



# Full wwPDB EM Validation Report ⓘ

May 26, 2024 – 11:34 AM EDT

PDB ID : 7SAX  
EMDB ID : EMD-24958  
Title : Structure of GldLM, the proton-powered motor that drives Type IX protein secretion and gliding motility in *Sphingobacterium wenxiniae*  
Authors : Hennell James, R.; Deme, J.C.; Lea, S.M.  
Deposited on : 2021-09-23  
Resolution : 3.00 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.dev92  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

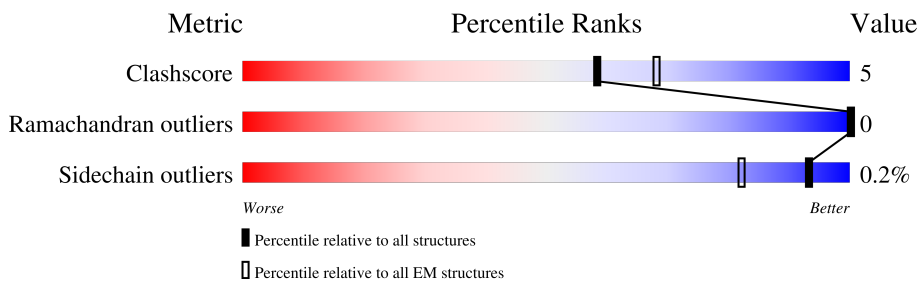
# 1 Overall quality at a glance

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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\geq 3$ , 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	263	
1	B	263	
2	C	212	
2	D	212	
2	E	212	
2	F	212	
2	G	212	

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 5305 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 GldM.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	213	1627	1015	284	324	4	0	0
1	B	211	1614	1007	281	322	4	0	0

There are 78 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	225	GLU	-	expression tag	UNP A0A1I6R6I5
A	226	ASN	-	expression tag	UNP A0A1I6R6I5
A	227	LEU	-	expression tag	UNP A0A1I6R6I5
A	228	TYR	-	expression tag	UNP A0A1I6R6I5
A	229	PHE	-	expression tag	UNP A0A1I6R6I5
A	230	GLN	-	expression tag	UNP A0A1I6R6I5
A	231	GLY	-	expression tag	UNP A0A1I6R6I5
A	232	GLN	-	expression tag	UNP A0A1I6R6I5
A	233	PHE	-	expression tag	UNP A0A1I6R6I5
A	234	GLY	-	expression tag	UNP A0A1I6R6I5
A	235	SER	-	expression tag	UNP A0A1I6R6I5
A	236	TRP	-	expression tag	UNP A0A1I6R6I5
A	237	SER	-	expression tag	UNP A0A1I6R6I5
A	238	HIS	-	expression tag	UNP A0A1I6R6I5
A	239	PRO	-	expression tag	UNP A0A1I6R6I5
A	240	GLN	-	expression tag	UNP A0A1I6R6I5
A	241	PHE	-	expression tag	UNP A0A1I6R6I5
A	242	GLU	-	expression tag	UNP A0A1I6R6I5
A	243	LYS	-	expression tag	UNP A0A1I6R6I5
A	244	GLY	-	expression tag	UNP A0A1I6R6I5
A	245	GLY	-	expression tag	UNP A0A1I6R6I5
A	246	GLY	-	expression tag	UNP A0A1I6R6I5
A	247	SER	-	expression tag	UNP A0A1I6R6I5
A	248	GLY	-	expression tag	UNP A0A1I6R6I5
A	249	GLY	-	expression tag	UNP A0A1I6R6I5
A	250	GLY	-	expression tag	UNP A0A1I6R6I5

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
A	251	SER	-	expression tag	UNP A0A1I6R6I5
A	252	GLY	-	expression tag	UNP A0A1I6R6I5
A	253	GLY	-	expression tag	UNP A0A1I6R6I5
A	254	GLY	-	expression tag	UNP A0A1I6R6I5
A	255	SER	-	expression tag	UNP A0A1I6R6I5
A	256	TRP	-	expression tag	UNP A0A1I6R6I5
A	257	SER	-	expression tag	UNP A0A1I6R6I5
A	258	HIS	-	expression tag	UNP A0A1I6R6I5
A	259	PRO	-	expression tag	UNP A0A1I6R6I5
A	260	GLN	-	expression tag	UNP A0A1I6R6I5
A	261	PHE	-	expression tag	UNP A0A1I6R6I5
A	262	GLU	-	expression tag	UNP A0A1I6R6I5
A	263	LYS	-	expression tag	UNP A0A1I6R6I5
B	225	GLU	-	expression tag	UNP A0A1I6R6I5
B	226	ASN	-	expression tag	UNP A0A1I6R6I5
B	227	LEU	-	expression tag	UNP A0A1I6R6I5
B	228	TYR	-	expression tag	UNP A0A1I6R6I5
B	229	PHE	-	expression tag	UNP A0A1I6R6I5
B	230	GLN	-	expression tag	UNP A0A1I6R6I5
B	231	GLY	-	expression tag	UNP A0A1I6R6I5
B	232	GLN	-	expression tag	UNP A0A1I6R6I5
B	233	PHE	-	expression tag	UNP A0A1I6R6I5
B	234	GLY	-	expression tag	UNP A0A1I6R6I5
B	235	SER	-	expression tag	UNP A0A1I6R6I5
B	236	TRP	-	expression tag	UNP A0A1I6R6I5
B	237	SER	-	expression tag	UNP A0A1I6R6I5
B	238	HIS	-	expression tag	UNP A0A1I6R6I5
B	239	PRO	-	expression tag	UNP A0A1I6R6I5
B	240	GLN	-	expression tag	UNP A0A1I6R6I5
B	241	PHE	-	expression tag	UNP A0A1I6R6I5
B	242	GLU	-	expression tag	UNP A0A1I6R6I5
B	243	LYS	-	expression tag	UNP A0A1I6R6I5
B	244	GLY	-	expression tag	UNP A0A1I6R6I5
B	245	GLY	-	expression tag	UNP A0A1I6R6I5
B	246	GLY	-	expression tag	UNP A0A1I6R6I5
B	247	SER	-	expression tag	UNP A0A1I6R6I5
B	248	GLY	-	expression tag	UNP A0A1I6R6I5
B	249	GLY	-	expression tag	UNP A0A1I6R6I5
B	250	GLY	-	expression tag	UNP A0A1I6R6I5
B	251	SER	-	expression tag	UNP A0A1I6R6I5
B	252	GLY	-	expression tag	UNP A0A1I6R6I5
B	253	GLY	-	expression tag	UNP A0A1I6R6I5

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
B	254	GLY	-	expression tag	UNP A0A1I6R6I5
B	255	SER	-	expression tag	UNP A0A1I6R6I5
B	256	TRP	-	expression tag	UNP A0A1I6R6I5
B	257	SER	-	expression tag	UNP A0A1I6R6I5
B	258	HIS	-	expression tag	UNP A0A1I6R6I5
B	259	PRO	-	expression tag	UNP A0A1I6R6I5
B	260	GLN	-	expression tag	UNP A0A1I6R6I5
B	261	PHE	-	expression tag	UNP A0A1I6R6I5
B	262	GLU	-	expression tag	UNP A0A1I6R6I5
B	263	LYS	-	expression tag	UNP A0A1I6R6I5

- Molecule 2 is a protein called GldL.

Mol	Chain	Residues	Atoms				AltConf	Trace	
2	C	60	Total	C	N	O	S	0	0
			473	318	74	77	4		
2	D	55	Total	C	N	O	S	0	0
			430	294	66	66	4		
2	E	50	Total	C	N	O	S	0	0
			387	266	59	58	4		
2	F	50	Total	C	N	O	S	0	0
			387	266	59	58	4		
2	G	50	Total	C	N	O	S	0	0
			387	265	59	59	4		





MET	ALA	ALA	F9	G10	I11	I15	L26	K34	M57	Q58	ALA	GLU	GLN	GLU	PRO	ASP	TRP	THR	ARG	VAL	TYR	PRO	GLU	LEU	ASP	GLU	ASP	TYR	ASN	GLY	LEU	PRO	THR	ARG	SER	VAL	ARG	ALA	VAL	ALA	GLN	PRO	PRO	VAL	ALA	THR	GLY	ASN	THR	ALA					
ALA	LEU	ASP	ALA	LYS	ILE	GLU	ASN	GLY	ASN	LEU	GLY	GLY	LEU	ARG	THR	PHE	SER	GLN	VAL	THR	ALA	SER	ILE	SER	VAL	ALA	ASP	ASP	THR	ALA	ALA	VAL	VAL	THR	ASN	GLN	PHE	SER	ALA	ASP	LYS	LEU	ASN	THR	ASN	ALA	ALA	ARG	SER	THR	GLY	ALA	ALA	GLN	LEU
SER	ASN	ALA	PHE	GLU	ARG	ALA	ALA	SER	ASP	GLN	GLN	GLN	PHE	LYS	GLU	GLU	VAL	SER	THR	PHE	ASN	LYS	ASN	LEU	SER	LEU	LEU	ASN	ASN	ALA	ILE	TYR	GLY	ASN	MET	LEU	SER	ALA	ALA	MET	ASN	THR	ASN	THR	ARG	SER	SER	SER							



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	111727	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 ( $e^-/\text{\AA}^2$ )	56	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.139	Depositor
Minimum map value	-0.079	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	212.992, 212.992, 212.992	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.832, 0.832, 0.832	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	0.34	0/1642	0.46	0/2214
1	B	0.31	0/1629	0.45	0/2198
2	C	0.37	0/485	0.47	0/656
2	D	0.38	0/440	0.49	0/590
2	E	0.36	0/396	0.49	0/532
2	F	0.39	0/396	0.46	0/532
2	G	0.38	0/396	0.46	0/533
All	All	0.35	0/5384	0.46	0/7255

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	1627	0	1674	22	0
1	B	1614	0	1658	18	0
2	C	473	0	483	7	0
2	D	430	0	454	6	0
2	E	387	0	413	8	0
2	F	387	0	413	4	0
2	G	387	0	408	2	0
All	All	5305	0	5503	53	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 5.

All (53) 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:210:HIS:HE1	1:A:214:LYS:HE2	1.54	0.71
1:B:9:ARG:NH1	2:C:47:GLU:OE2	2.17	0.71
1:A:51:GLN:NE2	1:A:55:ASP:OD1	2.24	0.71
1:A:210:HIS:CE1	1:A:214:LYS:HE2	2.27	0.70
1:B:138:ARG:NH2	1:B:164:ASP:OD1	2.30	0.65
1:A:39:LEU:HD23	1:B:195:LYS:HD3	1.84	0.58
1:A:9:ARG:NH1	1:A:13:ILE:HD11	2.17	0.58
2:D:44:LEU:HD22	2:E:23:ILE:HG23	1.86	0.58
1:A:12:MET:HE3	2:E:51:PHE:CD1	2.39	0.57
1:A:138:ARG:NH2	1:A:164:ASP:OD1	2.37	0.57
1:A:149:LEU:O	1:A:153:ASN:N	2.38	0.57
1:A:9:ARG:O	1:A:13:ILE:HG12	2.09	0.53
2:F:46:VAL:O	2:F:50:LEU:HD23	2.10	0.52
1:B:47:THR:HG23	1:B:201:LYS:HG3	1.91	0.51
1:A:34:ASP:CG	1:B:168:ARG:HH12	2.13	0.51
2:E:28:PHE:HB3	2:E:36:GLY:HA2	1.94	0.50
2:C:45:ALA:HB2	2:D:27:MET:SD	2.52	0.50
1:A:101:LEU:HD23	1:A:127:LEU:HD23	1.95	0.48
1:A:114:ASP:N	1:A:114:ASP:OD1	2.46	0.48
2:D:18:GLY:O	2:D:22:VAL:HG23	2.14	0.48
1:A:61:PHE:HE2	1:A:77:LEU:HB2	1.77	0.48
1:B:16:LEU:HD11	2:C:23:ILE:HD11	1.95	0.47
1:A:49:ASN:ND2	1:B:202:ASN:OD1	2.47	0.47
1:A:100:LEU:HG	1:A:127:LEU:HD21	1.97	0.46
1:A:34:ASP:OD2	1:B:168:ARG:NH1	2.43	0.46
1:B:87:VAL:HG21	1:B:204:GLU:HB2	1.98	0.46
1:A:126:ARG:HB3	2:C:32:HIS:HB3	1.96	0.46
2:E:17:TRP:HA	2:E:20:THR:HG22	1.96	0.46
1:B:25:ALA:O	2:F:29:LYS:HE3	2.16	0.45
1:A:135:LYS:NZ	1:A:139:GLU:OE2	2.47	0.45
1:A:148:LEU:HD22	1:A:207:VAL:HG21	1.99	0.45
2:D:11:ILE:HD11	2:D:50:LEU:HD22	1.99	0.44
2:E:9:PHE:HD2	2:E:13:THR:HG21	1.82	0.44
2:F:18:GLY:O	2:F:22:VAL:HG12	2.17	0.44
1:B:105:GLY:O	1:B:117:TYR:HB2	2.17	0.44
2:C:44:LEU:HD22	2:D:23:ILE:HG23	1.99	0.44
2:E:12:ASN:O	2:E:16:ASN:ND2	2.50	0.44

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:128:MET:HB3	1:B:134:ALA:HB2	1.99	0.43
1:A:53:GLY:O	1:A:57:MET:HG3	2.18	0.43
1:B:19:VAL:HA	2:G:26:LEU:HD11	2.01	0.43
2:G:11:ILE:O	2:G:15:ILE:HG12	2.19	0.42
1:B:160:LEU:HD23	1:B:160:LEU:HA	1.78	0.42
1:A:21:LEU:HD11	2:C:47:GLU:HG2	1.99	0.42
2:E:14:LEU:HD23	2:E:14:LEU:HA	1.80	0.41
1:A:72:ARG:NH2	1:A:215:MET:HB2	2.35	0.41
1:B:101:LEU:HD23	1:B:101:LEU:HA	1.84	0.41
2:F:12:ASN:HA	2:F:15:ILE:HG12	2.02	0.41
1:B:123:ILE:HB	1:B:186:LEU:HD12	2.03	0.41
1:B:141:ILE:HG23	1:B:160:LEU:HD22	2.02	0.41
2:C:53:ILE:HD13	2:C:53:ILE:HA	1.89	0.40
2:E:17:TRP:O	2:E:20:THR:HG22	2.20	0.40
1:B:6:GLU:HG3	1:B:11:ARG:HG3	2.03	0.40
2:D:54:MET:HE3	2:D:54:MET:HB2	1.94	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	211/263 (80%)	205 (97%)	6 (3%)	0	100	100
1	B	209/263 (80%)	200 (96%)	9 (4%)	0	100	100
2	C	58/212 (27%)	57 (98%)	1 (2%)	0	100	100
2	D	53/212 (25%)	51 (96%)	2 (4%)	0	100	100
2	E	48/212 (23%)	47 (98%)	1 (2%)	0	100	100
2	F	48/212 (23%)	46 (96%)	2 (4%)	0	100	100
2	G	48/212 (23%)	47 (98%)	1 (2%)	0	100	100
All	All	675/1586 (43%)	653 (97%)	22 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	175/212 (82%)	175 (100%)	0	100	100
1	B	174/212 (82%)	173 (99%)	1 (1%)	86	95
2	C	48/170 (28%)	48 (100%)	0	100	100
2	D	43/170 (25%)	43 (100%)	0	100	100
2	E	39/170 (23%)	39 (100%)	0	100	100
2	F	39/170 (23%)	39 (100%)	0	100	100
2	G	39/170 (23%)	39 (100%)	0	100	100
All	All	557/1274 (44%)	556 (100%)	1 (0%)	93	98

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	27	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	210	HIS

### 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 monosaccharides 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.

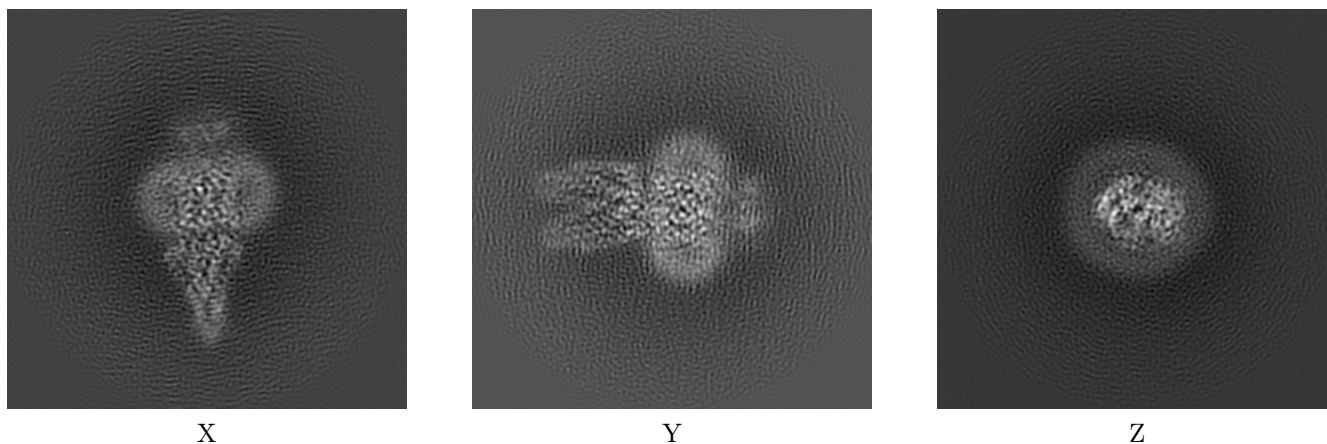
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24958. These allow visual inspection of the internal detail of the map and identification of artifacts.

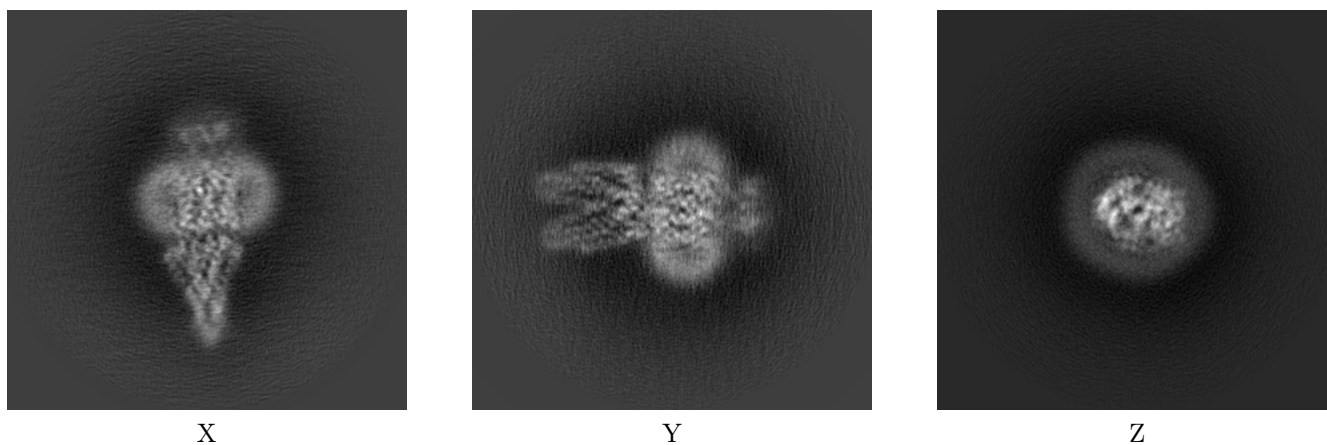
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

#### 6.1.1 Primary map



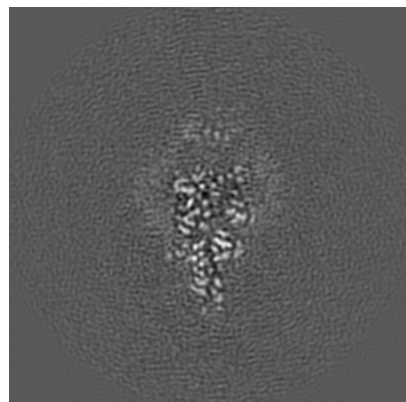
#### 6.1.2 Raw map



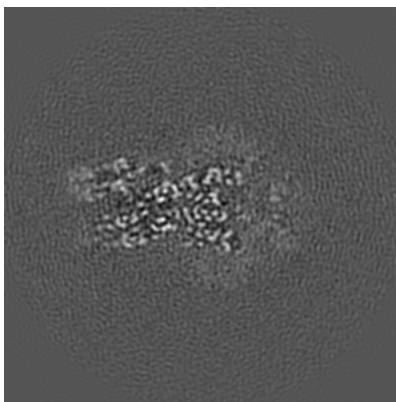
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

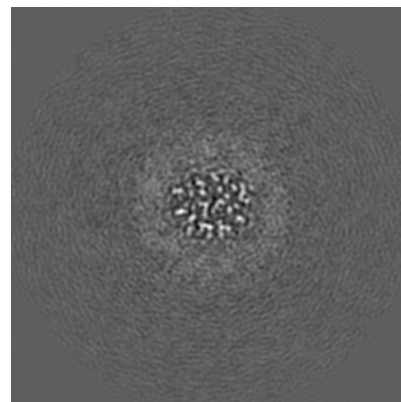
### 6.2.1 Primary map



X Index: 128

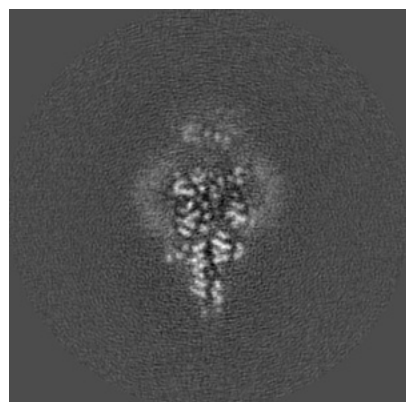


Y Index: 128

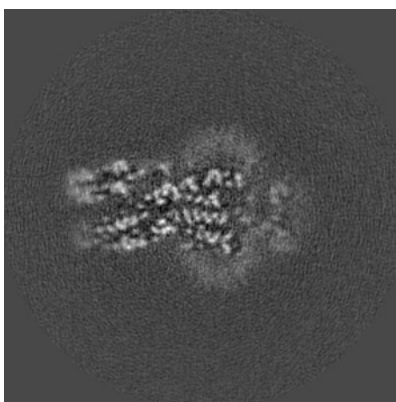


Z Index: 128

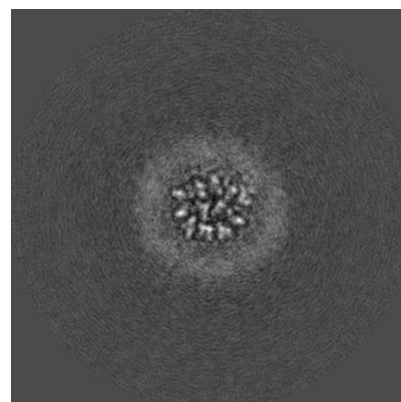
### 6.2.2 Raw map



X Index: 128



Y Index: 128



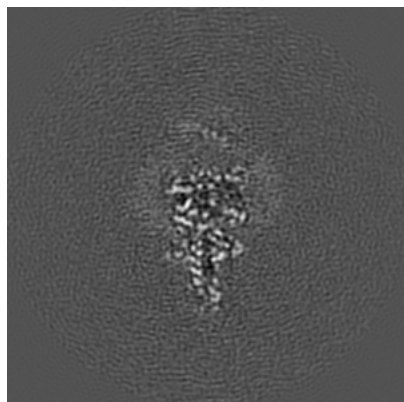
Z Index: 128

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

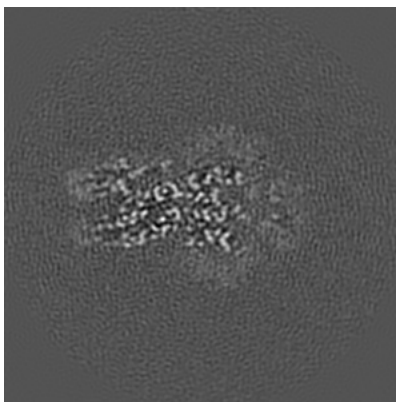


## 6.3 Largest variance slices [i](#)

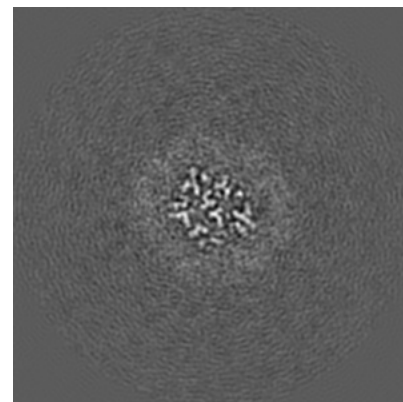
### 6.3.1 Primary map



X Index: 127

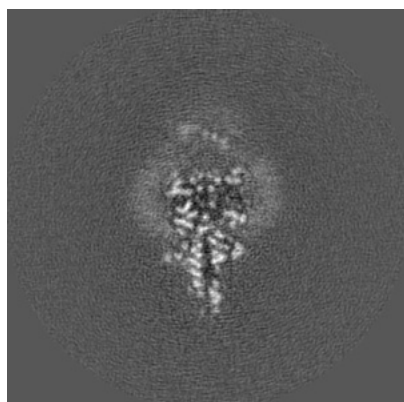


Y Index: 129

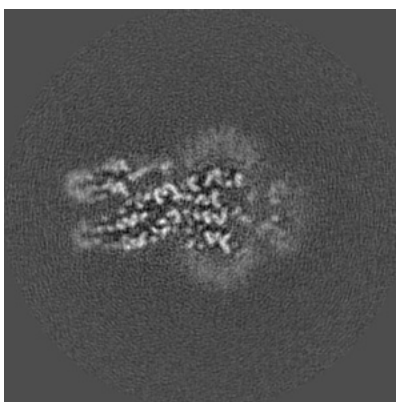


Z Index: 141

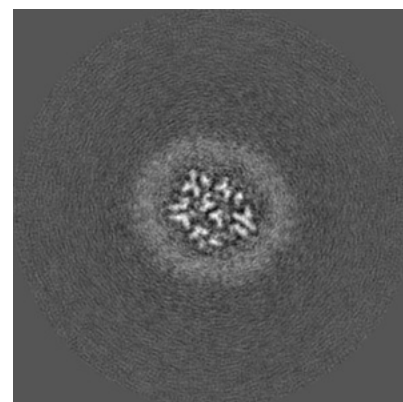
### 6.3.2 Raw map



X Index: 127



Y Index: 129

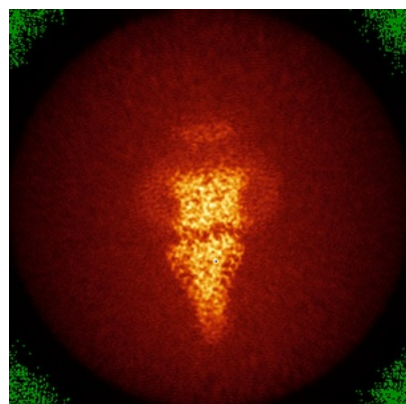


Z Index: 141

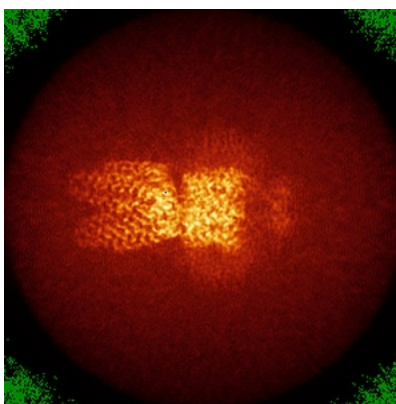
The images above show the largest variance slices of the map in three orthogonal directions.

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

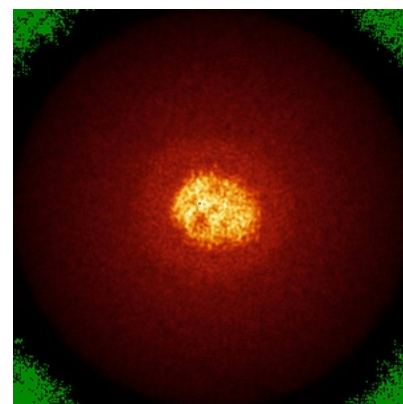
### 6.4.1 Primary map



X

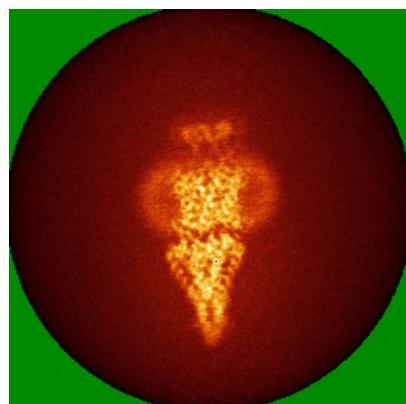


Y

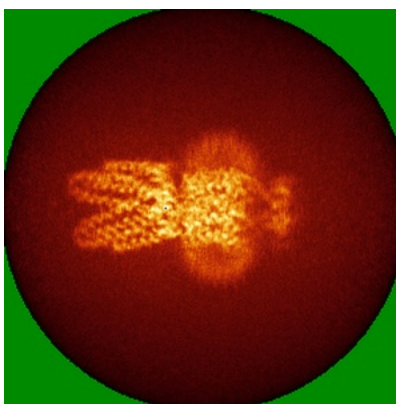


Z

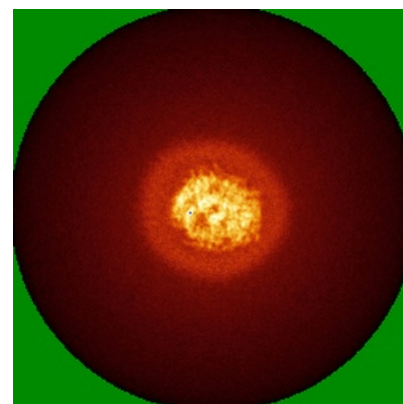
### 6.4.2 Raw map



X



Y

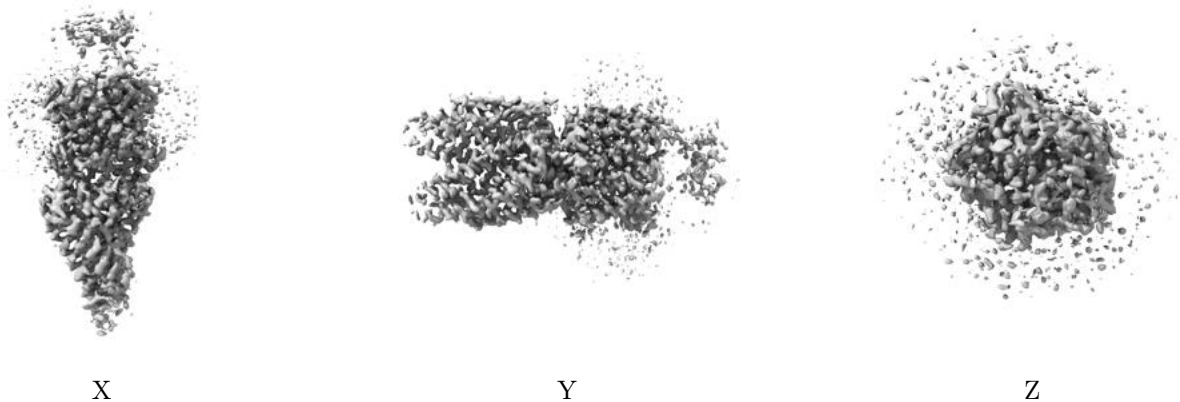


Z

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.

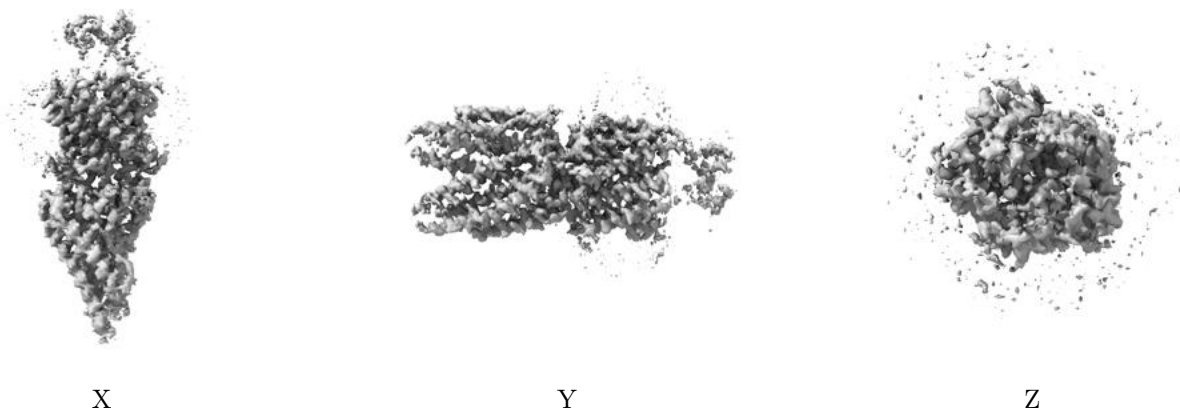
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. 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.

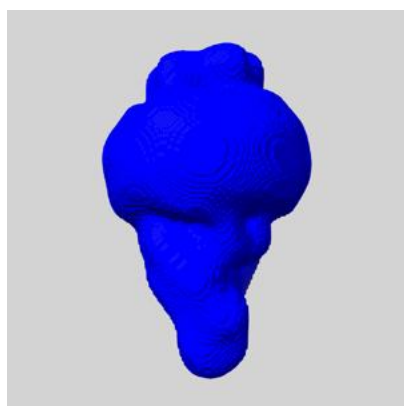
## 6.6 Mask visualisation [i](#)

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

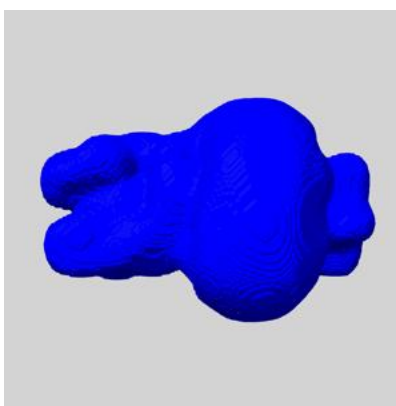
A mask typically either:

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

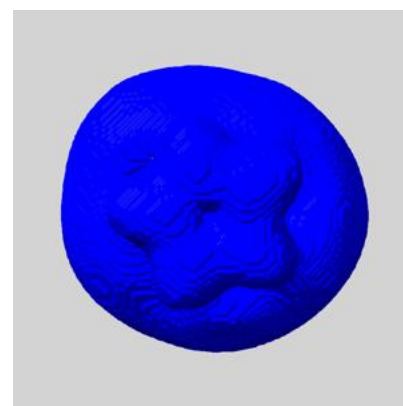
### 6.6.1 emd\_24958\_msk\_1.map [i](#)



X



Y

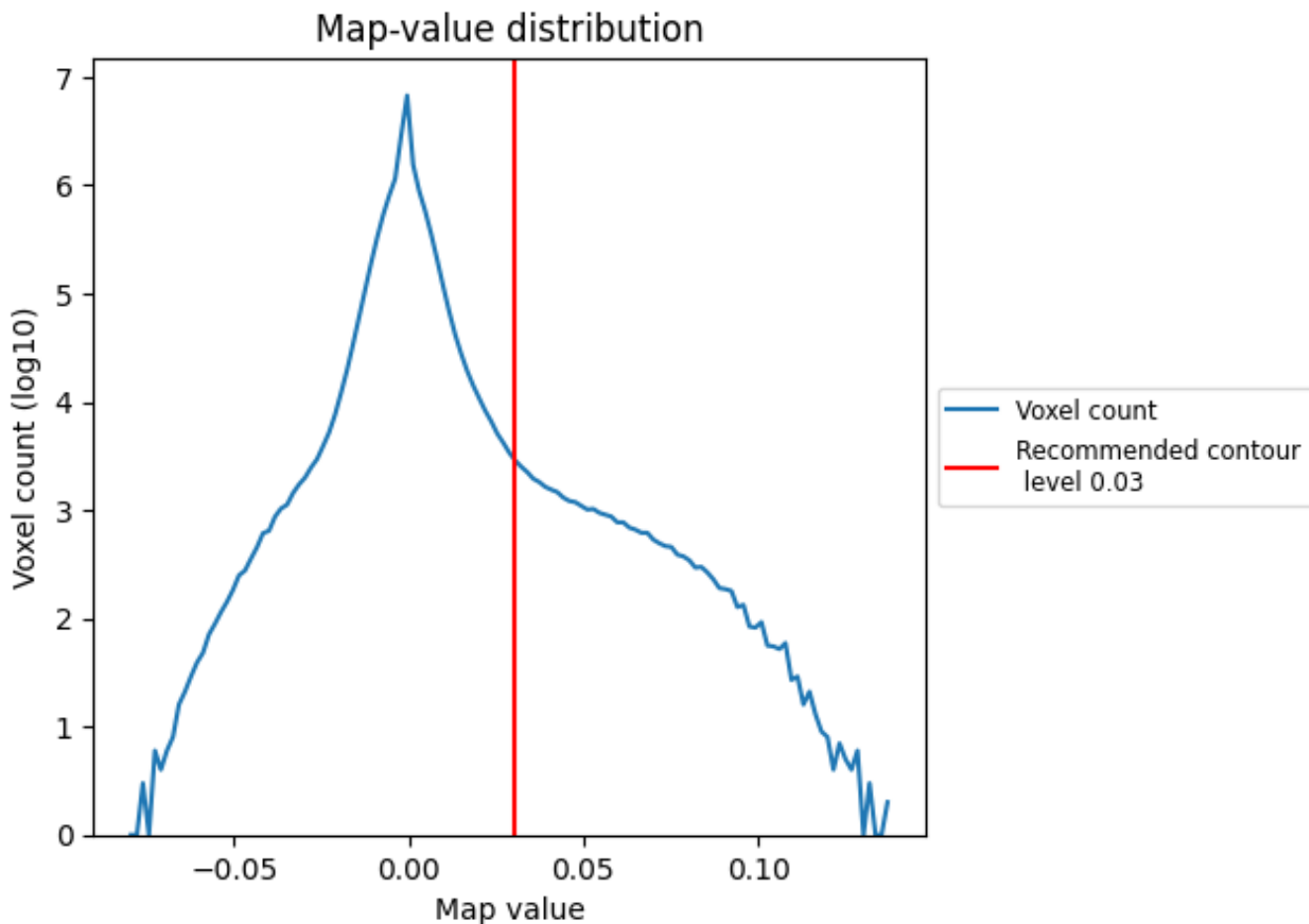


Z

## 7 Map analysis [i](#)

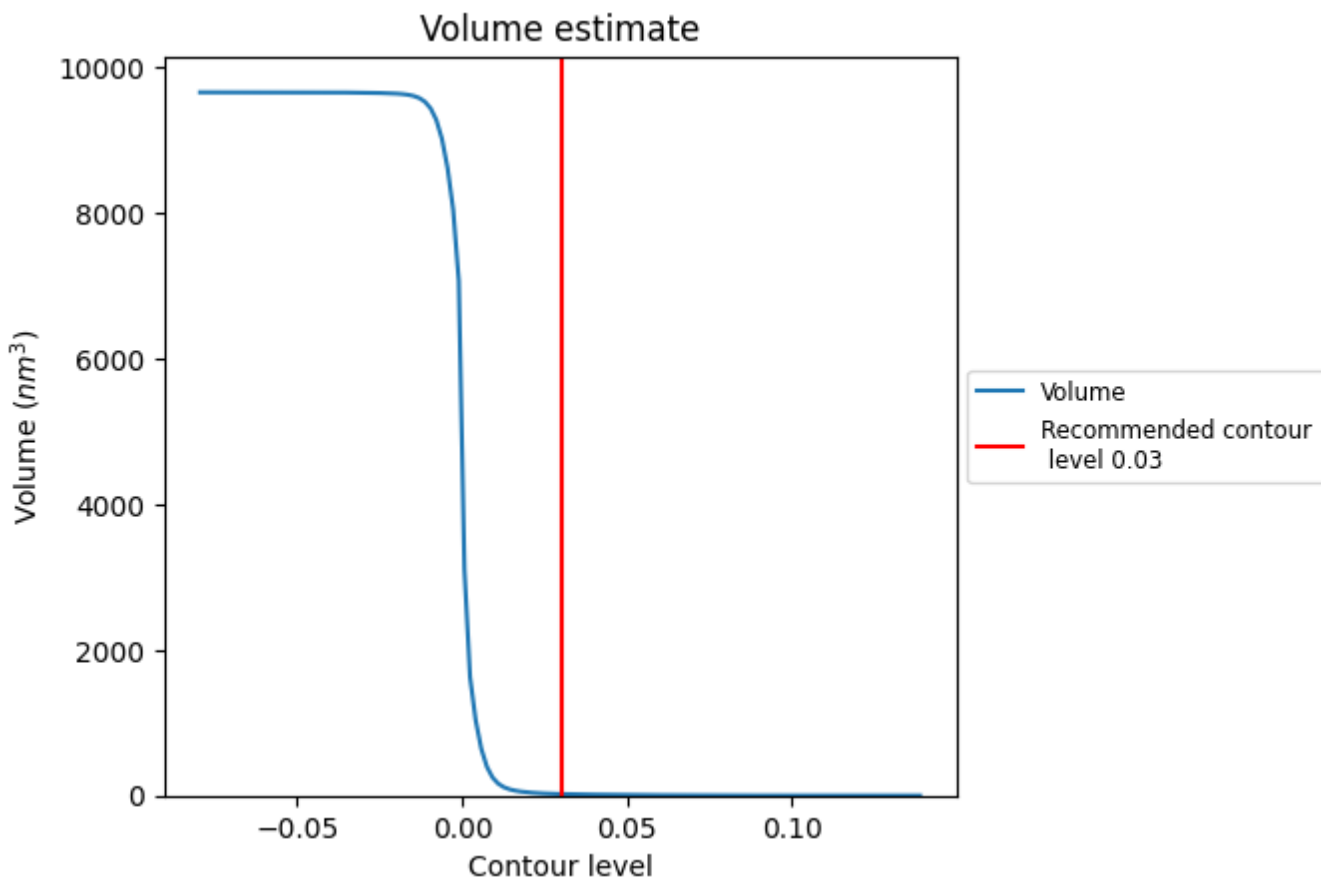
This section contains the results of statistical analysis of the map.

### 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.

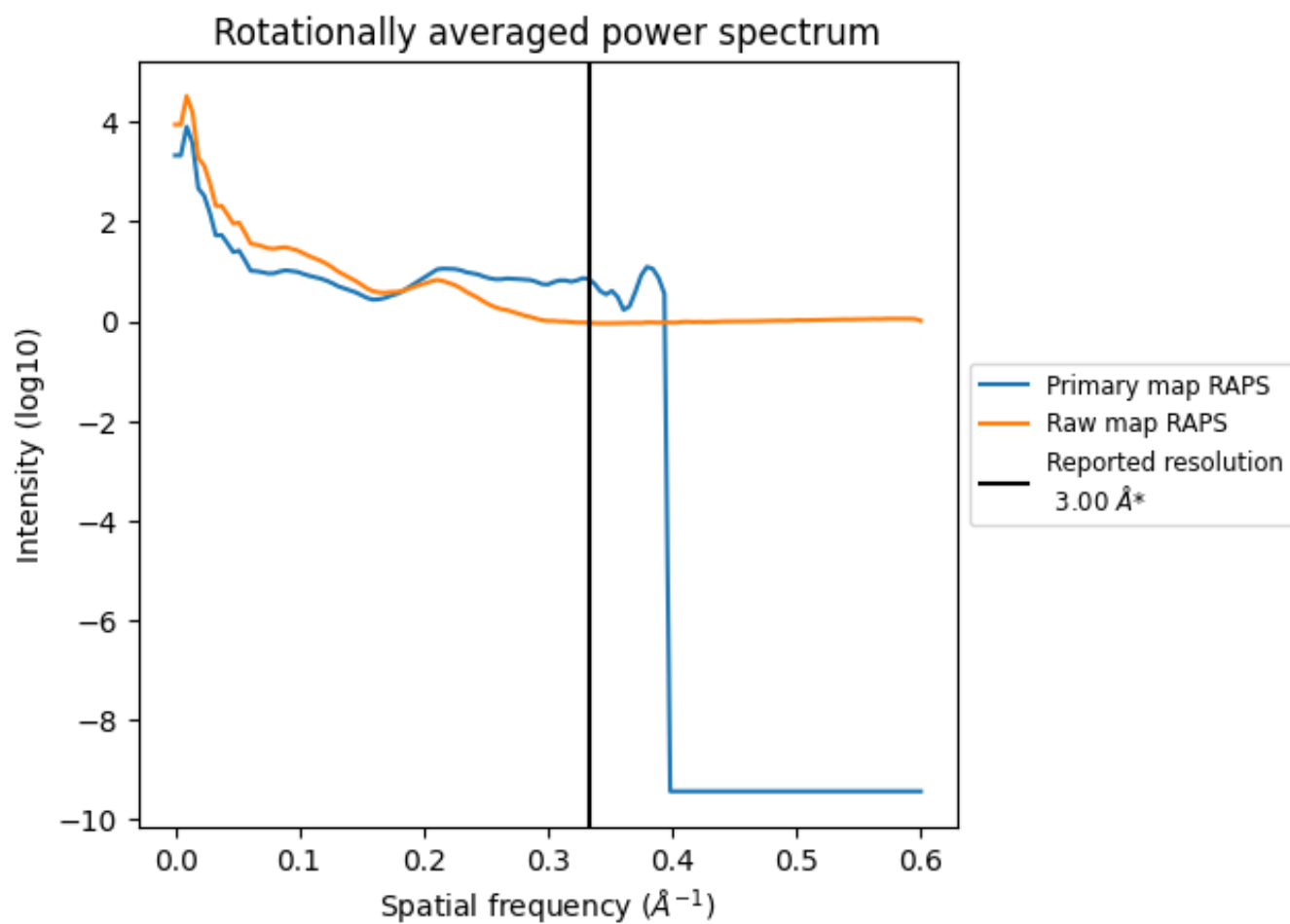
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 21 nm<sup>3</sup>; this corresponds to an approximate mass of 19 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](#)

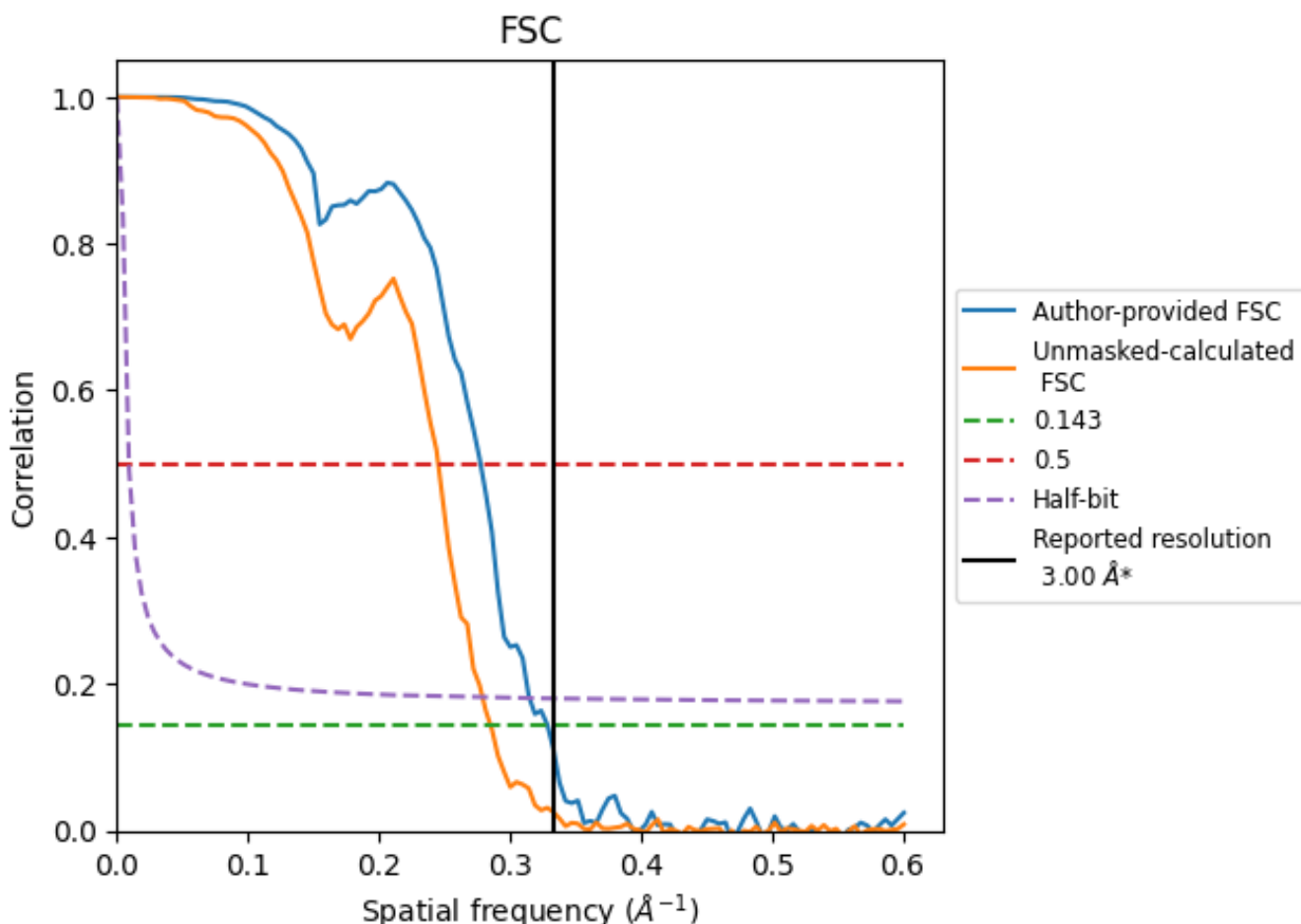


\*Reported resolution corresponds to spatial frequency of 0.333 Å<sup>-1</sup>

## 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 Å<sup>-1</sup>



## 8.2 Resolution estimates [i](#)

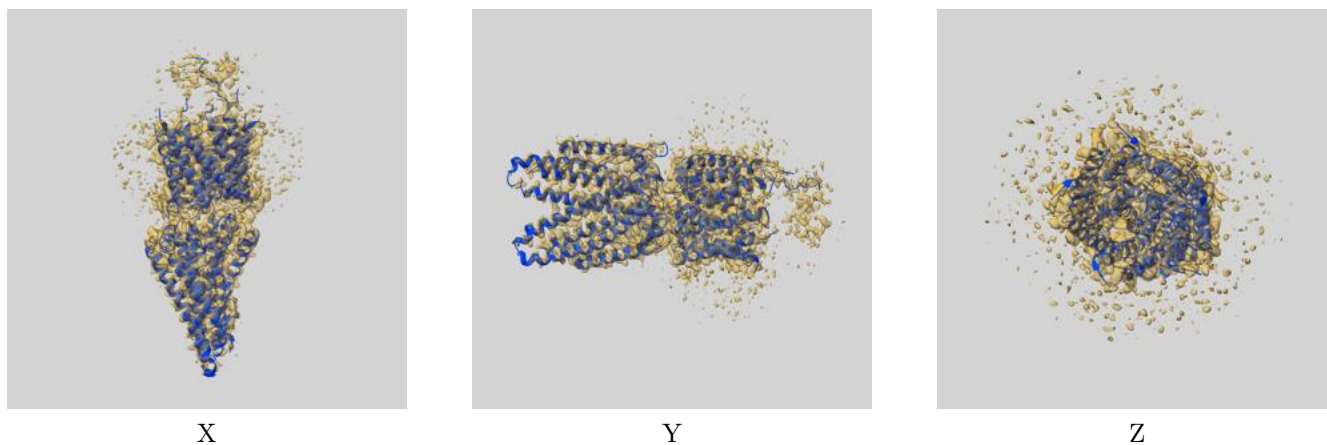
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.04	3.60	3.17
Unmasked-calculated*	3.50	4.07	3.58

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.50 differs from the reported value 3.0 by more than 10 %

## 9 Map-model fit [i](#)

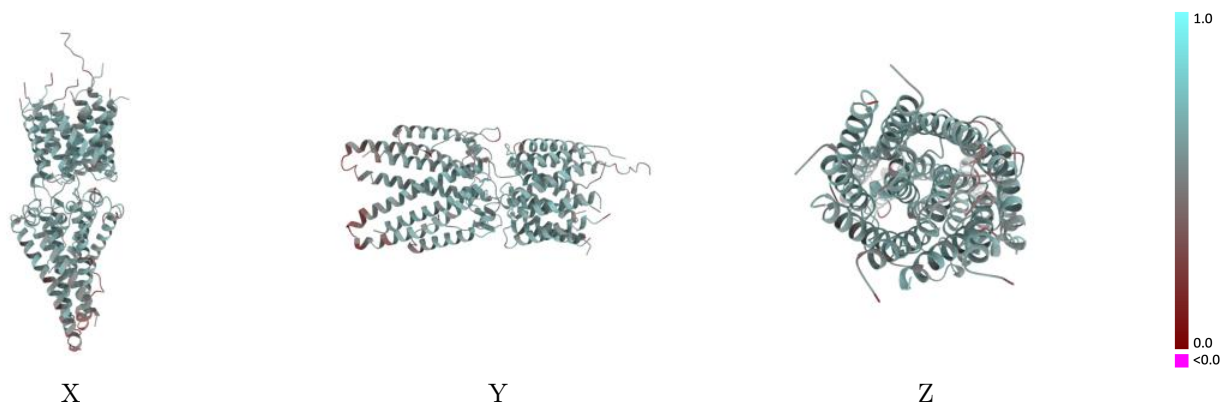
This section contains information regarding the fit between EMDB map EMD-24958 and PDB model 7SAX. Per-residue inclusion information can be found in section 3 on page 6.

### 9.1 Map-model overlay [i](#)



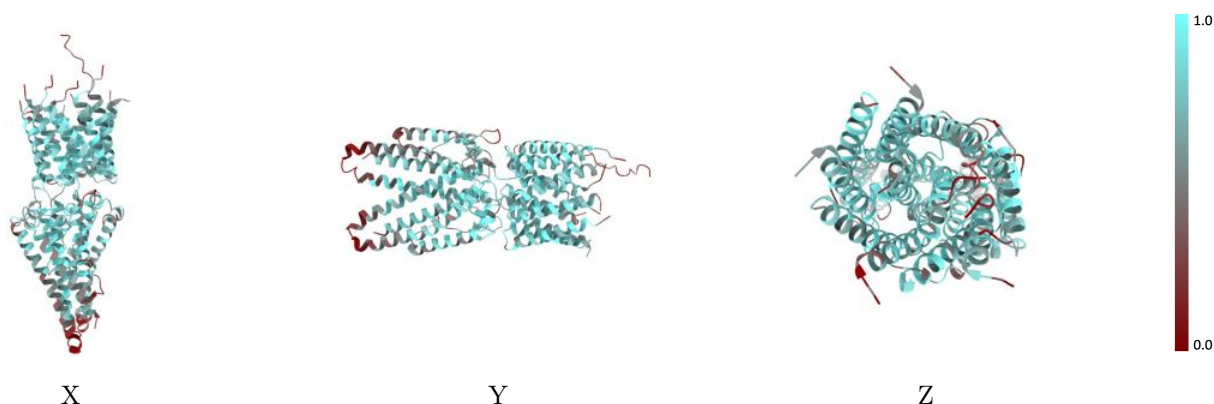
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



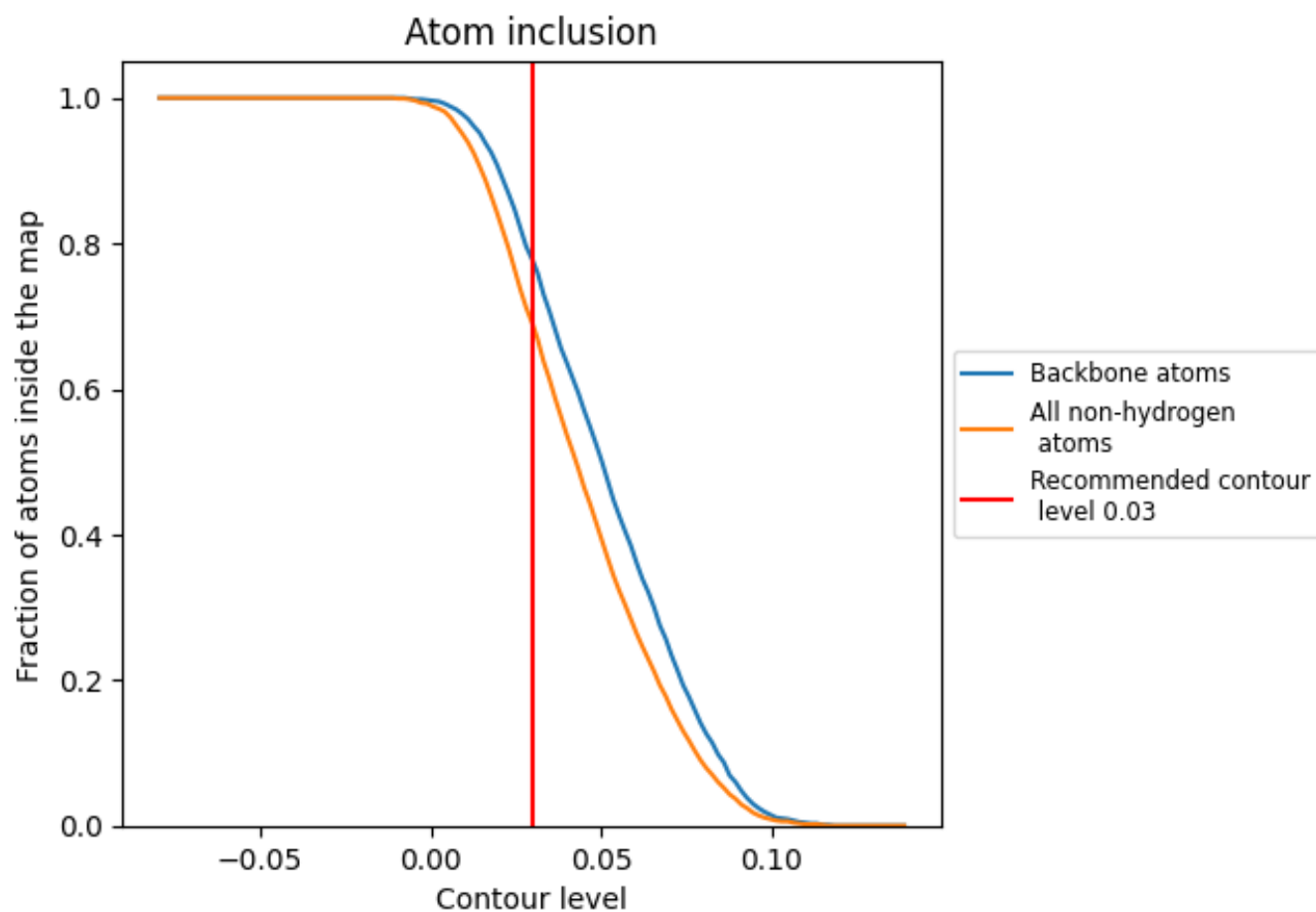
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

















## 9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 69% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6870	 0.5590
A	 0.6930	 0.5570
B	 0.6250	 0.5390
C	 0.6710	 0.5670
D	 0.7100	 0.5630
E	 0.7690	 0.5930
F	 0.7330	 0.5820
G	 0.7840	 0.5810

