



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 11:15 AM UTC

PDB ID : 9QZC / pdb_00009qzc
EMDB ID : EMD-53467
Title : Proximal A-C linker of Tetrahymena centriole, one repeating unit
Authors : Cai, B.; Xu, J.W.; Luo, L.; Aarts, E.; Leitner, A.; Ishikawa, T.; Beltro, P.;
Pillhofer, M.; Wieczorek, M.
Deposited on : 2025-04-22
Resolution : 3.80 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:

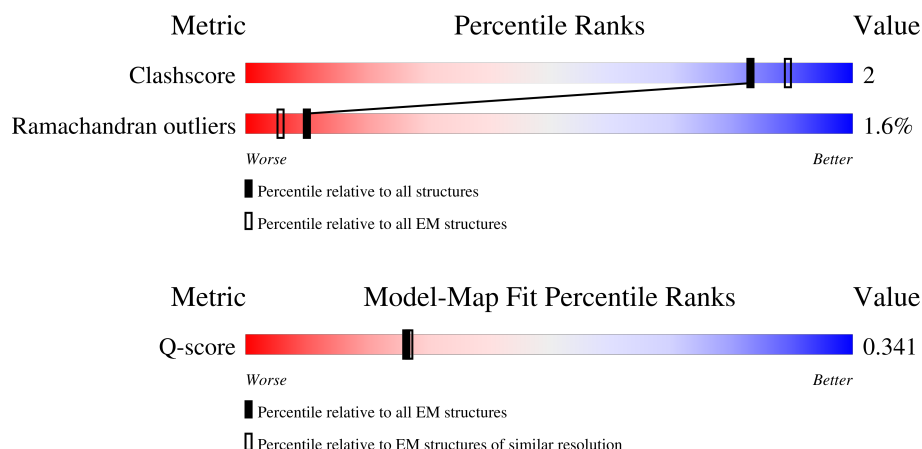
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.80 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	-
Q-score	-	25397	10198 (3.30 - 4.30)

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	i	452	
2	q	380	
2	y	380	
3	7	937	
4	AE	1202	

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Mol	Chain	Length	Quality of chain
4	AU	1202	
5	AM	634	
6	Ac	32	
7	As	153	
8	A7	230	
8	Az	230	
9	Bw	151	
10	B4	164	
11	CA	167	
12	CH	161	
13	CO	105	
14	CV	127	
15	Cc	102	

2 Entry composition

There are 15 unique types of molecules in this entry. The entry contains 22355 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 WD repeat WRAP73-like protein, putative.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	i	429	Total	C	N	O	0	0
			2129	1271	429	429		

- Molecule 2 is a protein called Centrosomal protein, putative.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	q	284	Total	C	N	O	0	0
			1415	847	284	284		
2	y	258	Total	C	N	O	0	0
			1288	772	258	258		

- Molecule 3 is a protein called Rab-GAP TBC domain-containing protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	7	813	Total	C	N	O	0	0
			4040	2414	813	813		

- Molecule 4 is a protein called TBC1 domain family member 31.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	AE	518	Total	C	N	O	0	0
			2584	1548	518	518		
4	AU	354	Total	C	N	O	0	0
			1752	1044	354	354		

- Molecule 5 is a protein called POC1 centriolar protein homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	AM	365	Total	C	N	O	0	0
			1806	1076	365	365		

- Molecule 6 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	Ac	32	Total	C	N	O	0	0
			160	96	32	32		

- Molecule 7 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	As	153	Total	C	N	O	0	0
			765	459	153	153		

- Molecule 8 is a protein called SWIM-type domain-containing protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	Az	151	Total	C	N	O	0	0
			748	446	151	151		
8	A7	158	Total	C	N	O	0	0
			783	467	158	158		

- Molecule 9 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	Bw	151	Total	C	N	O	0	0
			755	453	151	151		

- Molecule 10 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	B4	164	Total	C	N	O	0	0
			820	492	164	164		

- Molecule 11 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	CA	167	Total	C	N	O	0	0
			835	501	167	167		

- Molecule 12 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	CH	161	Total	C	N	O	0	0
			805	483	161	161		

- Molecule 13 is a protein called Unknown Protein Chain.

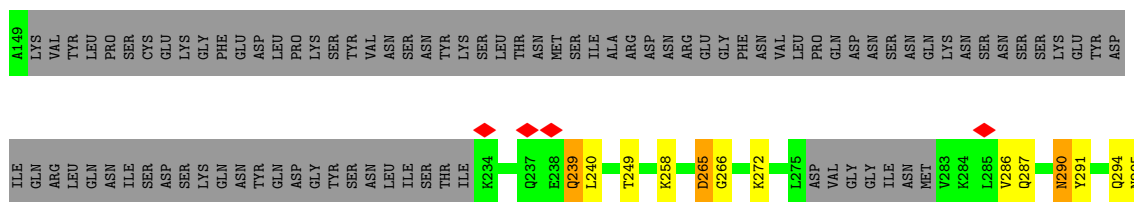
Mol	Chain	Residues	Atoms				AltConf	Trace
13	CO	105	Total	C	N	O	0	0
			525	315	105	105		

- Molecule 14 is a protein called Unknown Protein Chain.

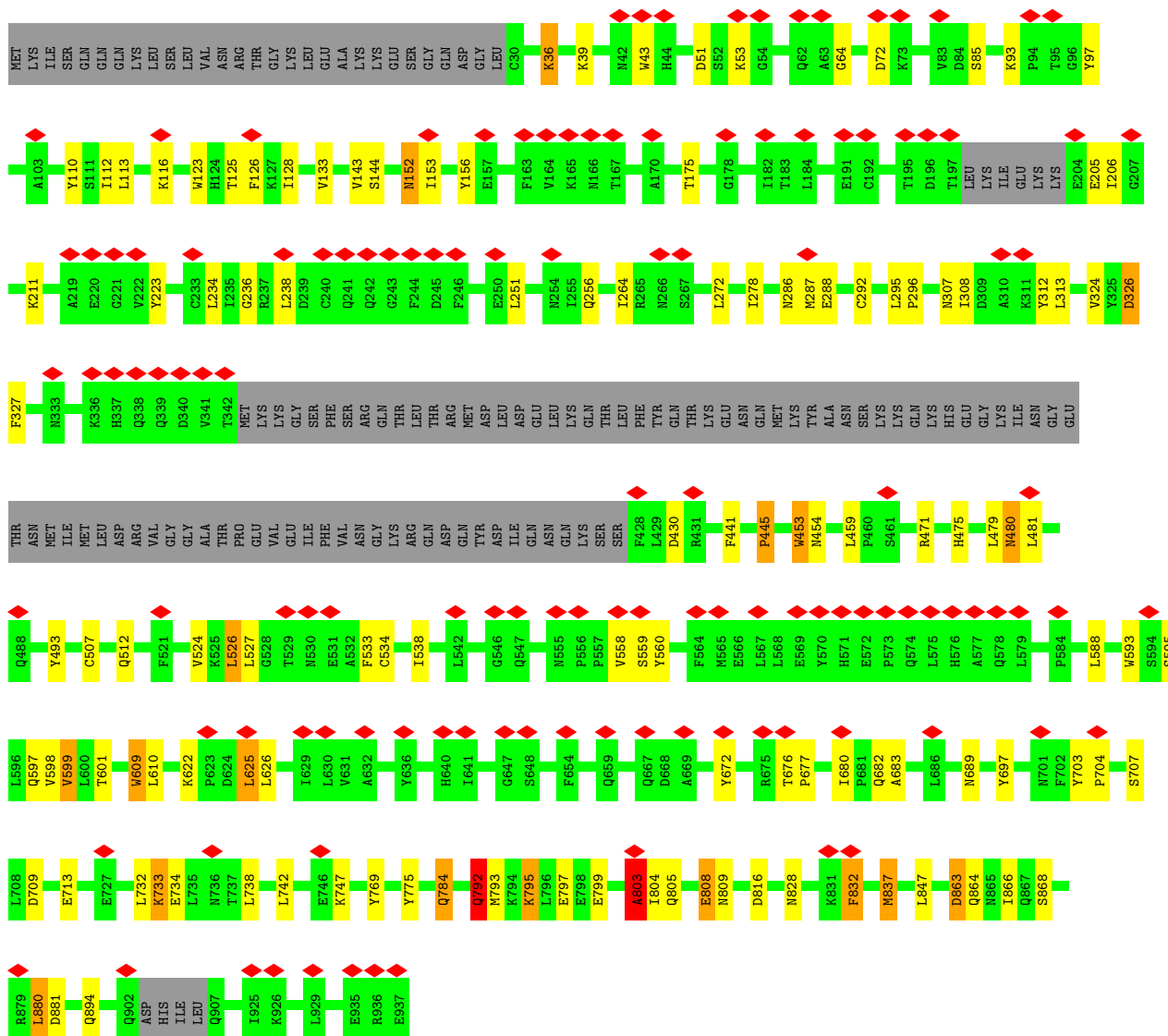
Mol	Chain	Residues	Atoms				AltConf	Trace
14	CV	127	Total	C	N	O	0	0
			635	381	127	127		

- Molecule 15 is a protein called Unknown Protein Chain.

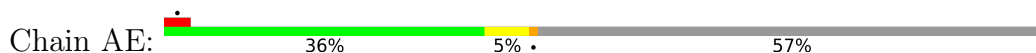
Mol	Chain	Residues	Atoms				AltConf	Trace
15	Cc	102	Total	C	N	O	0	0
			510	306	102	102		

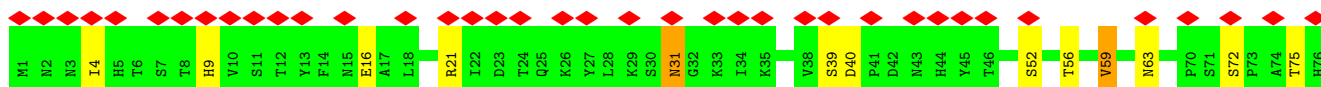


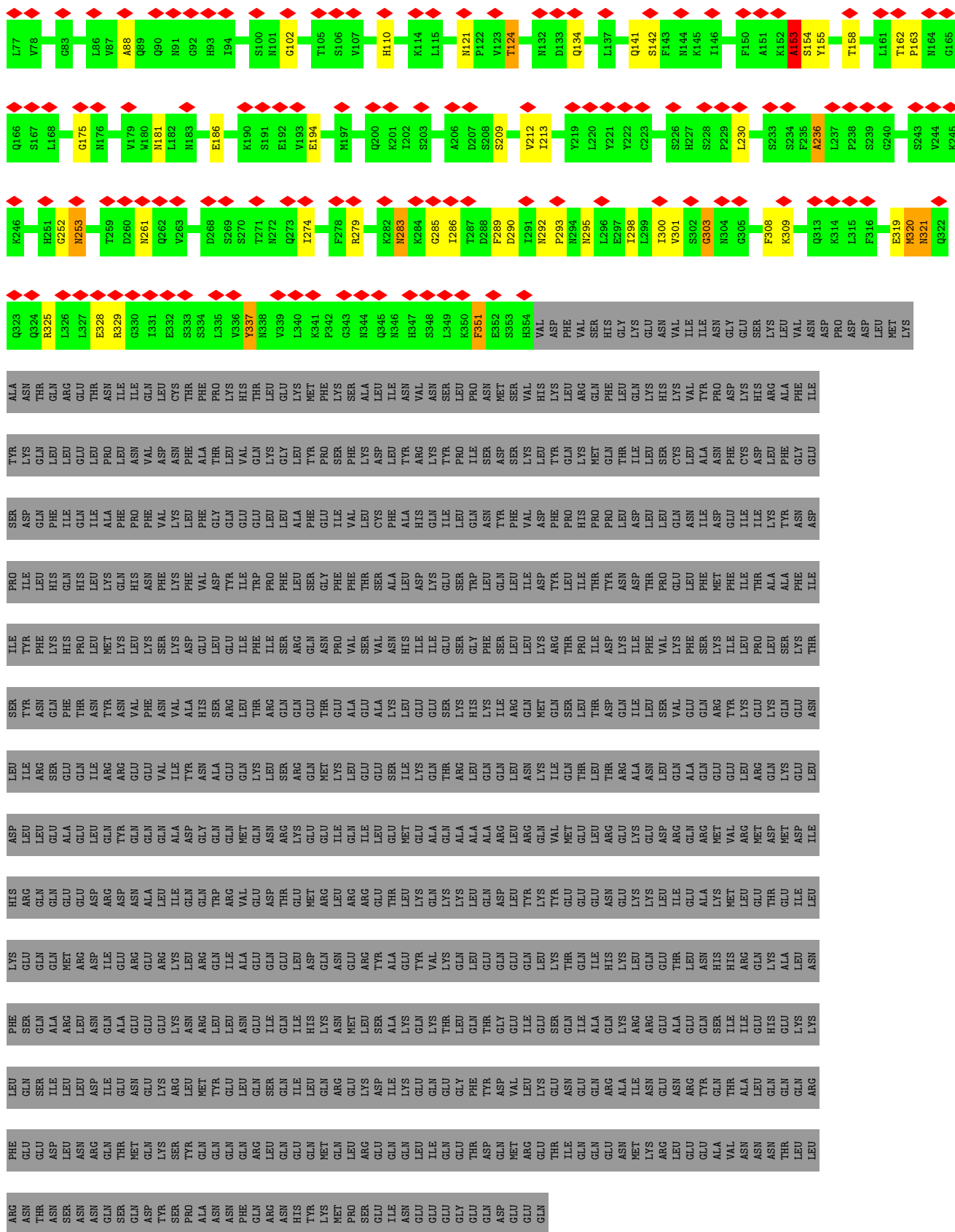
• Molecule 3: Rab-GAP TBC domain-containing protein



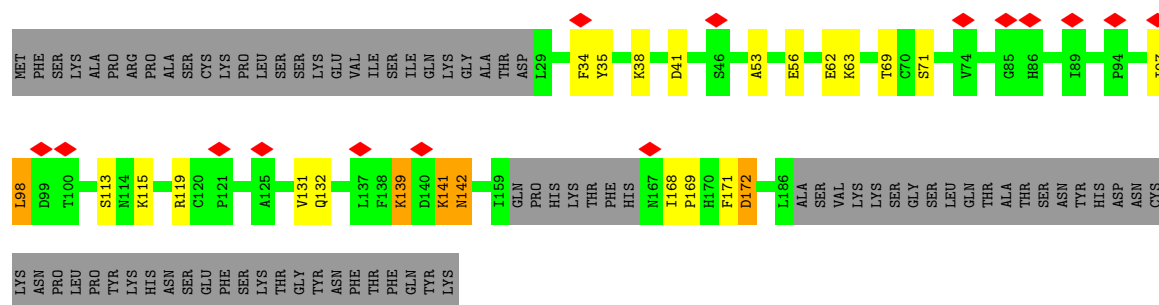
• Molecule 4: TBC1 domain family member 31



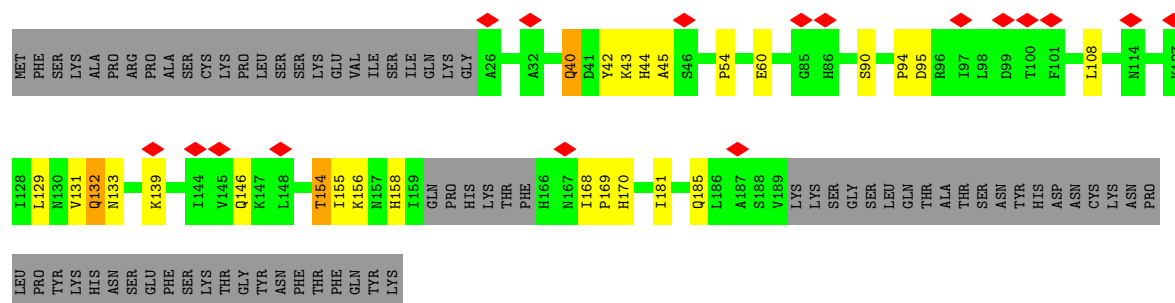




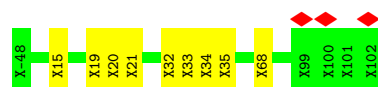
- Molecule 5: POC1 centriolar protein homolog



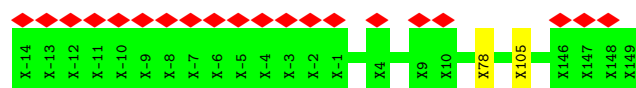
• Molecule 8: SWIM-type domain-containing protein



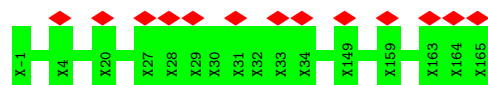
• Molecule 9: Unknown Protein Chain



• Molecule 10: Unknown Protein Chain



• Molecule 11: Unknown Protein Chain

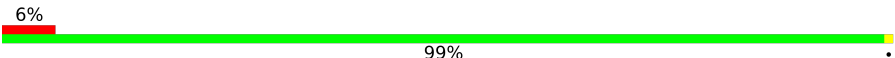


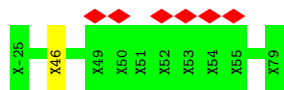
• Molecule 12: Unknown Protein Chain



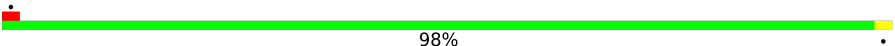
There are no outlier residues recorded for this chain.

• Molecule 13: Unknown Protein Chain

Chain CO:  6% 99% .

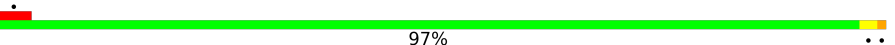


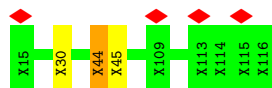
• Molecule 14: Unknown Protein Chain

Chain CV:  98% .



• Molecule 15: Unknown Protein Chain

Chain Cc:  97% ..



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	155485	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 ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	13.599	Depositor
Minimum map value	0.000	Depositor
Average map value	0.223	Depositor
Map value standard deviation	1.035	Depositor
Recommended contour level	5	Depositor
Map size (Å)	631.2, 631.2, 631.2	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.315, 1.315, 1.315	Depositor

5 Model quality

5.1 Standard geometry

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	i	1.59	4/2127 (0.2%)	1.88	38/2965 (1.3%)
2	q	1.30	0/1412	1.65	21/1969 (1.1%)
2	y	1.42	0/1285	2.07	44/1793 (2.5%)
3	7	1.34	6/4036 (0.1%)	1.84	112/5629 (2.0%)
4	AE	1.33	1/2582 (0.0%)	1.91	82/3608 (2.3%)
4	AU	1.38	9/1751 (0.5%)	1.99	70/2439 (2.9%)
5	AM	1.55	2/1803 (0.1%)	2.05	74/2508 (3.0%)
8	A7	1.49	1/781 (0.1%)	2.03	26/1086 (2.4%)
8	Az	1.35	0/746	2.02	25/1037 (2.4%)
All	All	1.41	23/16523 (0.1%)	1.92	492/23034 (2.1%)

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	i	0	6
2	q	0	7
2	y	0	11
3	7	0	18
4	AE	0	18
4	AU	0	9
5	AM	0	13
7	As	0	3
8	A7	0	5
8	Az	0	3
9	Bw	0	1
10	B4	0	3
13	CO	0	1
15	Cc	0	2
All	All	0	100

The worst 5 of 23 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	i	198	SER	CA-C	-6.23	1.45	1.52
4	AU	300	ILE	CA-C	-6.17	1.45	1.52
4	AU	181	ASN	CA-CB	-6.10	1.45	1.52
4	AU	301	VAL	CA-C	-5.87	1.45	1.52
4	AU	295	ASN	CA-C	-5.83	1.45	1.52

The worst 5 of 492 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	i	301	GLU	CA-C-O	-33.51	84.04	121.58
2	y	294	GLN	CA-C-N	19.38	146.80	120.44
2	y	294	GLN	C-N-CA	19.38	146.80	120.44
2	y	29	ILE	CA-C-N	18.04	153.47	122.26
2	y	29	ILE	C-N-CA	18.04	153.47	122.26

There are no chirality outliers.

5 of 100 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	i	155	ASP	Mainchain
1	i	222	TYR	Mainchain
1	i	301	GLU	Mainchain
1	i	349	VAL	Mainchain
1	i	94	LEU	Mainchain

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	i	2129	0	926	1	0
2	q	1415	0	597	4	0
2	y	1288	0	542	5	0
3	7	4040	0	1741	15	0
4	AE	2584	0	1093	11	0
4	AU	1752	0	772	5	0
5	AM	1806	0	792	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	Ac	160	0	35	0	0
7	As	765	0	158	3	0
8	A7	783	0	350	3	0
8	Az	748	0	330	1	0
9	Bw	755	0	158	5	0
10	B4	820	0	167	0	0
11	CA	835	0	169	0	0
12	CH	805	0	165	0	0
13	CO	525	0	107	0	0
14	CV	635	0	129	1	0
15	Cc	510	0	104	1	0
All	All	22355	0	8335	72	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 2.

The worst 5 of 72 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)
2:q:152:TYR:O	2:q:153:LEU:C	2.41	0.60
7:As:72:UNK:O	7:As:73:UNK:C	2.49	0.58
7:As:5:UNK:HA	7:As:6:UNK:C	2.36	0.56
4:AU:230:LEU:N	4:AU:351:PHE:O	2.40	0.55
5:AM:553:TYR:O	5:AM:557:LEU:N	2.40	0.55

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	i	425/452 (94%)	371 (87%)	45 (11%)	9 (2%)	5 31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	q	278/380 (73%)	266 (96%)	8 (3%)	4 (1%)	9	37
2	y	252/380 (66%)	244 (97%)	6 (2%)	2 (1%)	16	48
3	7	805/937 (86%)	761 (94%)	28 (4%)	16 (2%)	6	32
4	AE	514/1202 (43%)	479 (93%)	27 (5%)	8 (2%)	7	35
4	AU	352/1202 (29%)	334 (95%)	15 (4%)	3 (1%)	14	45
5	AM	359/634 (57%)	319 (89%)	36 (10%)	4 (1%)	11	41
8	A7	154/230 (67%)	143 (93%)	9 (6%)	2 (1%)	9	38
8	Az	147/230 (64%)	129 (88%)	13 (9%)	5 (3%)	3	23
All	All	3286/5647 (58%)	3046 (93%)	187 (6%)	53 (2%)	10	35

5 of 53 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	i	68	SER
3	7	72	ASP
3	7	430	ASP
4	AE	583	PHE
4	AE	598	LEU

5.3.2 Protein sidechains [i](#)

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

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.

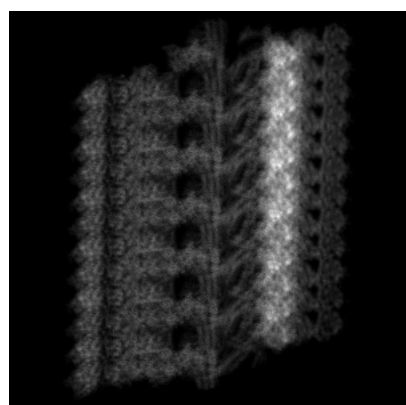
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53467. These allow visual inspection of the internal detail of the map and identification of artifacts.

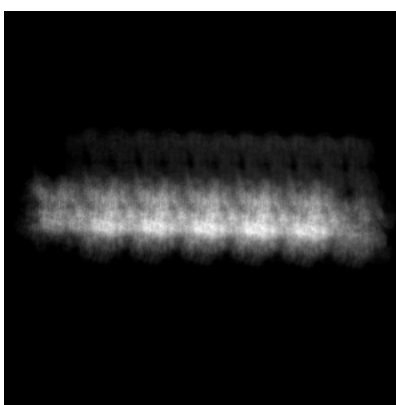
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y

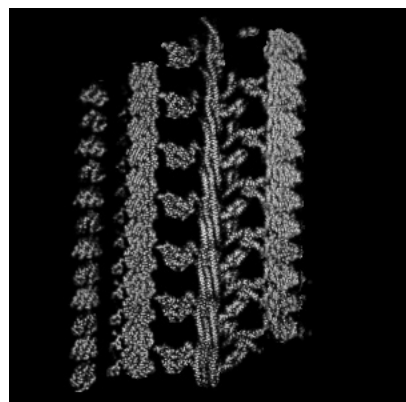


Z

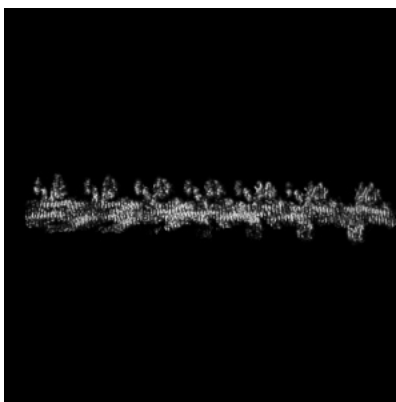
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 240



Y Index: 240

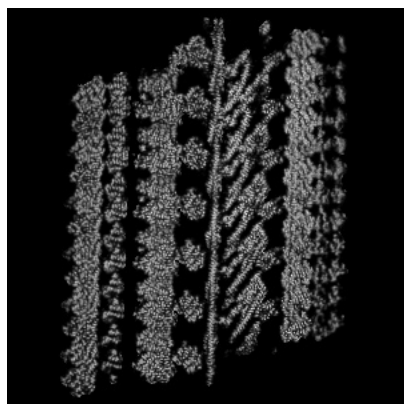


Z Index: 240

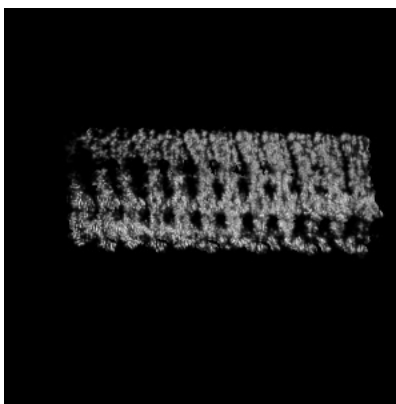
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

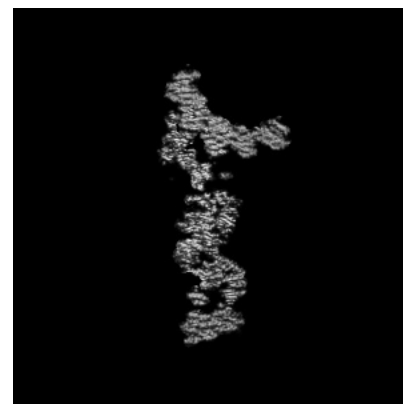
6.3.1 Primary map



X Index: 218



Y Index: 335

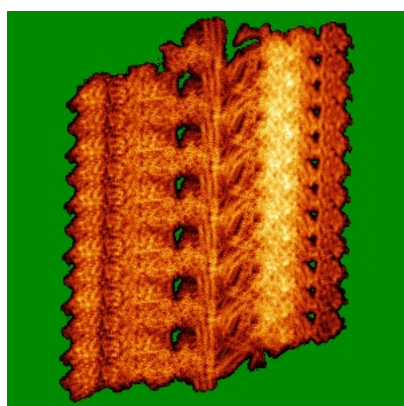


Z Index: 311

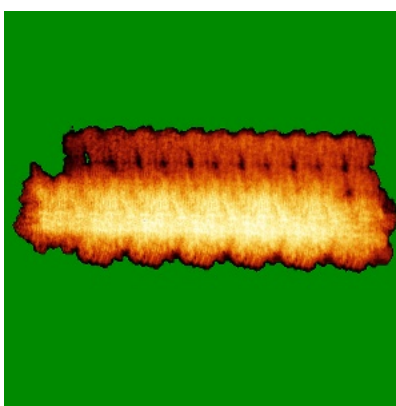
The images above show the largest variance slices of the map in three orthogonal directions.

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

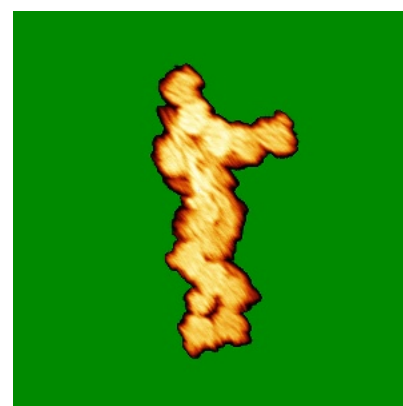
6.4.1 Primary map



X



Y

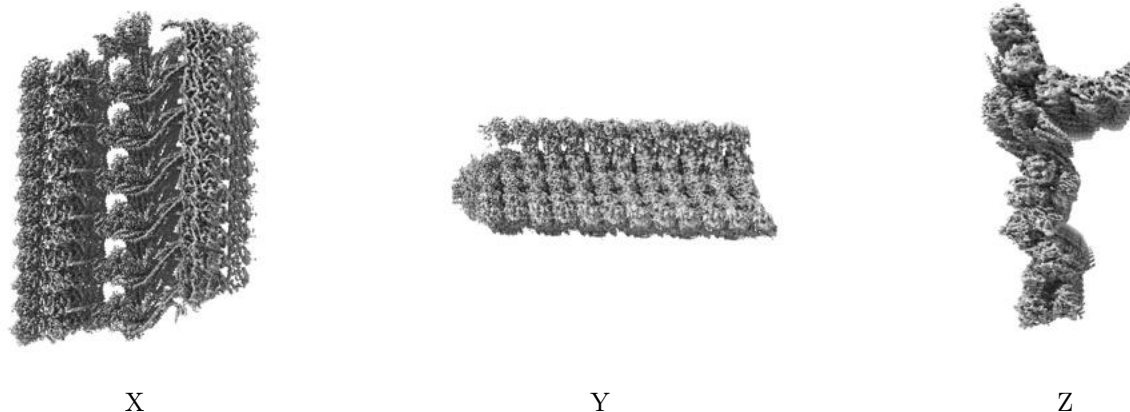


Z

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 [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 5.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

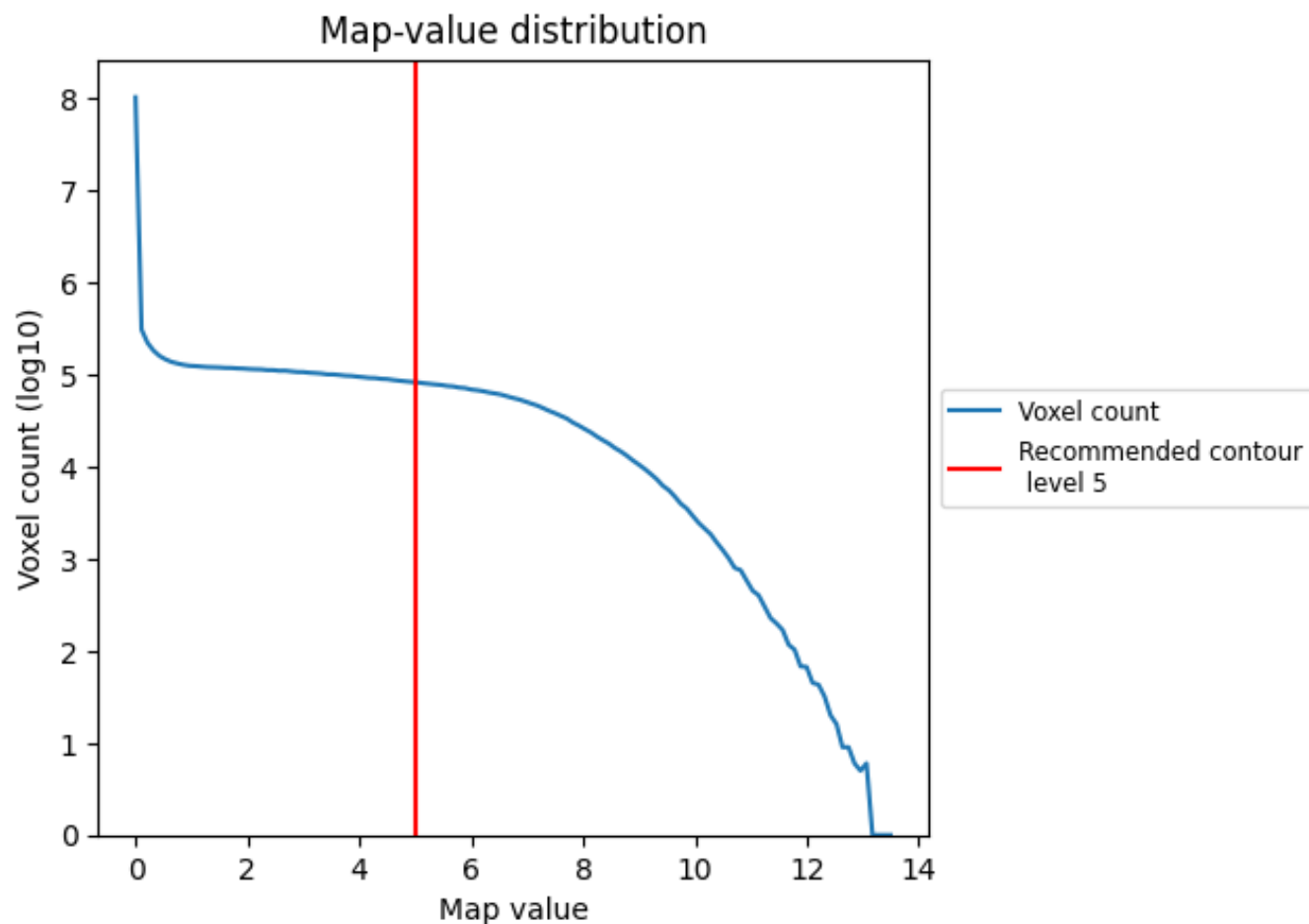
6.6 Mask visualisation [i](#)

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

7 Map analysis ⓘ

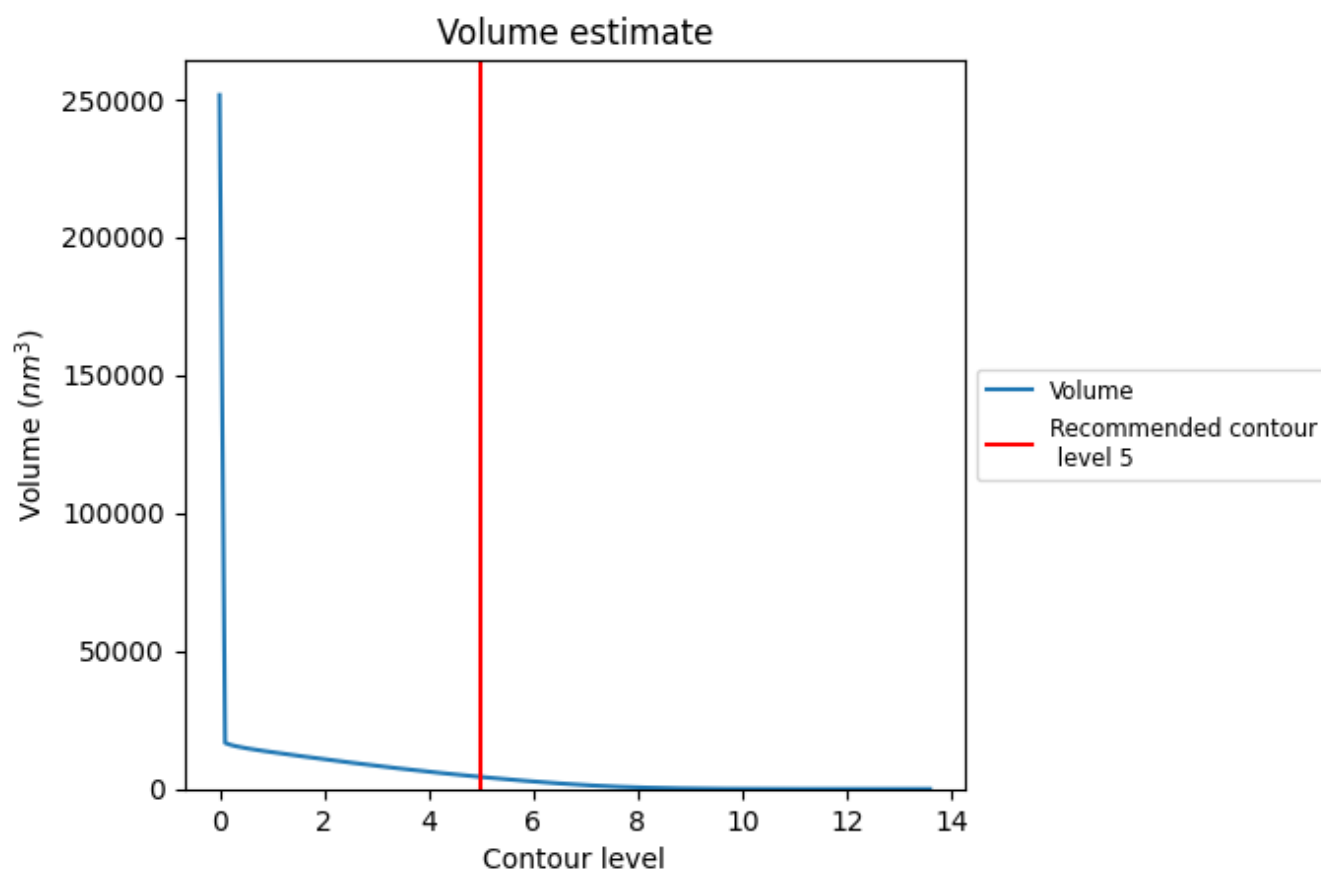
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ



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.

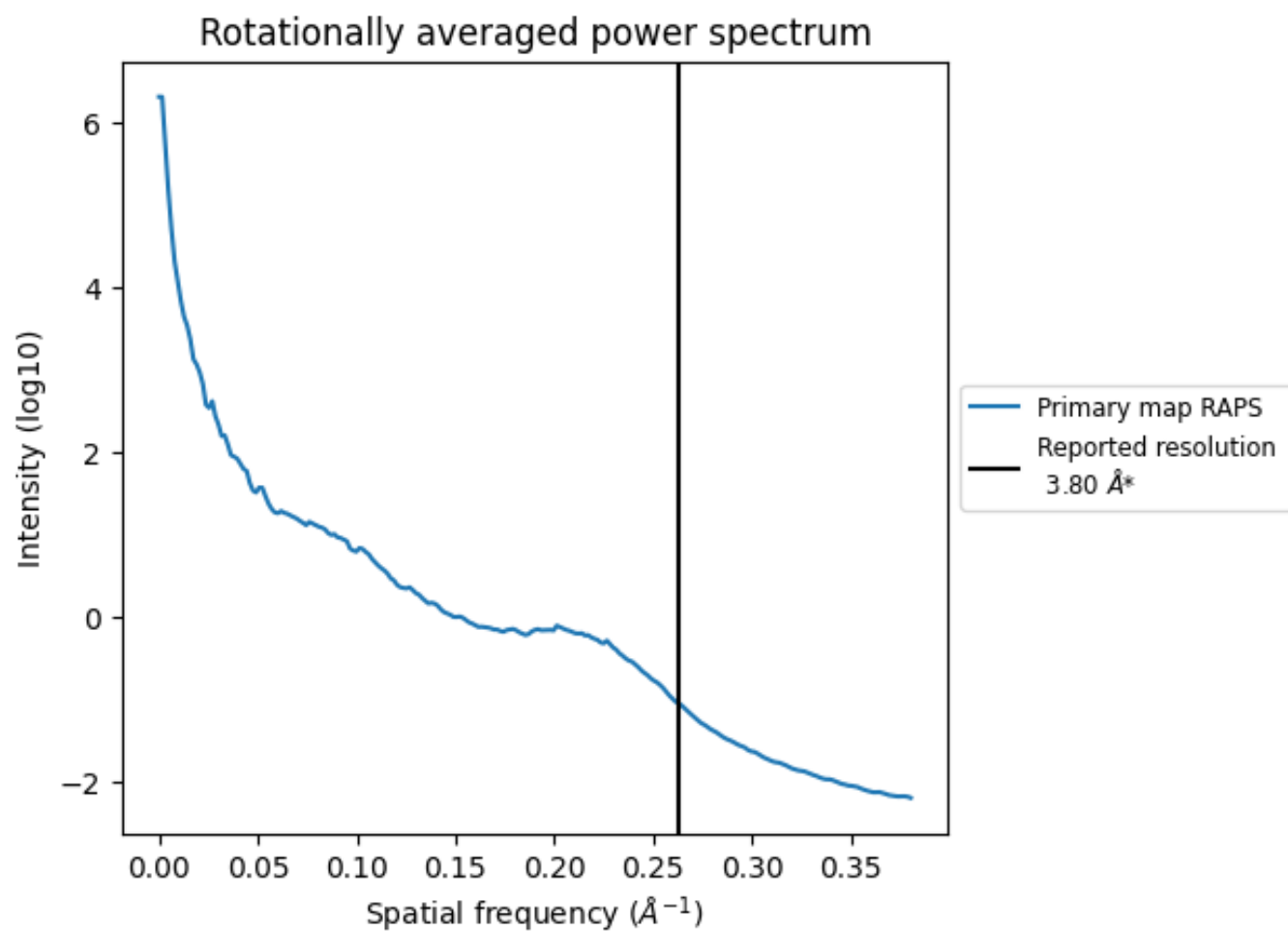
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4355 nm^3 ; this corresponds to an approximate mass of 3934 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 0.263 Å⁻¹

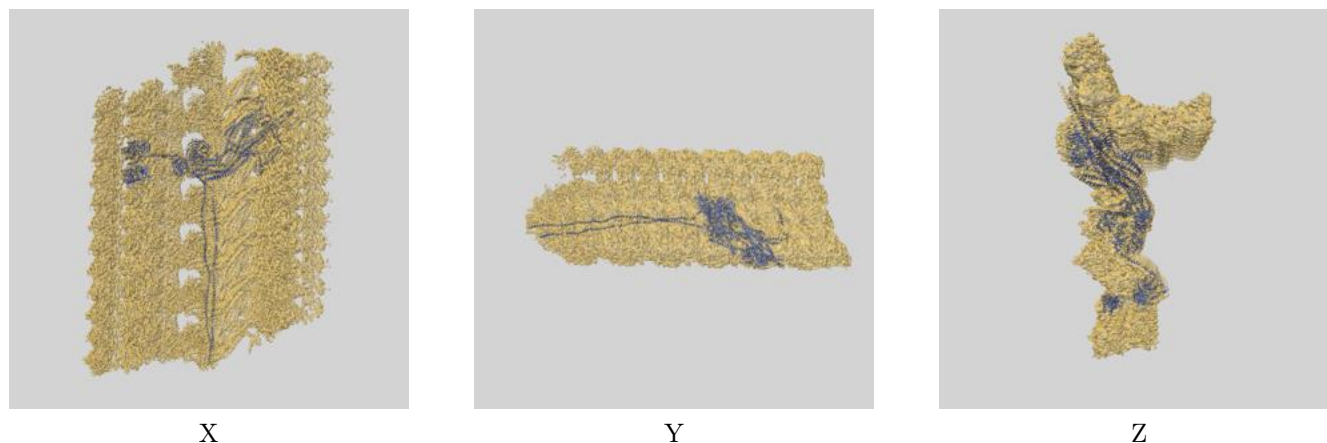
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-53467 and PDB model 9QZC. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 5.0 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](#)

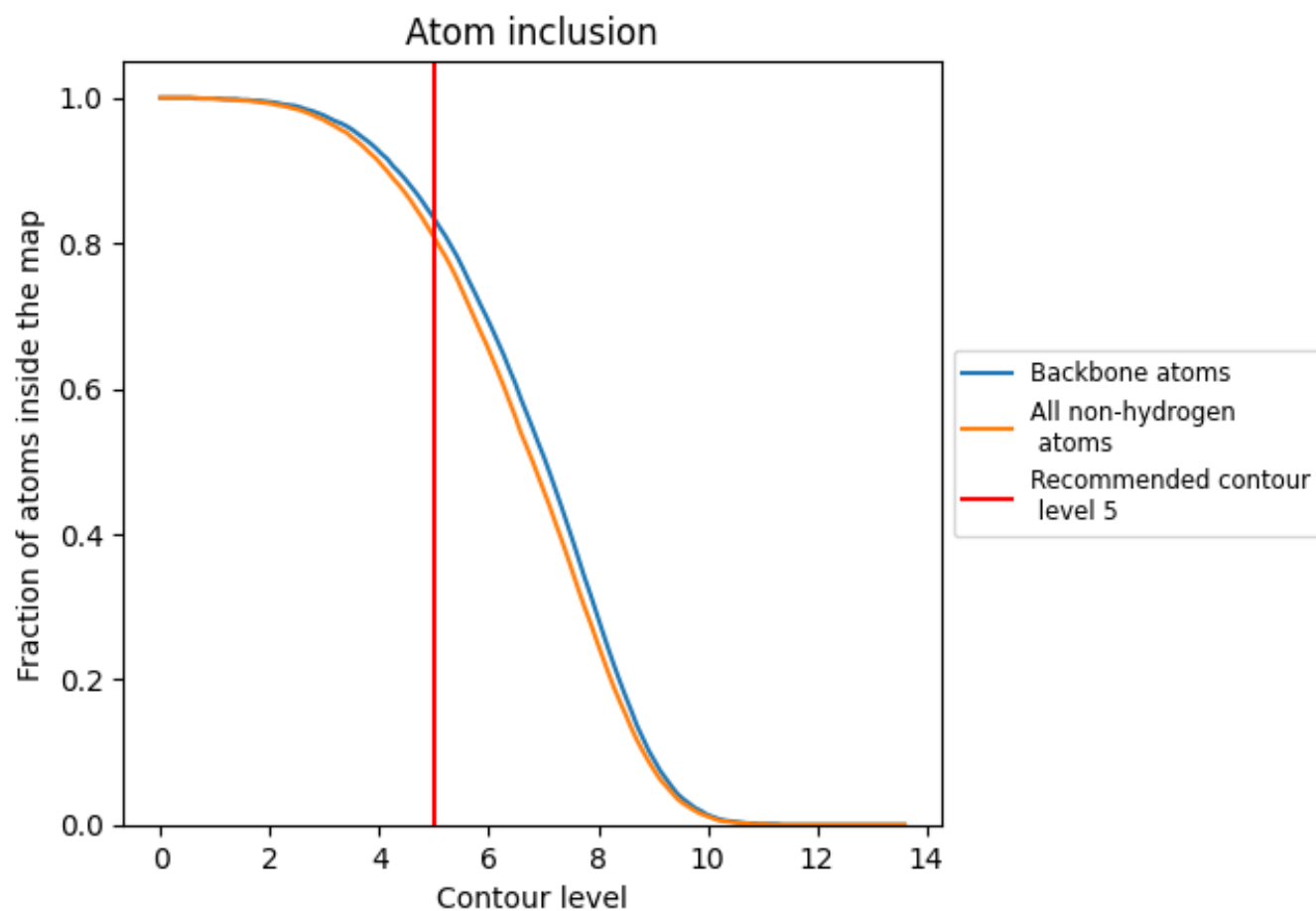


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 81% 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 (5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8080	 0.3410
7	 0.7440	 0.3410
A7	 0.7940	 0.3400
AE	 0.8500	 0.3580
AM	 0.7320	 0.2870
AU	 0.5010	 0.2140
Ac	 0.8440	 0.4140
As	 0.8990	 0.3380
Az	 0.7940	 0.3240
B4	 0.8520	 0.3670
Bw	 0.9430	 0.3710
CA	 0.8520	 0.3760
CH	 0.9430	 0.3910
CO	 0.9330	 0.3750
CV	 0.9200	 0.3590
Cc	 0.9250	 0.3730
i	 0.8760	 0.3990
q	 0.8820	 0.3490
y	 0.8370	 0.3210

