



wwPDB EM Validation Summary Report ⓘ

Nov 27, 2024 – 06:22 PM JST

PDB ID : 8XDA
EMDB ID : EMD-38271
Title : Cryo-EM structure of urea bound human urea transporter A2.
Authors : Huang, S.; Liu, L.; Sun, J.; Zhizheng, H.
Deposited on : 2023-12-10
Resolution : 3.00 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.dev113
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

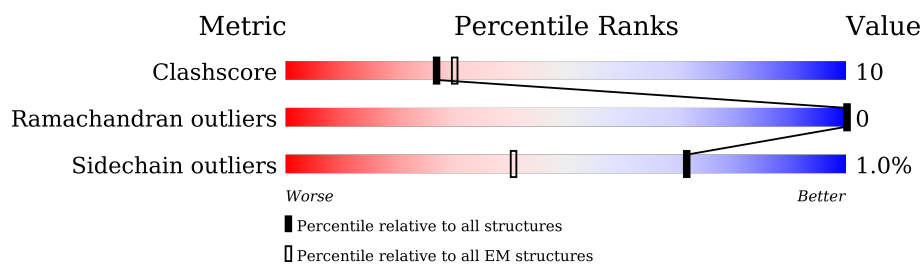
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	397	 63% 19% 17%
1	B	397	 63% 20% 17%
1	C	397	 62% 21% 17%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	URE	A	401[A]	-	X	-	-
2	URE	A	402	-	X	-	-
2	URE	B	401[A]	-	X	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	URE	B	402	-	X	-	-
2	URE	C	401[A]	-	X	-	-
2	URE	C	402	-	X	-	-

2 Entry composition [i](#)

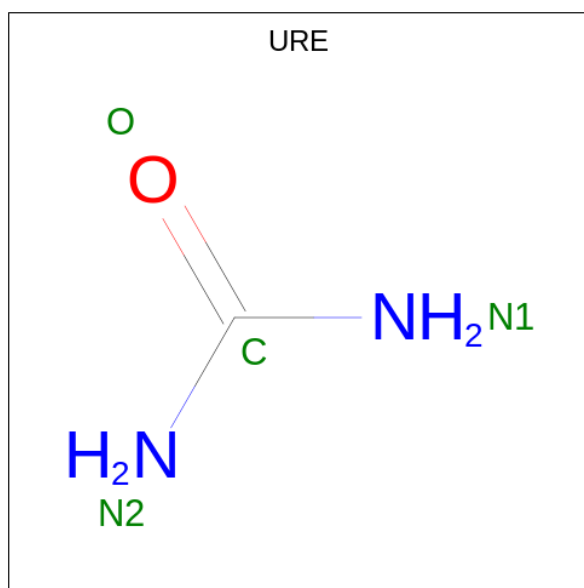
There are 3 unique types of molecules in this entry. The entry contains 7620 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Urea transporter 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	328	Total	C	N	O	S	2	0
			2530	1698	382	431	19		
1	B	328	Total	C	N	O	S	2	0
			2530	1698	382	431	19		
1	C	328	Total	C	N	O	S	2	0
			2530	1698	382	431	19		

- Molecule 2 is UREA (three-letter code: URE) (formula: CH₄N₂O).



Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total	C	N	O	1
			4	1	2	1	
2	A	1	Total	C	N	O	0
			4	1	2	1	
2	B	1	Total	C	N	O	1
			4	1	2	1	
2	B	1	Total	C	N	O	0
			4	1	2	1	

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Mol	Chain	Residues	Atoms				AltConf
2	C	1	Total	C	N	O	1
			4	1	2	1	
2	C	1	Total	C	N	O	0
			4	1	2	1	

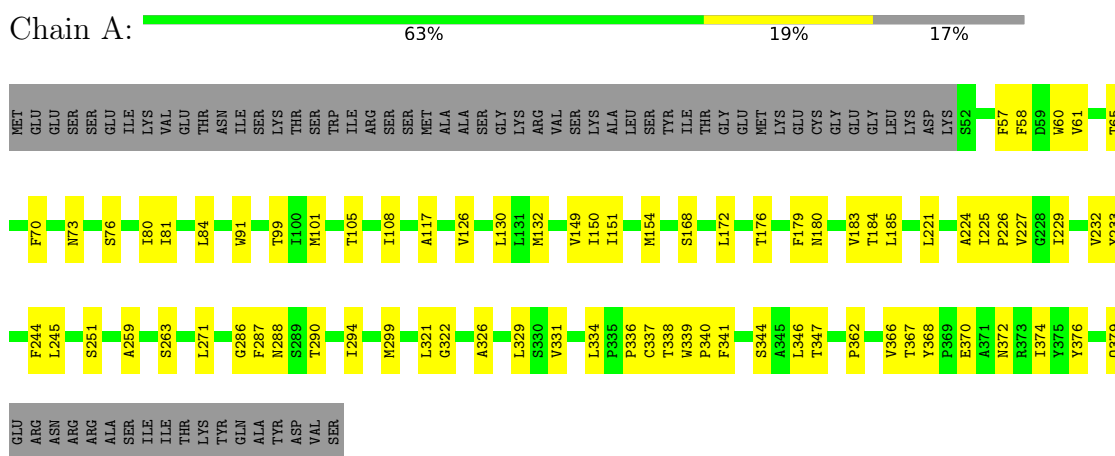
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		AltConf
3	A	2	Total	O	0
			2	2	
3	B	2	Total	O	0
			2	2	
3	C	2	Total	O	0
			2	2	

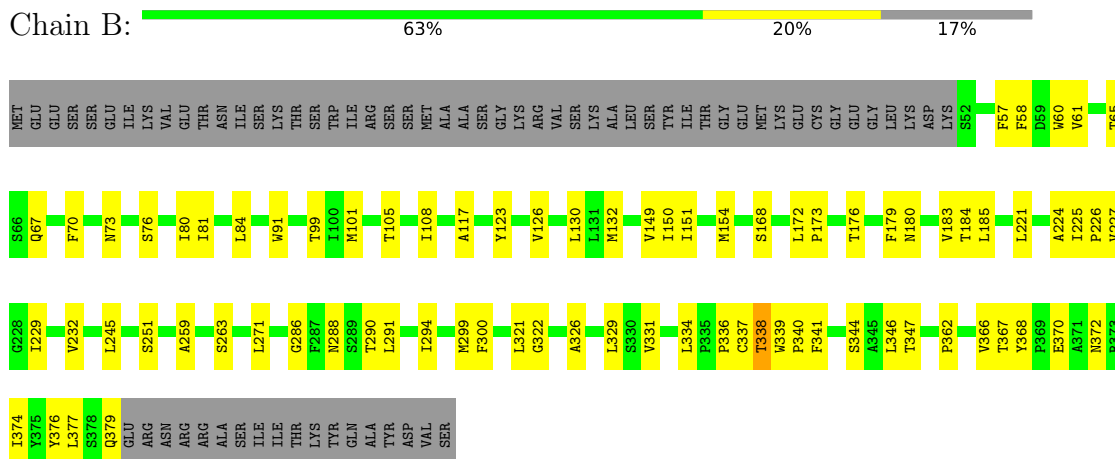
3 Residue-property plots

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: Urea transporter 2



• Molecule 1: Urea transporter 2



• Molecule 1: Urea transporter 2



T367	A224	S66	MET
Y368	I225	Q67	GLU
P369	P226	F70	GLU
E370	V227	N73	SER
A371	G228	S76	GLU
N372	I229	I80	ILE
H373	V232	I81	LYS
I374	L245	L84	VAL
Y375	S251	W91	GLU
Y376	A259	T99	THR
L377	S263	I100	SER
S378	L271	M101	TRP
Q379	G286	S102	ILE
GLU	F287	T105	ARG
ARG	N288	I108	SER
ASN	S289	A117	SER
ASN	T290	H121	ALA
ARG	L291	G122	GLY
ARG	I294	Y123	LYS
ALA	M299	V126	ARG
SER	F300	L127	VAL
ILE	C314	V128	SER
ILE	L321	G129	LYS
THR	G322	L130	TYR
THR	A326	I131	ILE
LYS	L329	M132	THR
LYS	S330	V149	GLY
GLN	V331	I151	GLU
ALA	L334	M154	MET
ALA	P335	S168	LYS
TYR	P336	L172	GLY
ASP	C337	P173	GLY
VAL	T338	W339	LEU
SER	P340	F341	LYS
	S344	T176	ASP
	A345	F179	LYS
	L346	N180	S52
	T347	V183	F57
	P362	T184	F58
	V366	L185	D59
		L221	W60
			V61
			T65

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	139996	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	7.297	Depositor
Minimum map value	-5.272	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.169	Depositor
Recommended contour level	1	Depositor
Map size (Å)	264.96, 264.96, 264.96	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.91999996, 0.91999996, 0.91999996	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: URE

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	0.39	0/2614	0.49	0/3590
1	B	0.39	0/2614	0.49	0/3590
1	C	0.39	0/2614	0.49	0/3590
All	All	0.39	0/7842	0.49	0/10770

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	2530	0	2564	50	0
1	B	2530	0	2564	51	0
1	C	2530	0	2564	54	0
2	A	8	0	8	0	0
2	B	8	0	8	0	0
2	C	8	0	8	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
All	All	7620	0	7716	149	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 10.

The worst 5 of 149 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:322:GLY:HA2	1:A:340:PRO:HG3	1.73	0.71
1:C:322:GLY:HA2	1:C:340:PRO:HG3	1.73	0.70
1:B:322:GLY:HA2	1:B:340:PRO:HG3	1.73	0.69
1:A:132:MET:HE3	1:A:149:VAL:HA	1.78	0.66
1:A:180:ASN:ND2	1:A:337:CYS:O	2.29	0.65

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	328/397 (83%)	318 (97%)	10 (3%)	0	100	100
1	B	328/397 (83%)	318 (97%)	10 (3%)	0	100	100
1	C	328/397 (83%)	318 (97%)	10 (3%)	0	100	100
All	All	984/1191 (83%)	954 (97%)	30 (3%)	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	273/332 (82%)	271 (99%)	2 (1%)	81	91
1	B	273/332 (82%)	270 (99%)	3 (1%)	70	87
1	C	273/332 (82%)	270 (99%)	3 (1%)	70	87
All	All	819/996 (82%)	811 (99%)	8 (1%)	71	88

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	338	THR
1	C	168	SER
1	B	338	THR
1	B	168	SER
1	C	73	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	ASN
1	B	72	ASN
1	C	72	ASN

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

6 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	URE	B	402	-	3,3,3	3.20	3 (100%)	3,3,3	3.32	2 (66%)
2	URE	B	401[A]	-	3,3,3	3.48	3 (100%)	3,3,3	1.47	1 (33%)
2	URE	C	401[A]	-	3,3,3	3.47	3 (100%)	3,3,3	1.47	1 (33%)
2	URE	A	401[A]	-	3,3,3	3.49	3 (100%)	3,3,3	1.46	1 (33%)
2	URE	A	402	-	3,3,3	3.21	3 (100%)	3,3,3	3.32	2 (66%)
2	URE	C	402	-	3,3,3	3.20	3 (100%)	3,3,3	3.33	2 (66%)

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	401[A]	URE	C-N1	4.06	1.45	1.34
2	A	401[A]	URE	C-N1	4.05	1.45	1.34
2	B	401[A]	URE	C-N1	4.05	1.45	1.34
2	A	402	URE	O-C	-3.86	1.11	1.26
2	C	402	URE	O-C	-3.85	1.11	1.26

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	402	URE	N2-C-N1	4.94	127.07	117.82
2	B	402	URE	N2-C-N1	4.93	127.05	117.82
2	A	402	URE	N2-C-N1	4.92	127.04	117.82
2	C	402	URE	O-C-N2	-2.64	115.06	121.02
2	B	402	URE	O-C-N2	-2.62	115.11	121.02

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

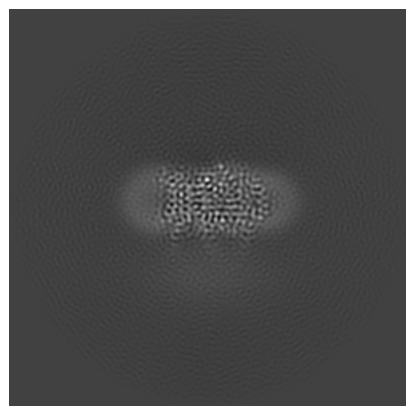
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38271. These allow visual inspection of the internal detail of the map and identification of artifacts.

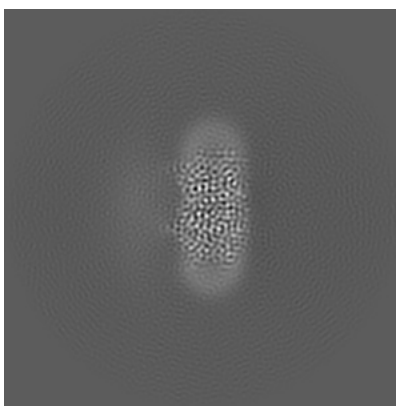
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

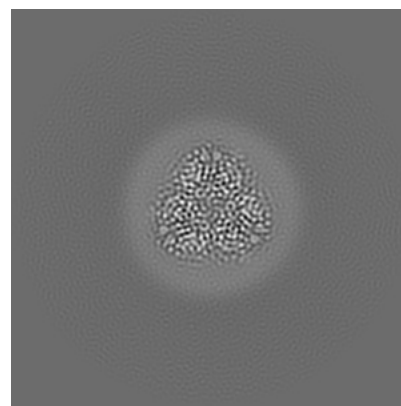
6.1.1 Primary map



X

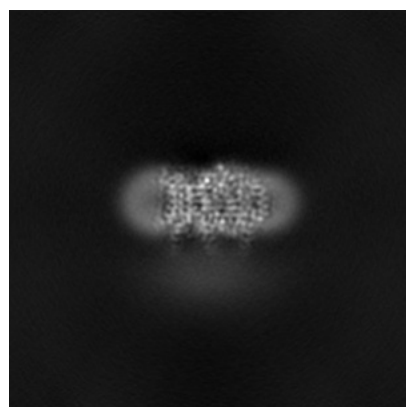


Y

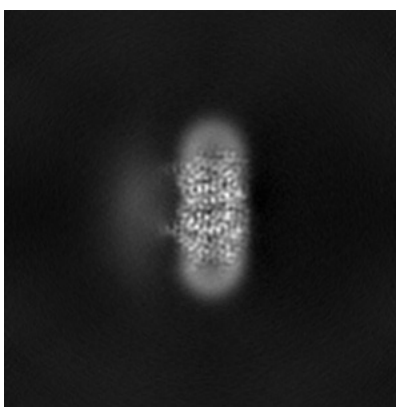


Z

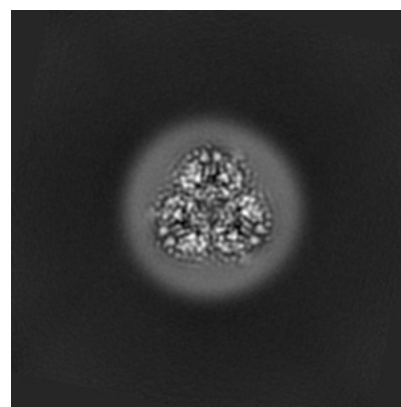
6.1.2 Raw map



X



Y

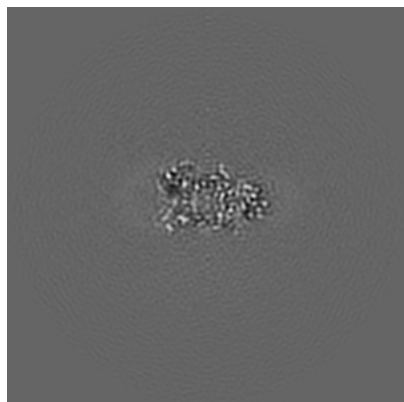


Z

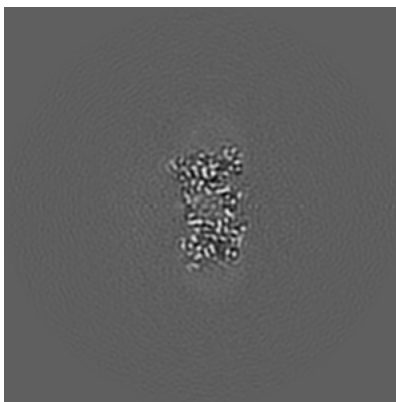
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

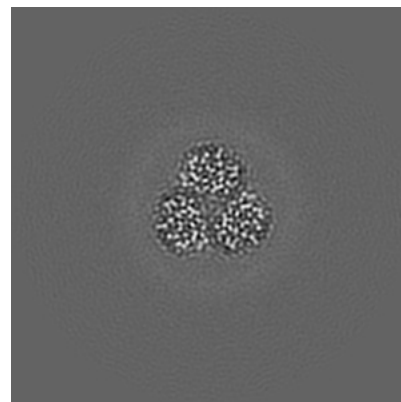
6.2.1 Primary map



X Index: 144

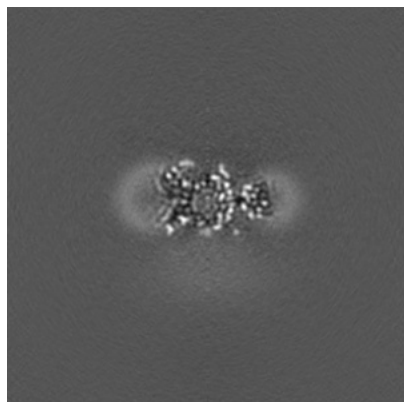


Y Index: 144

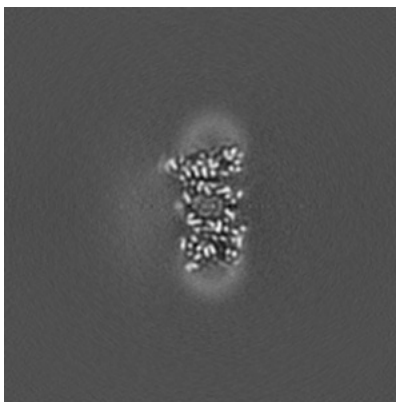


Z Index: 144

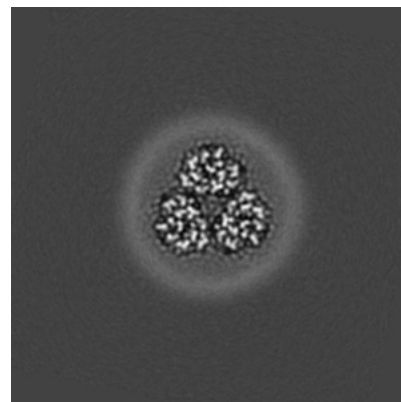
6.2.2 Raw map



X Index: 144



Y Index: 144

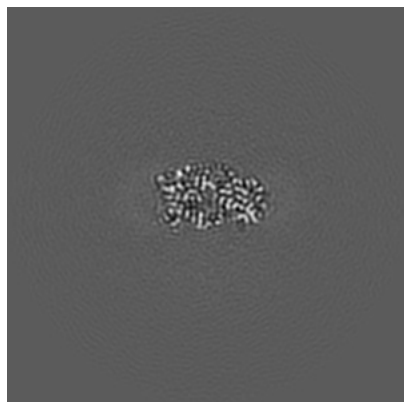


Z Index: 144

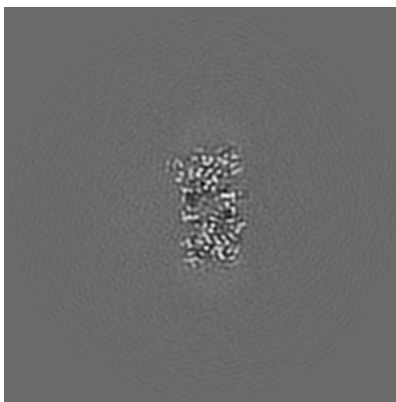
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

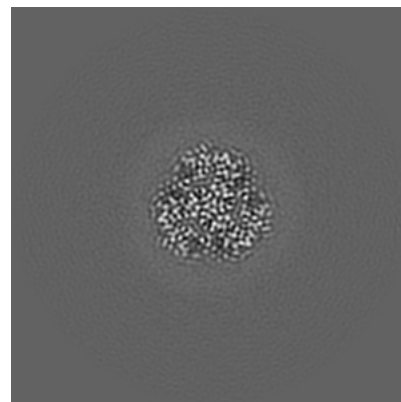
6.3.1 Primary map



X Index: 151

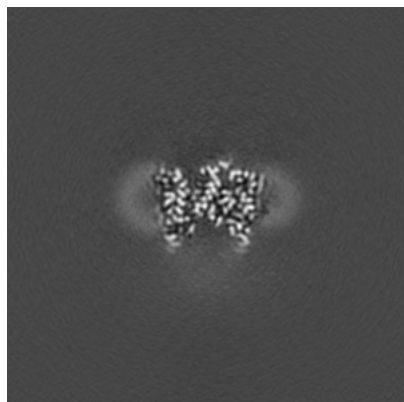


Y Index: 141

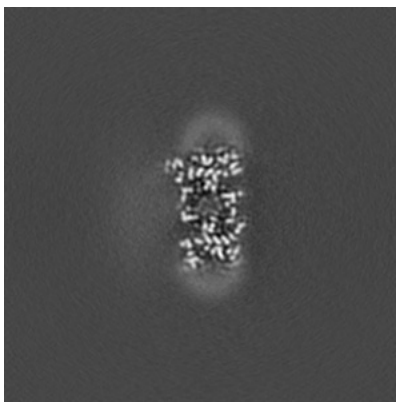


Z Index: 160

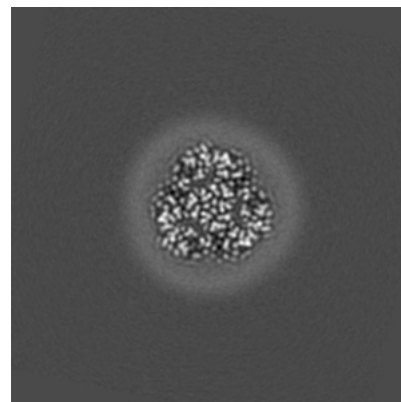
6.3.2 Raw map



X Index: 129



Y Index: 141

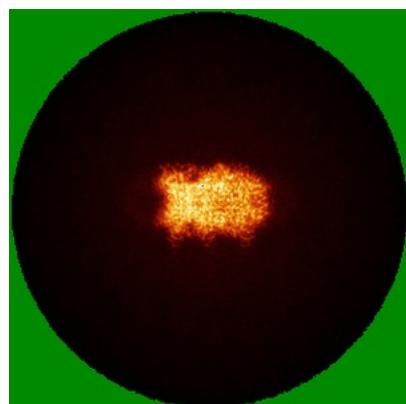


Z Index: 160

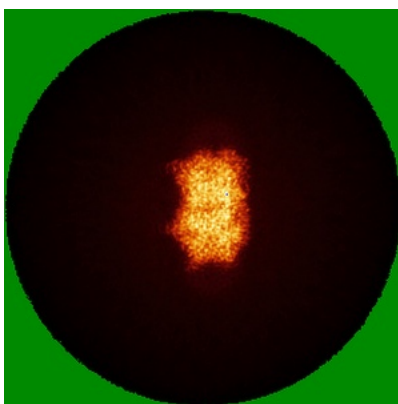
The images above show the largest variance slices of the map in three orthogonal directions.

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

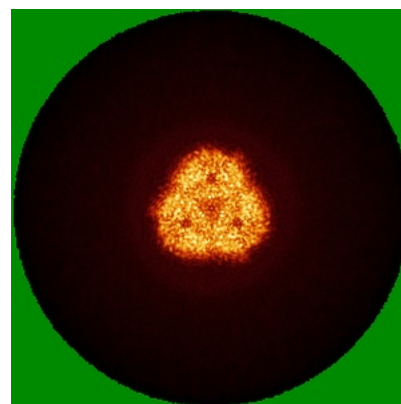
6.4.1 Primary map



X

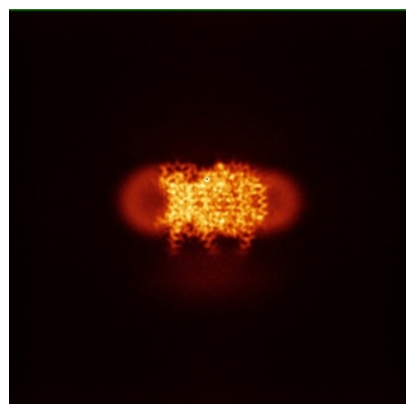


Y

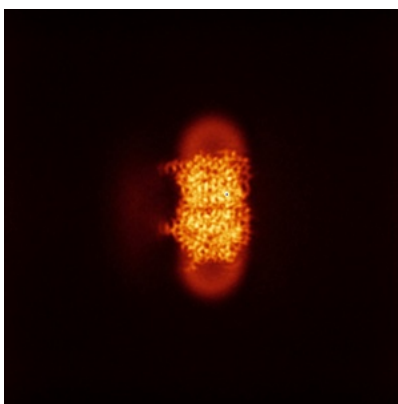


Z

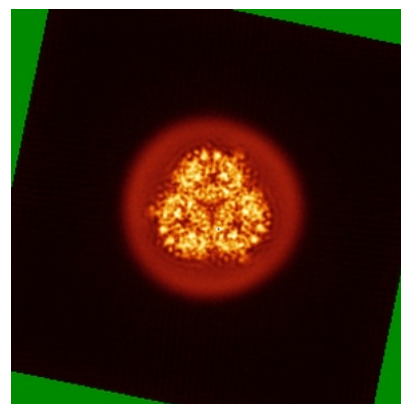
6.4.2 Raw map



X



Y

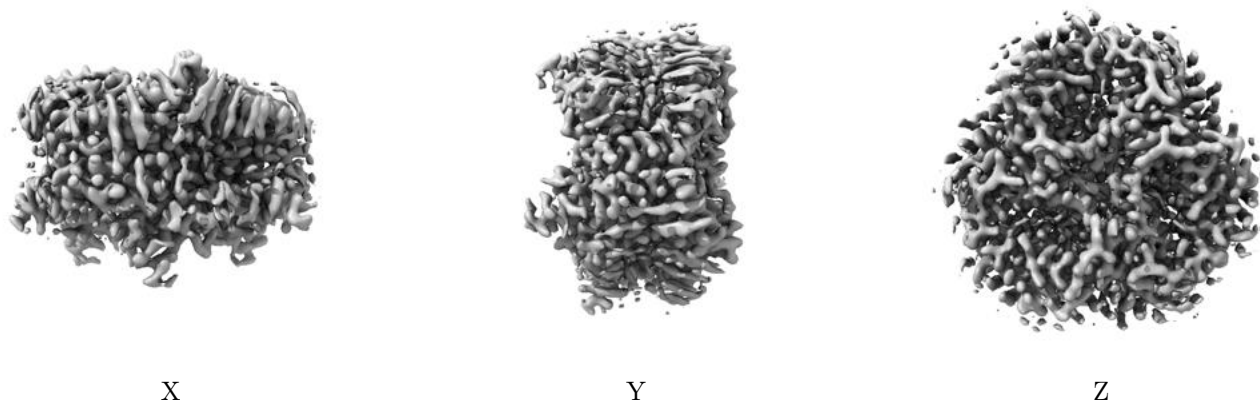


Z

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.

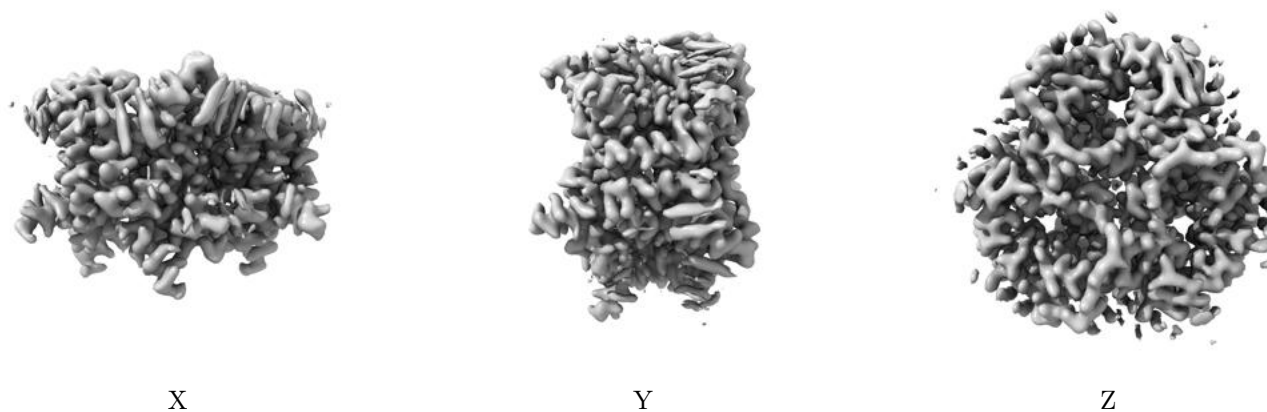
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.0. 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



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

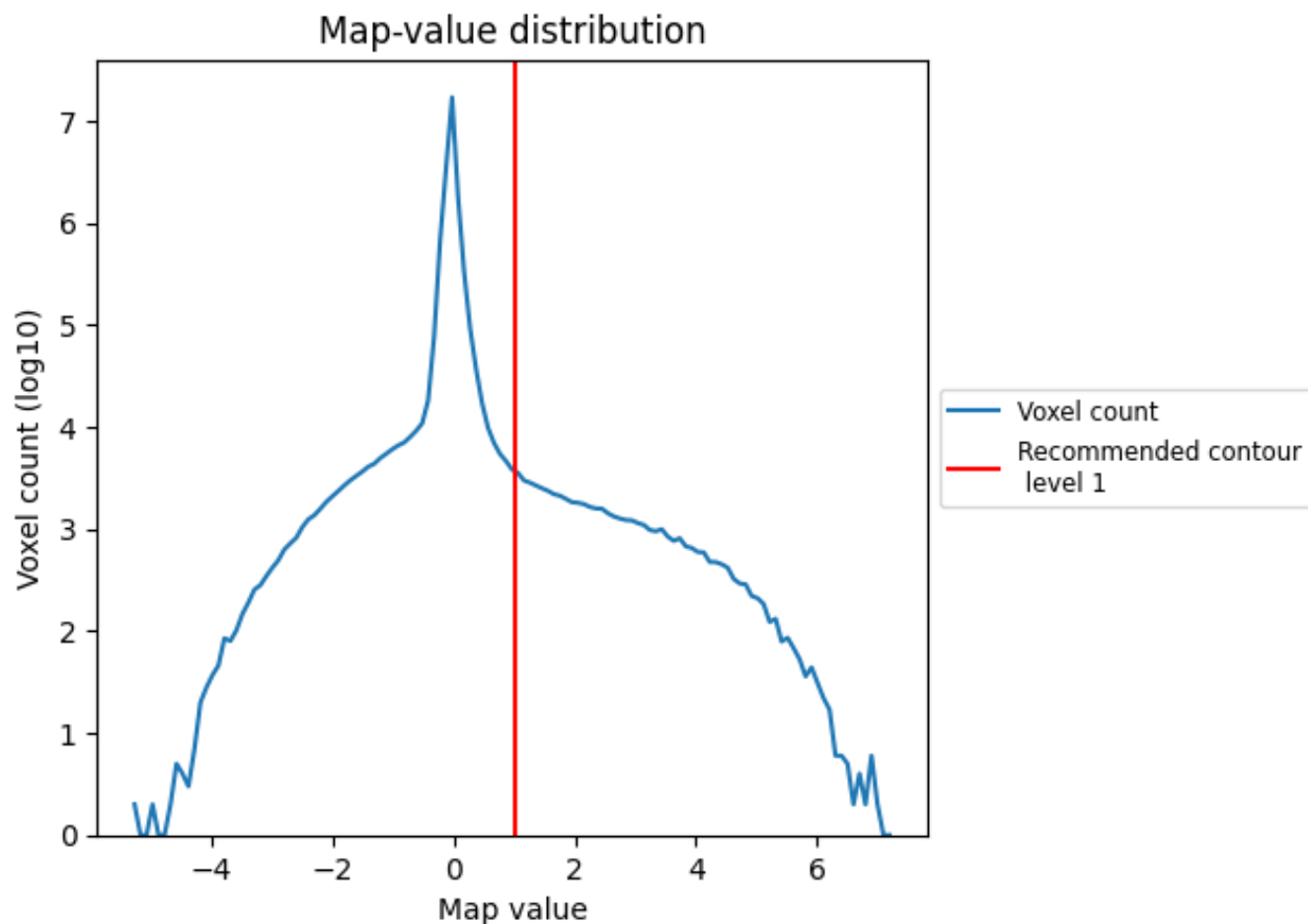
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

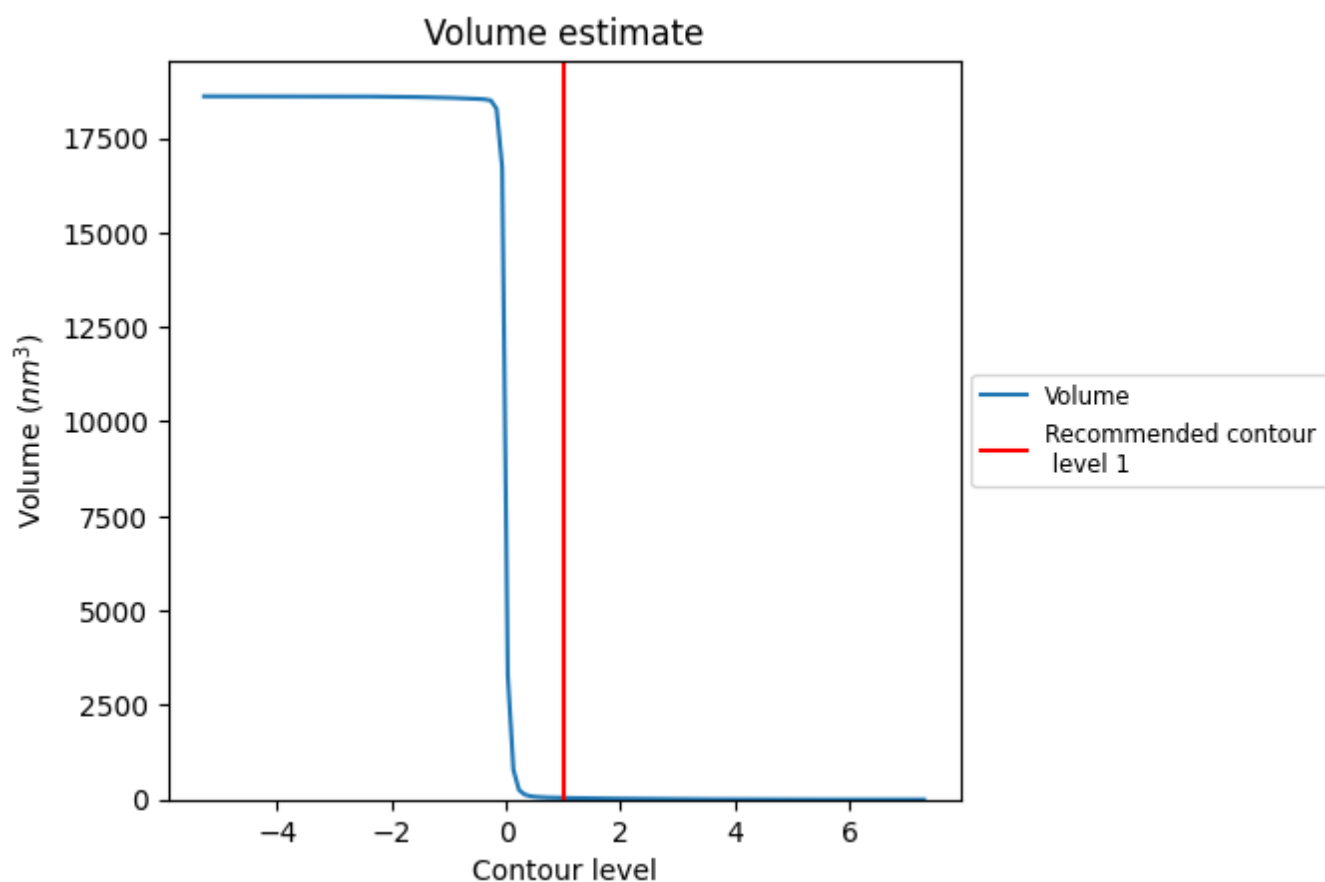
This section contains the results of statistical analysis of the map.

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.

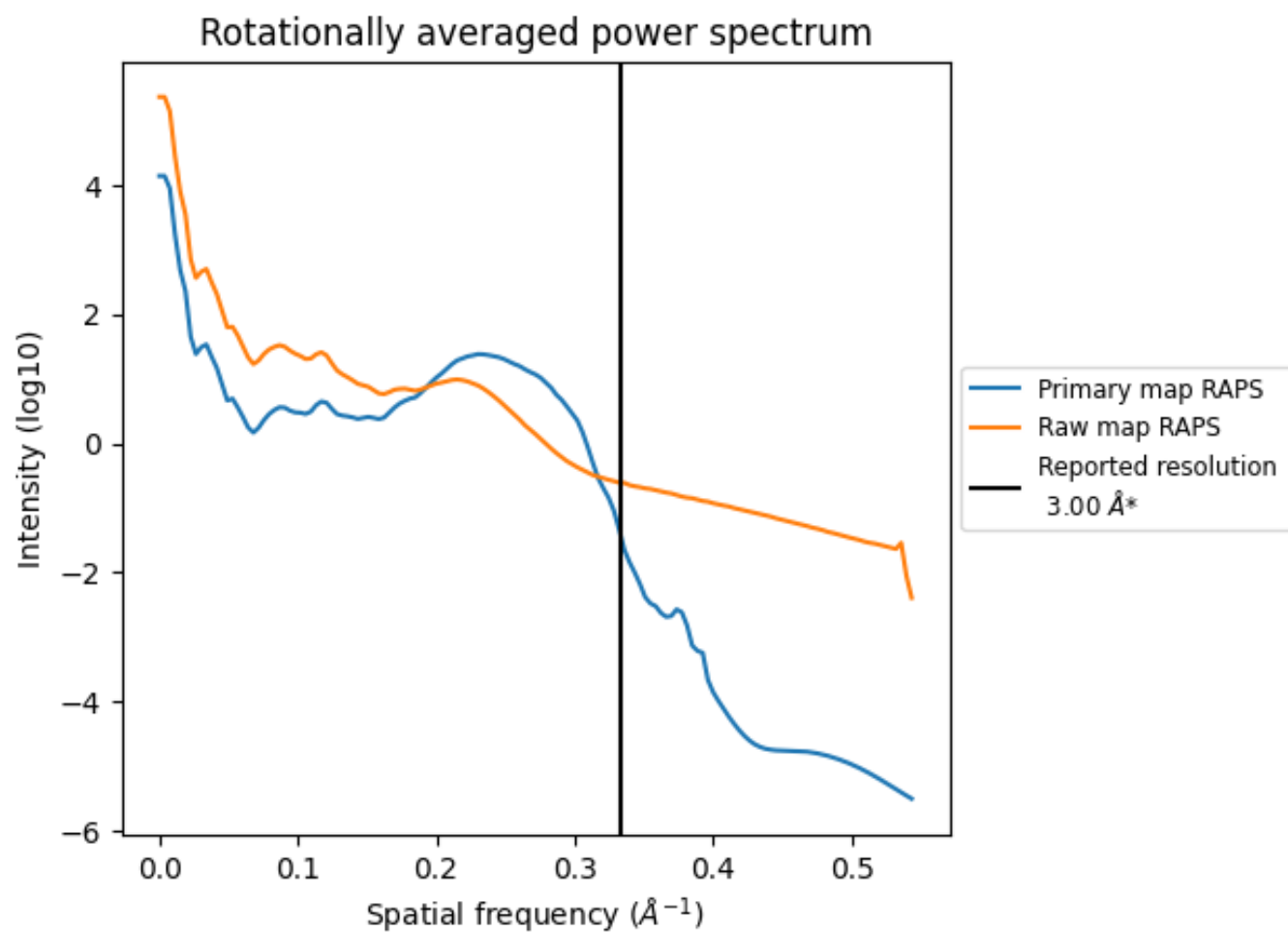
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 44 nm³; this corresponds to an approximate mass of 40 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 ⓘ

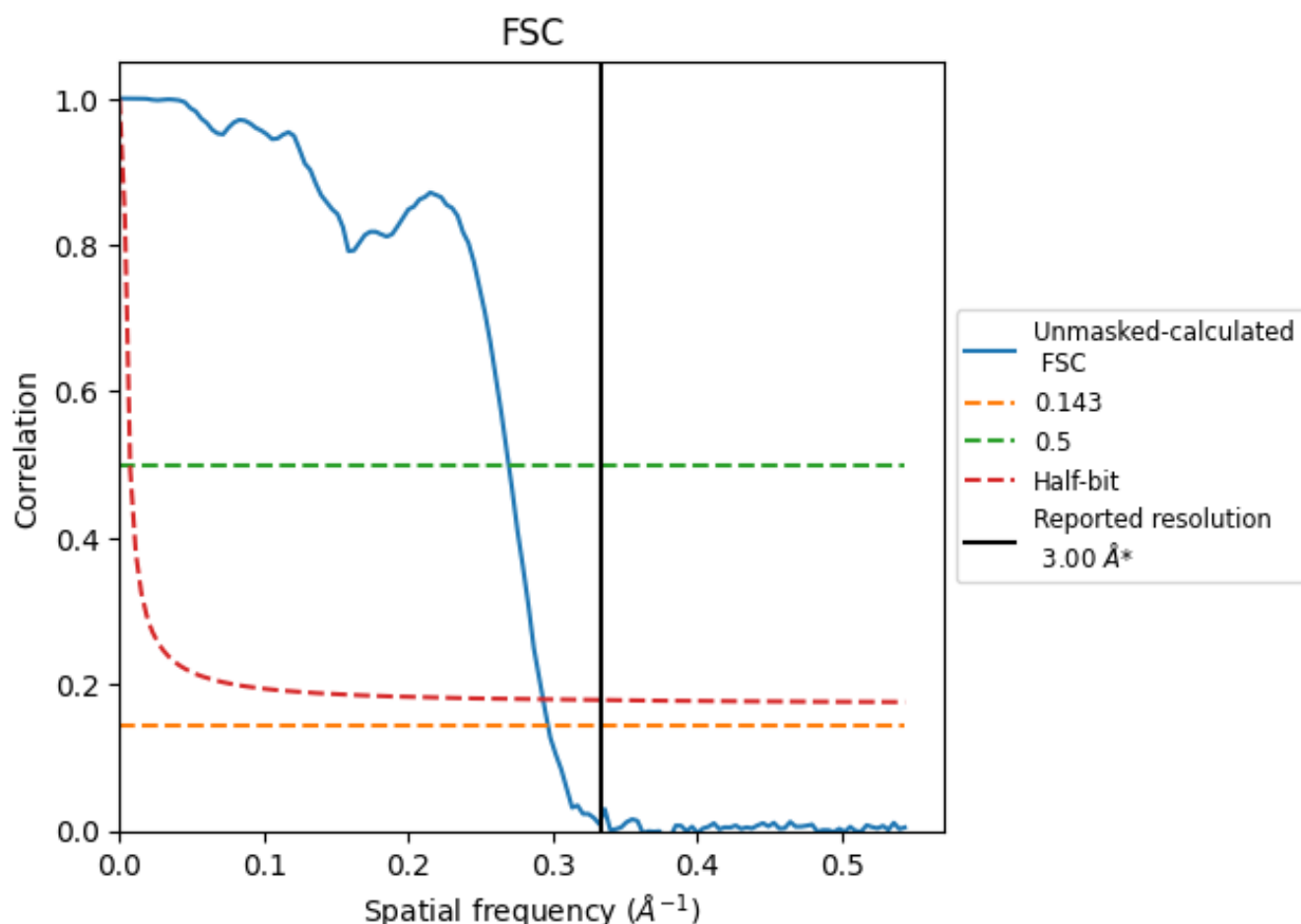


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 \AA^{-1}

8.2 Resolution estimates [i](#)

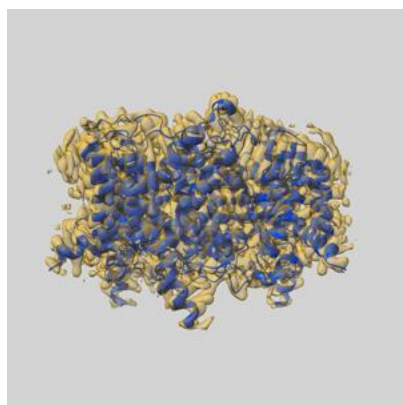
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.37	3.71	3.41

*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 3.37 differs from the reported value 3.0 by more than 10 %

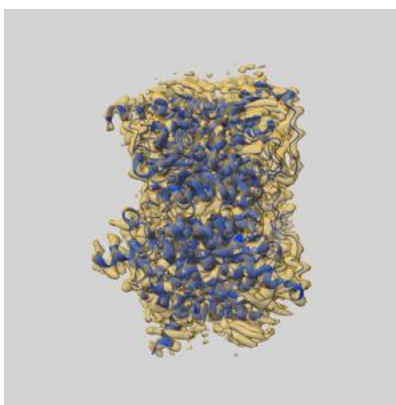
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-38271 and PDB model 8XDA. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

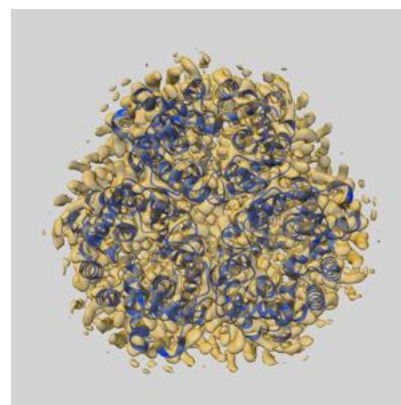
9.1 Map-model overlay [i](#)



X



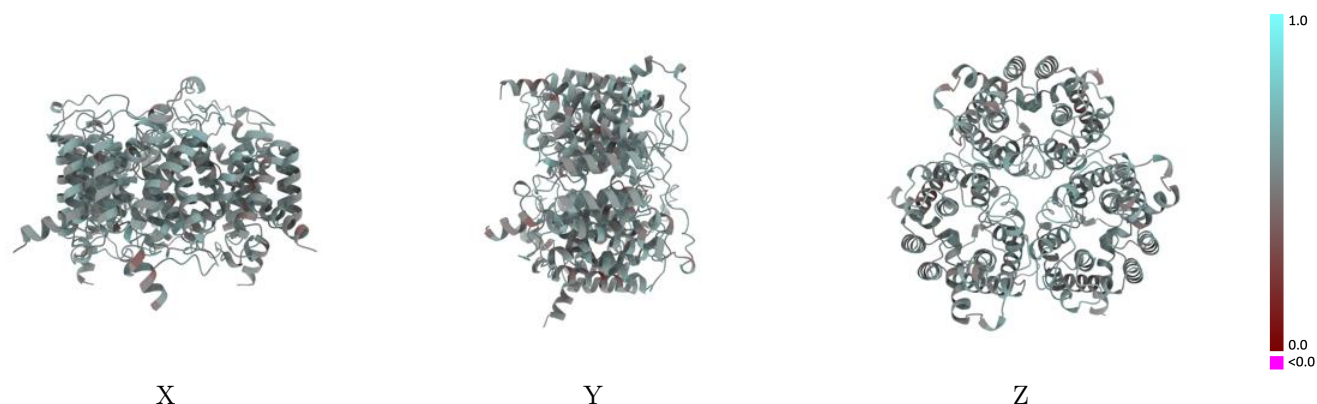
Y



Z

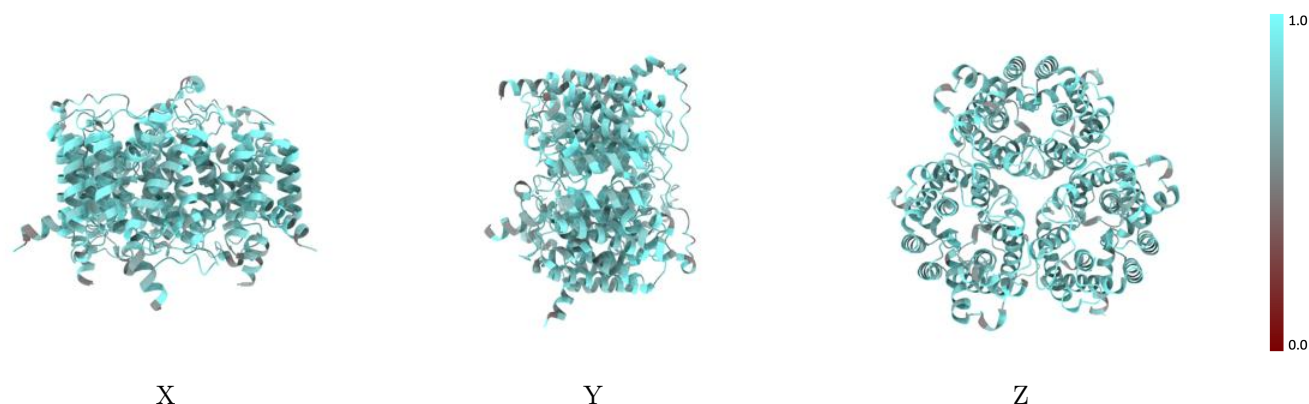
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



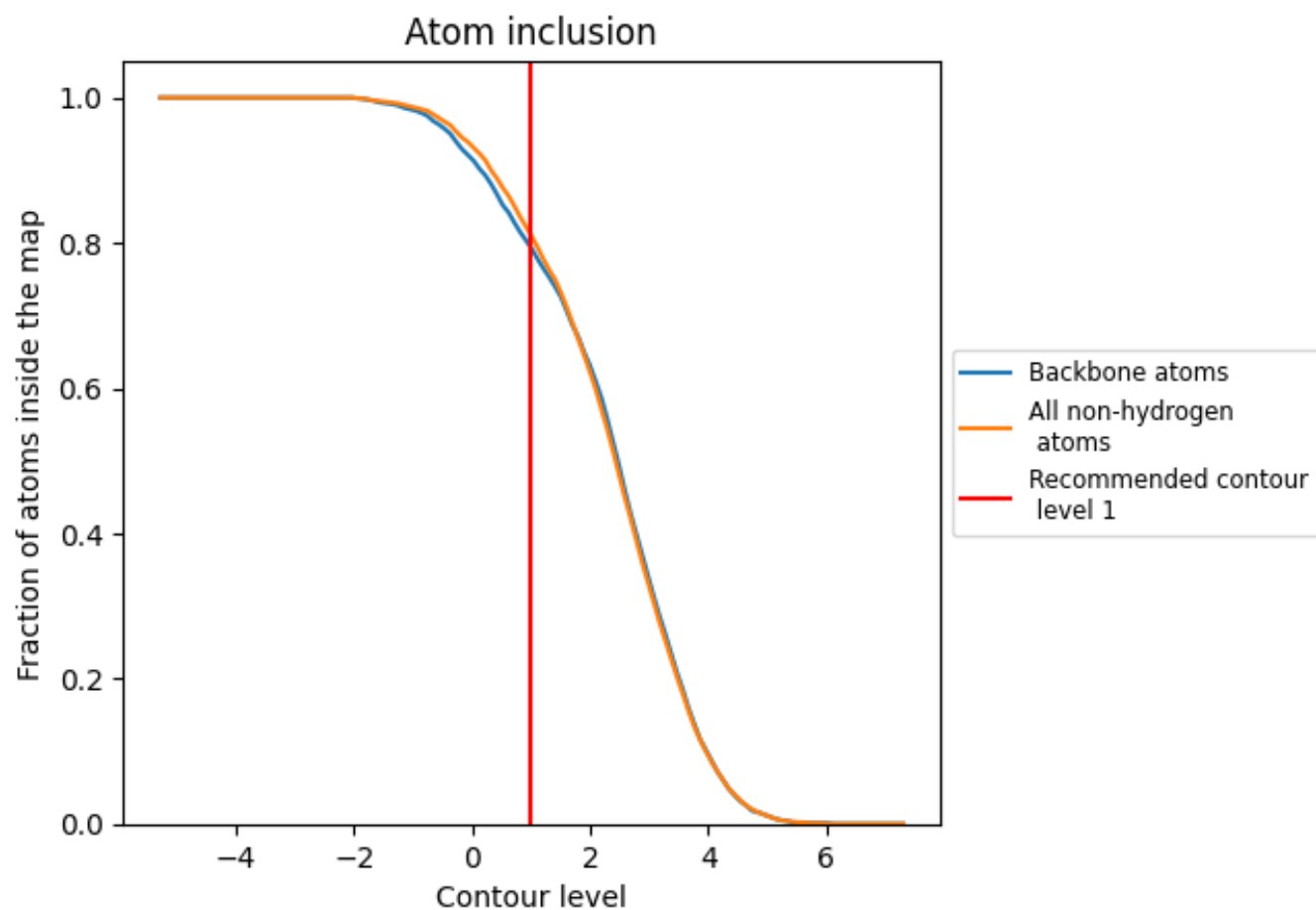
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 81% 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 (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.8110	<div><div></div></div> 0.5400
A	<div><div></div></div> 0.8060	<div><div></div></div> 0.5370
B	<div><div></div></div> 0.8160	<div><div></div></div> 0.5450
C	<div><div></div></div> 0.8090	<div><div></div></div> 0.5360

