



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 01:25 AM UTC

PDB ID : 8DTF / pdb_00008dtf
EMDB ID : EMD-27696
Title : Cryo-EM structure of the full length Arabidopsis SPY with complete TPRs
Authors : Kumar, S.; Zhou, Y.; Dillard, L.; Borgnia, M.J.; Bartesaghi, A.; Zhou, P.
Deposited on : 2022-07-25
Resolution : 3.70 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

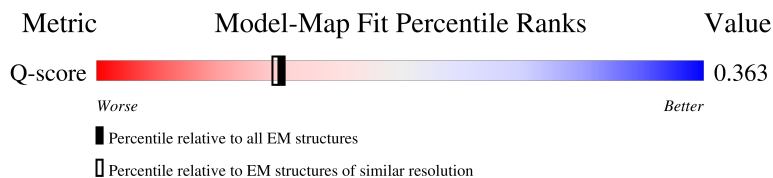
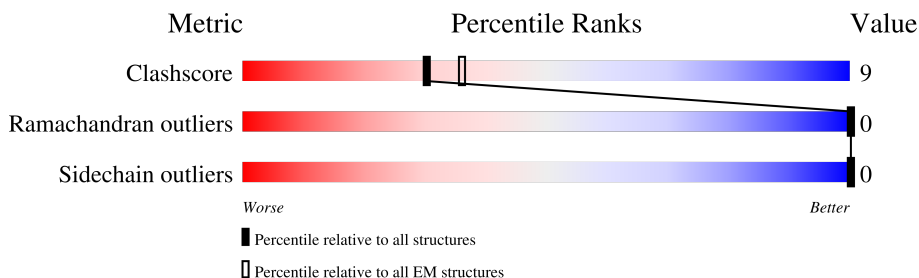
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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	11569 (3.20 - 4.20)

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	946	 68% 16% 15%
1	B	946	 68% 17% 15%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 12414 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 Probable UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase SPINDLY.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	803	Total	C	N	O	S	0	0
			6203	3951	1035	1169	48		
1	B	803	Total	C	N	O	S	0	0
			6211	3956	1036	1171	48		

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	915	GLY	-	expression tag	UNP Q96301
A	916	GLY	-	expression tag	UNP Q96301
A	917	SER	-	expression tag	UNP Q96301
A	918	GLU	-	expression tag	UNP Q96301
A	919	ASN	-	expression tag	UNP Q96301
A	920	LEU	-	expression tag	UNP Q96301
A	921	TYR	-	expression tag	UNP Q96301
A	922	PHE	-	expression tag	UNP Q96301
A	923	GLN	-	expression tag	UNP Q96301
A	924	GLY	-	expression tag	UNP Q96301
A	925	GLY	-	expression tag	UNP Q96301
A	926	SER	-	expression tag	UNP Q96301
A	927	HIS	-	expression tag	UNP Q96301
A	928	HIS	-	expression tag	UNP Q96301
A	929	HIS	-	expression tag	UNP Q96301
A	930	HIS	-	expression tag	UNP Q96301
A	931	HIS	-	expression tag	UNP Q96301
A	932	HIS	-	expression tag	UNP Q96301
A	933	HIS	-	expression tag	UNP Q96301
A	934	HIS	-	expression tag	UNP Q96301
A	935	HIS	-	expression tag	UNP Q96301
A	936	HIS	-	expression tag	UNP Q96301
A	937	GLY	-	expression tag	UNP Q96301
A	938	GLY	-	expression tag	UNP Q96301
A	939	TRP	-	expression tag	UNP Q96301

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Chain	Residue	Modelled	Actual	Comment	Reference
A	940	SER	-	expression tag	UNP Q96301
A	941	HIS	-	expression tag	UNP Q96301
A	942	PRO	-	expression tag	UNP Q96301
A	943	GLN	-	expression tag	UNP Q96301
A	944	PHE	-	expression tag	UNP Q96301
A	945	GLU	-	expression tag	UNP Q96301
A	946	LYS	-	expression tag	UNP Q96301
B	915	GLY	-	expression tag	UNP Q96301
B	916	GLY	-	expression tag	UNP Q96301
B	917	SER	-	expression tag	UNP Q96301
B	918	GLU	-	expression tag	UNP Q96301
B	919	ASN	-	expression tag	UNP Q96301
B	920	LEU	-	expression tag	UNP Q96301
B	921	TYR	-	expression tag	UNP Q96301
B	922	PHE	-	expression tag	UNP Q96301
B	923	GLN	-	expression tag	UNP Q96301
B	924	GLY	-	expression tag	UNP Q96301
B	925	GLY	-	expression tag	UNP Q96301
B	926	SER	-	expression tag	UNP Q96301
B	927	HIS	-	expression tag	UNP Q96301
B	928	HIS	-	expression tag	UNP Q96301
B	929	HIS	-	expression tag	UNP Q96301
B	930	HIS	-	expression tag	UNP Q96301
B	931	HIS	-	expression tag	UNP Q96301
B	932	HIS	-	expression tag	UNP Q96301
B	933	HIS	-	expression tag	UNP Q96301
B	934	HIS	-	expression tag	UNP Q96301
B	935	HIS	-	expression tag	UNP Q96301
B	936	HIS	-	expression tag	UNP Q96301
B	937	GLY	-	expression tag	UNP Q96301
B	938	GLY	-	expression tag	UNP Q96301
B	939	TRP	-	expression tag	UNP Q96301
B	940	SER	-	expression tag	UNP Q96301
B	941	HIS	-	expression tag	UNP Q96301
B	942	PRO	-	expression tag	UNP Q96301
B	943	GLN	-	expression tag	UNP Q96301
B	944	PHE	-	expression tag	UNP Q96301
B	945	GLU	-	expression tag	UNP Q96301
B	946	LYS	-	expression tag	UNP Q96301

HIS	Q90	E319	T506	L650	E792
HIS	L95	E330	H507	F660	Q795
GLY	R126	N334	H508	N661	V798
TRP	E129	L338	Y510	N662	A806
SER	Y134	R342	Y513	K665	A807
HIS	L151	D380	R530	S684	L807
PRO	V154	A381	K538	L686	K809
LEU	S161	R408	I548	K689	S812
LYS	L164	D409	D549	C690	S813
ALA	N412	N415	E550	K691	L814
ASN	M167	Y420	K551	P692	N818
GLY	E170	L424	K552	D696	S821
SER	Q173	M436	M556	S697	P822
PRO	K174	N445	E559	L706	V823
VAL	A186	L452	K561	L711	S828
LEU	Y189	R457	I564	R715	F829
PRO	L192	D468	L565	V716	A830
GLN	Y202	W469	L568	L723	V831
SER	D203	G460	G570	F724	R838
LYS	N204	W461	T579	M729	N839
ARG	A205	R462	M580	Y732	K843
ASP	L206	F463	R583	M735	K846
LEU	E210	T464	A585	S738	GLY
THR	L214	R465	P586	T748	GLU
GLY	E215	L476	Q588	C751	VAL
GLY	R216	P479	W591	Y755	HIS
SER	L229	E480	Y594	M756	ASP
ASN	M238	R481	I607	G757	ASP
LEU	N258	I483	T608	V758	PRO
PHE	L273	I484	D609	H768	LEU
GLY	G280	S489	L628	V772	GLN
GLY	Y284	D491	F632	L776	ASP
SER	Y289	S496	L633	G783	LEU
HIS	Y290	W497	C634	V786	HIS
HIS	N291	S498	Y635	A787	HIS
HIS	W292	I501	A641	K788	HIS
		E502	T647		PRO

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	91837	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	55	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	54900	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	61.923	Depositor
Minimum map value	-32.947	Depositor
Average map value	0.001	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	4	Depositor
Map size (Å)	337.91998, 337.91998, 337.91998	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.87999994, 0.87999994, 0.87999994	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	A	0.15	0/6345	0.42	0/8638
1	B	0.15	0/6353	0.42	0/8647
All	All	0.15	0/12698	0.42	0/17285

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

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	6203	0	6018	109	0
1	B	6211	0	6033	114	0
All	All	12414	0	12051	219	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 9.

The worst 5 of 219 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:B:87:LEU:HD23	1:B:95:LEU:HB2	1.83	0.59
1:A:87:LEU:HD23	1:A:95:LEU:HB2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:170:GLU:HA	1:A:173:GLN:OE1	2.04	0.58
1:B:170:GLU:HA	1:B:173:GLN:OE1	2.04	0.58
1:A:506:THR:O	1:A:538:LYS:NZ	2.37	0.57

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	801/946 (85%)	765 (96%)	36 (4%)	0	100	100
1	B	801/946 (85%)	767 (96%)	34 (4%)	0	100	100
All	All	1602/1892 (85%)	1532 (96%)	70 (4%)	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	652/800 (82%)	652 (100%)	0	100	100
1	B	654/800 (82%)	654 (100%)	0	100	100
All	All	1306/1600 (82%)	1306 (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 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	191	ASN
1	B	367	ASN
1	B	725	ASN
1	B	376	GLN
1	A	376	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.

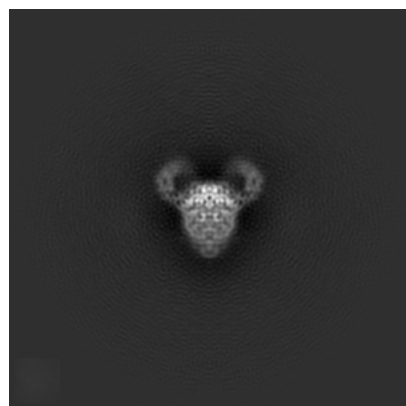
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27696. These allow visual inspection of the internal detail of the map and identification of artifacts.

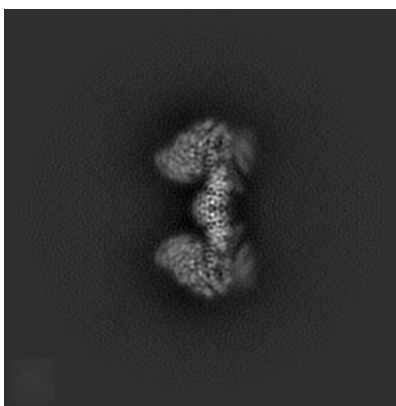
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

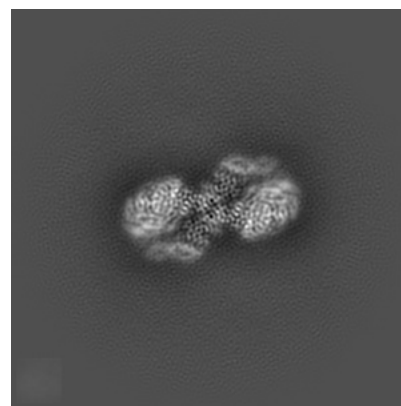
6.1.1 Primary map



X

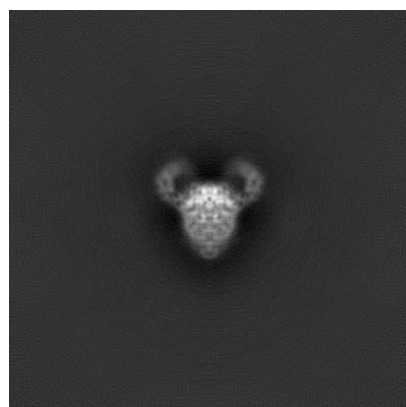


Y

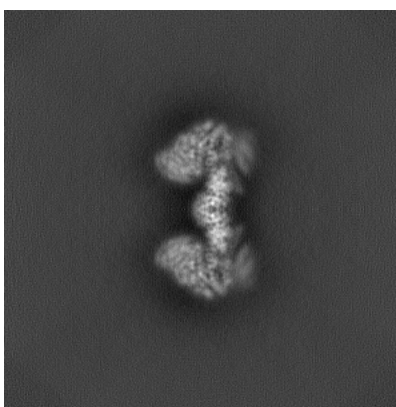


Z

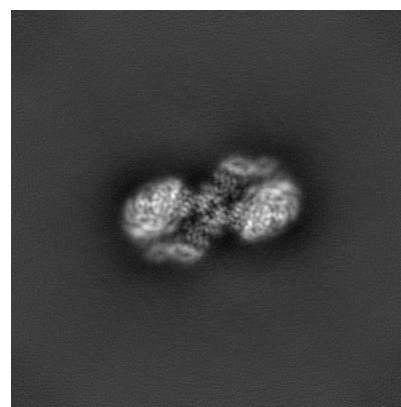
6.1.2 Raw map



X



Y

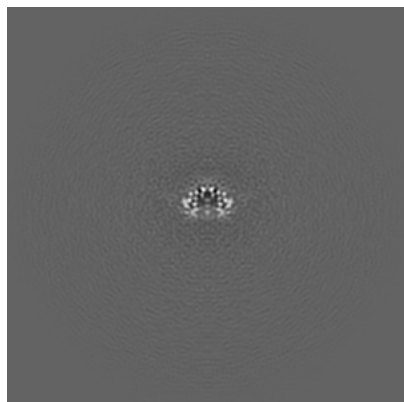


Z

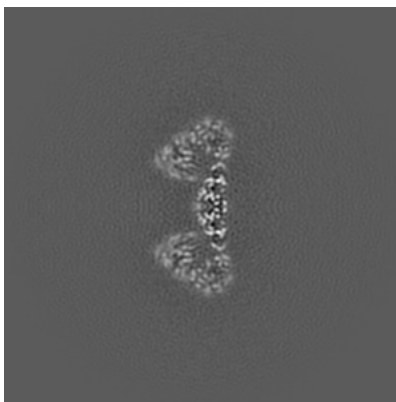
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

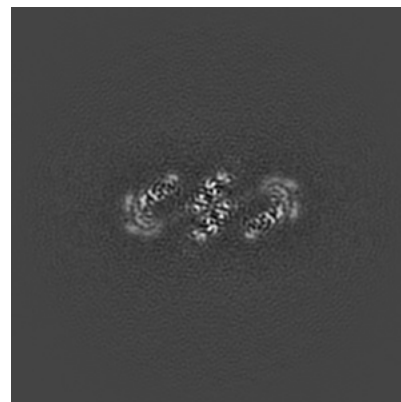
6.2.1 Primary map



X Index: 192

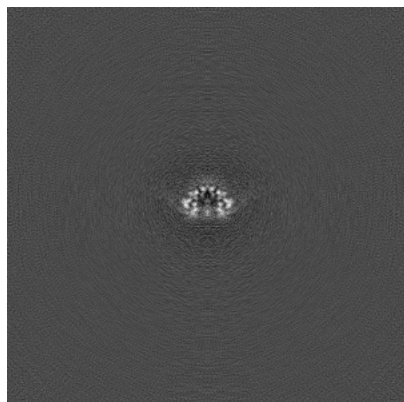


Y Index: 192

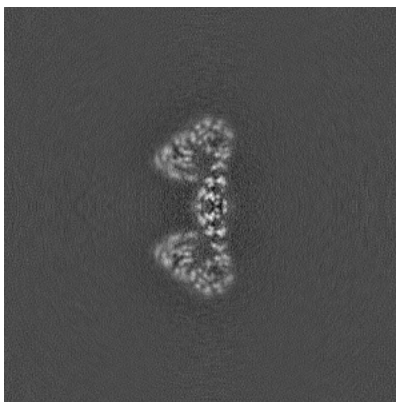


Z Index: 192

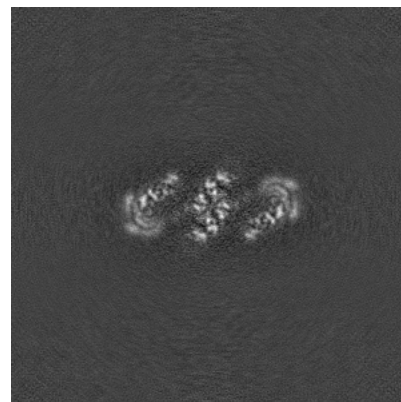
6.2.2 Raw map



X Index: 192



Y Index: 192

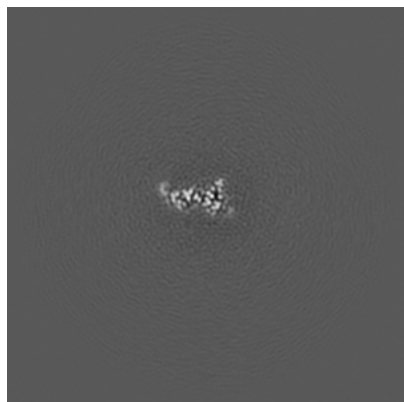


Z Index: 192

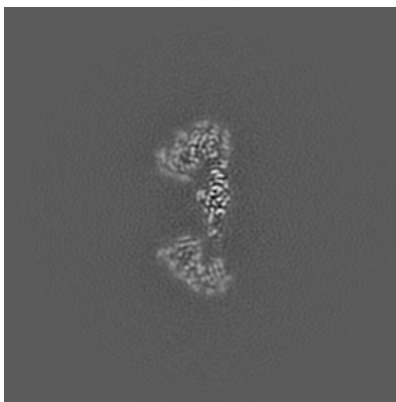
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

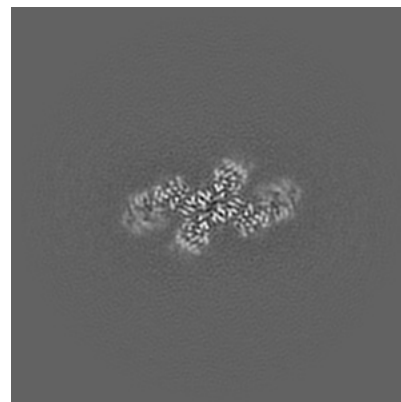
6.3.1 Primary map



X Index: 182

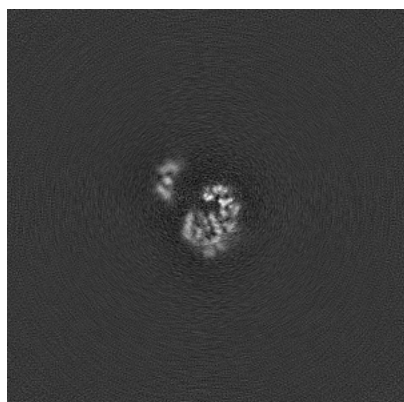


Y Index: 185

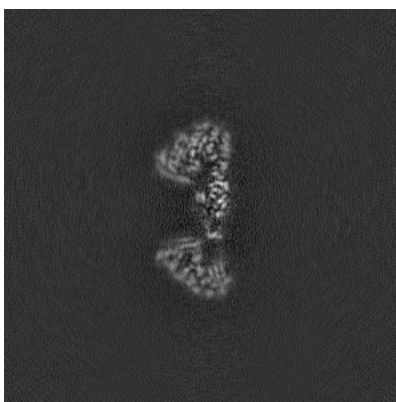


Z Index: 201

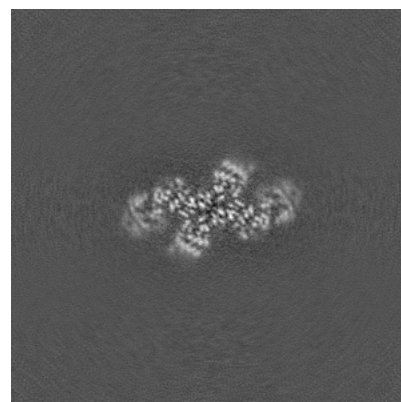
6.3.2 Raw map



X Index: 154



Y Index: 186

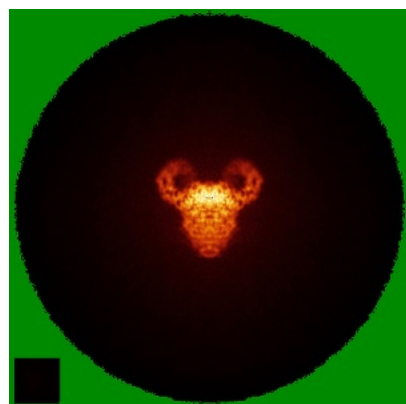


Z Index: 202

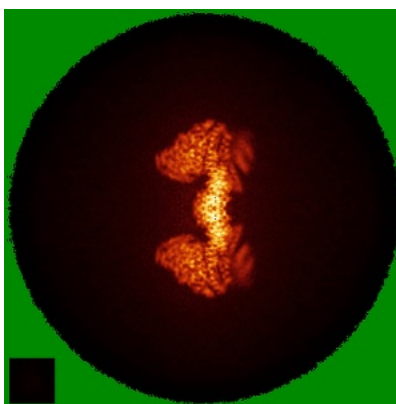
The images above show the largest variance slices of the map in three orthogonal directions.

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

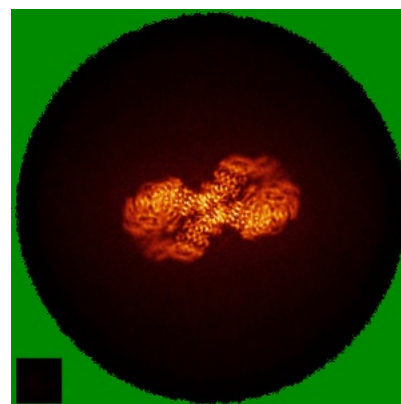
6.4.1 Primary map



X

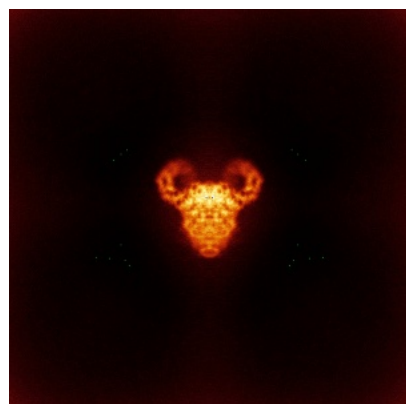


Y

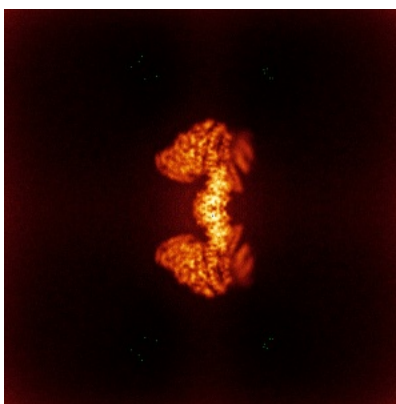


Z

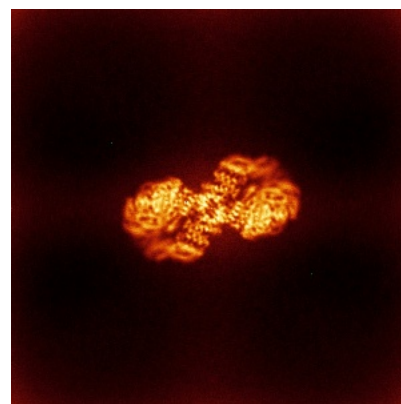
6.4.2 Raw map



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 4.0. 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.

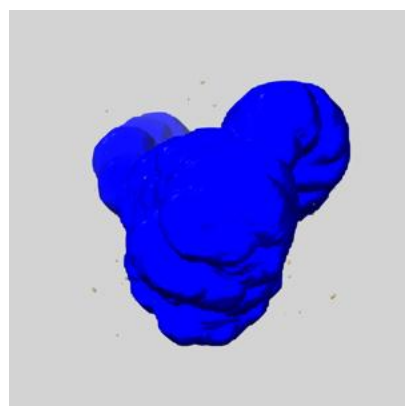
6.6 Mask visualisation [i](#)

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

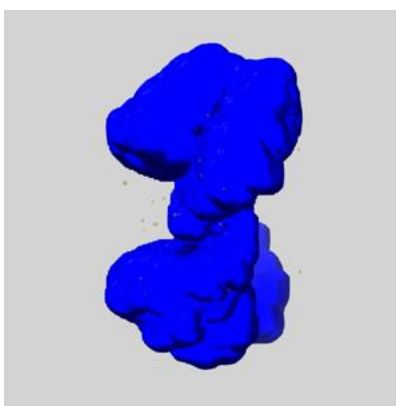
A mask typically either:

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

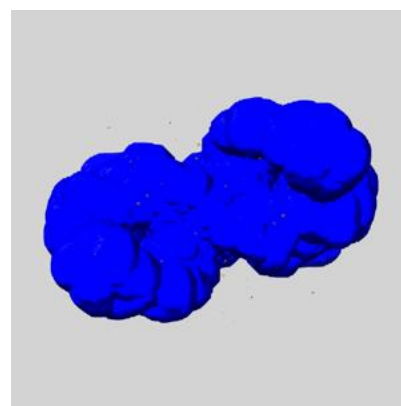
6.6.1 emd_27696_msk_1.map [i](#)



X



Y

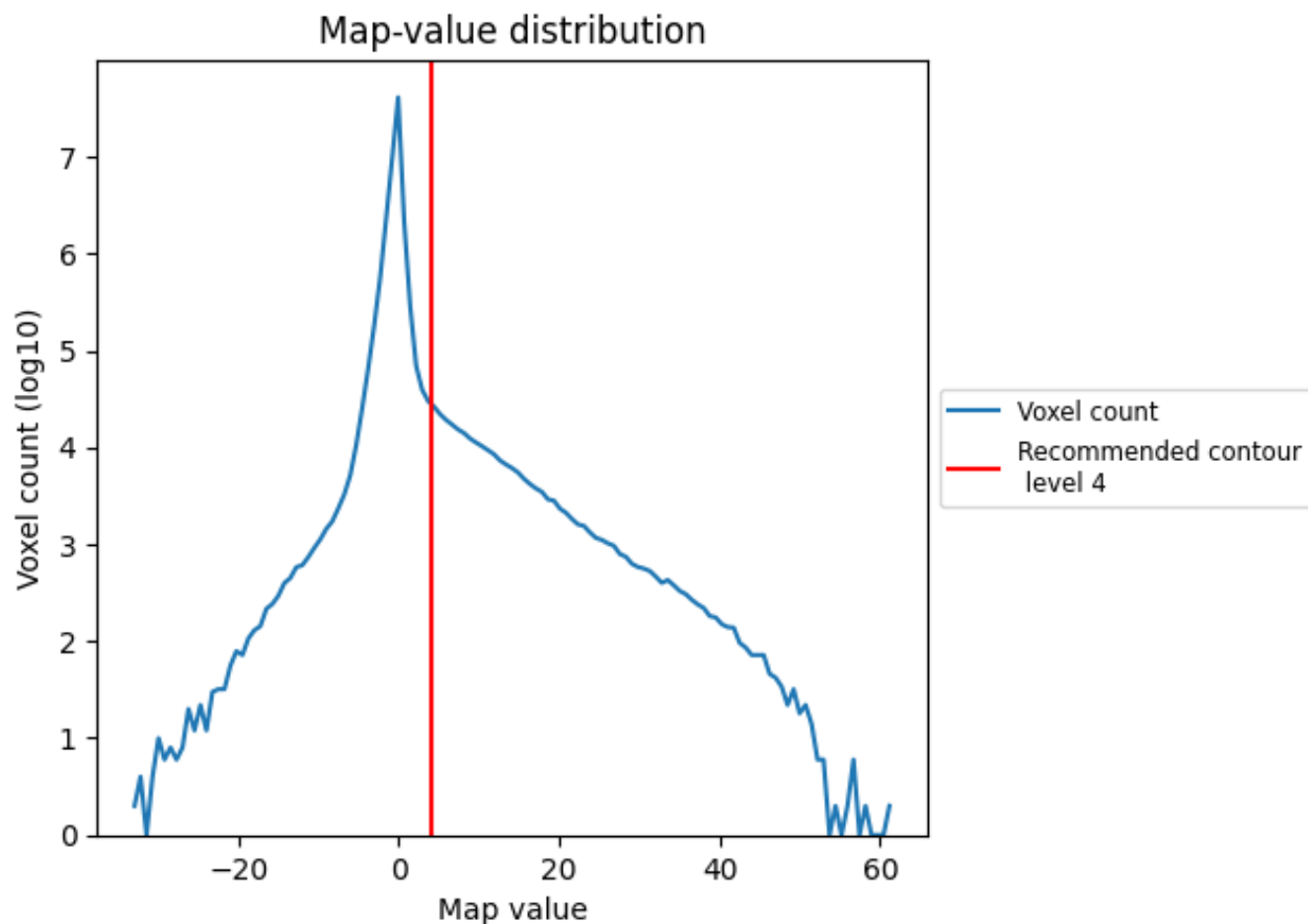


Z

7 Map analysis [i](#)

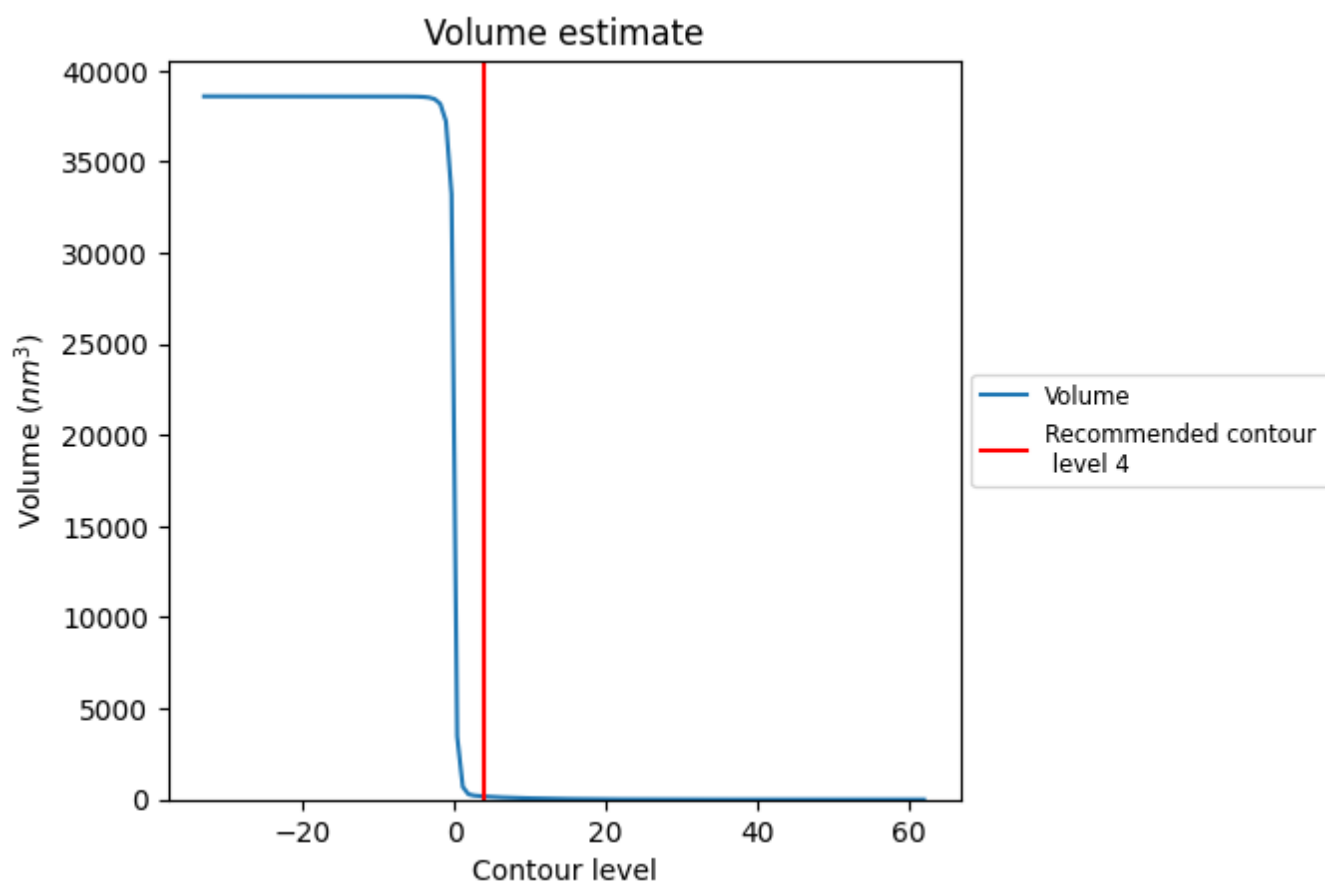
This section contains the results of statistical analysis of the map.

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.

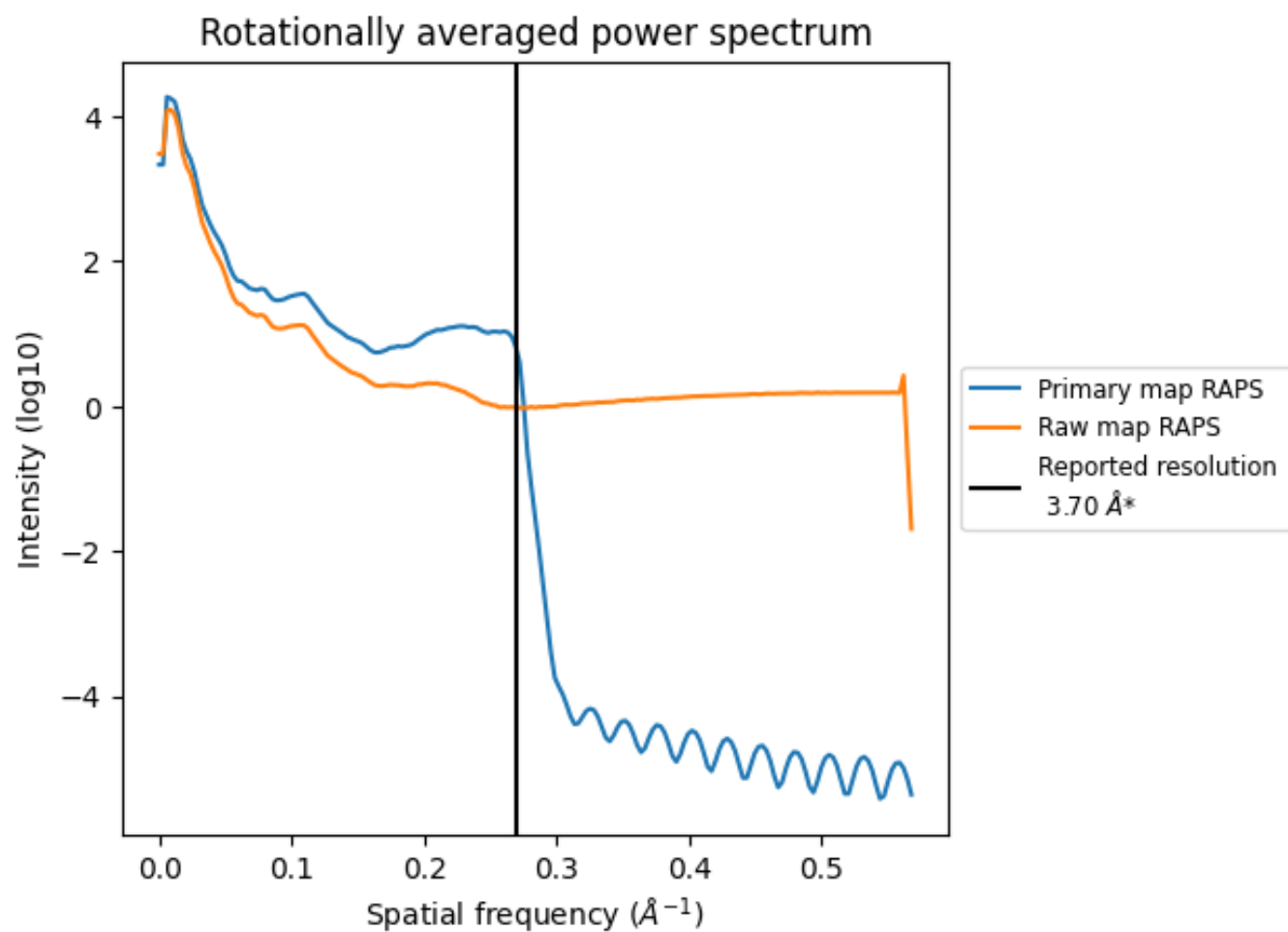
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 172 nm³; this corresponds to an approximate mass of 155 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](#)

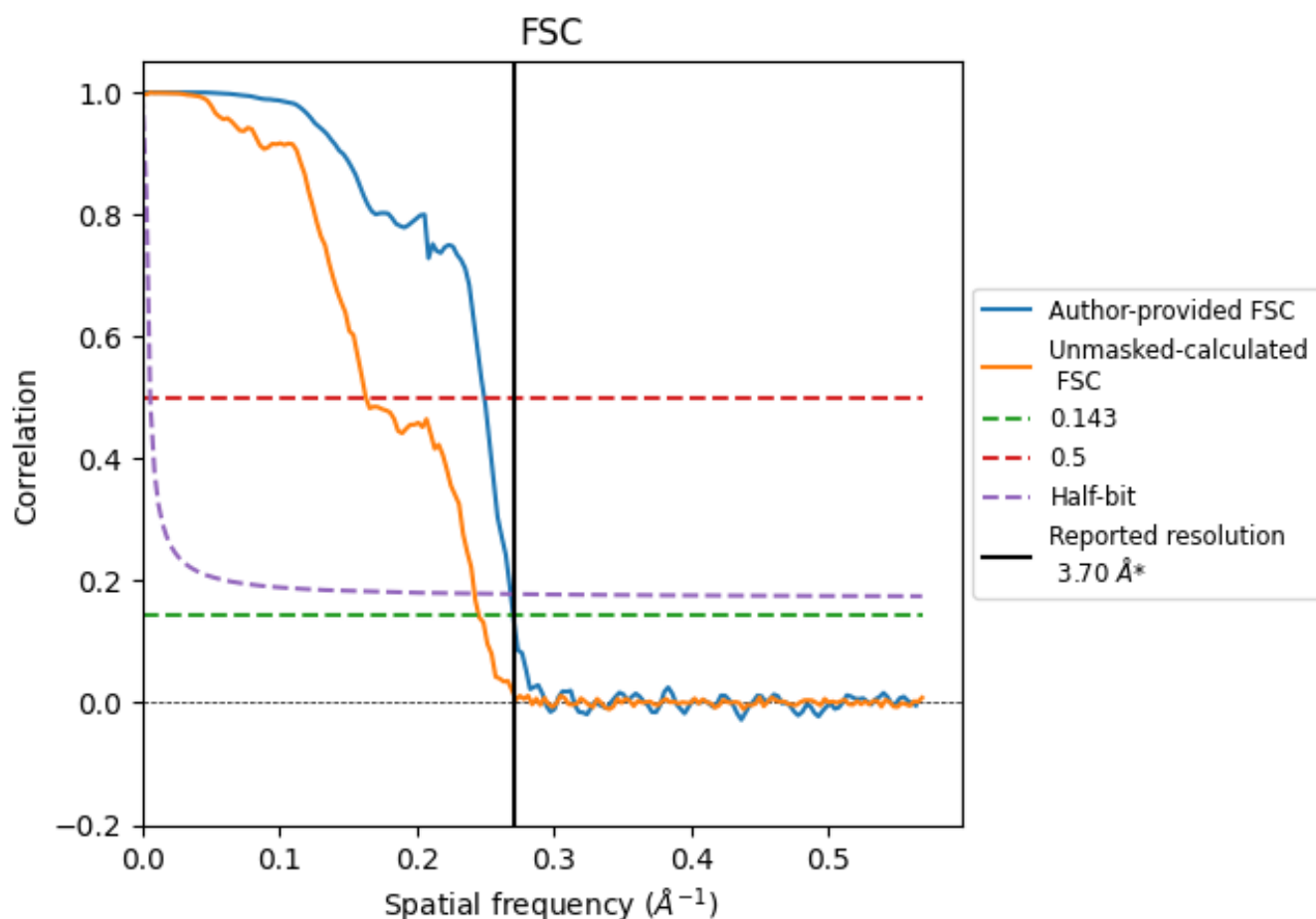


*Reported resolution corresponds to spatial frequency of 0.270 $\text{\AA}^{-1}$

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 0.270 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

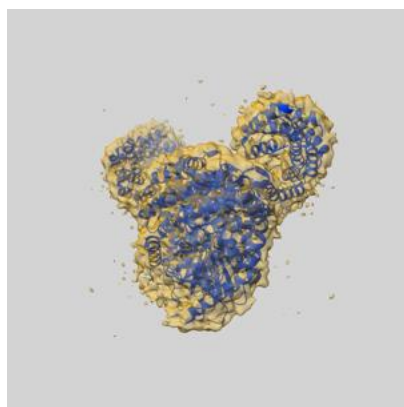
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.70	4.01	3.72
Unmasked-calculated*	4.08	6.14	4.13

*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 4.08 differs from the reported value 3.7 by more than 10 %

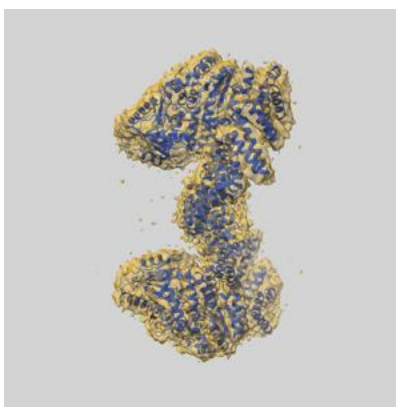
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-27696 and PDB model 8DTF. Per-residue inclusion information can be found in section [3](#) on page [5](#).

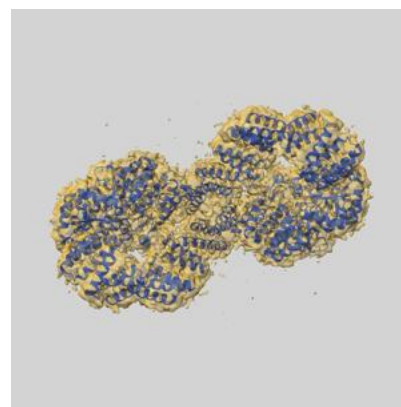
9.1 Map-model overlay [i](#)



X



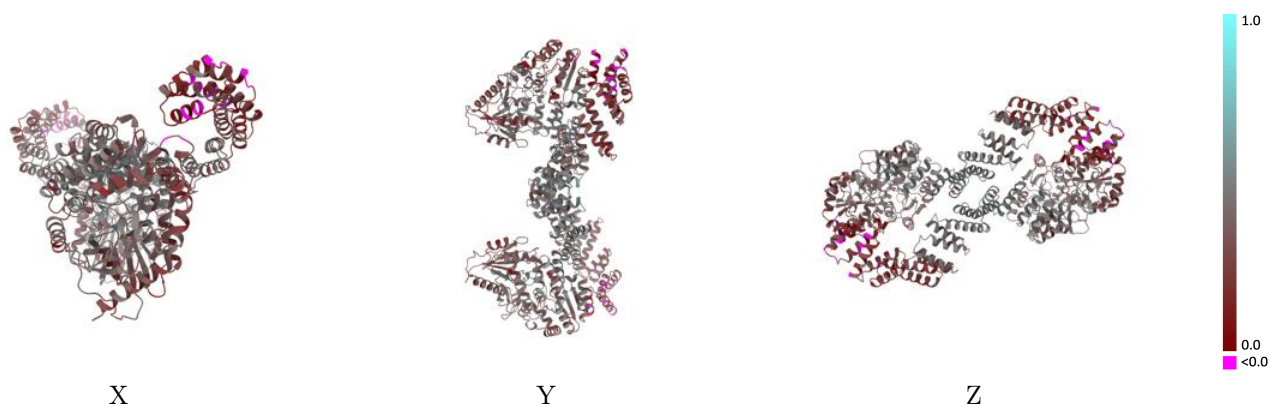
Y



Z

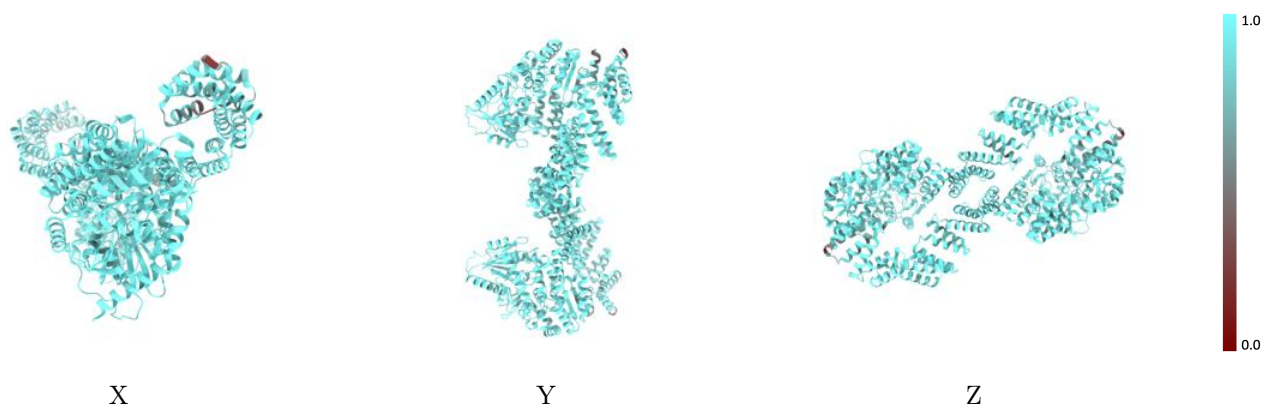
The images above show the 3D surface view of the map at the recommended contour level 4.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



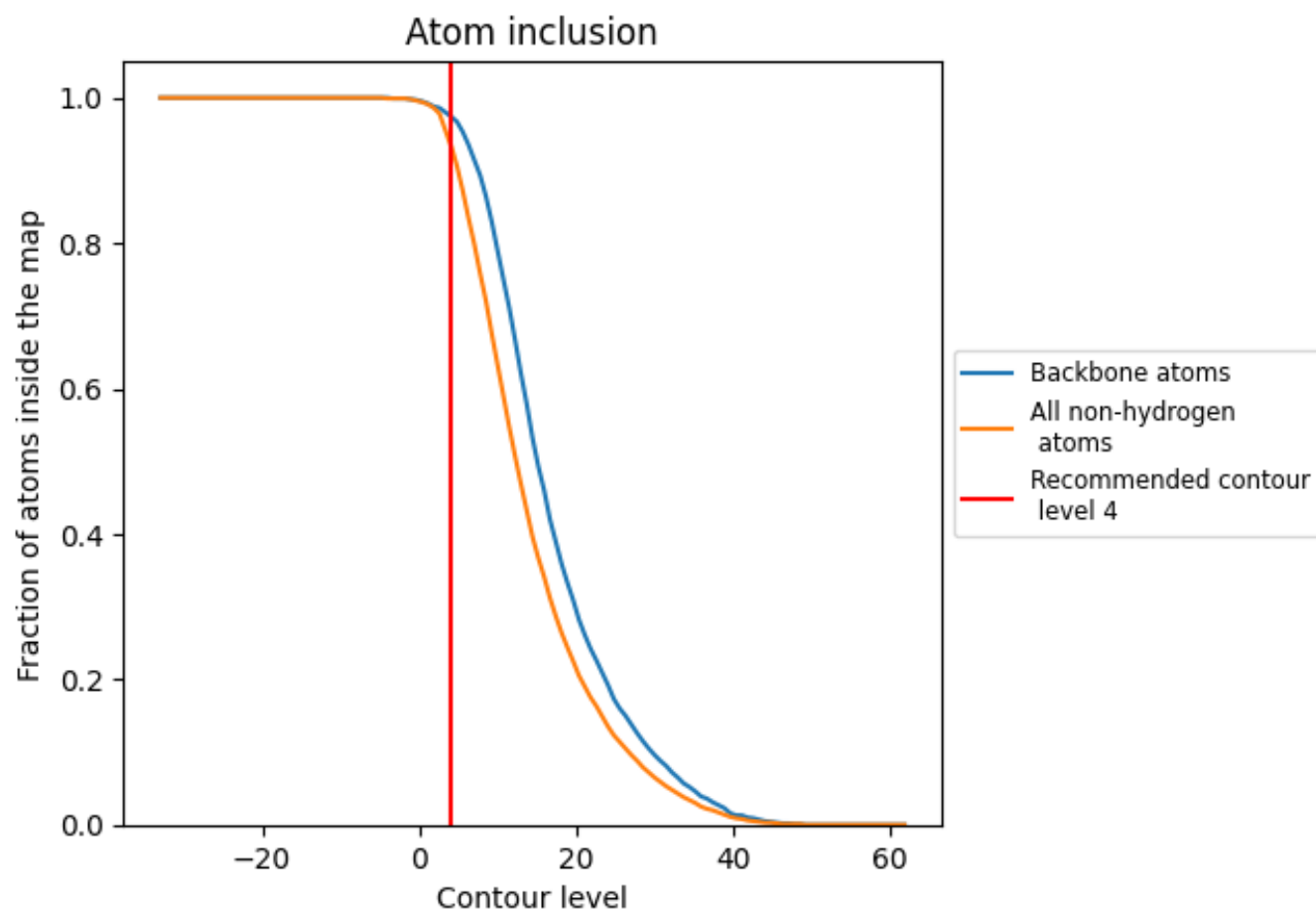
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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 (4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 94% 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 (4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9360	0.3630
A	0.9370	0.3630
B	0.9360	0.3620

