



wwPDB EM Validation Summary Report ⓘ

Aug 30, 2025 – 02:54 PM EDT

PDB ID : 9NXO / pdb_00009nxo
EMDB ID : EMD-49909
Title : Pseudomonas phage Pa223 periplasmic tunnel (pre-ejection, dodecameric assembly)
Authors : Hou, C.F.D.; Cingolani, G.; Lokareddy, K.R.
Deposited on : 2025-03-25
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.dev126
MolProbity : 4-5-2 with Phenix2.0rc1
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) : 2.45.1

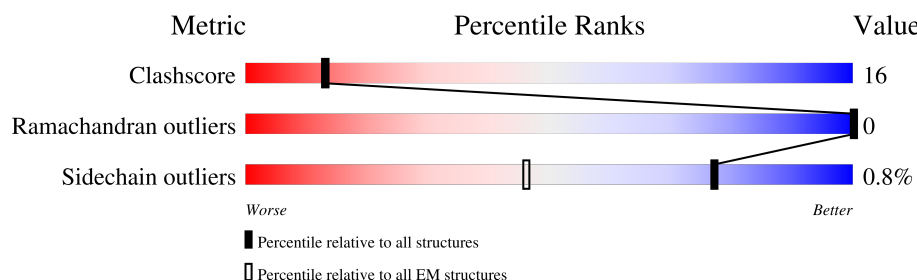
1 Overall quality at a glance

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.



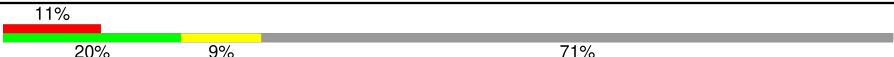



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	505	<div> <div>11%</div> <div>21% 8%</div> <div>71%</div> </div>
1	B	505	<div> <div>12%</div> <div>21% 8%</div> <div>71%</div> </div>
1	C	505	<div> <div>12%</div> <div>20% 9%</div> <div>71%</div> </div>
1	D	505	<div> <div>11%</div> <div>20% 9%</div> <div>71%</div> </div>
1	E	505	<div> <div>12%</div> <div>18% 10%</div> <div>71%</div> </div>
1	F	505	<div> <div>11%</div> <div>20% 9%</div> <div>71%</div> </div>
1	G	505	<div> <div>12%</div> <div>20% 9%</div> <div>71%</div> </div>
1	H	505	<div> <div>12%</div> <div>21% 8%</div> <div>71%</div> </div>

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Mol	Chain	Length	Quality of chain
1	I	505	
1	J	505	
1	K	505	
1	L	505	

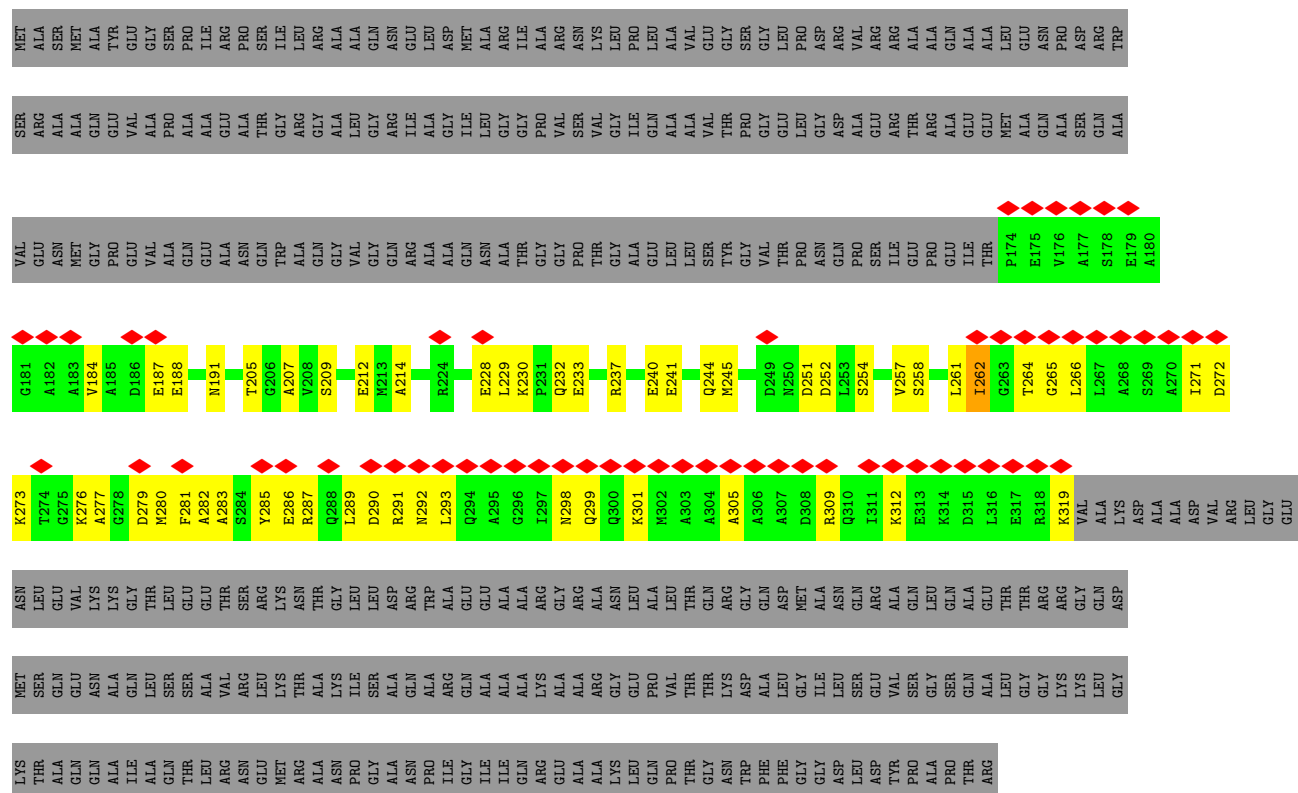
2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 13296 atoms, of which 0 are hydrogens and 0 are deuteriums.

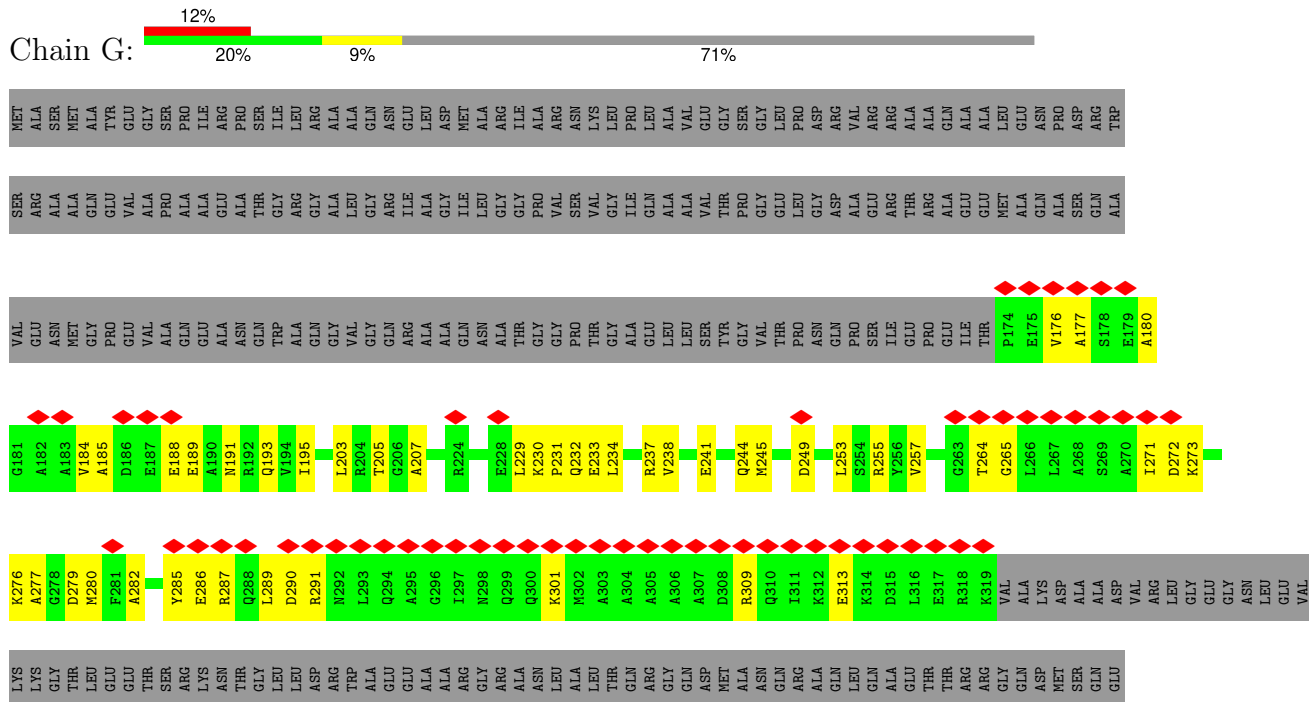
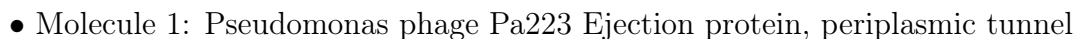
In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Pseudomonas phage Pa223 Ejection protein, periplasmic tunnel.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	146	Total	C	N	O	S	0	0
			1108	668	205	230	5		
1	B	146	Total	C	N	O	S	0	0
			1108	668	205	230	5		
1	C	146	Total	C	N	O	S	0	0
			1108	668	205	230	5		
1	D	146	Total	C	N	O	S	0	0
			1108	668	205	230	5		
1	E	146	Total	C	N	O	S	0	0
			1108	668	205	230	5		
1	F	146	Total	C	N	O	S	0	0
			1108	668	205	230	5		
1	G	146	Total	C	N	O	S	0	0
			1108	668	205	230	5		
1	H	146	Total	C	N	O	S	0	0
			1108	668	205	230	5		
1	I	146	Total	C	N	O	S	0	0
			1108	668	205	230	5		
1	J	146	Total	C	N	O	S	0	0
			1108	668	205	230	5		
1	K	146	Total	C	N	O	S	0	0
			1108	668	205	230	5		
1	L	146	Total	C	N	O	S	0	0
			1108	668	205	230	5		



- Chain F:



[illegible]

- Molecule 1: Pseudomonas phage Pa223 Ejection protein, periplasmic tunnel

[illegible]

VAL	GLU	ASN	MET	GLY	PRO	GLU	VAL	ALA	ALA	GLN	GLU	ALA	ALA	ASN	GLN	TRP	ALA	ALA	GLN	GLY	VAL	GLY	GLN	ARG	ALA	ALA	ALA	GLN	ASN	ALA	ALA	THR	GLY	GLY	PRO	THR	THR	GLY	ALA	ALA	GLU	LEU	LEU	SER	TYR	GLY	VAL	THR	THR	ASN	GLN	PRO	SER	ILE	GLU	PRO	GLU	GLU	ILE	THR	P174	E175	V176	A177	S178	E179	I180
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G181	A192	A193	V184	A195	D186	E187	E188	R192	T205	G206	A207	A214	R224	E228	L229	K230	P231	Q232	E233	L234	K235	M236	R237	E241	Q244	M245	D249	M250	D251	L261	L262	G263	T264	G265	L266	L267	A268	S269	A270	L271	D272	K273	T274	G275	K276	D279	M280	F281	L282
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Y285	Y286	Y287	Y288	Y289	Y290	Y291	Y292	Y293	Y294	Y295	Y296	Y297	Y298	Y299	Y300	Y301	Y302	Y303	Y304	Y305	Y306	Y307	Y308	Y309	Y310	Y311	Y312	Y313	Y314	Y315	Y316	Y317	Y318	Y319	VAL	ALA	LYS	ASP	ALA	ALA	ASP	VAL	ARG	LEU	GLY	GLY	ASN	LEU	GLU	VAL	LYS	LYS	GLY	THR	LEU	GLU	GLU
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[illegible]

VAL	ARG	LEU	LYS	THR	ALA	LYS	ILE	SER	ALA	GLN	ALA	ARG	GLN	ALA	ALA	ALA	LYS	ALA	ARG	GLY	GLU	PRO	VAL	THR	THR	ASP	LYS	ALA	ALA	LEU	ILE	LEU	SER	GLU	VAL	SER	GLY	SER	SER	GLN	ALA	LEU	GLY	GLY	LYS	LYS	ALA	GLN	ALA	GLN	ILE	ALA	GLN	THR	THR
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ARG	ASN	GLU	MET	ARG	ALA	ASN	PRO	GLY	ALA	ASN	PRO	GLY	ILE	ILE	ILE	GLN	ARG	GLU	ALA	ALA	LYS	LEU	GLN	THR	THR	GLY	ASN	PHE	PHE	GLY	ASP	GLY	LEU	ASP	TYR	PRO	ALA	PRO	THR	ARG
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- Molecule 1: Pseudomonas phage Pa223 Ejection protein, periplasmic tunnel



MET	ALA	SER	MET	ALA	TYR	GLU	GLY	PRO	SER	ILE	ARG	PRO	ALA	ALA	GLN	ASN	GLU	LEU	ASP	MET	ALA	ARG	ILE	ALA	ALA	ARG	ASN	LYS	LEU	PRO	PRO	LEU	ALA	ALA	VAL	LEU	PRO	ASP	ARG	VAL	ARG	ARG	ALA	ALA	GLN	ALA	ALA	ALA	ALA	LEU	GLU	ASN	PRO	PRO	ASP	ARG	TRP
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[illegible]

VAL	GLU	ASN	MET	GLY	PRO	GIU	VAL	ALA	GLN	GLU	ALA	ALA	ASN	GLN	TRP	ALA	GLN	GLY	VAL	GLY	GLN	ARG	ALA	ALA	GLN	ASN	ALA	THR	GLY	GLY	GLY	PRO	THR	THR	GLY	ALA	GLU	LEU	LEU	SER	SER	TYR	GLY	VAL	THR	PRO	ASN	GLN	GLN	PRO	SER	SER	ILE	GLU	PRO	PRO	GLU	ILE	GLU	THR	P174	E175	V176	A177	S178	F179
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Year	Country	Value
2012	Algeria	152
2013	Algeria	133
2014	Algeria	133
2015	Algeria	133
2016	Algeria	133
2017	Algeria	133
2018	Algeria	133
2019	Algeria	133
2020	Algeria	133
2021	Algeria	133
2022	Algeria	133
2023	Algeria	133
2024	Algeria	133
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2026	Algeria	133
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2062	Algeria	133
2063	Algeria	133
2064	Algeria	133
2065	Algeria	133
2066	Algeria	133
2067	Algeria	133
2068	Algeria	133
2069	Algeria	133
2070	Algeria	133



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	46120	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.056	Depositor
Minimum map value	-0.024	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	484.352, 484.352, 484.352	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.946, 0.946, 0.946	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	0.17	0/1114	0.47	0/1495
1	B	0.19	0/1114	0.51	0/1495
1	C	0.17	0/1114	0.43	0/1495
1	D	0.18	0/1114	0.50	0/1495
1	E	0.19	0/1114	0.52	0/1495
1	F	0.19	0/1114	0.54	0/1495
1	G	0.18	0/1114	0.52	0/1495
1	H	0.18	0/1114	0.54	0/1495
1	I	0.19	0/1114	0.50	0/1495
1	J	0.19	0/1114	0.55	0/1495
1	K	0.20	0/1114	0.55	0/1495
1	L	0.17	0/1114	0.48	0/1495
All	All	0.18	0/13368	0.51	0/17940

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	1108	0	1094	31	0
1	B	1108	0	1094	38	0
1	C	1108	0	1094	34	0
1	D	1108	0	1094	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	1108	0	1094	48	0
1	F	1108	0	1094	38	0
1	G	1108	0	1094	34	0
1	H	1108	0	1094	34	0
1	I	1108	0	1094	32	0
1	J	1108	0	1094	39	0
1	K	1108	0	1094	47	0
1	L	1108	0	1094	31	0
All	All	13296	0	13128	424	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 16.

The worst 5 of 424 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:B:230:LYS:HE3	1:B:231:PRO:HD2	1.63	0.80
1:L:176:VAL:HG13	1:L:276:LYS:HE2	1.63	0.80
1:H:180:ALA:O	1:H:184:VAL:HB	1.83	0.78
1:F:287:ARG:HH12	1:F:291:ARG:HD2	1.49	0.77
1:H:241:GLU:HG3	1:H:245:MET:HE3	1.70	0.72

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	144/505 (28%)	136 (94%)	8 (6%)	0	100	100
1	B	144/505 (28%)	133 (92%)	11 (8%)	0	100	100
1	C	144/505 (28%)	135 (94%)	9 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	144/505 (28%)	136 (94%)	8 (6%)	0	100	100
1	E	144/505 (28%)	131 (91%)	13 (9%)	0	100	100
1	F	144/505 (28%)	135 (94%)	9 (6%)	0	100	100
1	G	144/505 (28%)	133 (92%)	11 (8%)	0	100	100
1	H	144/505 (28%)	134 (93%)	10 (7%)	0	100	100
1	I	144/505 (28%)	136 (94%)	8 (6%)	0	100	100
1	J	144/505 (28%)	135 (94%)	9 (6%)	0	100	100
1	K	144/505 (28%)	133 (92%)	11 (8%)	0	100	100
1	L	144/505 (28%)	134 (93%)	10 (7%)	0	100	100
All	All	1728/6060 (28%)	1611 (93%)	117 (7%)	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	111/369 (30%)	109 (98%)	2 (2%)	54	80
1	B	111/369 (30%)	110 (99%)	1 (1%)	75	89
1	C	111/369 (30%)	109 (98%)	2 (2%)	54	80
1	D	111/369 (30%)	110 (99%)	1 (1%)	75	89
1	E	111/369 (30%)	109 (98%)	2 (2%)	54	80
1	F	111/369 (30%)	111 (100%)	0	100	100
1	G	111/369 (30%)	110 (99%)	1 (1%)	75	89
1	H	111/369 (30%)	111 (100%)	0	100	100
1	I	111/369 (30%)	111 (100%)	0	100	100
1	J	111/369 (30%)	111 (100%)	0	100	100
1	K	111/369 (30%)	110 (99%)	1 (1%)	75	89
1	L	111/369 (30%)	110 (99%)	1 (1%)	75	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1332/4428 (30%)	1321 (99%)	11 (1%)	77 90

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	319	LYS
1	G	249	ASP
1	L	319	LYS
1	K	215	GLN
1	C	261	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	299	GLN
1	J	299	GLN
1	J	193	GLN
1	K	232	GLN
1	C	299	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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

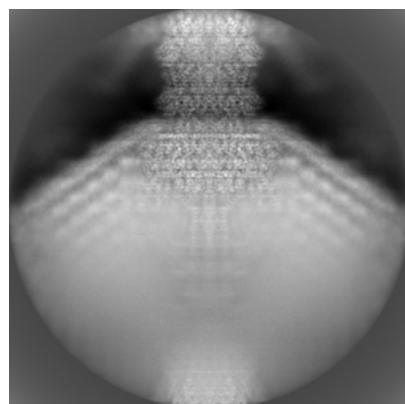
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-49909. These allow visual inspection of the internal detail of the map and identification of artifacts.

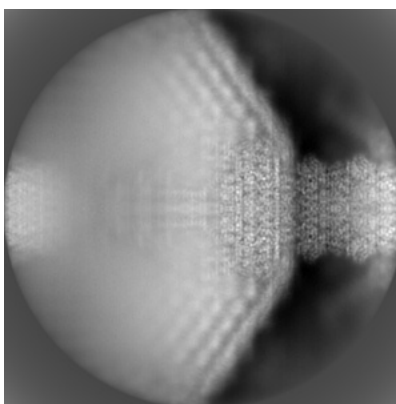
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

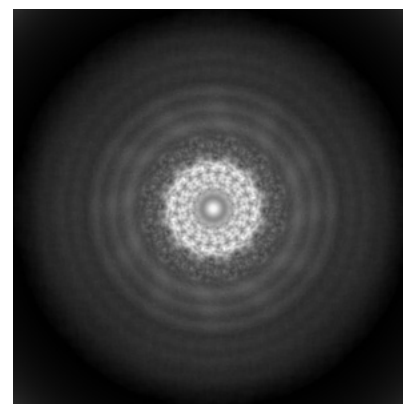
6.1.1 Primary map



X

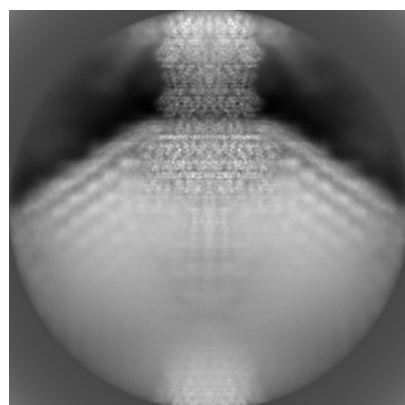


Y

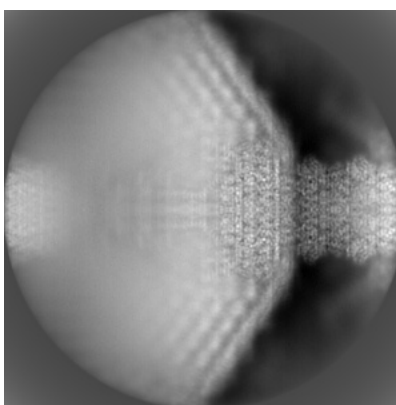


Z

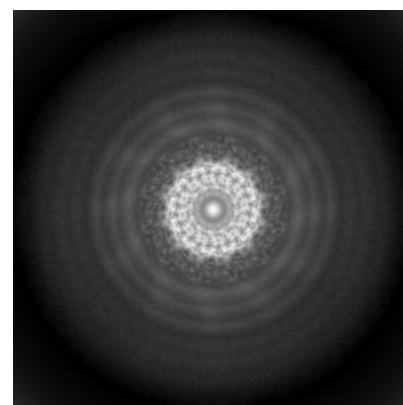
6.1.2 Raw map



X



Y

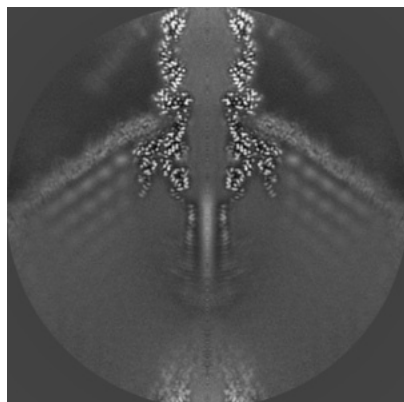


Z

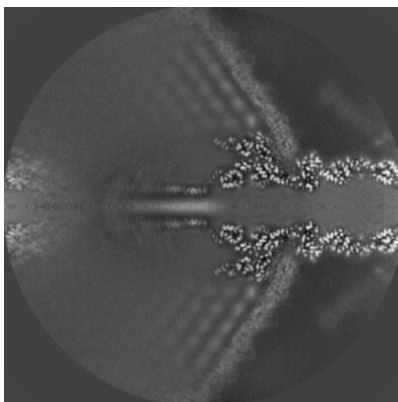
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

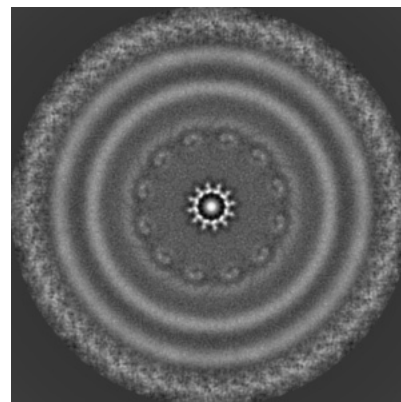
6.2.1 Primary map



X Index: 256

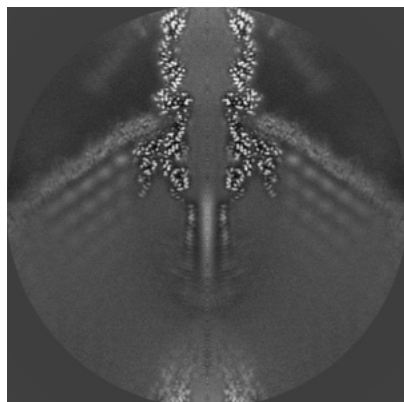


Y Index: 256

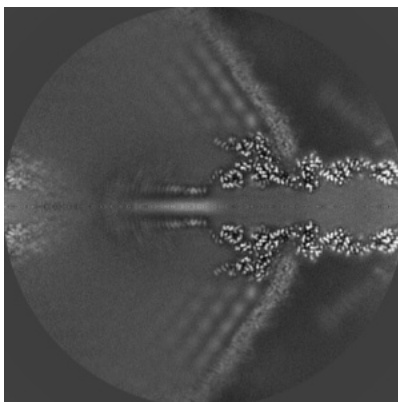


Z Index: 256

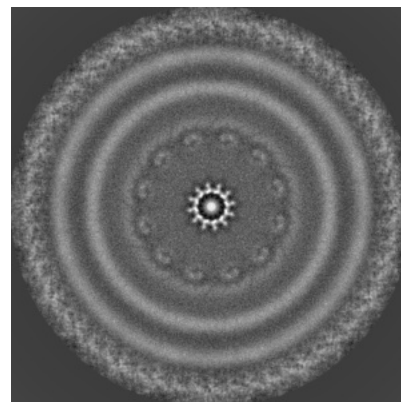
6.2.2 Raw map



X Index: 256



Y Index: 256

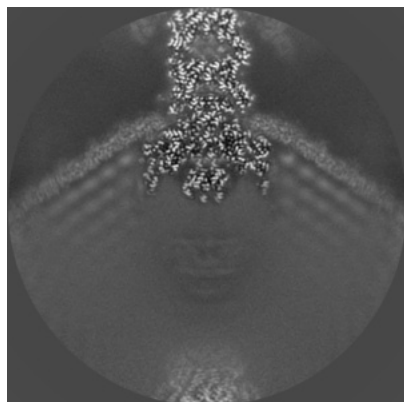


Z Index: 256

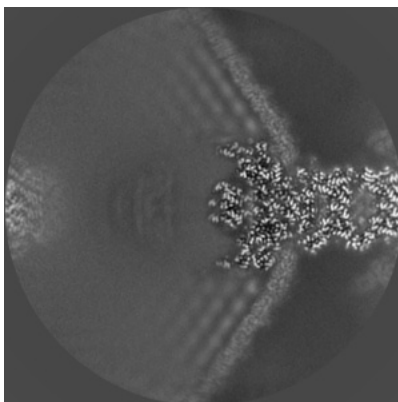
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

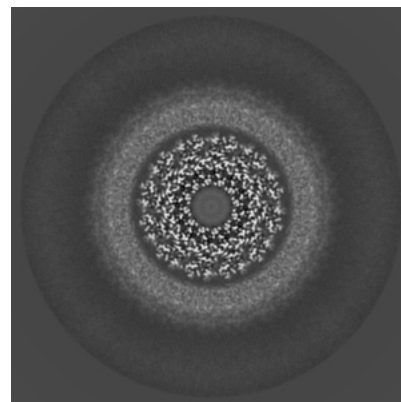
6.3.1 Primary map



X Index: 221

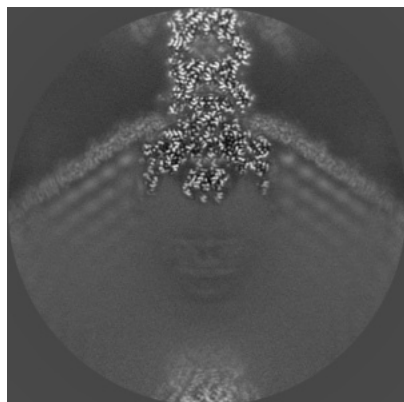


Y Index: 221

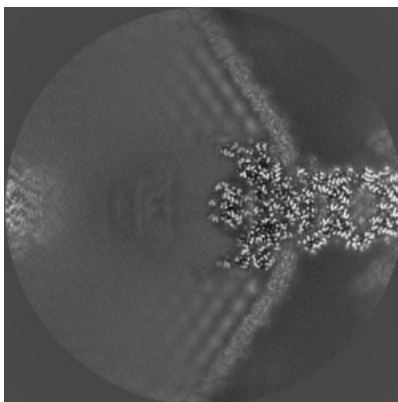


Z Index: 337

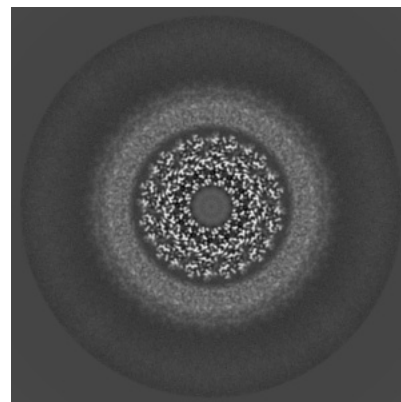
6.3.2 Raw map



X Index: 221



Y Index: 221

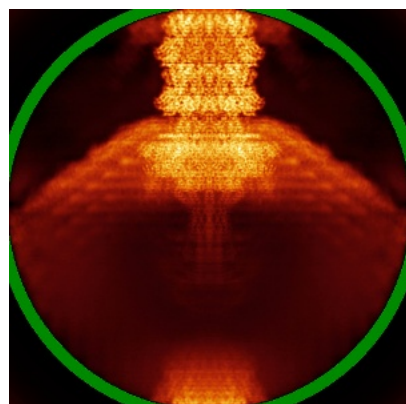


Z Index: 337

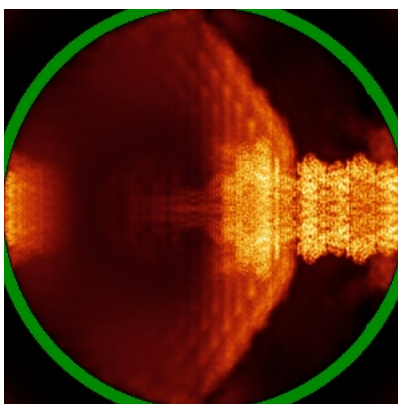
The images above show the largest variance slices of the map in three orthogonal directions.

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

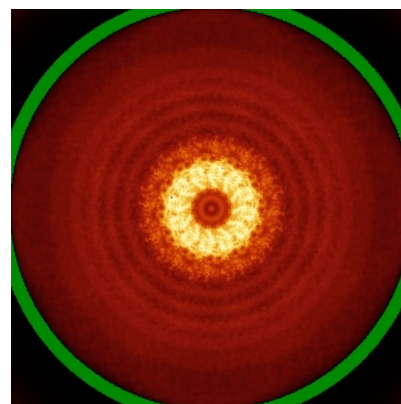
6.4.1 Primary map



X

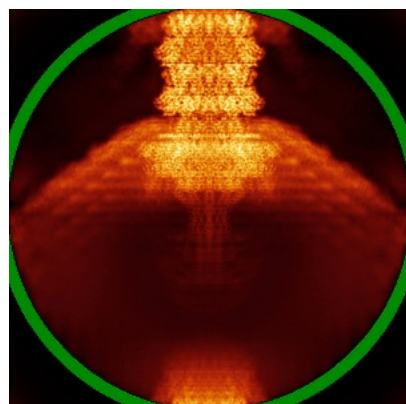


Y

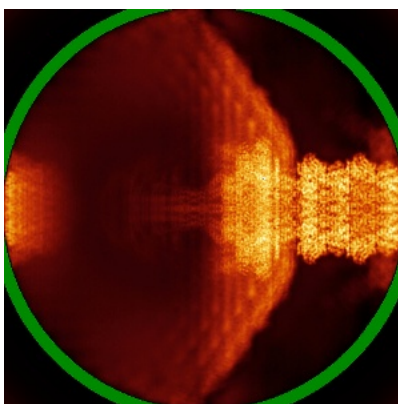


Z

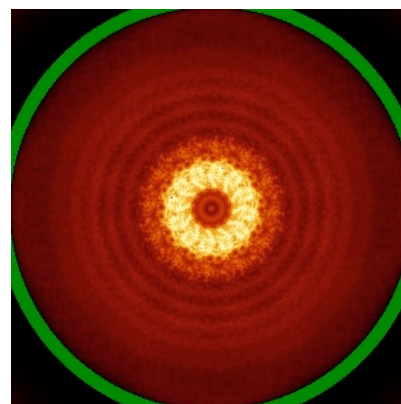
6.4.2 Raw map



X



Y

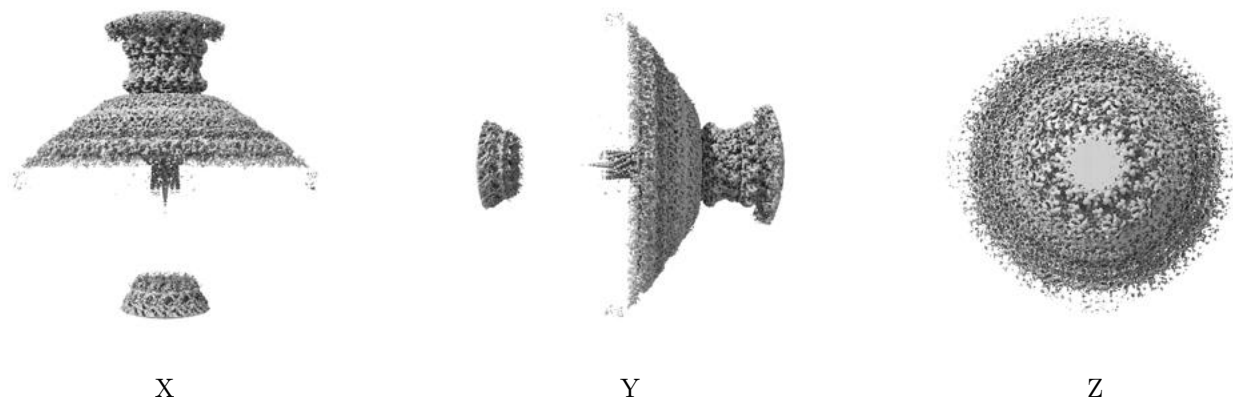


Z

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.

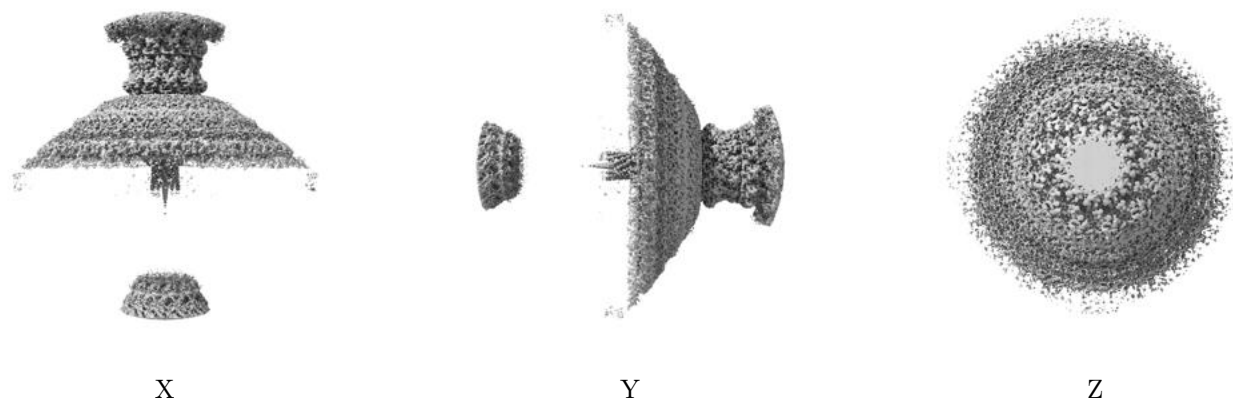
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. 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.

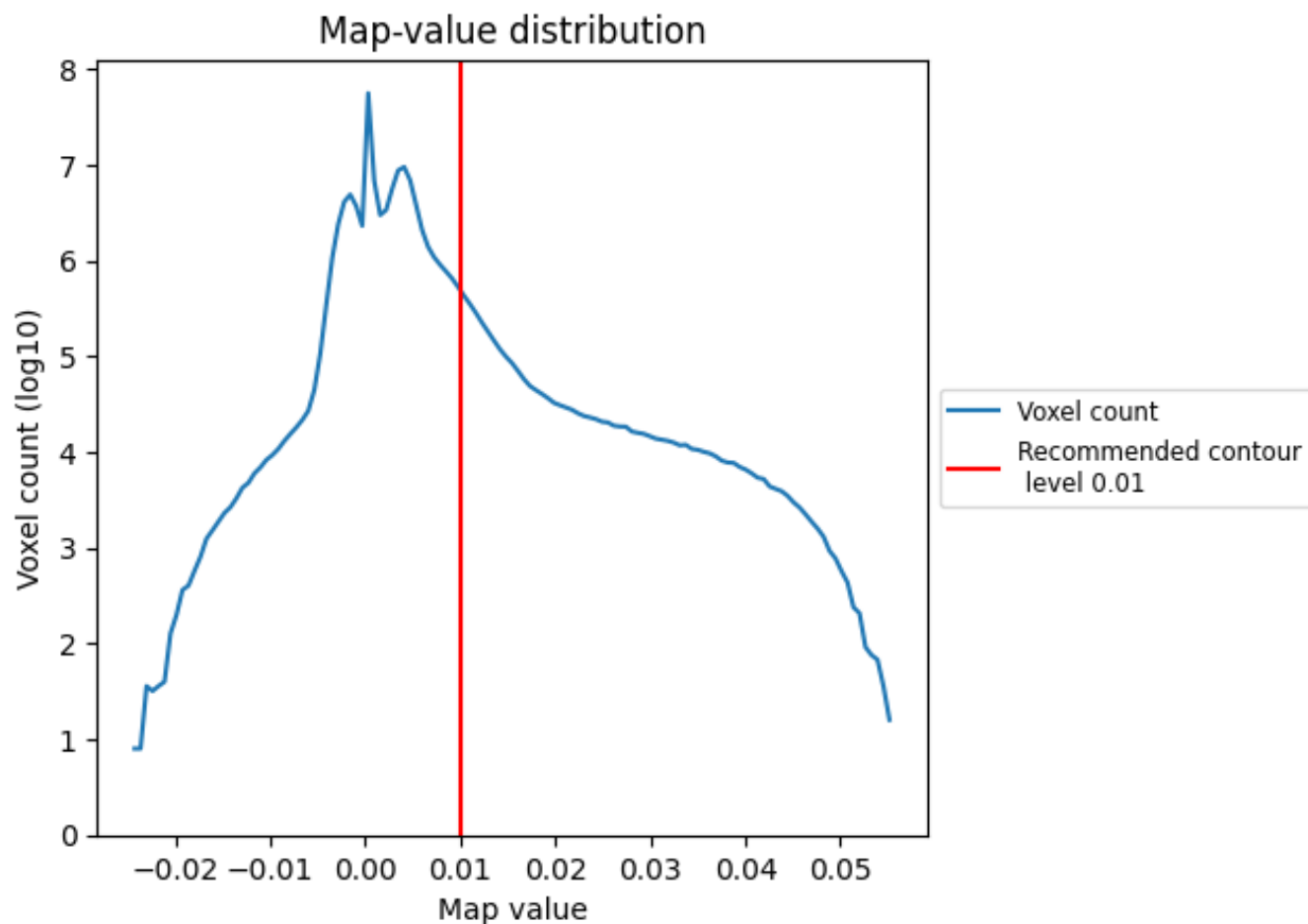
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

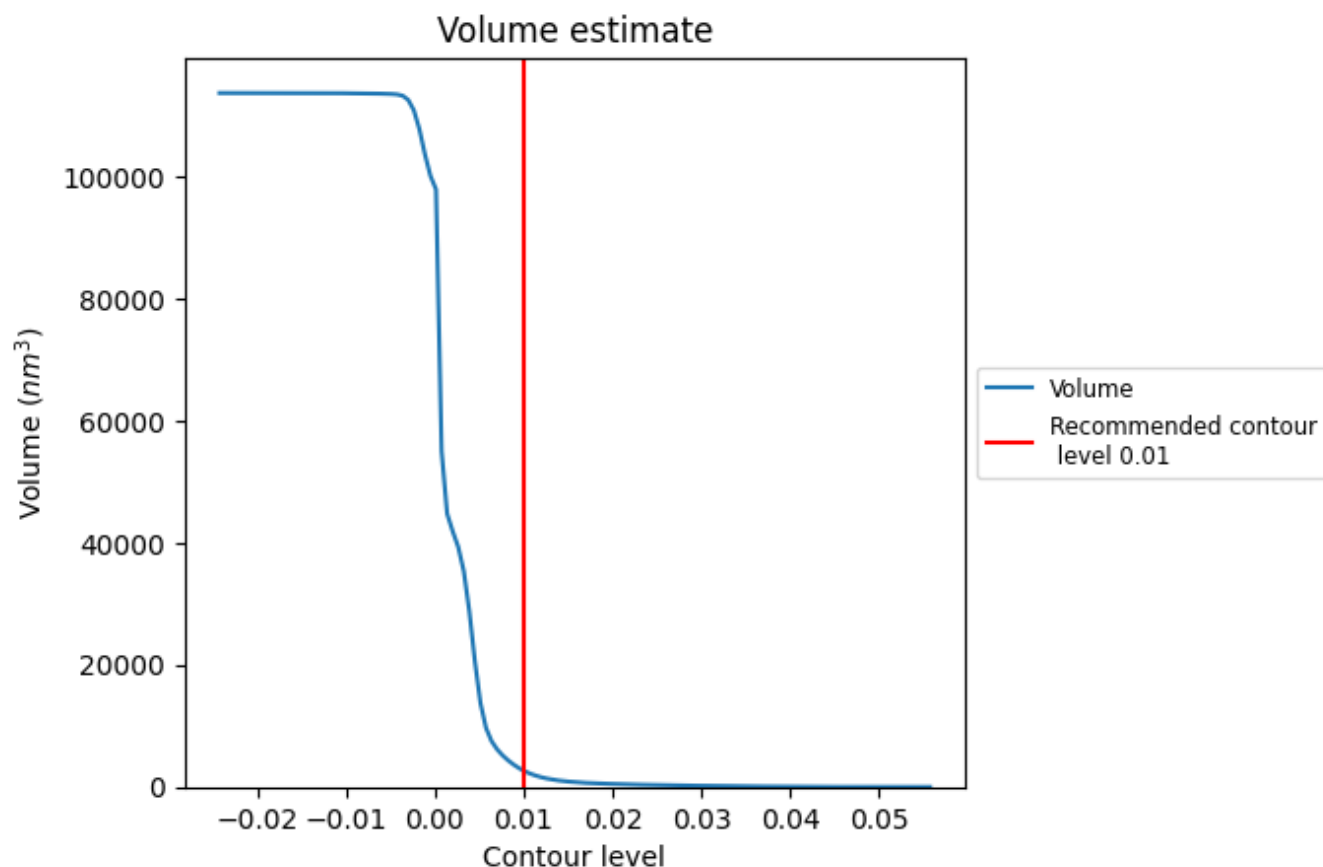
This section contains the results of statistical analysis of the map.

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.

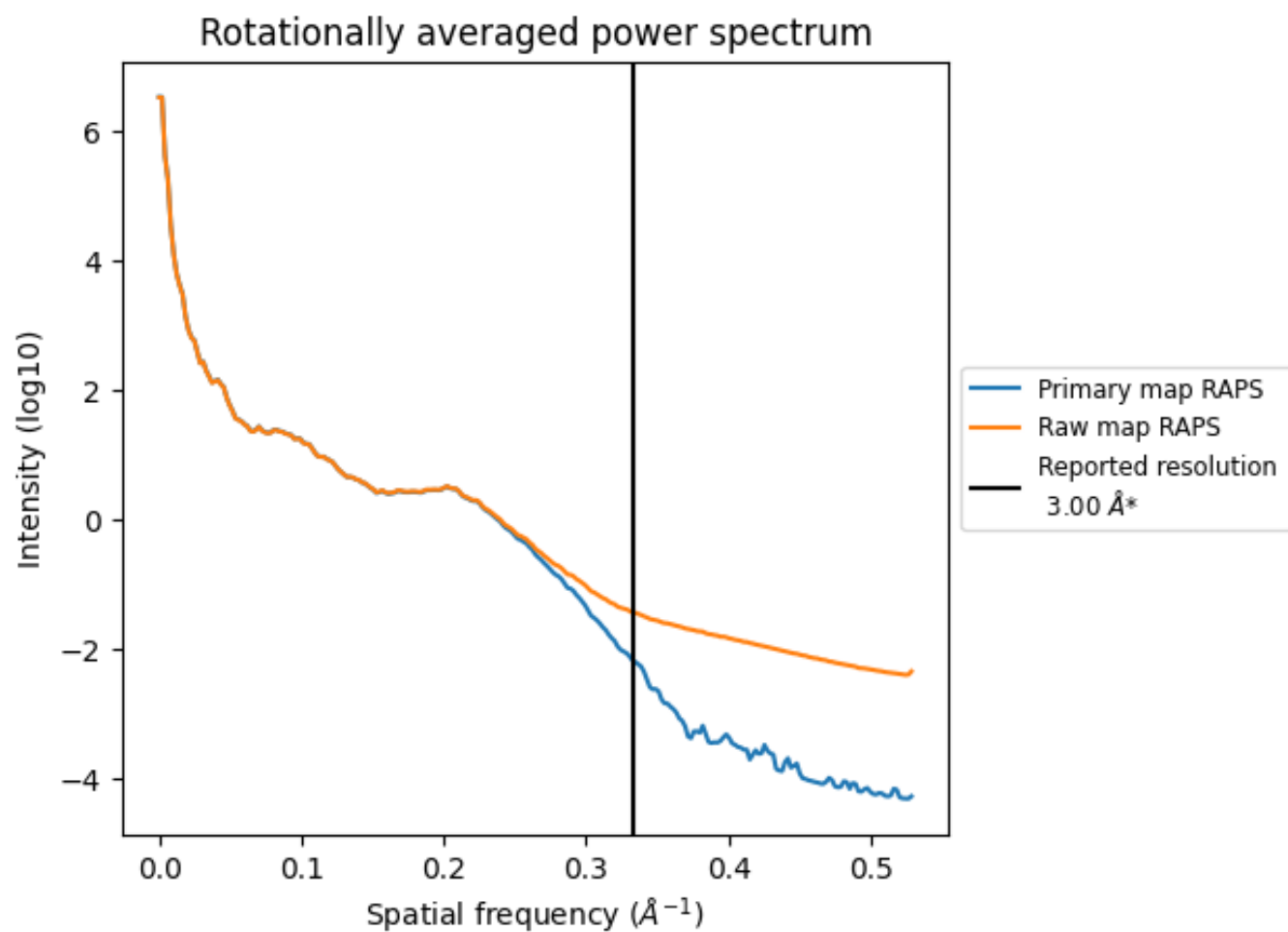
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2673 nm³; this corresponds to an approximate mass of 2414 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 ⓘ

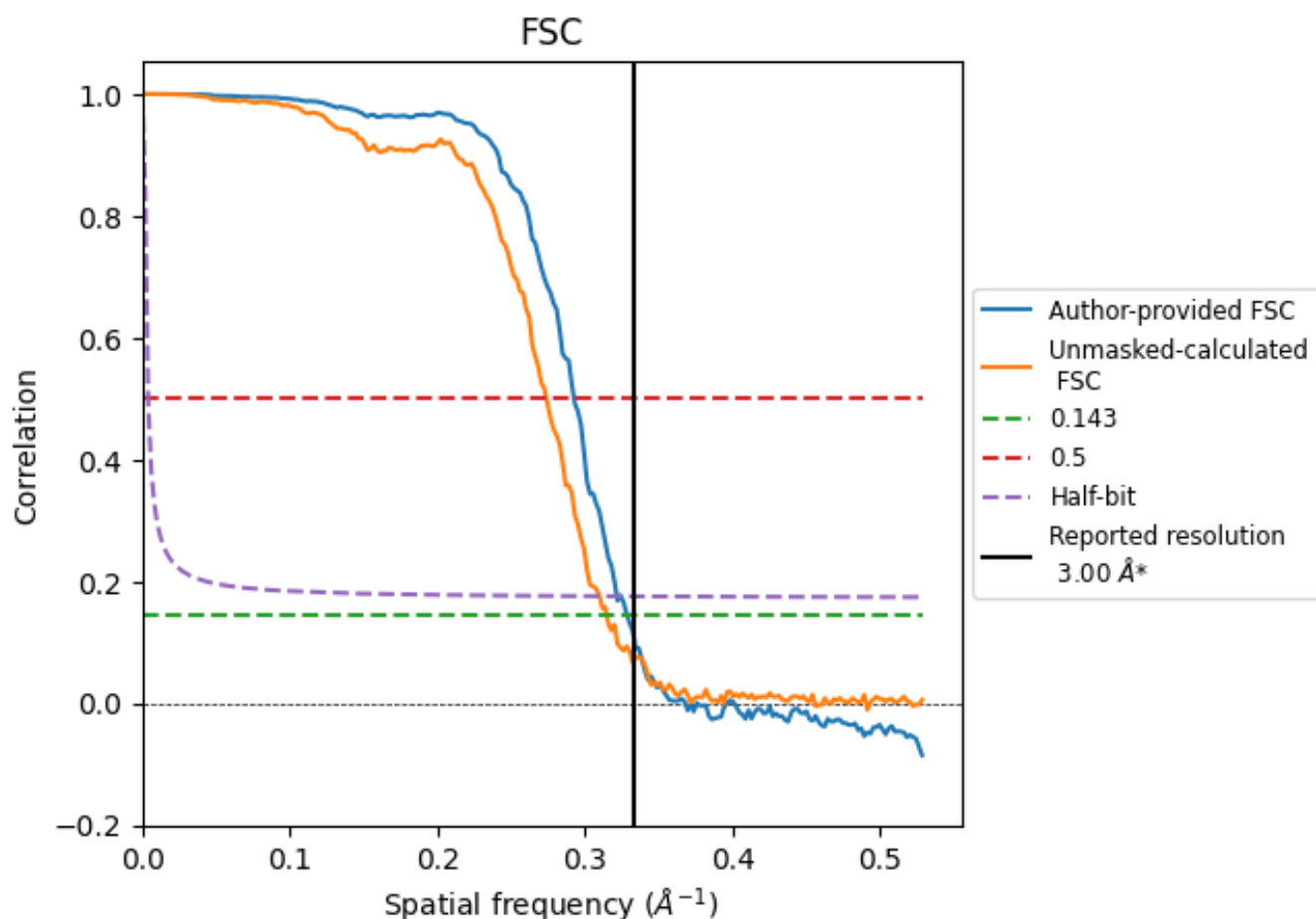


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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](#)

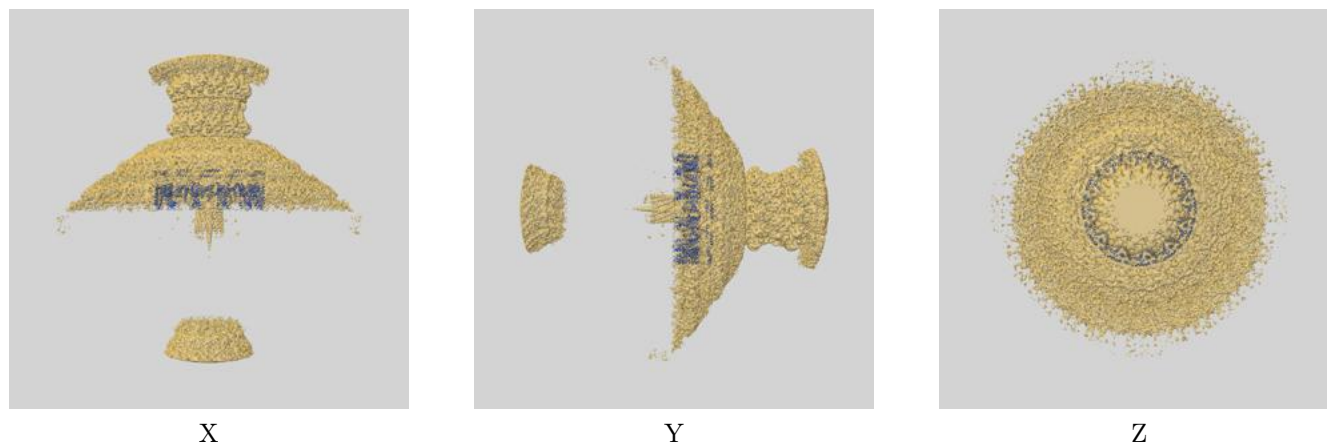
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.04	3.42	3.11
Unmasked-calculated*	3.18	3.65	3.23

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

9 Map-model fit [i](#)

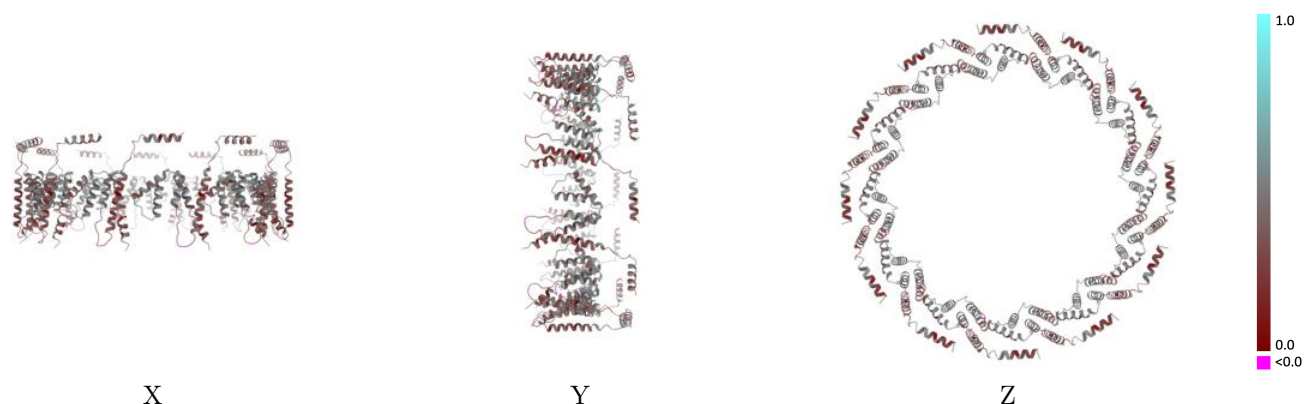
This section contains information regarding the fit between EMDB map EMD-49909 and PDB model 9NXO. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



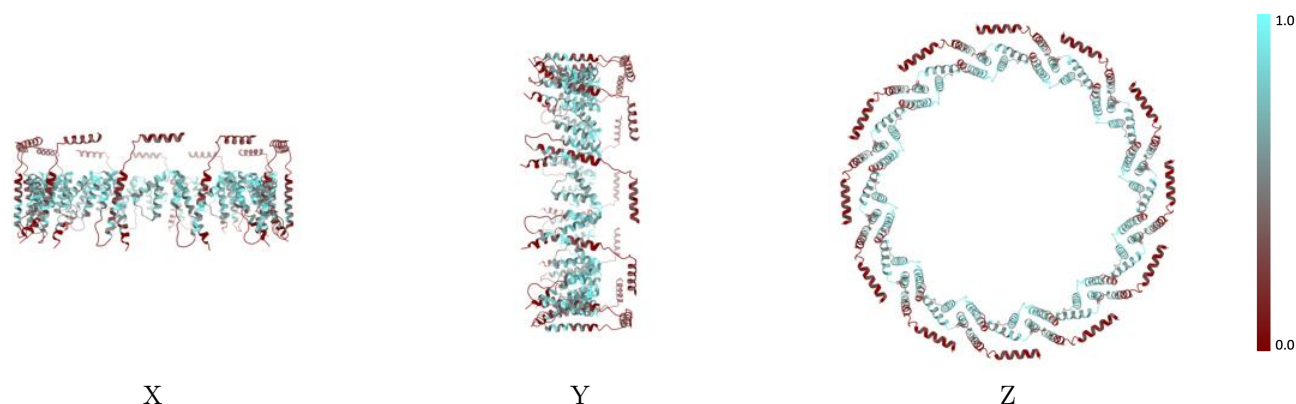
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



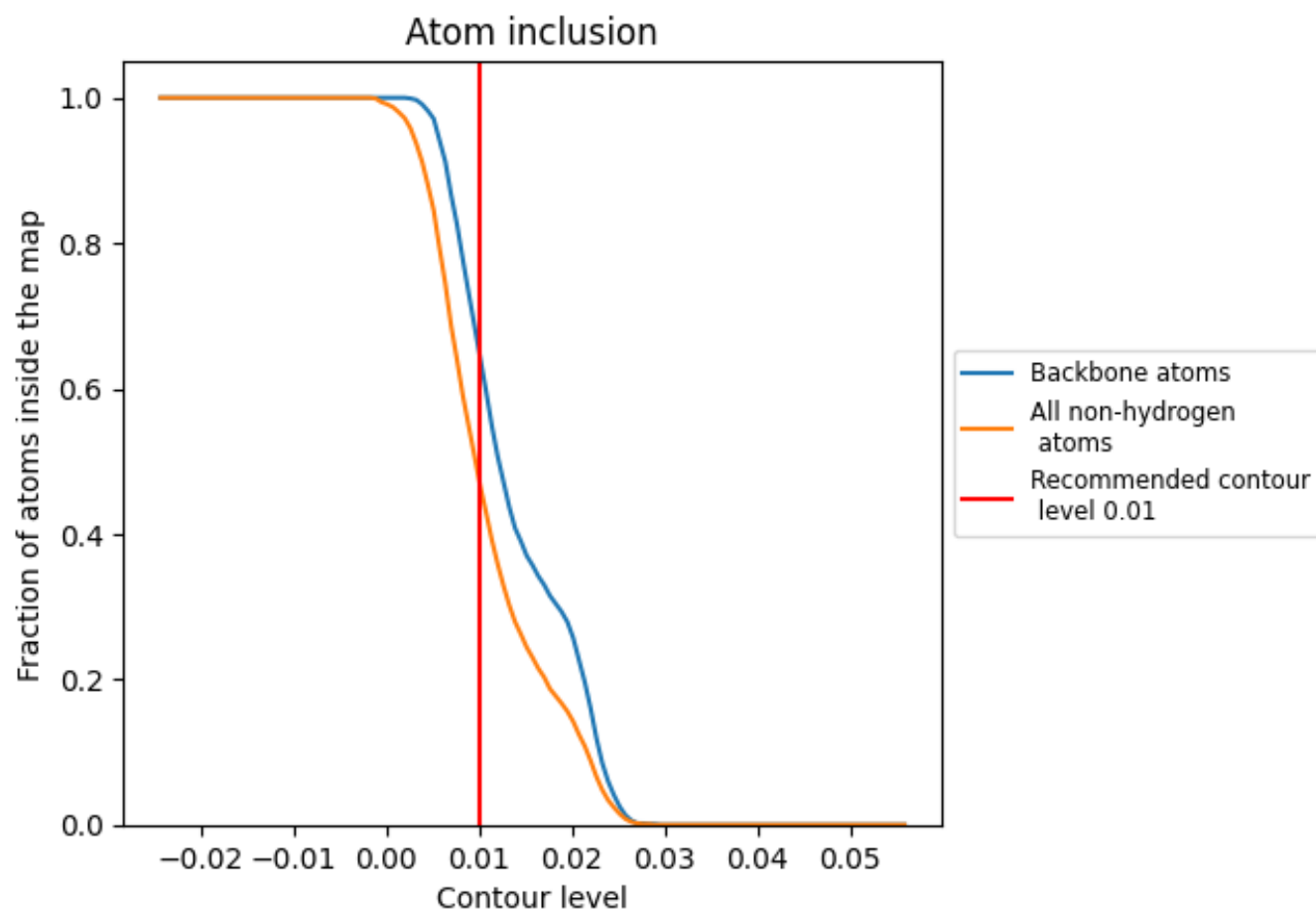
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 48% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.4750	<div></div> 0.3900
A	<div></div> 0.4810	<div></div> 0.3960
B	<div></div> 0.4760	<div></div> 0.3910
C	<div></div> 0.4660	<div></div> 0.3900
D	<div></div> 0.4870	<div></div> 0.3970
E	<div></div> 0.4700	<div></div> 0.3860
F	<div></div> 0.4750	<div></div> 0.3930
G	<div></div> 0.4750	<div></div> 0.3930
H	<div></div> 0.4780	<div></div> 0.3890
I	<div></div> 0.4710	<div></div> 0.3920
J	<div></div> 0.4830	<div></div> 0.3920
K	<div></div> 0.4650	<div></div> 0.3800
L	<div></div> 0.4660	<div></div> 0.3860

1.0

0.0

<0.0