



## Full wwPDB EM Validation Report ⓘ

Oct 15, 2025 – 02:19 pm BST

PDB ID : 9QPQ / pdb\_00009qpq  
EMDB ID : EMD-53278  
Title : The structure of the COPI leaf bound to GOLPH3  
Authors : Taylor, R.J.; Tagiltsev, G.; Ciazynska, K.A.; Briggs, J.A.G.  
Deposited on : 2025-03-28  
Resolution : 7.50 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](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>.

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

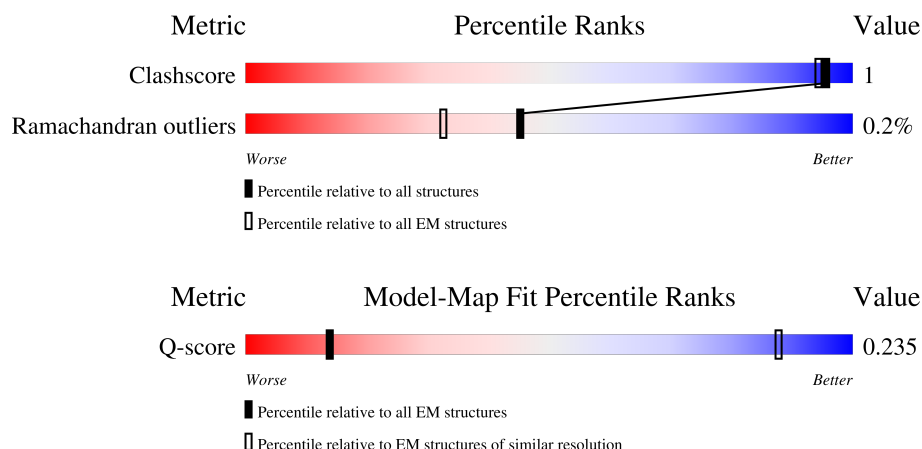
EMDB validation analysis : 0.0.1.dev129  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.46

# 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 7.50 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.







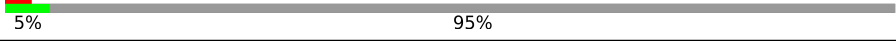

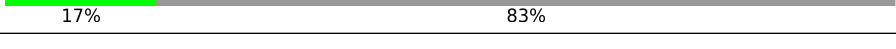
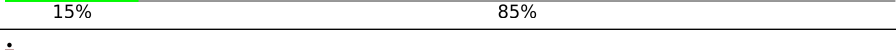
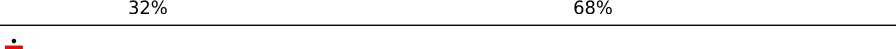
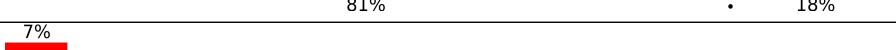
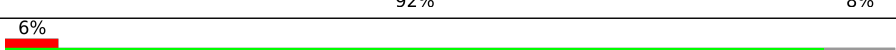
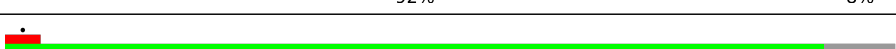
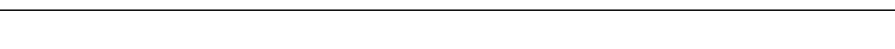
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Q-score	-	25397	436 ( 7.00 - 8.00 )

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	298	5% 95%
1	B	298	82% 18%
2	D	1224	5% 48% 52%
2	E	1224	19% 81%
3	F	905	64% 35%

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Mol	Chain	Length	Quality of chain
3	G	905	 27%72%
4	H	953	 25%75%
4	I	953	 32%67%
4	J	953	 32%67%
4	K	953	 5%95%
5	L	511	 39%61%
6	M	874	 17%83%
6	N	874	 15%85%
6	O	874	 32%68%
7	P	177	 81%18%
8	R	181	 7%92%8%
8	S	181	 6%92%8%
8	T	181	 92%8%

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 17013 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 Golgi phosphoprotein 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	16	Total	C	N	O	0	0
			64	32	16	16		
1	B	244	Total	C	N	O	0	0
			977	488	244	245		

- Molecule 2 is a protein called Coatomer subunit alpha.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	D	591	Total	C	N	O	0	0
			2364	1182	591	591		
2	E	233	Total	C	N	O	0	0
			932	466	233	233		

- Molecule 3 is a protein called Coatomer subunit beta'.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	F	586	Total	C	N	O	0	0
			2344	1172	586	586		
3	G	252	Total	C	N	O	0	0
			1008	504	252	252		

- Molecule 4 is a protein called Coatomer subunit beta.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	H	243	Total	C	N	O	0	0
			973	486	243	244		
4	I	313	Total	C	N	O	0	0
			1252	626	313	313		
4	J	311	Total	C	N	O	0	0
			1244	622	311	311		
4	K	51	Total	C	N	O	0	0
			204	102	51	51		

- Molecule 5 is a protein called Coatomer subunit delta.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	L	201	Total	C	N	O	0	0
			804	402	201	201		

- Molecule 6 is a protein called Coatomer subunit gamma-1.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	M	149	Total	C	N	O	0	0
			596	298	149	149		
6	N	133	Total	C	N	O	0	0
			532	266	133	133		
6	O	283	Total	C	N	O	0	0
			1132	566	283	283		

- Molecule 7 is a protein called Coatomer subunit zeta-1.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	P	145	Total	C	N	O	0	0
			580	290	145	145		

- Molecule 8 is a protein called ADP-ribosylation factor 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	R	167	Total	C	N	O	0	0
			669	334	167	168		
8	S	167	Total	C	N	O	0	0
			669	334	167	168		
8	T	167	Total	C	N	O	0	0
			669	334	167	168		









- Molecule 3: Coatomer subunit beta'

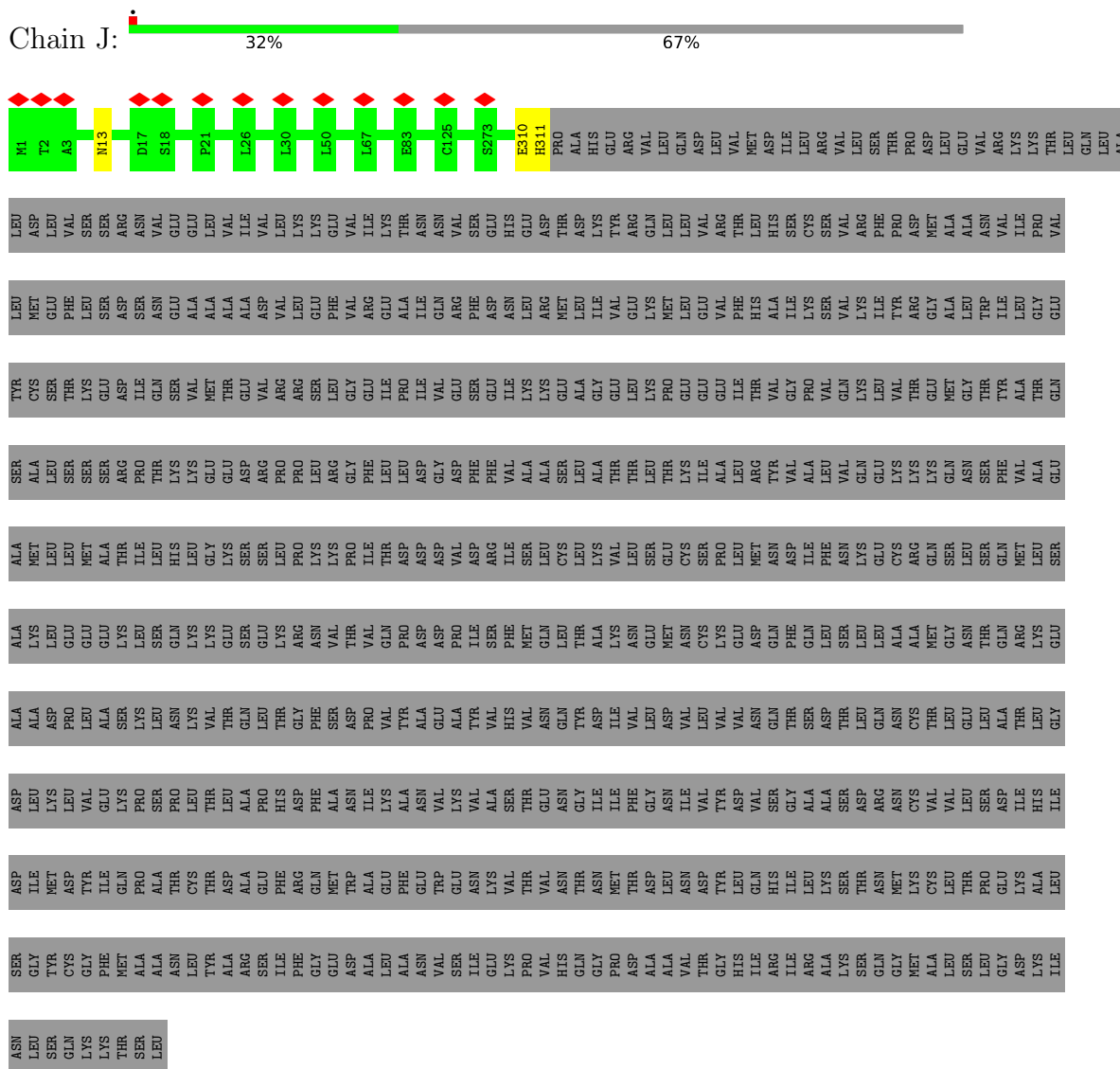
- Molecule 4: Coatomer subunit beta

[illegible]

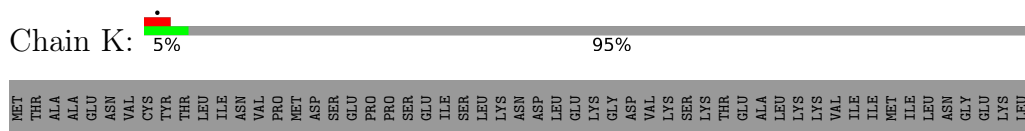


[illegible]

- Molecule 4: Coatomer subunit beta



- Molecule 4: Coatomer subunit beta





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

- Molecule 6: Coatomer subunit gamma-1

[illegible]

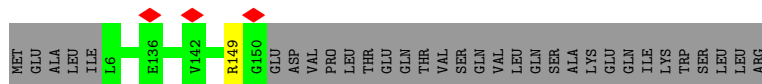
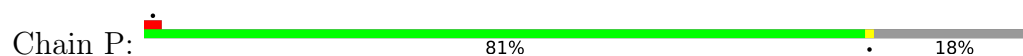
- Molecule 6: Coatomer subunit gamma-1



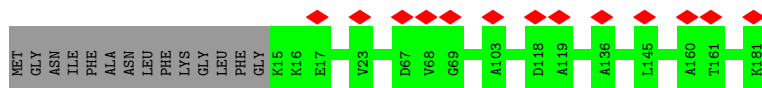
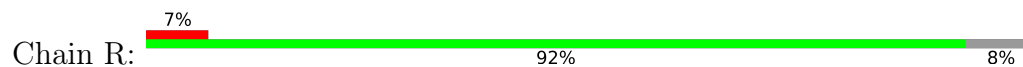


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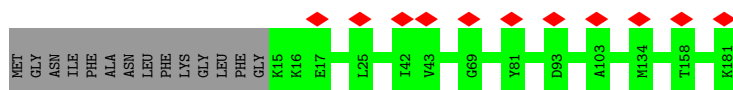
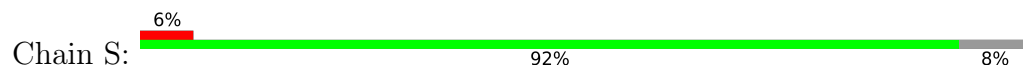
- Molecule 7: Coatomer subunit zeta-1



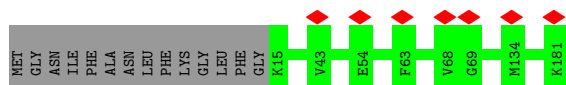
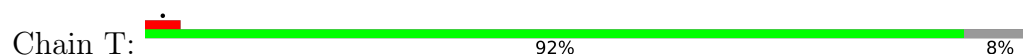
- Molecule 8: ADP-ribosylation factor 1



- Molecule 8: ADP-ribosylation factor 1



- Molecule 8: ADP-ribosylation factor 1



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	108432	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 ( $e^-/\text{\AA}^2$ )	125	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	53000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.042	Depositor
Minimum map value	-0.023	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0053	Depositor
Map size (Å)	499.32, 499.32, 499.32	wwPDB
Map dimensions	292, 292, 292	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.71, 1.71, 1.71	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	0.60	0/63	0.92	0/77
1	B	0.77	0/976	1.10	0/1217
2	D	0.73	0/2363	0.93	0/2952
2	E	0.75	0/931	1.22	0/1162
3	F	0.69	0/2343	0.91	0/2927
3	G	0.78	0/1007	1.24	0/1257
4	H	0.65	0/972	0.97	0/1212
4	I	0.73	0/1250	1.24	0/1559
4	J	0.72	0/1243	1.20	0/1552
4	K	0.69	0/203	1.06	0/252
5	L	0.69	0/802	1.08	0/999
6	M	0.75	0/595	1.23	0/742
6	N	0.73	0/531	1.23	0/662
6	O	0.78	0/1131	1.21	0/1412
7	P	0.75	0/579	1.01	0/722
8	R	0.69	0/668	1.05	0/832
8	S	0.68	0/668	1.05	0/832
8	T	0.73	0/668	1.02	0/832
All	All	0.72	0/16993	1.09	0/21200

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	64	0	17	0	0
1	B	977	0	253	0	0
2	D	2364	0	637	2	0
2	E	932	0	246	3	0
3	F	2344	0	650	2	0
3	G	1008	0	260	4	0
4	H	973	0	258	0	0
4	I	1252	0	315	10	0
4	J	1244	0	312	10	0
4	K	204	0	49	0	0
5	L	804	0	215	1	0
6	M	596	0	154	0	0
6	N	532	0	139	0	0
6	O	1132	0	287	0	0
7	P	580	0	155	0	0
8	R	669	0	185	0	0
8	S	669	0	185	0	0
8	T	669	0	185	0	0
All	All	17013	0	4502	19	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 1.

All (19) 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)
4:I:311:HIS:CA	4:J:310:GLU:O	1.72	1.35
4:I:311:HIS:N	4:J:310:GLU:O	1.82	1.13
4:I:314:HIS:CA	4:J:311:HIS:O	2.10	0.99
4:I:311:HIS:N	4:J:310:GLU:C	2.36	0.84
2:E:793:LYS:CA	3:G:819:TRP:O	2.31	0.79
4:I:314:HIS:N	4:J:311:HIS:O	2.18	0.76
4:I:311:HIS:CA	4:J:310:GLU:C	2.60	0.75
2:E:764:THR:O	3:G:821:ALA:O	2.09	0.69
2:E:764:THR:O	3:G:821:ALA:C	2.35	0.69
4:I:311:HIS:N	4:J:310:GLU:CA	2.65	0.59
3:F:37:GLY:HA3	3:F:56:CYS:O	2.08	0.54
3:F:251:GLY:HA2	3:F:272:GLU:O	2.09	0.52
2:D:181:VAL:C	2:D:183:GLY:H	2.18	0.51
4:I:314:HIS:H	4:J:311:HIS:C	2.19	0.51
4:I:537:GLU:O	4:I:539:ARG:N	2.47	0.48
4:I:314:HIS:N	4:J:311:HIS:C	2.72	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:31:GLY:HA2	2:D:52:GLY:O	2.17	0.44
3:G:758:ALA:O	3:G:762:LEU:C	2.63	0.42
4:J:13:ASN:N	5:L:16:ILE:O	2.43	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	14/298 (5%)	13 (93%)	1 (7%)	0	100	100
1	B	242/298 (81%)	237 (98%)	5 (2%)	0	100	100
2	D	589/1224 (48%)	560 (95%)	25 (4%)	4 (1%)	19	57
2	E	231/1224 (19%)	227 (98%)	4 (2%)	0	100	100
3	F	584/905 (64%)	565 (97%)	19 (3%)	0	100	100
3	G	250/905 (28%)	248 (99%)	2 (1%)	0	100	100
4	H	241/953 (25%)	237 (98%)	4 (2%)	0	100	100
4	I	309/953 (32%)	307 (99%)	1 (0%)	1 (0%)	37	73
4	J	309/953 (32%)	304 (98%)	5 (2%)	0	100	100
4	K	49/953 (5%)	46 (94%)	2 (4%)	1 (2%)	6	32
5	L	197/511 (39%)	194 (98%)	3 (2%)	0	100	100
6	M	147/874 (17%)	146 (99%)	1 (1%)	0	100	100
6	N	131/874 (15%)	131 (100%)	0	0	100	100
6	O	281/874 (32%)	279 (99%)	2 (1%)	0	100	100
7	P	143/177 (81%)	138 (96%)	4 (3%)	1 (1%)	19	57
8	R	165/181 (91%)	162 (98%)	3 (2%)	0	100	100
8	S	165/181 (91%)	162 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	T	165/181 (91%)	163 (99%)	2 (1%)	0	100	100
All	All	4212/12519 (34%)	4119 (98%)	86 (2%)	7 (0%)	45	78

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	178	GLU
2	D	180	ASP
2	D	182	ARG
4	I	538	ASP
7	P	149	ARG
2	D	187	VAL
4	K	684	CYS

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

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

### 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 ⓘ

There are no chain breaks in this entry.

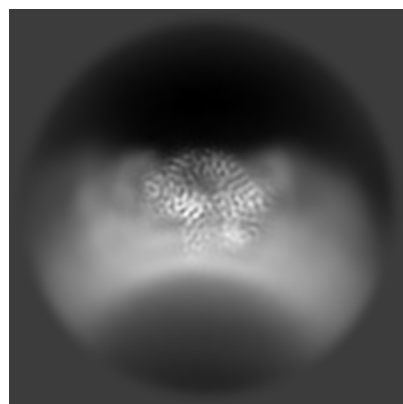
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53278. These allow visual inspection of the internal detail of the map and identification of artifacts.

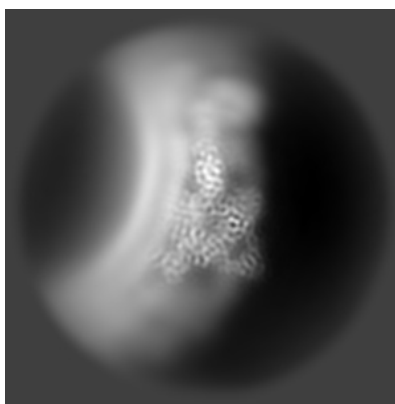
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

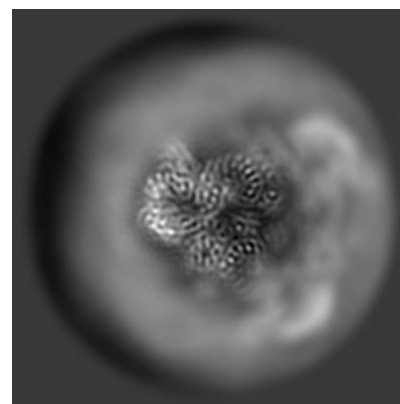
#### 6.1.1 Primary map



X

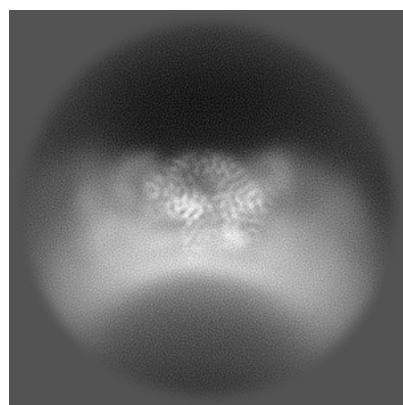


Y

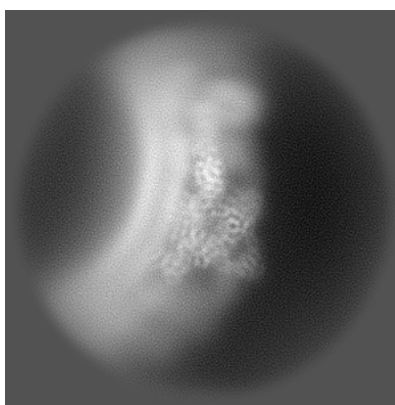


Z

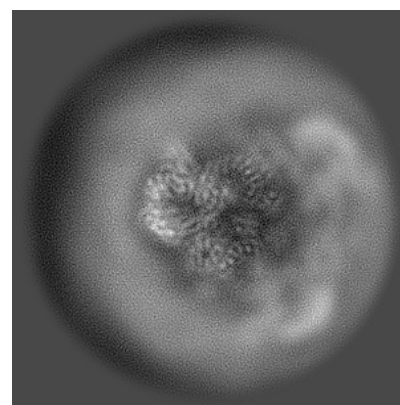
#### 6.1.2 Raw map



X



Y

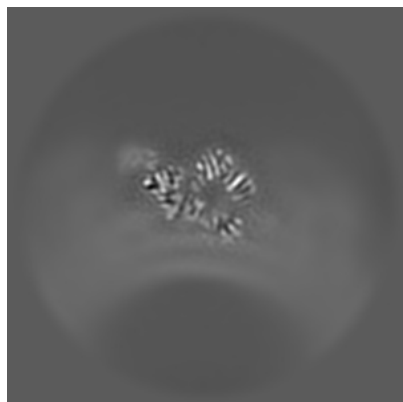


Z

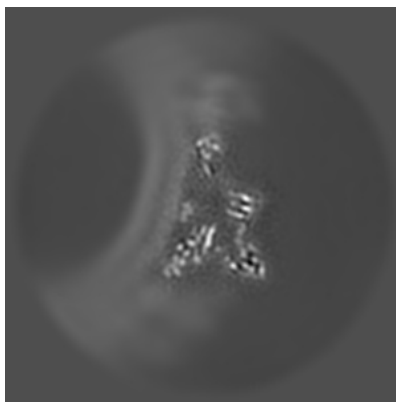
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

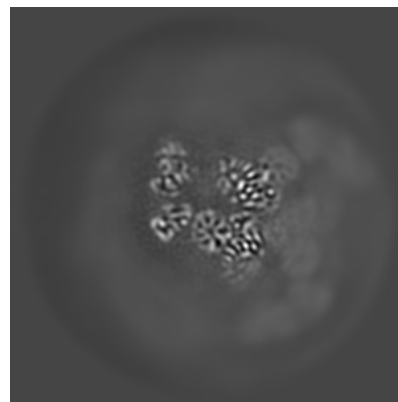
### 6.2.1 Primary map



X Index: 146

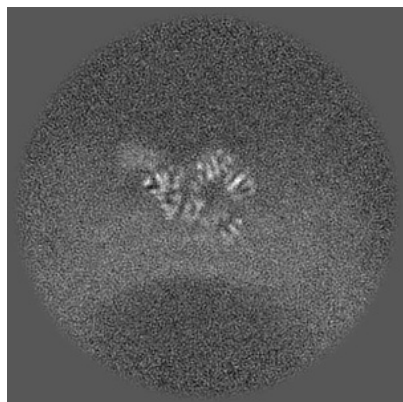


Y Index: 146

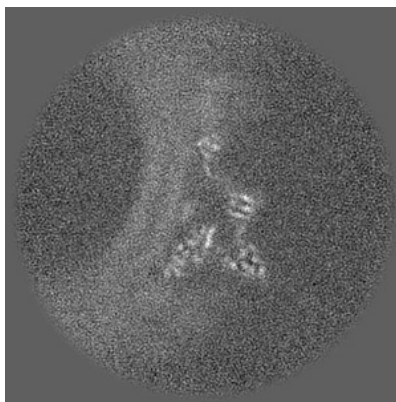


Z Index: 146

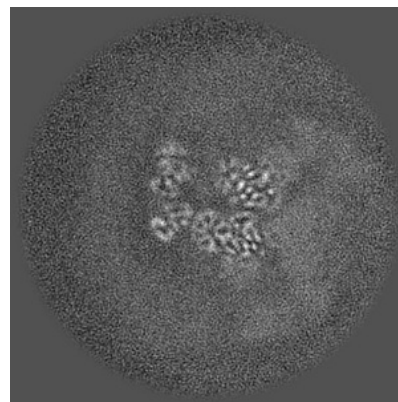
### 6.2.2 Raw map



X Index: 146



Y Index: 146

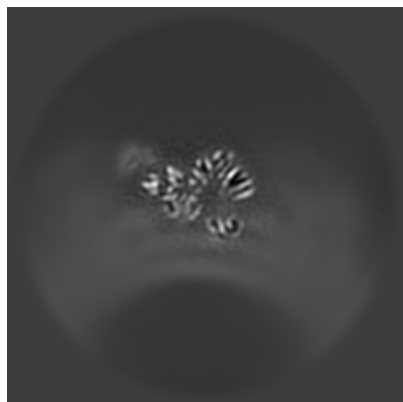


Z Index: 146

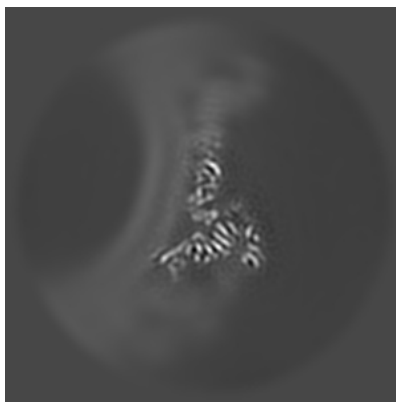
The images above show central slices of the map in three orthogonal directions.

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

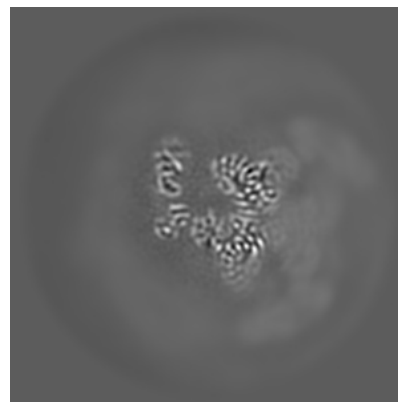
### 6.3.1 Primary map



X Index: 143

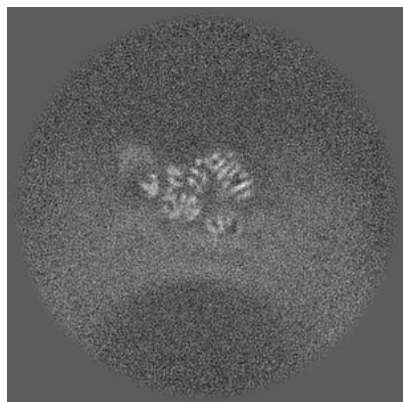


Y Index: 129

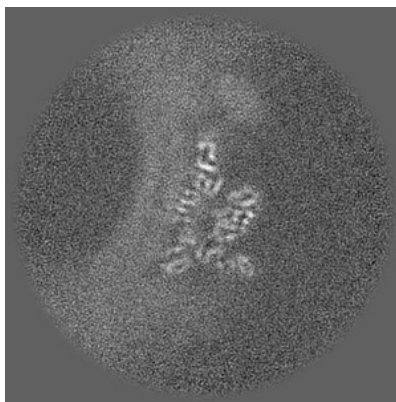


Z Index: 149

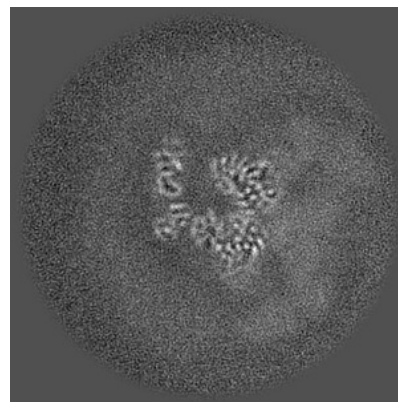
### 6.3.2 Raw map



X Index: 142



Y Index: 158



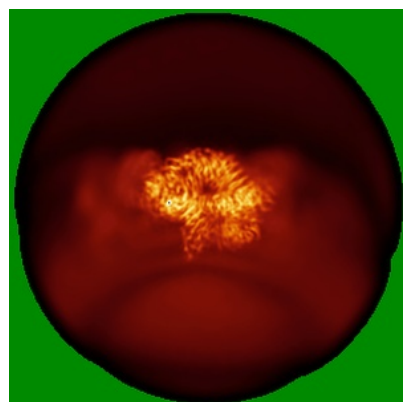
Z Index: 149

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

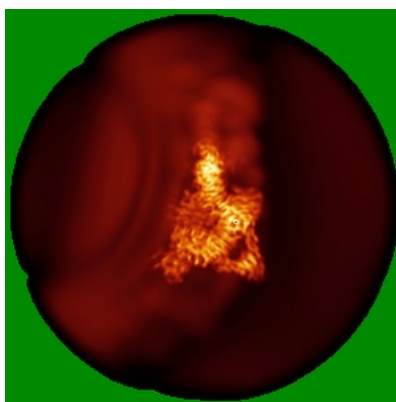


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

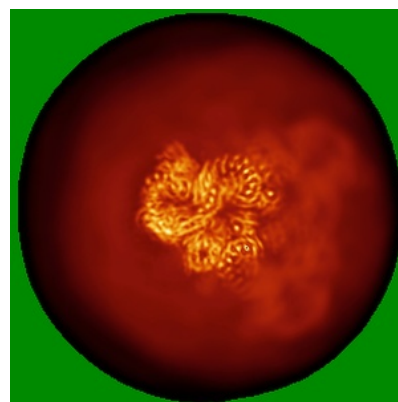
### 6.4.1 Primary map



X

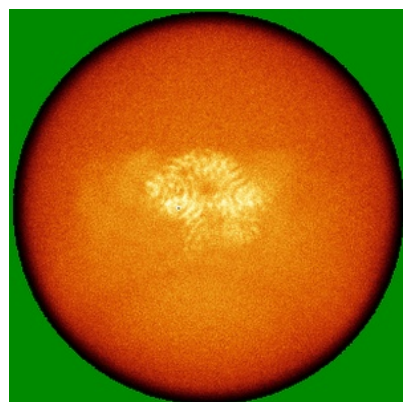


Y

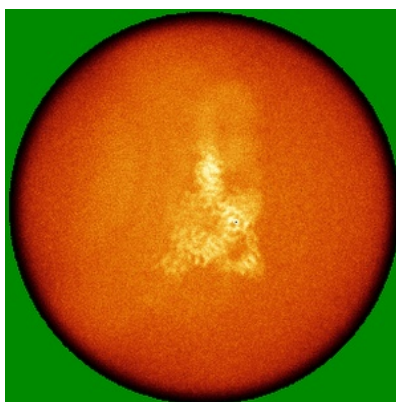


Z

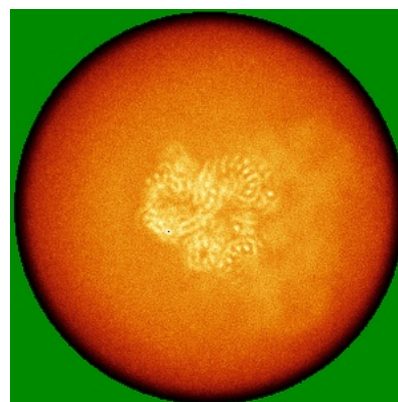
### 6.4.2 Raw map



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.

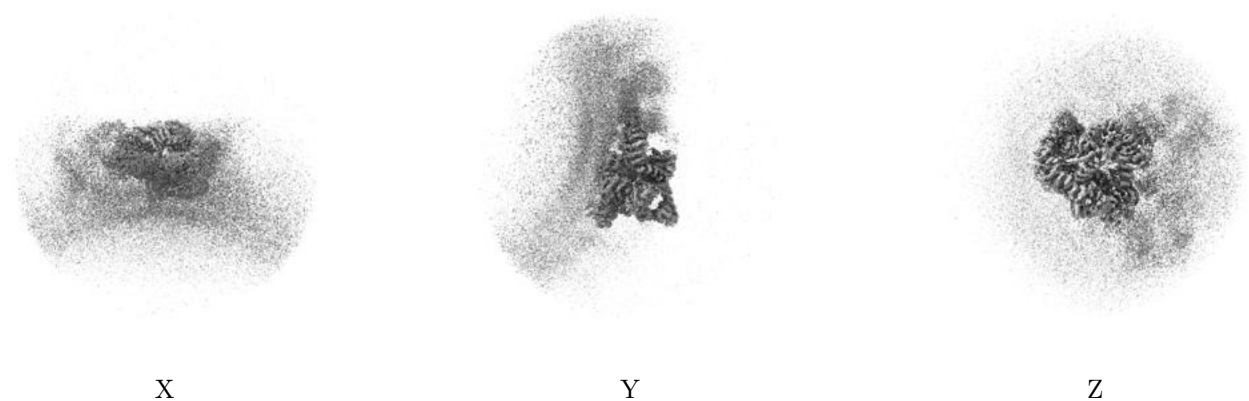
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0053. 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.

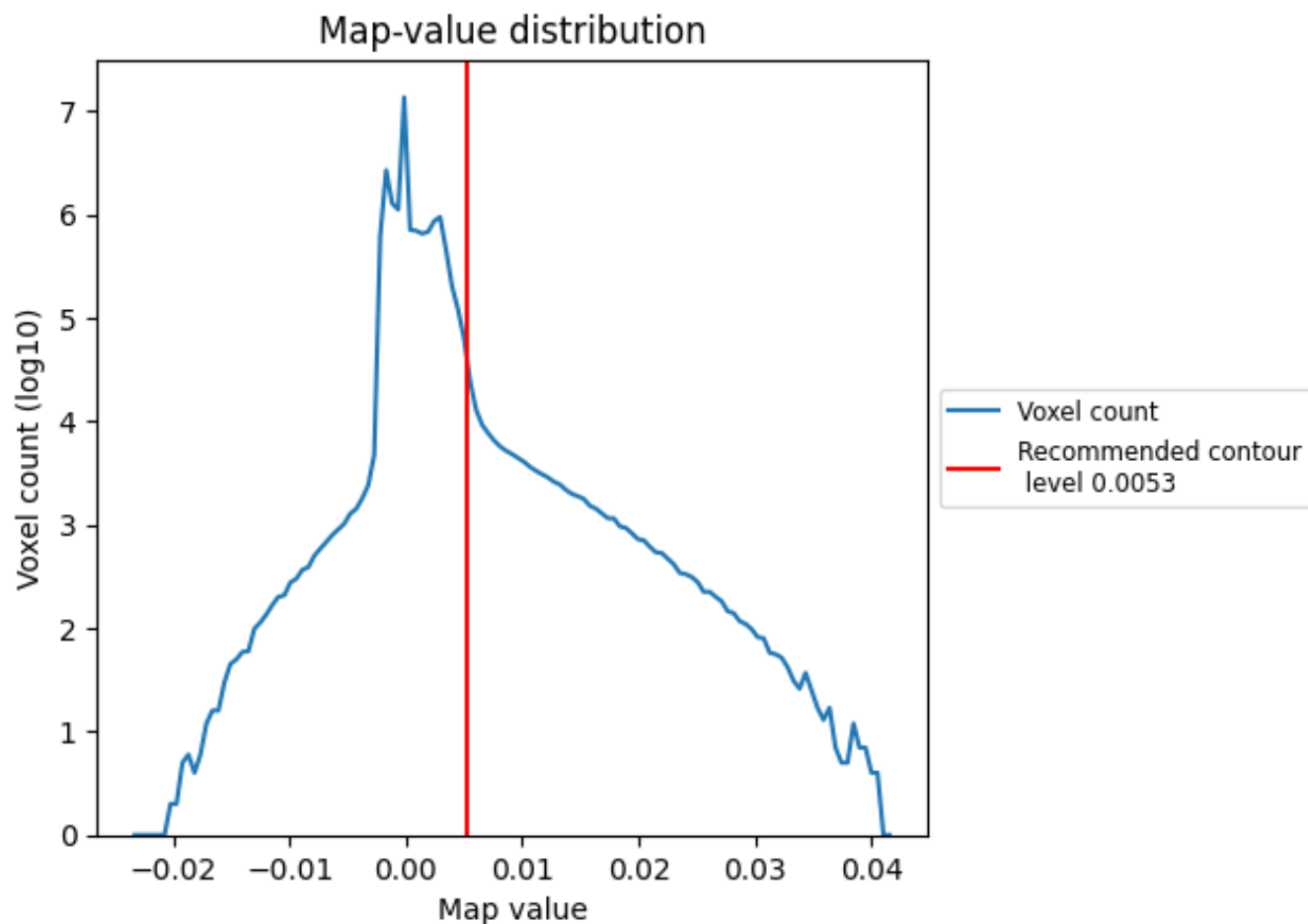
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

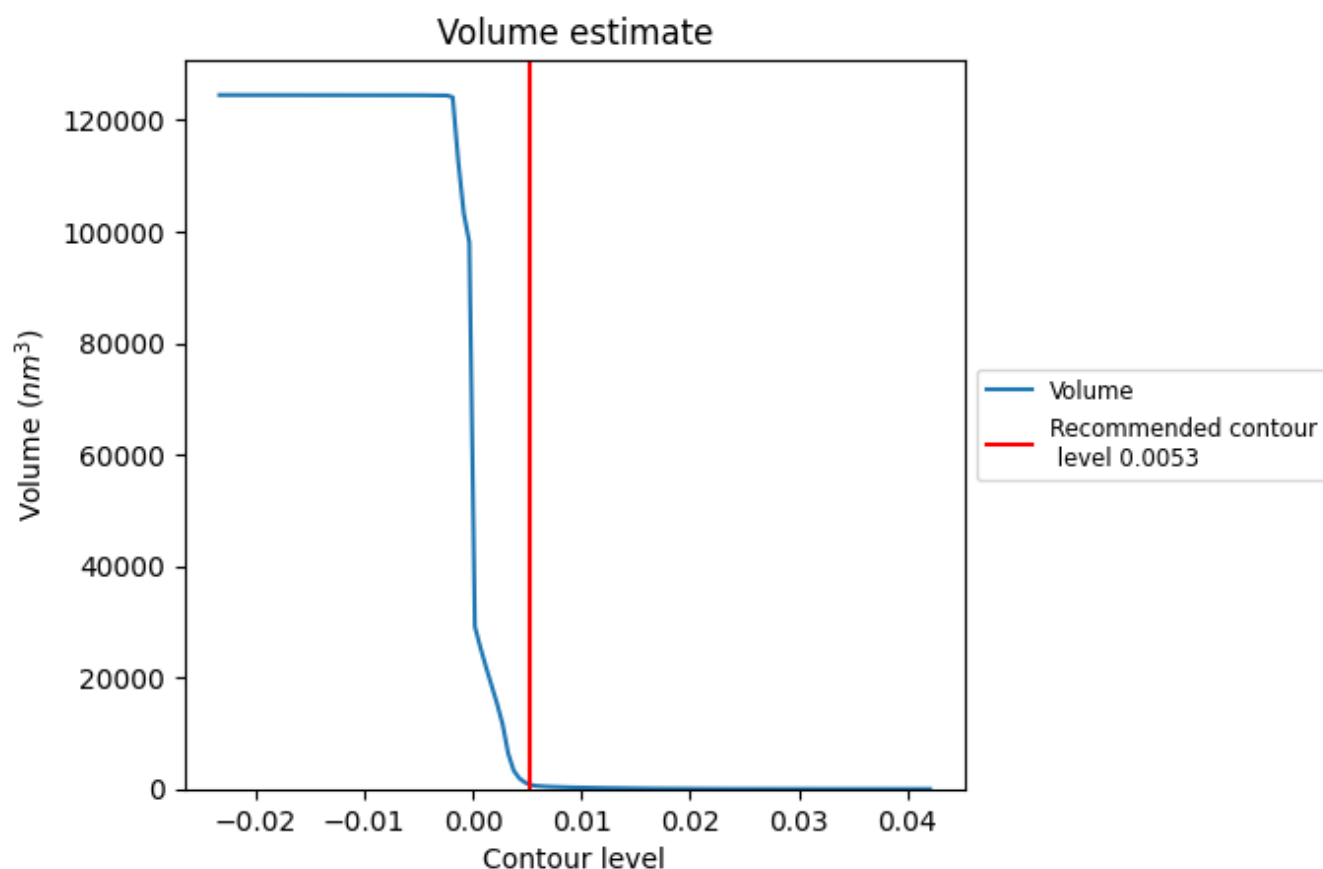
This section contains the results of statistical analysis of the map.

### 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.

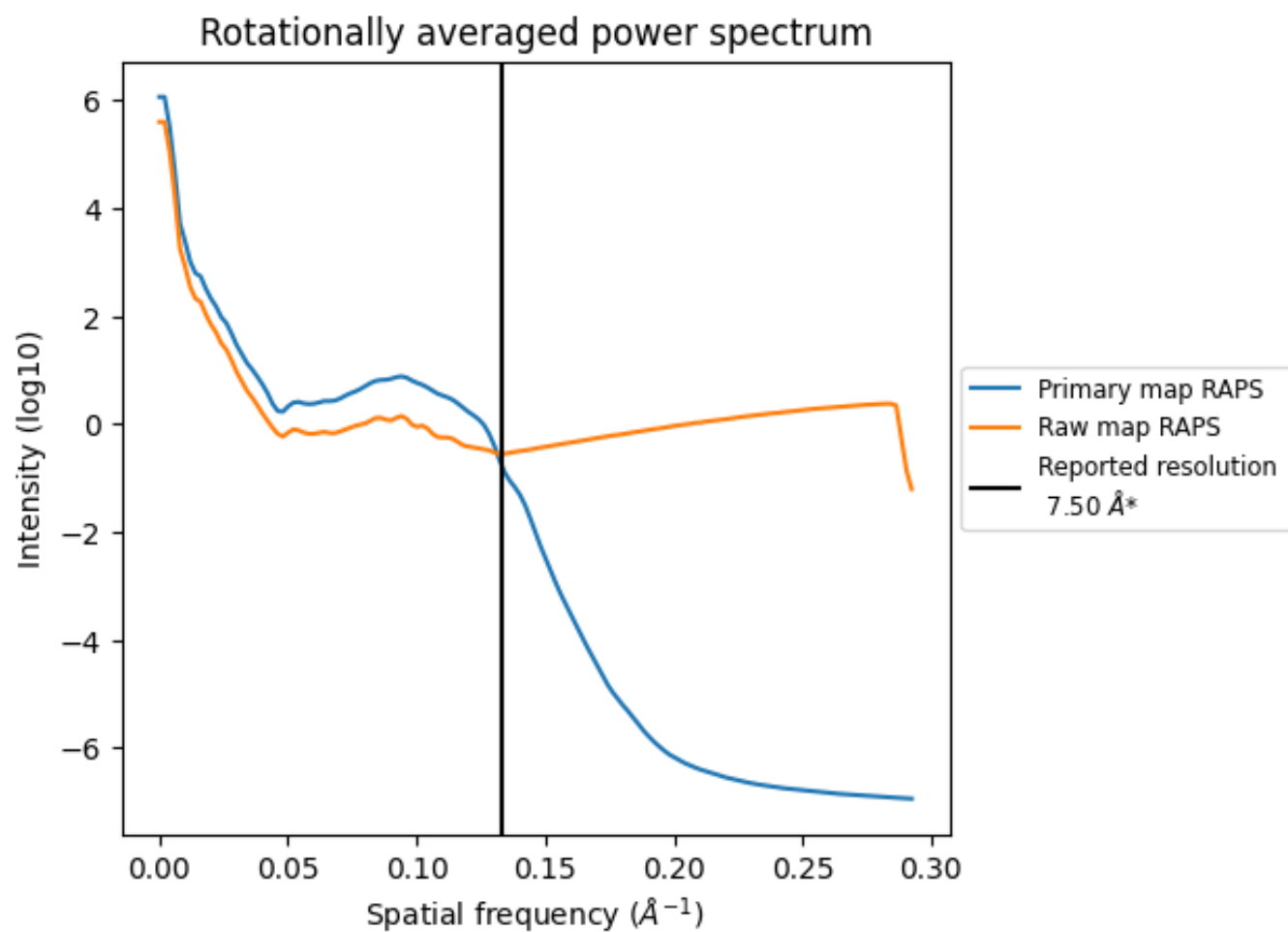
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 742 nm<sup>3</sup>; this corresponds to an approximate mass of 670 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 ⓘ

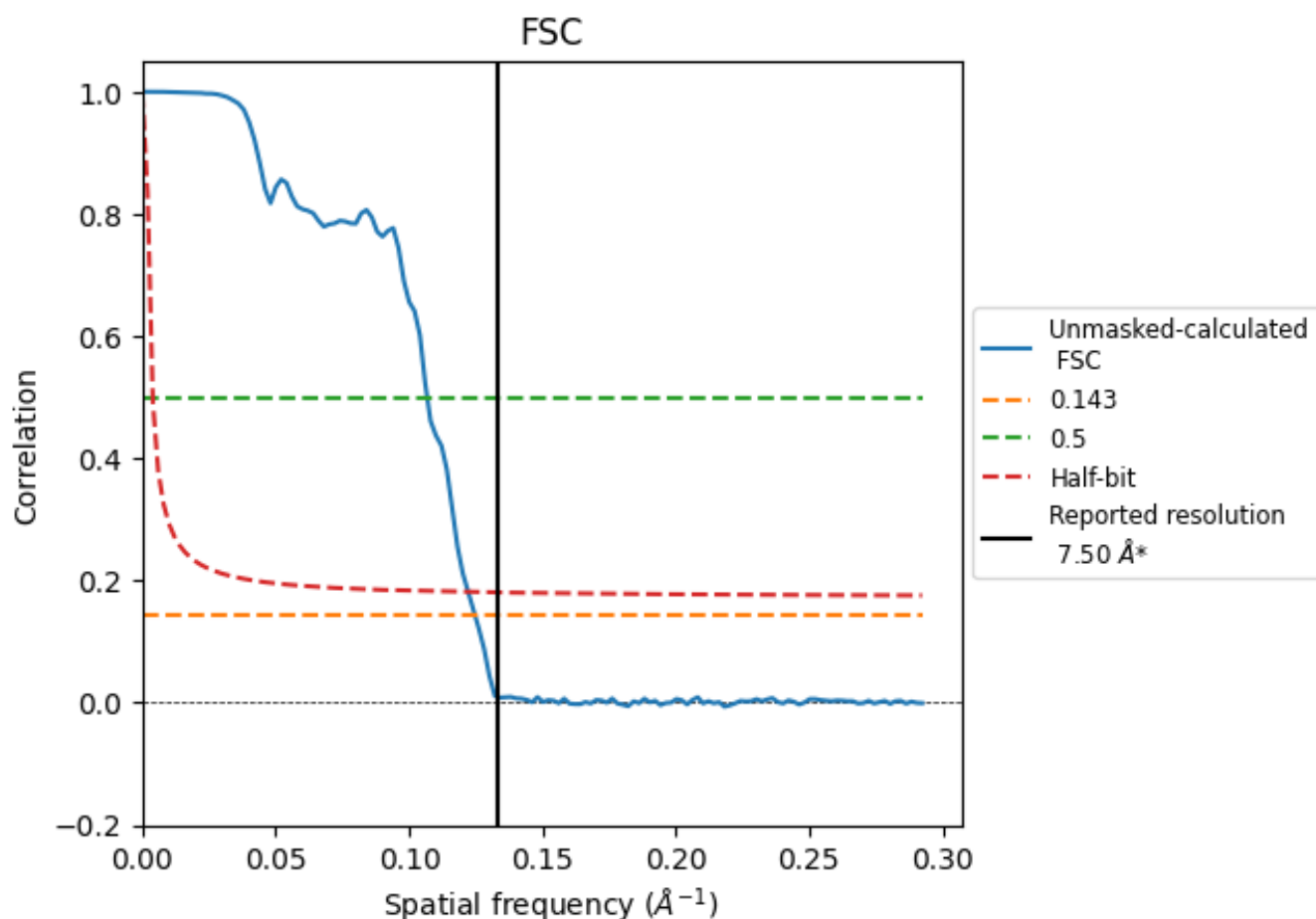


\*Reported resolution corresponds to spatial frequency of 0.133 Å<sup>-1</sup>

## 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 0.133  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

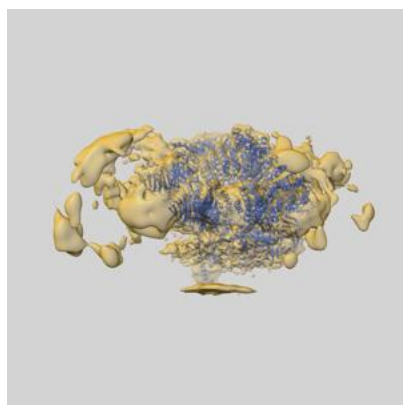
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	8.01	9.35	8.18

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

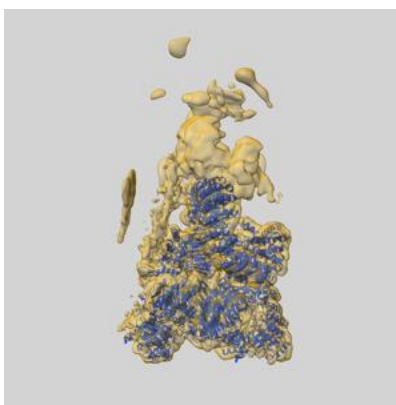
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-53278 and PDB model 9QPQ. Per-residue inclusion information can be found in section [3](#) on page [6](#).

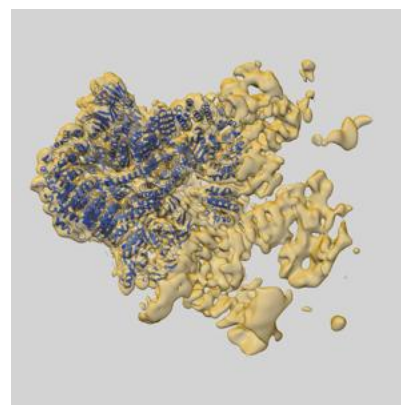
### 9.1 Map-model overlay [i](#)



X



Y

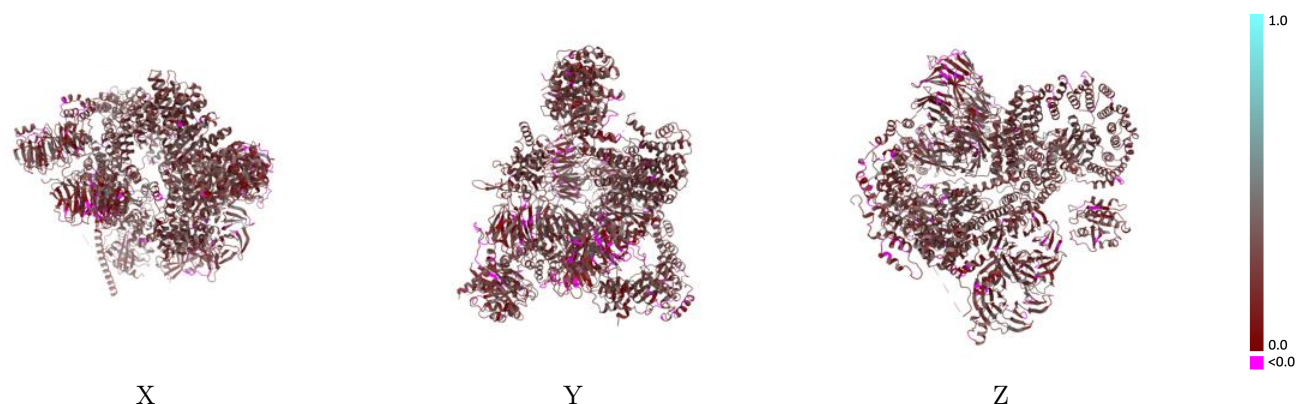


Z

The images above show the 3D surface view of the map at the recommended contour level 0.0053 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.

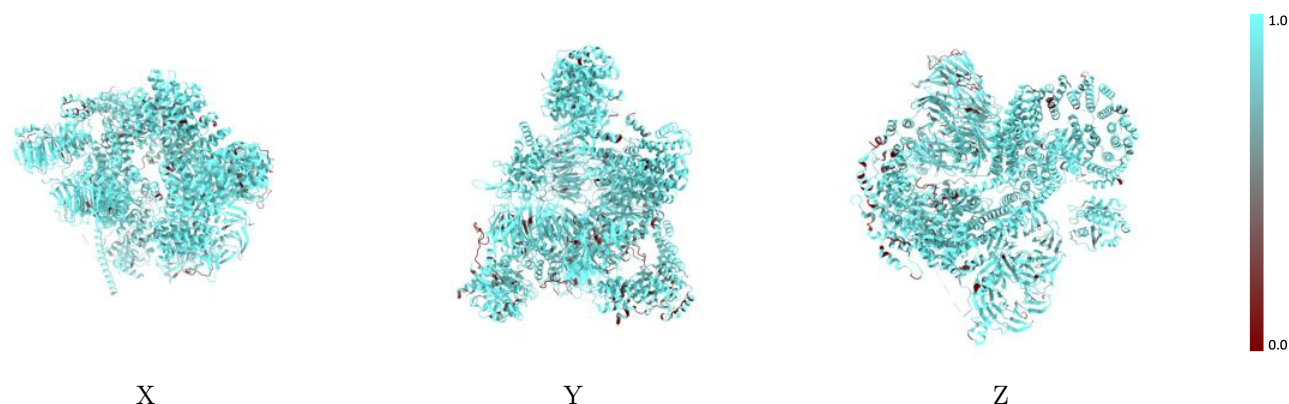


## 9.2 Q-score mapped to coordinate model [i](#)



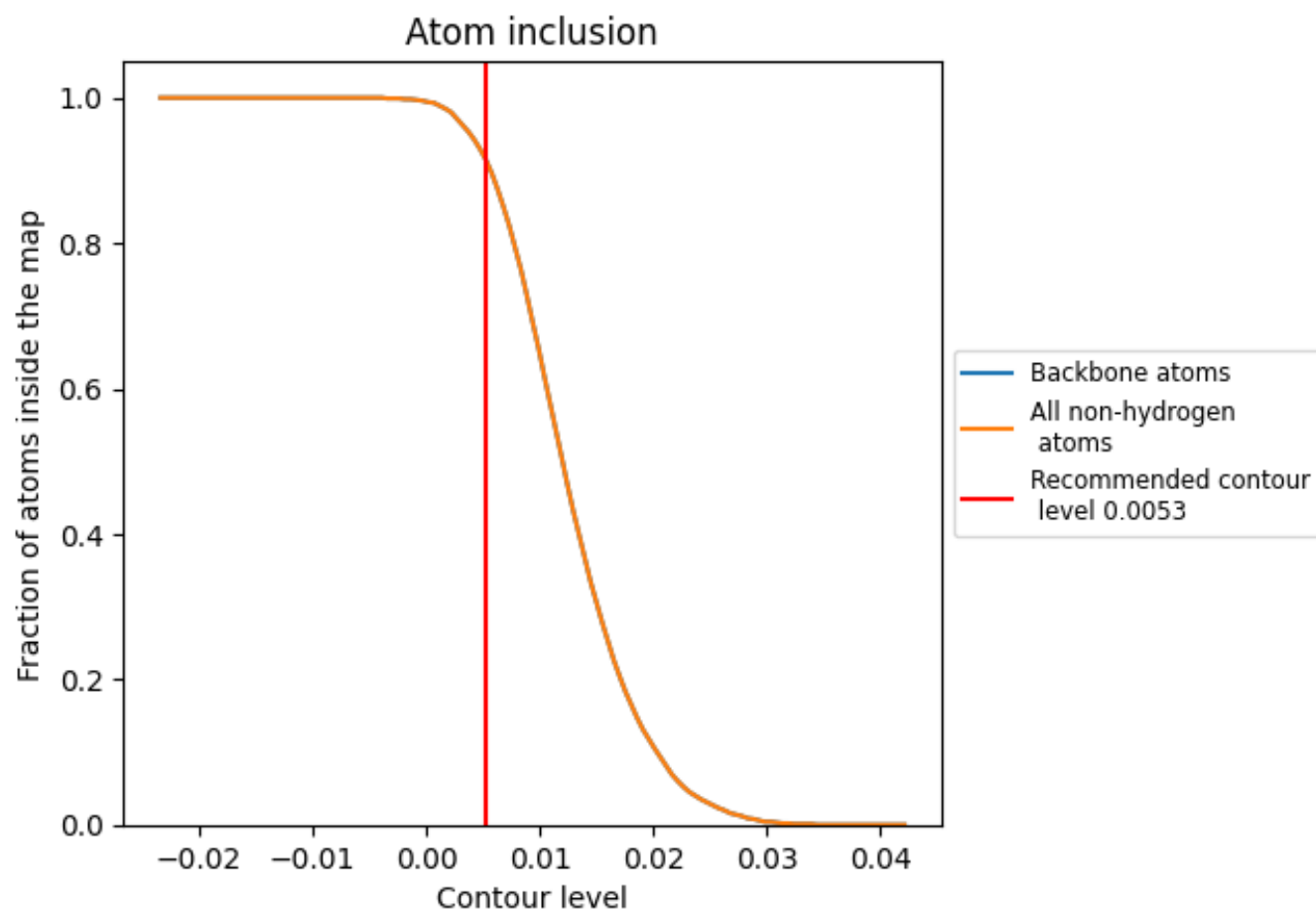
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0053).







































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 91% 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 (0.0053) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9140	 0.2350
A	 0.7810	 0.1970
B	 0.9580	 0.2620
D	 0.8570	 0.1850
E	 0.8460	 0.2290
F	 0.9510	 0.2260
G	 0.8640	 0.2190
H	 0.9290	 0.2440
I	 0.9520	 0.2650
J	 0.9410	 0.2690
K	 0.4220	 0.0920
L	 0.9520	 0.2670
M	 0.9510	 0.2630
N	 0.9830	 0.2830
O	 0.9440	 0.2520
P	 0.9710	 0.2820
R	 0.8790	 0.2240
S	 0.8910	 0.2110
T	 0.9310	 0.2090

