



Full wwPDB EM Validation Report ⓘ

Mar 27, 2026 – 04:58 PM UTC

PDB ID : 9QNO / pdb_00009qno
EMDB ID : EMD-53248
Title : Ternary complex of the human 20S proteasome in complex with Importin-9 and two homodimers of Akirin-2 - focussed refinement on Importin-9 and Akirin-2
Authors : Brunner, H.L.; Grundmann, L.; David, H.
Deposited on : 2025-03-25
Resolution : 4.20 Å(reported)

This is a Full wwPDB EM Validation 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

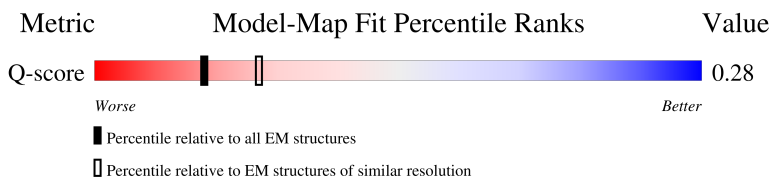
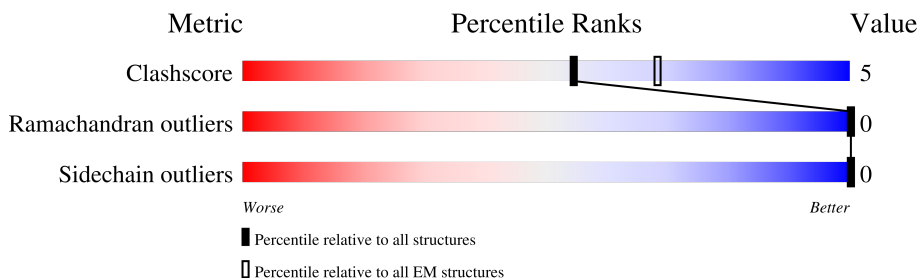
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 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	5410 (3.70 - 4.70)

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	D	203	 22% 78%
1	E	203	 20% 79%
2	A	1041	 59% 37%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6271 atoms, of which 2306 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 Akirin-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	D	45	Total	C	H	N	O	0	0
			321	134	97	45	45		
1	E	42	Total	C	H	N	O	0	0
			300	125	91	42	42		

- Molecule 2 is a protein called Importin-9.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	A	660	Total	C	H	N	O	S	0	0
			5650	2156	2118	678	692	6		

PRO	THR	LEU	GLN	ASP	GLN	THR	ALA
LEU	PRO	ASP	LEU	LEU	THR	GLN	CYS
TYR	ALA	GLU	ILE	GLN	ALA	THR	CYS
ILE	TRP	ARG	GLU	PHE	VAL	PHE	LEU
ASP	SER	VAL	PHE	LEU	GLY	HIS	THR
LEU	GLN	LYS	VAL	LEU	ARG	ASP	THR
GLN	ASP	GLY	CYS	CYS	ARG	ASP	THR
ALA	ASP	GLU	GLU	SER	LEU	VAL	ASN
LEU	SER	GLU	GLU	LEU	VAL	ASN	ASN
THR	ASP	ILE	PRO	GLY	THR	THR	ALA
ASP	MET	SER	PRO	PRO	LEU	MET	THR
PHE	TRP	MET	THR	THR	ILE	GLN	THR
LEU	GLU	ASP	GLY	GLY	SER	GLY	GLN
CYS	ASP	GLU	LYS	LYS	LYS	GLY	GLY
PHE	GLU	ILE	ALA	ALA	GLY	ARG	CYS
ALA	GLU	ARG	LEU	LEU	ARG	GLU	LEU
GLN	GLU	THR	THR	GLU	GLU	LEU	LEU
GLU	GLU	ARG	PHE	VAL	GLY	ALA	ARG
PRO	GLU	SER	VAL	VAL	GLY	ALA	ALA
CYS	GLU	LYS	MET	GLY	TYR	GLY	TYR
GLY	GLU	SER	ALA	ASN	ASN	VAL	VAL
TYR	GLU	SER	ALA	GLU	LEU	SER	SER
ILE	GLU	ALA	LYS	TRP	THR	ILE	ALA
MET	ASP	LYS	TRP	THR	ASN	GLN	ALA
PHE	GLY	ASN	ASN	PHE	PHE	LEU	ALA
GLY	LEU	ILE	ILE	TYR	SER	TRP	GLN
GLU	ASP	PRO	PRO	GLY	TRP	GLN	TRP
GLU	ILE	GLU	GLU	GLN	GLY	HIS	HIS
ASP	ILE	LEU	LEU	ARG	GLY	ASP	ASP
ASN	SER	ILE	ILE	ARG	ASP	GLY	GLY
GLU	ASP	GLU	GLU	GLN	GLY	GLY	GLY
GLU	ILE	GLU	GLU	GLN	GLN	GLN	GLN
ASP	ASP	LEU	LEU	THR	THR	HIS	HIS
ASN	SER	ILE	LEU	ASN	LEU	ASN	ASN
GLU	ASP	PRO	PRO	PRO	THR	GLY	GLY
GLU	ILE	GLU	GLU	GLN	GLY	LEU	LEU
ASP	GLU	GLU	ILE	VAL	VAL	TRP	TRP
GLU	ASP	ILE	ASN	ALA	GLN	VAL	VAL
THR	TYR	ILE	ASN	LYS	GLU	VAL	VAL
GLN	SER	ILE	ASN	VAL	THR	GLN	GLN
THR	LYS	LEU	LEU	VAL	THR	ASN	ASN
ILE	ILE	LEU	SER	SER	LEU	GLY	GLY
GLY	GLU	GLU	LEU	SER	LEU	LEU	LEU
ILE	ASP	ILE	ILE	VAL	MET	TRP	TRP

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	61470	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 ($e^-/\text{\AA}^2$)	44.4	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1900	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.569	Depositor
Minimum map value	-0.000	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.239	Depositor
Map size (Å)	428.99997, 428.99997, 428.99997	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.43, 1.43, 1.43	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	D	0.16	0/223	0.21	0/310
1	E	0.16	0/208	0.25	0/289
2	A	0.13	0/3567	0.34	0/4980
All	All	0.13	0/3998	0.33	0/5579

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	D	224	97	96	1	0
1	E	209	91	90	1	0
2	A	3532	2118	2117	31	0
All	All	3965	2306	2303	32	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 5.

All (32) 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:A:637:GLU:N	2:A:637:GLU:OE1	2.18	0.76

Continued on next page...

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:567:GLY:O	2:A:571:LEU:N	2.25	0.69
2:A:384:GLN:O	2:A:388:ASP:N	2.27	0.68
2:A:660:ASP:OD1	2:A:661:LYS:N	2.29	0.66
2:A:603:SER:O	2:A:646:ARG:NH2	2.35	0.60
2:A:651:LEU:O	2:A:654:ILE:HG22	2.03	0.58
2:A:473:ASP:O	2:A:477:PHE:N	2.30	0.57
1:D:180:ALA:HB1	2:A:661:LYS:HE2	1.87	0.56
1:E:143:THR:O	1:E:147:VAL:N	2.35	0.55
2:A:230:LYS:O	2:A:234:LYS:N	2.33	0.54
2:A:652:VAL:O	2:A:656:GLN:OE1	2.28	0.52
2:A:293:ILE:O	2:A:297:THR:N	2.40	0.51
2:A:636:ILE:HG23	2:A:636:ILE:O	2.13	0.48
2:A:651:LEU:CD1	2:A:670:ALA:HB1	2.43	0.48
2:A:656:GLN:OE1	2:A:656:GLN:N	2.47	0.48
2:A:654:ILE:HD11	2:A:662:ILE:HG12	1.96	0.47
2:A:237:ILE:O	2:A:241:VAL:N	2.41	0.47
2:A:671:ILE:O	2:A:675:THR:HG23	2.15	0.47
2:A:619:ASP:O	2:A:620:PRO:C	2.58	0.46
2:A:618:ASN:OD1	2:A:666:LEU:HB2	2.17	0.44
2:A:662:ILE:HG13	2:A:663:PRO:HD2	2.00	0.44
2:A:618:ASN:O	2:A:618:ASN:ND2	2.51	0.44
2:A:649:PRO:HA	2:A:652:VAL:HG22	2.00	0.43
2:A:346:ASN:O	2:A:350:LYS:N	2.51	0.43
2:A:634:SER:HB3	2:A:643:MET:HE2	2.01	0.43
2:A:680:ASN:O	2:A:680:ASN:OD1	2.37	0.43
2:A:669:THR:O	2:A:673:ILE:HG12	2.19	0.42
2:A:631:LYS:O	2:A:634:SER:OG	2.30	0.42
2:A:625:LEU:O	2:A:629:ILE:HG12	2.20	0.42
2:A:651:LEU:HD13	2:A:670:ALA:HB1	2.02	0.41
2:A:661:LYS:HD2	2:A:661:LYS:C	2.46	0.41
2:A:640:GLN:O	2:A:644:GLN:HG2	2.22	0.40

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	D	43/203 (21%)	43 (100%)	0	0	100	100
1	E	40/203 (20%)	40 (100%)	0	0	100	100
2	A	656/1041 (63%)	627 (96%)	29 (4%)	0	100	100
All	All	739/1447 (51%)	710 (96%)	29 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	
2	A	95/894 (11%)	95 (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. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	680	ASN
2	A	687	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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-53248. These allow visual inspection of the internal detail of the map and identification of artifacts.

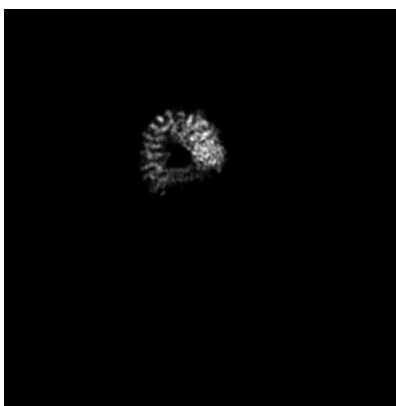
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X

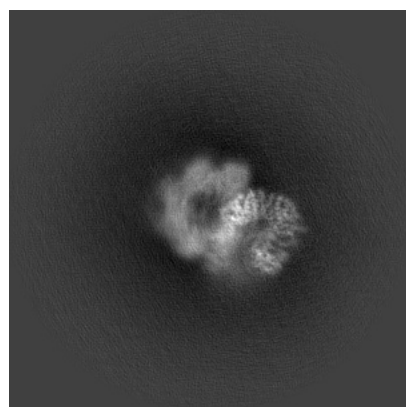


Y

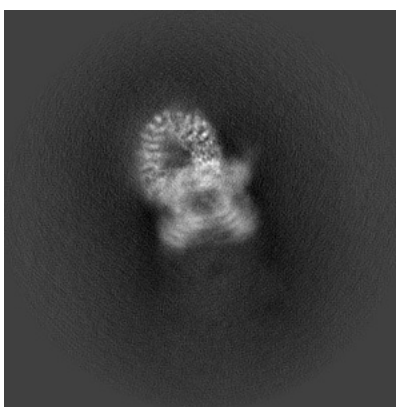


Z

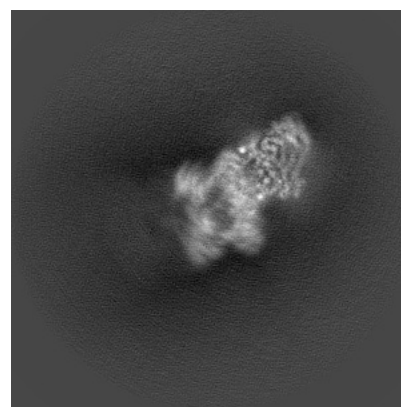
6.1.2 Raw map



X



Y

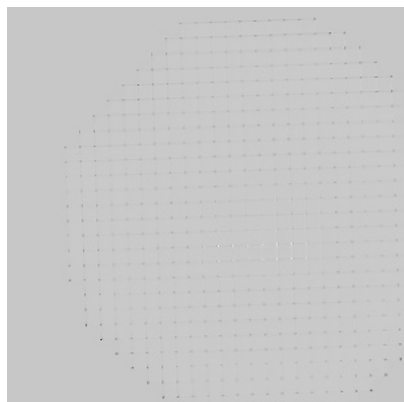


Z

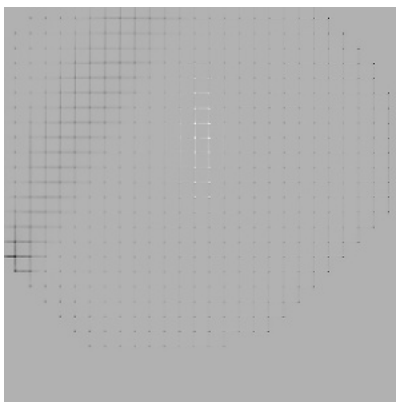
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

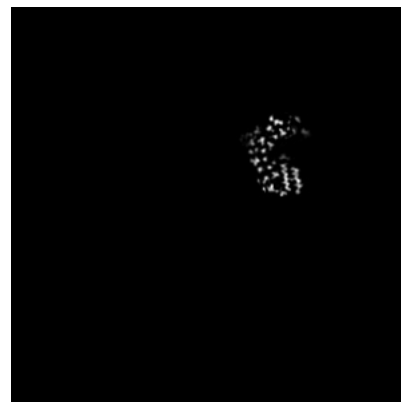
6.2.1 Primary map



X Index: 150

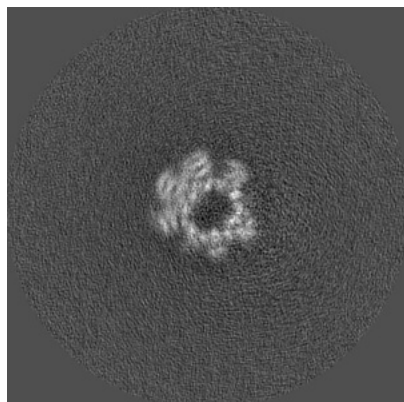


Y Index: 150

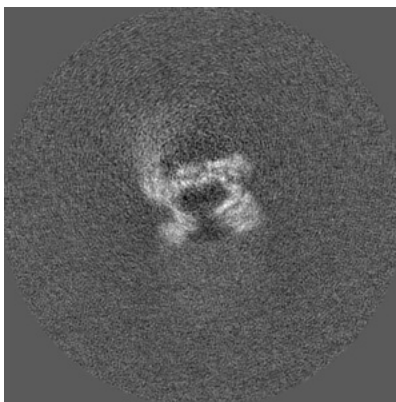


Z Index: 150

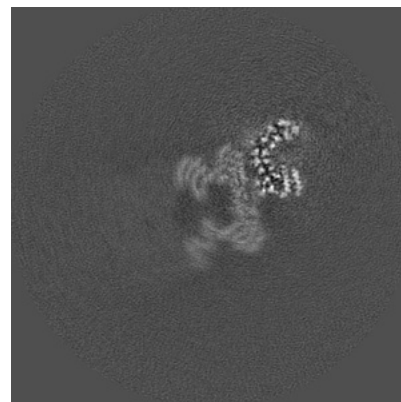
6.2.2 Raw map



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: 195

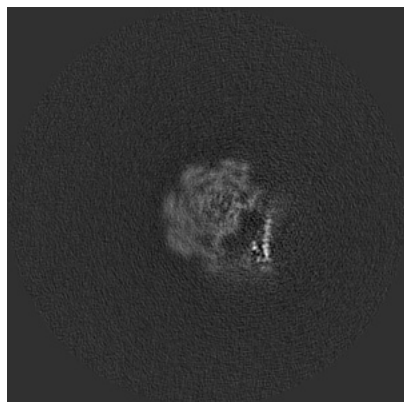


Y Index: 196

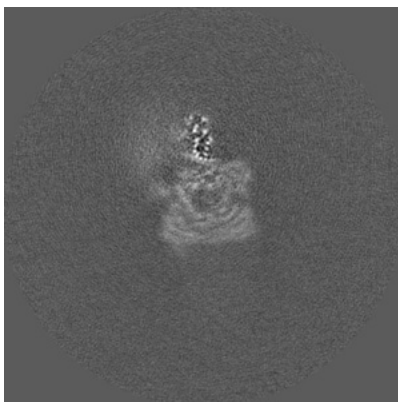


Z Index: 144

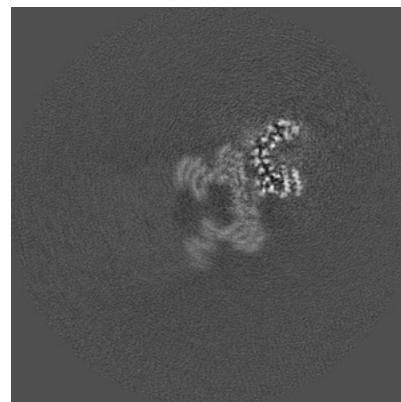
6.3.2 Raw map



X Index: 173



Y Index: 167



Z Index: 150

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

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

6.4.1 Primary map



X

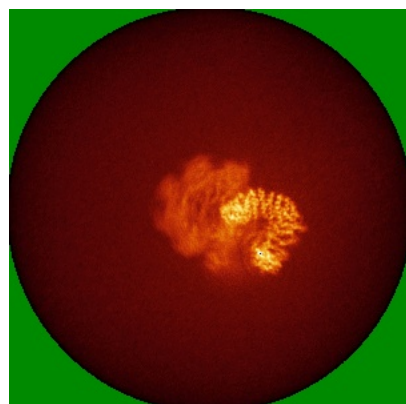


Y

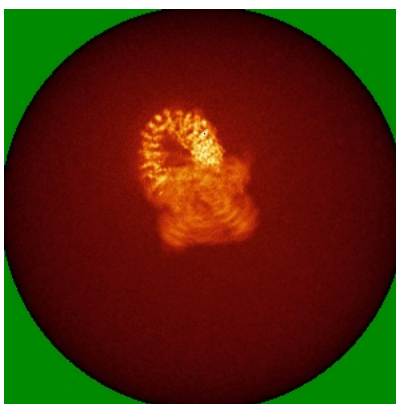


Z

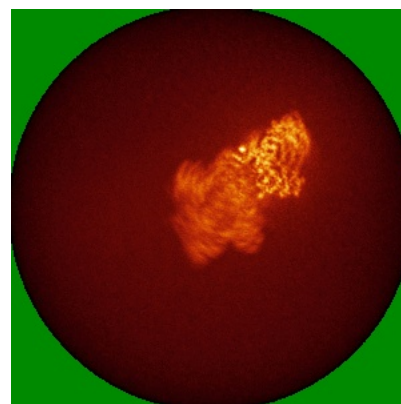
6.4.2 Raw map



X



Y

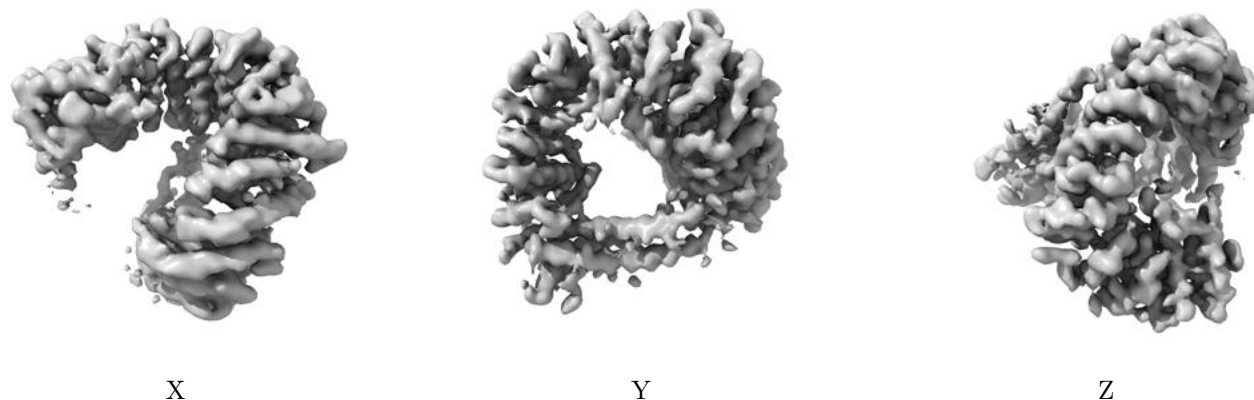


Z

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 0.239. 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



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.

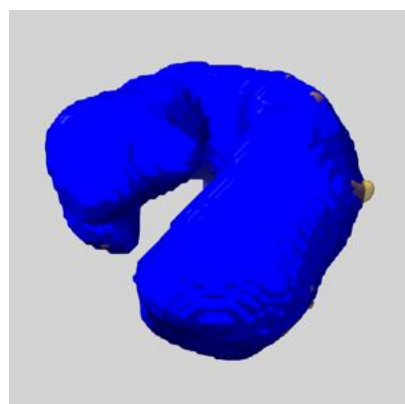
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

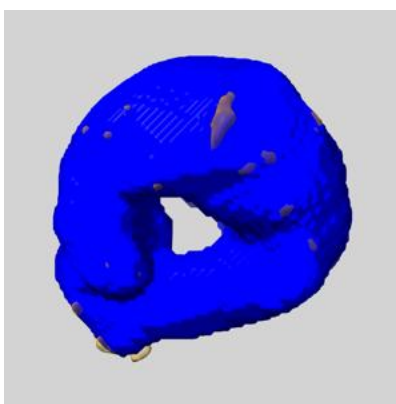
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

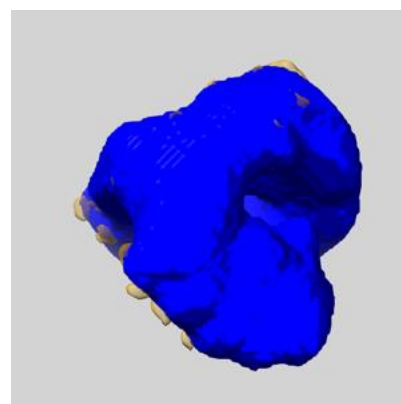
6.6.1 emd_53248_msk_1.map [i](#)



X



Y

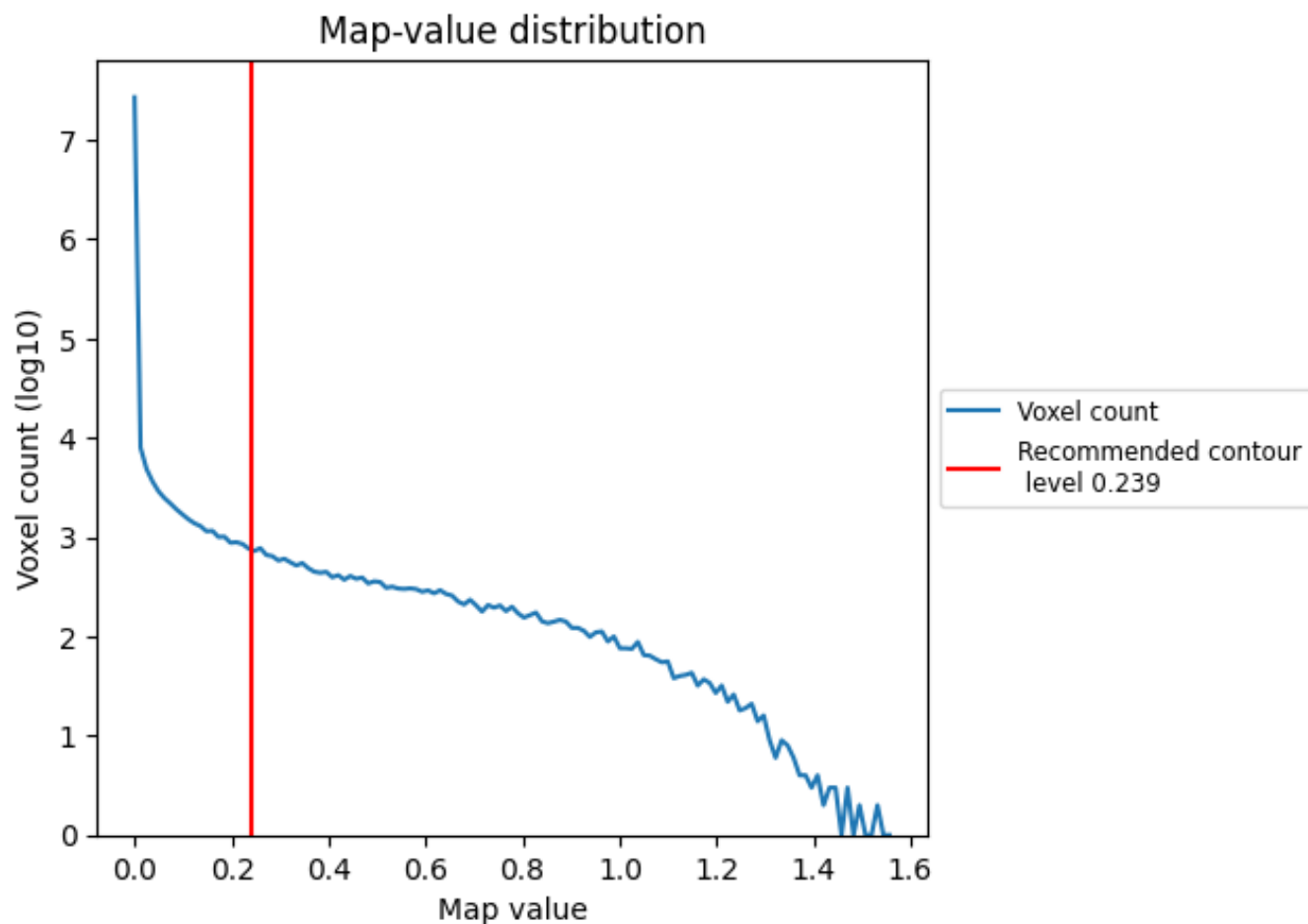


Z

7 Map analysis [i](#)

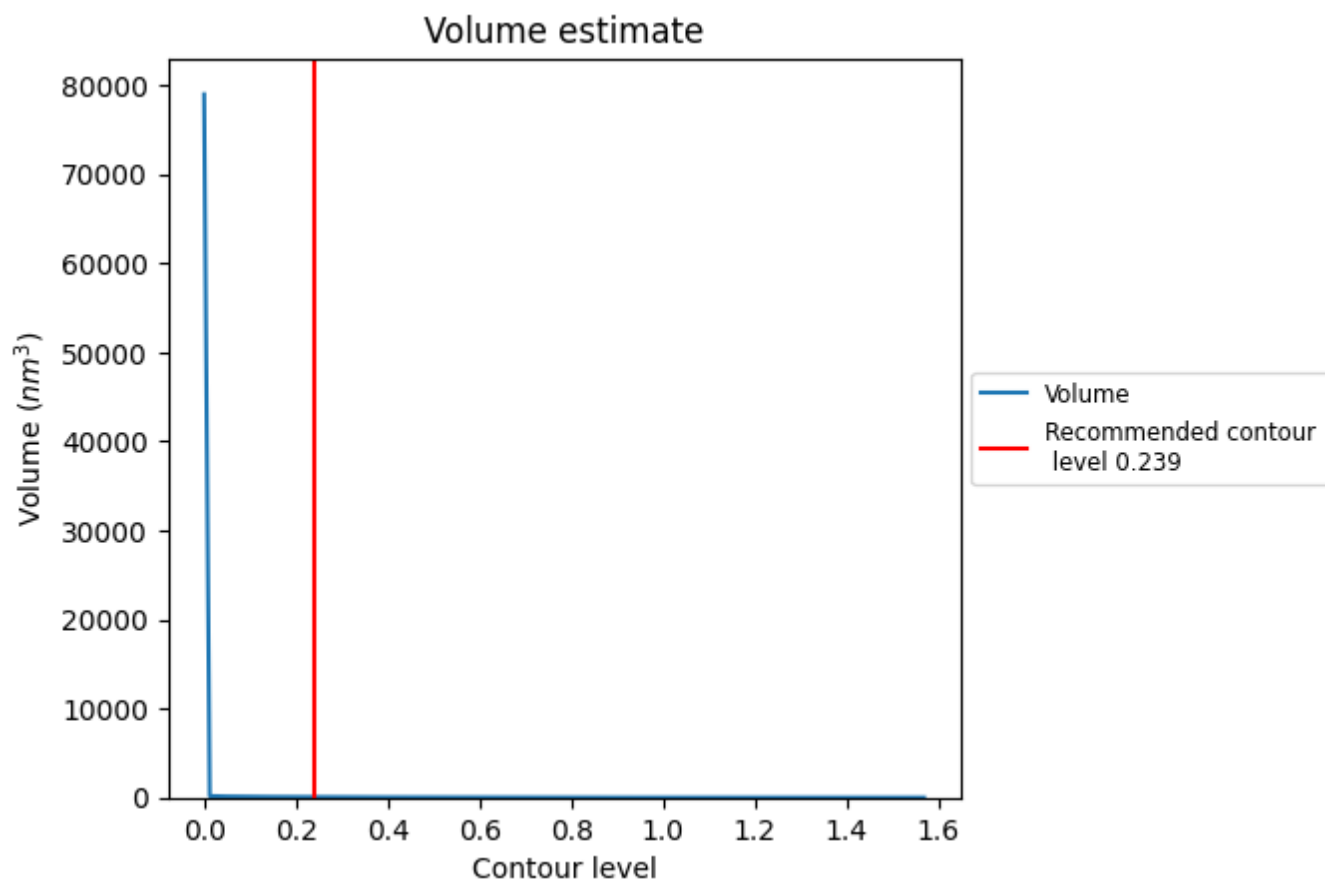
This section contains the results of statistical analysis of the map.

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.

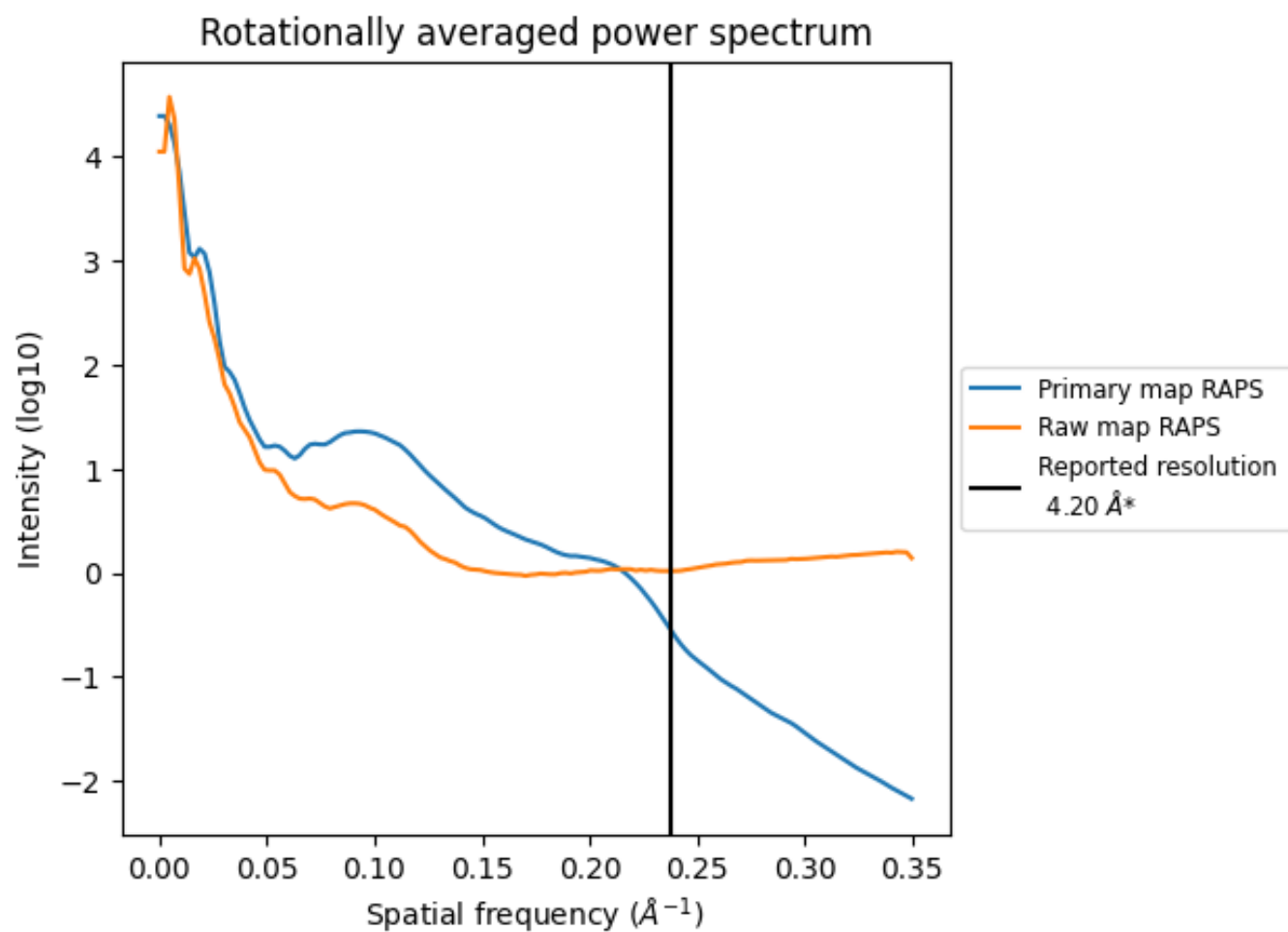
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 59 nm^3 ; this corresponds to an approximate mass of 54 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 ⓘ

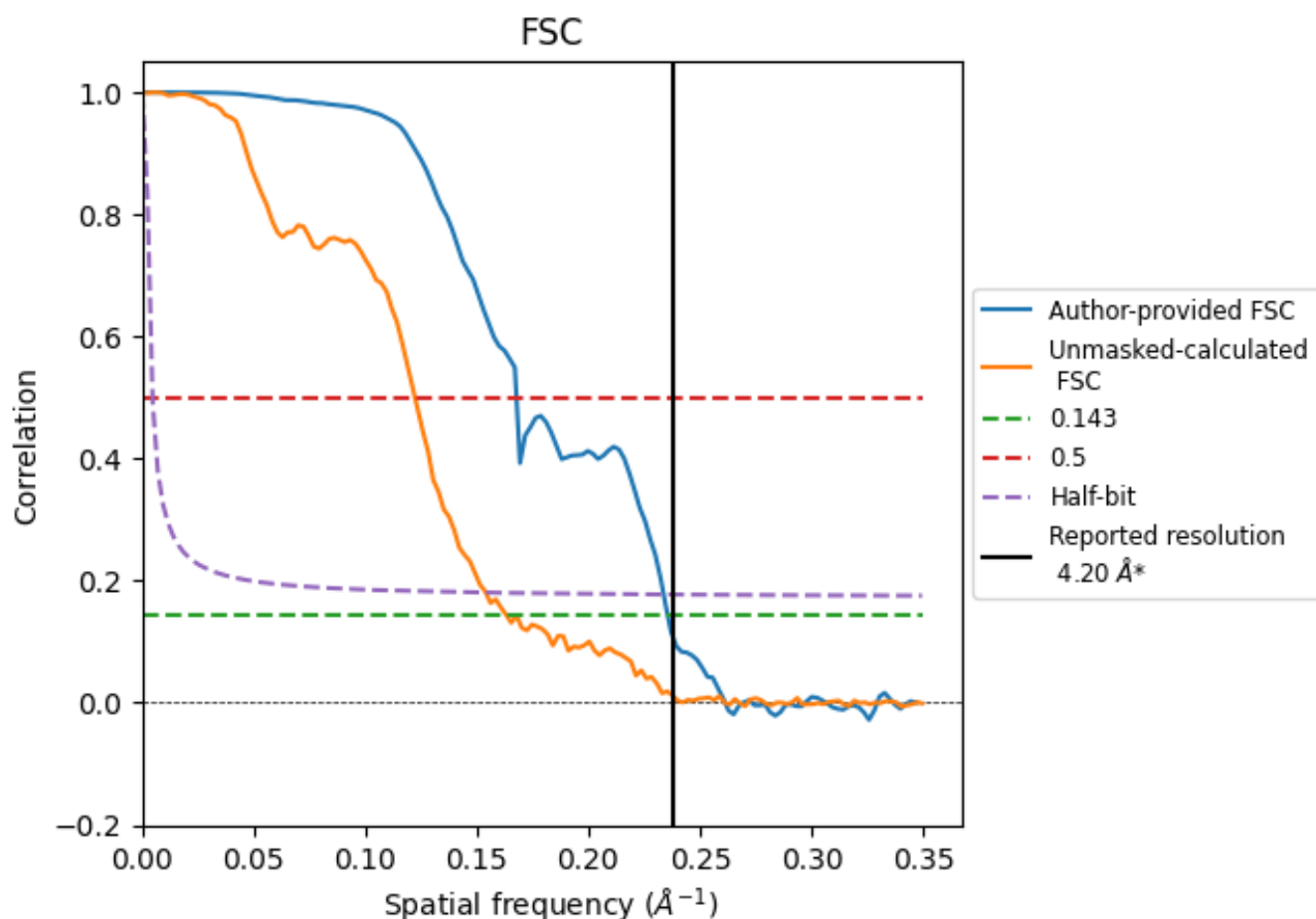


*Reported resolution corresponds to spatial frequency of 0.238 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.238 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

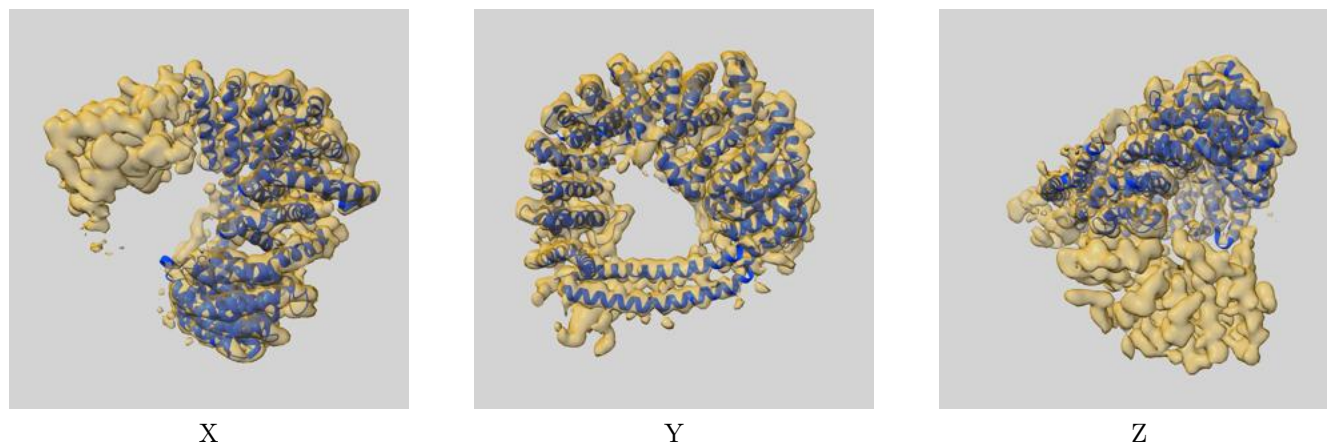
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.20	-	-
Author-provided FSC curve	4.24	5.96	4.28
Unmasked-calculated*	6.12	8.17	6.49

*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 6.12 differs from the reported value 4.2 by more than 10 %

9 Map-model fit [i](#)

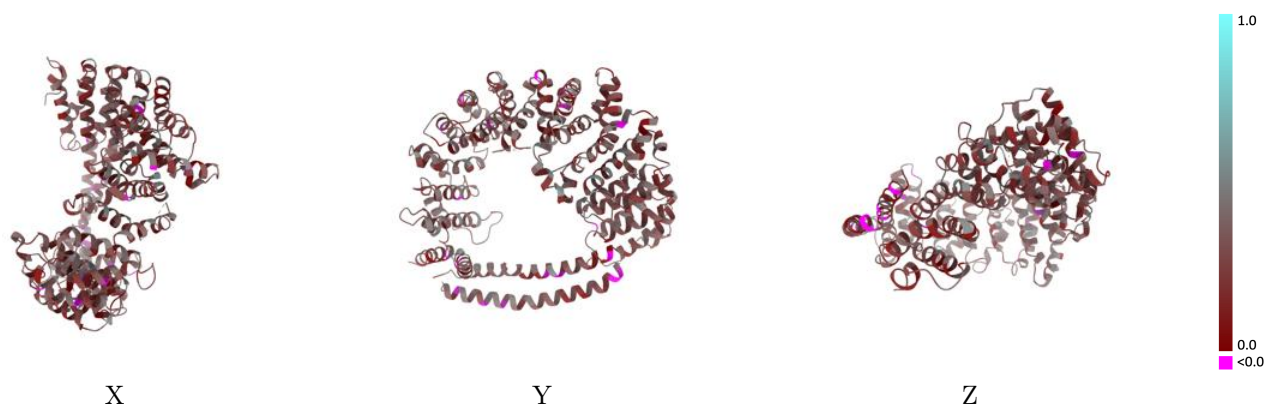
This section contains information regarding the fit between EMDB map EMD-53248 and PDB model 9QNO. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



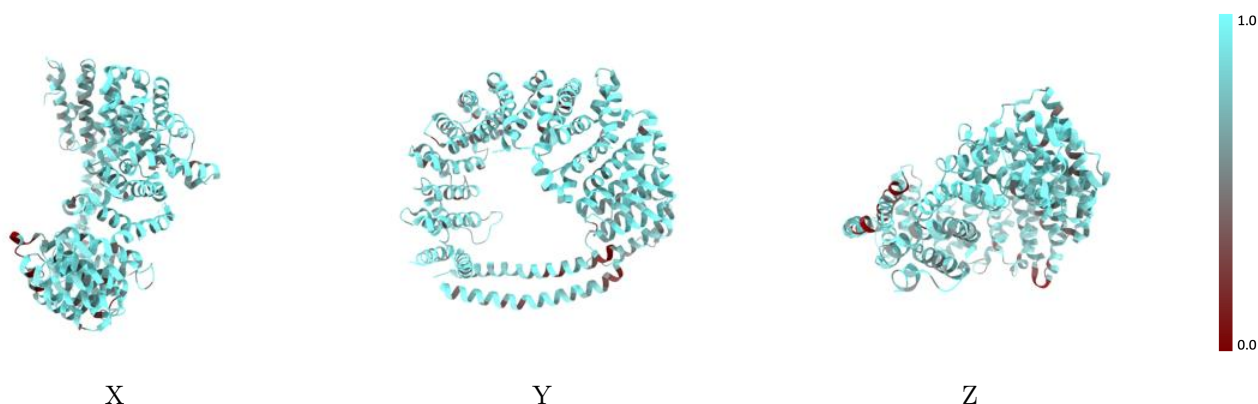
The images above show the 3D surface view of the map at the recommended contour level 0.239 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



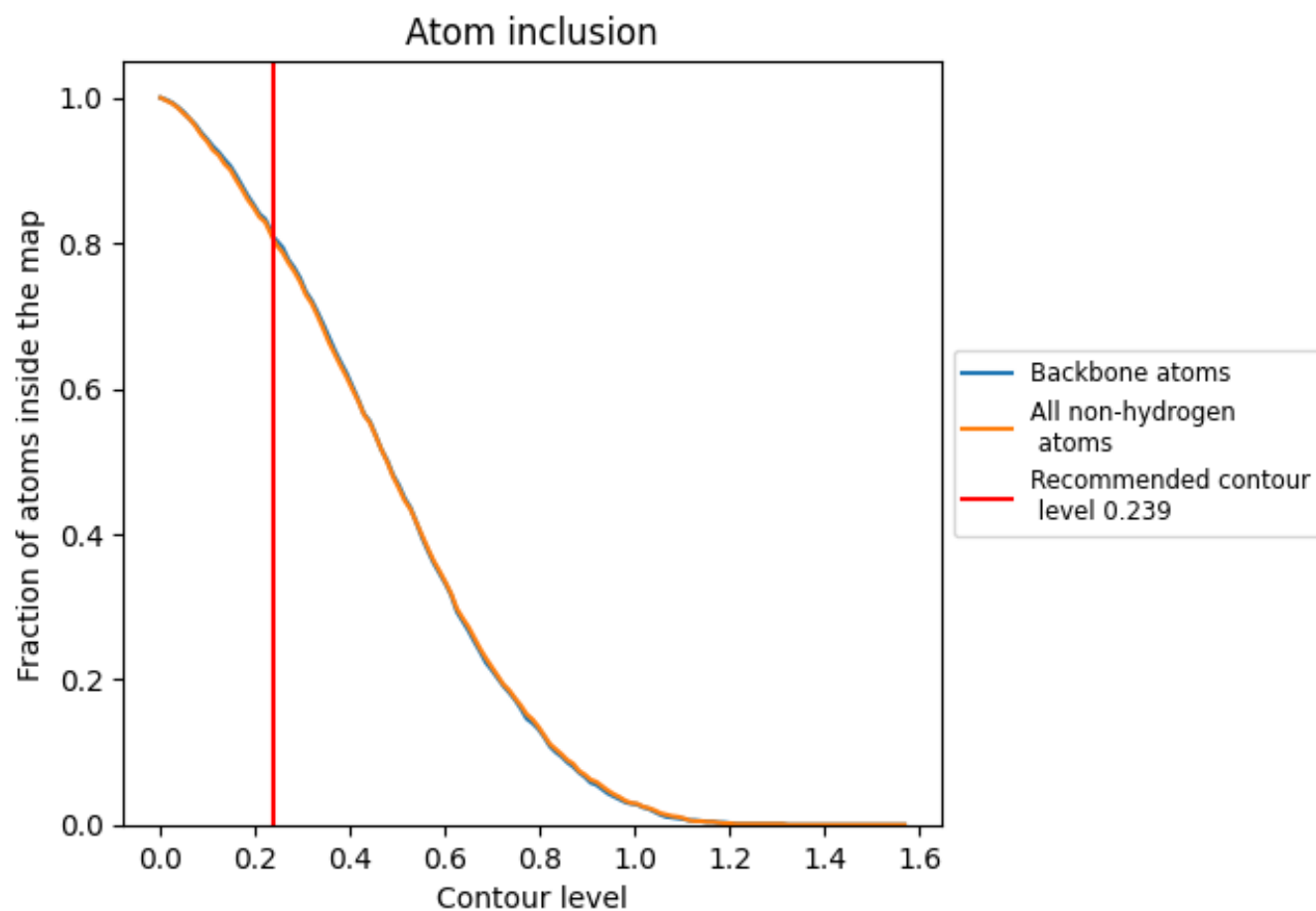
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.239).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 80% 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 (0.239) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8030	0.2800
A	0.8070	0.2840
D	0.7770	0.2540
E	0.7270	0.2440

