



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 10:14 AM UTC

PDB ID : 8DTG / pdb_00008dtg
EMDB ID : EMD-27697
Title : Cryo-EM structure of Arabidopsis SPY alternative conformation 1
Authors : Kumar, S.; Zhou, Y.; Dillard, L.; Borgnia, M.J.; Bartesaghi, A.; Zhou, P.
Deposited on : 2022-07-25
Resolution : 3.90 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

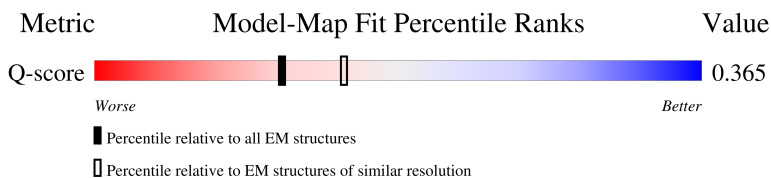
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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	8855 (3.40 - 4.40)

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	 69% 16% 15%
1	B	946	 65% 13% 22%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 11451 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	802	Total	C	N	O	S	0	0
			5985	3812	1005	1126	42		
1	B	737	Total	C	N	O	S	0	0
			5466	3478	930	1020	38		

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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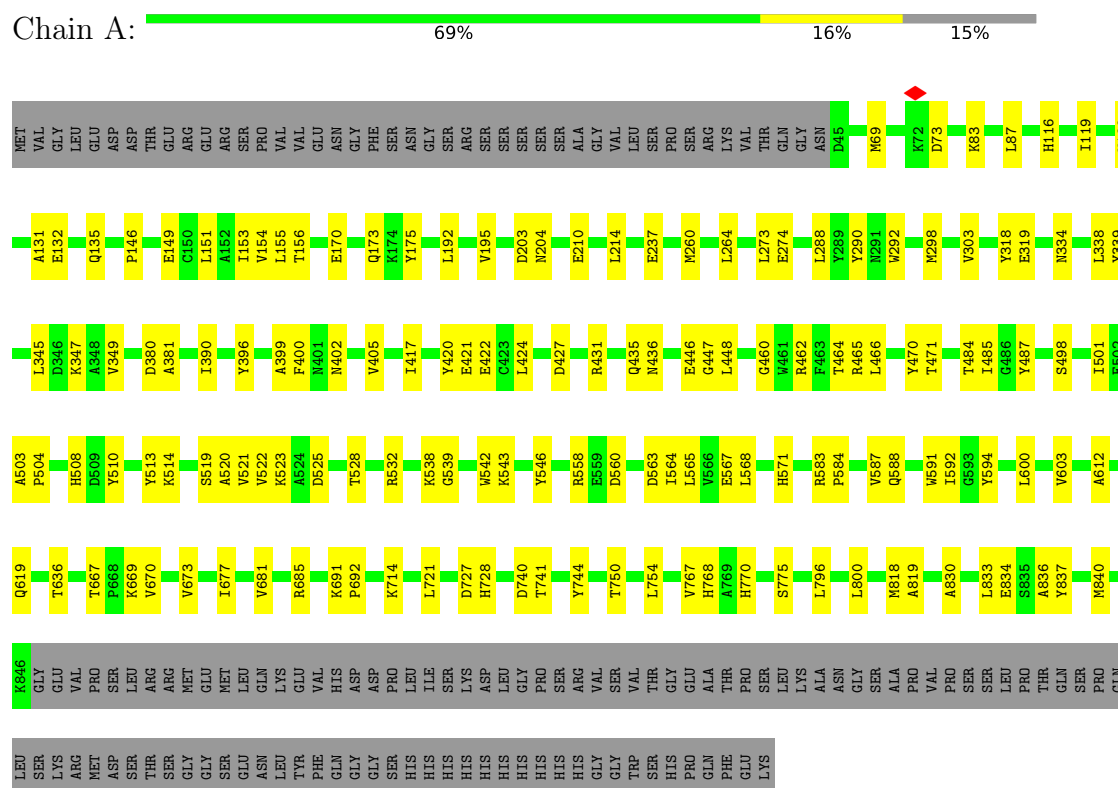
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Chain	Residue	Modelled	Actual	Comment	Reference
A	940	SER	-	expression tag	UNP Q96301
A	941	HIS	-	expression tag	UNP Q96301
A	942	PRO	-	expression tag	UNP Q96301
A	943	GLN	-	expression tag	UNP Q96301
A	944	PHE	-	expression tag	UNP Q96301
A	945	GLU	-	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

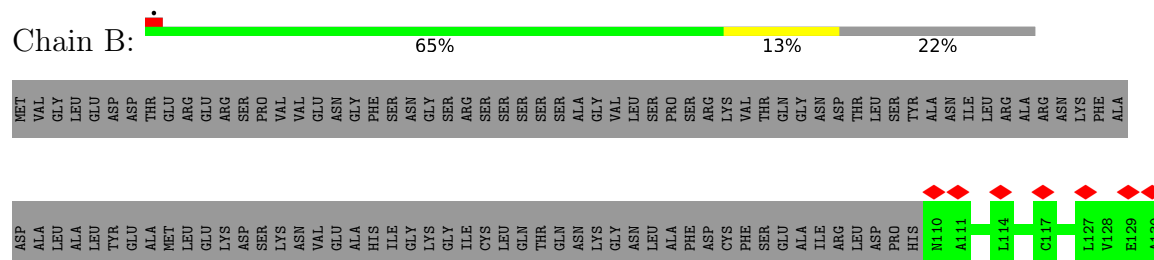
3 Residue-property plots

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: Probable UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase SPINDLY



- Molecule 1: Probable UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase SPINDLY



LEU	S133	M354	H495	L628	K246
SER	Y134	L369	P504	P629	GLY
LYS	Q135	V372	L505	D630	GLU
ARG	K136	N402	T506	Y635	VAL
MET	M139	V405	H507	T647	PRO
ASP	A140	L406	H508	L650	SER
SER	D141	D409	K514	F657	LEU
THR	A142	I413	Y529	M662	ARG
ARG	S143	T414	R532	W674	ARG
GLY	Y144	M415	K535	R685	MET
MET	I181	A416	G539	L686	GLY
GLU	E210	I417	I548	V687	MET
ASN	L214	D418	K552	C690	LEU
LEU	A222	E422	R558	R691	GLN
TYR	M226	D427	E559	P692	PHE
PHE	Y230	G434	D560	I722	GLY
GLN	R233	L438	K561	M729	GLY
GLY	L236	K451	I562	S738	GLY
GLY	E237	E454	D563	L739	SER
TRP	M238	A455	E567	E752	PRO
SER	A239	H456	T569	M756	ARG
SER	I240	R457	G570	C760	VAL
HIS	E254	D458	H571	T778	SER
GLU	I255	W459	T572	S808	THR
ALA	A256	G460	M580	R811	LEU
THR	K257	F463	A585	M812	LYS
SER	W292	T464	Q588	S813	ALA
LEU	H293	R465	W591	L814	ASN
LYS	N291	L466	I592	D816	GLY
ALA	D296	Q469	T597	L817	SER
VAL	N300	S472	L600	M818	ALA
VAL	V303	N475	V603	S821	PRO
SER	E319	P479	D604	P822	SER
LEU	N325	R481	Y605	V823	LEU
THR	P326	P482	L611	Y837	PRO
GLN	H327	S489	Q621	R838	THR
SER	C328	F492	V622	M839	GLN
PRO	N333	T494	E624	M840	SER
GLN	N334				PRO
	L338				GLN

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	80304	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	56.629	Depositor
Minimum map value	-38.190	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	0.18	0/6120	0.37	0/8359
1	B	0.17	0/5588	0.35	0/7623
All	All	0.17	0/11708	0.36	0/15982

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	5985	0	5641	102	0
1	B	5466	0	5135	80	0
All	All	11451	0	10776	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 8.

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:A:380:ASP:OD1	1:A:381:ALA:N	2.29	0.64
1:B:457:ARG:NH1	1:B:458:ASP:OD1	2.29	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:647:THR:OG1	1:B:811:ARG:NE	2.30	0.64
1:A:612:ALA:N	1:A:775:SER:OG	2.32	0.63
1:B:635:TYR:OH	1:B:752:GLU:OE2	2.14	0.63

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	800/946 (85%)	758 (95%)	42 (5%)	0	100	100
1	B	735/946 (78%)	691 (94%)	44 (6%)	0	100	100
All	All	1535/1892 (81%)	1449 (94%)	86 (6%)	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	592/800 (74%)	592 (100%)	0	100	100
1	B	532/800 (66%)	532 (100%)	0	100	100
All	All	1124/1600 (70%)	1124 (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 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	784	HIS
1	B	325	ASN
1	B	726	HIS
1	A	191	ASN
1	A	167	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.

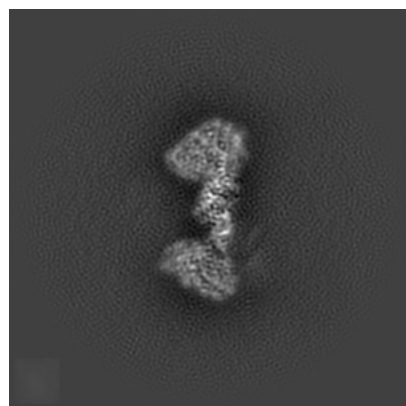
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27697. These allow visual inspection of the internal detail of the map and identification of artifacts.

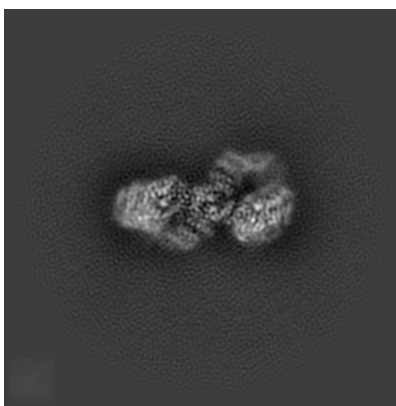
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

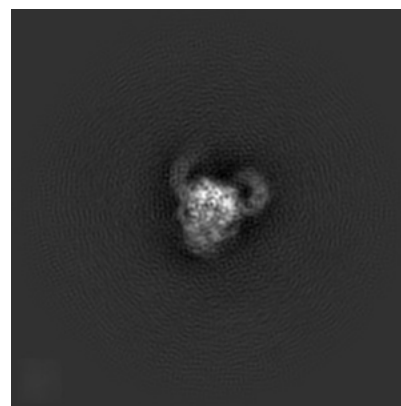
6.1.1 Primary map



X

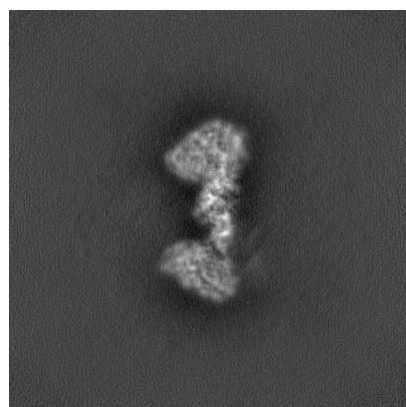


Y

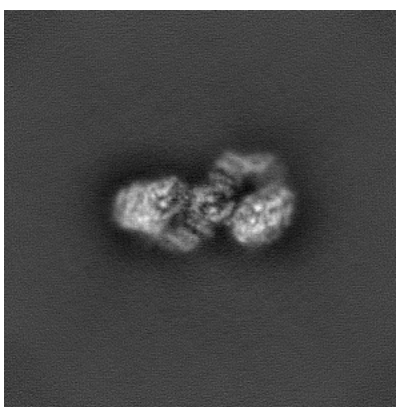


Z

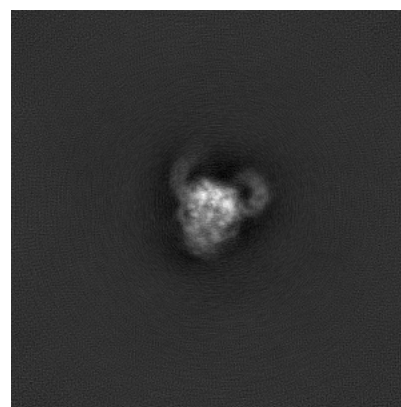
6.1.2 Raw map



X



Y

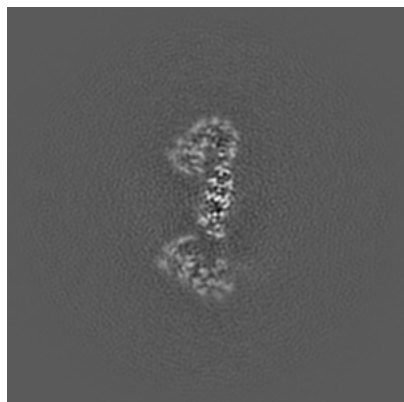


Z

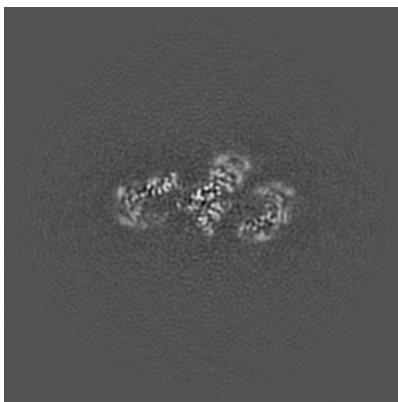
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

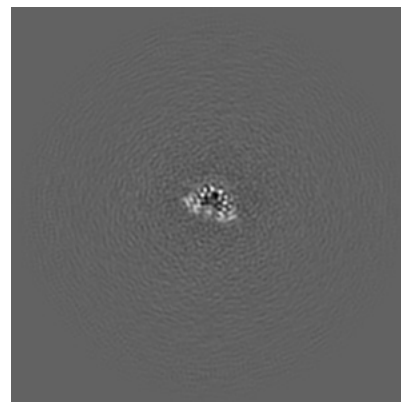
6.2.1 Primary map



X Index: 192

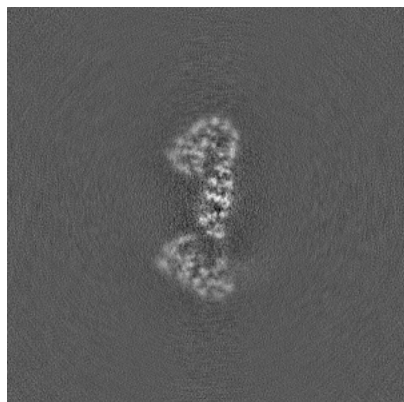


Y Index: 192

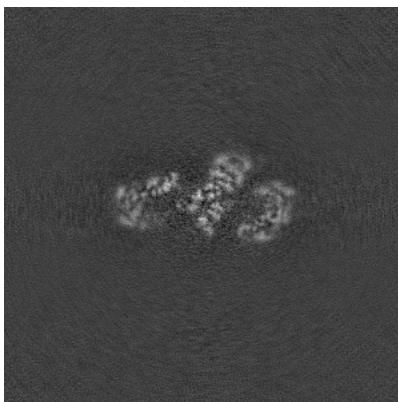


Z Index: 192

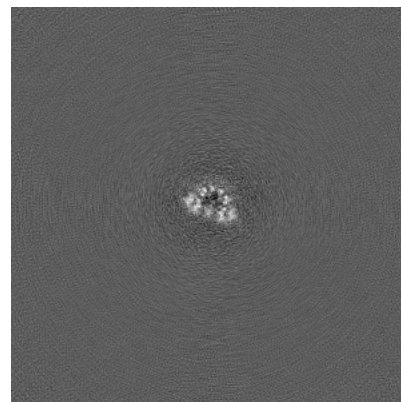
6.2.2 Raw map



X Index: 192



Y Index: 192

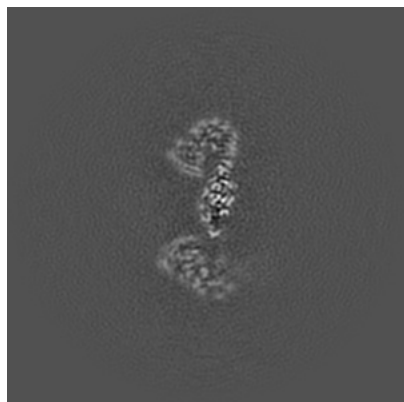


Z Index: 192

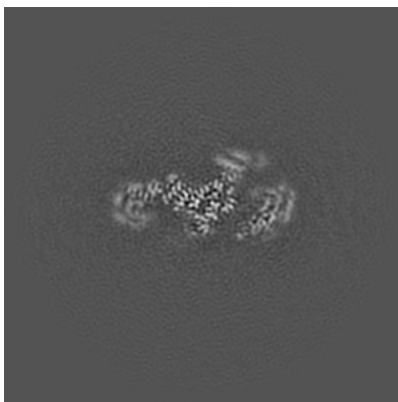
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

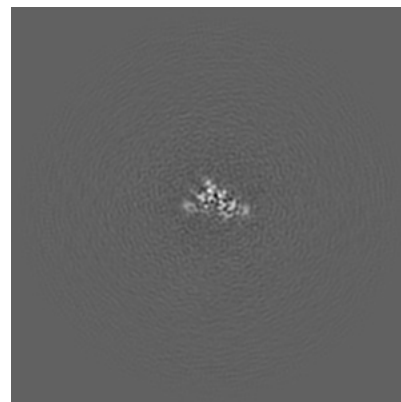
6.3.1 Primary map



X Index: 190

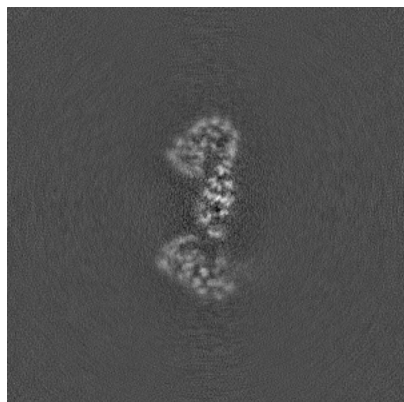


Y Index: 198

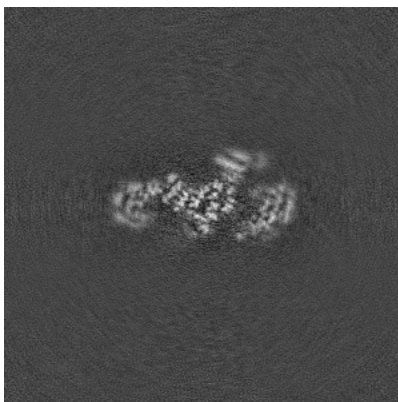


Z Index: 198

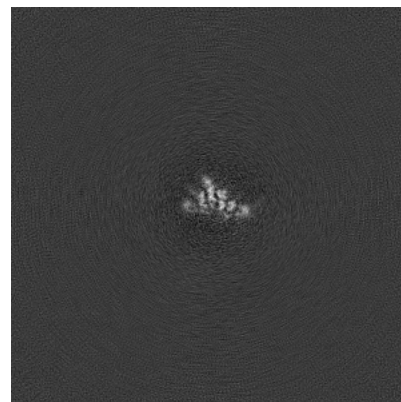
6.3.2 Raw map



X Index: 191



Y Index: 198

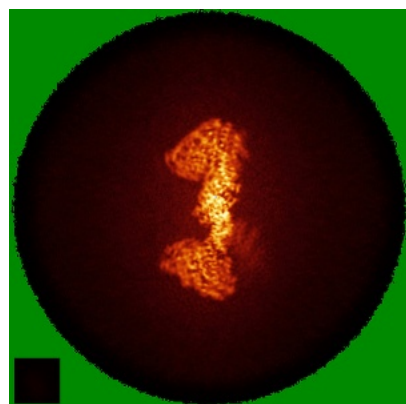


Z Index: 199

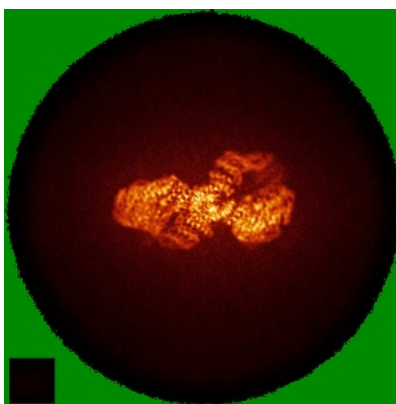
The images above show the largest variance slices of the map in three orthogonal directions.

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

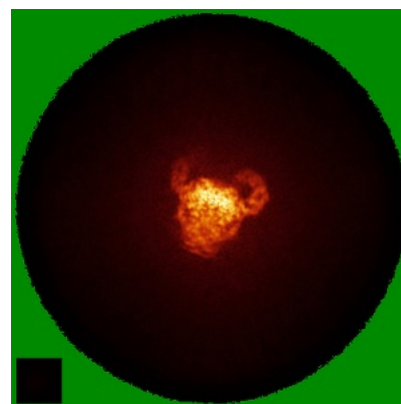
6.4.1 Primary map



X

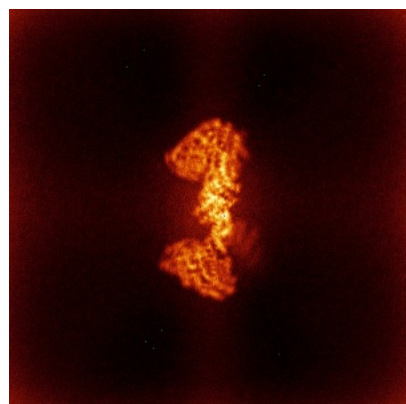


Y

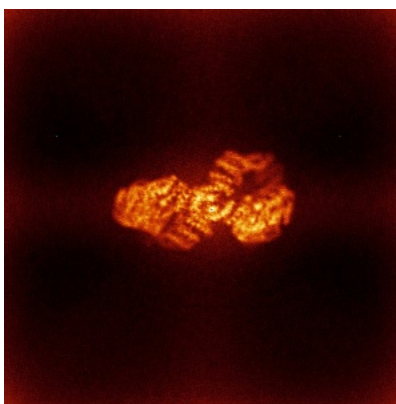


Z

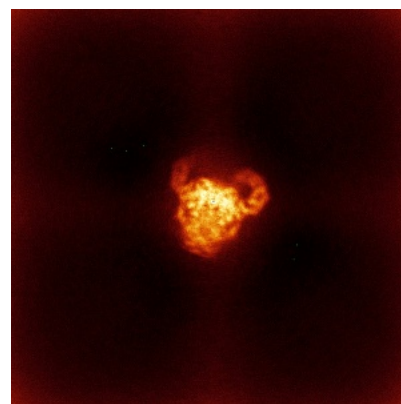
6.4.2 Raw map



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](#)

This section was not generated.

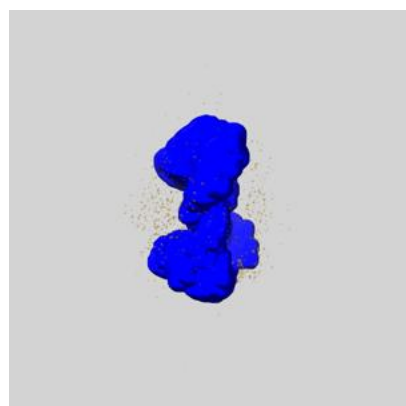
6.6 Mask visualisation [i](#)

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

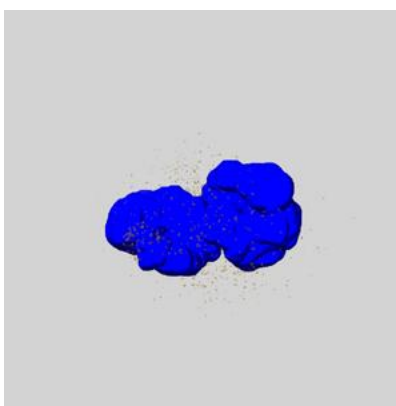
A mask typically either:

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

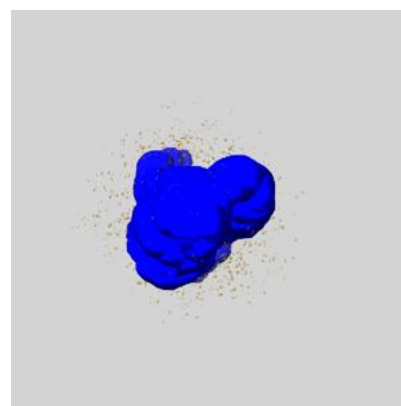
6.6.1 emd_27697_msk_1.map [i](#)



X



Y

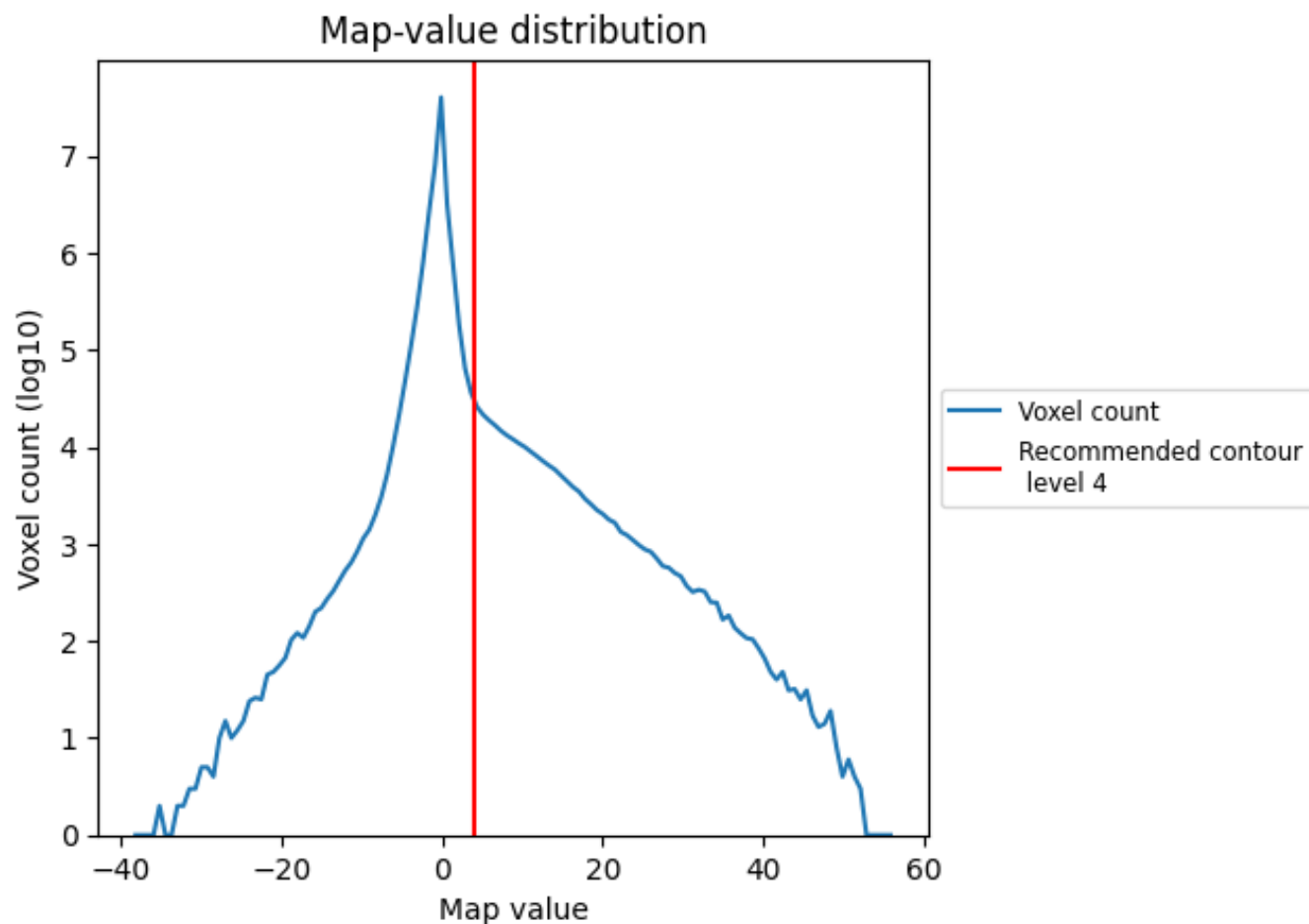


Z

7 Map analysis [i](#)

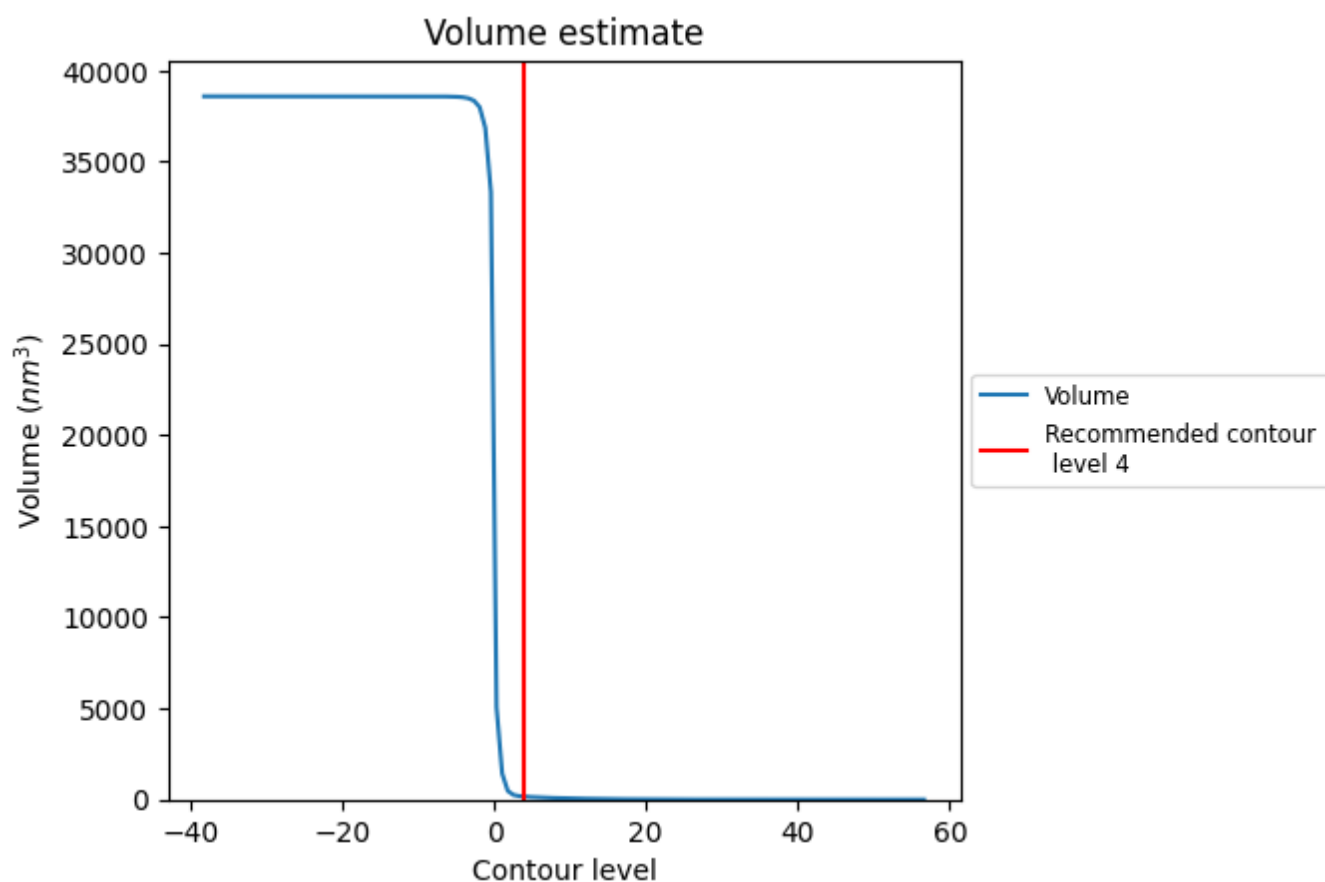
This section contains the results of statistical analysis of the map.

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.

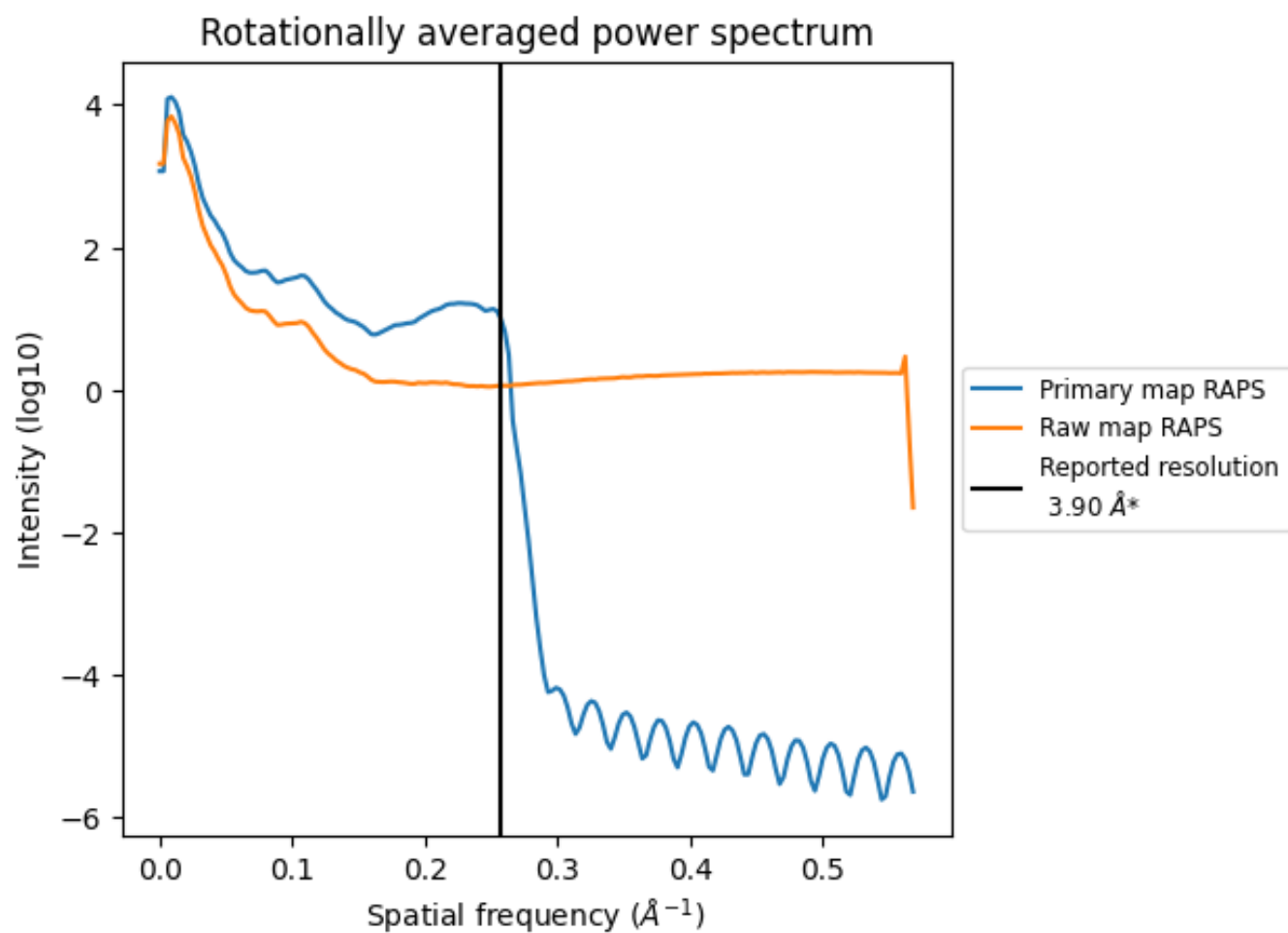
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 162 nm³; this corresponds to an approximate mass of 147 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 ⓘ

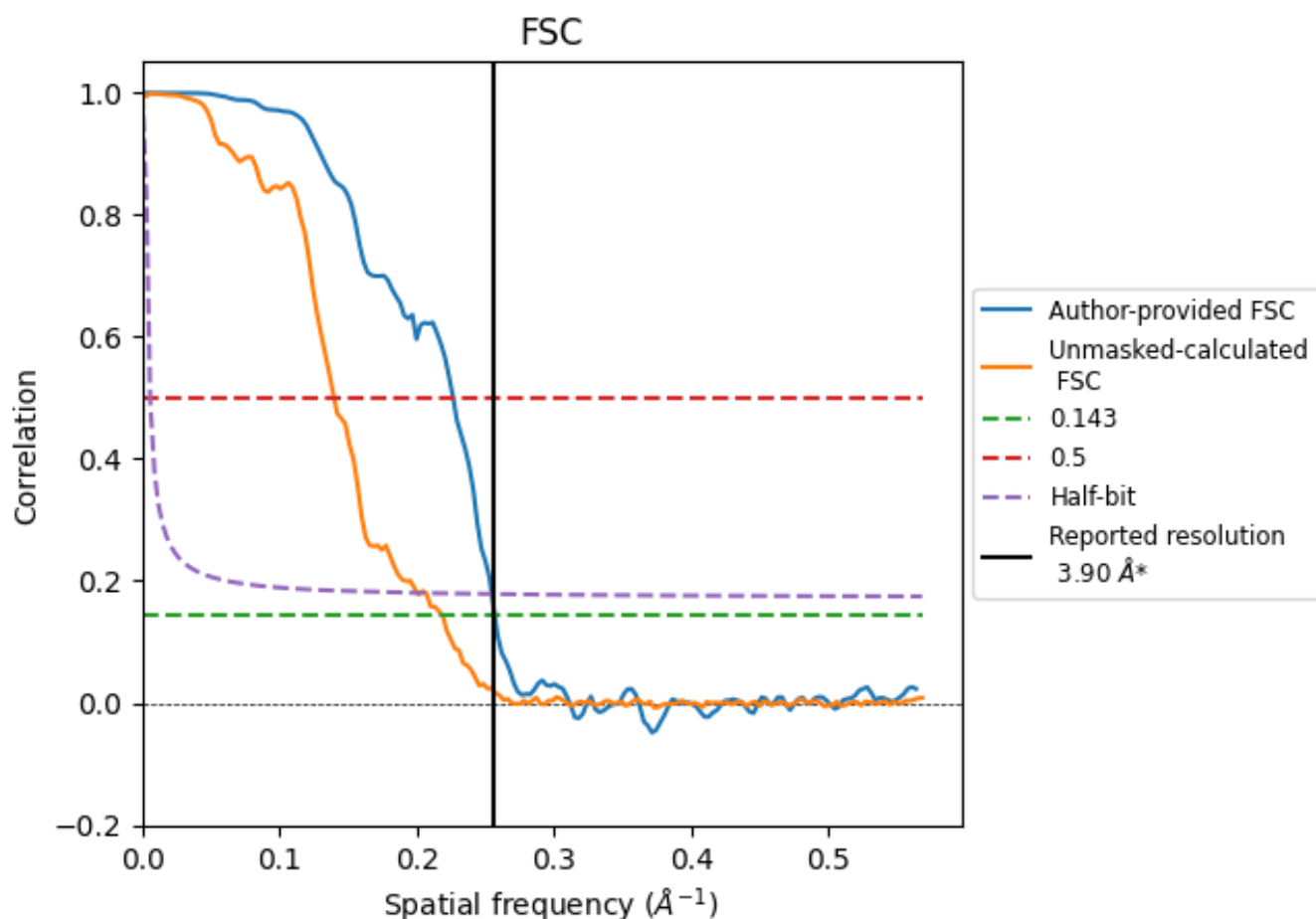


*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

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 0.256 Å⁻¹

8.2 Resolution estimates [i](#)

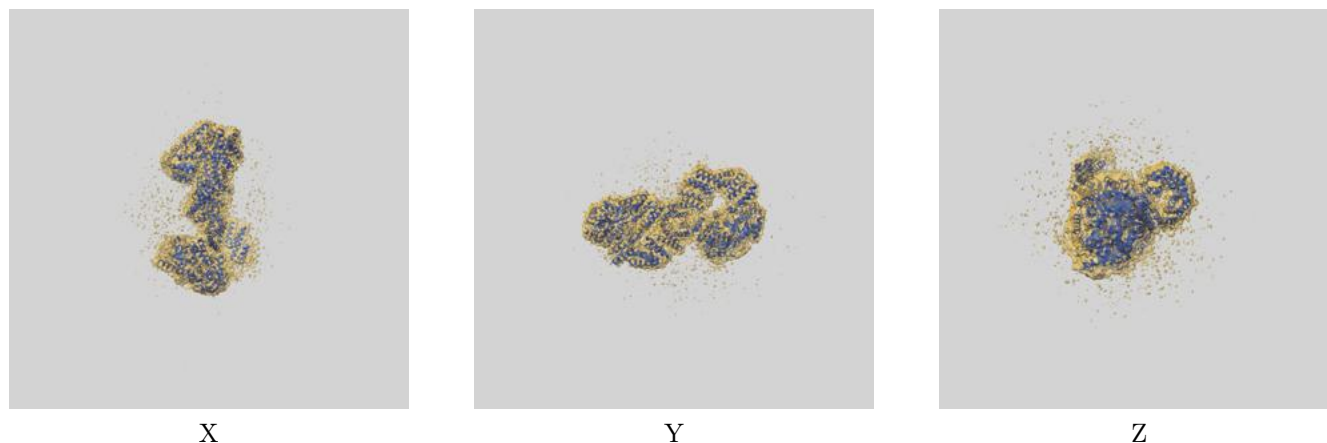
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.89	4.42	3.93
Unmasked-calculated*	4.57	7.15	4.99

*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 4.57 differs from the reported value 3.9 by more than 10 %

9 Map-model fit [i](#)

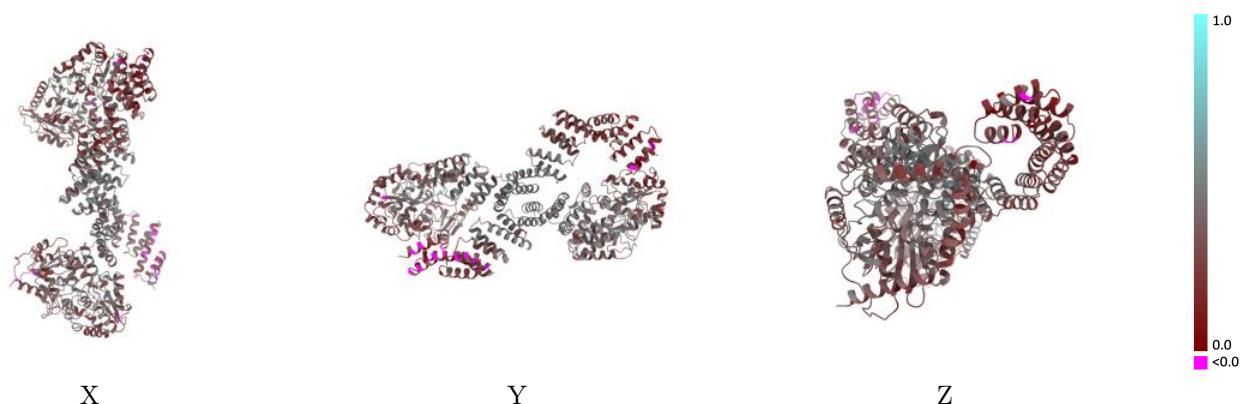
This section contains information regarding the fit between EMDB map EMD-27697 and PDB model 8DTG. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



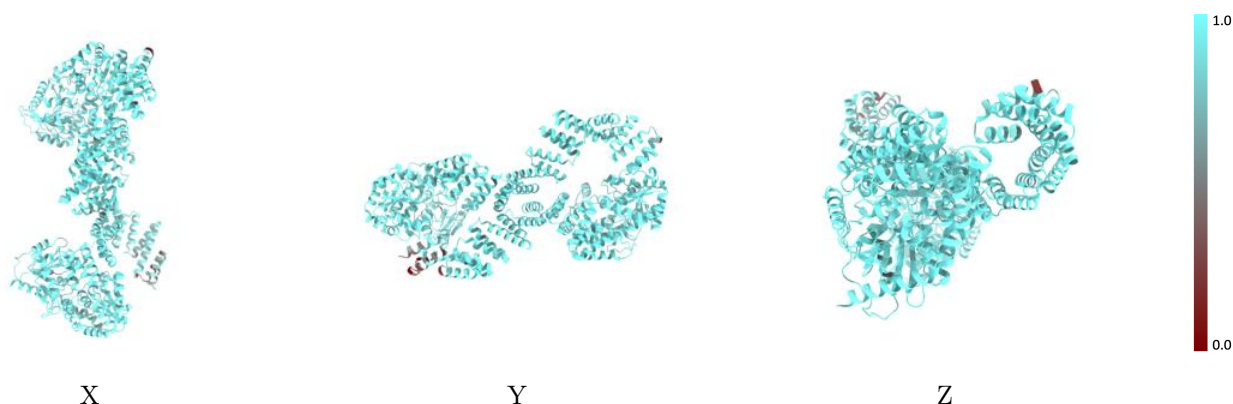
The images above show the 3D surface view of the map at the recommended contour level 4.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



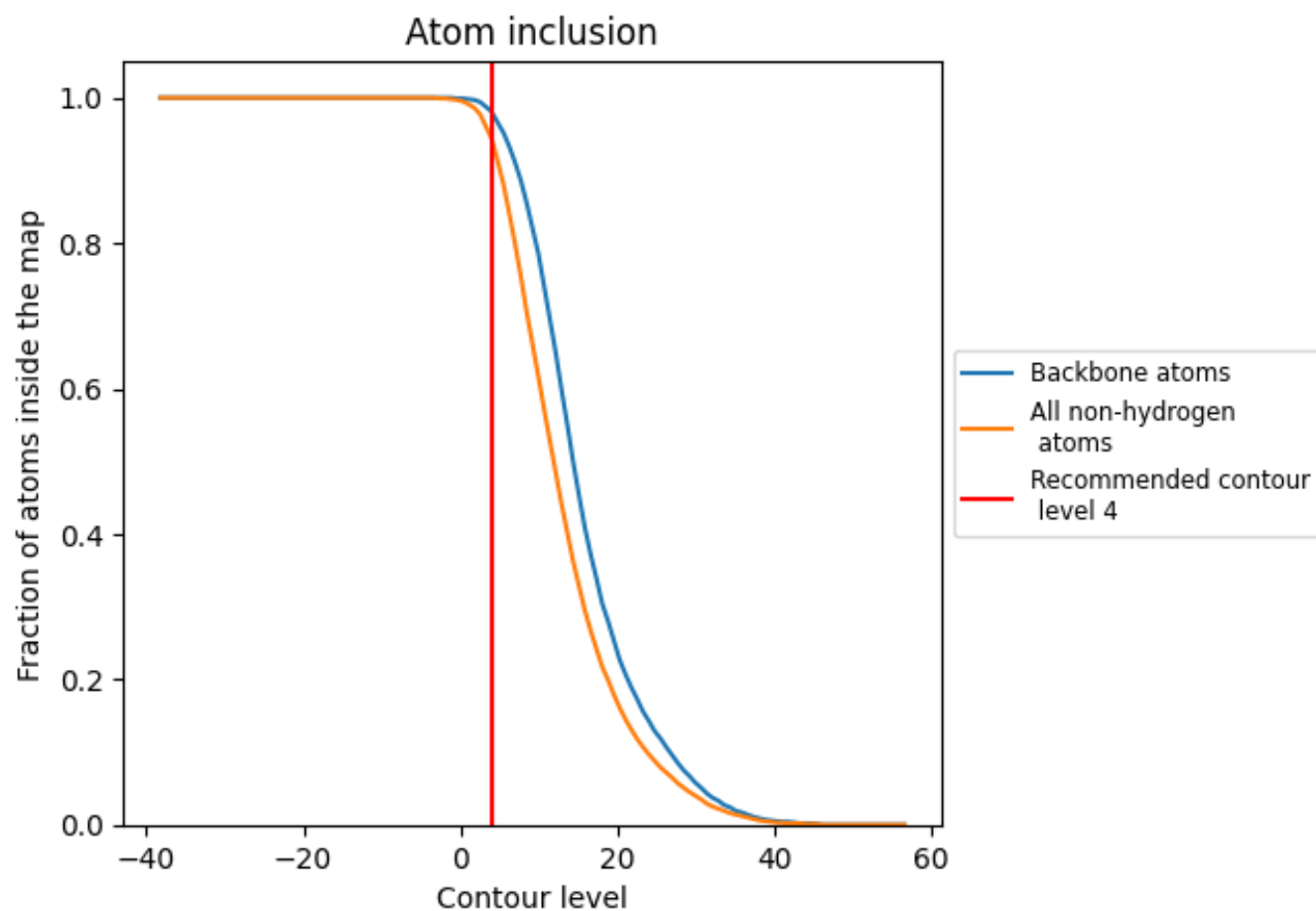
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	0.9440	0.3650
A	0.9460	0.3570
B	0.9430	0.3730

