wwPDB EM Validation Summary Report (i)

May 7, 2025 – 12:12 PM JST

PDB ID	:	9IVW / pdb_00009ivw
EMDB ID	:	EMD-60935
Title	:	Structure of Adenovirus serotype 2 100K
Authors	:	Liu, Q.; Li, H.; Xiang, Y.
Deposited on	:	2024-07-24
Resolution	:	3.79 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 (i) 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 (i)) were used in the production of this report:

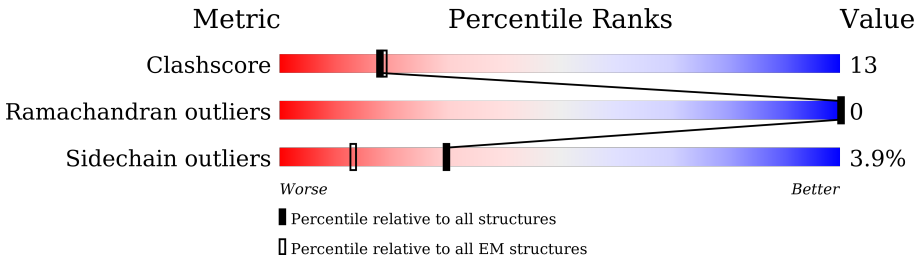
EMDB validation analysis	:	0.0.1.dev118
MolProbity	:	4-5-2 with Phenix2.0rc1
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.43.1

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 3.79 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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 <=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	F	849	38% 16% · 45%
1	G	849	31% 13% · 55%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 6852 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 Shutoff protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	G	380	Total	C	N	O	S	0	0
			3074	1954	544	555	21		
1	F	469	Total	C	N	O	S	0	0
			3778	2412	661	680	25		

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	806	GLY	-	expression tag	UNP P24932
G	807	SER	-	expression tag	UNP P24932
G	808	LEU	-	expression tag	UNP P24932
G	809	GLU	-	expression tag	UNP P24932
G	810	VAL	-	expression tag	UNP P24932
G	811	LEU	-	expression tag	UNP P24932
G	812	PHE	-	expression tag	UNP P24932
G	813	GLN	-	expression tag	UNP P24932
G	814	GLY	-	expression tag	UNP P24932
G	815	PRO	-	expression tag	UNP P24932
G	816	ARG	-	expression tag	UNP P24932
G	817	SER	-	expression tag	UNP P24932
G	818	MET	-	expression tag	UNP P24932
G	819	GLY	-	expression tag	UNP P24932
G	820	TRP	-	expression tag	UNP P24932
G	821	SER	-	expression tag	UNP P24932
G	822	HIS	-	expression tag	UNP P24932
G	823	PRO	-	expression tag	UNP P24932
G	824	GLN	-	expression tag	UNP P24932
G	825	PHE	-	expression tag	UNP P24932
G	826	GLU	-	expression tag	UNP P24932
G	827	LYS	-	expression tag	UNP P24932
G	828	GLY	-	expression tag	UNP P24932
G	829	GLY	-	expression tag	UNP P24932
G	830	GLY	-	expression tag	UNP P24932
G	831	ALA	-	expression tag	UNP P24932

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Chain	Residue	Modelled	Actual	Comment	Reference
G	832	ARG	-	expression tag	UNP P24932
G	833	GLY	-	expression tag	UNP P24932
G	834	GLY	-	expression tag	UNP P24932
G	835	SER	-	expression tag	UNP P24932
G	836	GLY	-	expression tag	UNP P24932
G	837	GLY	-	expression tag	UNP P24932
G	838	GLY	-	expression tag	UNP P24932
G	839	SER	-	expression tag	UNP P24932
G	840	TRP	-	expression tag	UNP P24932
G	841	SER	-	expression tag	UNP P24932
G	842	HIS	-	expression tag	UNP P24932
G	843	PRO	-	expression tag	UNP P24932
G	844	GLN	-	expression tag	UNP P24932
G	845	PHE	-	expression tag	UNP P24932
G	846	GLU	-	expression tag	UNP P24932
G	847	LYS	-	expression tag	UNP P24932
G	848	GLY	-	expression tag	UNP P24932
G	849	PHE	-	expression tag	UNP P24932
F	806	GLY	-	expression tag	UNP P24932
F	807	SER	-	expression tag	UNP P24932
F	808	LEU	-	expression tag	UNP P24932
F	809	GLU	-	expression tag	UNP P24932
F	810	VAL	-	expression tag	UNP P24932
F	811	LEU	-	expression tag	UNP P24932
F	812	PHE	-	expression tag	UNP P24932
F	813	GLN	-	expression tag	UNP P24932
F	814	GLY	-	expression tag	UNP P24932
F	815	PRO	-	expression tag	UNP P24932
F	816	ARG	-	expression tag	UNP P24932
F	817	SER	-	expression tag	UNP P24932
F	818	MET	-	expression tag	UNP P24932
F	819	GLY	-	expression tag	UNP P24932
F	820	TRP	-	expression tag	UNP P24932
F	821	SER	-	expression tag	UNP P24932
F	822	HIS	-	expression tag	UNP P24932
F	823	PRO	-	expression tag	UNP P24932
F	824	GLN	-	expression tag	UNP P24932
F	825	PHE	-	expression tag	UNP P24932
F	826	GLU	-	expression tag	UNP P24932
F	827	LYS	-	expression tag	UNP P24932
F	828	GLY	-	expression tag	UNP P24932
F	829	GLY	-	expression tag	UNP P24932

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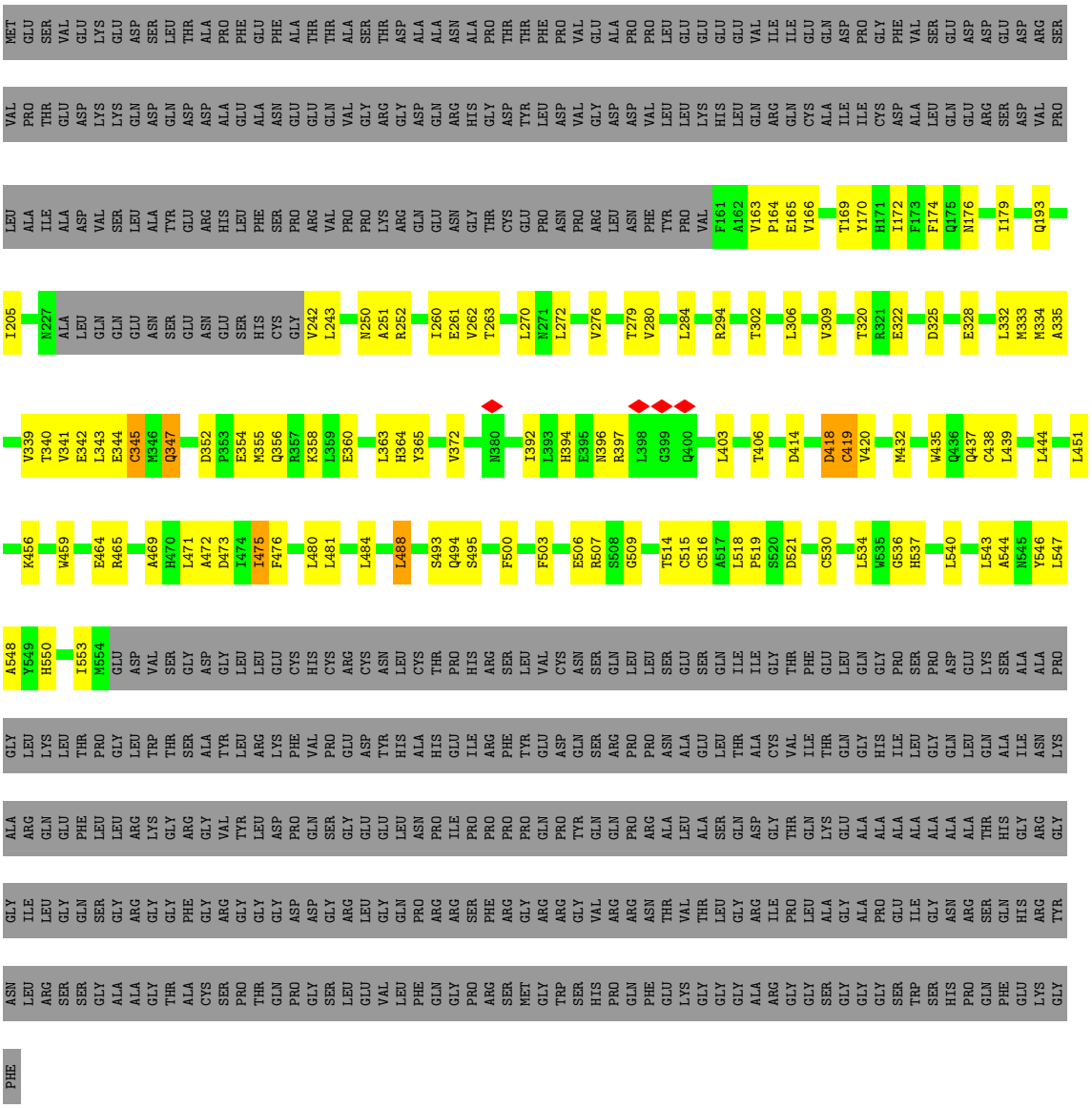
Chain	Residue	Modelled	Actual	Comment	Reference
F	830	GLY	-	expression tag	UNP P24932
F	831	ALA	-	expression tag	UNP P24932
F	832	ARG	-	expression tag	UNP P24932
F	833	GLY	-	expression tag	UNP P24932
F	834	GLY	-	expression tag	UNP P24932
F	835	SER	-	expression tag	UNP P24932
F	836	GLY	-	expression tag	UNP P24932
F	837	GLY	-	expression tag	UNP P24932
F	838	GLY	-	expression tag	UNP P24932
F	839	SER	-	expression tag	UNP P24932
F	840	TRP	-	expression tag	UNP P24932
F	841	SER	-	expression tag	UNP P24932
F	842	HIS	-	expression tag	UNP P24932
F	843	PRO	-	expression tag	UNP P24932
F	844	GLN	-	expression tag	UNP P24932
F	845	PHE	-	expression tag	UNP P24932
F	846	GLU	-	expression tag	UNP P24932
F	847	LYS	-	expression tag	UNP P24932
F	848	GLY	-	expression tag	UNP P24932
F	849	PHE	-	expression tag	UNP P24932

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

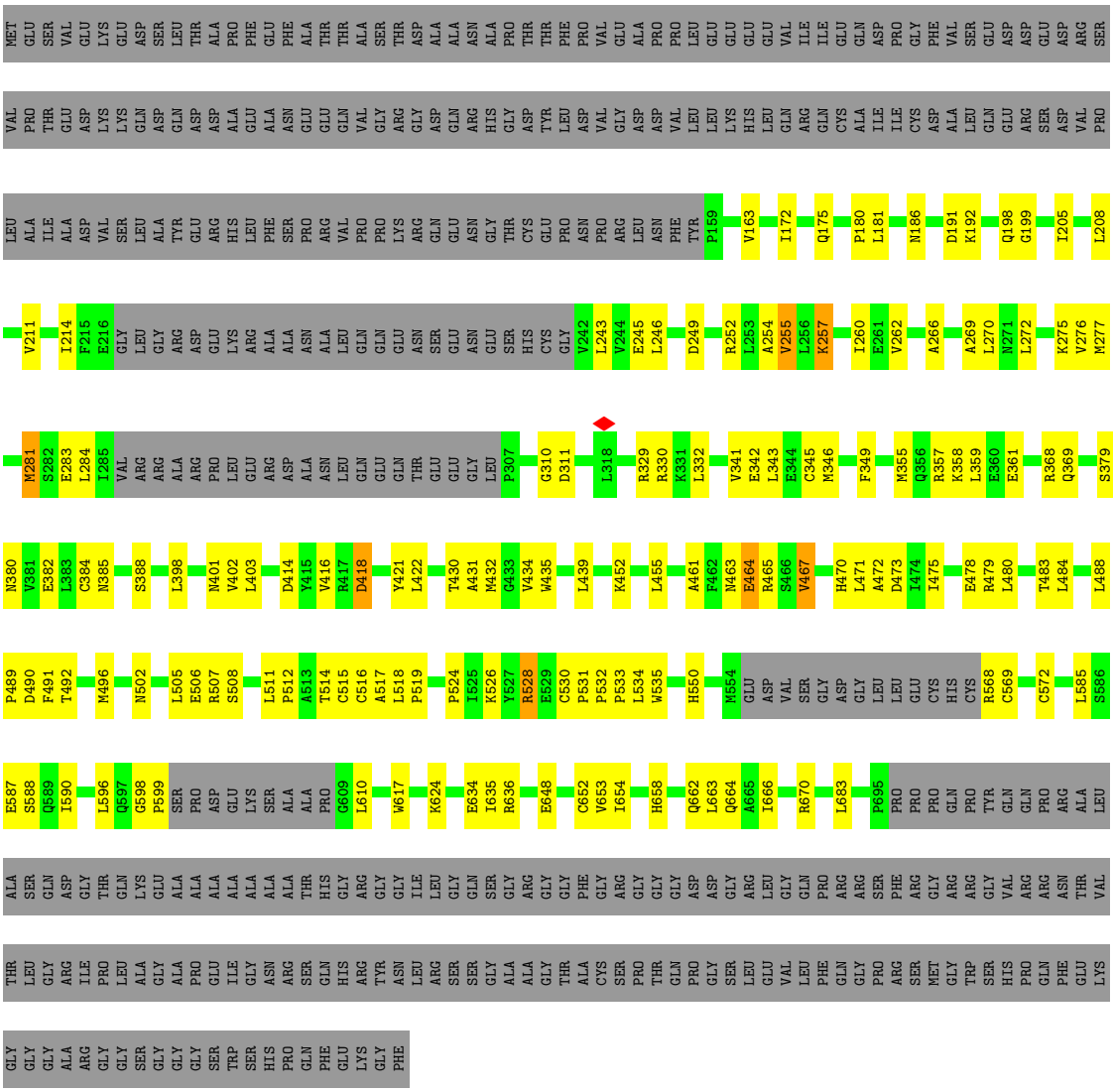
- Molecule 1: Shutoff protein

Chain G:



• Molecule 1: Shutoff protein

Chain F: 38% 16% • 45%



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	251682	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 ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.802	Depositor
Minimum map value	-0.042	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.0108	Depositor
Map size (Å)	300.0, 300.0, 300.0	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.25, 1.25, 1.25	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	F	0.48	4/3860 (0.1%)	0.72	7/5230 (0.1%)
1	G	0.49	3/3136 (0.1%)	0.73	8/4246 (0.2%)
All	All	0.48	7/6996 (0.1%)	0.73	15/9476 (0.2%)

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	521	ASP	C-N	10.51	1.45	1.33
1	F	470	HIS	C-O	-7.93	1.14	1.24
1	F	416	VAL	C-O	-6.74	1.16	1.24
1	F	255	VAL	C-O	5.65	1.30	1.24
1	G	418	ASP	C-O	-5.45	1.17	1.24

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	G	345	CYS	N-CA-C	-6.82	103.84	111.28
1	G	262	VAL	CA-C-O	-6.32	115.77	121.97
1	G	506	GLU	N-CA-C	-6.31	104.09	110.97
1	G	347	GLN	N-CA-C	-6.29	103.35	111.02
1	F	464	GLU	CB-CG-CD	6.20	123.13	112.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	3778	0	3796	108	0
1	G	3074	0	3094	80	0
All	All	6852	0	6890	180	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 13.

The worst 5 of 180 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:F:524:PRO:HG2	1:F:530:CYS:HB2	1.69	0.75
1:F:254:ALA:HA	1:F:257:LYS:HE3	1.71	0.71
1:G:503:PHE:CZ	1:F:398:LEU:HD21	2.29	0.67
1:G:260:ILE:HD11	1:G:514:THR:HG21	1.75	0.67
1:F:311:ASP:OD1	1:F:330:ARG:NH2	2.29	0.67

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	F	459/849 (54%)	431 (94%)	28 (6%)	0	100	100
1	G	376/849 (44%)	361 (96%)	15 (4%)	0	100	100
All	All	835/1698 (49%)	792 (95%)	43 (5%)	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	F	415/714 (58%)	399 (96%)	16 (4%)	27 51
1	G	334/714 (47%)	321 (96%)	13 (4%)	27 51
All	All	749/1428 (52%)	720 (96%)	29 (4%)	30 51

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	252	ARG
1	F	528	ARG
1	F	275	LYS
1	F	478	GLU
1	F	257	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	537	HIS
1	F	570	ASN
1	G	545	ASN
1	F	658	HIS
1	F	429	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.

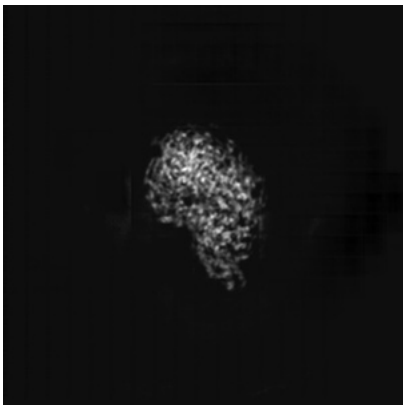
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-60935. These allow visual inspection of the internal detail of the map and identification of artifacts.

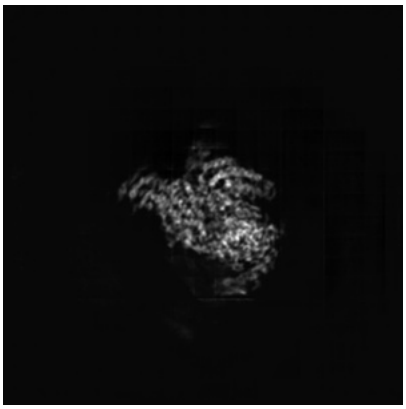
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

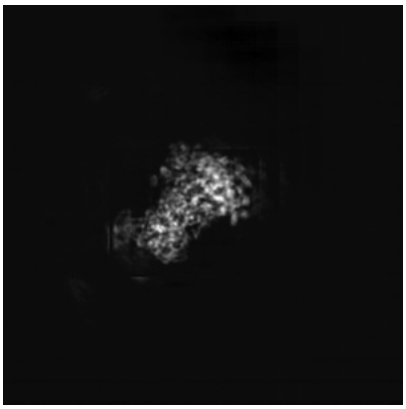
6.1.1 Primary map



X

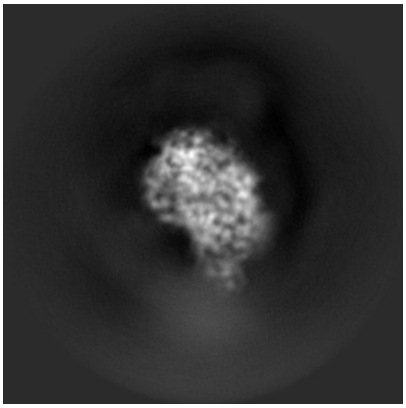


Y

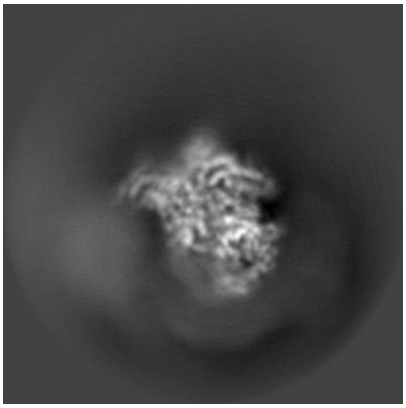


Z

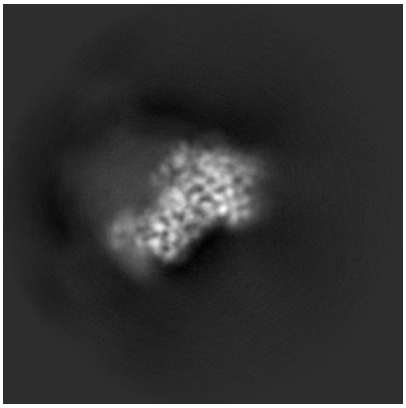
6.1.2 Raw map



X



Y



Z

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

6.2 Central slices (i)

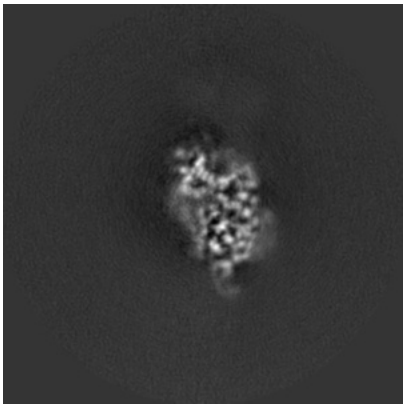
6.2.1 Primary map

X Index: 120

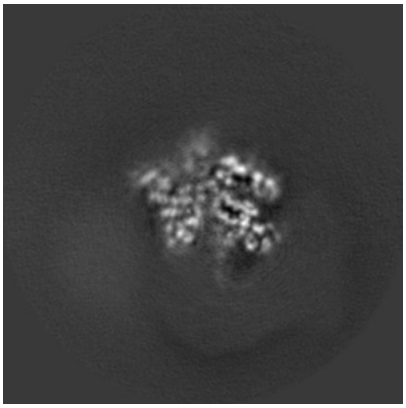
Y Index: 120

Z Index: 120

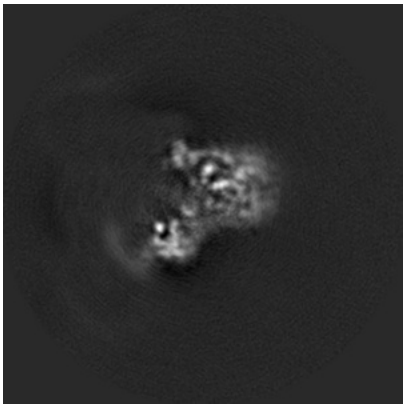
6.2.2 Raw map



X Index: 120



Y Index: 120



Z Index: 120

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

6.3 Largest variance slices (i)

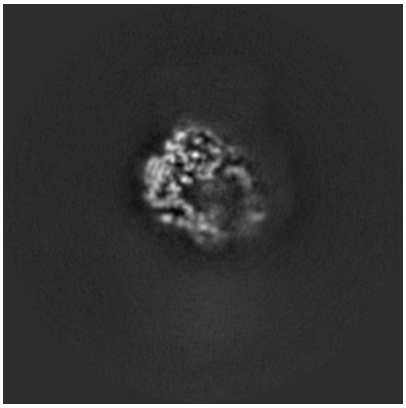
6.3.1 Primary map

X Index: 101

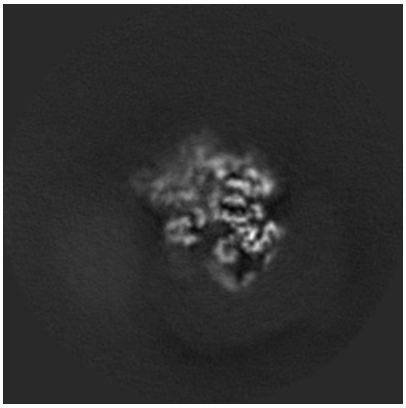
Y Index: 124

Z Index: 134

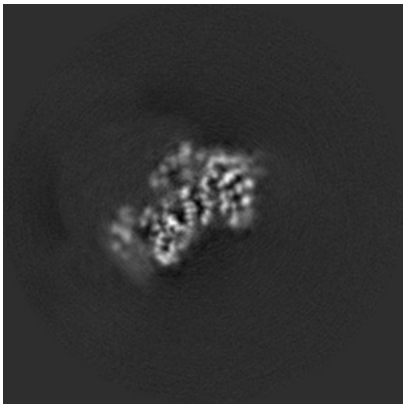
6.3.2 Raw map



X Index: 101



Y Index: 115

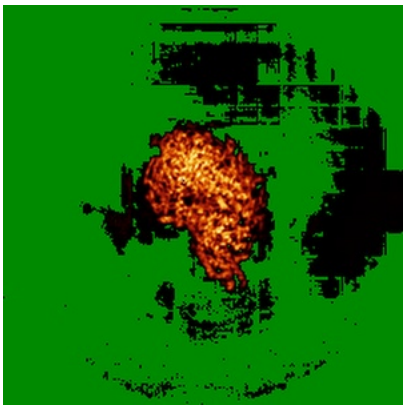


Z Index: 134

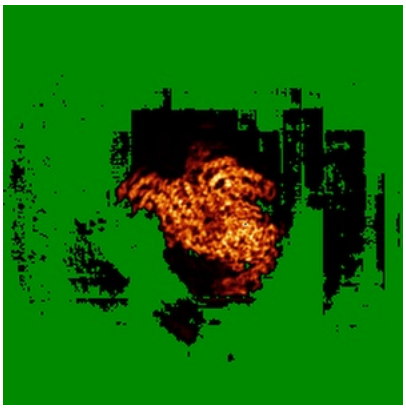
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

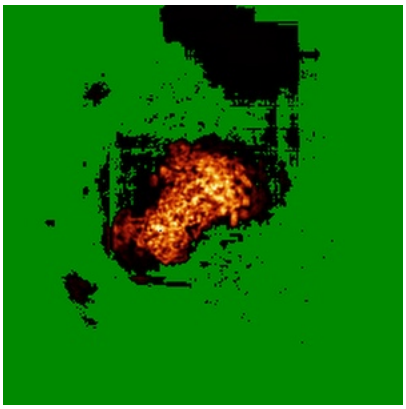
6.4.1 Primary map



X

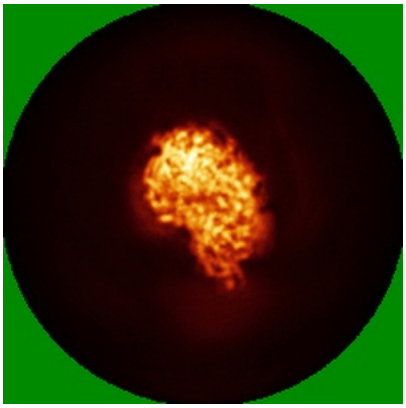


Y

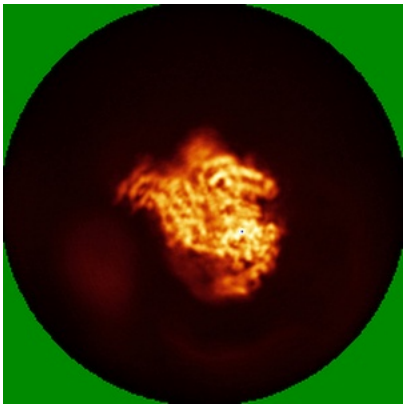


Z

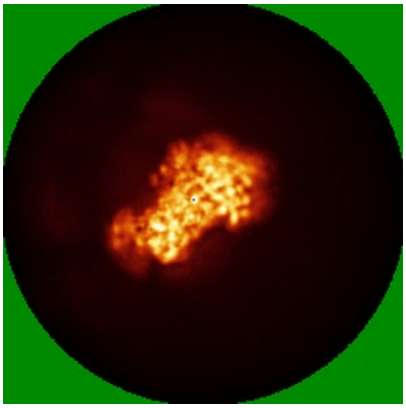
6.4.2 Raw map



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.

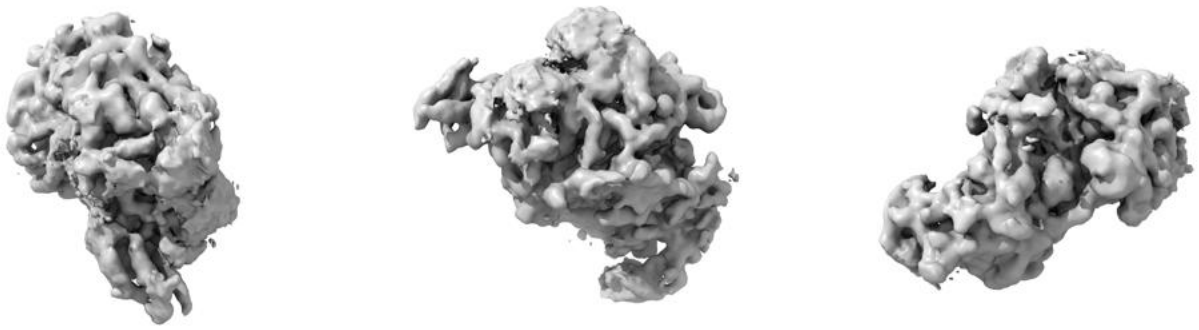
6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.0108. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

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

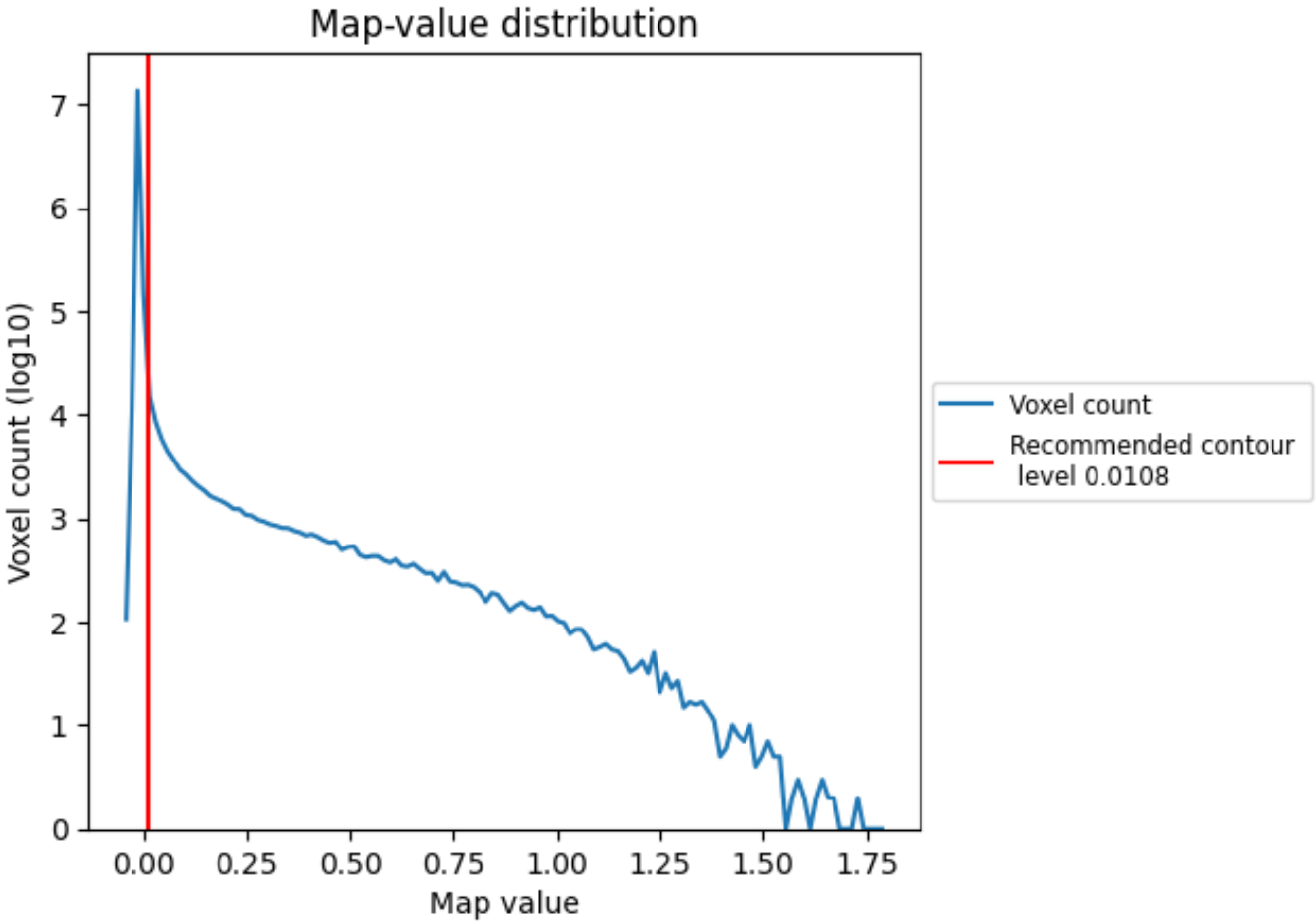
6.6 Mask visualisation (i)

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

7 Map analysis

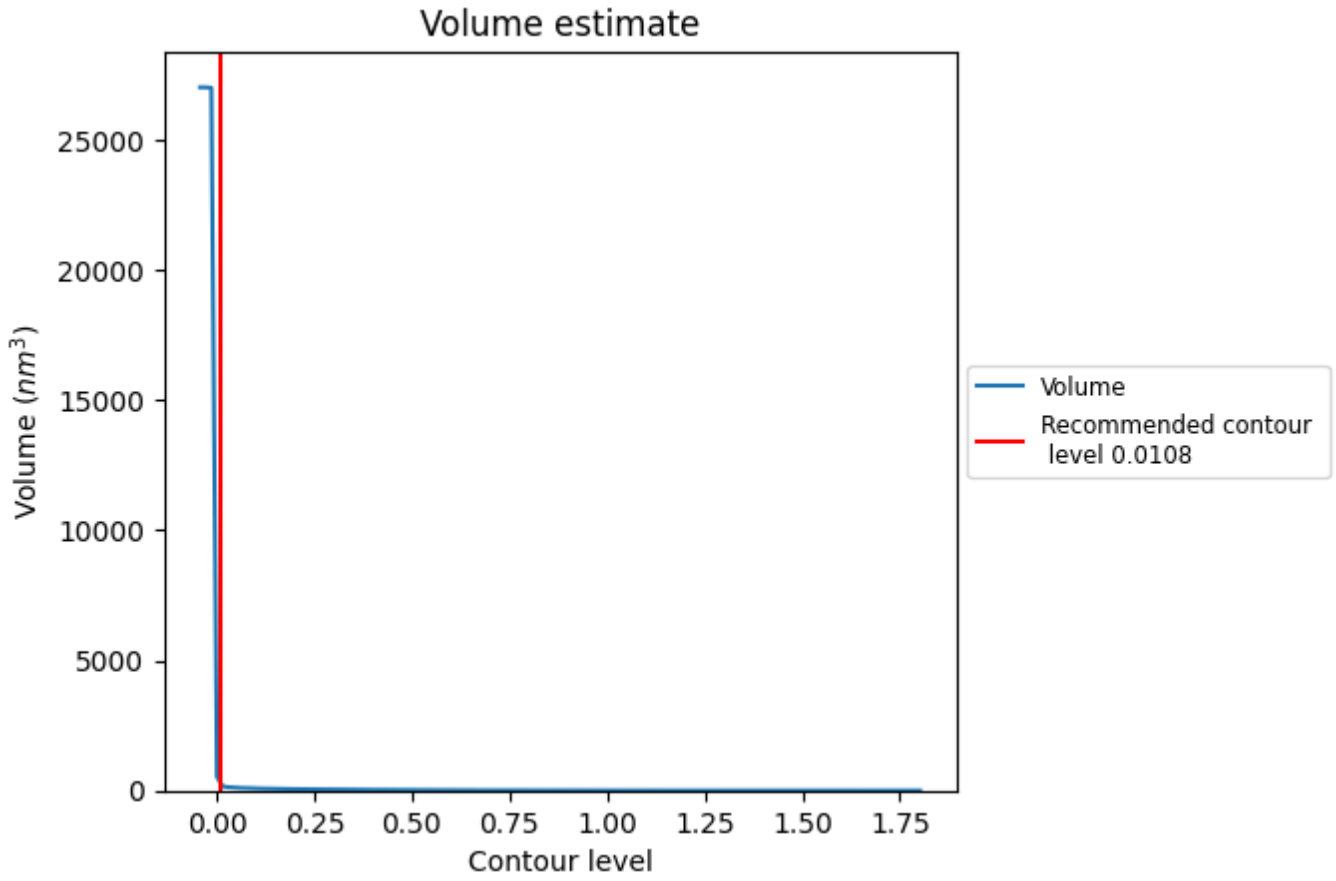
This section contains the results of statistical analysis of the map.

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.

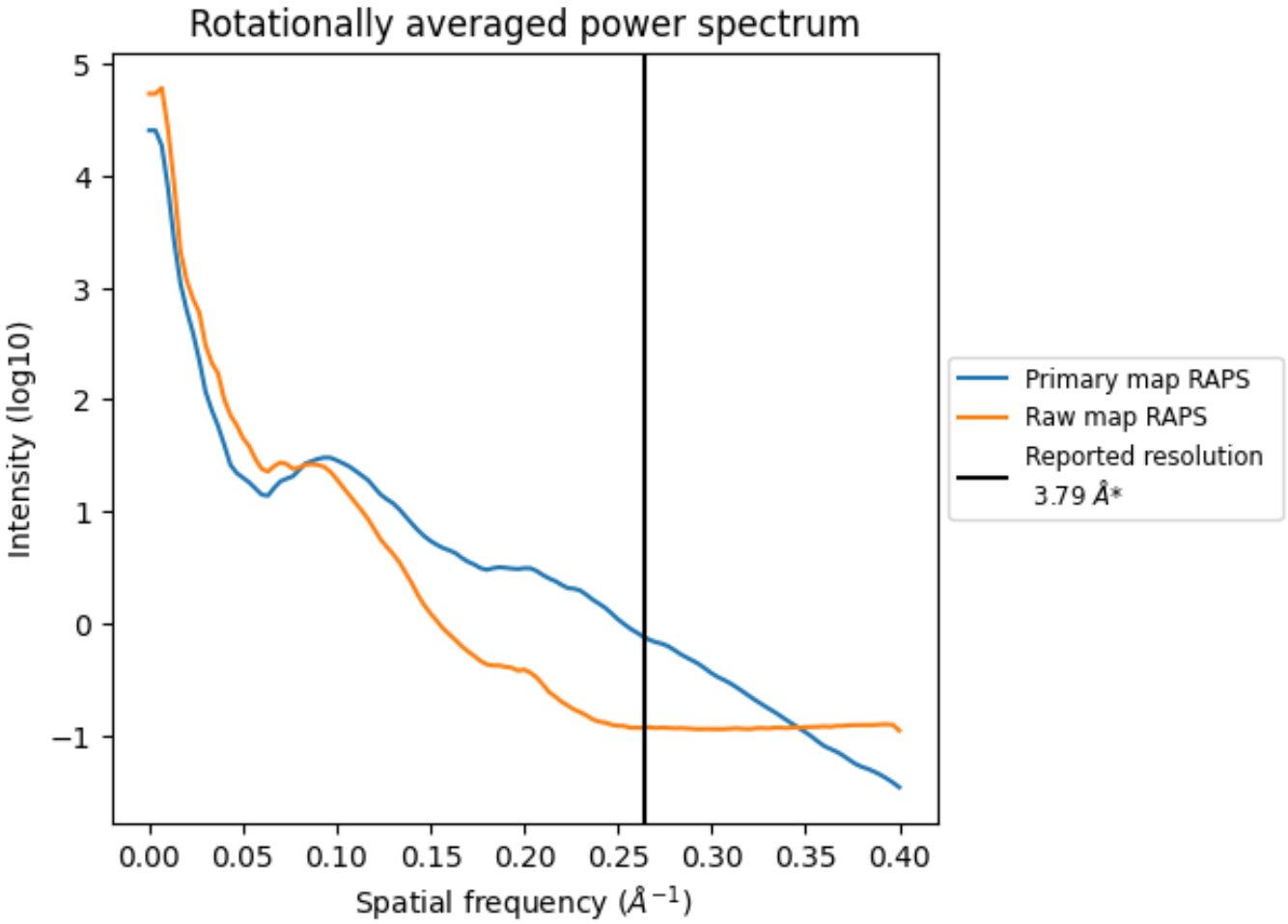
7.2 Volume estimate (i)



The volume at the recommended contour level is 280 nm^3; this corresponds to an approximate mass of 253 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)

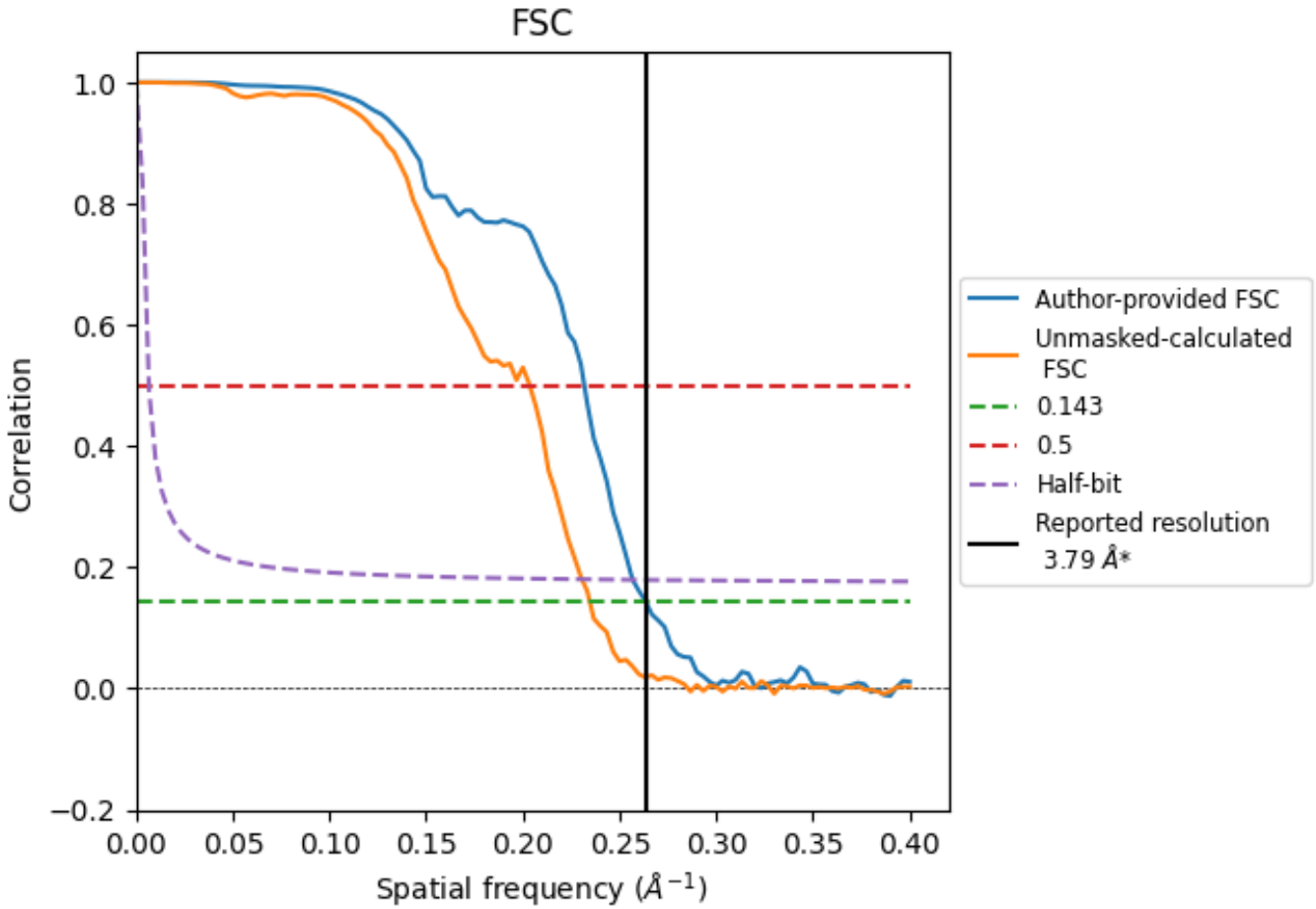


*Reported resolution corresponds to spatial frequency of 0.264 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.264 Å^{-1}

8.2 Resolution estimates (i)

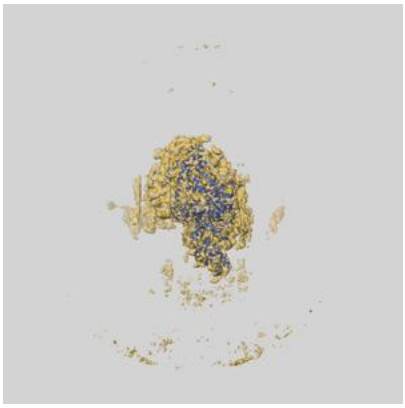
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.79	-	-
Author-provided FSC curve	3.79	4.31	3.90
Unmasked-calculated*	4.26	4.91	4.34

*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 4.26 differs from the reported value 3.79 by more than 10 %

9 Map-model fit

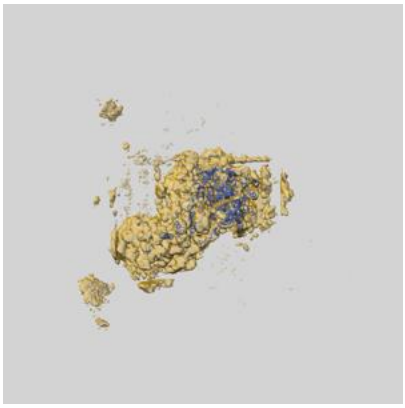
This section contains information regarding the fit between EMDB map EMD-60935 and PDB model 9IVW. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay



X

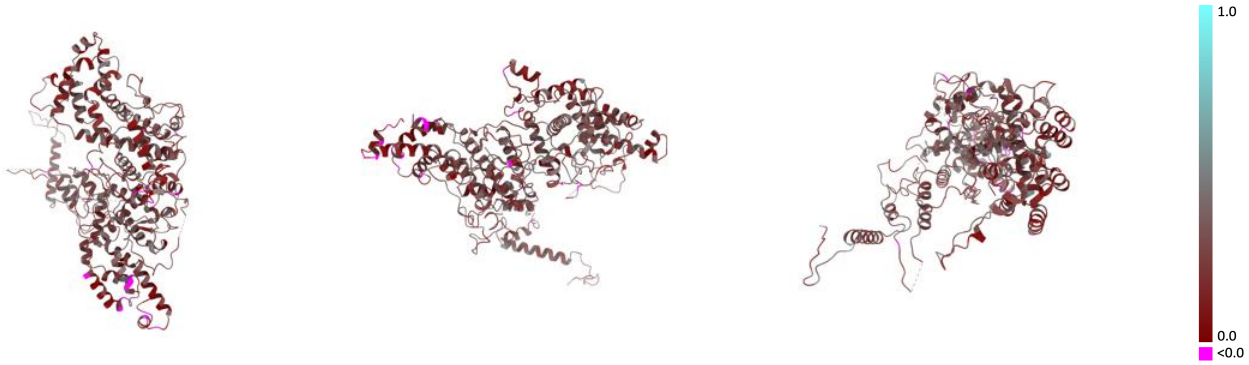
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0108 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.

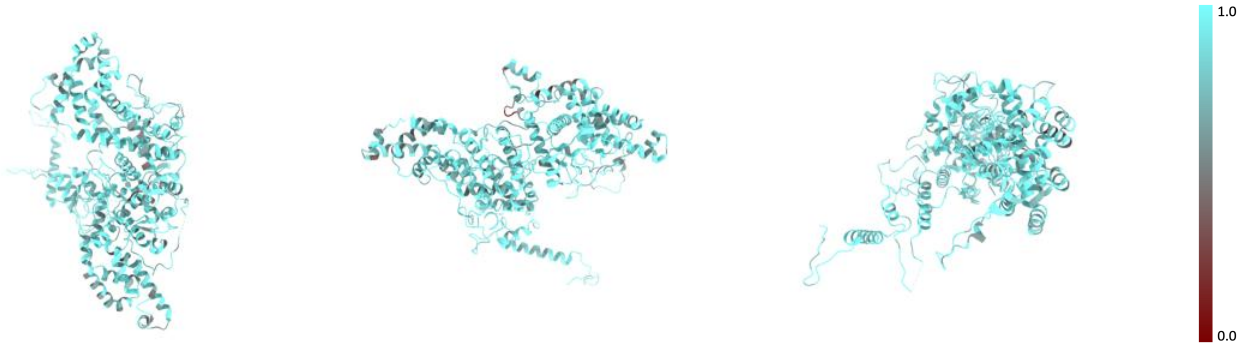
9.2 Q-score mapped to coordinate model



X Y Z

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.

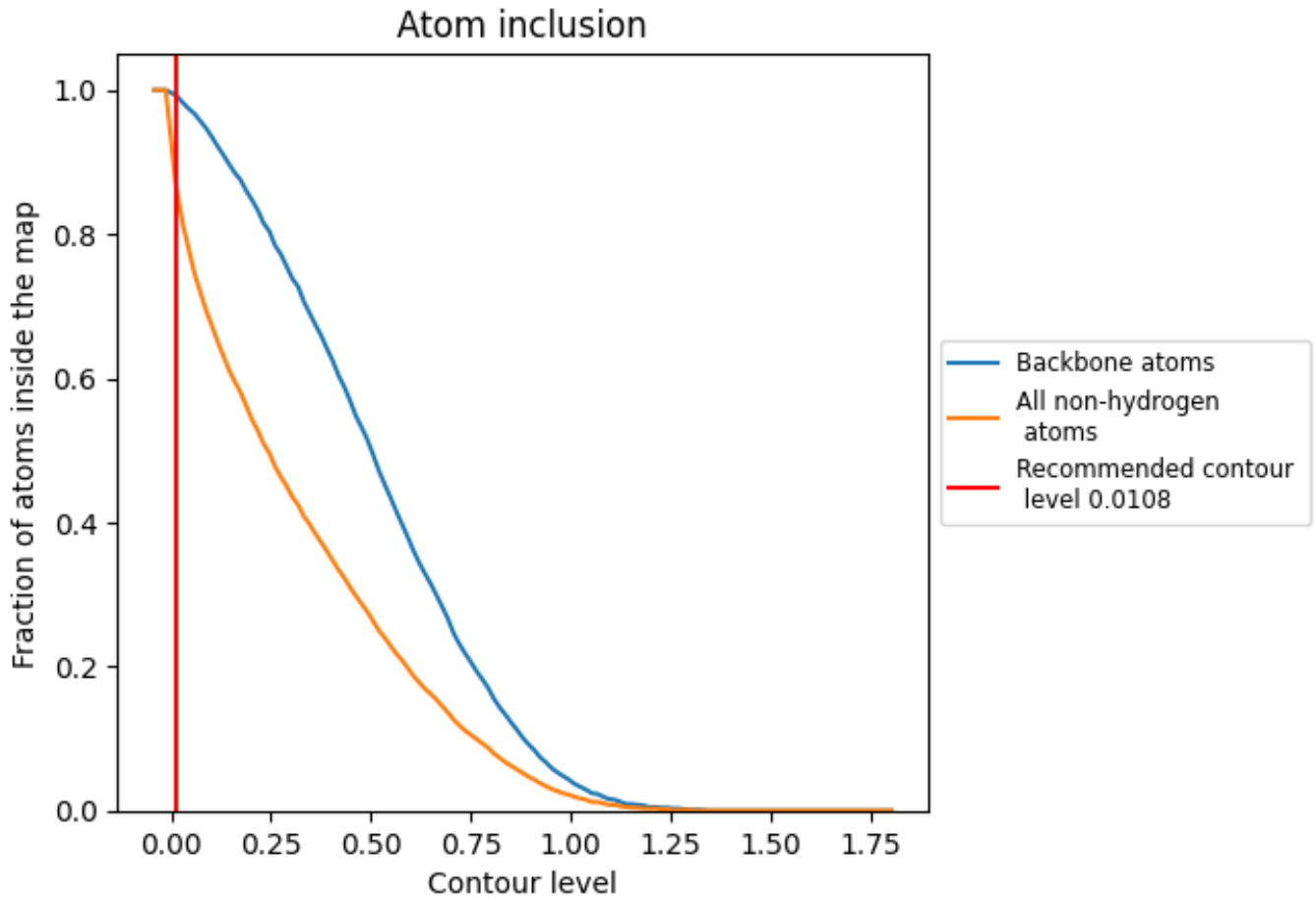
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (0.0108).

9.4 Atom inclusion (i)



At the recommended contour level, 99% of all backbone atoms, 87% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.0108) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8730	0.2740
F	0.8790	0.2750
G	0.8650	0.2740