



Full wwPDB EM Validation Report ⓘ

May 11, 2026 – 04:49 PM EDT

PDB ID : 13HS / pdb_000013hs
EMDB ID : EMD-77073
Title : Cryo-EM structure of Pseudomonas aeruginosa outer-membrane lipoprotein PA3214 in the open conformation
Authors : Giacometti, S.I.; Coudray, N.; Bhabha, G.; Ekiert, D.C.
Deposited on : 2026-05-06
Resolution : 3.70 Å(reported)
Based on initial model : .

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

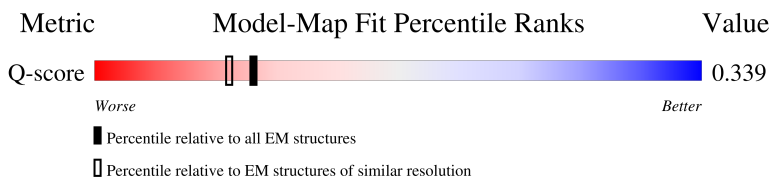
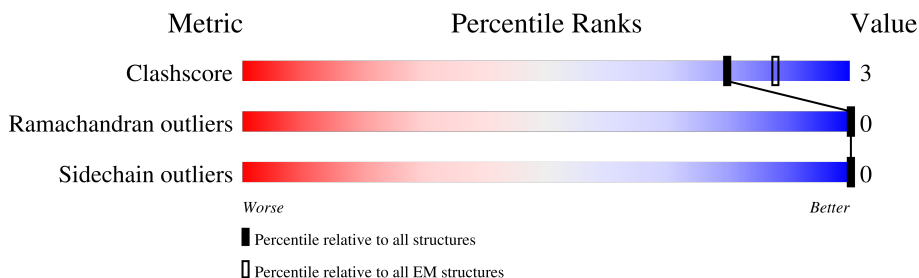
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11569 (3.20 - 4.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	214	
1	B	214	
1	C	214	
1	D	214	

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Mol	Chain	Length	Quality of chain
1	E	214	<div><div><div></div><div></div><div></div></div><div>81%17%</div></div>
1	F	214	<div><div><div></div><div></div><div></div></div><div>6%79%17%</div></div>
1	G	214	<div><div><div></div><div></div><div></div></div><div>24%71%12%17%</div></div>
1	H	214	<div><div><div></div><div></div><div></div></div><div>69%74%9%17%</div></div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 11040 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.

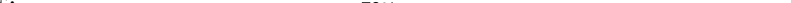
- Molecule 1 is a protein called ABC-type transport auxiliary lipoprotein component domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	178	Total	C	N	O	S	0	0
			1380	860	261	258	1		
1	B	178	Total	C	N	O	S	0	0
			1380	860	261	258	1		
1	C	178	Total	C	N	O	S	0	0
			1380	860	261	258	1		
1	D	178	Total	C	N	O	S	0	0
			1380	860	261	258	1		
1	E	178	Total	C	N	O	S	0	0
			1380	860	261	258	1		
1	F	178	Total	C	N	O	S	0	0
			1380	860	261	258	1		
1	G	178	Total	C	N	O	S	0	0
			1380	860	261	258	1		
1	H	178	Total	C	N	O	S	0	0
			1380	860	261	258	1		

[illegible]

- Chain E: 81% 17%

MET	ARG	LEU	LEU	ARG	PRO	LEU	ARG	ARG	LEU	SER	SER	LEU	ALA	ALA	GLY	LEU	ALA	ALA	LEU	LEU	THR	THR	LEU	GLY	ALA	ALA	CYS	SER	SER	ILE	LEU	PRO	GLU	ALA	ALA	Q33	A49	A50	W56	I74	W91	D120	Y151	D152	A153	D176	G177	K178	P210	ALA	VAL	GLN	PRO
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- Chain F:  6% 79% 17%

MET	ARG	LEU	ALA	LEU	ARG	PRO	LEU	ARG	ARG	LEU	SER	LEU	ALA	ALA	GLY	LEU	ALA	ALA	ALA	CYS	SER	ILE	PRO	GLU	ALA	Q33	L40	P41	S48	A49	A50	A51	L69	I74	A75	W91	R114	D119	D120	G131	R134	Y151	D152
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ALA
VAL
GLN
PRO

- Chain G: 

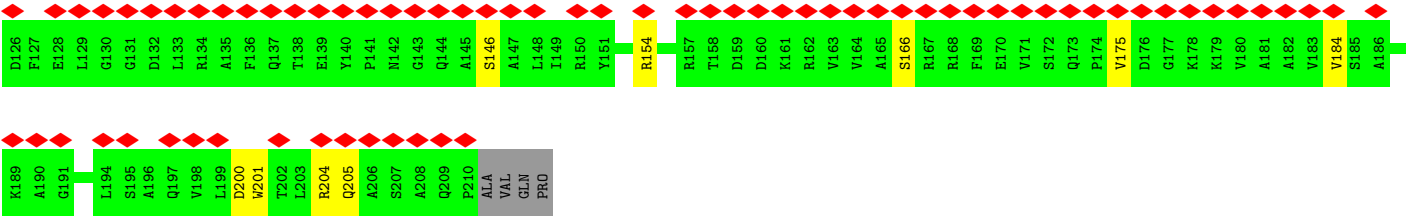
NET	ARG	LEU	ALA	LEU	ARG	PRO	LEU	ARG	ARG	LEU	SER	LEU	ALA	ALA	GLY	LEU	ALA	ALA	ALA	THR	LEU	GLY	CYS	ILE	LEU	PRO	GLU	ALA	Q33	V34	L35	L39	L40	P41	V42	P46	A47	S48	A49	A50	A51	R52	I60	A61	R62	P63	R64	L67	V68	L69	E70
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Category	Item	Value	Color	Label
A	I74	100	Red	100
	A75	100	Red	100
	V76	100	Red	100
	R77	100	Red	100
	G80	100	Green	100
	D81	100	Red	100
	E82	100	Red	100
	I83	100	Red	100
	S84	100	Red	100
	V85	100	Red	100
B	Y86	100	Red	100
	K87	100	Red	100
	G88	100	Green	100
	W91	100	Yellow	100
	S92	100	Yellow	100
	D93	100	Red	100
	P94	100	Yellow	100
	L99	100	Yellow	100
	R102	100	Yellow	100
	Q105	100	Yellow	100
C	R114	100	Red	100
	G115	100	Red	100
	L116	100	Red	100
	D119	100	Red	100
	M122	100	Red	100
	E128	100	Red	100
	L129	100	Red	100
	G130	100	Red	100
	G131	100	Red	100
	R134	100	Yellow	100
D	A135	100	Red	100
	F136	100	Red	100
	M142	100	Red	100
	S146	100	Yellow	100
	Y151	100	Red	100
	R154	100	Yellow	100
	R157	100	Red	100
	T158	100	Red	100
	D159	100	Red	100
	R162	100	Red	100
E	S166	100	Yellow	100
	R167	100	Red	100
	P168	100	Red	100

- Chain H:  69% 9% 22%

NET	ARG	LEU	ALA	LEU	ARG	PRO	LEU	ARG	ARG	LEU	LEU	ALA	ALA	GLY	LEU	ALA	ALA	ALA	THR	LEU	GLY	CYS	SER	ILE	LEU	PRO	GLU	ALA	Q33	V34	L35	Y38	L39	L40	P41	V42	H43	M44	P45	P46	A47	S48	A49	A50	A51	R52	P53	V54	D55	W56	R59	I60	A61
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P63	R64	T65	S66	L67	V68	L69	E70	S71	F72	R73	I74	A75	V76	R77	F78	H79	G80	D81	E82	I83	S84	V85	Y86	Q87	G88	A89	R90	W91	S92	D93	P94	A95	L99	R102	L103	Q104	Q105	A106	F107	Q108	A109	D110	G111	R112	V113	R114	G115	L116	S117	S118	D119	D120	S121	M122	L123	Q124	L125
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	187311	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	51.51, 51.43	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k), GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.121	Depositor
Minimum map value	-0.390	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.044	Depositor
Recommended contour level	0.399	Depositor
Map size (\AA)	277.248, 277.248, 277.248	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.083, 1.083, 1.083	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	0.15	0/1408	0.31	0/1915
1	B	0.24	0/1408	0.48	0/1915
1	C	0.24	0/1408	0.41	0/1915
1	D	0.24	0/1408	0.38	0/1915
1	E	0.24	0/1408	0.43	0/1915
1	F	0.22	0/1408	0.38	0/1915
1	G	0.18	0/1408	0.33	0/1915
1	H	0.12	0/1408	0.28	0/1915
All	All	0.21	0/11264	0.38	0/15320

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	1380	0	1375	13	0
1	B	1380	0	1375	7	0
1	C	1380	0	1375	4	0
1	D	1380	0	1375	3	0
1	E	1380	0	1375	3	0
1	F	1380	0	1375	6	0
1	G	1380	0	1375	14	0
1	H	1380	0	1375	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	11040	0	11000	59	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 3.

All (59) 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:G:40:LEU:HD12	1:G:41:PRO:HD2	1.82	0.62
1:A:40:LEU:HD12	1:A:41:PRO:HD2	1.83	0.60
1:B:151:TYR:CE2	1:B:153:ALA:HB2	2.40	0.57
1:F:134:ARG:HD2	1:G:105:GLN:HE21	1.69	0.57
1:D:74:ILE:HG12	1:D:91:TRP:NE1	2.20	0.56
1:G:134:ARG:HD3	1:H:105:GLN:HE21	1.73	0.53
1:C:151:TYR:CE2	1:C:153:ALA:HB2	2.43	0.53
1:E:74:ILE:HG12	1:E:91:TRP:CE2	2.44	0.53
1:C:74:ILE:HG12	1:C:91:TRP:NE1	2.23	0.52
1:H:146:SER:HA	1:H:175:VAL:HG23	1.93	0.51
1:E:151:TYR:CE2	1:E:153:ALA:HB2	2.46	0.51
1:H:63:PRO:HG2	1:H:99:LEU:HD23	1.92	0.51
1:H:154:ARG:HG2	1:H:166:SER:OG	2.11	0.51
1:A:41:PRO:HG2	1:A:188:GLY:HA3	1.93	0.50
1:D:74:ILE:HG12	1:D:91:TRP:CE2	2.47	0.49
1:A:63:PRO:HG2	1:A:99:LEU:HD23	1.95	0.49
1:B:76:VAL:HG23	1:B:138:THR:HB	1.95	0.48
1:A:42:VAL:HG13	1:A:102:ARG:CZ	2.44	0.48
1:B:129:LEU:HD11	1:B:153:ALA:HB1	1.96	0.47
1:G:33:GLN:HE22	1:G:87:GLN:HG2	1.79	0.47
1:F:74:ILE:HG12	1:F:91:TRP:CE2	2.50	0.46
1:C:56:TRP:CD1	1:C:56:TRP:H	2.34	0.46
1:G:42:VAL:HG13	1:G:102:ARG:CZ	2.45	0.46
1:G:146:SER:HA	1:G:175:VAL:HG23	1.97	0.46
1:B:51:ALA:HB1	1:B:112:ARG:HG2	1.98	0.46
1:F:151:TYR:HE2	1:F:153:ALA:HB2	1.81	0.46
1:G:62:ARG:HH21	1:G:94:PRO:HB2	1.81	0.45
1:H:35:LEU:HD23	1:H:88:GLY:HA2	1.98	0.45
1:A:35:LEU:HD23	1:A:88:GLY:HA2	1.99	0.44
1:G:63:PRO:HG2	1:G:99:LEU:HD23	1.99	0.44
1:G:35:LEU:HD23	1:G:88:GLY:HA2	2.00	0.44
1:H:41:PRO:HD3	1:H:184:VAL:HG12	2.00	0.44
1:H:60:ILE:HD12	1:H:104:MET:SD	2.58	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:40:LEU:HD12	1:F:41:PRO:HD2	1.99	0.44
1:H:62:ARG:HH21	1:H:94:PRO:HB2	1.83	0.44
1:A:41:PRO:HD3	1:A:184:VAL:HG12	1.99	0.43
1:E:56:TRP:CD1	1:E:56:TRP:H	2.36	0.43
1:D:56:TRP:CD1	1:D:56:TRP:H	2.36	0.43
1:G:154:ARG:HG2	1:G:166:SER:OG	2.18	0.43
1:G:74:ILE:HG12	1:G:91:TRP:CD1	2.53	0.43
1:A:60:ILE:HD12	1:A:104:MET:SD	2.59	0.43
1:F:151:TYR:CE2	1:F:153:ALA:HB2	2.53	0.43
1:B:95:ALA:HA	1:B:98:LEU:HD12	2.01	0.43
1:H:40:LEU:HD12	1:H:41:PRO:HD2	2.01	0.42
1:A:201:TRP:O	1:A:205:GLN:HG2	2.19	0.42
1:F:175:VAL:HG12	1:F:177:GLY:H	1.85	0.42
1:A:154:ARG:HG2	1:A:166:SER:OG	2.20	0.42
1:A:146:SER:HA	1:A:175:VAL:HG23	2.02	0.42
1:B:155:LEU:HD12	1:B:155:LEU:HA	1.77	0.41
1:C:114:ARG:HA	1:C:114:ARG:HD3	1.86	0.41
1:H:200:ASP:O	1:H:204:ARG:HG3	2.20	0.41
1:H:201:TRP:O	1:H:205:GLN:HG2	2.20	0.41
1:G:201:TRP:O	1:G:205:GLN:HG2	2.20	0.41
1:A:167:ARG:HD3	1:A:169:PHE:CZ	2.56	0.41
1:A:200:ASP:O	1:A:204:ARG:HG3	2.21	0.41
1:G:167:ARG:HD3	1:G:169:PHE:CZ	2.56	0.40
1:A:157:ARG:HG2	1:A:159:ASP:OD1	2.22	0.40
1:B:157:ARG:HG2	1:B:159:ASP:OD1	2.21	0.40
1:G:200:ASP:O	1:G:204:ARG:HG3	2.21	0.40

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	176/214 (82%)	173 (98%)	3 (2%)	0	100	100
1	B	176/214 (82%)	172 (98%)	4 (2%)	0	100	100
1	C	176/214 (82%)	171 (97%)	5 (3%)	0	100	100
1	D	176/214 (82%)	173 (98%)	3 (2%)	0	100	100
1	E	176/214 (82%)	172 (98%)	4 (2%)	0	100	100
1	F	176/214 (82%)	173 (98%)	3 (2%)	0	100	100
1	G	176/214 (82%)	173 (98%)	3 (2%)	0	100	100
1	H	176/214 (82%)	173 (98%)	3 (2%)	0	100	100
All	All	1408/1712 (82%)	1380 (98%)	28 (2%)	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	145/170 (85%)	145 (100%)	0	100	100
1	B	145/170 (85%)	145 (100%)	0	100	100
1	C	145/170 (85%)	145 (100%)	0	100	100
1	D	145/170 (85%)	145 (100%)	0	100	100
1	E	145/170 (85%)	145 (100%)	0	100	100
1	F	145/170 (85%)	145 (100%)	0	100	100
1	G	145/170 (85%)	145 (100%)	0	100	100
1	H	145/170 (85%)	145 (100%)	0	100	100
All	All	1160/1360 (85%)	1160 (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. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	GLN
1	A	124	GLN
1	A	137	GLN
1	B	36	GLN
1	C	105	GLN
1	D	173	GLN
1	E	108	GLN
1	F	43	HIS
1	F	105	GLN
1	F	173	GLN
1	G	33	GLN
1	G	124	GLN
1	H	33	GLN
1	H	87	GLN
1	H	124	GLN
1	H	137	GLN

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 ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

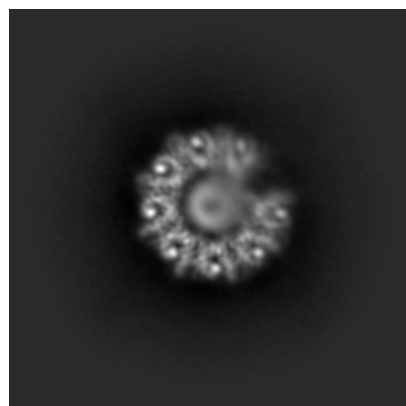
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-77073. These allow visual inspection of the internal detail of the map and identification of artifacts.

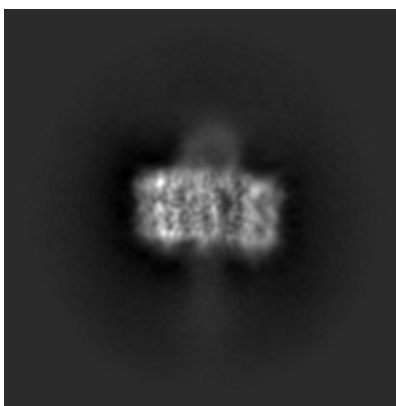
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

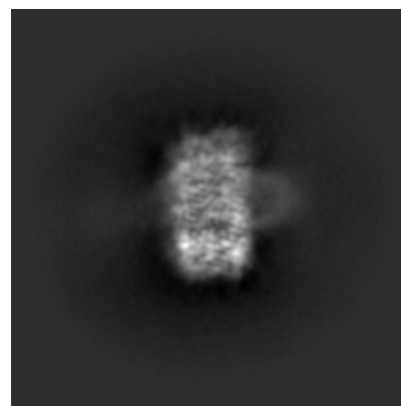
6.1.1 Primary map



X

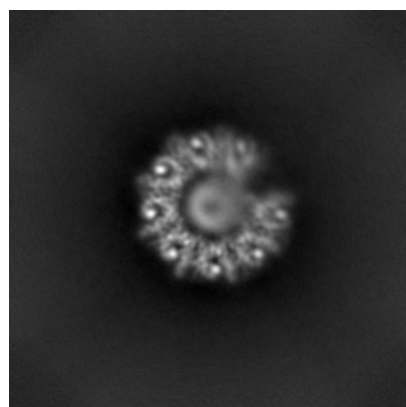


Y

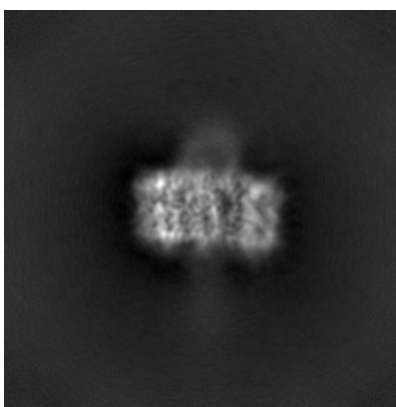


Z

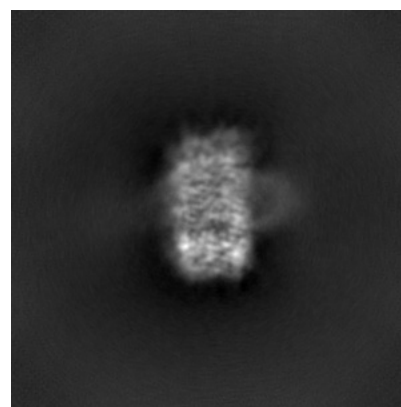
6.1.2 Raw map



X



Y

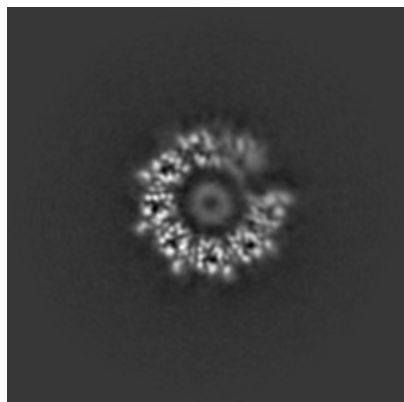


Z

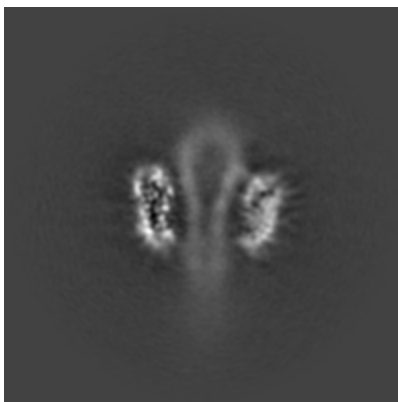
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

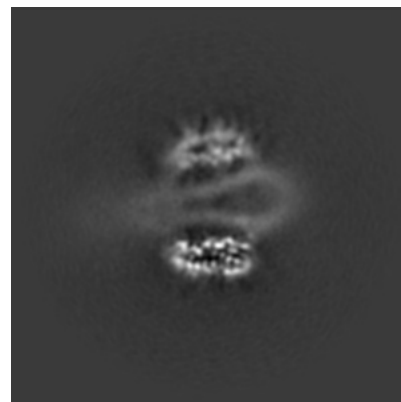
6.2.1 Primary map



X Index: 128

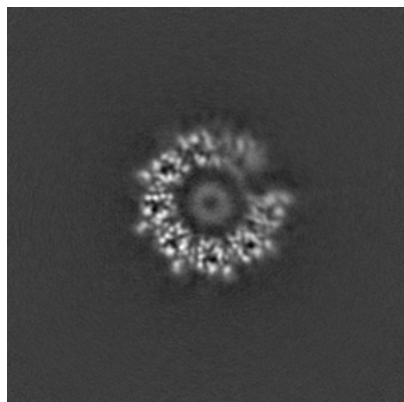


Y Index: 128

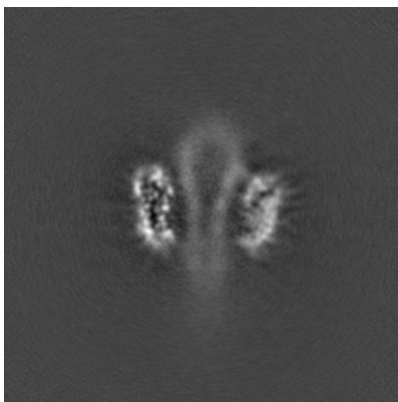


Z Index: 128

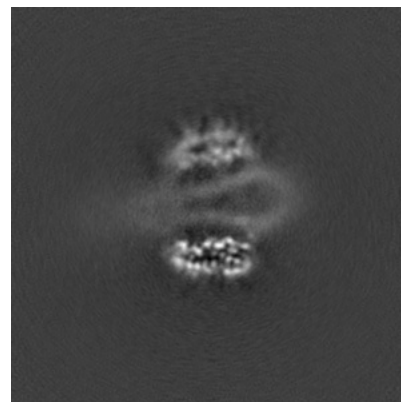
6.2.2 Raw map



X Index: 128



Y Index: 128

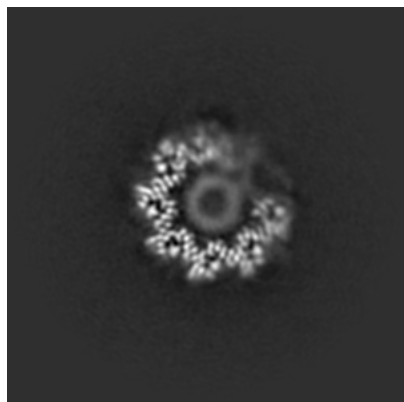


Z Index: 128

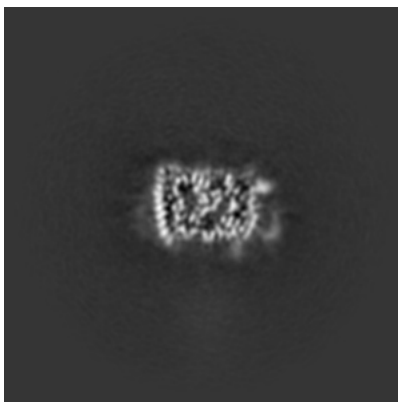
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

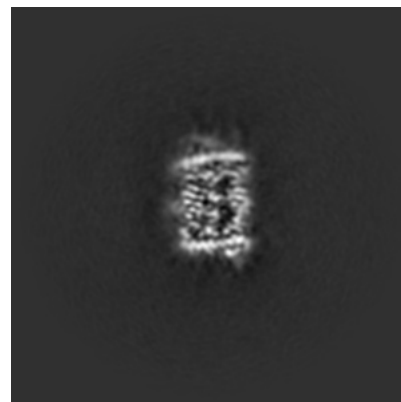
6.3.1 Primary map



X Index: 143

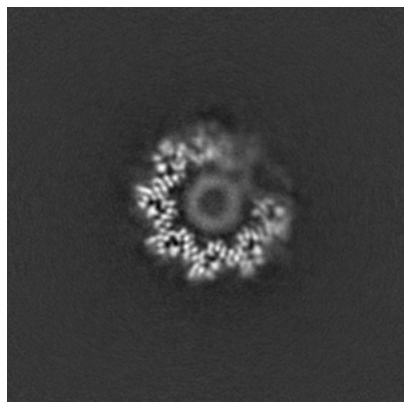


Y Index: 104

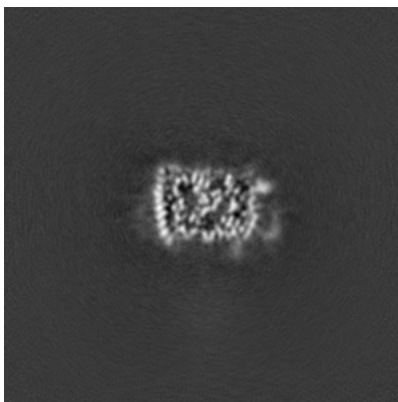


Z Index: 100

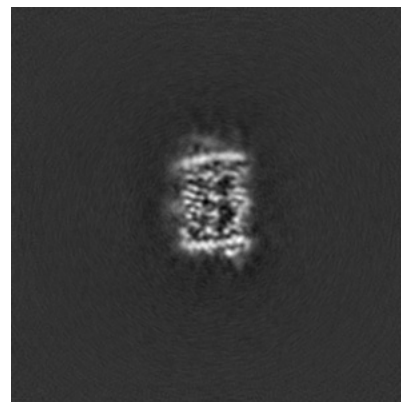
6.3.2 Raw map



X Index: 143



Y Index: 104

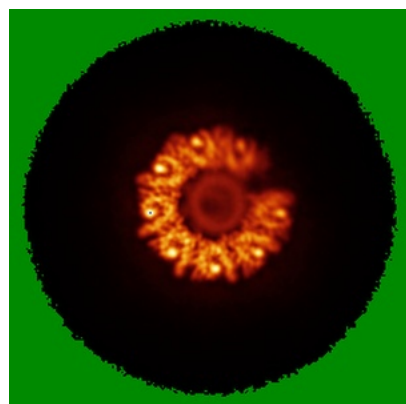


Z Index: 100

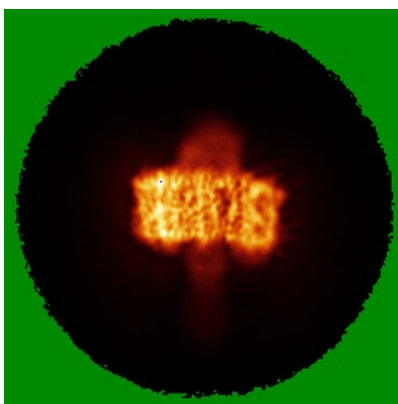
The images above show the largest variance slices of the map in three orthogonal directions.

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

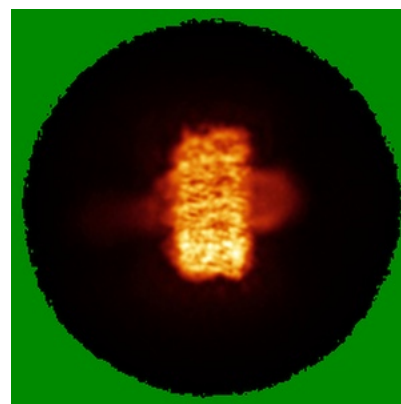
6.4.1 Primary map



X

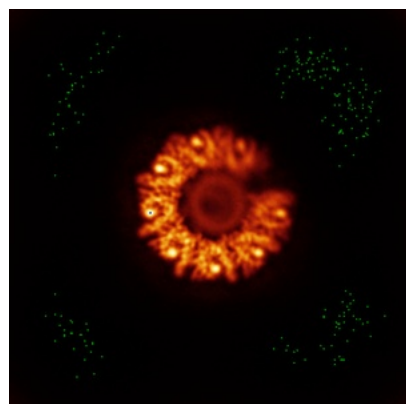


Y

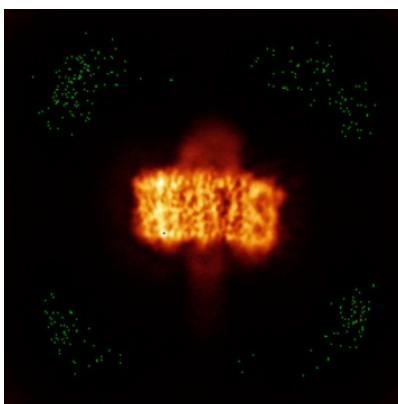


Z

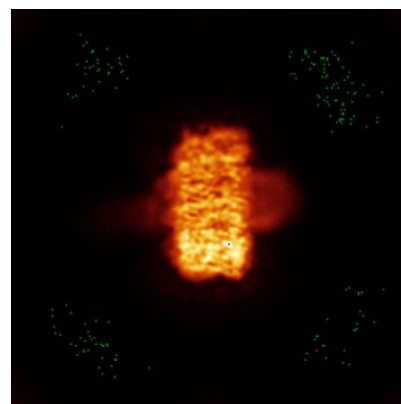
6.4.2 Raw map



X



Y

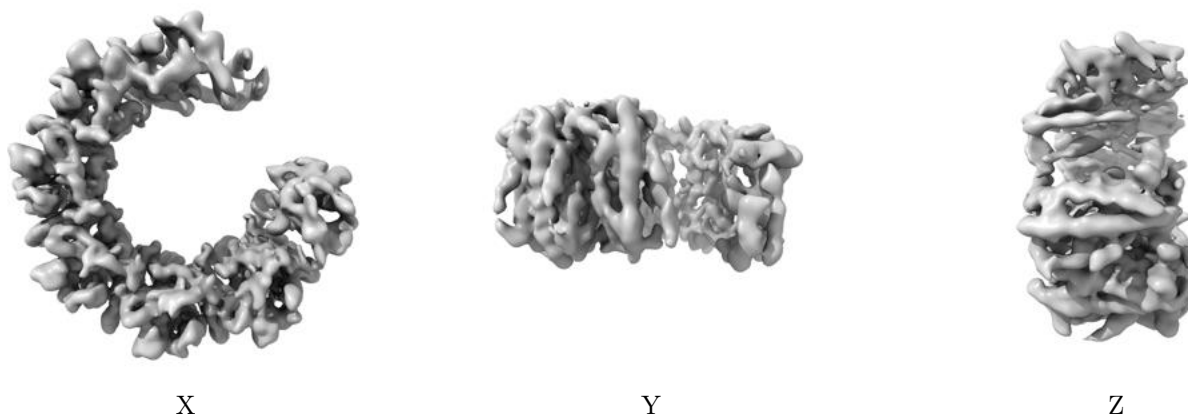


Z

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.

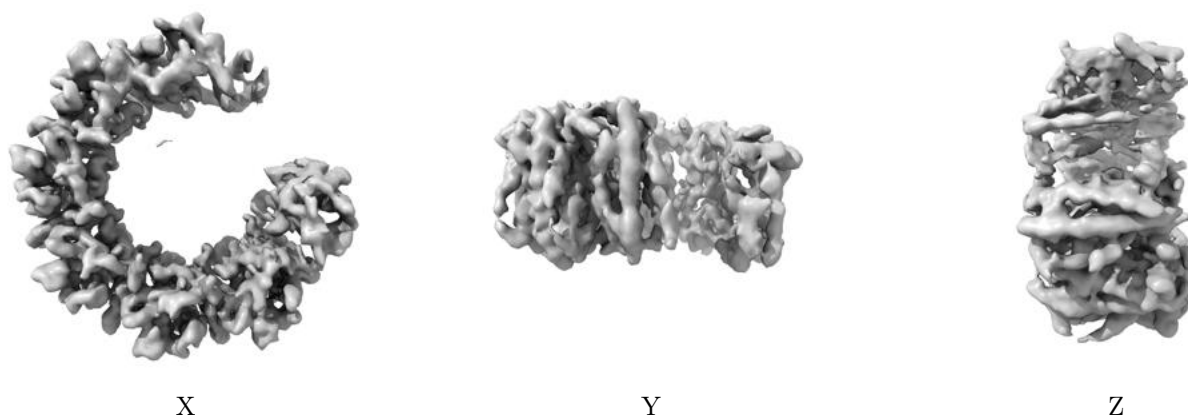
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.399. 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.

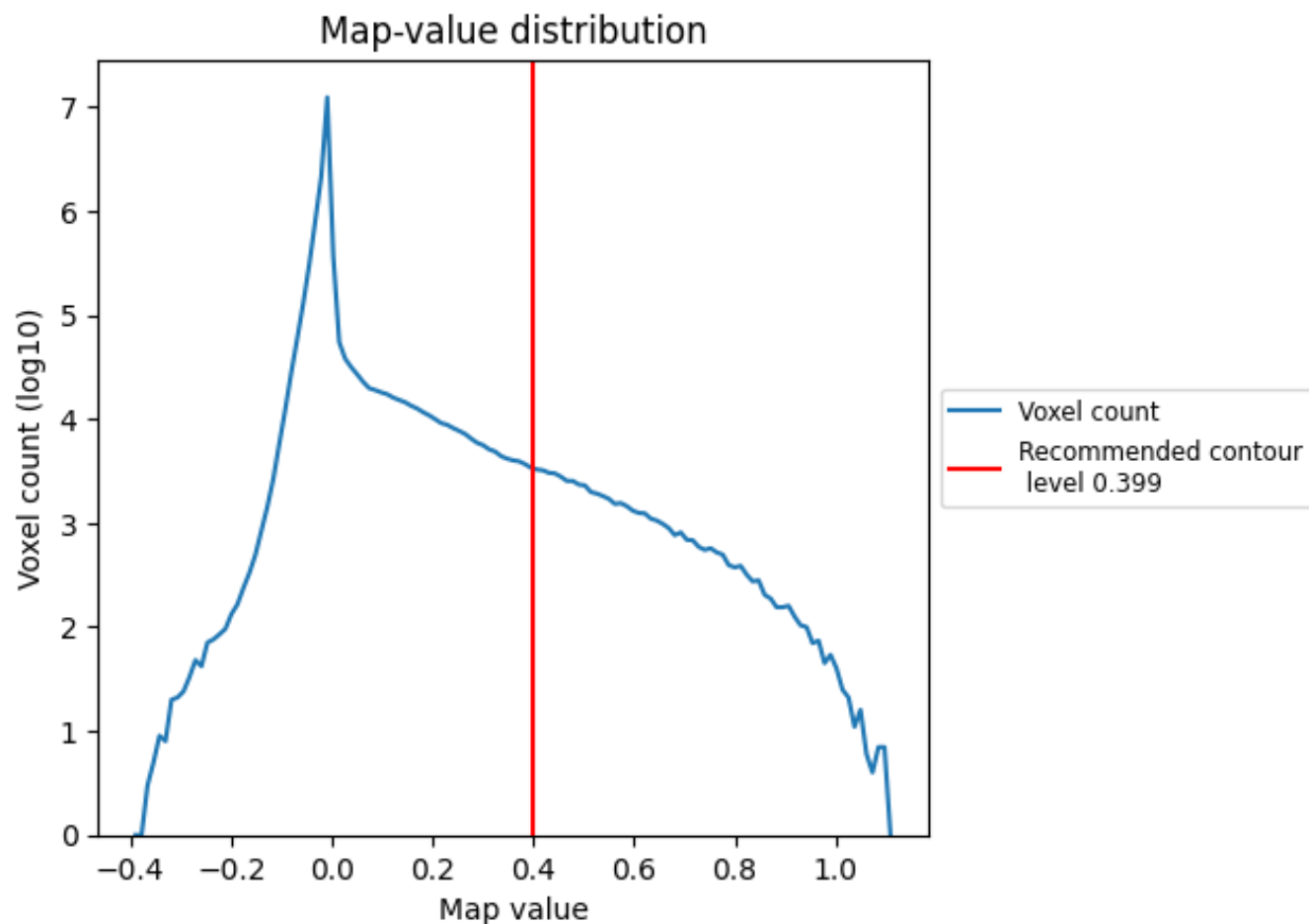
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

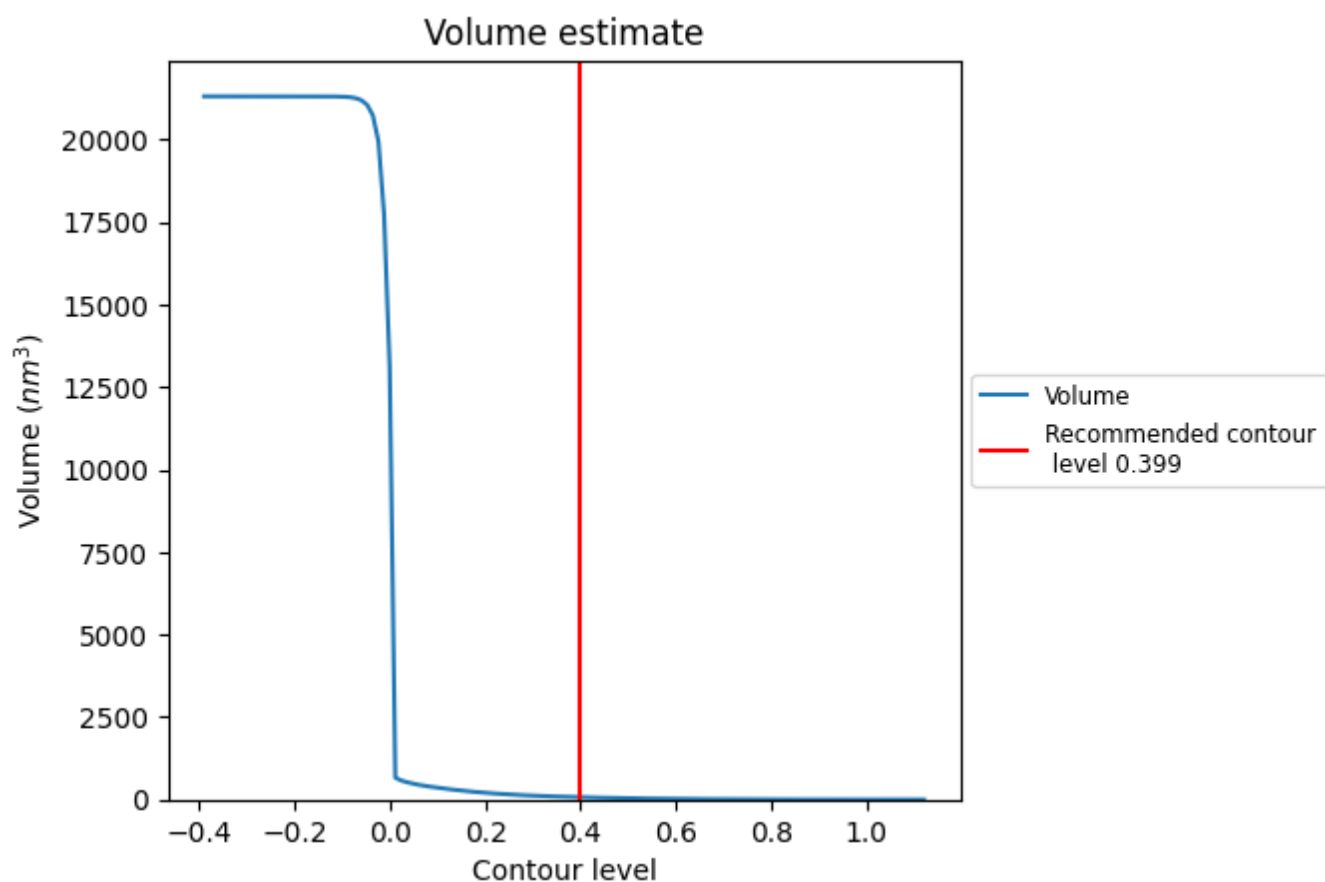
This section contains the results of statistical analysis of the map.

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.

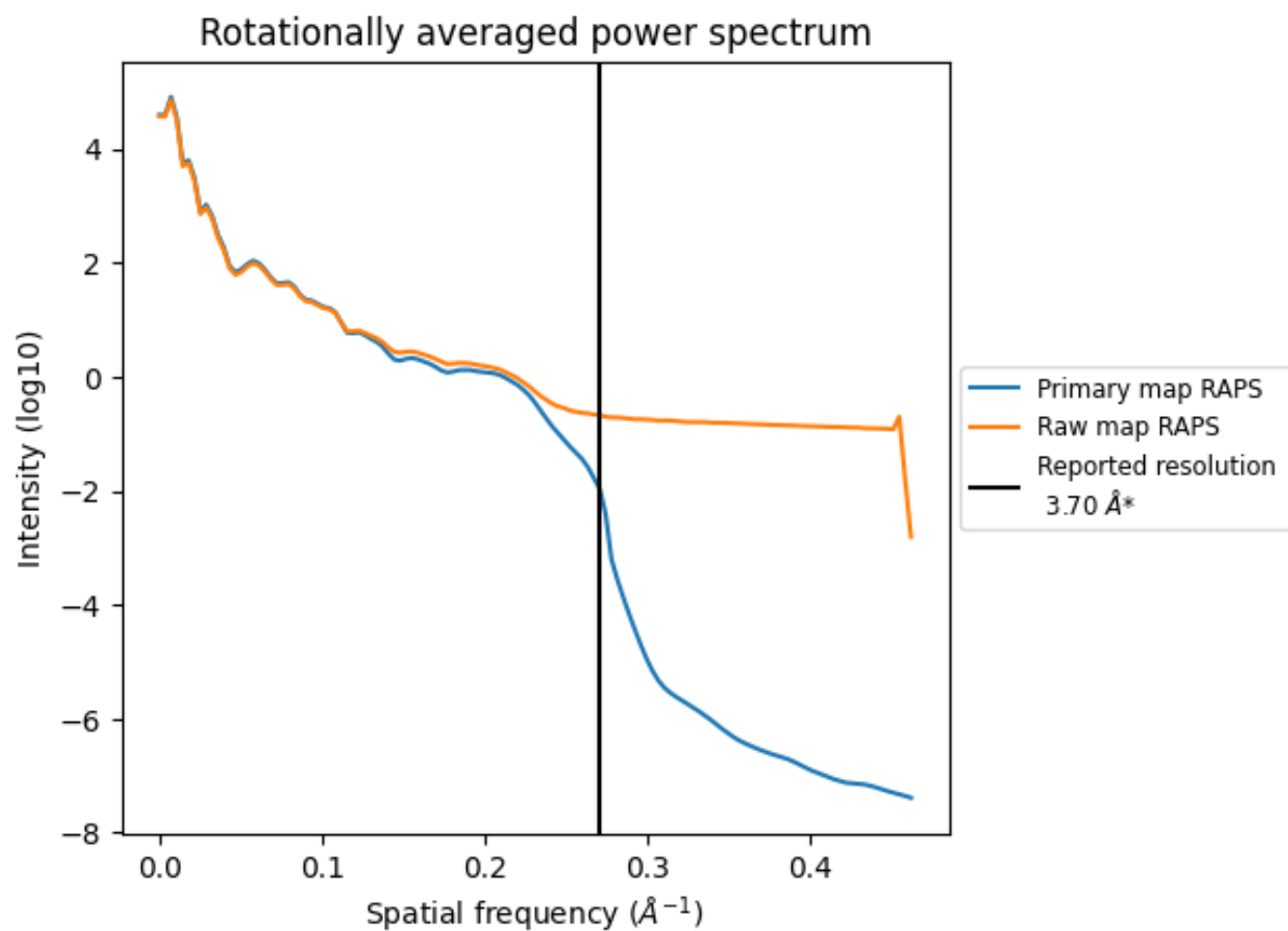
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 72 nm³; this corresponds to an approximate mass of 65 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 ⓘ

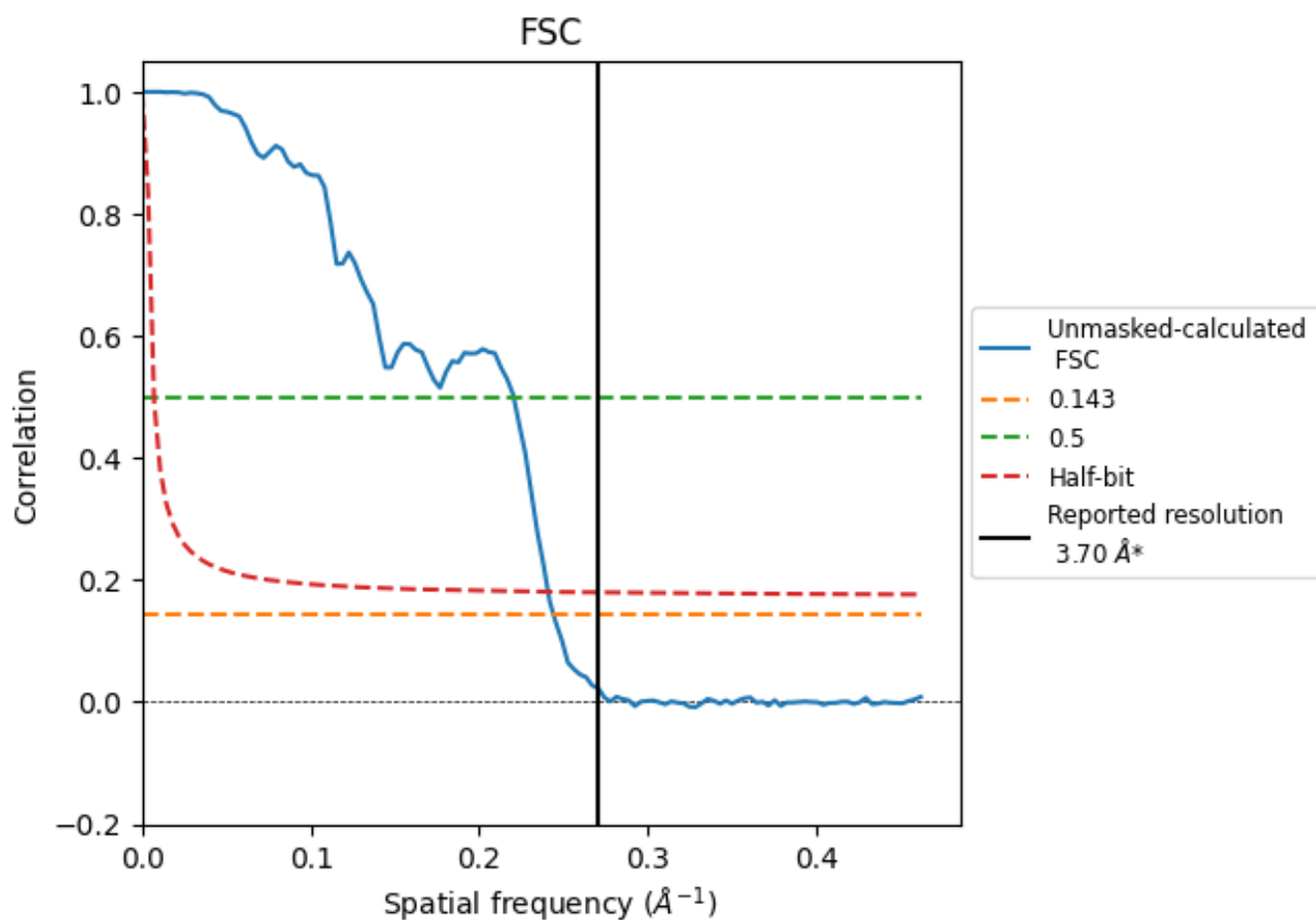


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

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 0.270 \AA^{-1}

8.2 Resolution estimates [i](#)

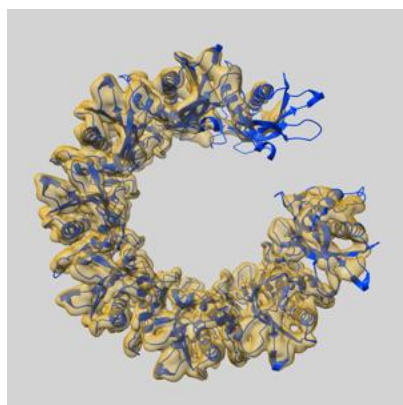
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.10	4.54	4.15

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

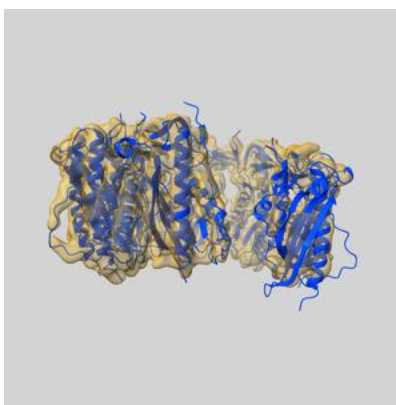
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-77073 and PDB model 13HS. Per-residue inclusion information can be found in section [3](#) on page [5](#).

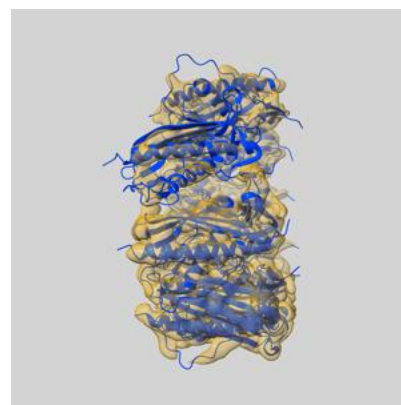
9.1 Map-model overlay [i](#)



X



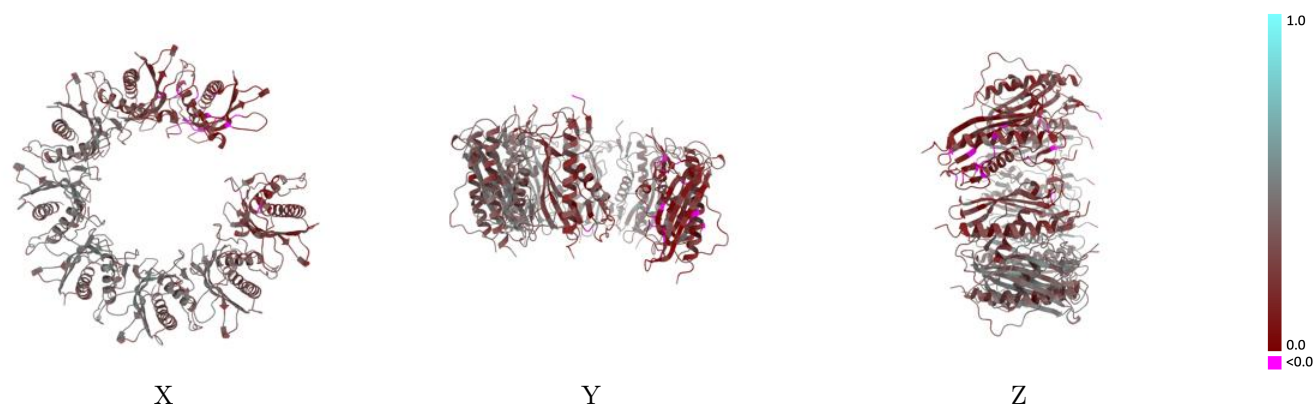
Y



Z

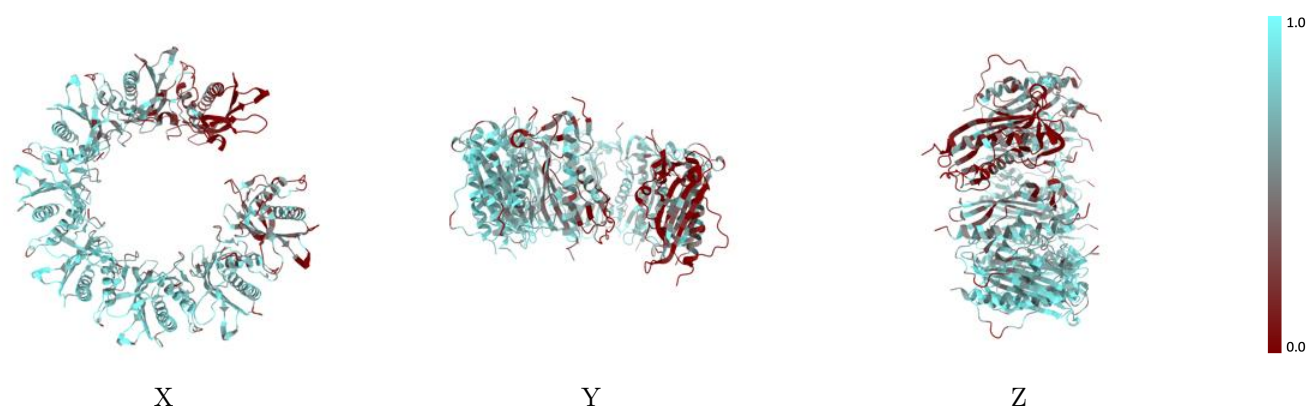
The images above show the 3D surface view of the map at the recommended contour level 0.399 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



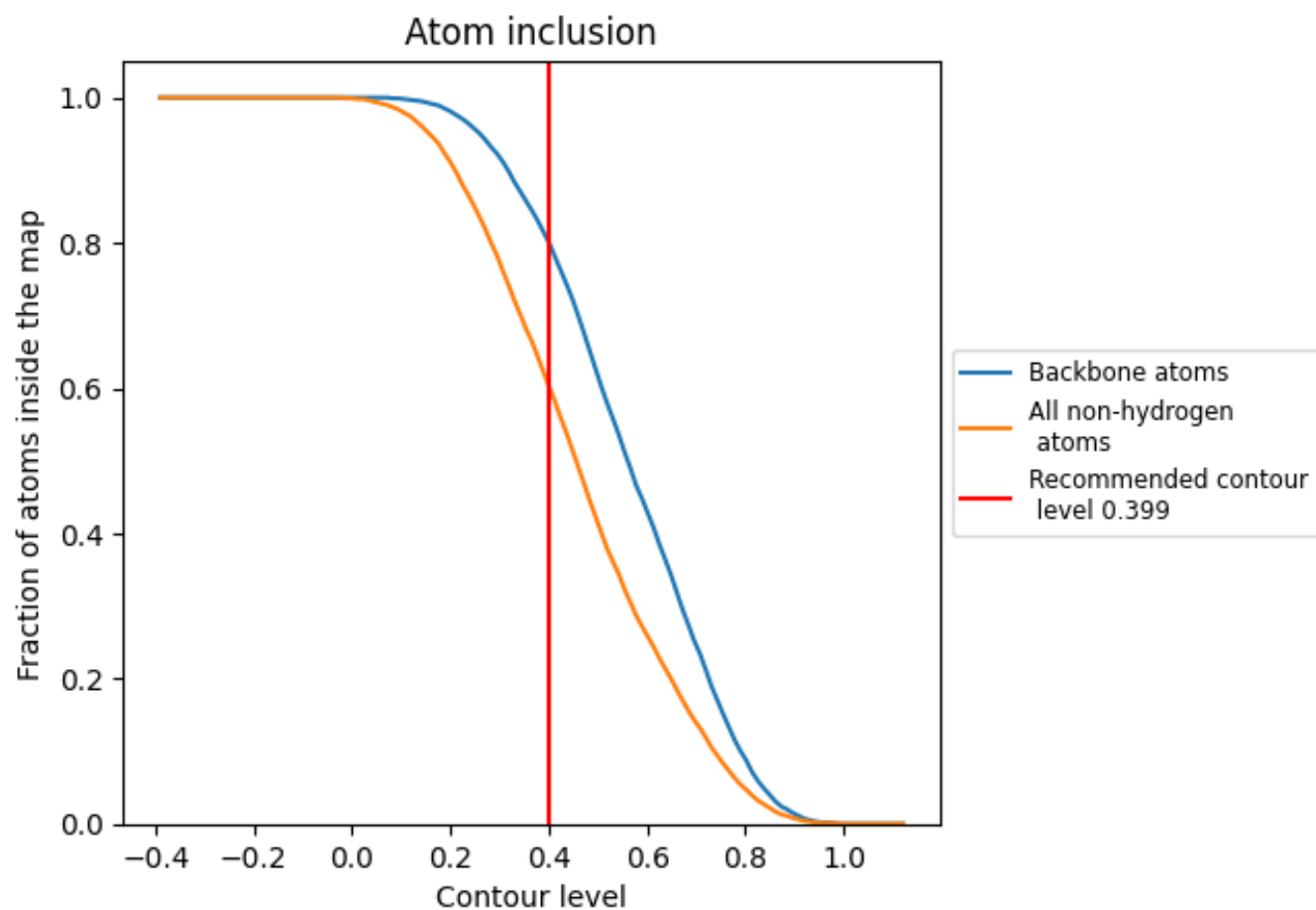
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.399).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 60% 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 (0.399) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6050	<div></div> 0.3390
A	<div></div> 0.4390	<div></div> 0.2530
B	<div></div> 0.6770	<div></div> 0.3800
C	<div></div> 0.7600	<div></div> 0.4190
D	<div></div> 0.7720	<div></div> 0.4280
E	<div></div> 0.7760	<div></div> 0.4220
F	<div></div> 0.7220	<div></div> 0.3950
G	<div></div> 0.5470	<div></div> 0.2730
H	<div></div> 0.1510	<div></div> 0.1430

1.0

0.0

<0.0