



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 10:54 PM UTC

PDB ID : 8P4A / pdb_00008p4a
EMDB ID : EMD-17403
Title : Structural insights into human co-transcriptional capping - structure 1
Authors : Garg, G.; Dienemann, C.; Farnung, L.; Schwarz, J.; Linden, A.; Urlaub, H.; Cramer, P.
Deposited on : 2023-05-20
Resolution : 3.60 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:

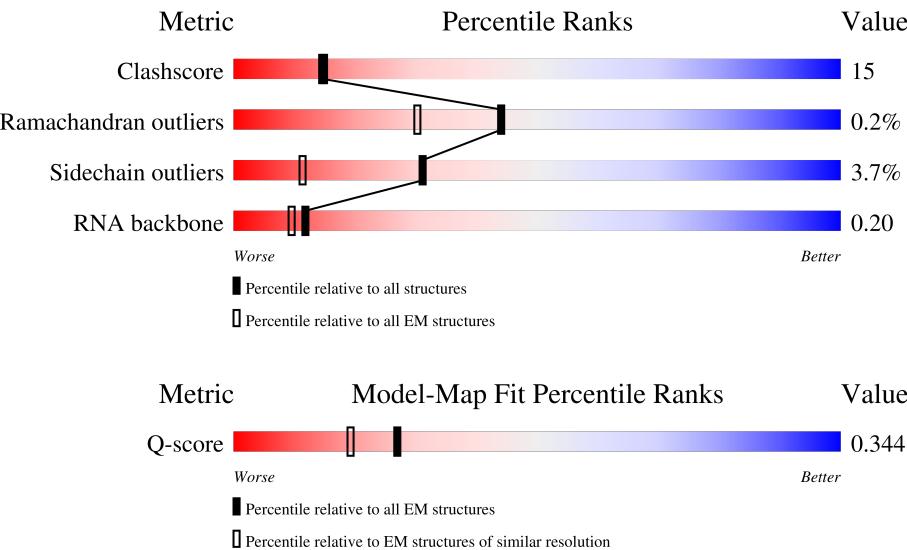
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.60 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.



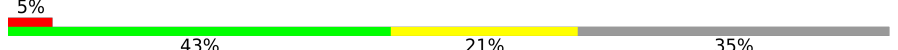
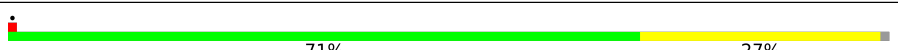
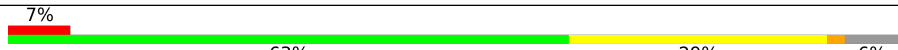
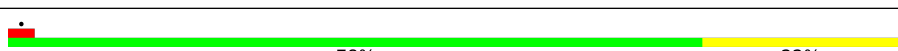
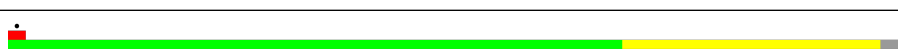
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12797 (3.10 - 4.10)

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	1984	
2	P	19	
3	B	1174	

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Mol	Chain	Length	Quality of chain
4	C	275	
5	D	142	
6	E	210	
7	F	127	
8	G	172	
9	H	150	
10	I	125	
11	J	67	
12	K	117	
13	L	58	
14	N	29	
15	T	38	
16	M	597	

2 Entry composition

There are 18 unique types of molecules in this entry. The entry contains 36673 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 subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1407	Total	C	N	O	S	0	0
			11142	7014	1997	2063	68		

- Molecule 2 is a RNA chain called RNA (5'-R(P*AP*AP*AP*AP*CP*CP*CP*AP*GP*GP*GP*AP*AP*CP*CP*CP*AP*CP*U)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
2	P	19	Total	C	N	O	P	0	0
			405	182	78	126	19		

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	1116	Total	C	N	O	S	0	0
			8928	5652	1568	1644	64		

- Molecule 4 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	258	Total	C	N	O	S	0	0
			2070	1301	352	411	6		

- Molecule 5 is a protein called RNA polymerase II subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	129	Total	C	N	O	S	0	1
			998	629	170	195	4		

- Molecule 6 is a protein called DNA-directed RNA polymerase II subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	209	Total	C	N	O	S	0	0
			1721	1089	300	324	8		

- Molecule 7 is a protein called DNA-directed RNA polymerase II subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	82	Total	C	N	O	S	0	0
			658	418	113	122	5		

- Molecule 8 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	171	Total	C	N	O	S	0	0
			1305	852	205	240	8		

- Molecule 9 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	148	Total	C	N	O	S	0	0
			1186	750	194	237	5		

- Molecule 10 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	117	Total	C	N	O	S	0	0
			950	587	169	183	11		

- Molecule 11 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	67	Total	C	N	O	S	0	0
			533	345	90	92	6		

- Molecule 12 is a protein called DNA-directed RNA polymerase II subunit RPB11-a.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	115	Total	C	N	O	S	0	0
			920	593	152	173	2		

- Molecule 13 is a protein called RNA polymerase II subunit K.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	46	Total	C	N	O	S	0	0
			389	241	75	67	6		

- Molecule 14 is a DNA chain called DNA (29-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	29	Total	C	N	O	P	0	0
			591	283	107	172	29		

- Molecule 15 is a DNA chain called DNA (38-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
15	T	38	Total	C	N	O	P	0	0
			785	374	142	231	38		

- Molecule 16 is a protein called mRNA-capping enzyme.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	507	Total	C	N	O	S	0	0
			4083	2602	714	738	29		

There is a discrepancy between the modelled and reference sequences:

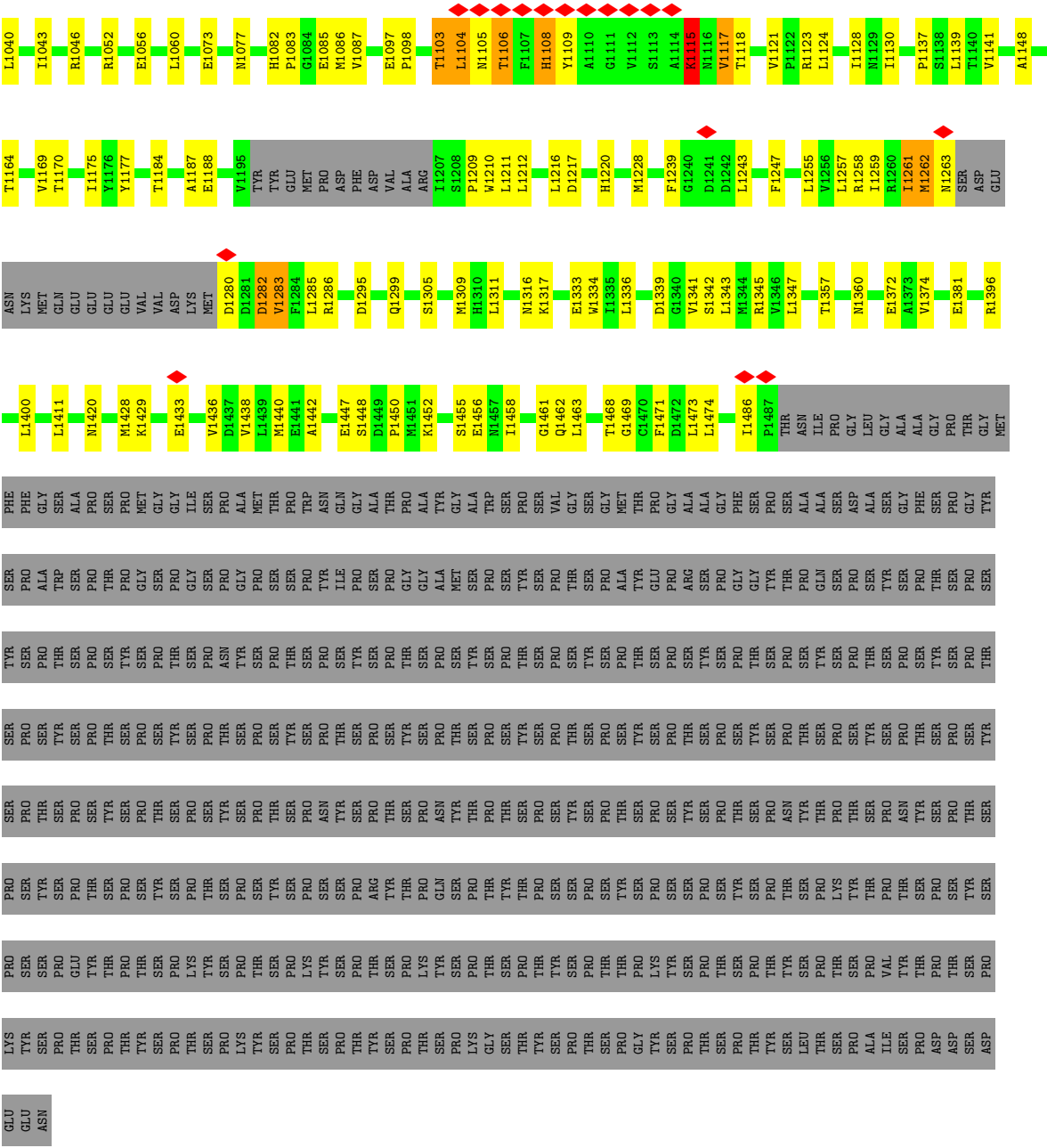
Chain	Residue	Modelled	Actual	Comment	Reference
M	126	SER	CYS	conflict	UNP O60942

- Molecule 17 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

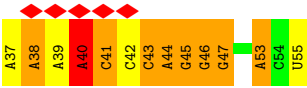
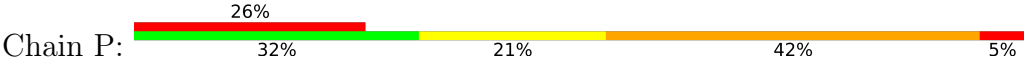
Mol	Chain	Residues	Atoms		AltConf
17	A	1	Total	Mg	0
			1	1	

- Molecule 18 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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



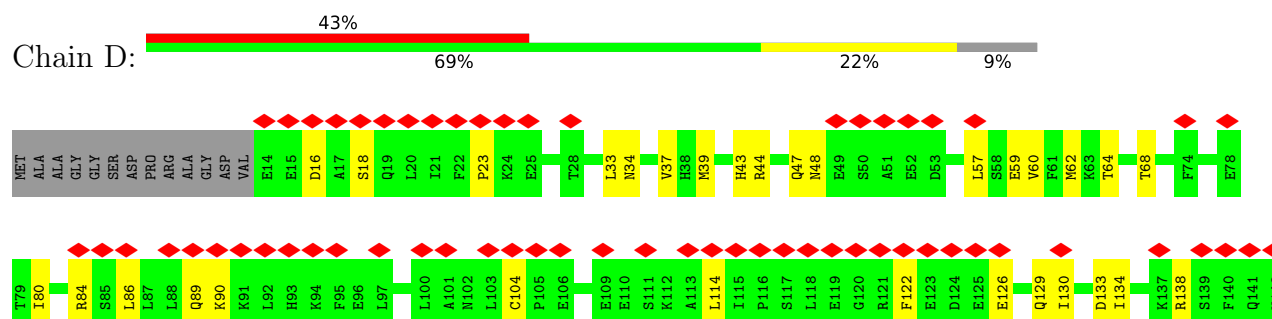
● Molecule 2: RNA (5'-R(P*AP*AP*AP*AP*CP*CP*CP*AP*GP*GP*GP*AP*AP*CP*CP*C
P*AP*CP*U)-3')



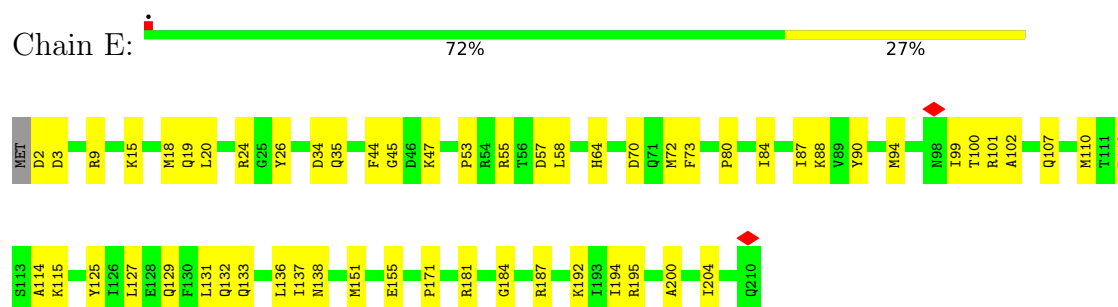
● Molecule 3: DNA-directed RNA polymerase subunit beta



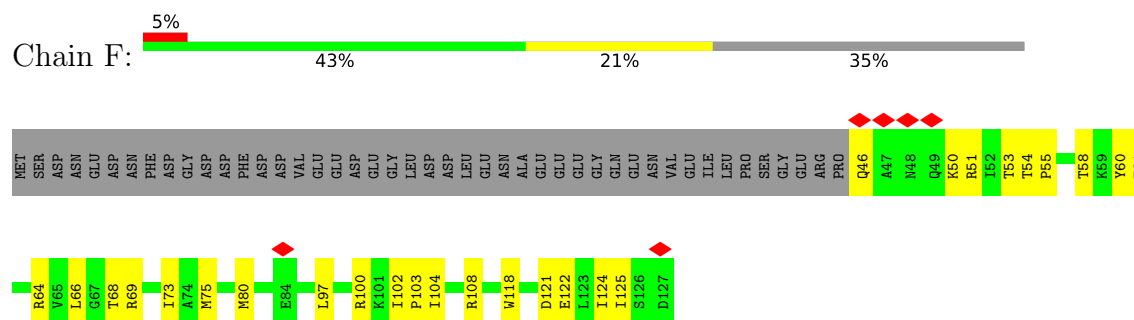
- Molecule 5: RNA polymerase II subunit D



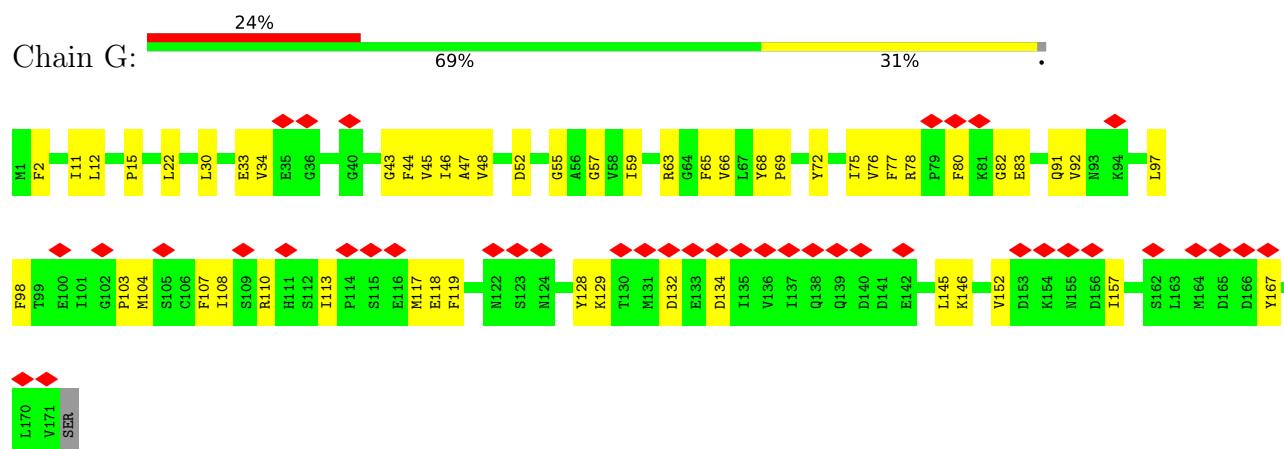
- Molecule 6: DNA-directed RNA polymerase II subunit E



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

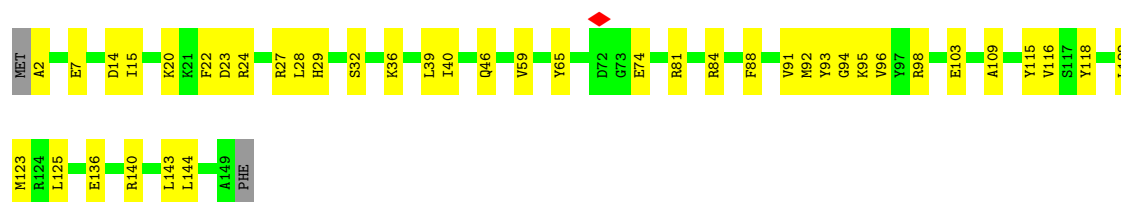


- Molecule 8: DNA-directed RNA polymerase II subunit RPB7



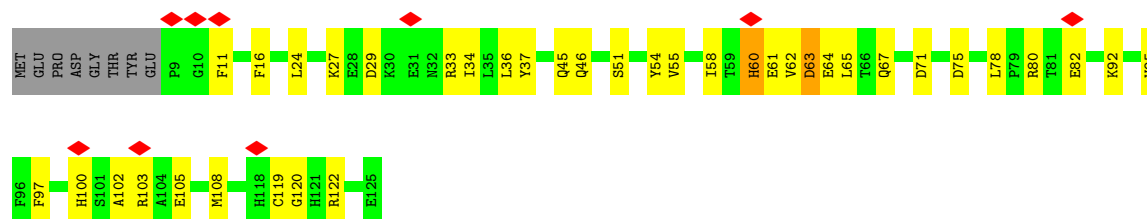
- Molecule 9: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Chain H:  71% 27%



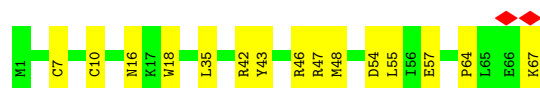
- Molecule 10: DNA-directed RNA polymerase II subunit RPB9

Chain I:  7% 63% 29% 6%



- Molecule 11: DNA-directed RNA polymerases I, II, and III subunit RPABC5

Chain J:  78% 22%



- Molecule 12: DNA-directed RNA polymerase II subunit RPB11-a

Chain K:  69% 29%

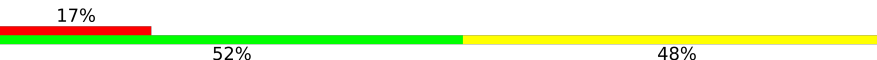


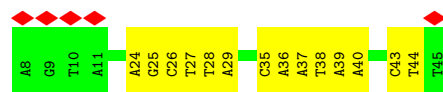
- Molecule 13: RNA polymerase II subunit K

Chain L:  48% 31% 21%

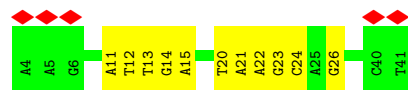


- Molecule 14: DNA (29-MER)

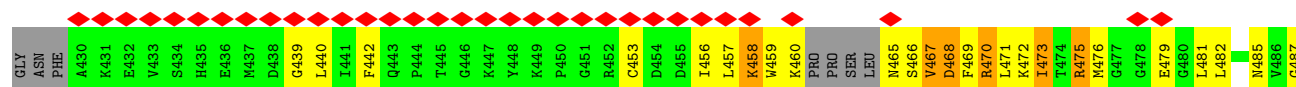
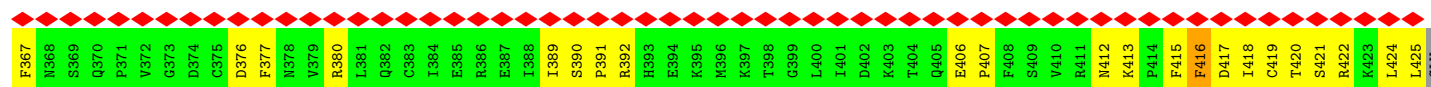
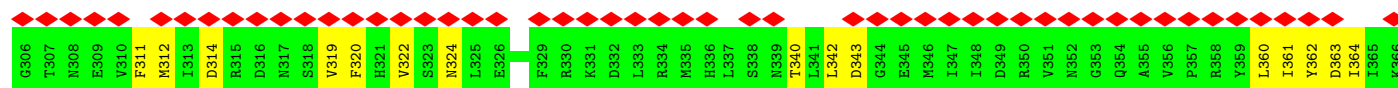
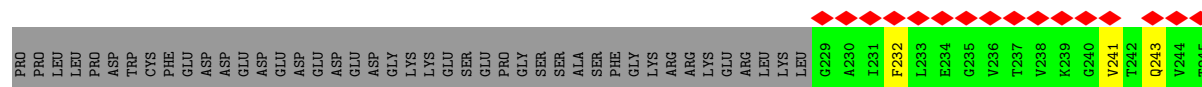
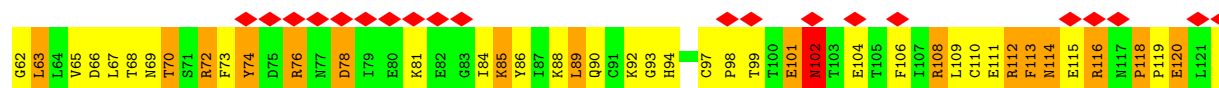
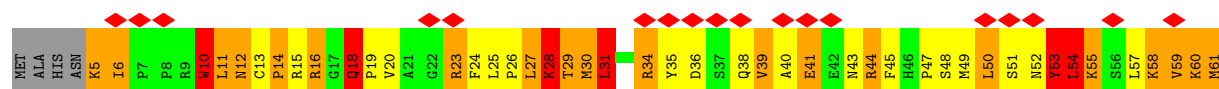
Chain N:  17% 52% 48%



• Molecule 15: DNA (38-MER)



• Molecule 16: mRNA-capping enzyme



N551	P552	V553	T554	K555	E556	M557	L558	F559	E560	F561	I562	D563	R564	C565	THR	ALA	ALA	SER	GLN	GLY	GLN	LYS	ARG	LYS	HIS	HIS	LEU	ASP	PRO	ASP	THR	GLU	LEU	MET	PRO	PRO	PRO	PRO	PRO	LYS	ARG	PRO	ARG	PRO	LEU	THR
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	34647	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	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.082	Depositor
Minimum map value	-0.024	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0257	Depositor
Map size (Å)	315.0, 315.0, 315.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor

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: 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	0/11347	0.44	7/15321 (0.0%)
2	P	0.39	0/453	0.80	2/703 (0.3%)
3	B	0.17	0/9105	0.36	0/12290
4	C	0.15	0/2112	0.31	0/2869
5	D	0.12	0/1012	0.31	0/1366
6	E	0.16	0/1752	0.34	0/2366
7	F	0.14	0/668	0.33	0/901
8	G	0.16	0/1336	0.40	0/1820
9	H	0.17	0/1207	0.37	0/1628
10	I	0.23	0/973	0.54	0/1316
11	J	0.16	0/542	0.33	0/730
12	K	0.20	0/939	0.42	0/1271
13	L	0.22	0/395	0.45	0/524
14	N	0.15	0/661	0.30	0/1014
15	T	0.18	0/880	0.35	0/1358
16	M	0.86	2/4173 (0.0%)	1.19	33/5622 (0.6%)
All	All	0.34	2/37555 (0.0%)	0.55	42/51099 (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
16	M	1	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	M	18	GLN	C-N	34.23	1.73	1.33
16	M	28	LYS	N-CA	5.74	1.53	1.46

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	M	30	MET	N-CA-C	14.41	129.95	110.35
16	M	118	PRO	N-CA-C	10.62	123.65	110.70
16	M	28	LYS	N-CA-CB	-7.43	97.92	110.49
16	M	132	ARG	CB-CA-C	7.38	117.14	109.83
16	M	27	LEU	CA-C-O	-7.26	113.07	120.77

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
16	M	30	MET	CA

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
16	M	416	PHE	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	11142	0	11293	323	0
2	P	405	0	209	17	0
3	B	8928	0	8950	247	0
4	C	2070	0	2013	43	0
5	D	998	0	953	24	0
6	E	1721	0	1737	42	0
7	F	658	0	684	24	0
8	G	1305	0	1267	41	0
9	H	1186	0	1147	34	0
10	I	950	0	880	36	0
11	J	533	0	553	12	0
12	K	920	0	942	29	0
13	L	389	0	395	15	0
14	N	591	0	329	8	0
15	T	785	0	431	8	0
16	M	4083	0	4067	301	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	A	1	0	0	0	0
18	A	2	0	0	0	0
18	B	1	0	0	0	0
18	C	1	0	0	0	0
18	I	2	0	0	0	0
18	J	1	0	0	0	0
18	L	1	0	0	0	0
All	All	36673	0	35850	1082	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 15.

The worst 5 of 1082 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)
16:M:18:GLN:C	16:M:19:PRO:N	1.73	1.47
16:M:153:VAL:HG13	16:M:173:LEU:HD13	1.33	1.07
5:D:86:LEU:O	5:D:90:LYS:NZ	1.96	0.98
3:B:230:ARG:HE	3:B:231:PRO:HD2	1.30	0.95
16:M:93:GLY:O	16:M:94:HIS:HB2	1.66	0.94

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	A	1399/1984 (70%)	1323 (95%)	74 (5%)	2 (0%)	48	79
3	B	1102/1174 (94%)	1047 (95%)	55 (5%)	0	100	100
4	C	254/275 (92%)	248 (98%)	6 (2%)	0	100	100
5	D	127/142 (89%)	123 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	E	207/210 (99%)	201 (97%)	6 (3%)	0	100	100
7	F	80/127 (63%)	79 (99%)	1 (1%)	0	100	100
8	G	169/172 (98%)	164 (97%)	5 (3%)	0	100	100
9	H	146/150 (97%)	139 (95%)	7 (5%)	0	100	100
10	I	115/125 (92%)	110 (96%)	5 (4%)	0	100	100
11	J	65/67 (97%)	63 (97%)	2 (3%)	0	100	100
12	K	113/117 (97%)	108 (96%)	5 (4%)	0	100	100
13	L	44/58 (76%)	43 (98%)	1 (2%)	0	100	100
16	M	499/597 (84%)	466 (93%)	27 (5%)	6 (1%)	10	41
All	All	4320/5198 (83%)	4114 (95%)	198 (5%)	8 (0%)	44	72

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1115	LYS
16	M	13	CYS
16	M	31	LEU
1	A	1263	ASN
16	M	519	PHE

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	1238/1763 (70%)	1213 (98%)	25 (2%)	48	66
3	B	979/1027 (95%)	979 (100%)	0	100	100
4	C	234/252 (93%)	234 (100%)	0	100	100
5	D	104/126 (82%)	104 (100%)	0	100	100
6	E	191/192 (100%)	191 (100%)	0	100	100
7	F	71/111 (64%)	71 (100%)	0	100	100
8	G	138/153 (90%)	138 (100%)	0	100	100

Continued on next page...

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	H	129/131 (98%)	129 (100%)	0	100	100
10	I	105/112 (94%)	102 (97%)	3 (3%)	37	60
11	J	56/56 (100%)	56 (100%)	0	100	100
12	K	104/106 (98%)	104 (100%)	0	100	100
13	L	43/55 (78%)	43 (100%)	0	100	100
16	M	447/534 (84%)	332 (74%)	115 (26%)	0	4
All	All	3839/4618 (83%)	3696 (96%)	143 (4%)	31	56

5 of 143 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	M	479	GLU
16	M	496	ARG
16	M	518	LYS
16	M	57	LEU
16	M	55	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 55 such sidechains are listed below:

Mol	Chain	Res	Type
3	B	749	HIS
5	D	129	GLN
16	M	547	ASN
16	M	280	ASN
3	B	797	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	P	18/19 (94%)	11 (61%)	2 (11%)

5 of 11 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	P	38	A
2	P	39	A
2	P	40	A
2	P	41	C

Continued on next page...

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Mol	Chain	Res	Type
2	P	42	C

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	P	40	A
2	P	41	C

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](#)

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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
14	N	1

Continued on next page...

Continued from previous page...

Mol	Chain	Number of breaks
16	M	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	N	14:DT	O3'	24:DA	P	38.36
1	M	18:GLN	C	19:PRO	N	1.73

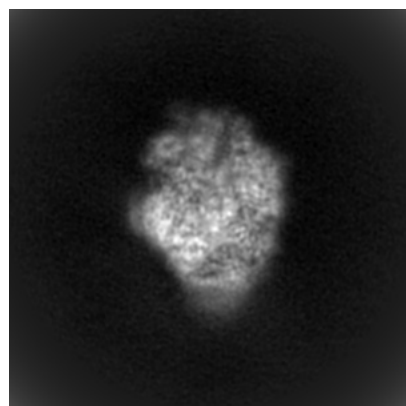
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17403. These allow visual inspection of the internal detail of the map and identification of artifacts.

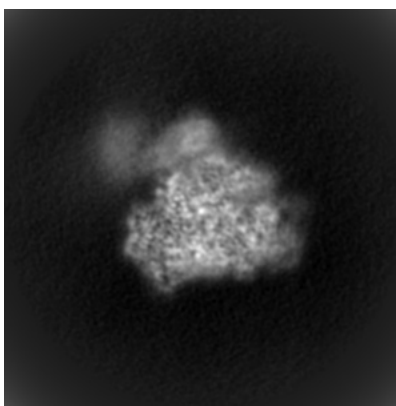
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

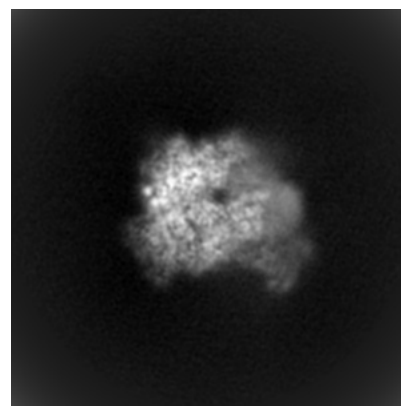
6.1.1 Primary map



X

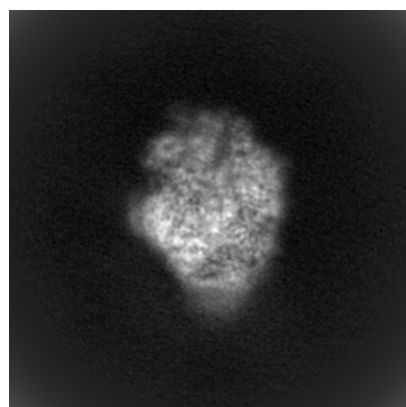


Y

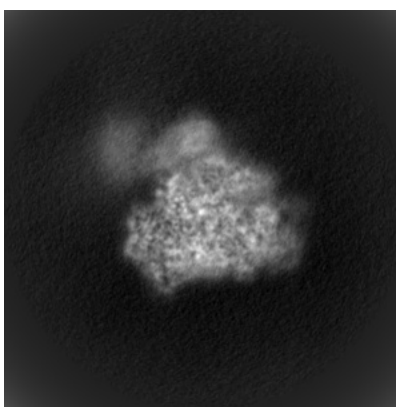


Z

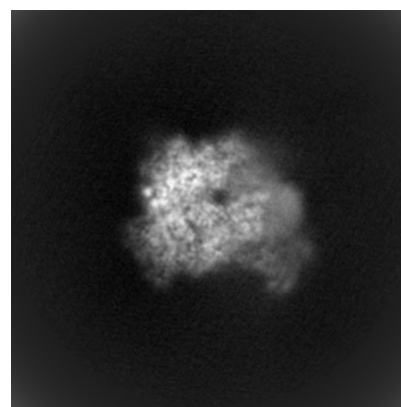
6.1.2 Raw map



X



Y

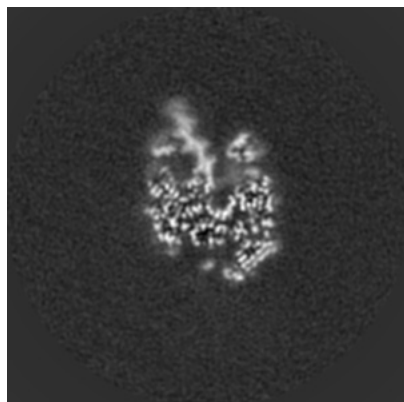


Z

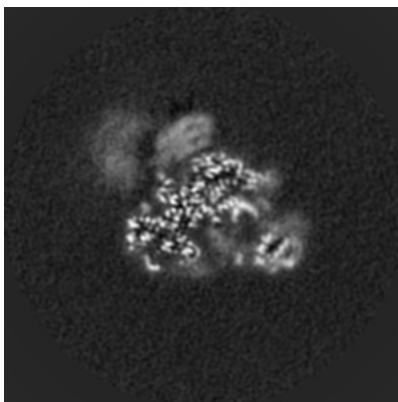
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

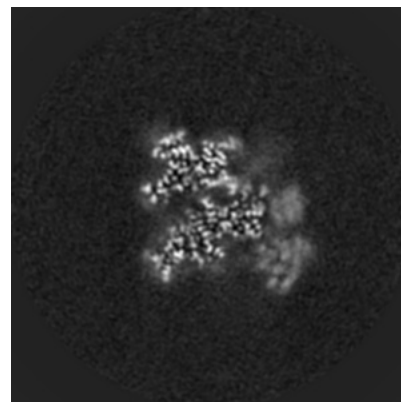
6.2.1 Primary map



X Index: 150

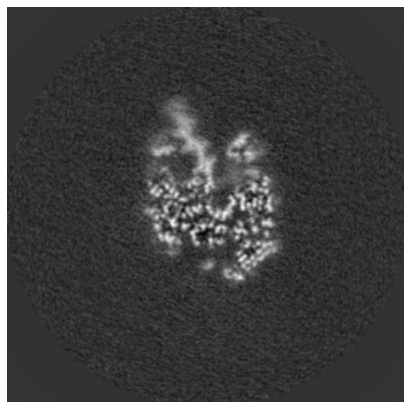


Y Index: 150

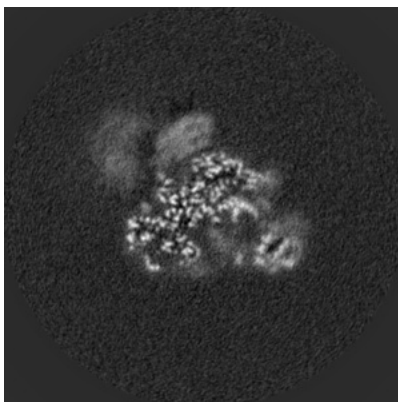


Z Index: 150

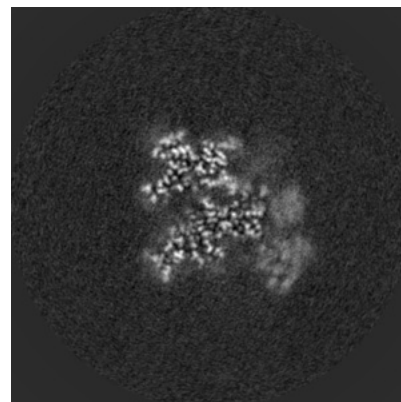
6.2.2 Raw map



X Index: 150



Y Index: 150

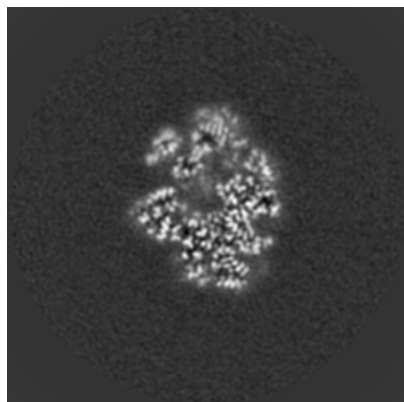


Z Index: 150

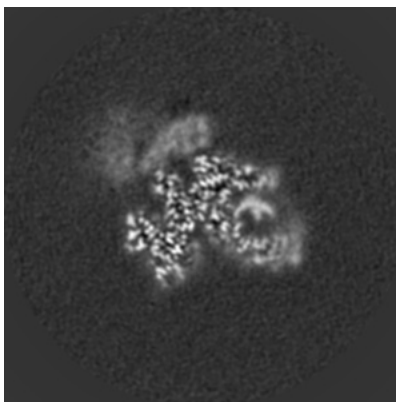
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

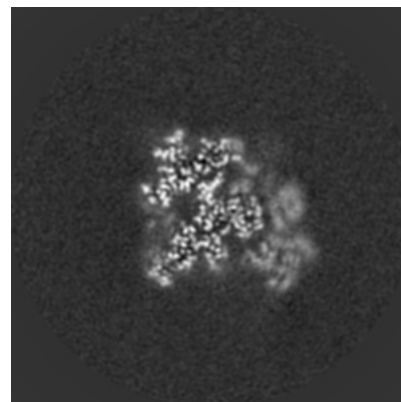
6.3.1 Primary map



X Index: 120

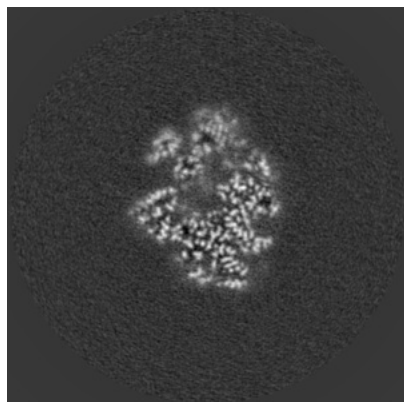


Y Index: 144

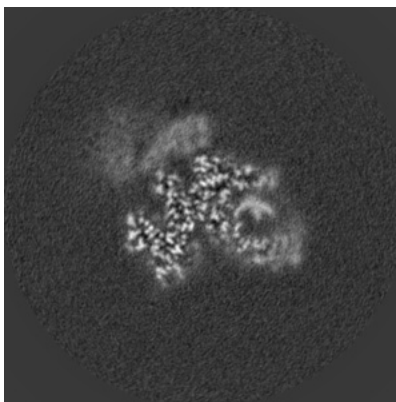


Z Index: 146

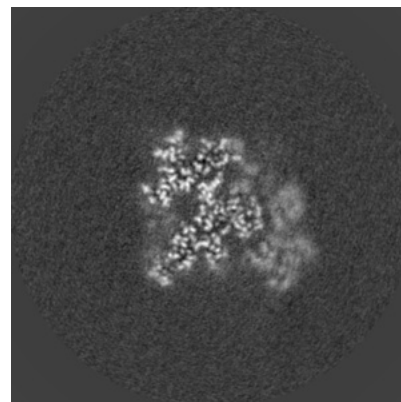
6.3.2 Raw map



X Index: 119



Y Index: 144

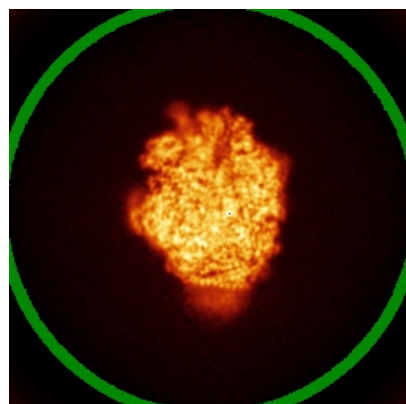


Z Index: 146

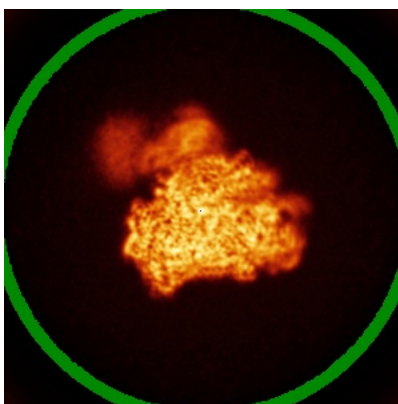
The images above show the largest variance slices of the map in three orthogonal directions.

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

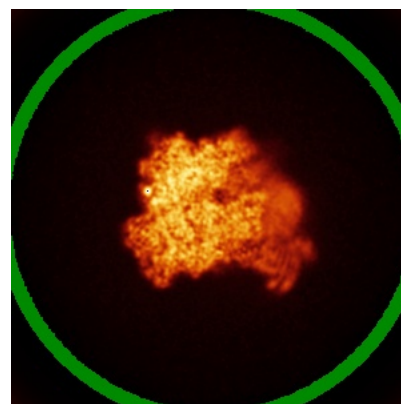
6.4.1 Primary map



X

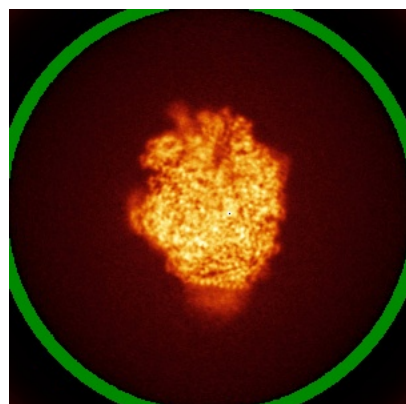


Y

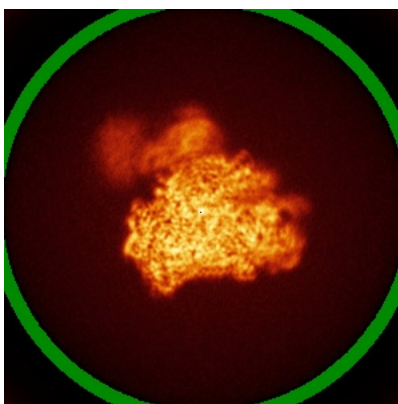


Z

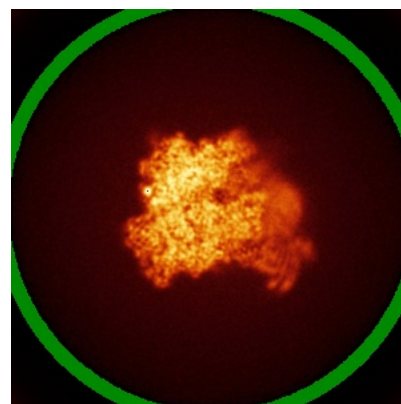
6.4.2 Raw map



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 0.0257. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

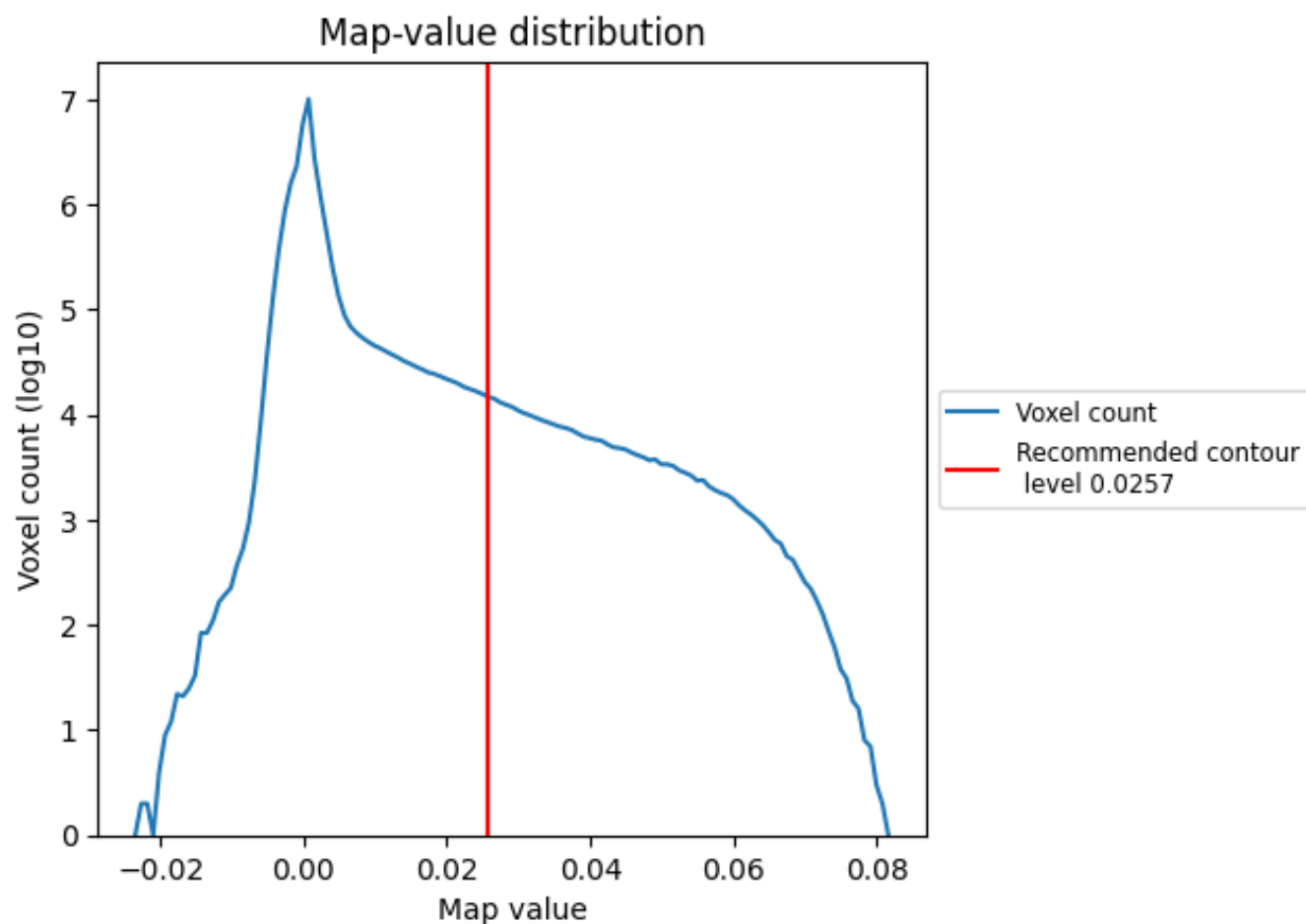
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

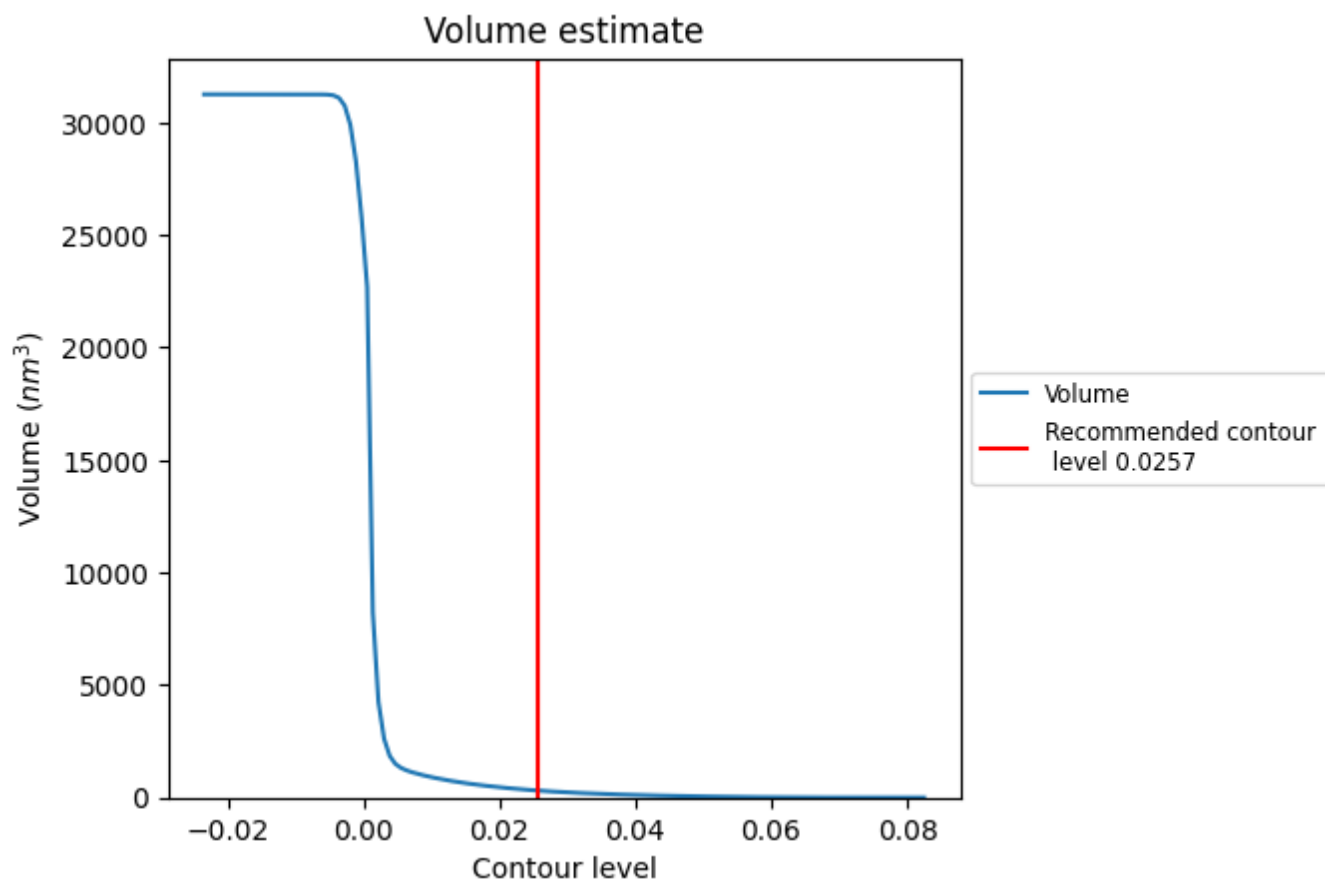
This section contains the results of statistical analysis of the map.

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.

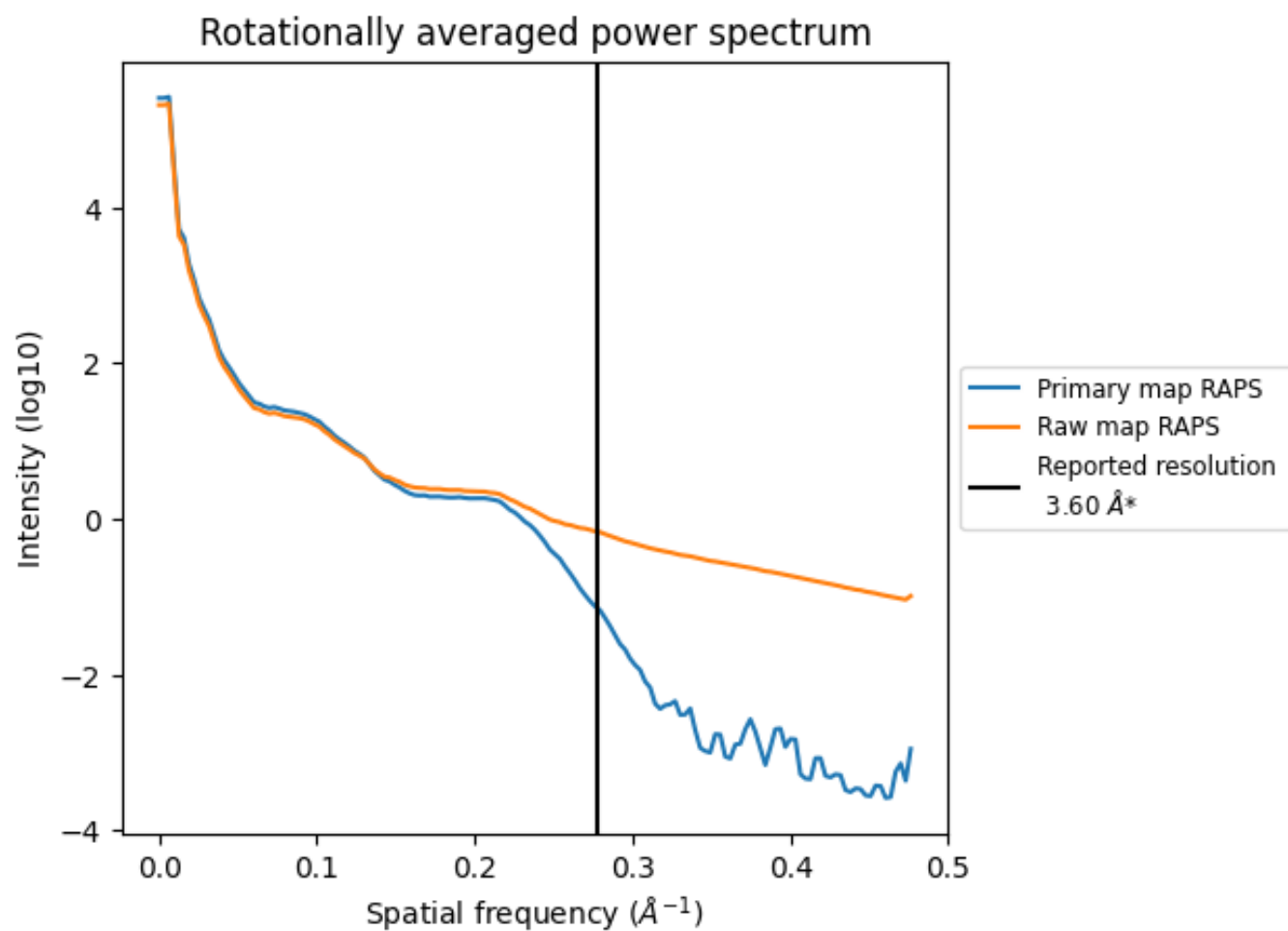
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 310 nm³; this corresponds to an approximate mass of 280 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 ⓘ

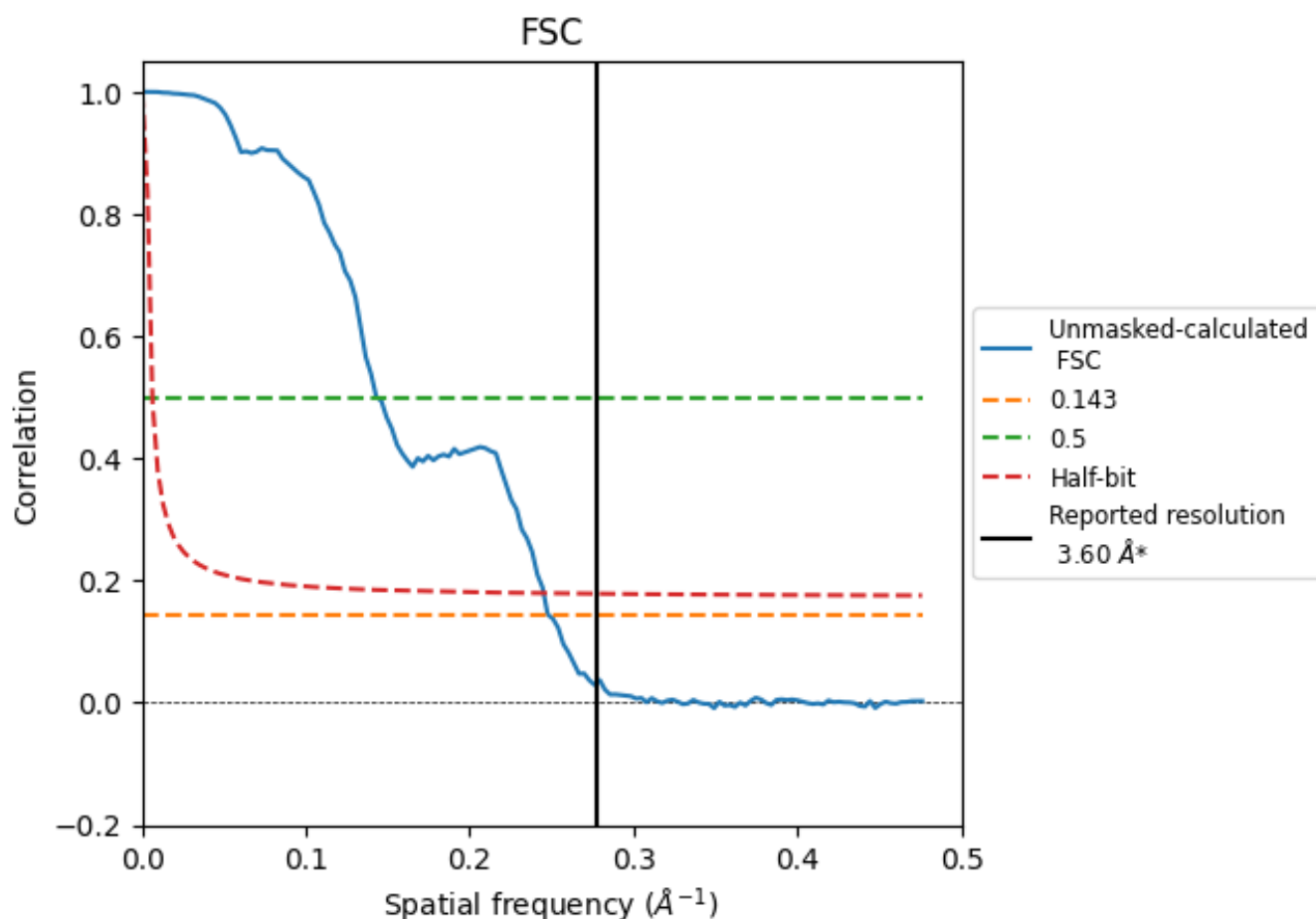


*Reported resolution corresponds to spatial frequency of 0.278 $\text{\AA}^{-1}$

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 0.278 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.03	6.98	4.08

*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 4.03 differs from the reported value 3.6 by more than 10 %

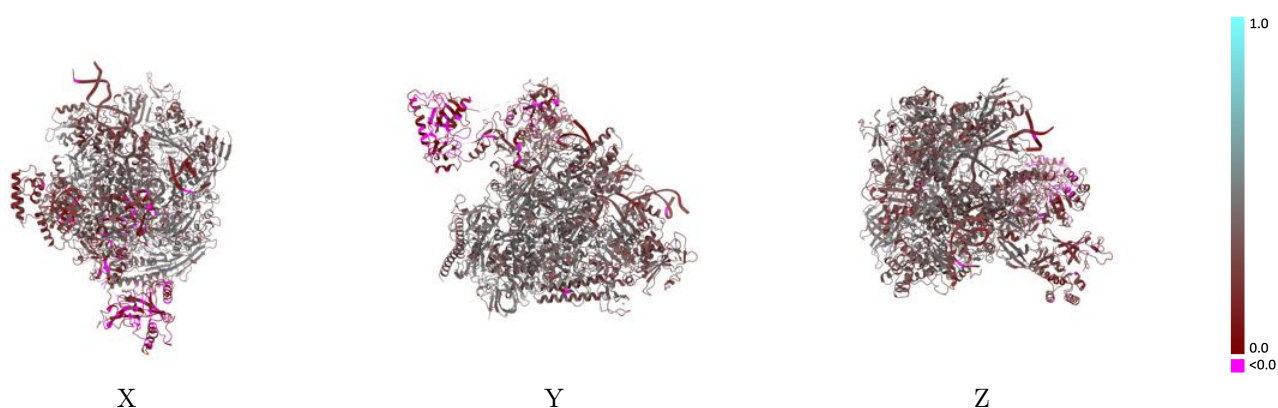
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-17403 and PDB model 8P4A. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)

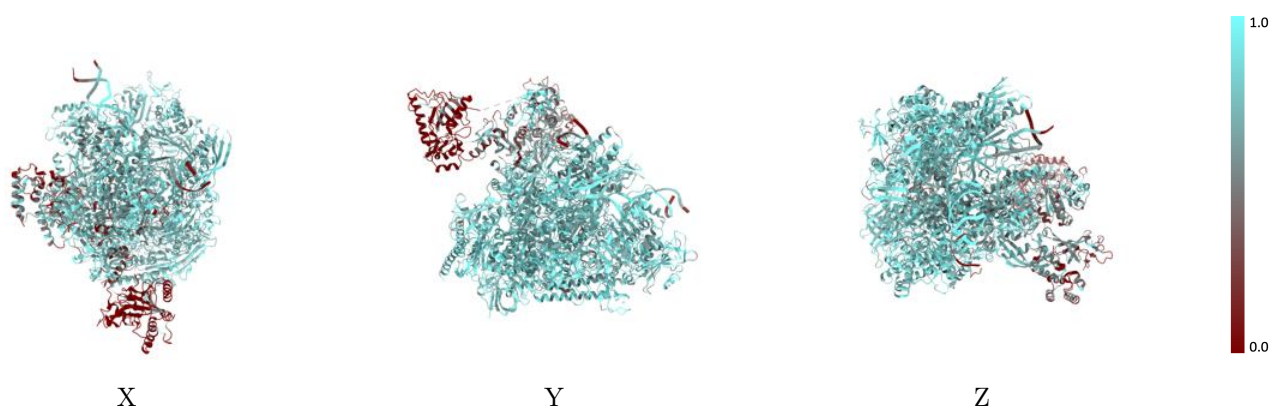
This section was not generated.

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



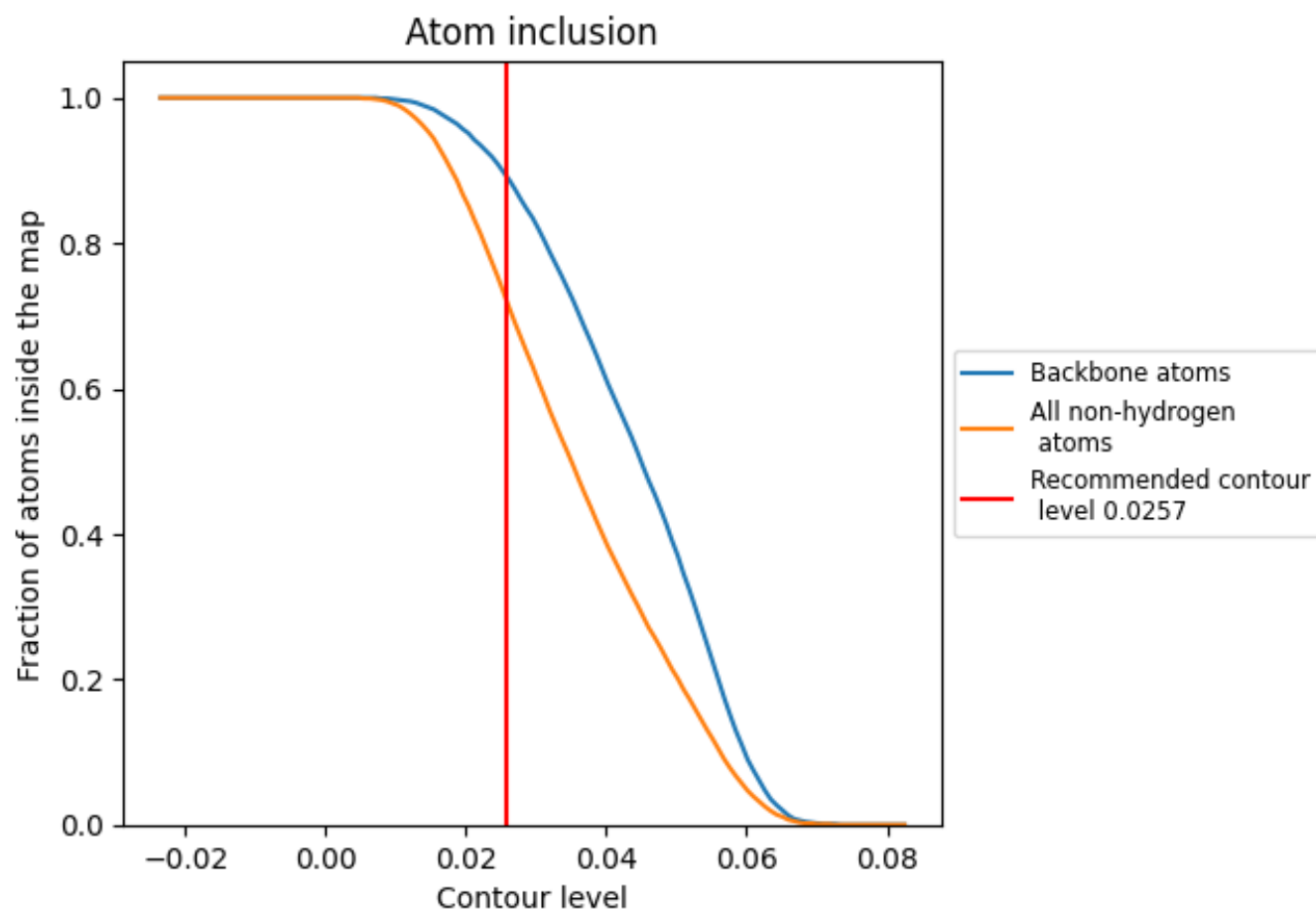
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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 (0.0257).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 72% 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 (0.0257) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7230	 0.3440
A	 0.7820	 0.3810
B	 0.7930	 0.3990
C	 0.8180	 0.4160
D	 0.4140	 0.2180
E	 0.8070	 0.3700
F	 0.7890	 0.4070
G	 0.5750	 0.2580
H	 0.8240	 0.4100
I	 0.7900	 0.3390
J	 0.8270	 0.4050
K	 0.8150	 0.4060
L	 0.7610	 0.3770
M	 0.3490	 0.1220
N	 0.6920	 0.2340
P	 0.6640	 0.2430
T	 0.7880	 0.2720

