



wwPDB EM Validation Summary Report ⓘ

Sep 24, 2026 – 02:23 PM EDT

PDB ID : 38RI / pdb_000038ri
EMDB ID : EMD-79080
Title : Structure of the DAB1 Complex in State B
Authors : Phillips, N.R.; Oltrogge, L.M.; Remis, J.P.; Savage, D.F.
Deposited on : 2026-09-15
Resolution : 2.29 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.dev133
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) : 2.50

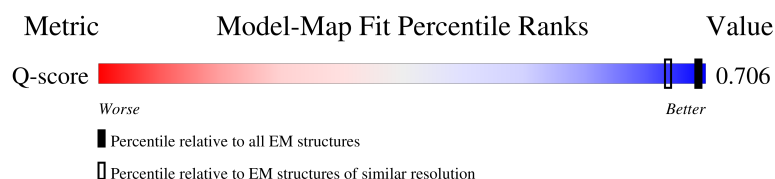
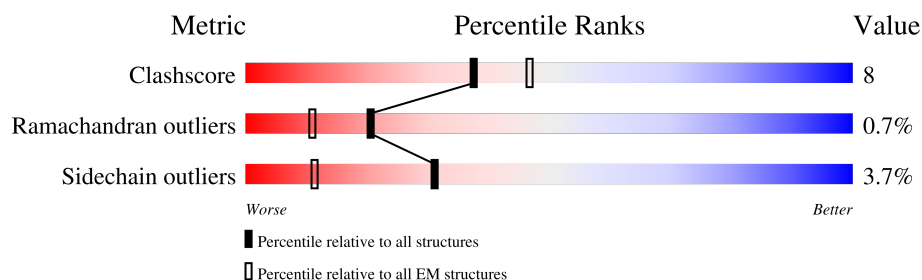
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.29 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	3699 (1.79 - 2.79)

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	1031	 69% 18% 10%
2	B	773	 69% 23% 5%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 28005 atoms, of which 13809 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 inorganic carbon transporter subunit DabA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	932	Total	C	H	N	O	S	1	0
			15264	4961	7637	1280	1363	23		

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1000	GLY	-	expression tag	UNP D3SP01
A	1001	GLY	-	expression tag	UNP D3SP01
A	1002	SER	-	expression tag	UNP D3SP01
A	1003	GLY	-	expression tag	UNP D3SP01
A	1004	TRP	-	expression tag	UNP D3SP01
A	1005	SER	-	expression tag	UNP D3SP01
A	1006	HIS	-	expression tag	UNP D3SP01
A	1007	PRO	-	expression tag	UNP D3SP01
A	1008	GLN	-	expression tag	UNP D3SP01
A	1009	PHE	-	expression tag	UNP D3SP01
A	1010	GLU	-	expression tag	UNP D3SP01
A	1011	LYS	-	expression tag	UNP D3SP01
A	1012	GLY	-	expression tag	UNP D3SP01
A	1013	GLY	-	expression tag	UNP D3SP01
A	1014	GLY	-	expression tag	UNP D3SP01
A	1015	SER	-	expression tag	UNP D3SP01
A	1016	GLY	-	expression tag	UNP D3SP01
A	1017	GLY	-	expression tag	UNP D3SP01
A	1018	GLY	-	expression tag	UNP D3SP01
A	1019	SER	-	expression tag	UNP D3SP01
A	1020	GLY	-	expression tag	UNP D3SP01
A	1021	GLY	-	expression tag	UNP D3SP01
A	1022	SER	-	expression tag	UNP D3SP01
A	1023	ALA	-	expression tag	UNP D3SP01
A	1024	TRP	-	expression tag	UNP D3SP01
A	1025	SER	-	expression tag	UNP D3SP01
A	1026	HIS	-	expression tag	UNP D3SP01
A	1027	PRO	-	expression tag	UNP D3SP01

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1028	GLN	-	expression tag	UNP D3SP01
A	1029	PHE	-	expression tag	UNP D3SP01
A	1030	GLU	-	expression tag	UNP D3SP01
A	1031	LYS	-	expression tag	UNP D3SP01

- Molecule 2 is a protein called NADH/Ubiquinone/plastoquinone (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	746	Total	C	H	N	O	S	
			12125	4009	6172	921	996	27	1 0

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	532	ALA	SER	conflict	UNP D3SP02
B	760	SER	-	expression tag	UNP D3SP02
B	761	GLY	-	expression tag	UNP D3SP02
B	762	SER	-	expression tag	UNP D3SP02
B	763	SER	-	expression tag	UNP D3SP02
B	764	ALA	-	expression tag	UNP D3SP02
B	765	HIS	-	expression tag	UNP D3SP02
B	766	HIS	-	expression tag	UNP D3SP02
B	767	HIS	-	expression tag	UNP D3SP02
B	768	HIS	-	expression tag	UNP D3SP02
B	769	HIS	-	expression tag	UNP D3SP02
B	770	HIS	-	expression tag	UNP D3SP02
B	771	HIS	-	expression tag	UNP D3SP02
B	772	HIS	-	expression tag	UNP D3SP02
B	773	HIS	-	expression tag	UNP D3SP02

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total	Zn	
			1	1	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		AltConf
4	A	394	Total	O	
			394	394	0

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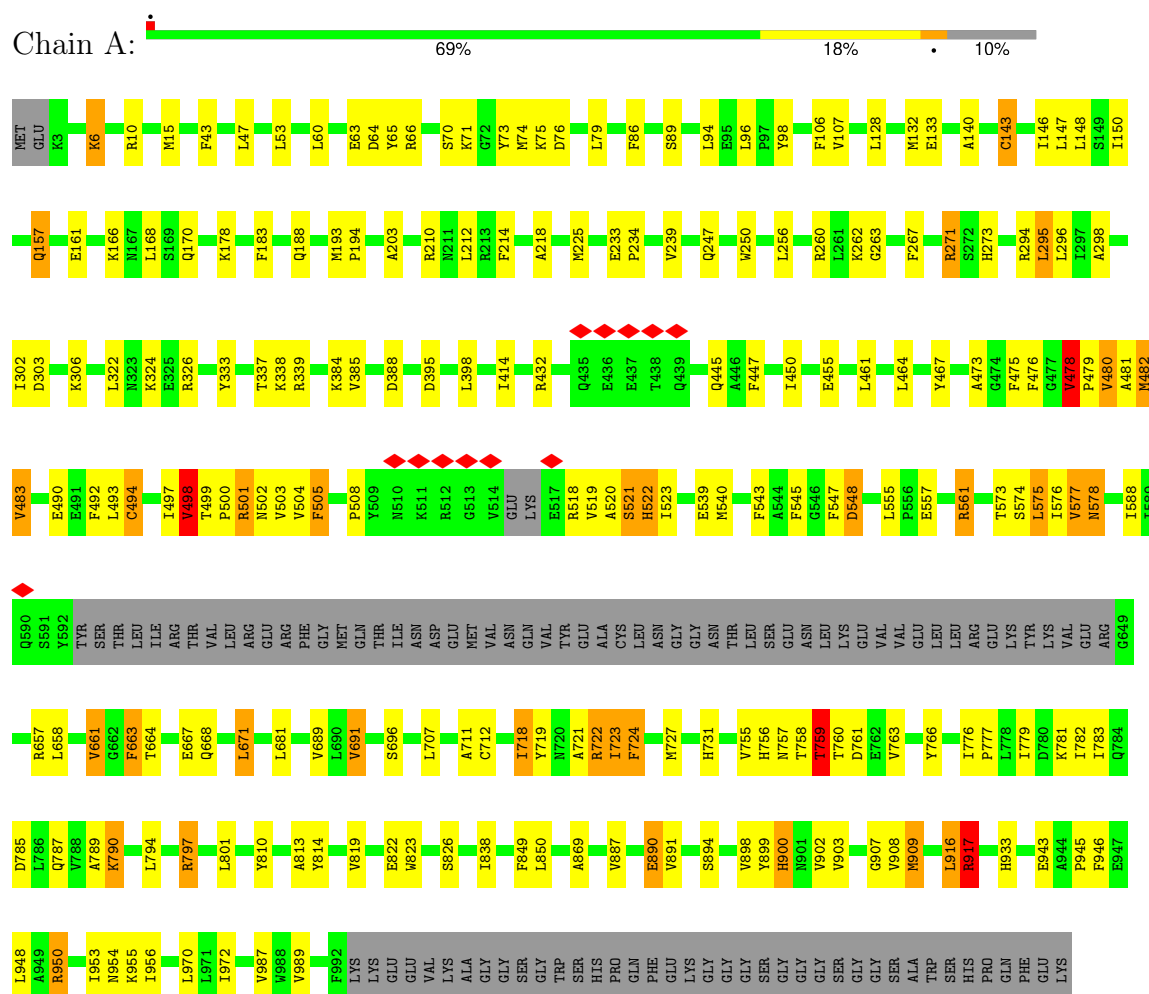
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Mol	Chain	Residues	Atoms		AltConf
4	B	221	Total	O	0
			221	221	

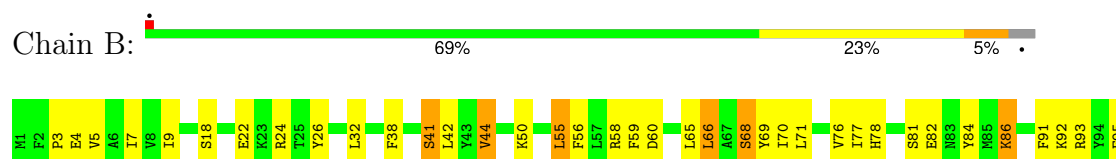
3 Residue-property plots

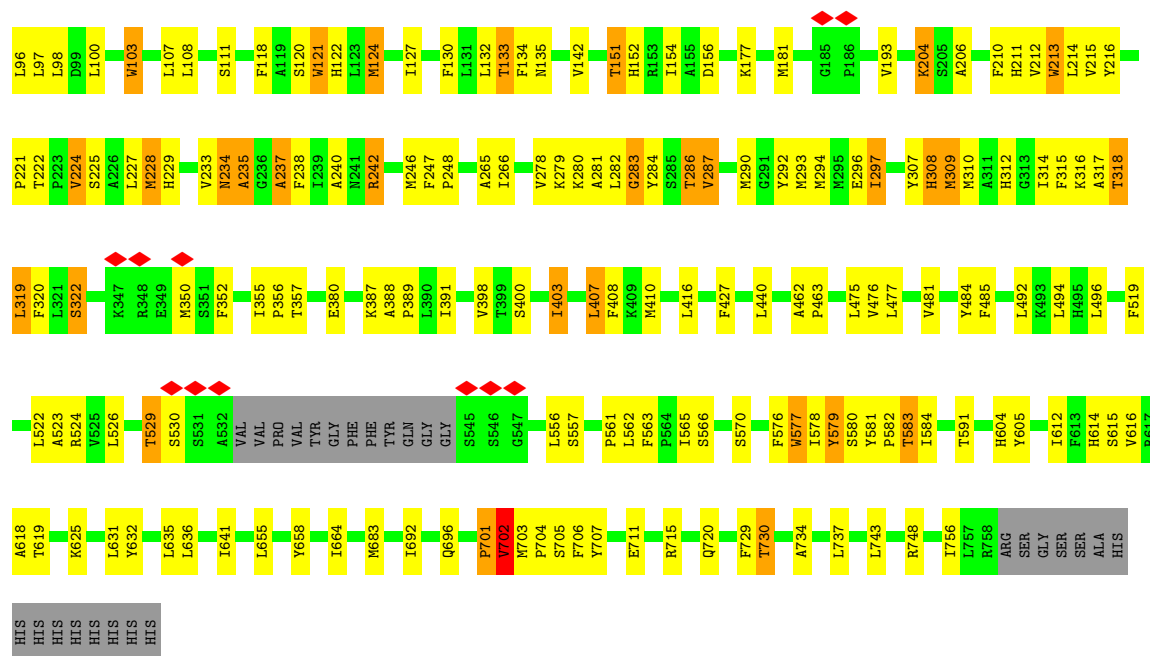
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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 inorganic carbon transporter subunit DabA



- Molecule 2: NADH/Ubiquinone/plastoquinone (Complex I)





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	168739	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; Patch CTF used in cryoSPARC	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	5.170	Depositor
Minimum map value	-2.764	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.336	Depositor
Recommended contour level	0.225	Depositor
Map size ($\text{\AA}$)	90.299995, 118.649994, 133.875	wwPDB
Map dimensions	255, 226, 172	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.525, 0.525, 0.525	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.85	42/7814 (0.5%)	0.97	59/10564 (0.6%)
2	B	1.05	60/6113 (1.0%)	1.12	60/8317 (0.7%)
All	All	0.94	102/13927 (0.7%)	1.04	119/18881 (0.6%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	7
2	B	0	4
All	All	0	11

The worst 5 of 102 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	96	LEU	C-O	-14.24	1.07	1.24
2	B	312	HIS	C-O	-13.58	1.07	1.24
2	B	222	THR	C-O	-12.16	1.12	1.24
2	B	66	LEU	C-O	-11.10	1.09	1.24
2	B	281	ALA	C-O	-10.19	1.12	1.24

The worst 5 of 119 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	478	VAL	N-CA-CB	10.00	125.21	111.21
1	A	548	ASP	CA-CB-CG	8.99	121.59	112.60
1	A	890	GLU	CB-CA-C	8.76	125.74	110.85
1	A	493	LEU	N-CA-C	-8.55	97.63	110.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	492	PHE	N-CA-CB	-8.18	98.62	110.56

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	518	ARG	Sidechain
1	A	561	ARG	Sidechain
1	A	657	ARG	Sidechain
1	A	759	THR	Mainchain
1	A	917	ARG	Sidechain

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	7627	7637	7633	102	0
2	B	5953	6172	6171	112	0
3	A	1	0	0	0	0
4	A	394	0	0	11	0
4	B	221	0	0	24	0
All	All	14196	13809	13804	206	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 206 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:850:LEU:HD12	4:A:1527:HOH:O	1.63	0.95
2:B:631:LEU:HD22	4:B:898:HOH:O	1.72	0.87
1:A:479:PRO:HB2	1:A:500:PRO:CG	2.07	0.85
2:B:703:MET:HB3	4:B:891:HOH:O	1.76	0.84
2:B:214[B]:LEU:HD12	2:B:233:VAL:HG21	1.60	0.82

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	927/1031 (90%)	888 (96%)	32 (4%)	7 (1%)	16	20
2	B	743/773 (96%)	712 (96%)	27 (4%)	4 (0%)	24	31
All	All	1670/1804 (93%)	1600 (96%)	59 (4%)	11 (1%)	20	23

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	478	VAL
1	A	483	VAL
1	A	520	ALA
1	A	522	HIS
2	B	235	ALA

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	806/896 (90%)	770 (96%)	36 (4%)	24	37
2	B	646/680 (95%)	629 (97%)	17 (3%)	40	59
All	All	1452/1576 (92%)	1399 (96%)	53 (4%)	31	45

5 of 53 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	759	THR

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Mol	Chain	Res	Type
1	A	989	VAL
2	B	440	LEU
1	A	790	LYS
1	A	955	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	438	HIS
2	B	441	GLN
1	A	578	ASN
1	A	668	GLN
1	A	954	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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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 [i](#)

There are no chain breaks in this entry.

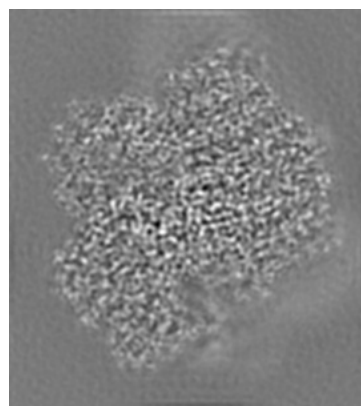
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-79080. These allow visual inspection of the internal detail of the map and identification of artifacts.

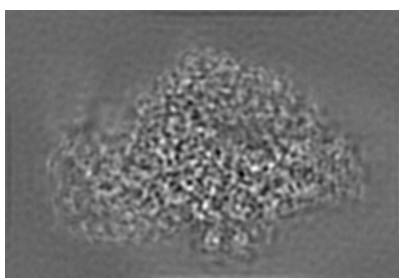
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

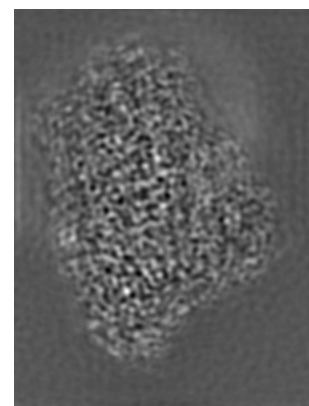
6.1.1 Primary map



X

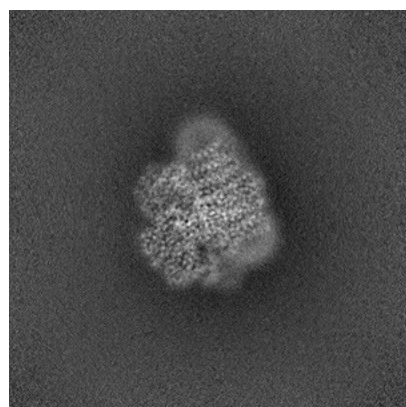


Y

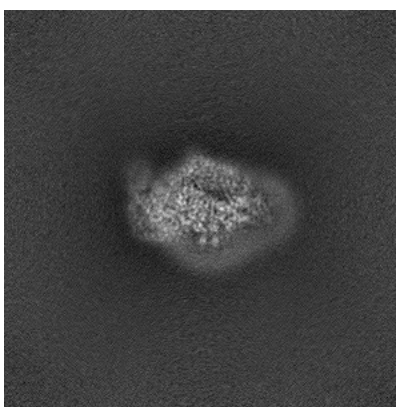


Z

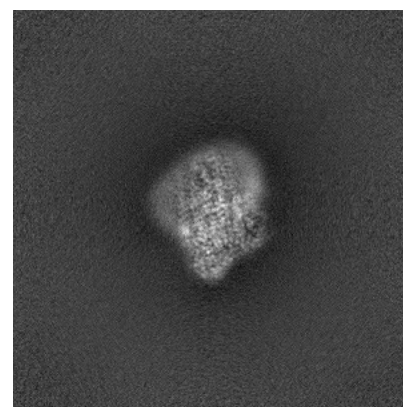
6.1.2 Raw map



X



Y

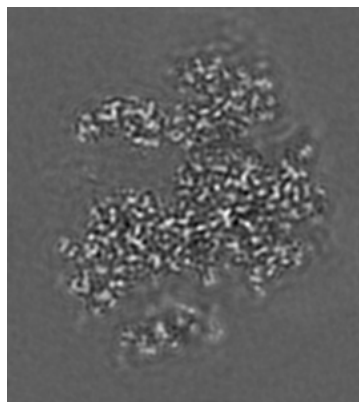


Z

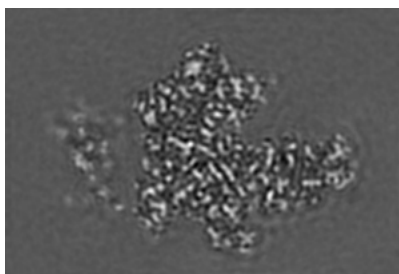
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

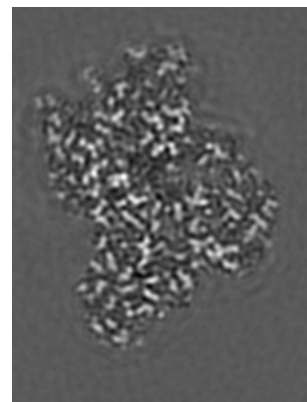
6.2.1 Primary map



X Index: 86

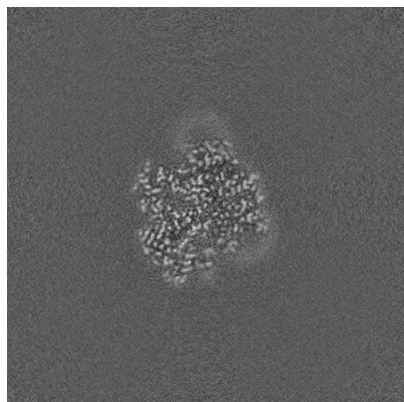


Y Index: 113

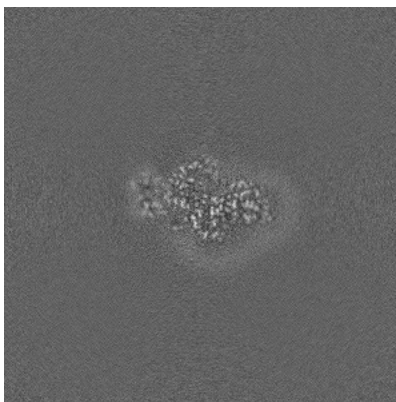


Z Index: 127

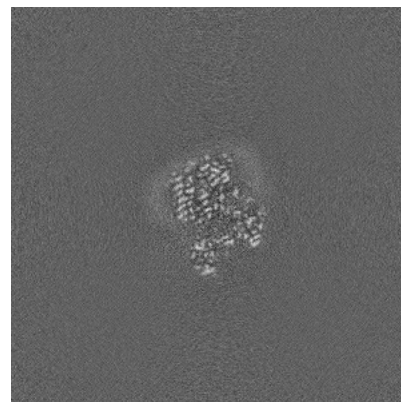
6.2.2 Raw map



X Index: 288



Y Index: 288

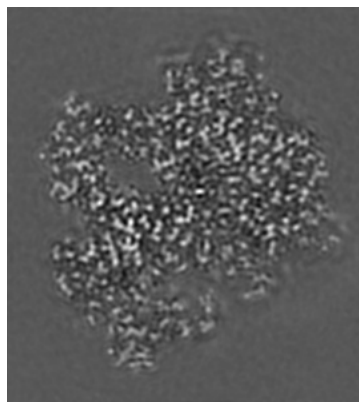


Z Index: 288

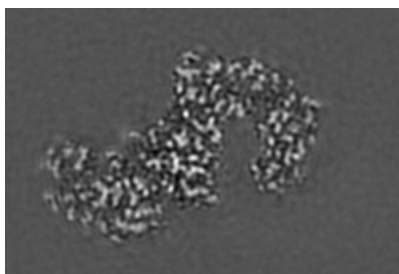
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

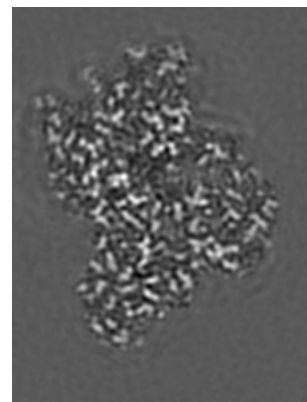
6.3.1 Primary map



X Index: 73

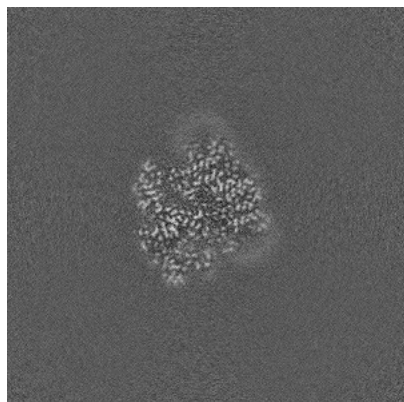


Y Index: 83

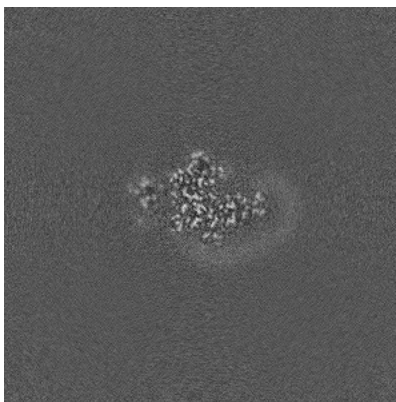


Z Index: 127

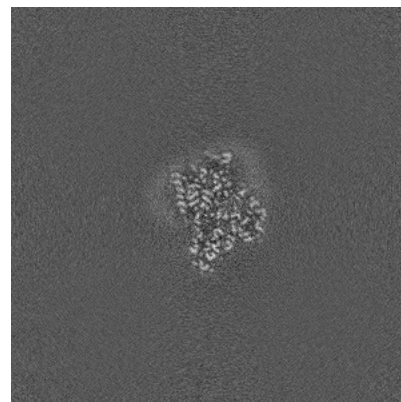
6.3.2 Raw map



X Index: 291



Y Index: 276

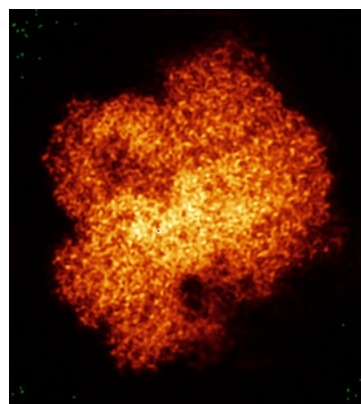


Z Index: 283

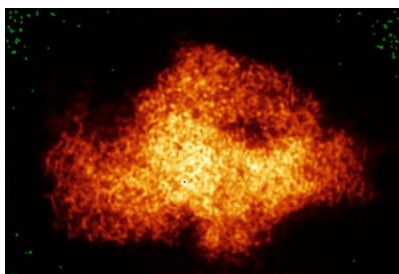
The images above show the largest variance slices of the map in three orthogonal directions.

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

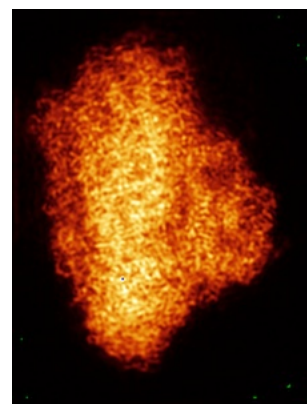
6.4.1 Primary map



X

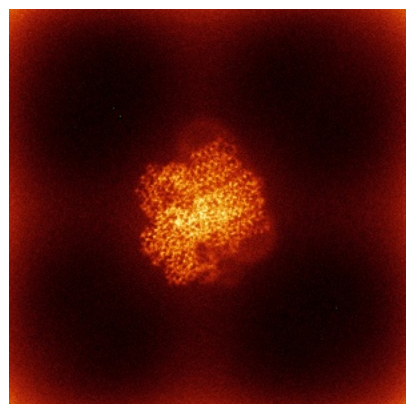


Y

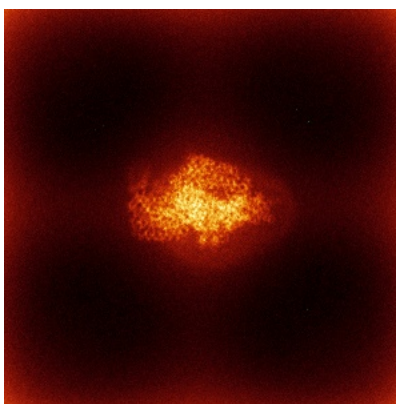


Z

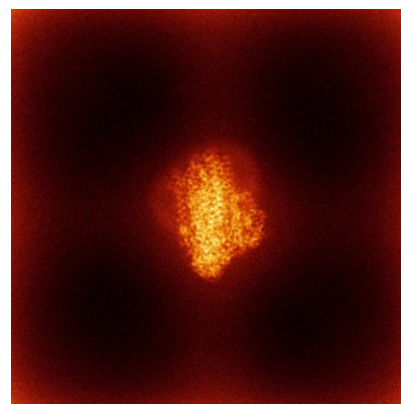
6.4.2 Raw map



X



Y

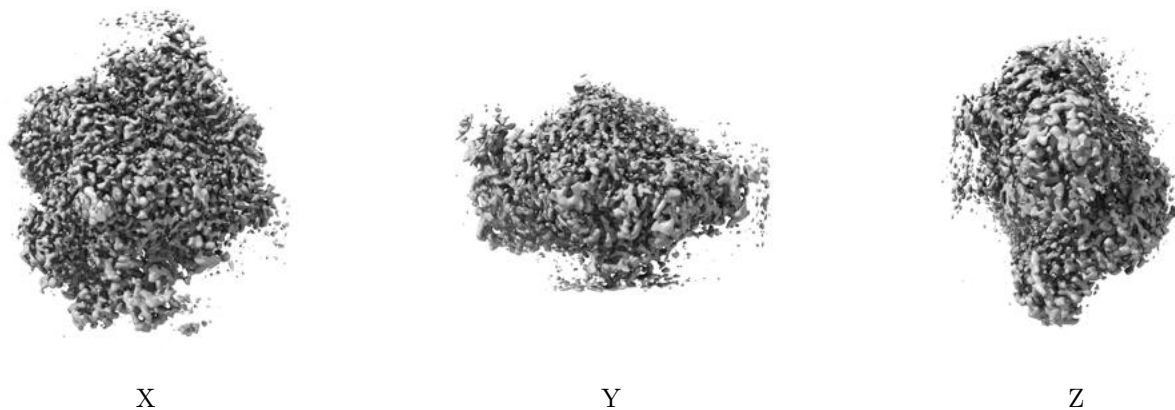


Z

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.

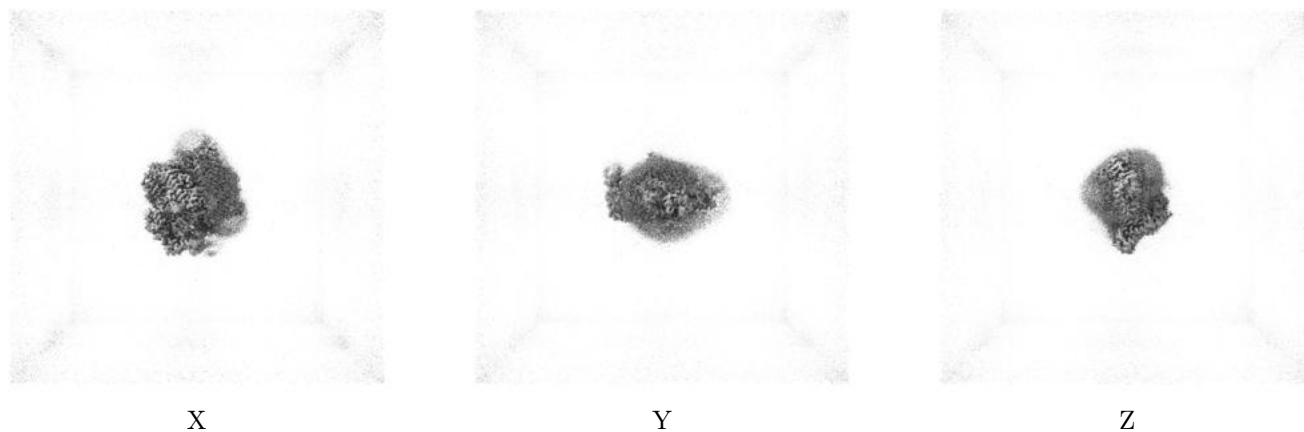
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.225. 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.

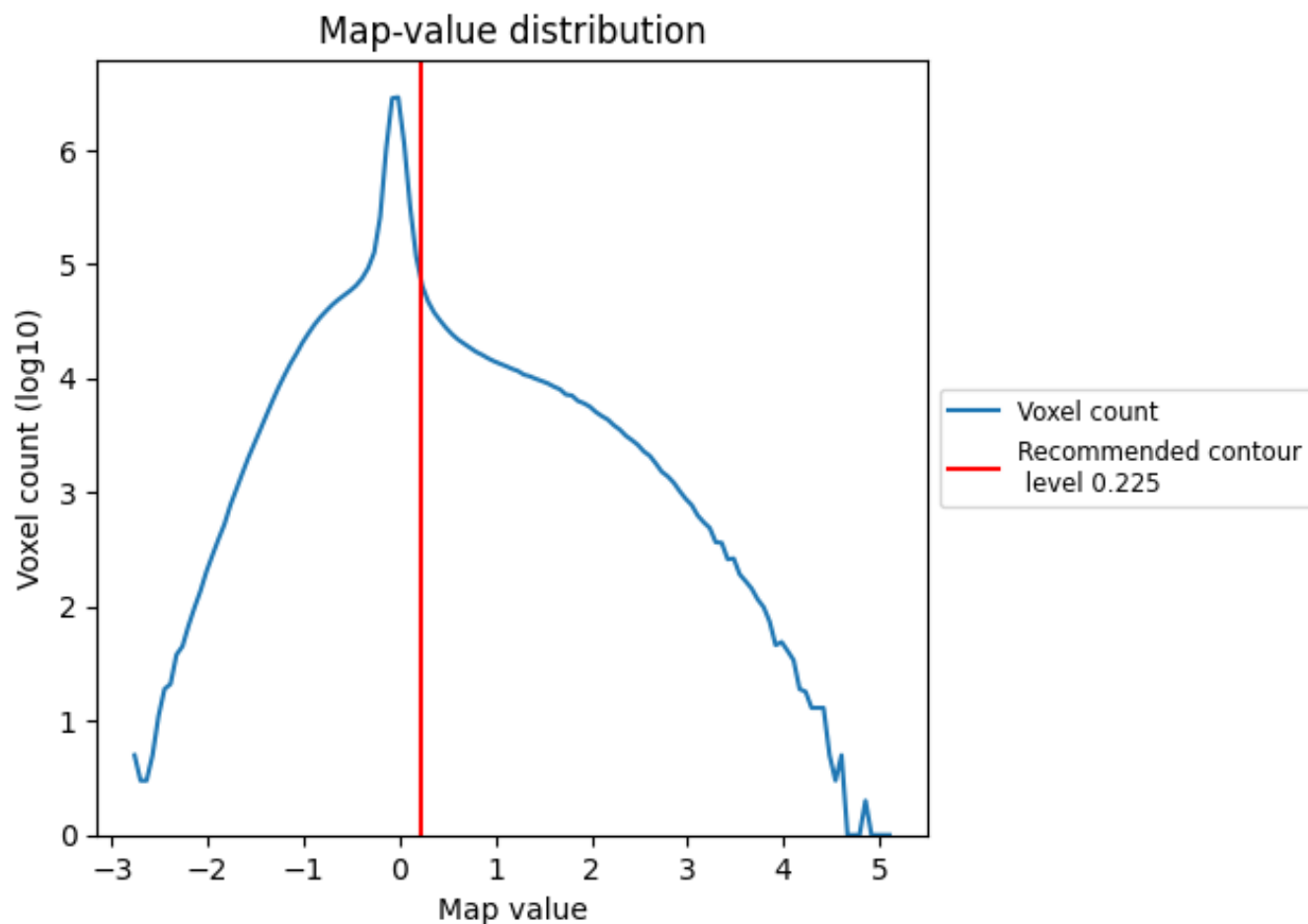
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

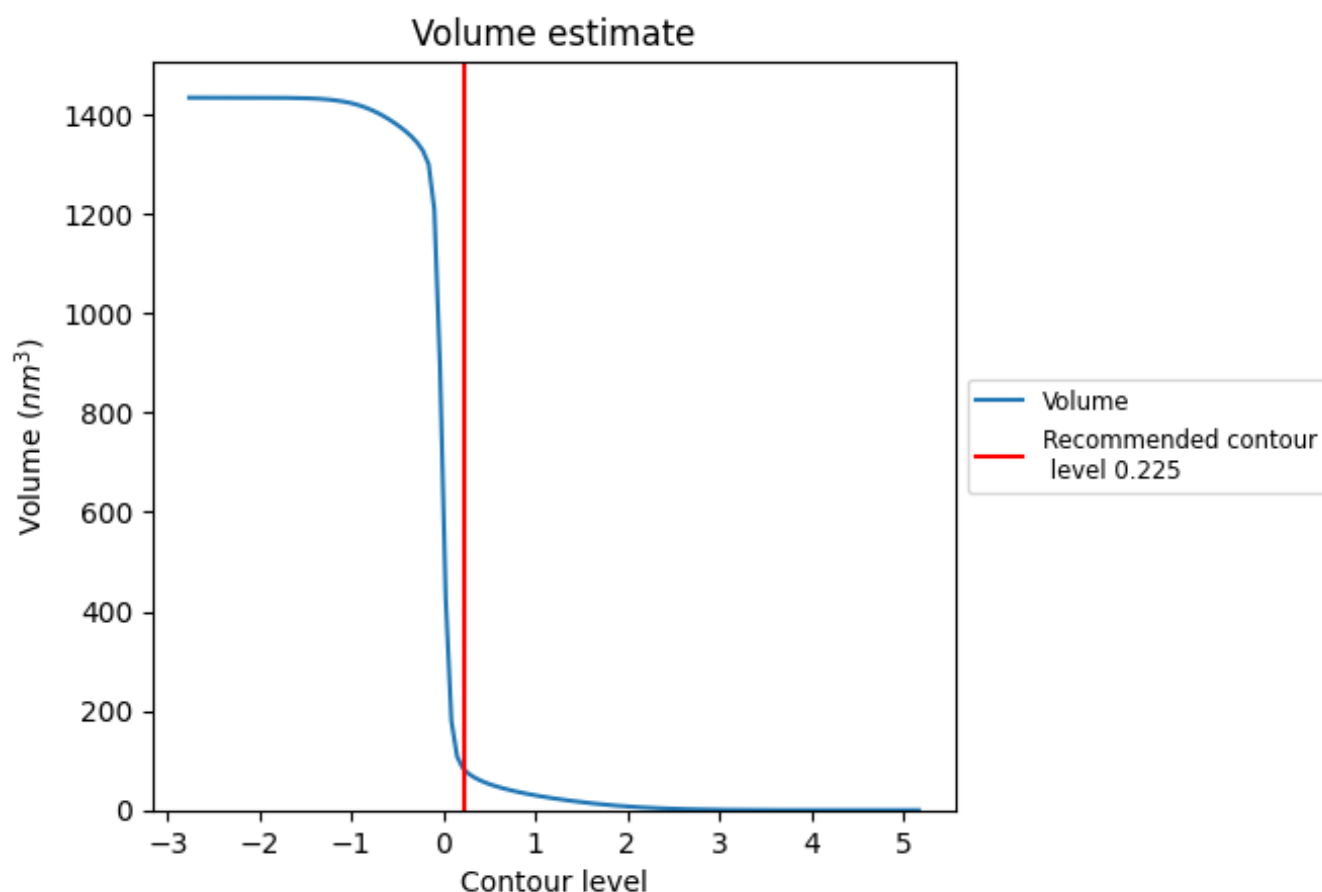
This section contains the results of statistical analysis of the map.

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 82 nm³; this corresponds to an approximate mass of 74 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.

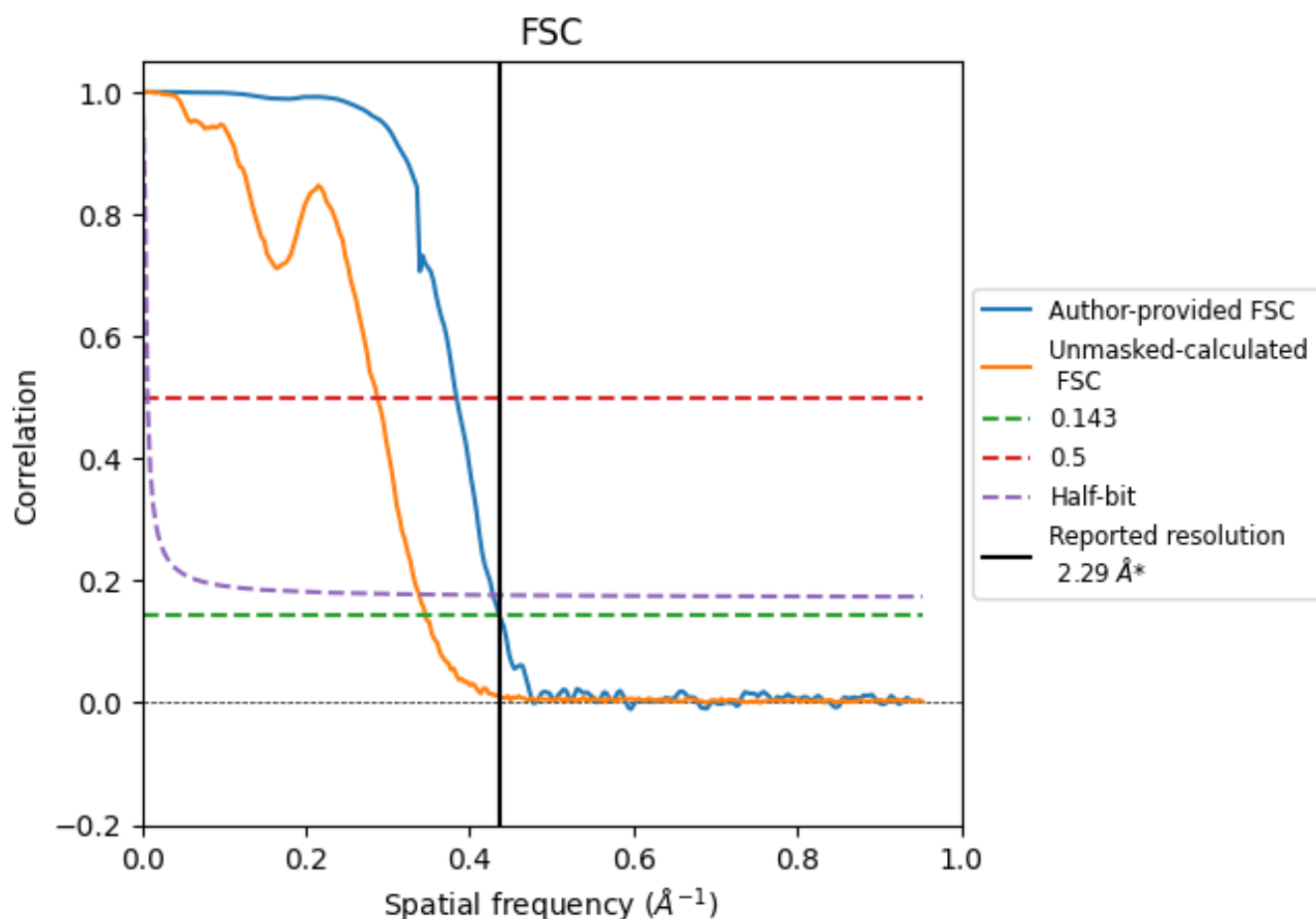
7.3 Rotationally averaged power spectrum [i](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

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 $0.437 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

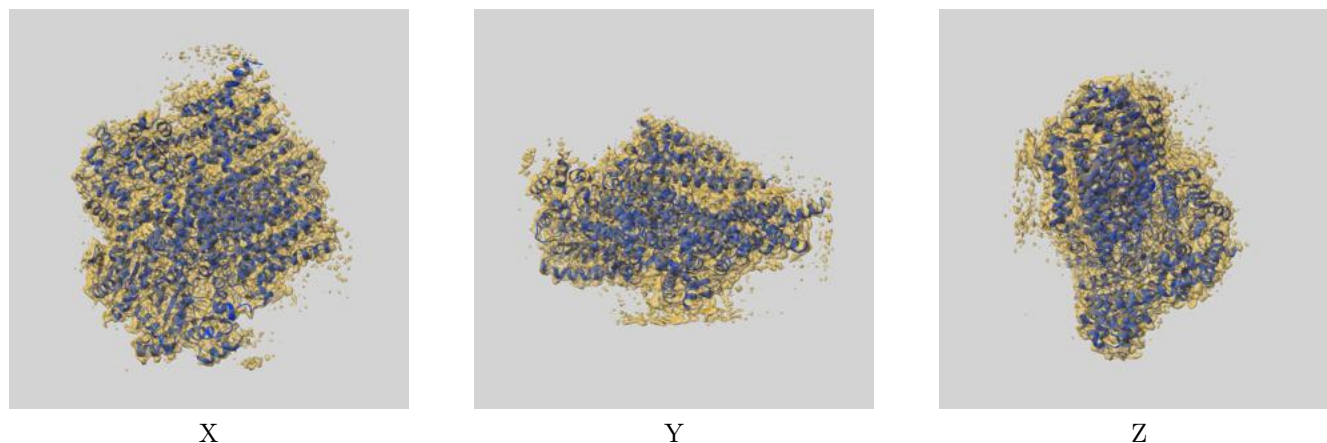
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.29	-	-
Author-provided FSC curve	2.29	2.61	2.33
Unmasked-calculated*	2.89	3.48	2.96

*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 2.89 differs from the reported value 2.29 by more than 10 %

9 Map-model fit [i](#)

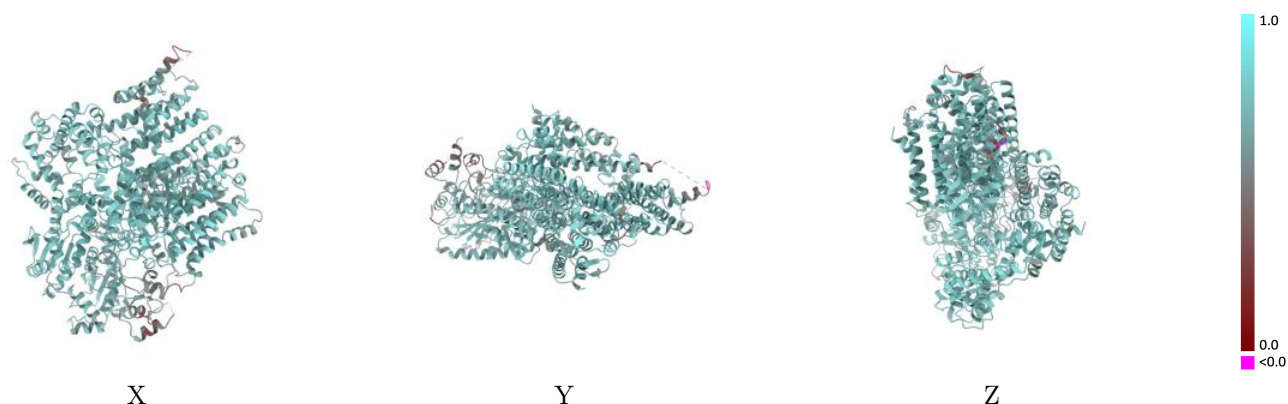
This section contains information regarding the fit between EMDB map EMD-79080 and PDB model 38RI. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



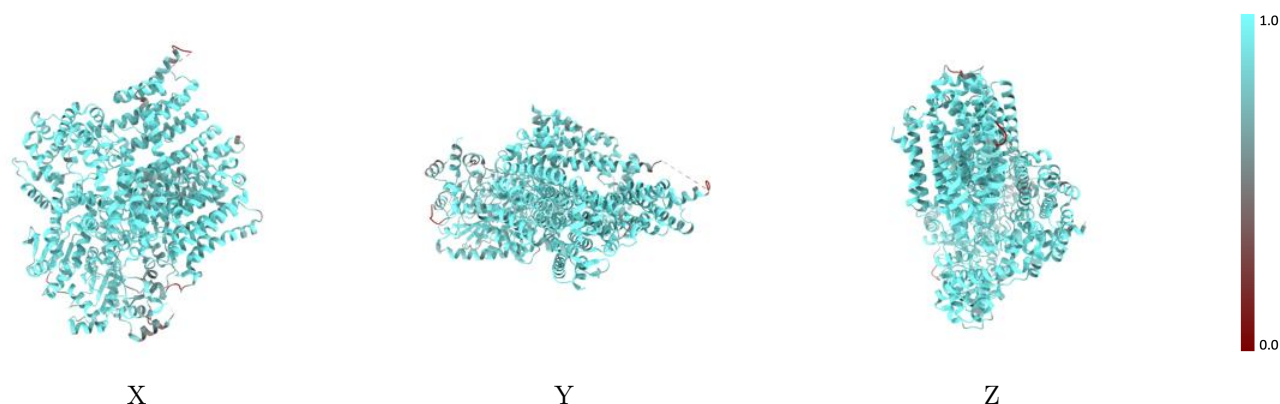
The images above show the 3D surface view of the map at the recommended contour level 0.225 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



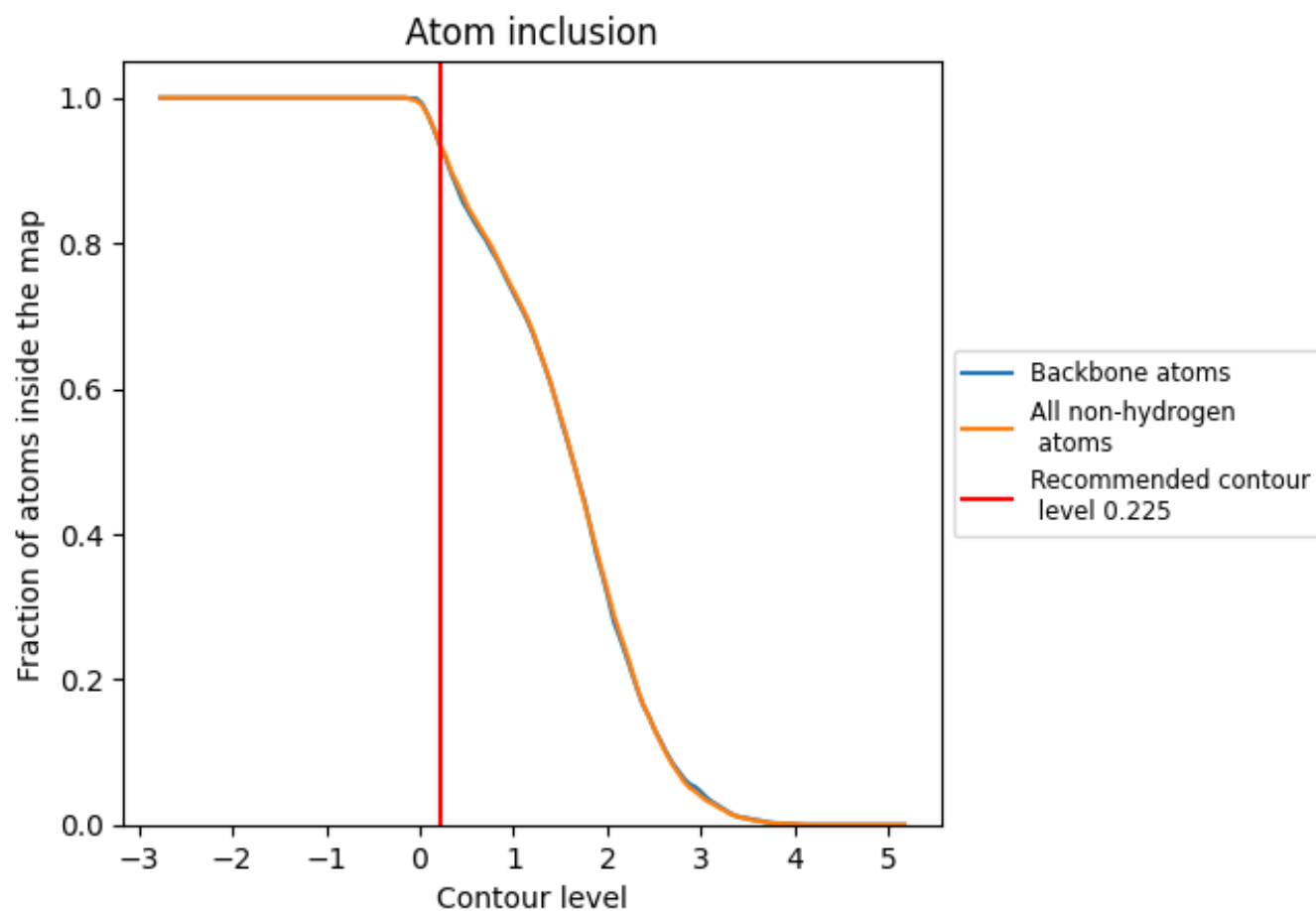
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.225).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 93% 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 (0.225) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9330	0.7060
A	0.9320	0.7030
B	0.9480	0.7110

