



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 09:36 AM UTC

PDB ID : 9FLS / pdb_00009fls
EMDB ID : EMD-50538
Title : CryoEM structure of the fragment-3 (2061-2397) in the grappling hook protein A (GhpA) in the bacterium *Aureispira* sp. CCB-QB1
Authors : Lien, Y.-W.; Amendola, D.; Lee, K.S.; Bartlau, N.; Xu, J.; Furusawa, G.; Polz, M.F.; Stocker, R.; Weiss, G.L.; Pilhofer, M.
Deposited on : 2024-06-05
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:

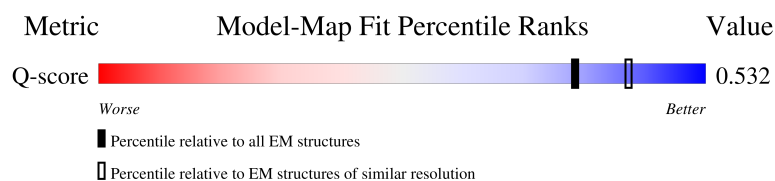
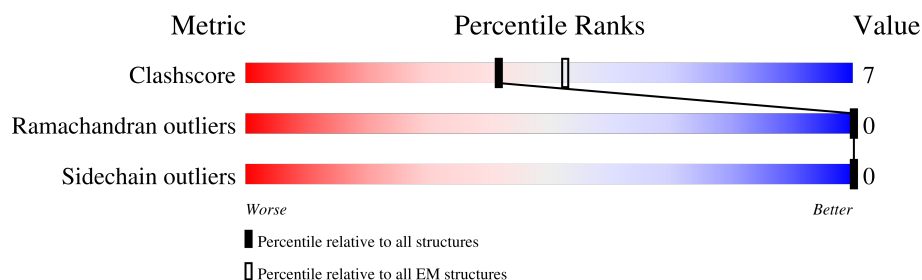
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.40 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.



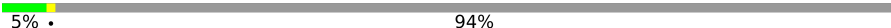


Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	5898	
1	B	5898	
1	C	5898	
1	D	5898	

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Mol	Chain	Length	Quality of chain
1	E	5898	 5% • 94%
1	F	5898	 5% • 94%
1	G	5898	 5% • 94%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 16604 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 The grappling hook protein A (GhpA) in the bacterium *Aureispira* sp. CCB-QB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	337	Total	C	N	O	S	0	0
			2372	1456	384	522	10		
1	B	337	Total	C	N	O	S	0	0
			2372	1456	384	522	10		
1	C	337	Total	C	N	O	S	0	0
			2372	1456	384	522	10		
1	D	337	Total	C	N	O	S	0	0
			2372	1456	384	522	10		
1	E	337	Total	C	N	O	S	0	0
			2372	1456	384	522	10		
1	F	337	Total	C	N	O	S	0	0
			2372	1456	384	522	10		
1	G	337	Total	C	N	O	S	0	0
			2372	1456	384	522	10		









TYR	PHE	TYR	ILE	MET	GLU	LEU	ALA	ASP	GLY	GLN	ARG	PHE	GLN	GLY	PHE	VAL	GLU	VAL	ARG	ARG
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- Molecule 1: The grappling hook protein A (GhpA) in the bacterium *Aureispira* sp. CCB-QB1

Chain B: 5% 94%

TYR	VAL	ARG	LEU	ILE	VAL	PRO	THR	GLY	PHE	THR	PHE	ASP	ASN	ALA	SER	PHE	GLY	GLY	SER	ILE	GLN	THR	VAL	GLN	ASN	LEU	VAL	GLY	ILE	VAL	SER	GLY	ALA	PRO	ASN	ASN	PHE	VAL	VAL	ILE	ILE	ASP	PRO	ILE	ALA	GLN	SER	ASN	ASN	THR	THR	SER	ASP	THR	ILE	PHE	ALA	ALA	PRO	VAL
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GLY	SER	THR	VAL	ILE	LEU	LEU	GLU	TYR	PRO	VAL	GLY	SER	SER	MET	VAL	GLN	GLY	GLY	VAL	SER	SER	LEU	ILE	ILE	THR	THR	VAL	ASP	PRO	ALA	ALA	ALA	THR	THR	THR	ILE	GLY	VAL	VAL	PRO	VAL	ASP	ASP	ILE	CYS	THR	THR	GLN	GLY	VAL	VAL	TYR	GLU	PHE	GLY	ASP	THR	PRO	THR	THR	GLY	ASP	ASN	GLY	GLY	PRO	ILE
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ALA GLY ALA ASN GLU CYS LEU PRO ILE LEU PHE ARG PHE ASP LYS LYS VAL ASN GLY SER ASP GLY VAL TYR ASN ASN VAL PRO GLY GLY GLY SER ALA LEU HIS ILE ILE GLN TYR GLU LEU ASN ILE ASP ALA ALA ALA GLY THR LEU ASN GLY PRO ILE THR

ILE	THR	ASP	VAL	LEU	PRO	GLY	GLU	LEU	ALA	ALA	TYR	PHE	GLY	ASN	ILE	SER	SER	GLY	PRO	ALA	GLY	CYS	SER	ALA	VAL	VAL	GLU	PRO	THR	THR	GLY	GLY	LEU	GLY	GLY	THR	THR	LEU	THR	VAL	VAL	CYS	THR	ASN	GLY	SER	TYR	PRO	PRO	GLY	THR	THR	THR	THR	PHE	ASP	ALA	ALA	VAL
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SER	ASP	THR	LEU	GLU	THR	ILE	CYS	ASP	ASP	THR	ASP	ILE	ASN	ASN	GLY	ALA	THR	VAL	ASN	VAL	VAL	PRO	PRO	GLY	ASN	PRO	SER	SER	GLN	ASP	THR	VAL	VAL	THR	THR	HIS	VAL	VAL	GLU	HIS	VAL	VAL	LEU	LEU	GLY	HIS	THR	THR	ASN	ASN	THR	THR	VAL	SER	VAL	PRO	PRO	THR	THR	ILE	GLY	GLN	THR	VAL	VAL	LEU	LEU	TYR	THR
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[illegible]

HIS	THR	GLN	ASN	GLY	ALA	ASN	ILE	LEU	PRO	CYS	SER	PRO	SER	LEU	GLN	TYR	THR	ALA	ASP	VAL	ASN	GLN	THR	TYR	ALA	ASN	GLY	ASP	PRO	VAL	LEU	SER	ARG	ASP	ARG	LEU	THR	HIS	SER	SER	THR	LEU	THR	TYR	ASP	LEU	VAL	GLY	ALA	ALA	THR	GLY	CYS	THR	THR	SER	THR	ALA	TYR
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THR	PRO	PRO	ILE	ASP	ASP	VAL	VAL	ILE	ASP	ASP	ILE	PHE	PHE	GLN	LYS	THR	THR	VAL	ASN	ASN	SER	PRO	PRO	THR	THR	PRO	PRO	GLY	GLY	GLN	TRP	TRP	TRP	PRO	PRO	GLY	ASP	VAL	VAL	GLN	TYR	GLN	ARG	ARG	LEU	GLU	LEU	LEU	LEU	ASP	ASP	ASP	ASP	VAL	VAL	ILE	ILE	THR	THR	ASP	PHE	PHE	PRO	PRO	LEU	LEU	PRO	PRO	ILE
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HIS	ASP	VAL	ALA	SER	LEU	ALA	ALA	THR	PHE	GLY	THR	ASP	VAL	ARG	PHE	ASP	PRO	ALA	THR	CYS	TRP	THR	THR	THR	ARG	ASP	ILE	PRO	PRO	THR	ASN	SER	SER	LEU	LEU	ASP	PHE	GLY	ASP	VAL	VAL	ILE	THR	GLY	CYS	VAL	ASP	ILE	VAL	LEU	LEU	THR	ILE
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ASP	ILE	PRO	PRO	THR	THR	LEU	PRO	PHE	ALA	ALA	ASP	GLY	LEU	PHE	HIS	SER	ASN	PHE	MET	GLN	VAL	ASN	ASP	ASN	SER	THR	THR	ALA	ALA	ASN	ASN	ILE	THR	THR	ASN	SER	LEU	THR	THR	GLN	VAL	GLY	ALA	PRO	ASP	LEU	GLU	THR	LYS	GLY	ILE	VAL	SER	ASP	ASN	PRO	ASN	ASN
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THR	ILE	SER	PRO	THR	VAL	VAL	PRO	PRO	ASP	GLY	ASN	ALA	THR	ASP	SER	SER	ALA	GLY	ASP	GLN	LEU	PHE	PHE	ASP	ILE	THR	ILE	ILE	GLU	ASN	VAL	GLY	GLY	GLY	ALA	ALA	ALA	PRO	PRO	GLU	LEU	THR	ASN	CYS	ALA	ALA	ALA	PRO	PRO	ASN	ASN	PRO	VAL
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VAL	ASP	GLY	GLY	SER	ASN	ASN	ALA	ALA	ALA	PHE	SER	GLY	GLY	PHE	VAL	GLY	THR	LEU	ILE	ASP	ASN	VAL	VAL	ALA	ALA	PRO	ASN	ASN	ASP	SER	ILE	ALA	PHE	THR	ALA	ALA	ALA	PRO	ASN	ASN	ASP	CYS	GLU	ALA	VAL	VAL	THR	ILE	LEU	THR	Tyr	SER	VAL	ARG	PHE
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ASP	ASN	THR	ALA	GLU	VAL	ASP	TRP	SER	SER	THR	ARG	GLY	GLY	VAL	LYS	PHE	PRO	PRO	VAL	GLU	ASP	ASP	ALA	ASN	GLY	GLY	ARG	ILE	ALA	ALA	ASP	PRO	THR	MET	ASN	LYS	VAL	VAL	VAL	ASP	ASP	Tyr	PHE	PHE	PRO	THR	ASN	SER	THR	THR	THR	THR	GLN	ALA	ALA	SER	ILE	ILE	GLY	GLU	VAL	VAL	VAL	TYR	THR	THR
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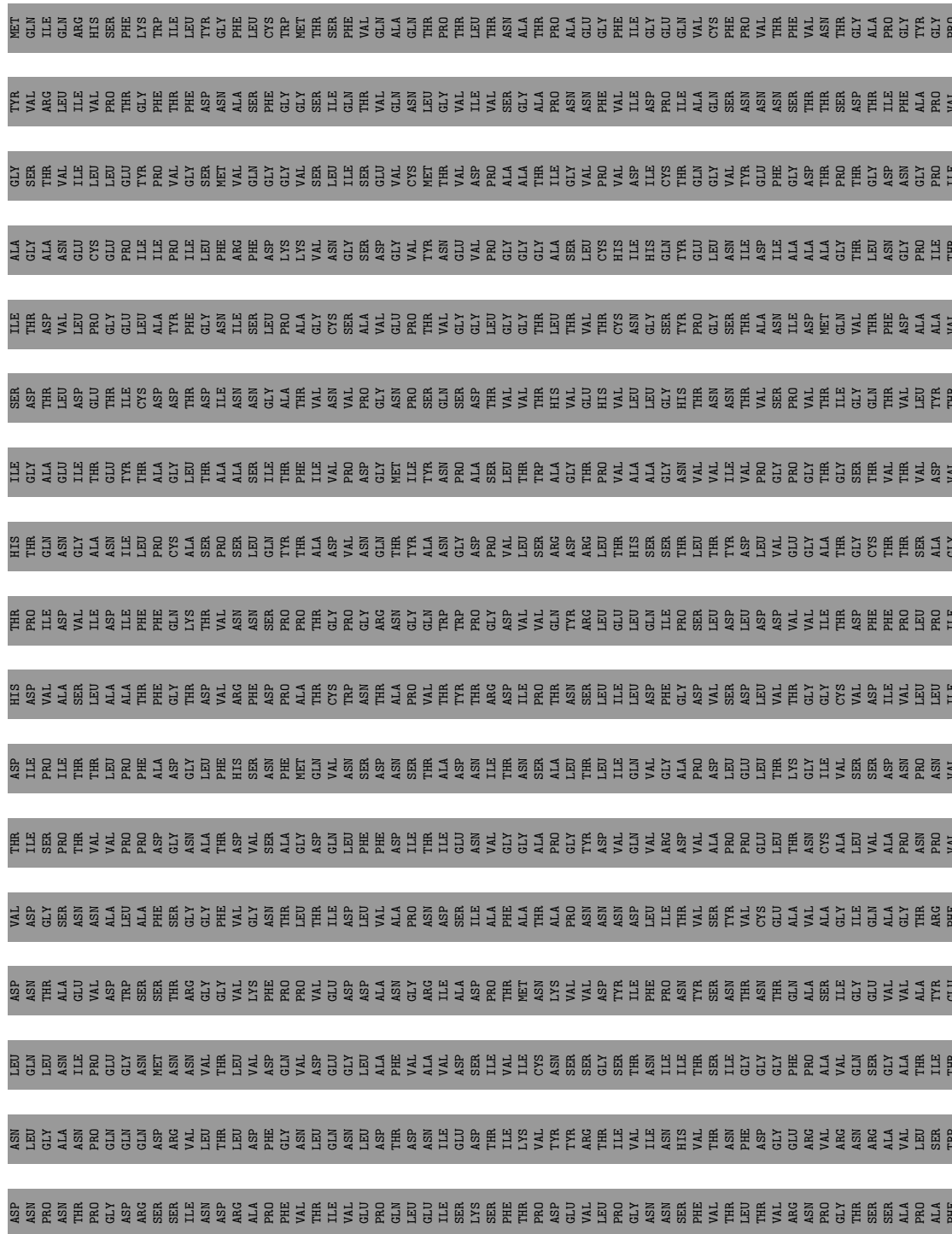
LEU GLN LEU LEU LEU ASN ASN PRO GLU GLY GLN MET MET ASN ASN VAL VAL THR LEU LEU ASP ASP GLN VAL ASP ASP GLU GLY GLY LEU ALA PHE VAL ALA ALA ALA ASP SER SER ILE VAL ILE CYS ASN SER ASN SER SER THR THR ILE ILE ILE ILE THR SER ILE ILE GLY GLY GLY GLY PHE PRO ALA ALA VAL VAL CLN SER GLY ALA THR ILE THR

















- Molecule 1: The grappling hook protein A (GhpA) in the bacterium *Aureispira* sp. CCB-QB1

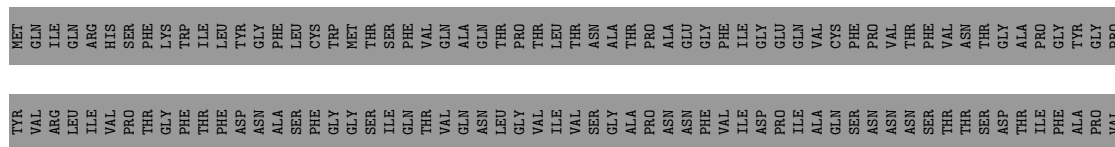
94%

[illegible]

















[illegible]

- Molecule 1: The grappling hook protein A (GhpA) in the bacterium *Aureispira* sp. CCB-QB1

Chain F:  5% .

94%

[illegible]









WORLDWIDE
PDB
PROTEIN DATA BANK







[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C7	Depositor
Number of particles used	151084	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	9.081	Depositor
Minimum map value	-6.311	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.168	Depositor
Recommended contour level	1	Depositor
Map size (Å)	319.50003, 319.50003, 319.50003	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.065, 1.065, 1.065	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	0.90	1/2421 (0.0%)	1.11	8/3352 (0.2%)
1	B	0.90	1/2421 (0.0%)	1.11	8/3352 (0.2%)
1	C	0.90	1/2421 (0.0%)	1.11	8/3352 (0.2%)
1	D	0.90	1/2421 (0.0%)	1.11	8/3352 (0.2%)
1	E	0.90	1/2421 (0.0%)	1.11	8/3352 (0.2%)
1	F	0.90	1/2421 (0.0%)	1.11	8/3352 (0.2%)
1	G	0.90	1/2421 (0.0%)	1.11	8/3352 (0.2%)
All	All	0.90	7/16947 (0.0%)	1.11	56/23464 (0.2%)

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2132	CYS	CB-SG	-5.20	1.64	1.81
1	D	2132	CYS	CB-SG	-5.20	1.64	1.81
1	F	2132	CYS	CB-SG	-5.20	1.64	1.81
1	G	2132	CYS	CB-SG	-5.20	1.64	1.81
1	C	2132	CYS	CB-SG	-5.20	1.64	1.81

The worst 5 of 56 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	2156	PHE	CA-CB-CG	7.08	120.88	113.80
1	A	2156	PHE	CA-CB-CG	7.03	120.83	113.80
1	C	2156	PHE	CA-CB-CG	7.01	120.81	113.80
1	G	2156	PHE	CA-CB-CG	7.01	120.81	113.80
1	F	2156	PHE	CA-CB-CG	7.00	120.80	113.80

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2372	0	2234	31	0
1	B	2372	0	2234	32	0
1	C	2372	0	2234	31	0
1	D	2372	0	2234	31	0
1	E	2372	0	2234	33	0
1	F	2372	0	2234	33	0
1	G	2372	0	2234	35	0
All	All	16604	0	15638	219	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 219 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:E:2255:ASN:HD21	1:E:2295:ALA:HA	1.57	0.69
1:F:2255:ASN:HD21	1:F:2295:ALA:HA	1.57	0.69
1:B:2255:ASN:ND2	1:B:2295:ALA:HA	2.08	0.69
1:D:2255:ASN:HD21	1:D:2295:ALA:HA	1.57	0.69
1:G:2255:ASN:HD21	1:G:2295:ALA:HA	1.57	0.69

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	335/5898 (6%)	321 (96%)	14 (4%)	0	100	100
1	B	335/5898 (6%)	321 (96%)	14 (4%)	0	100	100
1	C	335/5898 (6%)	321 (96%)	14 (4%)	0	100	100
1	D	335/5898 (6%)	321 (96%)	14 (4%)	0	100	100
1	E	335/5898 (6%)	321 (96%)	14 (4%)	0	100	100
1	F	335/5898 (6%)	321 (96%)	14 (4%)	0	100	100
1	G	335/5898 (6%)	321 (96%)	14 (4%)	0	100	100
All	All	2345/41286 (6%)	2247 (96%)	98 (4%)	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	274/4919 (6%)	274 (100%)	0	100	100
1	B	274/4919 (6%)	274 (100%)	0	100	100
1	C	274/4919 (6%)	274 (100%)	0	100	100
1	D	274/4919 (6%)	274 (100%)	0	100	100
1	E	274/4919 (6%)	274 (100%)	0	100	100
1	F	274/4919 (6%)	274 (100%)	0	100	100
1	G	274/4919 (6%)	274 (100%)	0	100	100
All	All	1918/34433 (6%)	1918 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	2186	ASN
1	F	2186	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	F	2062	ASN
1	F	2255	ASN
1	C	2062	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

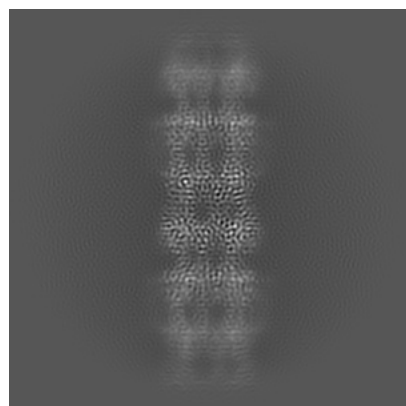
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-50538. These allow visual inspection of the internal detail of the map and identification of artifacts.

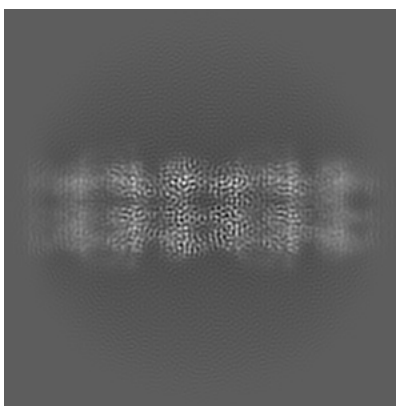
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

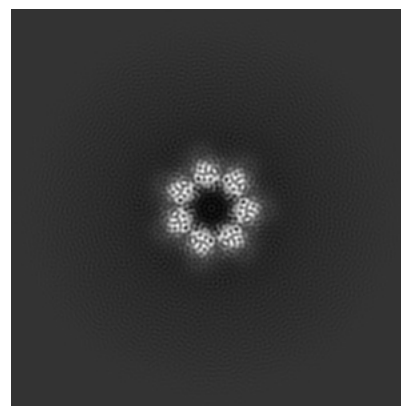
6.1.1 Primary map



X

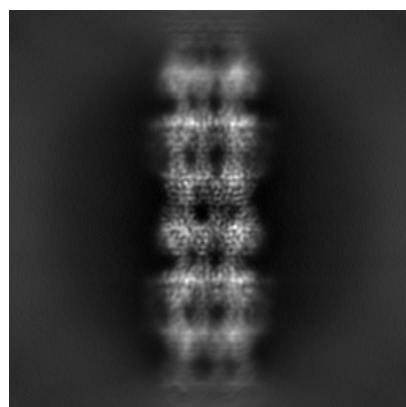


Y

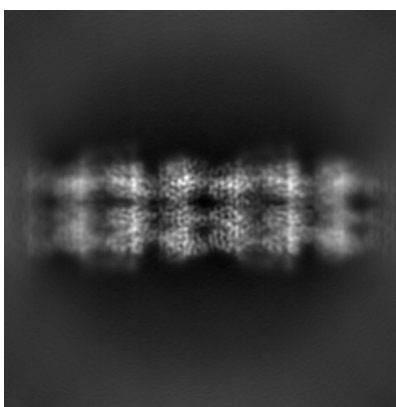


Z

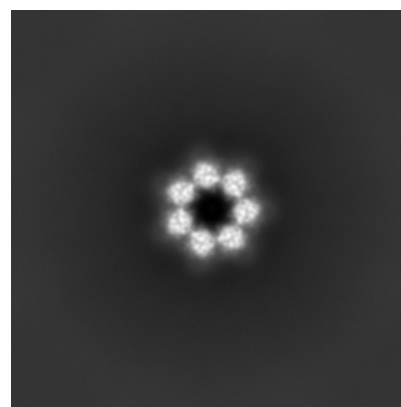
6.1.2 Raw map



X



Y

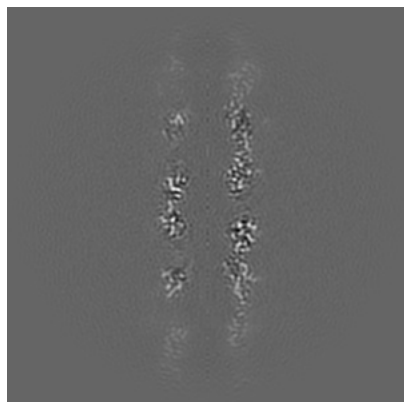


Z

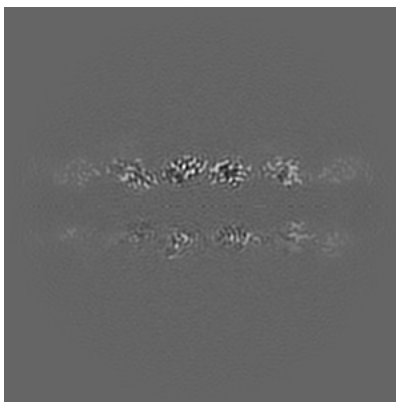
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

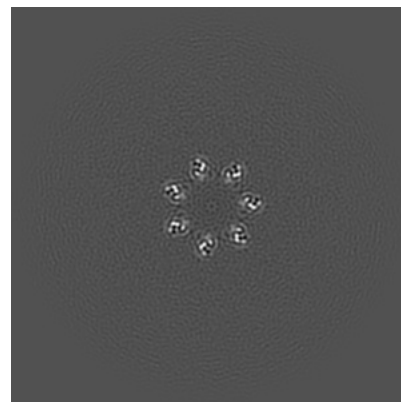
6.2.1 Primary map



X Index: 150

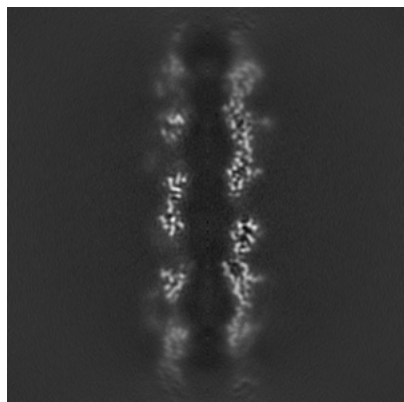


Y Index: 150

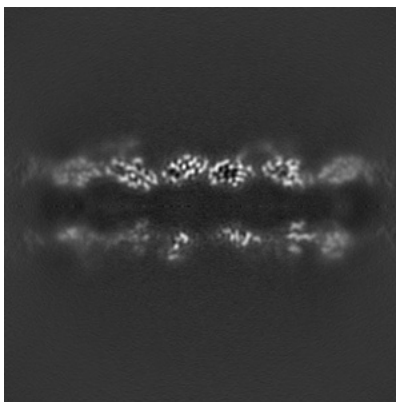


Z Index: 150

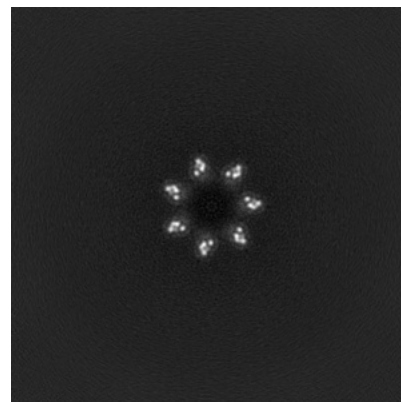
6.2.2 Raw map



X Index: 150



Y Index: 150

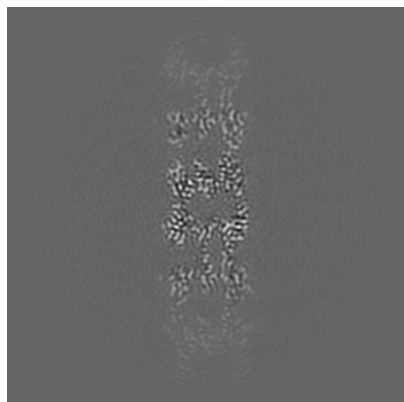


Z Index: 150

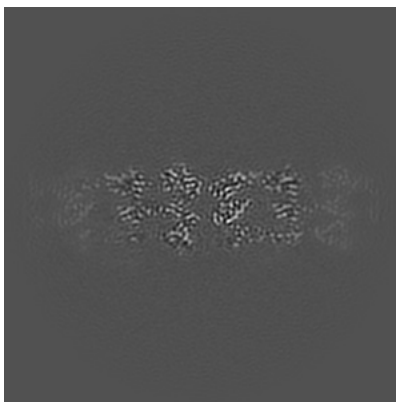
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

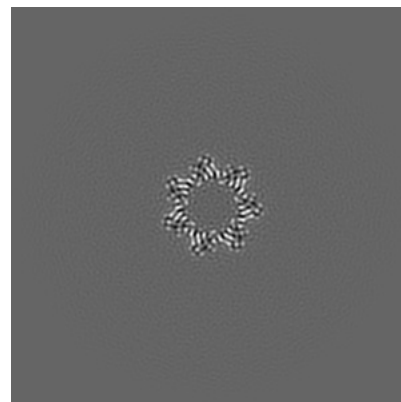
6.3.1 Primary map



X Index: 169

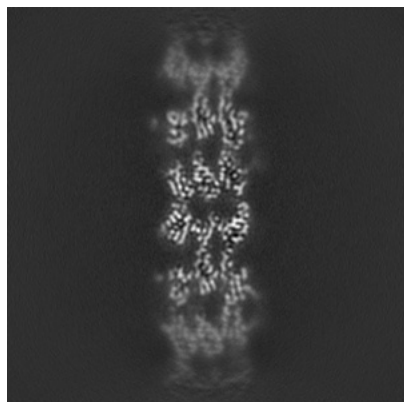


Y Index: 170

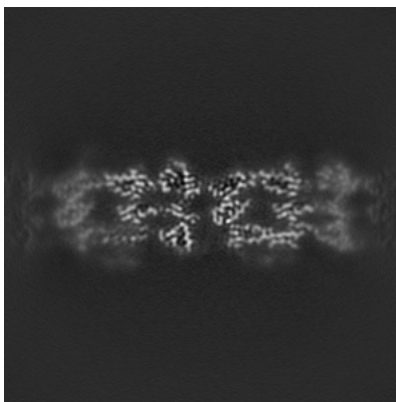


Z Index: 136

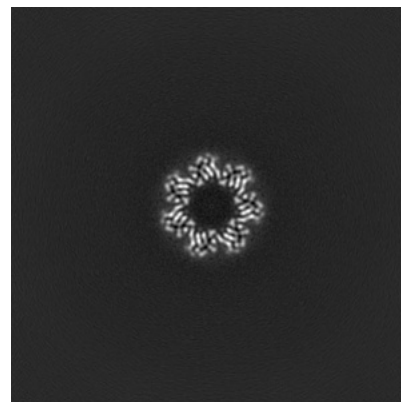
6.3.2 Raw map



X Index: 170



Y Index: 169

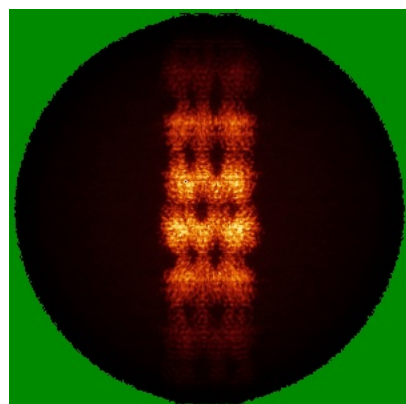


Z Index: 136

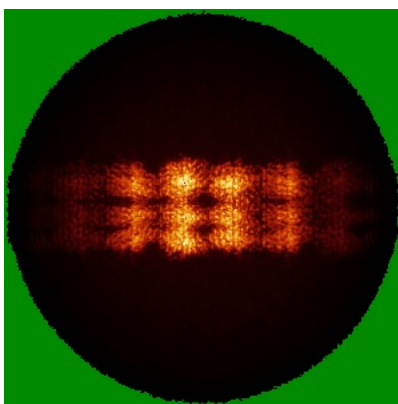
The images above show the largest variance slices of the map in three orthogonal directions.

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

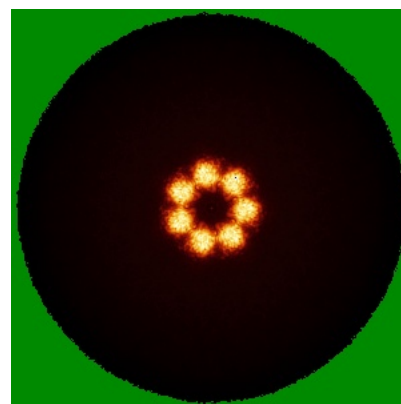
6.4.1 Primary map



X

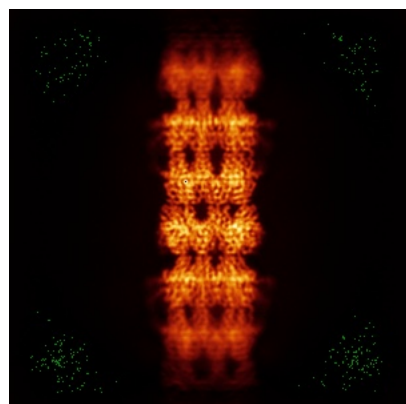


Y

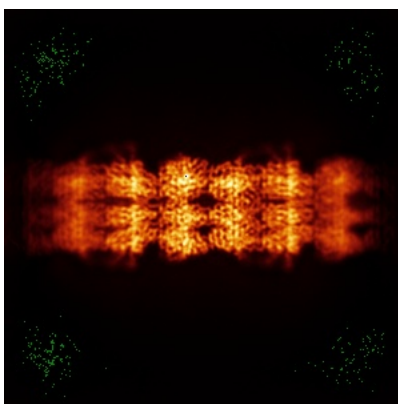


Z

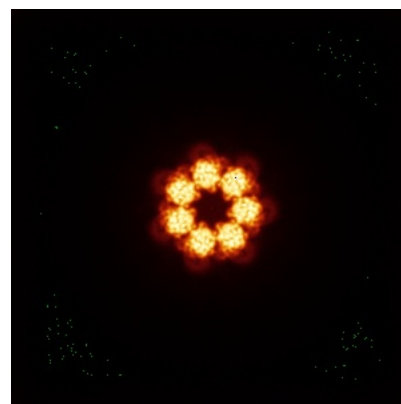
6.4.2 Raw map



X



Y

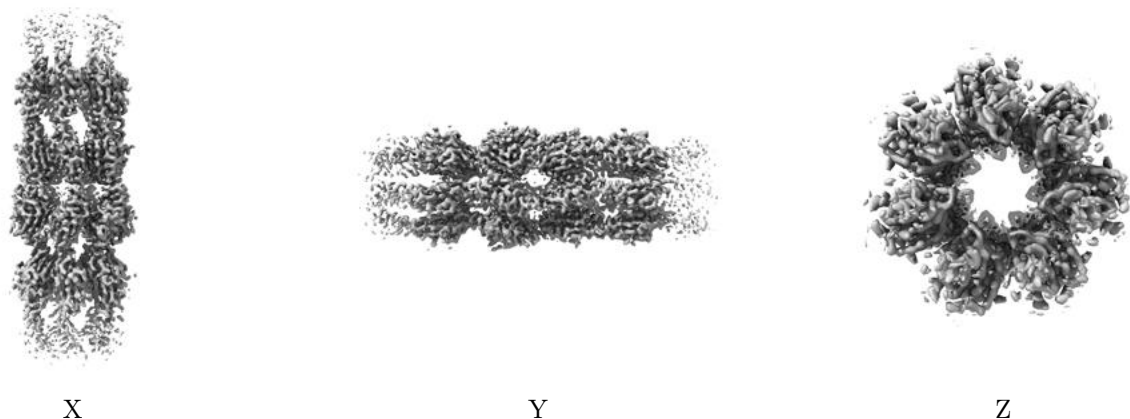


Z

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.

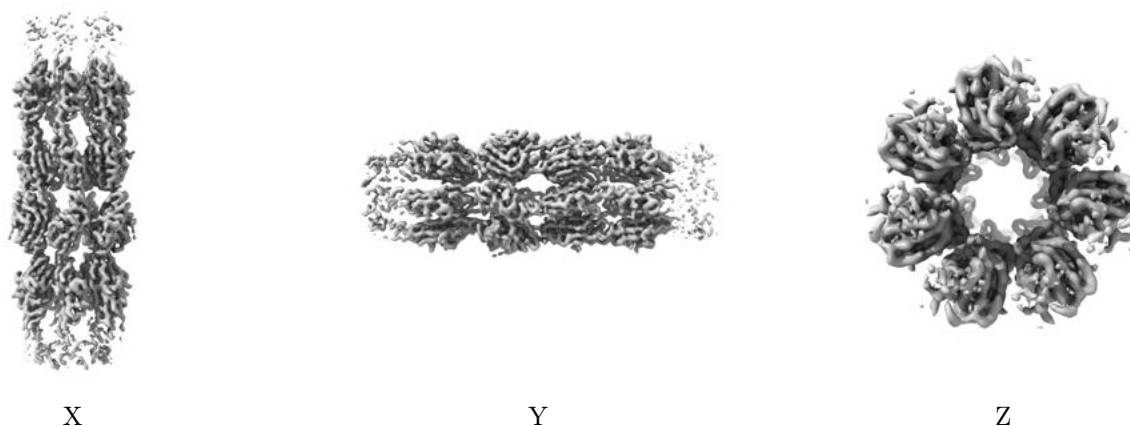
6.5 Orthogonal surface views [i](#)

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.

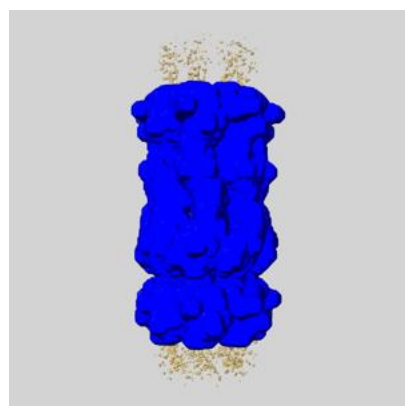
6.6 Mask visualisation [i](#)

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

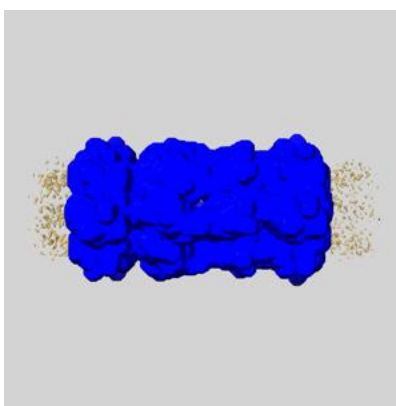
A mask typically either:

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

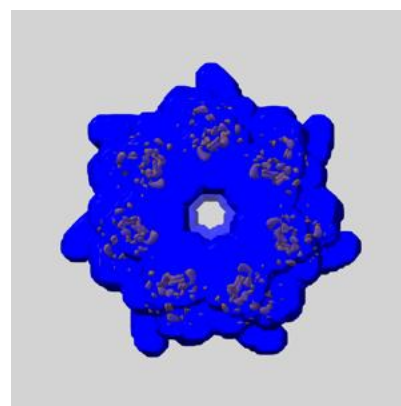
6.6.1 emd_50538_msk_1.map [i](#)



X



Y

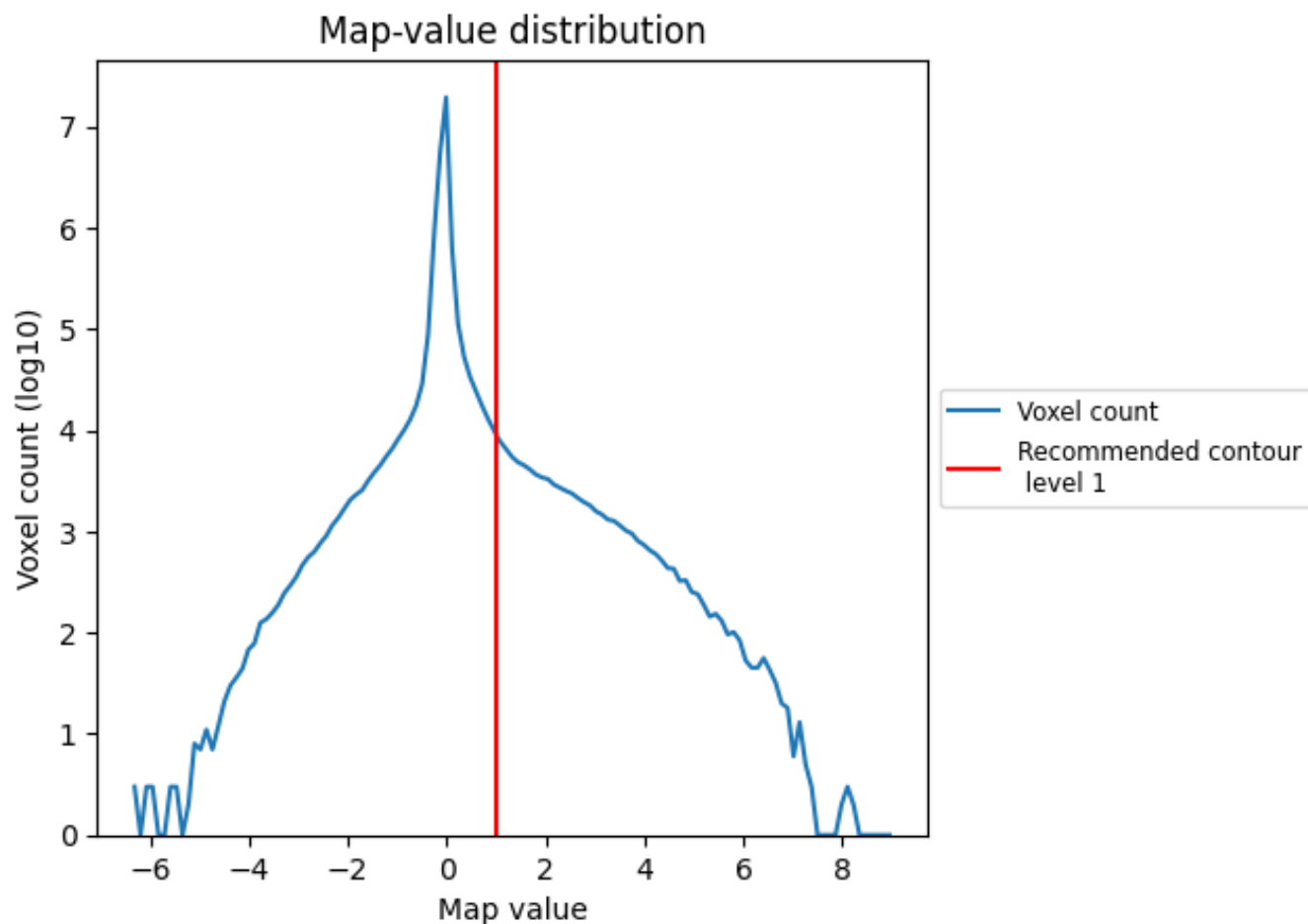


Z

7 Map analysis [i](#)

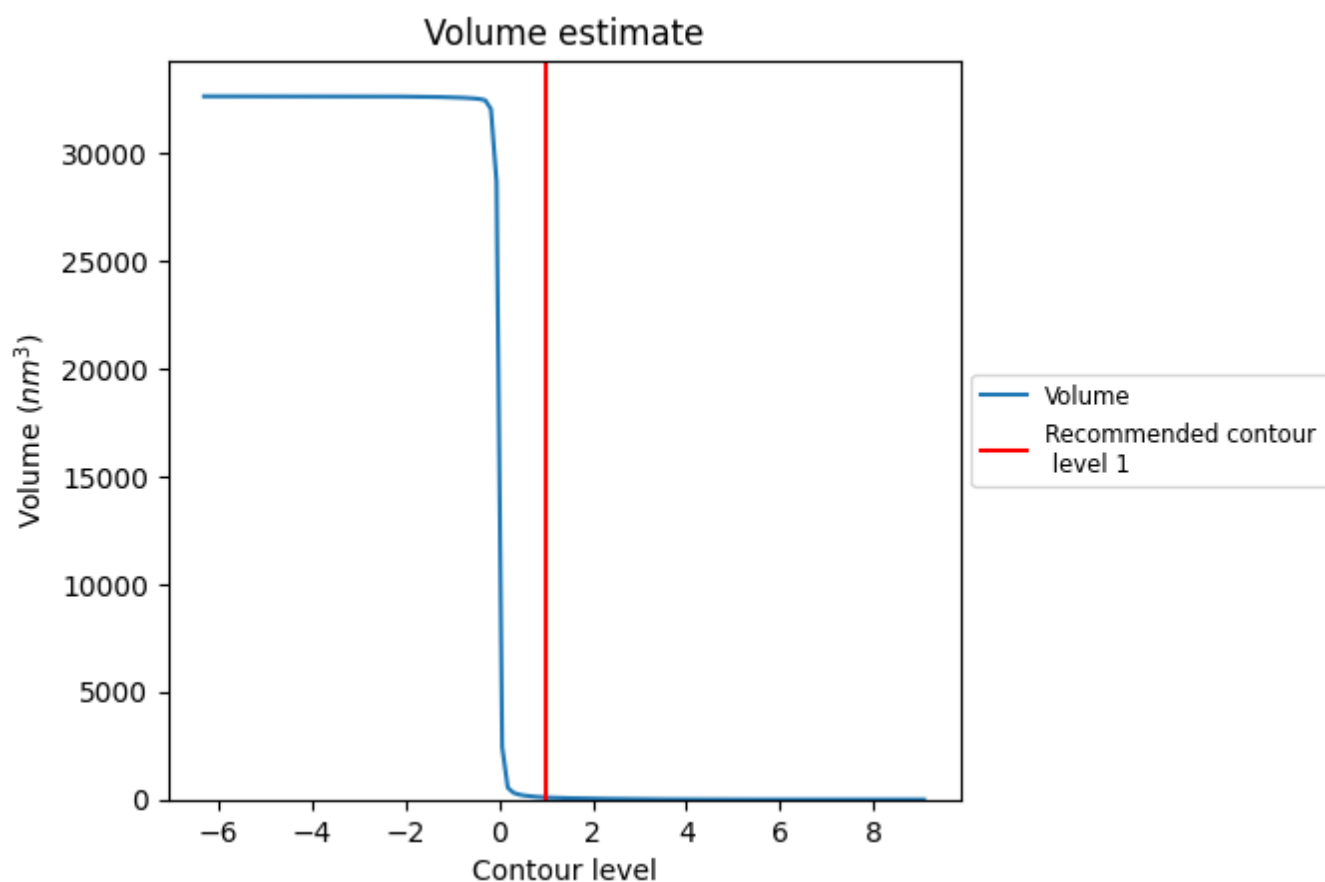
This section contains the results of statistical analysis of the map.

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.

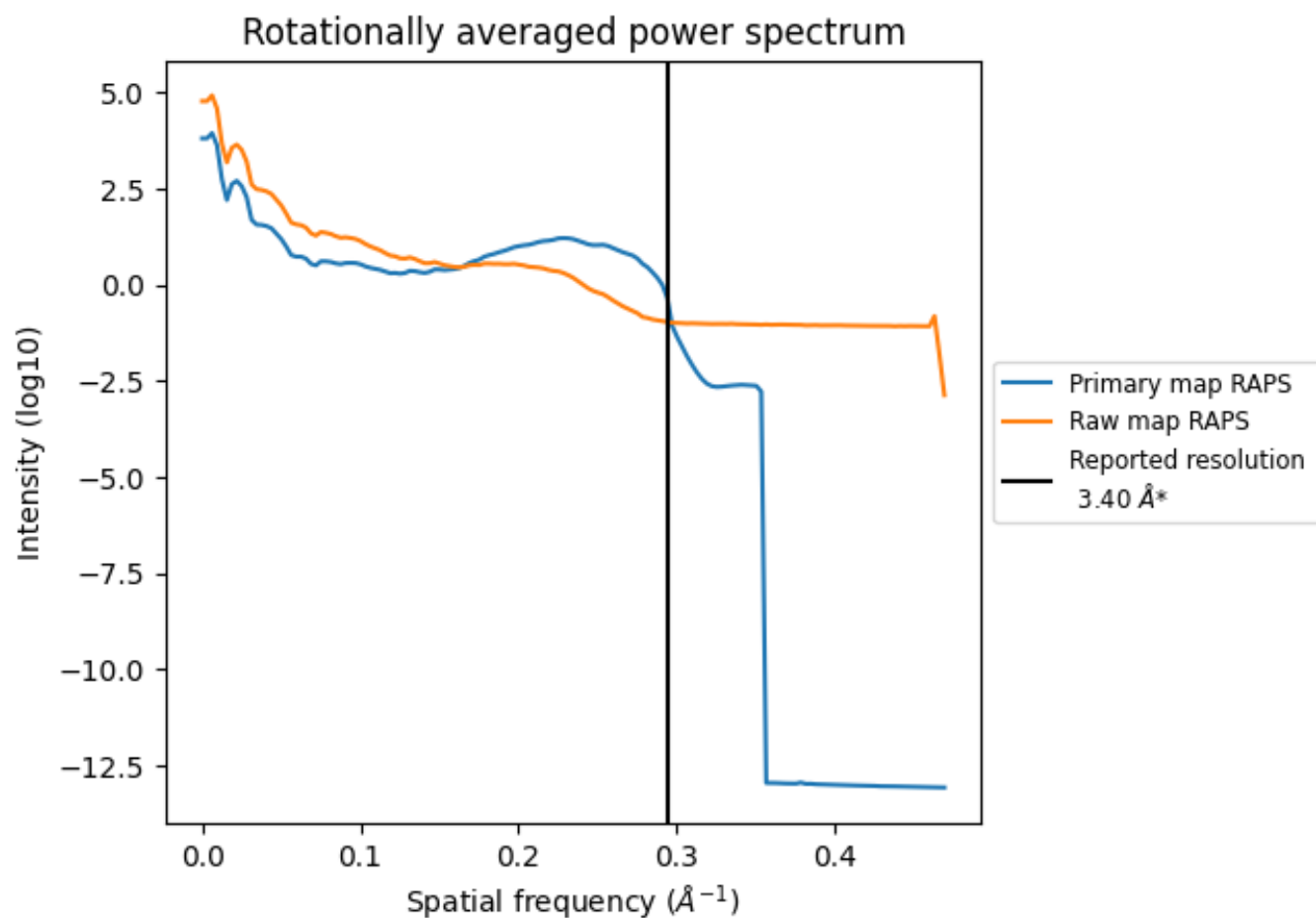
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 99 nm³; this corresponds to an approximate mass of 89 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 ⓘ

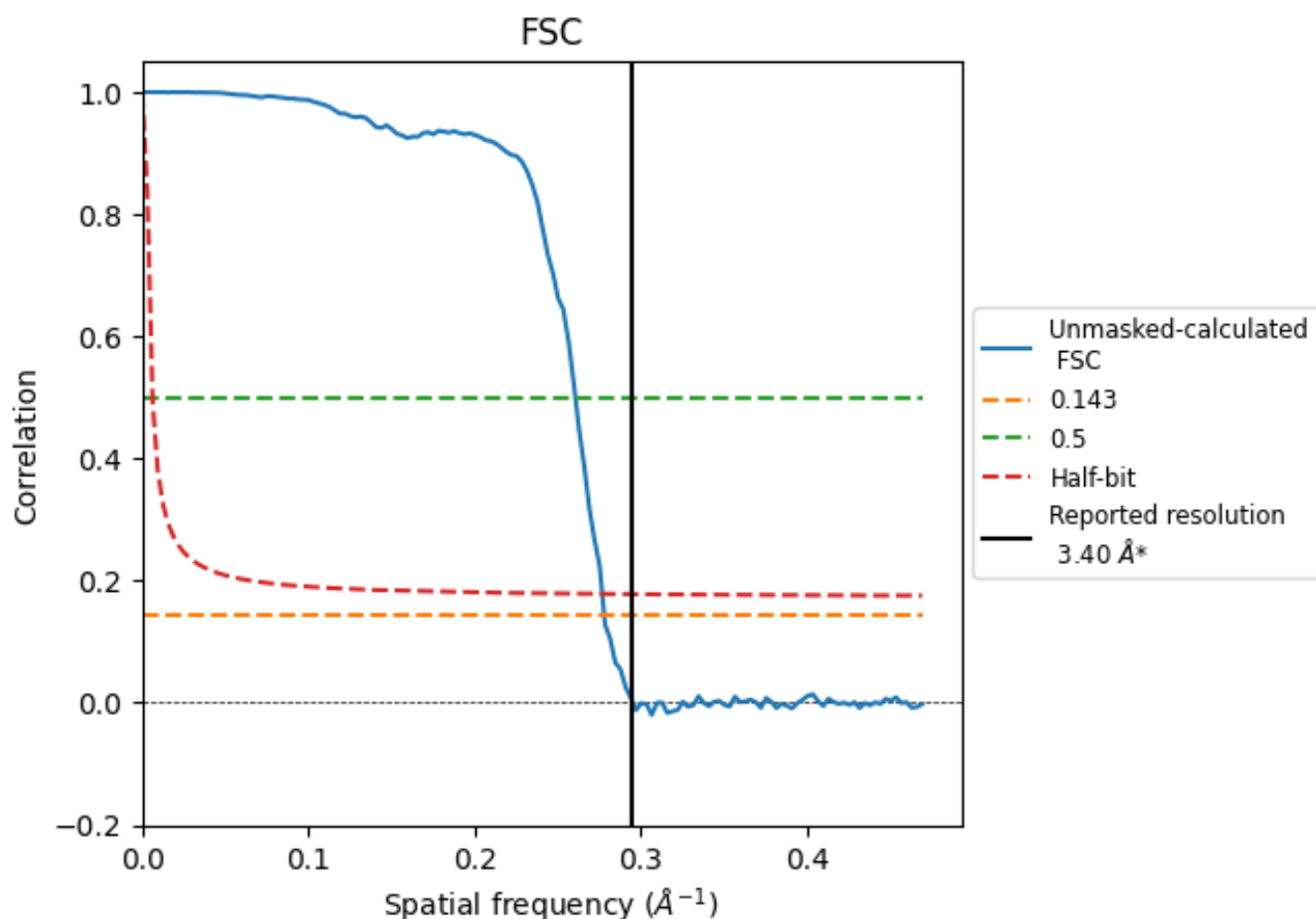


*Reported resolution corresponds to spatial frequency of 0.294 \AA^{-1}

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 \AA^{-1}

8.2 Resolution estimates [i](#)

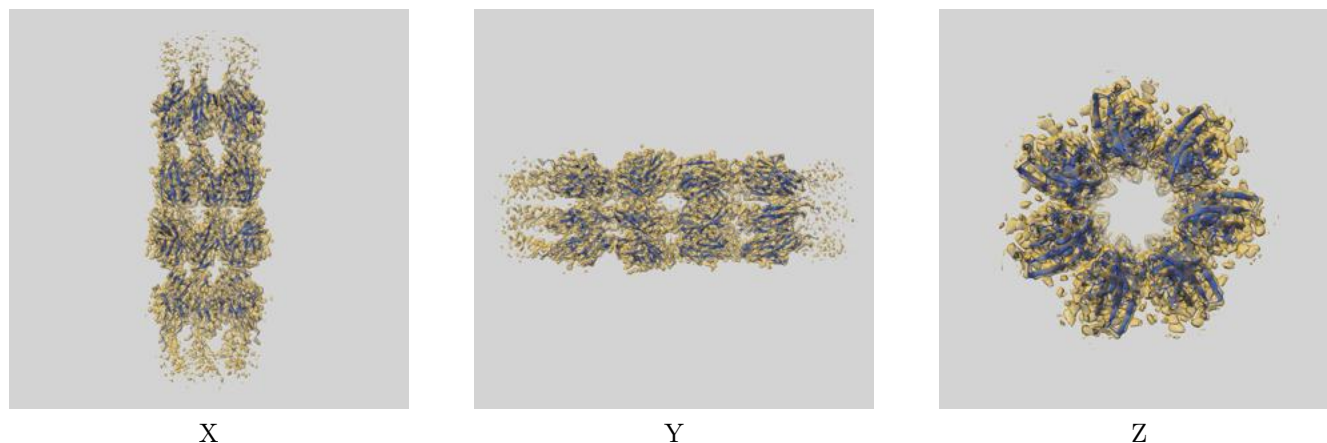
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.60	3.83	3.61

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

9 Map-model fit [i](#)

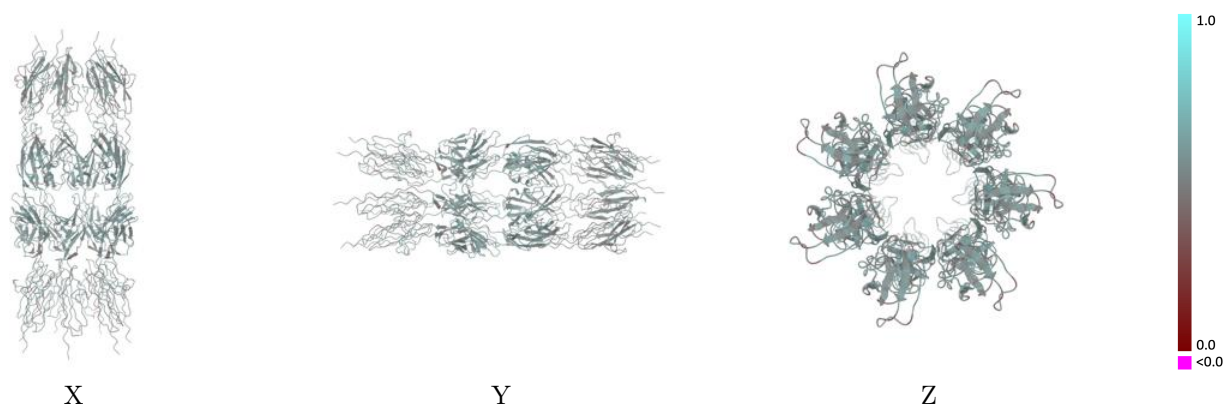
This section contains information regarding the fit between EMDB map EMD-50538 and PDB model 9FLS. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



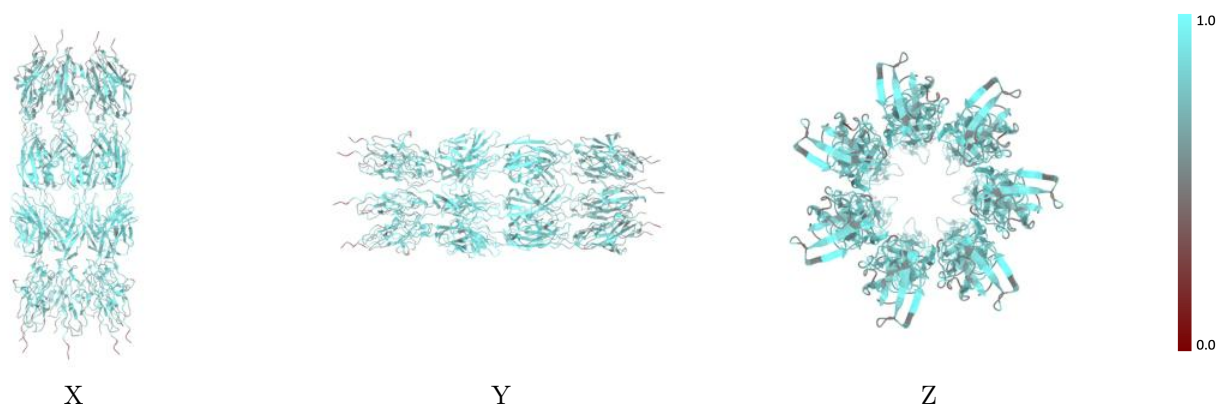
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



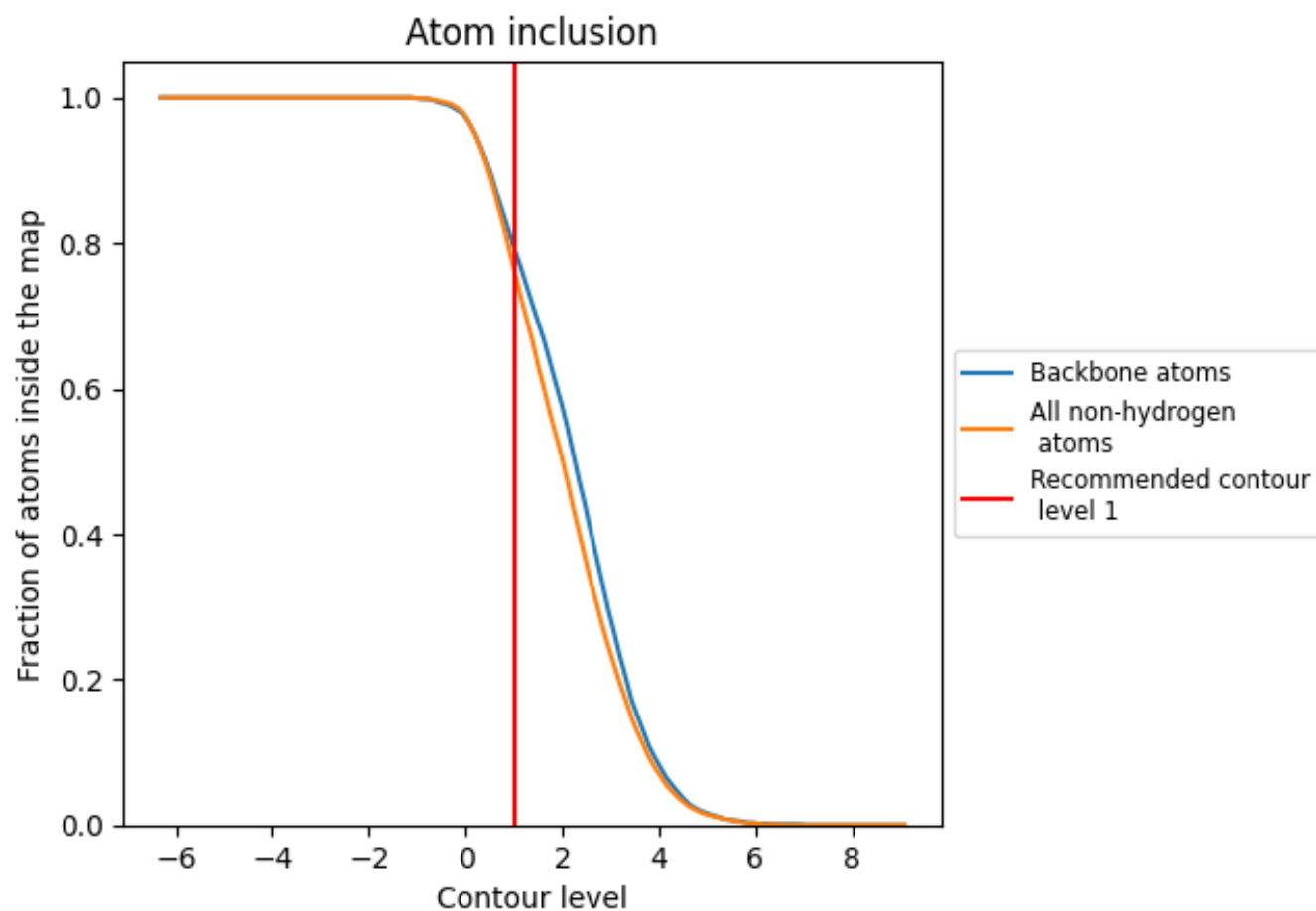
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 80% of all backbone atoms, 76% 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> 0.7640	<div><div></div></div> 0.5320
A	<div><div></div></div> 0.7640	<div><div></div></div> 0.5310
B	<div><div></div></div> 0.7630	<div><div></div></div> 0.5330
C	<div><div></div></div> 0.7650	<div><div></div></div> 0.5320
D	<div><div></div></div> 0.7630	<div><div></div></div> 0.5320
E	<div><div></div></div> 0.7610	<div><div></div></div> 0.5320
F	<div><div></div></div> 0.7650	<div><div></div></div> 0.5320
G	<div><div></div></div> 0.7670	<div><div></div></div> 0.5310

1.0

0.0

<0.0