



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 03:07 AM UTC

PDB ID : 7VF5 / pdb_00007vf5
EMDB ID : EMD-31947
Title : Human m6A-METTL associated complex (WTAP, VIRMA, and HAKAI)
Authors : Su, S.; Li, S.; Deng, T.; Gao, M.; Yin, Y.; Wu, B.; Peng, C.; Liu, J.; Ma, J.; Zhang, K.
Deposited on : 2021-09-10
Resolution : 3.00 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

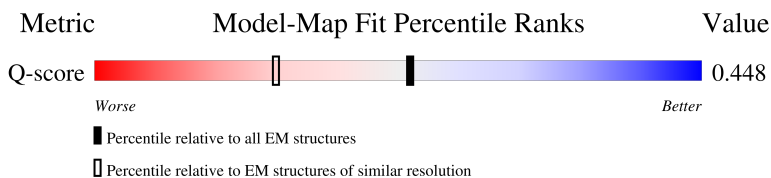
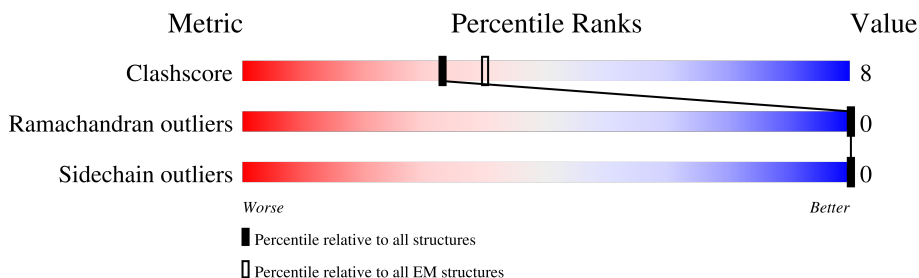
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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	14081 (2.50 - 3.50)

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
1	A	1812	7% 51% 15% 34%
2	C	396	5% 36% 10% 54%
2	D	396	5% 36% 10% 54%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12313 atoms, of which 0 are hydrogens and 0 are deuteriums.

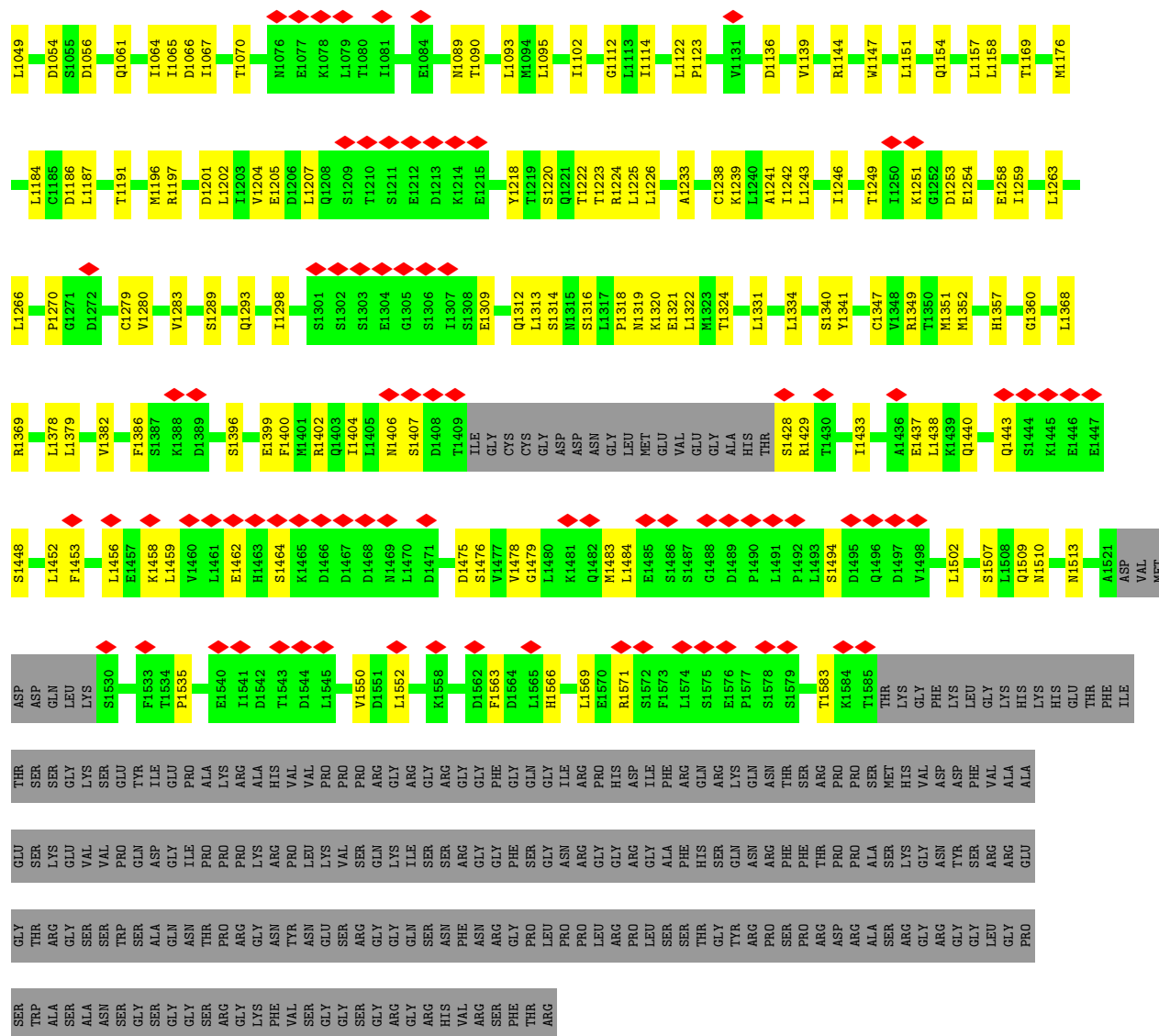
In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Protein virilizer homolog.

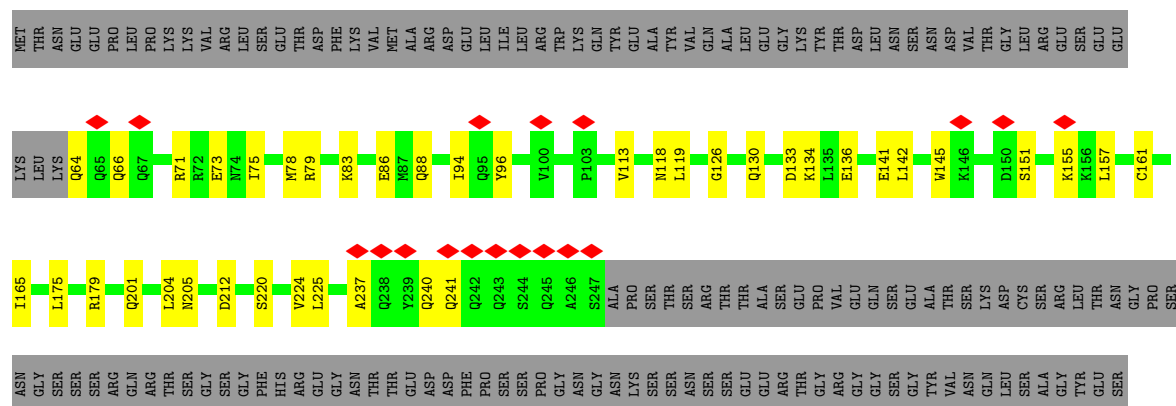
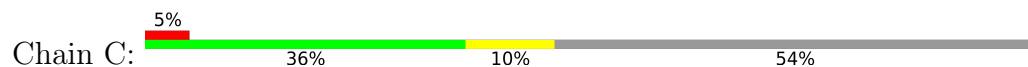
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1188	Total	C	N	O	S	0	0
			9325	5920	1548	1802	55		

- Molecule 2 is a protein called Pre-mRNA-splicing regulator WTAP.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	184	Total	C	N	O	S	0	0
			1494	920	264	301	9		
2	D	184	Total	C	N	O	S	0	0
			1494	920	264	301	9		

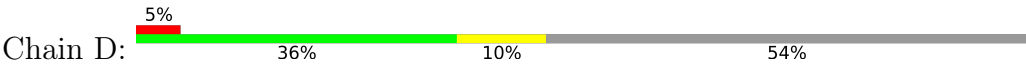


• Molecule 2: Pre-mRNA-splicing regulator WTAP



VAL	ASP	THR	ASP	PRO	THR	GLY	SER	GLU	ASN	SER	LEU	THR	HIS	GLN	SER	ASN	ASP	THR	ASP	SER	SER	HIS	ASP	PRO	GLN	GLU	GLY	LYS	ALA	VAL	SER	GLY	LYS	GLY	ASN	ARG	THR	VAL	GLY	SER	ARG	HIS	VAL	GLN	ASN	GLY	LEU	ASP	SER	SER	VAL	ASN	VAL	GLN	GLY	SER	VAL	LEU
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● Molecule 2: Pre-mRNA-splicing regulator WTAP



MET	THR	ASN	GLU	GLU	PRO	LEU	PRO	LYS	LYS	VAL	ARG	LEU	SER	GLU	THR	THR	ASP	PHE	LYS	VAL	MET	ALA	ARG	ASP	GLU	LEU	ILE	LEU	ARG	TRP	LYS	GLN	TYR	GLU	ALA	TYR	VAL	GLN	ALA	LEU	GLY	GLY	LYS	THR	TYR	ASN	ASP	VAL	GLY	ARG	GLU	SER	GLU
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LYS	LEU	LYS	Q64	Q65	Q66	Q67	F68	S69	A70	R71	N74	T82	R83	E84	Q85	F86	H87	Q88	E89	C90	T91	T92	Q93	I94	V100	P103	L108	M112	G126	E127	L128	F129	Q130	T131	K132	D133	K134	L135	E136	Q137	N140	F141	L142	K146	F147	S151	L157
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L164	L176	R179	I180	A181	Q182	L204	I209	Q210	L211	D212	E213	M218	L229	R233	Q238	Y239	Q240	Q241	Q242	Q243	S244	Q245	A246	S247	ALA	PRO	SER	THR	SER	ASN	ARG	THR	THR	ALA	SER	THR	GLY	PRO	VAL	GLY	GLN	SER	GLY	ALA	THR	SER	LYS	ASP	CYS	ARG	LEU	THR
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ASN	GLY	PRO	SER	ASN	GLY	SER	SER	ARG	GLN	ARG	THR	ASN	SER	GLY	GLY	PHE	HIS	ARG	GLU	GLY	ASN	THR	SER	THR	GLU	ASP	PRO	PHE	GLN	GLU	GLY	SER	SER	ALA	PRO	ASN	GLY	ASN	LYS	SER	ASN	THR	VAL	SER	GLY	GLY	THR	VAL	GLY	THR	VAL	ASN	GLN	LEU	SER	ALA
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GLY	TYR	GLU	SER	VAL	ASP	SER	PRO	THR	GLY	SER	GLU	ASN	SER	THR	HIS	GLN	SER	ASN	ASP	THR	ASP	SER	SER	HIS	ASP	PRO	GLN	GLU	GLY	LYS	ALA	VAL	SER	GLY	LYS	GLY	ASN	ARG	THR	VAL	GLY	THR	VAL	SER	GLY	THR	VAL	ASN	VAL	GLN	LEU	GLY	SER
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VAL	LEU
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	282821	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 ($e^-/\text{\AA}^2$)	56	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	4.503	Depositor
Minimum map value	-2.787	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.085	Depositor
Recommended contour level	0.36	Depositor
Map size (Å)	275.52, 275.52, 275.52	wwPDB
Map dimensions	336, 336, 336	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82, 0.82, 0.82	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	A	0.15	0/9479	0.37	0/12846
2	C	0.13	0/1505	0.34	0/2015
2	D	0.15	0/1505	0.37	0/2015
All	All	0.15	0/12489	0.36	0/16876

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	9325	0	9473	167	0
2	C	1494	0	1507	35	0
2	D	1494	0	1507	33	0
All	All	12313	0	12487	209	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 8.

The worst 5 of 209 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:C:86:GLU:HB2	2:D:87:MET:HE1	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:145:TRP:HD1	2:D:151:SER:HB2	1.51	0.74
1:A:1318:PRO:HB3	1:A:1322:LEU:HD23	1.69	0.74
1:A:689:LEU:HD22	1:A:738:PHE:HE2	1.52	0.74
1:A:1270:PRO:HB3	1:A:1280:VAL:HG11	1.69	0.72

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	1180/1812 (65%)	1140 (97%)	40 (3%)	0	100	100
2	C	182/396 (46%)	180 (99%)	2 (1%)	0	100	100
2	D	182/396 (46%)	180 (99%)	2 (1%)	0	100	100
All	All	1544/2604 (59%)	1500 (97%)	44 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	A	1074/1613 (67%)	1074 (100%)	0	100	100
2	C	167/351 (48%)	167 (100%)	0	100	100
2	D	167/351 (48%)	167 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	1408/2315 (61%)	1408 (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 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1496	GLN
2	D	64	GLN
2	C	201	GLN
2	D	107	GLN
1	A	921	ASN

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.

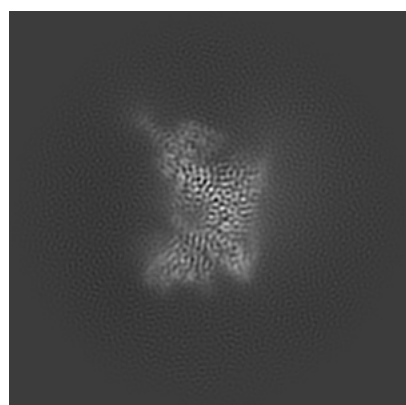
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31947. These allow visual inspection of the internal detail of the map and identification of artifacts.

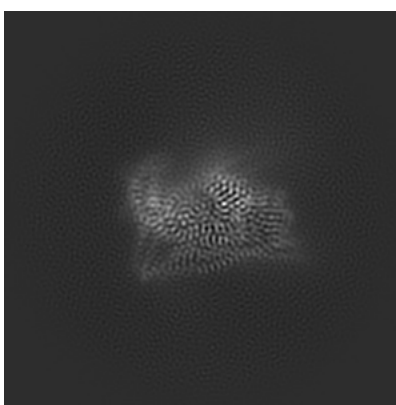
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

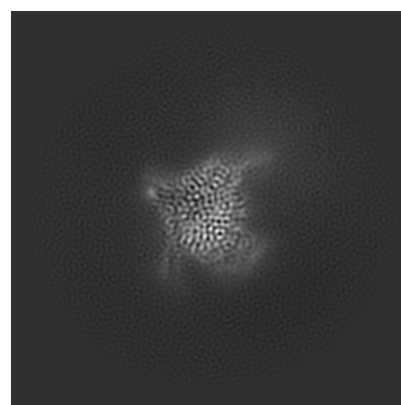
6.1.1 Primary map



X



Y

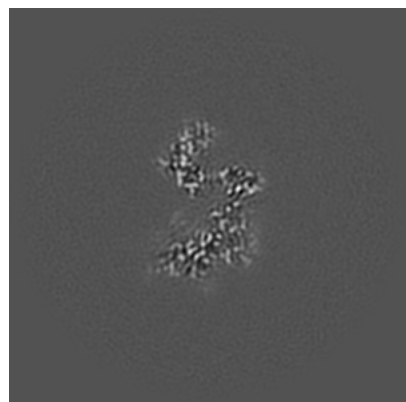


Z

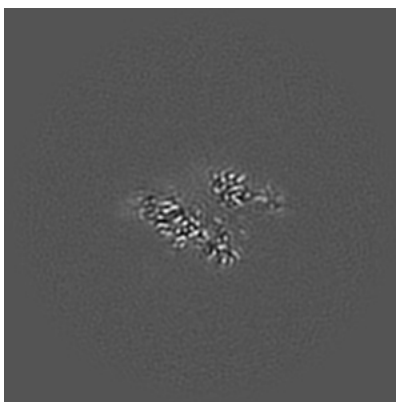
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

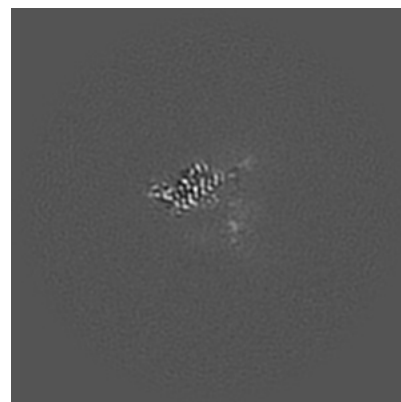
6.2.1 Primary map



X Index: 168



Y Index: 168

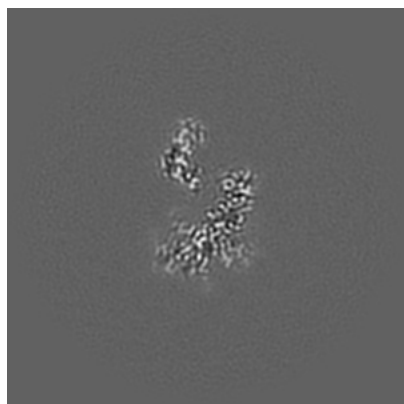


Z Index: 168

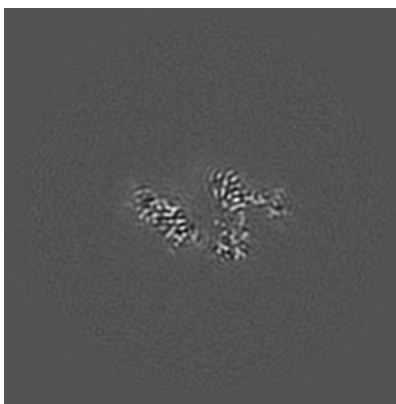
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

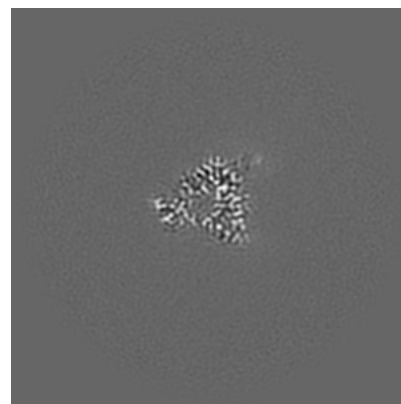
6.3.1 Primary map



X Index: 162



Y Index: 162

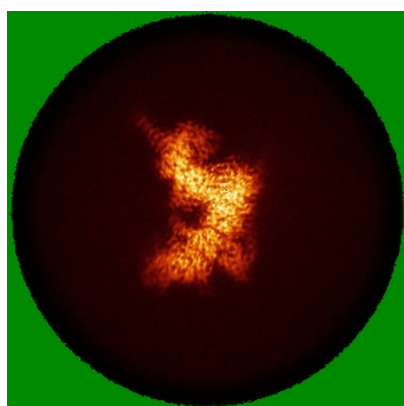


Z Index: 185

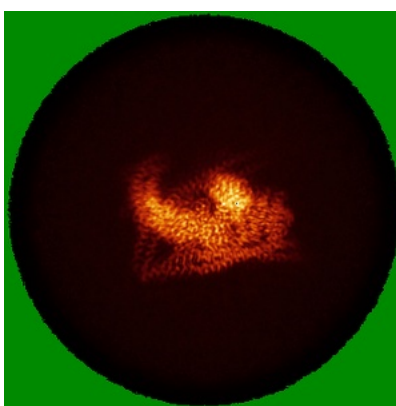
The images above show the largest variance slices of the map in three orthogonal directions.

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

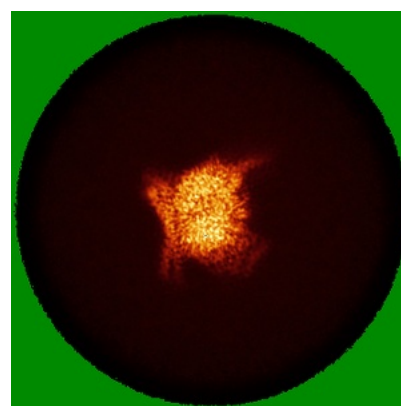
6.4.1 Primary map



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.

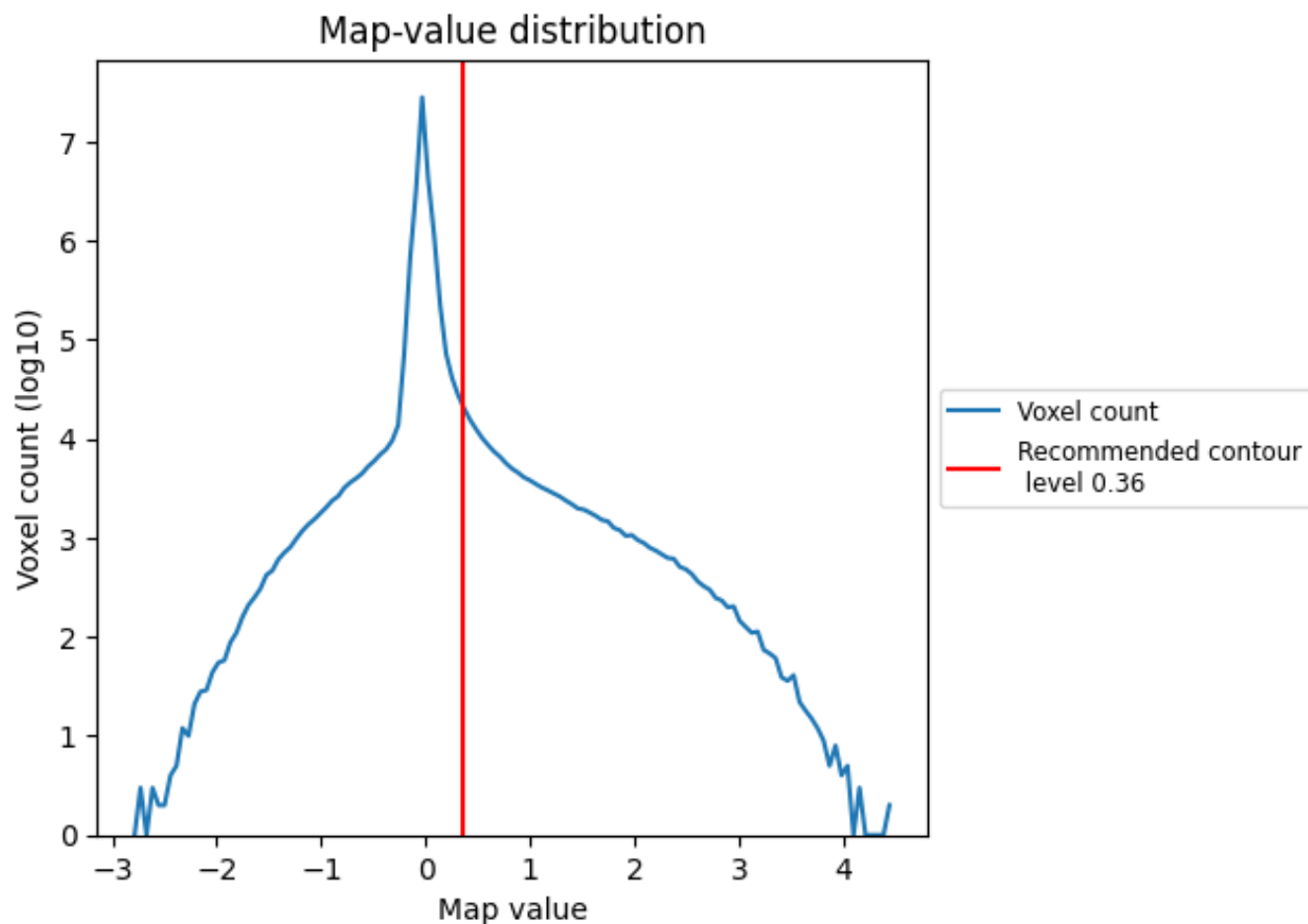
6.6 Mask visualisation

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

7 Map analysis [i](#)

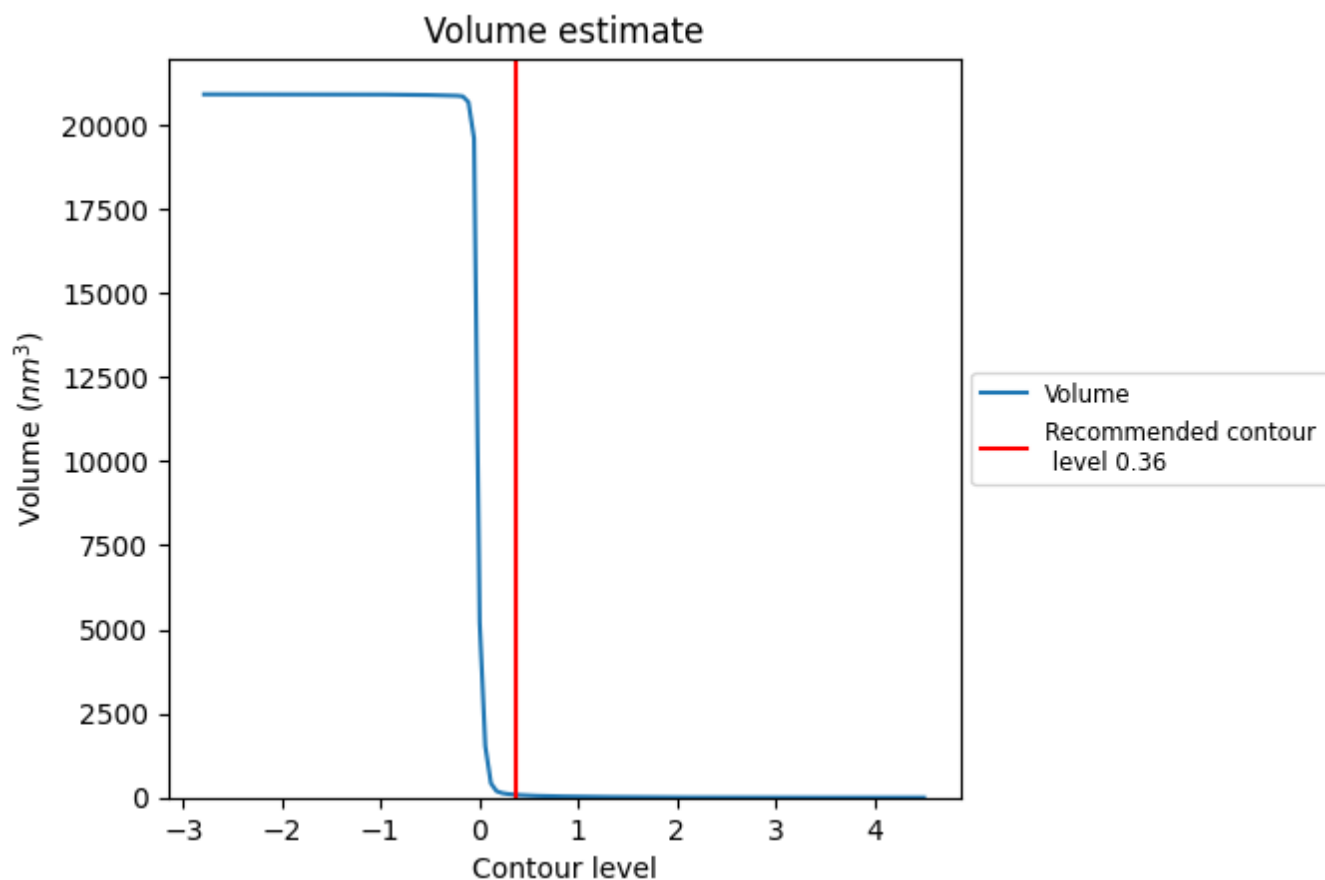
This section contains the results of statistical analysis of the map.

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.

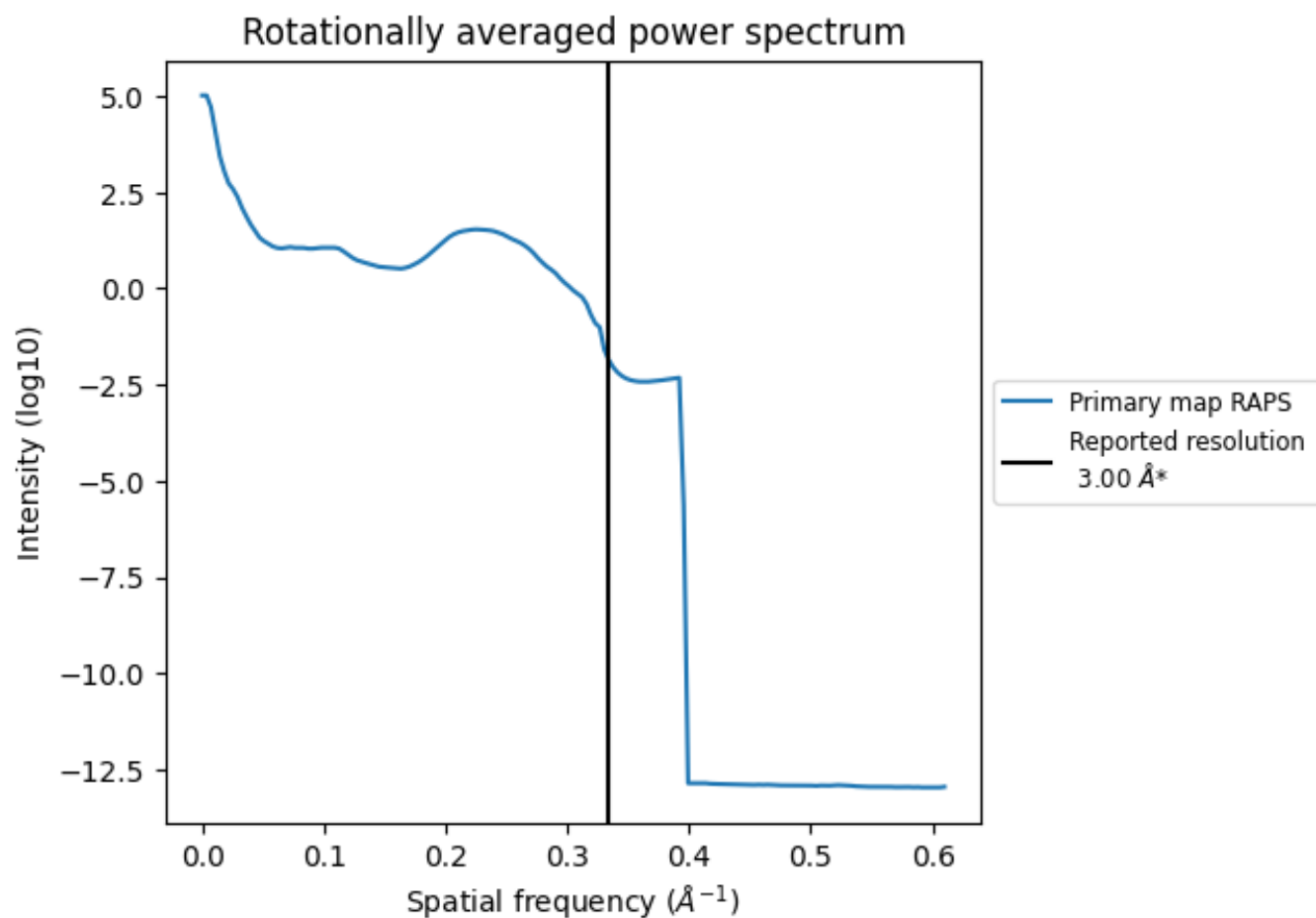
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 84 nm^3 ; this corresponds to an approximate mass of 76 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 0.333 Å⁻¹

8 Fourier-Shell correlation

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

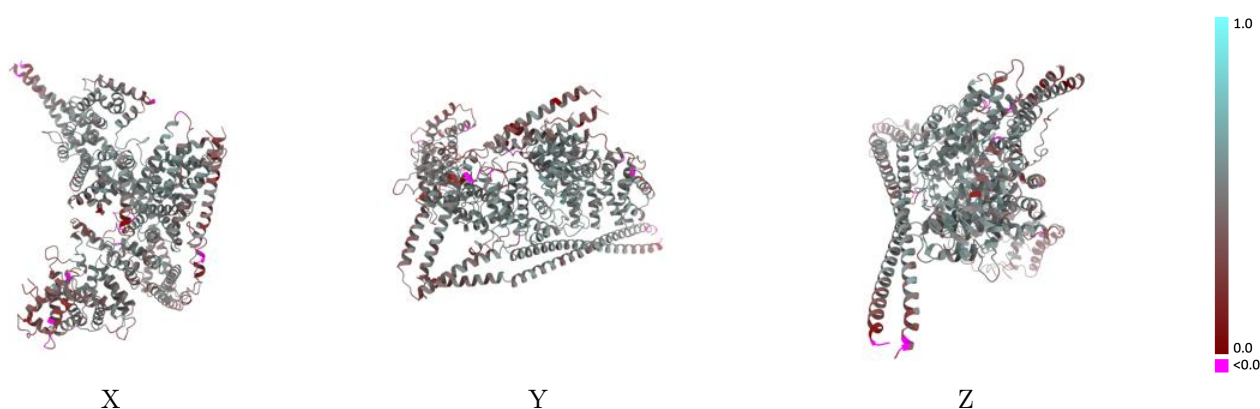
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-31947 and PDB model 7VF5. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)

This section was not generated.

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

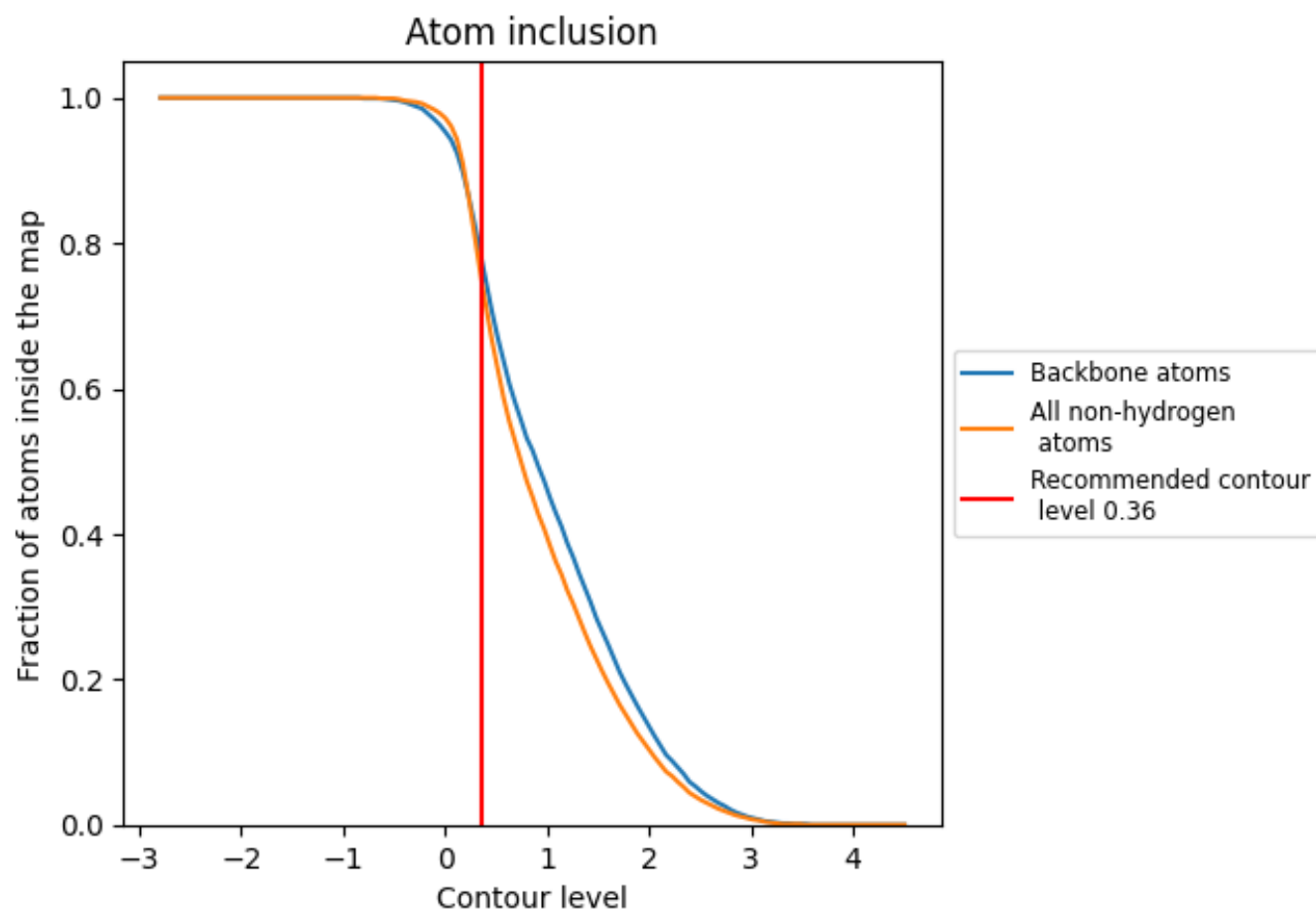


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 78% of all backbone atoms, 75% 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 (0.36) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7470	0.4480
A	0.7620	0.4550
C	0.7170	0.4380
D	0.6840	0.4190

