



wwPDB EM Validation Summary Report ⓘ

May 26, 2024 – 07:07 PM EDT

PDB ID : 7SQR
EMDB ID : EMD-25391
Title : 201phi2-1 Chimallin localized tetramer reconstruction
Authors : Laughlin, T.G.; Deep, A.; Prichard, A.M.; Seitz, C.; Gu, Y.; Enustun, E.;
Suslov, S.; Khanna, K.; Birkholz, E.A.; Amaro, R.E.; Pogliano, J.; Corbett,
K.D.; Villa, E.
Deposited on : 2021-11-06
Resolution : 3.40 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.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

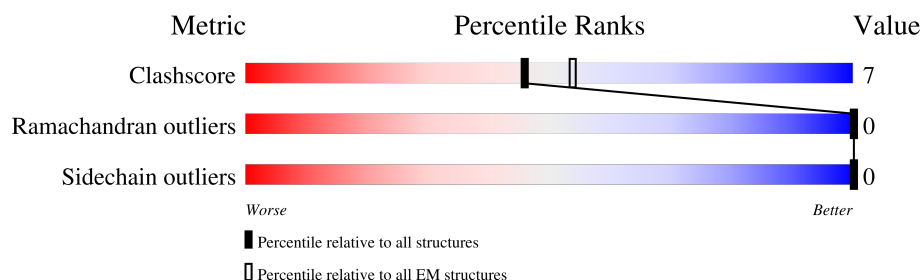
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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.



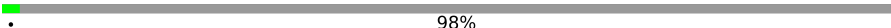

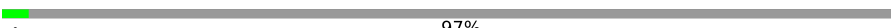
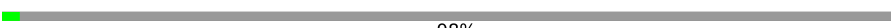
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	634	
1	B	634	
1	C	634	
1	D	634	
1	E	634	
1	F	634	
1	G	634	
1	H	634	

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Mol	Chain	Length	Quality of chain
1	I	634	 98%
1	J	634	 69% 13% 18%
1	K	634	 97%
1	L	634	 98%

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 17272 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 Chimallin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	522	Total	C	N	O	S	0	0
			4072	2542	737	781	12		
1	B	22	Total	C	N	O	S	0	0
			163	97	33	31	2		
1	C	10	Total	C	N	O		0	0
			83	54	12	17			
1	D	522	Total	C	N	O	S	0	0
			4072	2542	737	781	12		
1	E	22	Total	C	N	O	S	0	0
			163	97	33	31	2		
1	F	10	Total	C	N	O		0	0
			83	54	12	17			
1	G	522	Total	C	N	O	S	0	0
			4072	2542	737	781	12		
1	H	22	Total	C	N	O	S	0	0
			163	97	33	31	2		
1	I	10	Total	C	N	O		0	0
			83	54	12	17			
1	J	522	Total	C	N	O	S	0	0
			4072	2542	737	781	12		
1	K	22	Total	C	N	O	S	0	0
			163	97	33	31	2		
1	L	10	Total	C	N	O		0	0
			83	54	12	17			

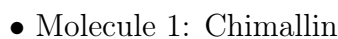
There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP B3FIW8
A	-1	ASN	-	expression tag	UNP B3FIW8
A	0	ALA	-	expression tag	UNP B3FIW8
B	-2	SER	-	expression tag	UNP B3FIW8
B	-1	ASN	-	expression tag	UNP B3FIW8
B	0	ALA	-	expression tag	UNP B3FIW8

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	SER	-	expression tag	UNP B3FIW8
C	-1	ASN	-	expression tag	UNP B3FIW8
C	0	ALA	-	expression tag	UNP B3FIW8
D	-2	SER	-	expression tag	UNP B3FIW8
D	-1	ASN	-	expression tag	UNP B3FIW8
D	0	ALA	-	expression tag	UNP B3FIW8
E	-2	SER	-	expression tag	UNP B3FIW8
E	-1	ASN	-	expression tag	UNP B3FIW8
E	0	ALA	-	expression tag	UNP B3FIW8
F	-2	SER	-	expression tag	UNP B3FIW8
F	-1	ASN	-	expression tag	UNP B3FIW8
F	0	ALA	-	expression tag	UNP B3FIW8
G	-2	SER	-	expression tag	UNP B3FIW8
G	-1	ASN	-	expression tag	UNP B3FIW8
G	0	ALA	-	expression tag	UNP B3FIW8
H	-2	SER	-	expression tag	UNP B3FIW8
H	-1	ASN	-	expression tag	UNP B3FIW8
H	0	ALA	-	expression tag	UNP B3FIW8
I	-2	SER	-	expression tag	UNP B3FIW8
I	-1	ASN	-	expression tag	UNP B3FIW8
I	0	ALA	-	expression tag	UNP B3FIW8
J	-2	SER	-	expression tag	UNP B3FIW8
J	-1	ASN	-	expression tag	UNP B3FIW8
J	0	ALA	-	expression tag	UNP B3FIW8
K	-2	SER	-	expression tag	UNP B3FIW8
K	-1	ASN	-	expression tag	UNP B3FIW8
K	0	ALA	-	expression tag	UNP B3FIW8
L	-2	SER	-	expression tag	UNP B3FIW8
L	-1	ASN	-	expression tag	UNP B3FIW8
L	0	ALA	-	expression tag	UNP B3FIW8



98%

[illegible]

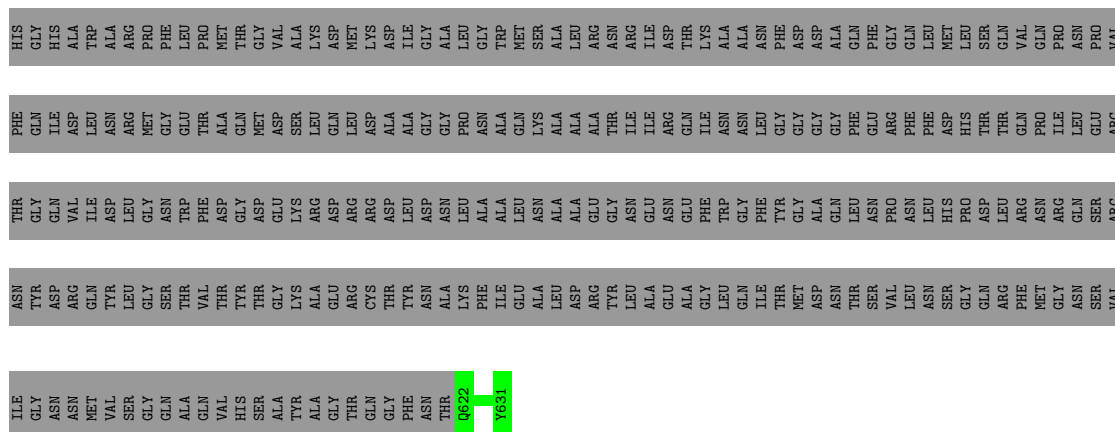
- Molecule 1: Chimallin

69%

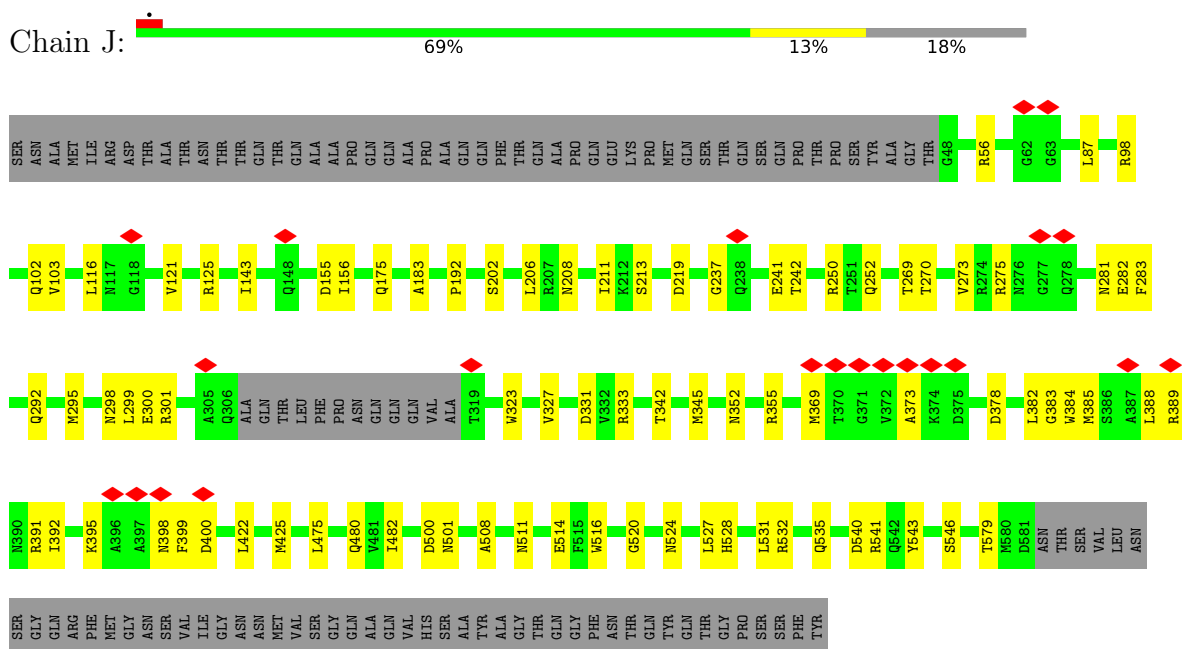
13%

18%

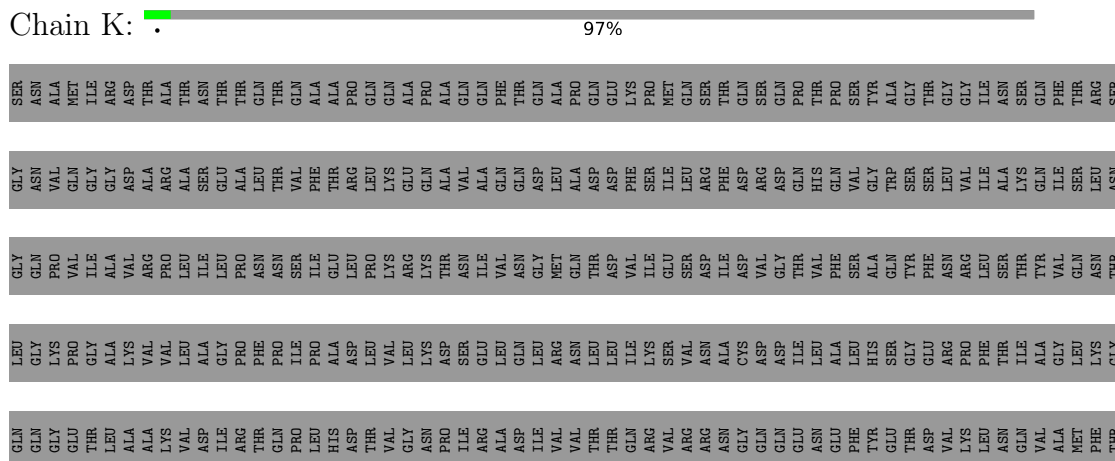
LEU	R391	E282	R98	SER
ASN	I392	F283		ASN
SER				ALA
GLN	R395	Q292	Y103	MET
GLY	A396	R295	L116	ILE
ARG	A397		N117	ARG
PHE	N398	M298	G118	ASP
MET	F399	L299		THR
GLY	D400	E300		ALA
ASN		R301		THR
SER	L422		V121	ASN
VAL	M425	A305	R125	ASN
ILE		Q306		THR
GLY	L475	ALA	I143	GLN
ASN		GLN		GLN
ASN		THR	Q148	ALA
MET		LEU		ALA
MET	Q480	PHE	D155	PRO
SER	V481	PRO	I156	GLN
GLY	L482	ASN	Q175	GLN
GLN		ALA	A183	ALA
GLN	D489	GLN		PRO
GLN	G490	GLN		ALA
VAL		GLN		ALA
HIS	D500	VAL		GLN
SER	N501	ALA	P192	PHE
SER		T319		PHE
ALA	A508		S202	THR
TYR		V327		GLN
ALA	N511		L206	ALA
GLY		D331	R207	PRO
THR	E514	V332	N208	GLN
GLN	F515	R333	I211	GLU
GLY	F516		K212	LYS
PHE		T342	S213	PRO
ASN		R345	D219	MET
THR	G520		G237	GLN
GLN	N524	N352	Q238	SER
TYR	L527	R355		GLN
THR	H528		E241	THR
GLY			T242	PRO
PRO	L531	M369	R250	SER
SER	E532	T370	T251	PRO
PHE		V371	Q252	SER
TYR	Q535	G371	G276	TYR
		A373	T269	GLY
	D540		T270	ALA
RS41		K374		THR
	D542	D375		G48
	Y543			
		D378	V273	R56
	S546		R274	
	T579	L382	R275	G62
		G383	N276	G53
	D581	W384	G277	A81
ASN			Q278	
THR		A387		L87
SER		L388		
VAL		R389		
		H390		



- Molecule 1: Chimallin



- Molecule 1: Chimallin





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	664363	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; CTF correction performed during 3D reconstruction	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	42.6	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.075	Depositor
Minimum map value	-0.028	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.014	Depositor
Map size (Å)	200.19205, 200.19205, 200.19205	wwPDB
Map dimensions	148, 148, 148	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.352649, 1.352649, 1.352649	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.25	0/4147	0.53	0/5627
1	B	0.25	0/164	0.64	0/218
1	C	0.25	0/86	0.34	0/116
1	D	0.25	0/4147	0.53	0/5627
1	E	0.26	0/164	0.64	0/218
1	F	0.26	0/86	0.34	0/116
1	G	0.25	0/4147	0.53	0/5627
1	H	0.26	0/164	0.64	0/218
1	I	0.26	0/86	0.34	0/116
1	J	0.25	0/4147	0.53	0/5627
1	K	0.25	0/164	0.64	0/218
1	L	0.25	0/86	0.34	0/116
All	All	0.25	0/17588	0.53	0/23844

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4072	0	3995	60	0
1	B	163	0	155	2	0
1	C	83	0	69	0	0
1	D	4072	0	3995	61	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	163	0	155	2	0
1	F	83	0	69	0	0
1	G	4072	0	3995	60	0
1	H	163	0	155	2	0
1	I	83	0	69	0	0
1	J	4072	0	3995	60	0
1	K	163	0	155	2	0
1	L	83	0	69	0	0
All	All	17272	0	16876	225	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 7.

The worst 5 of 225 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:540:ASP:OD2	1:A:541:ARG:N	2.28	0.67
1:A:527:LEU:HD22	1:A:532:ARG:HG2	1.77	0.67
1:D:540:ASP:OD2	1:D:541:ARG:N	2.28	0.67
1:J:527:LEU:HD22	1:J:532:ARG:HG2	1.77	0.67
1:A:281:ASN:ND2	1:J:102:GLN:OE1	2.26	0.66

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	518/634 (82%)	501 (97%)	17 (3%)	0	100	100
1	B	20/634 (3%)	20 (100%)	0	0	100	100
1	C	8/634 (1%)	8 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	518/634 (82%)	501 (97%)	17 (3%)	0	100	100
1	E	20/634 (3%)	20 (100%)	0	0	100	100
1	F	8/634 (1%)	8 (100%)	0	0	100	100
1	G	518/634 (82%)	501 (97%)	17 (3%)	0	100	100
1	H	20/634 (3%)	20 (100%)	0	0	100	100
1	I	8/634 (1%)	8 (100%)	0	0	100	100
1	J	518/634 (82%)	501 (97%)	17 (3%)	0	100	100
1	K	20/634 (3%)	20 (100%)	0	0	100	100
1	L	8/634 (1%)	8 (100%)	0	0	100	100
All	All	2184/7608 (29%)	2116 (97%)	68 (3%)	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	
1	A	431/522 (83%)	431 (100%)	0	100	100
1	B	18/522 (3%)	18 (100%)	0	100	100
1	C	9/522 (2%)	9 (100%)	0	100	100
1	D	431/522 (83%)	431 (100%)	0	100	100
1	E	18/522 (3%)	18 (100%)	0	100	100
1	F	9/522 (2%)	9 (100%)	0	100	100
1	G	431/522 (83%)	431 (100%)	0	100	100
1	H	18/522 (3%)	18 (100%)	0	100	100
1	I	9/522 (2%)	9 (100%)	0	100	100
1	J	431/522 (83%)	431 (100%)	0	100	100
1	K	18/522 (3%)	18 (100%)	0	100	100
1	L	9/522 (2%)	9 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	1832/6264 (29%)	1832 (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. There are no such sidechains identified.

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 monosaccharides 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.

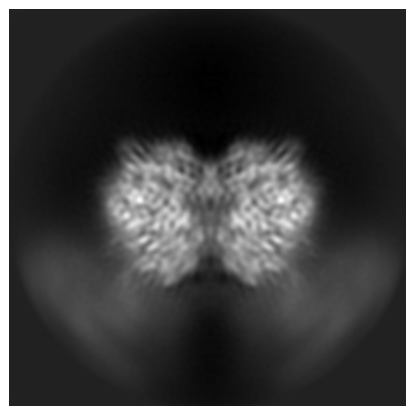
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25391. These allow visual inspection of the internal detail of the map and identification of artifacts.

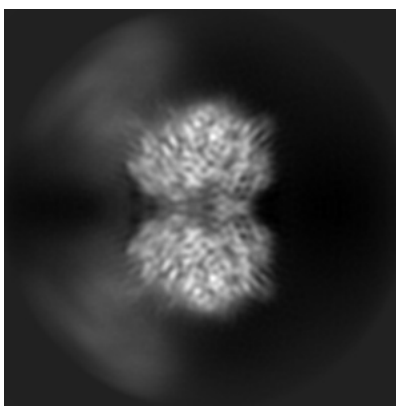
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

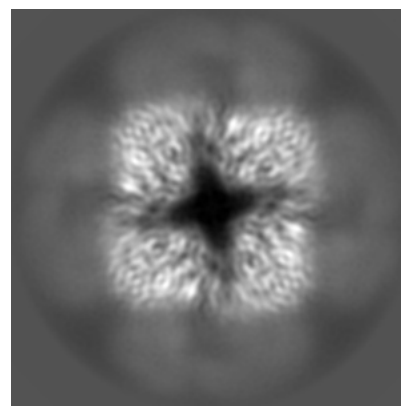
6.1.1 Primary map



X

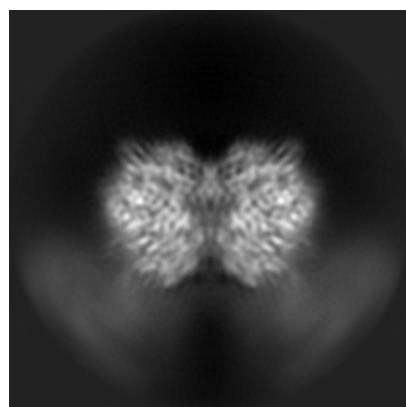


Y

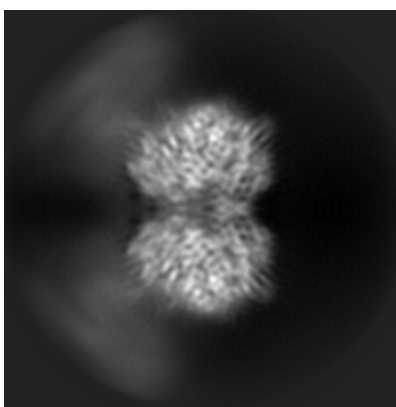


Z

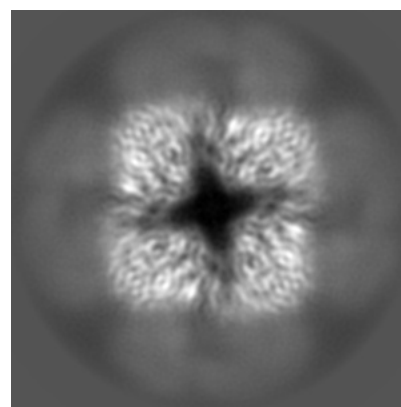
6.1.2 Raw map



X



Y

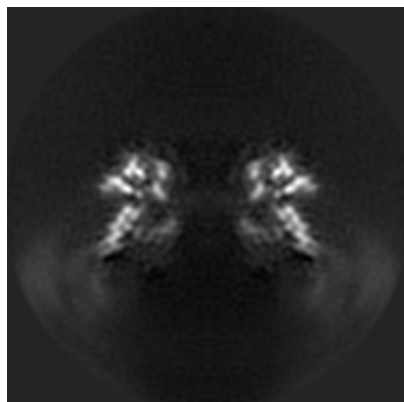


Z

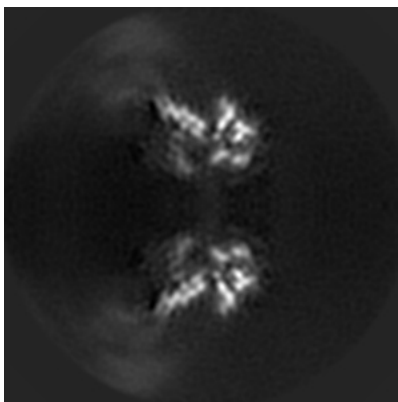
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

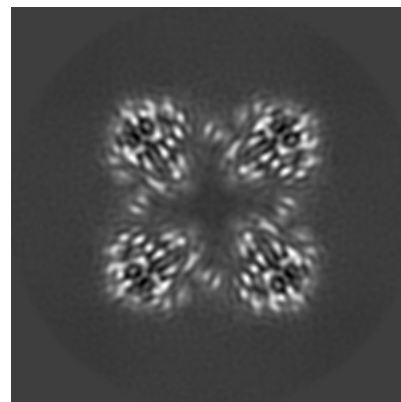
6.2.1 Primary map



X Index: 74

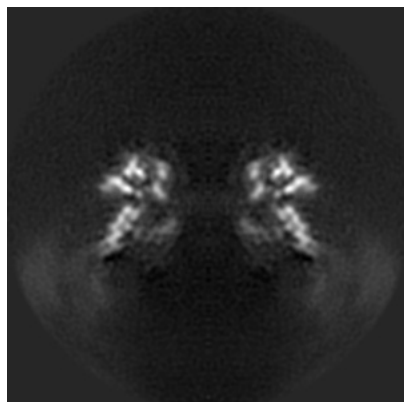


Y Index: 74

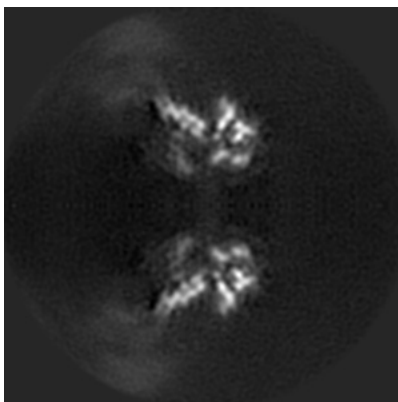


Z Index: 74

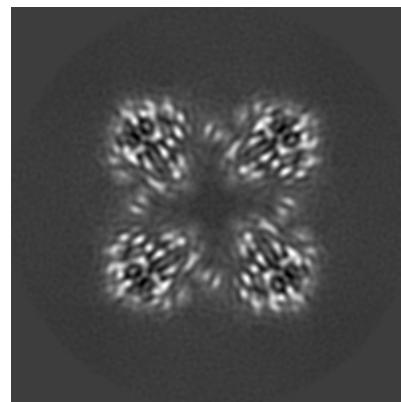
6.2.2 Raw map



X Index: 74



Y Index: 74

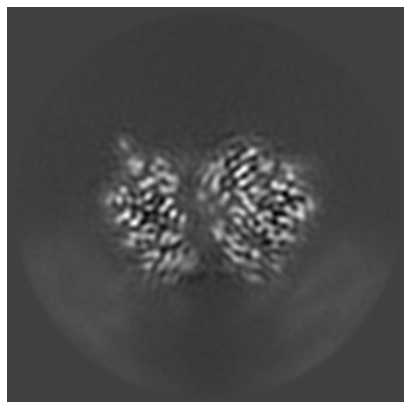


Z Index: 74

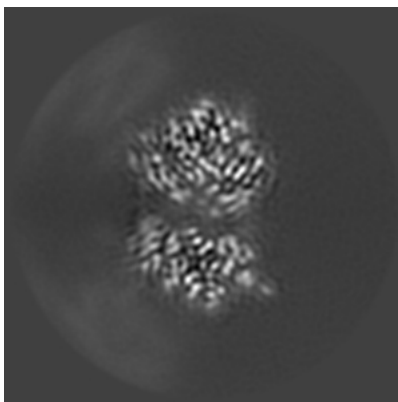
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

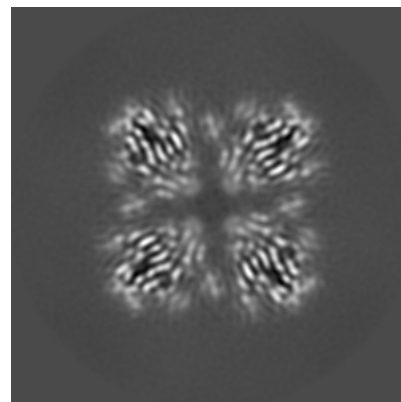
6.3.1 Primary map



X Index: 50

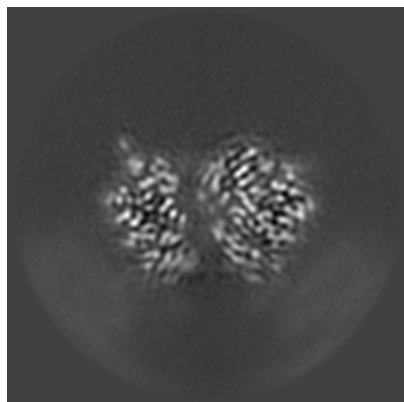


Y Index: 98

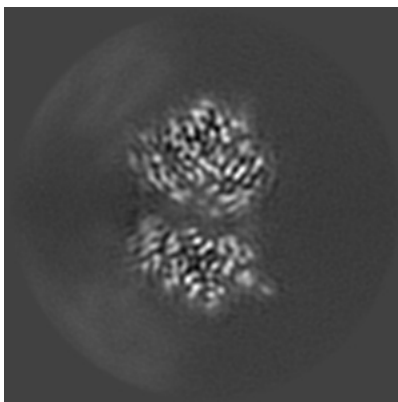


Z Index: 71

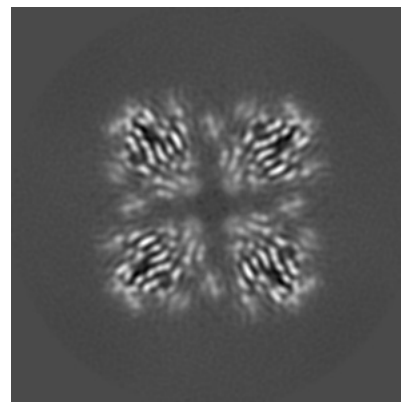
6.3.2 Raw map



X Index: 50



Y Index: 98

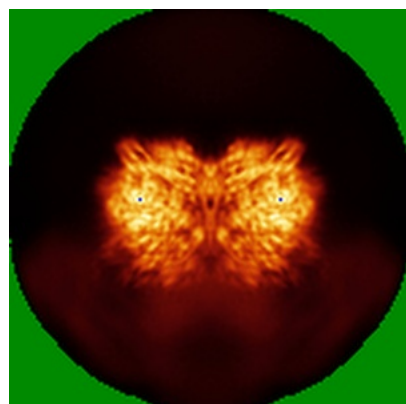


Z Index: 71

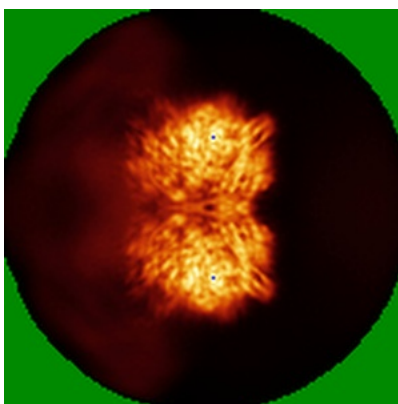
The images above show the largest variance slices of the map in three orthogonal directions.

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

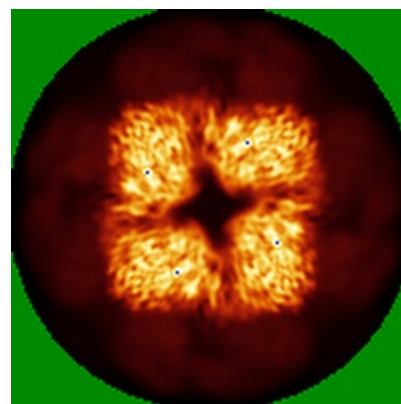
6.4.1 Primary map



X

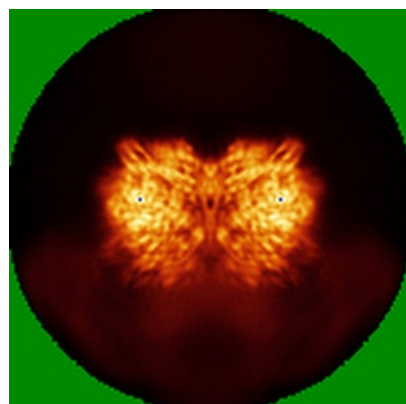


Y

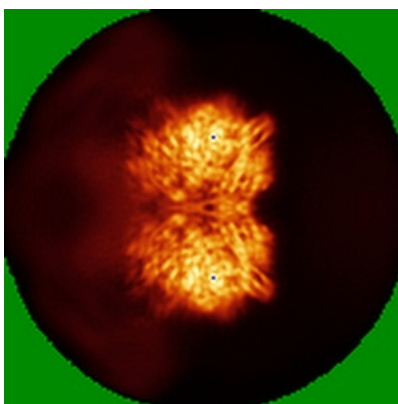


Z

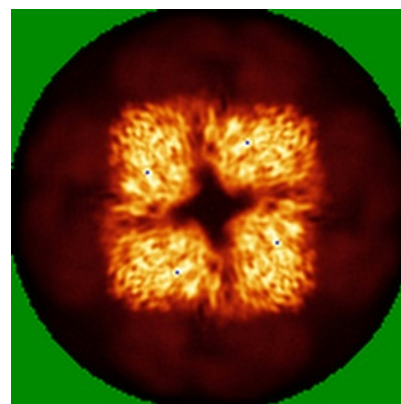
6.4.2 Raw map



X



Y

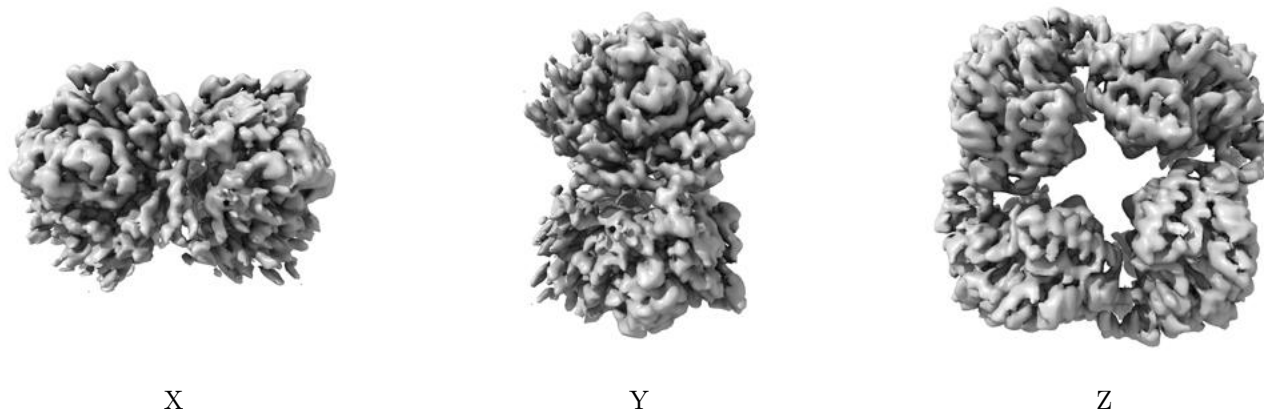


Z

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.

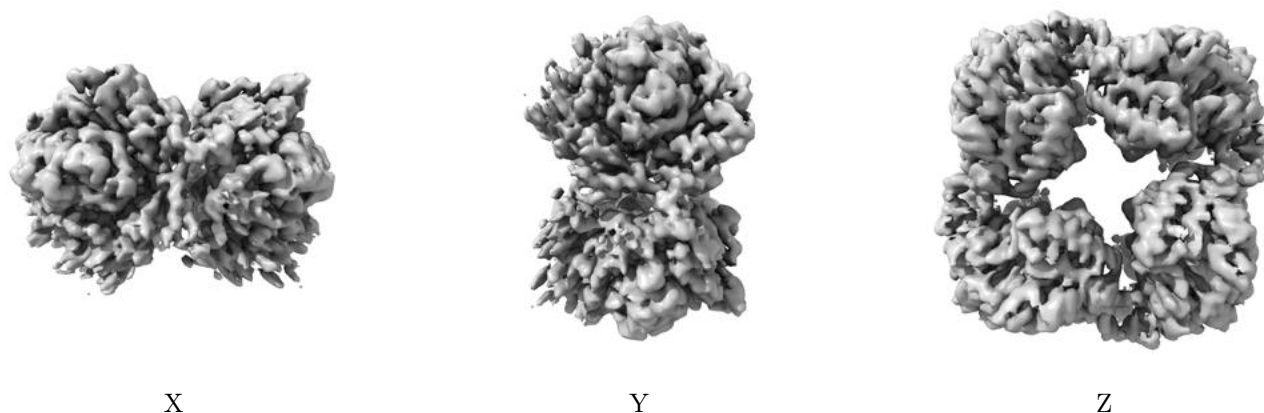
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.014. 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.

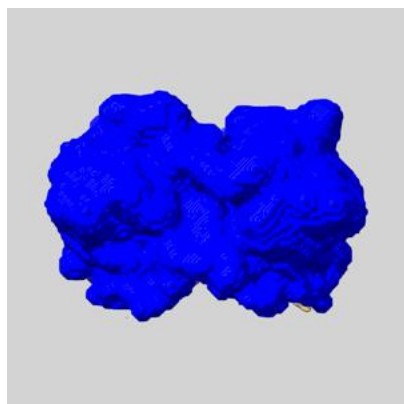
6.6 Mask visualisation [i](#)

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

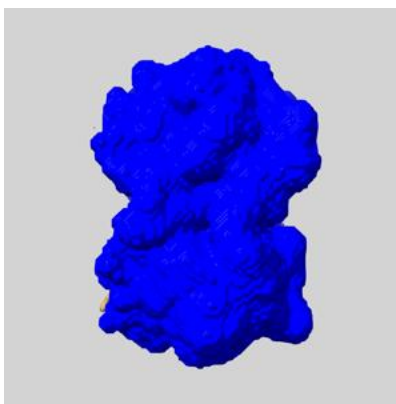
A mask typically either:

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

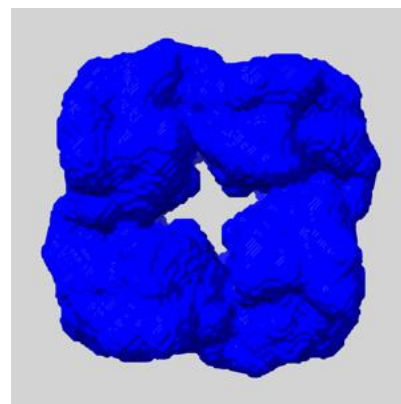
6.6.1 emd_25391_msk_1.map [i](#)



X



Y

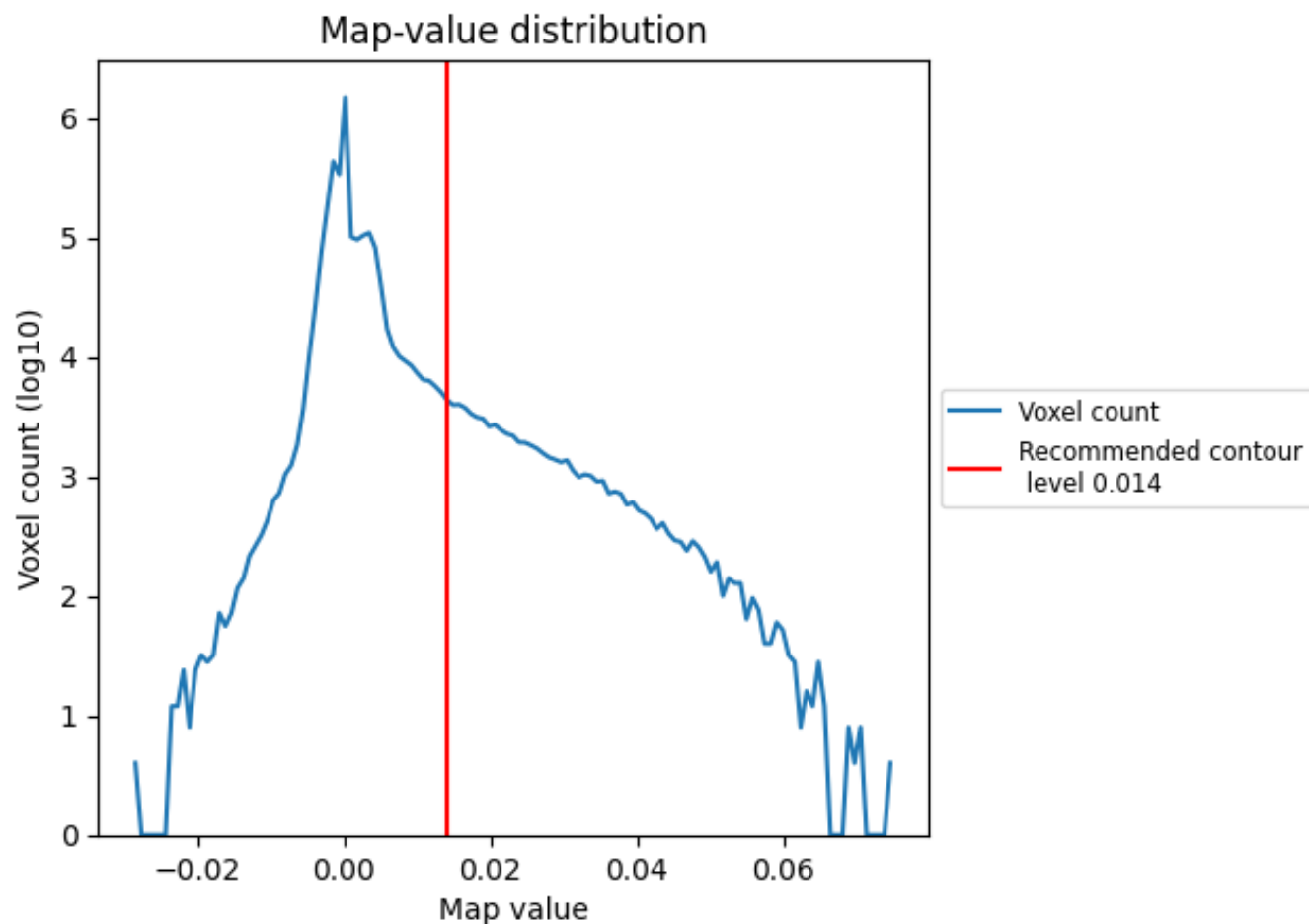


Z

7 Map analysis [i](#)

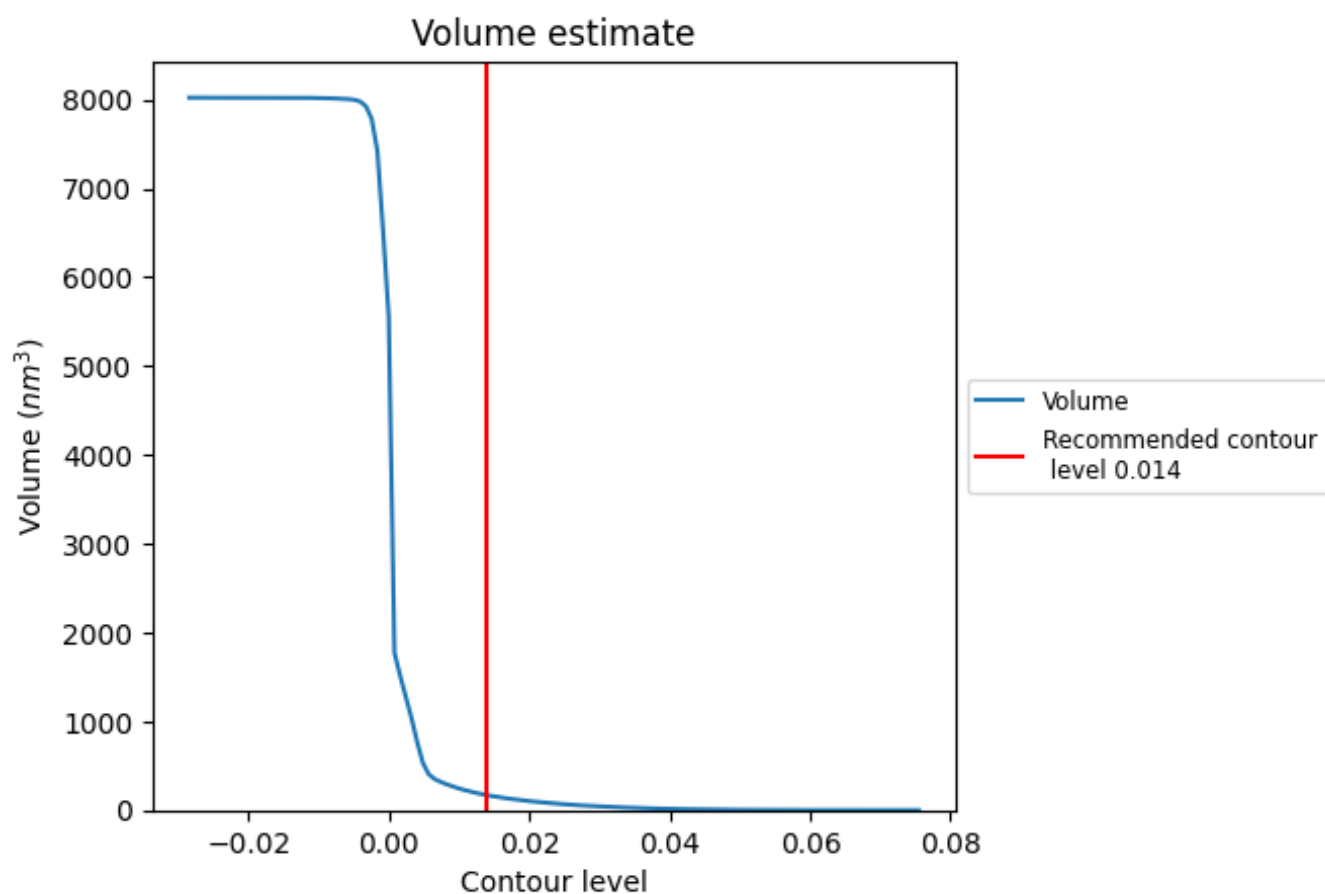
This section contains the results of statistical analysis of the map.

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.

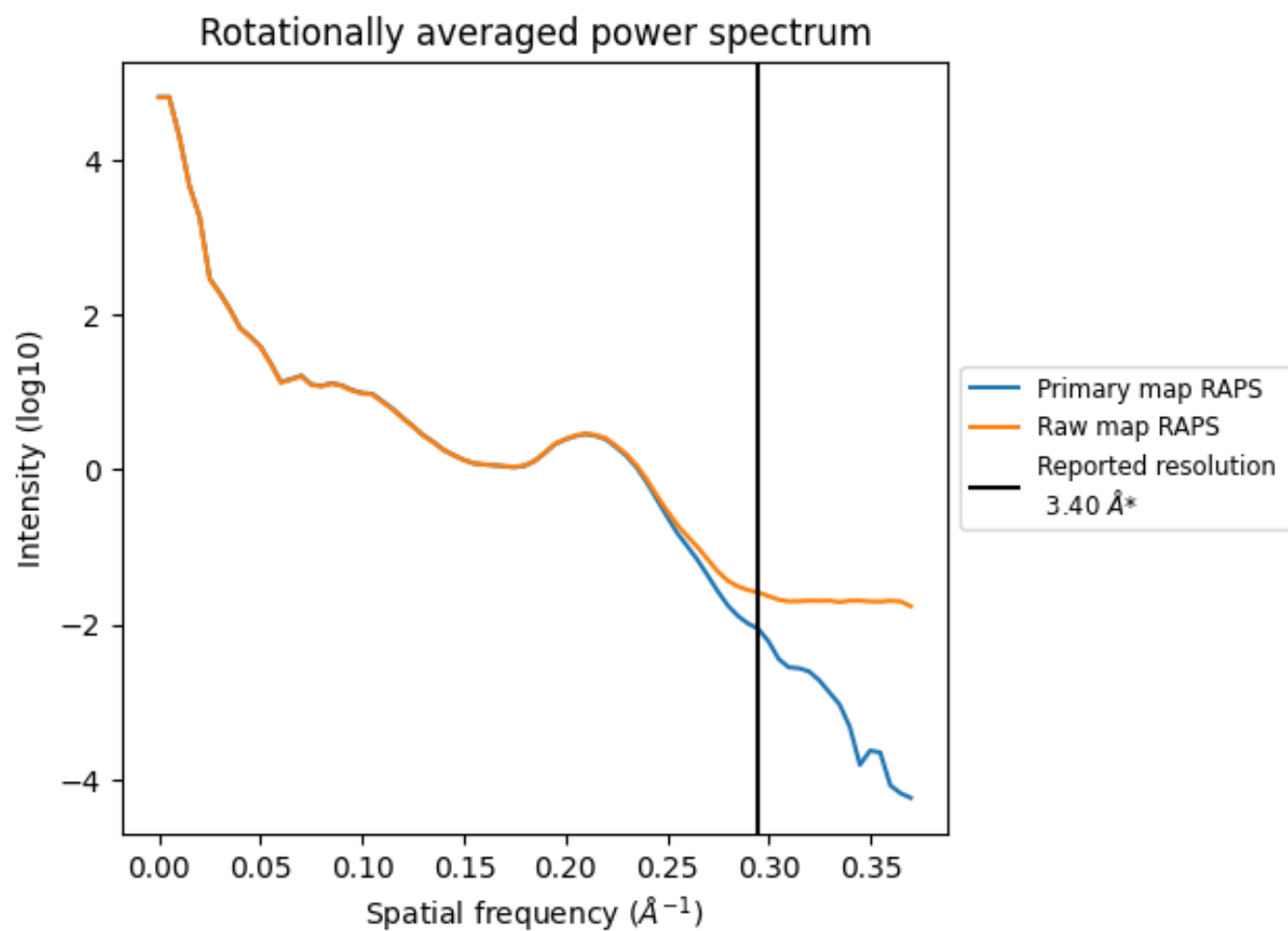
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 168 nm^3 ; this corresponds to an approximate mass of 152 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 ⓘ

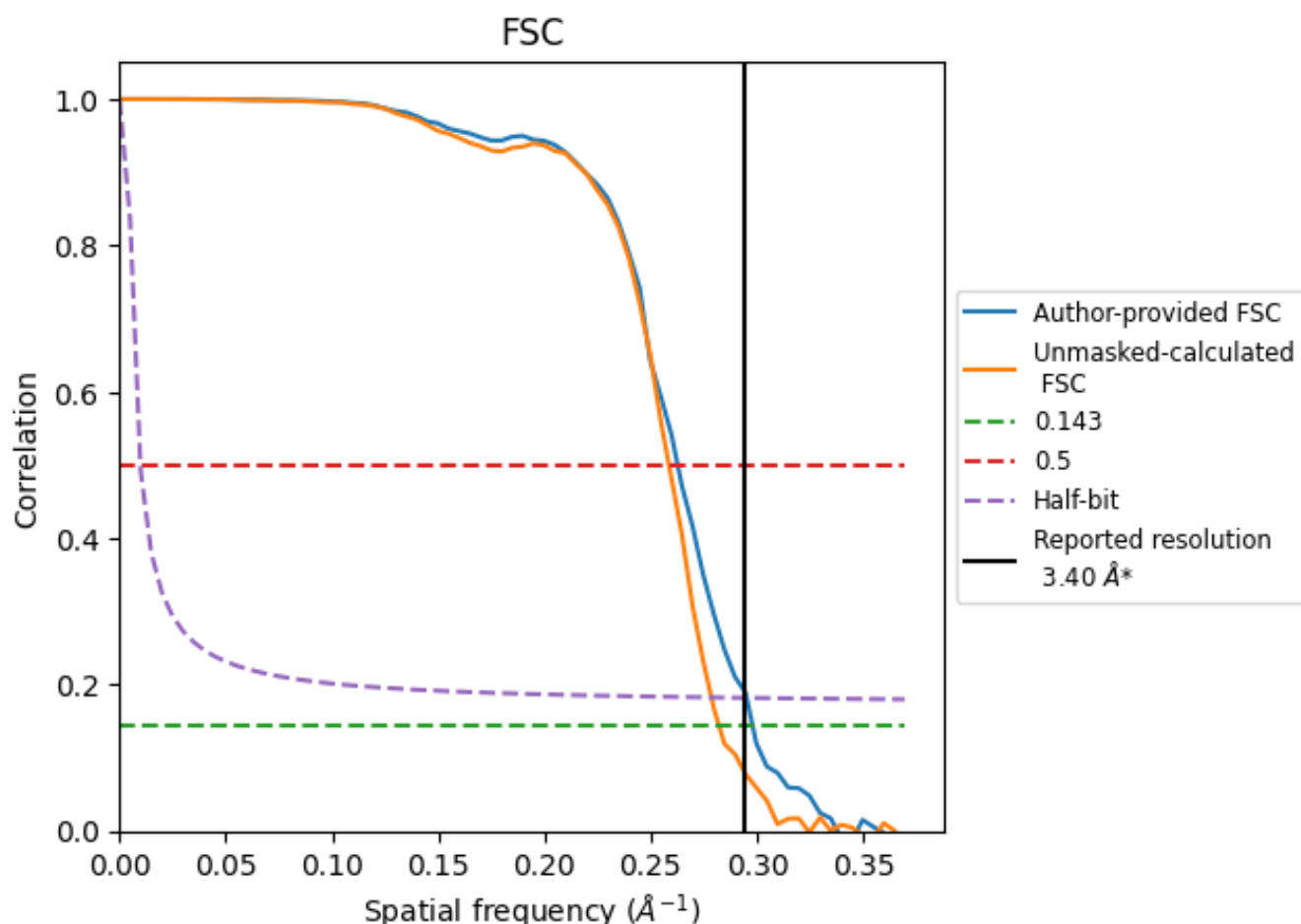


*Reported resolution corresponds to spatial frequency of 0.294 \AA^{-1}

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 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

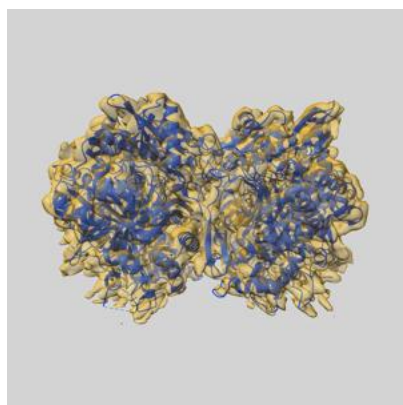
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.36	3.81	3.39
Unmasked-calculated*	3.54	3.87	3.59

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

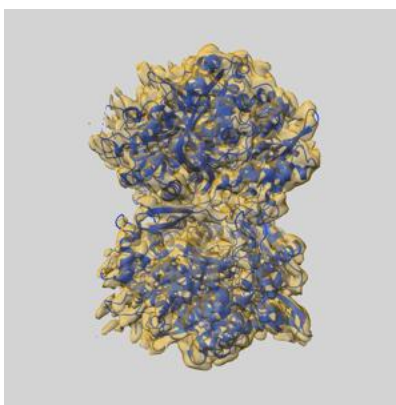
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-25391 and PDB model 7SQR. Per-residue inclusion information can be found in section [3](#) on page [6](#).

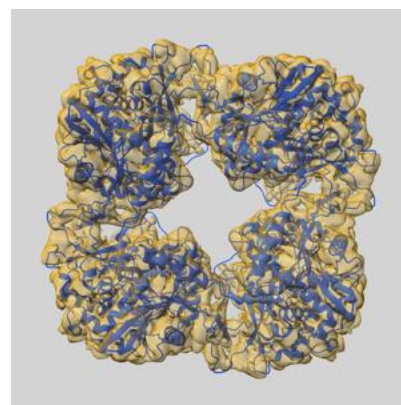
9.1 Map-model overlay [i](#)



X



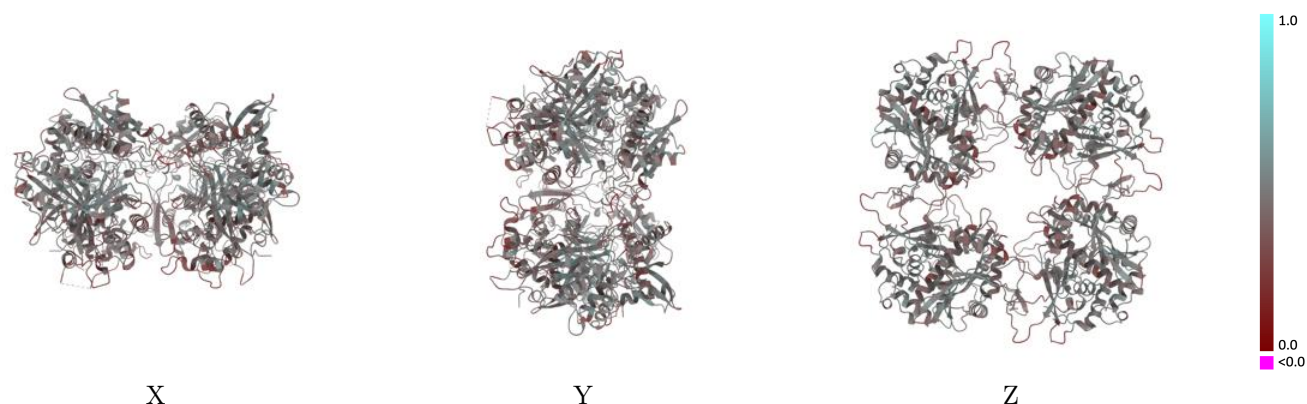
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.014 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](#)



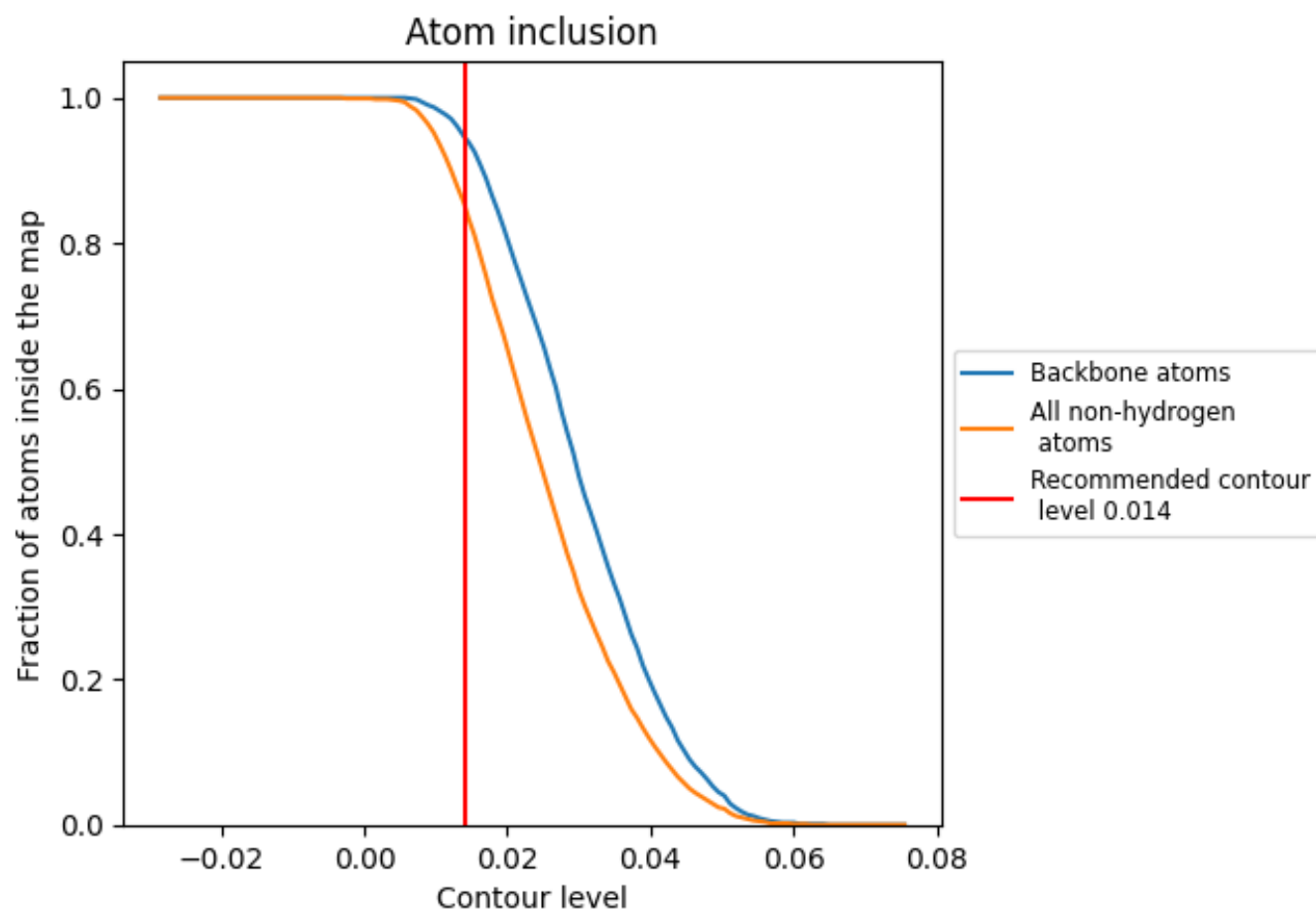
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.014).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 85% 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 (0.014) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.8540</div>	<div><div></div>0.4330</div>
A	<div><div></div>0.8550</div>	<div><div></div>0.4340</div>
B	<div><div></div>0.8010</div>	<div><div></div>0.4260</div>
C	<div><div></div>0.9140</div>	<div><div></div>0.4470</div>
D	<div><div></div>0.8550</div>	<div><div></div>0.4330</div>
E	<div><div></div>0.8010</div>	<div><div></div>0.4210</div>
F	<div><div></div>0.9140</div>	<div><div></div>0.4480</div>
G	<div><div></div>0.8550</div>	<div><div></div>0.4330</div>
H	<div><div></div>0.8010</div>	<div><div></div>0.4230</div>
I	<div><div></div>0.9140</div>	<div><div></div>0.4410</div>
J	<div><div></div>0.8550</div>	<div><div></div>0.4330</div>
K	<div><div></div>0.8010</div>	<div><div></div>0.4310</div>
L	<div><div></div>0.9140</div>	<div><div></div>0.4350</div>

1.0

0.0

<0.0