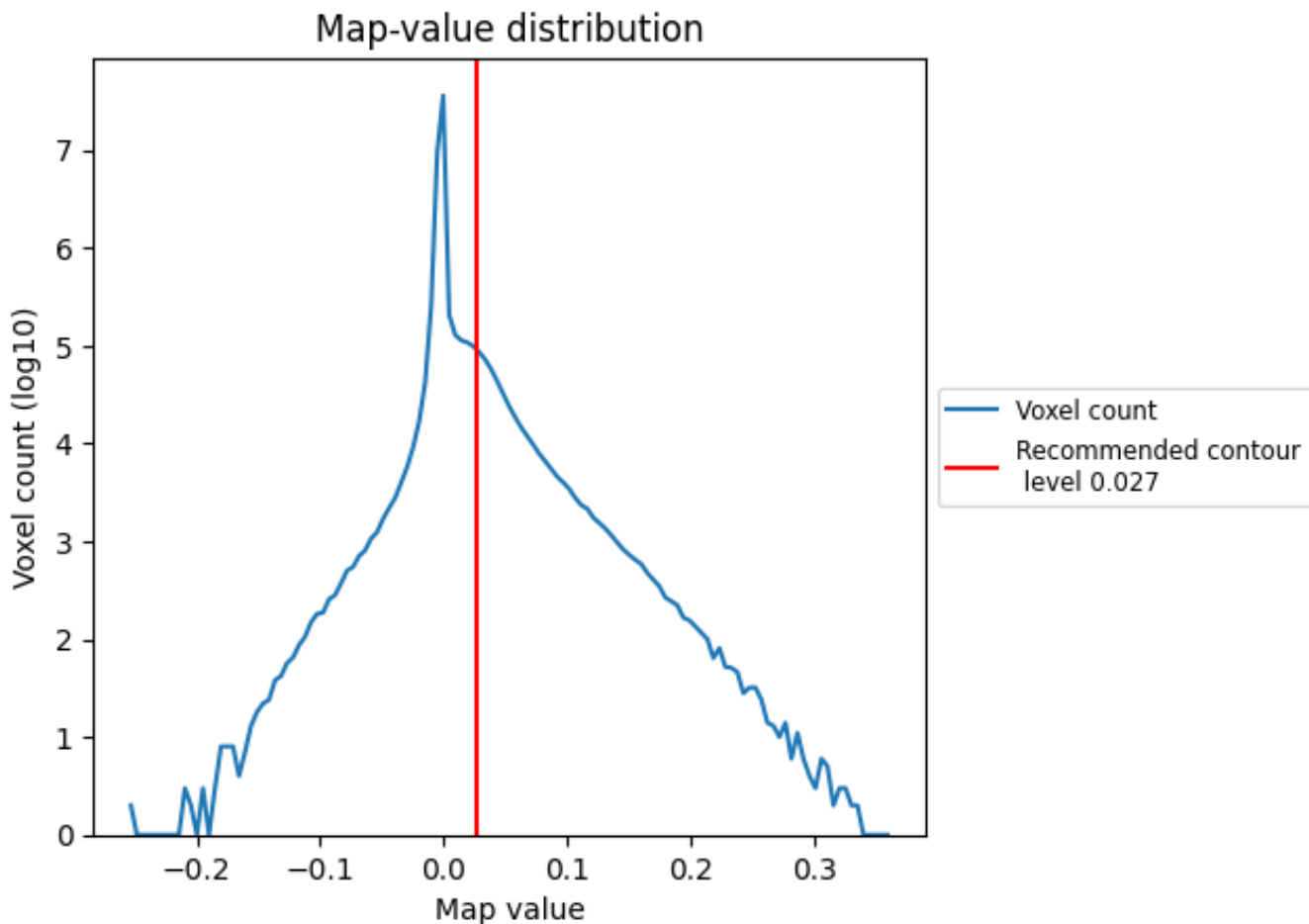
6.6 Mask visualisation

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

7 Map analysis [i](#)

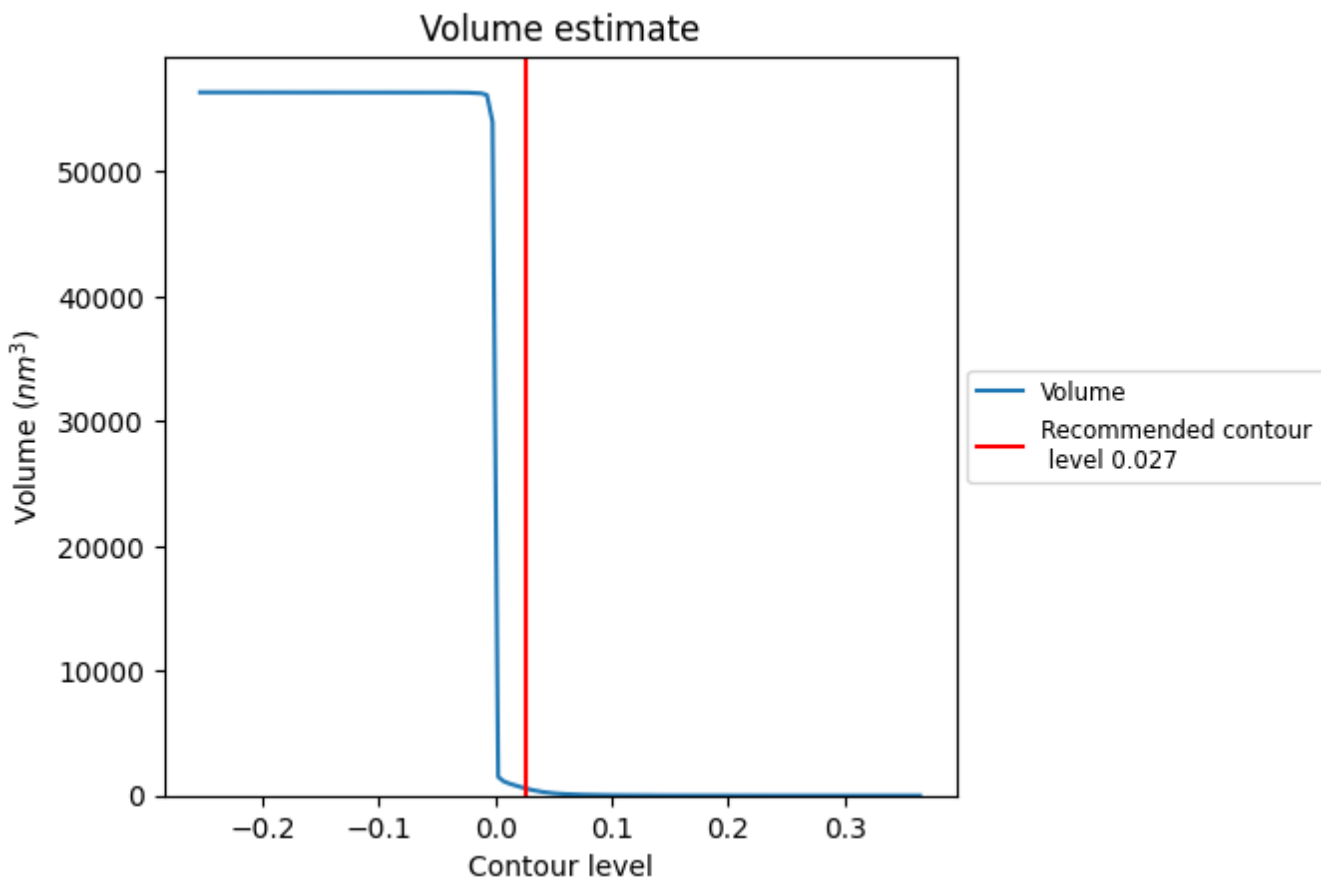
This section contains the results of statistical analysis of the map.

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.

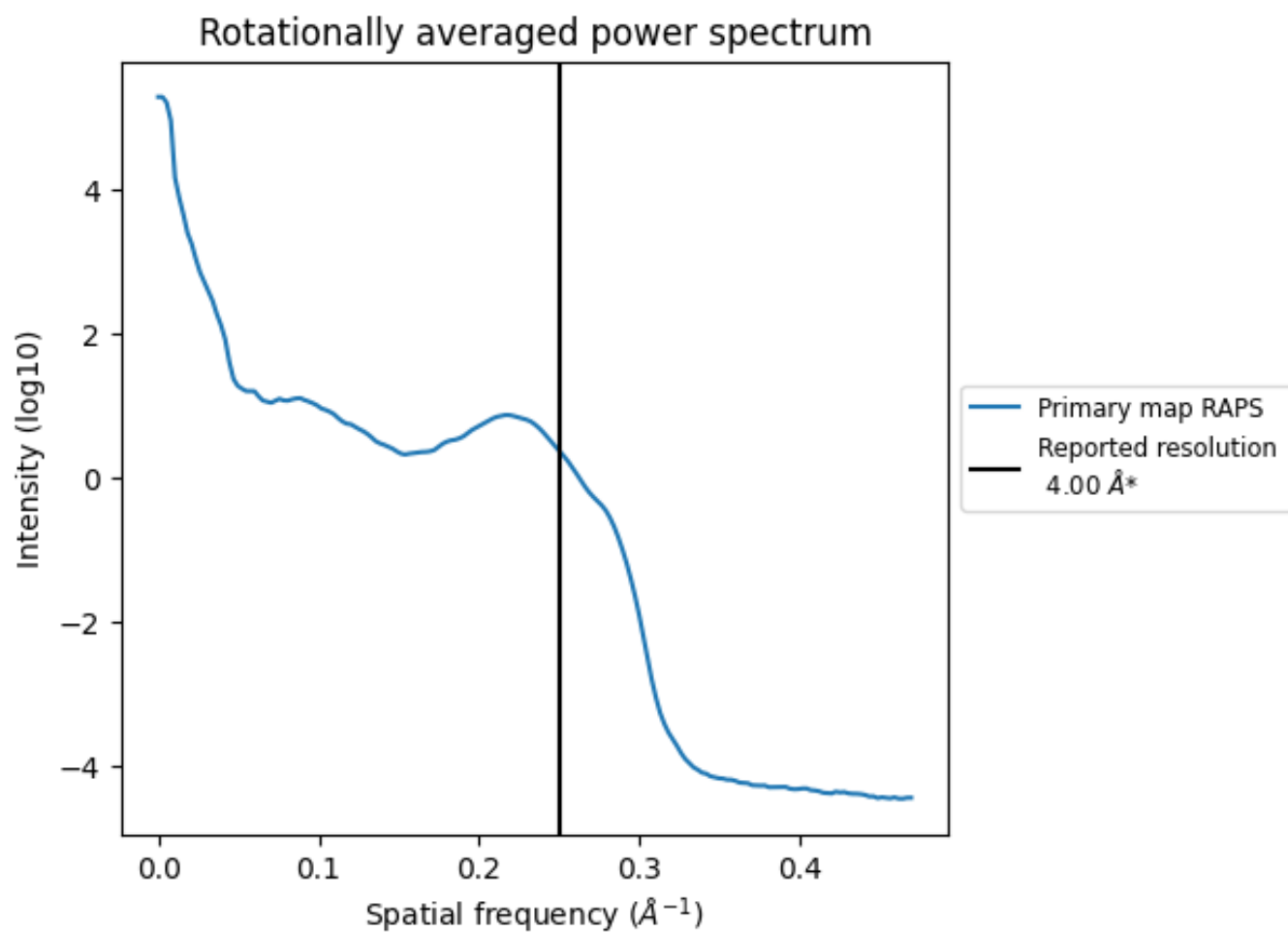
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 555 nm³; this corresponds to an approximate mass of 501 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 [i](#)

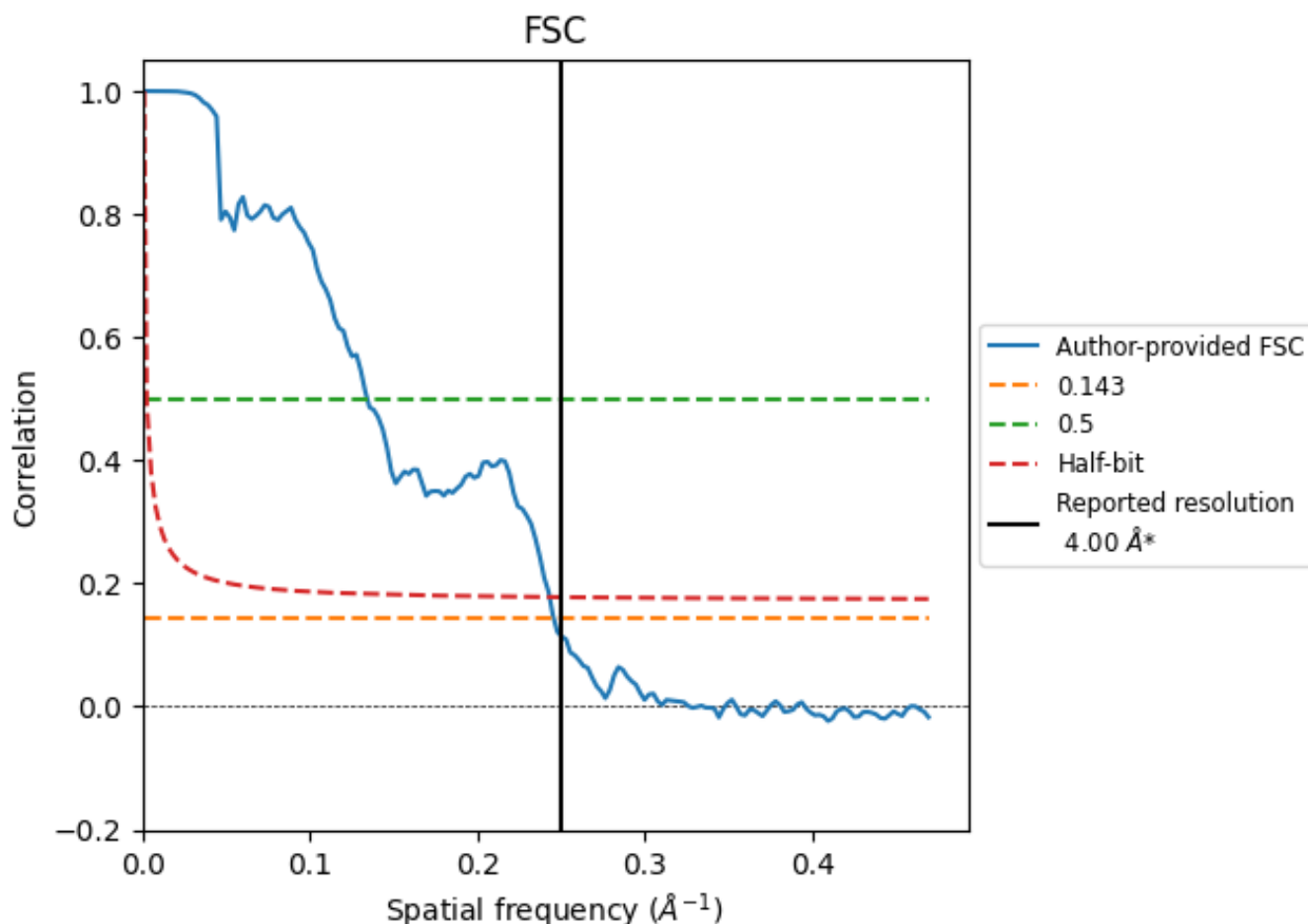


*Reported resolution corresponds to spatial frequency of 0.250 Å⁻¹

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 0.250 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	4.07	7.45	4.11
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

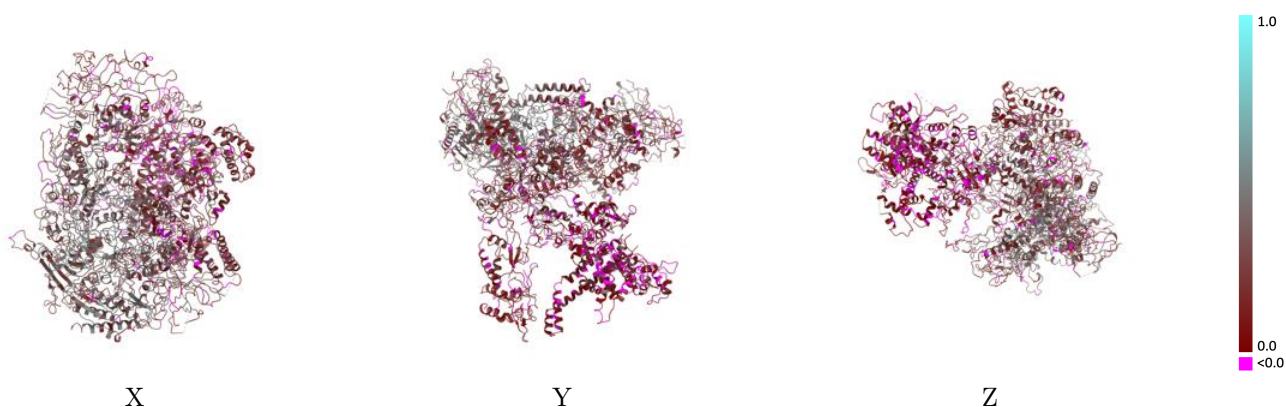
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11904 and PDB model 7AST. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)

This section was not generated.

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

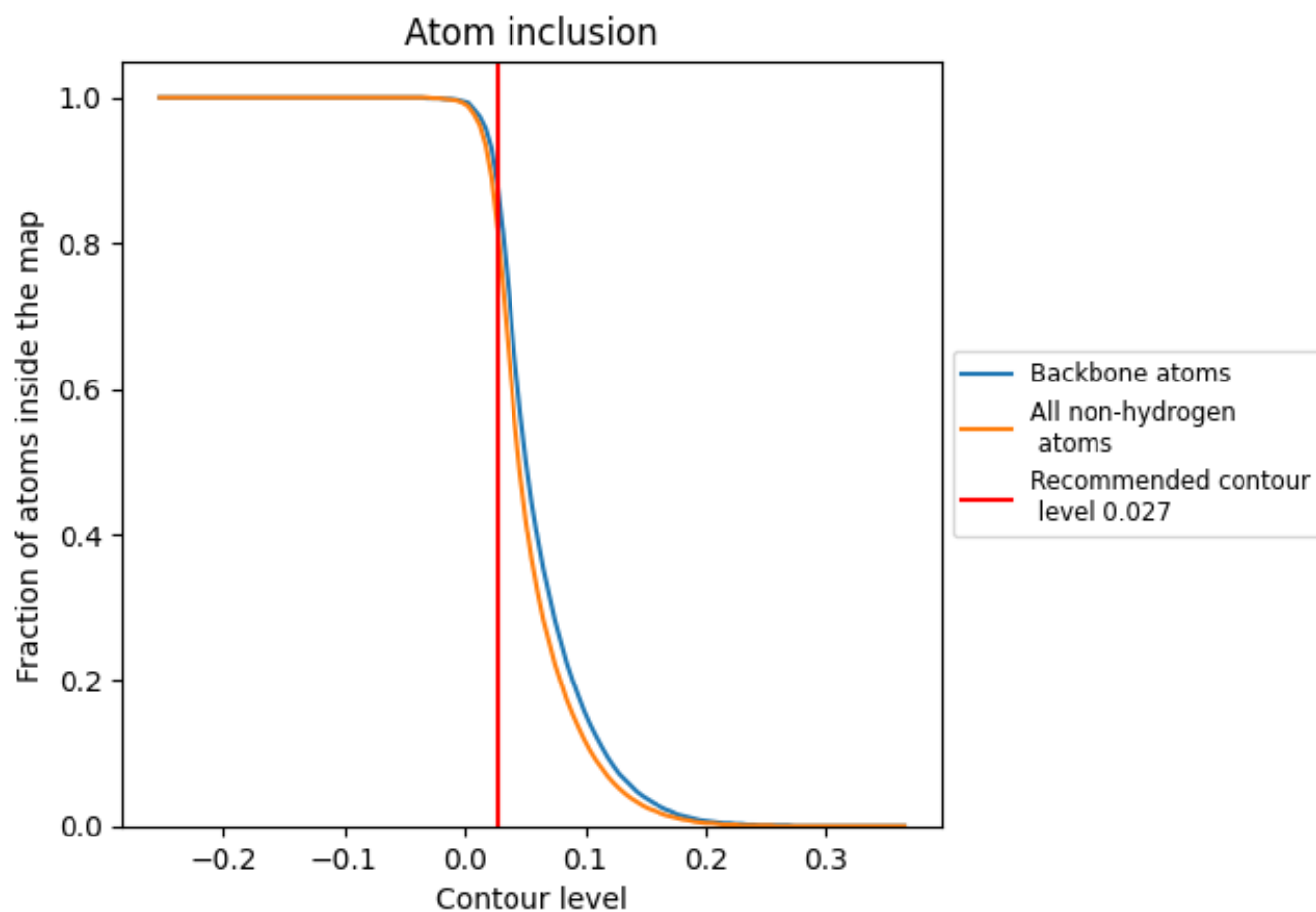


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)

This section was not generated.





































9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 82% 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 (0.027) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8200	 0.2400
A	 0.9960	 0.2280
B	 0.9190	 0.3890
C	 0.9270	 0.2890
D	 0.8980	 0.2860
E	 0.8180	 0.2110
F	 0.8750	 0.1970
G	 0.9240	 0.3620
H	 0.9170	 0.3520
I	 0.5670	 0.1330
J	 0.6800	 0.1370
K	 0.9380	 0.2130
L	 0.9480	 0.2860
M	 0.8720	 0.3090
N	 0.8270	 0.2280
X	 0.5860	 0.0820
Y	 0.5280	 0.0640
Z	 0.7230	 0.0750

