



wwPDB EM Validation Summary Report ⓘ

Mar 30, 2025 – 04:02 am BST

PDB ID : 9EUJ / pdb_00009euj
EMDB ID : EMD-19972
Title : Cryo-EM structure of Staphylococcus aureus bacteriophage phi812 baseplate in the post-contraction state - sheath initiator, wedge module, inner tripod, arm segment, and proximal tail sheath proteins
Authors : Binovsky, J.; Siborova, M.; Baska, R.; Pichel-Beleiro, A.; Skubnik, K.; Novacek, J.; van Raaij, M.J.; Plevka, P.
Deposited on : 2024-03-27
Resolution : 4.00 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.dev117
MolProbity : 4.02b-467
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) : 2.42

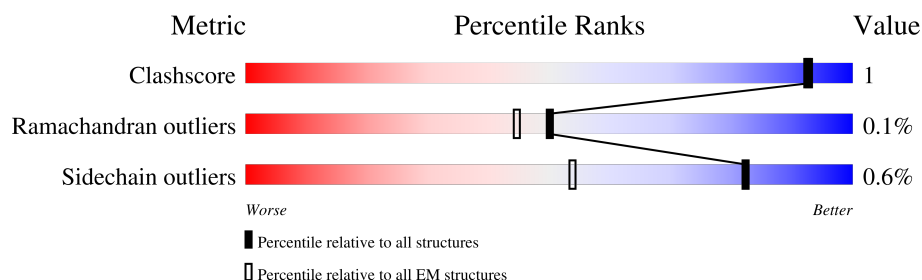
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 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	H	194	
2	I	587	
2	J	587	
2	K	587	
2	L	587	
2	M	587	
2	N	587	
3	A	234	

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Mol	Chain	Length	Quality of chain
4	B	348	<div><div></div><div>95%</div><div>5%</div></div>
4	C	348	<div><div></div><div>97%</div><div></div></div>
5	D	1019	<div><div></div><div>18%</div><div>81%</div></div>
6	E	1152	<div><div></div><div>77%</div><div>21%</div></div>
6	F	1152	<div><div></div><div>77%</div><div>21%</div></div>
6	G	1152	<div><div></div><div>69%</div><div>29%</div></div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 56898 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 Baseplate protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	H	172	Total	C	N	O	S	0	0
			1349	858	221	269	1		

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	174	ASP	-	expression tag	UNP A0A0U1WQQ5
H	175	PRO	-	expression tag	UNP A0A0U1WQQ5
H	176	ASN	-	expression tag	UNP A0A0U1WQQ5
H	177	SER	-	expression tag	UNP A0A0U1WQQ5
H	178	SER	-	expression tag	UNP A0A0U1WQQ5
H	179	SER	-	expression tag	UNP A0A0U1WQQ5
H	180	VAL	-	expression tag	UNP A0A0U1WQQ5
H	181	ASP	-	expression tag	UNP A0A0U1WQQ5
H	182	LYS	-	expression tag	UNP A0A0U1WQQ5
H	183	LEU	-	expression tag	UNP A0A0U1WQQ5
H	184	ALA	-	expression tag	UNP A0A0U1WQQ5
H	185	ALA	-	expression tag	UNP A0A0U1WQQ5
H	186	ALA	-	expression tag	UNP A0A0U1WQQ5
H	187	LEU	-	expression tag	UNP A0A0U1WQQ5
H	188	GLU	-	expression tag	UNP A0A0U1WQQ5
H	189	HIS	-	expression tag	UNP A0A0U1WQQ5
H	190	HIS	-	expression tag	UNP A0A0U1WQQ5
H	191	HIS	-	expression tag	UNP A0A0U1WQQ5
H	192	HIS	-	expression tag	UNP A0A0U1WQQ5
H	193	HIS	-	expression tag	UNP A0A0U1WQQ5
H	194	HIS	-	expression tag	UNP A0A0U1WQQ5

- Molecule 2 is a protein called Major tail sheath protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	I	540	Total	C	N	O	S	0	0
			4213	2653	714	839	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	J	553	Total	C	N	O	S	0	0
			4321	2723	734	857	7		
2	K	553	Total	C	N	O	S	0	0
			4321	2723	734	857	7		
2	L	553	Total	C	N	O	S	0	0
			4321	2723	734	857	7		
2	M	553	Total	C	N	O	S	0	0
			4321	2723	734	857	7		
2	N	553	Total	C	N	O	S	0	0
			4321	2723	734	857	7		

- Molecule 3 is a protein called Baseplate wedge subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	234	Total	C	N	O	S	0	0
			1871	1174	314	377	6		

- Molecule 4 is a protein called Baseplate component.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	348	Total	C	N	O	S	0	0
			2760	1734	459	560	7		
4	C	347	Total	C	N	O	S	0	0
			2752	1729	458	559	6		

- Molecule 5 is a protein called TmpF.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	189	Total	C	N	O	S	0	0
			1547	991	259	295	2		

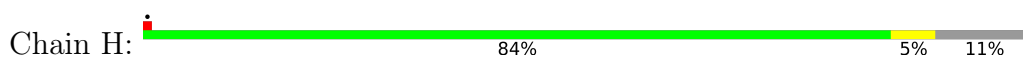
- Molecule 6 is a protein called DUF4815 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	908	Total	C	N	O	S	0	0
			7166	4511	1184	1453	18		
6	F	908	Total	C	N	O	S	0	0
			7166	4511	1184	1453	18		
6	G	821	Total	C	N	O	S	0	0
			6469	4077	1066	1308	18		

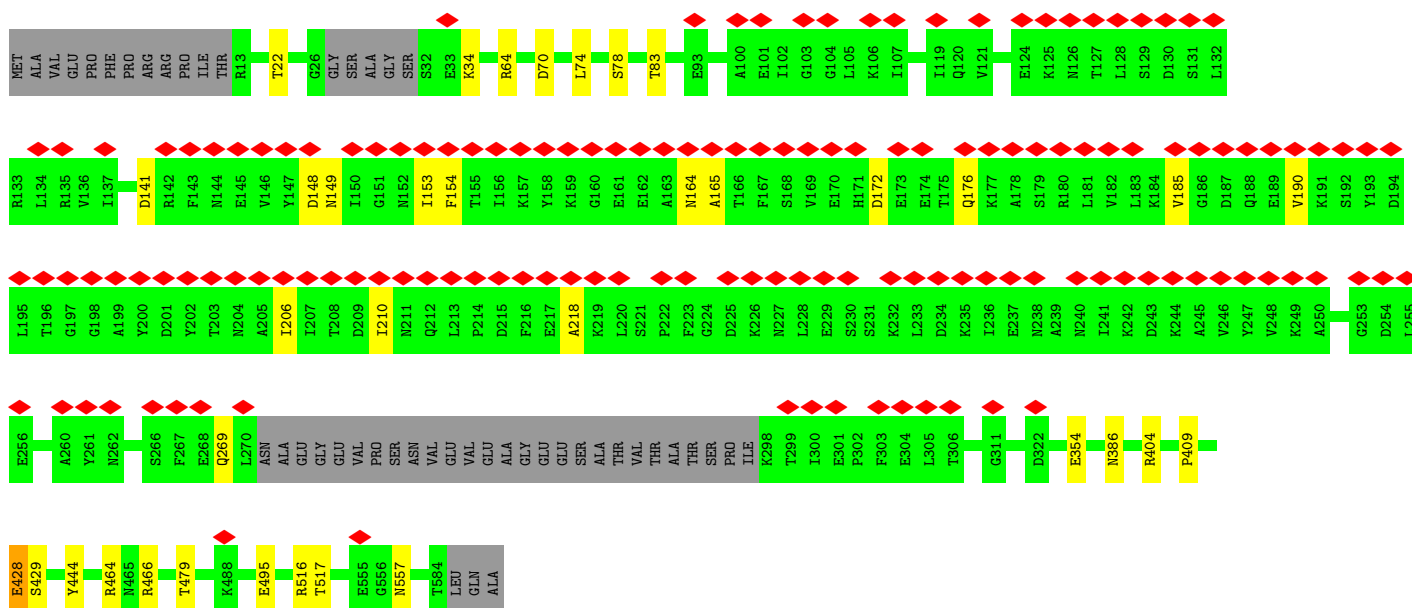
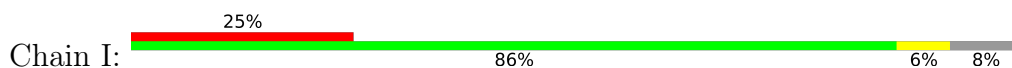
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

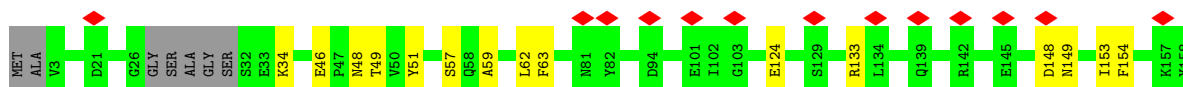
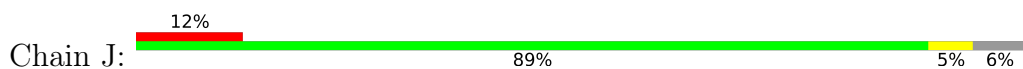
- Molecule 1: Baseplate protein

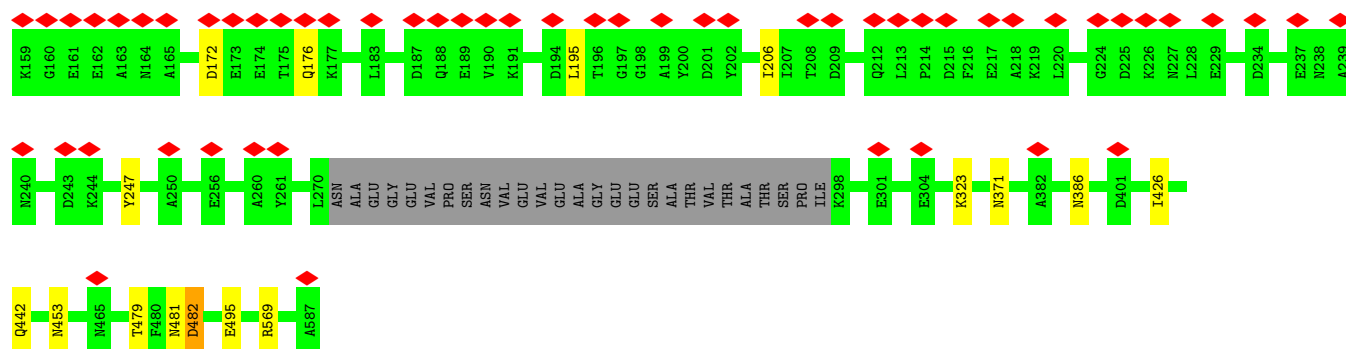


- Molecule 2: Major tail sheath protein

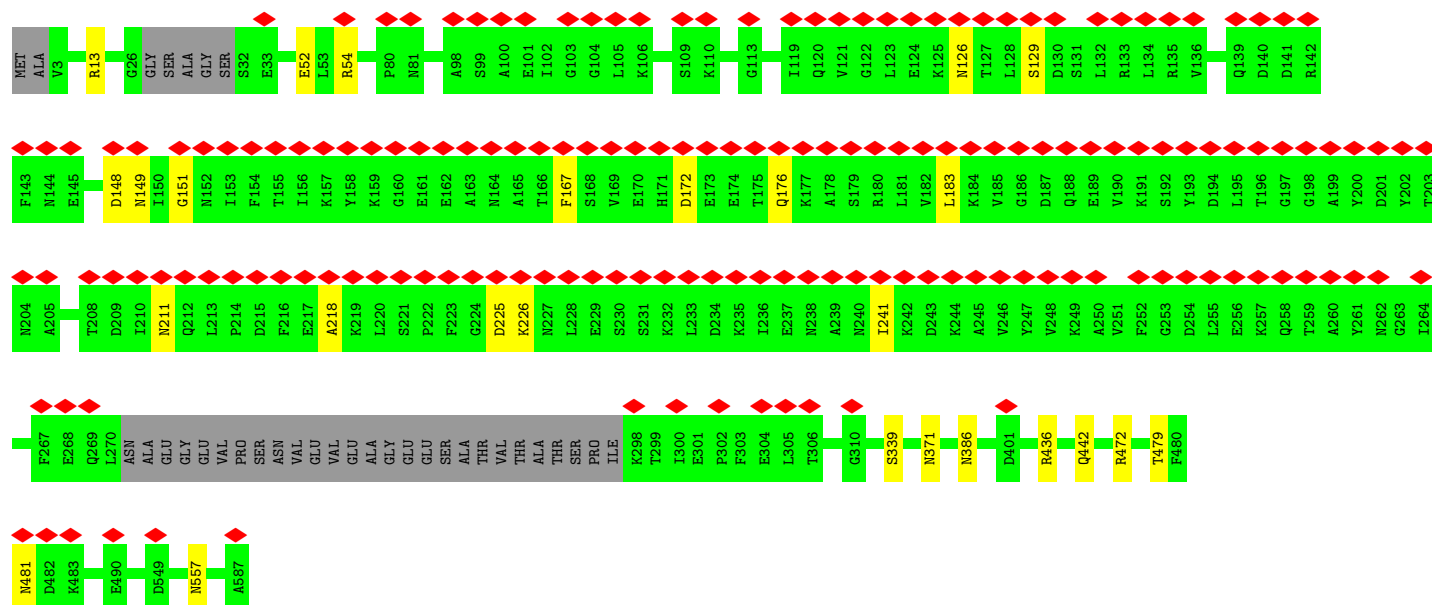


- Molecule 2: Major tail sheath protein

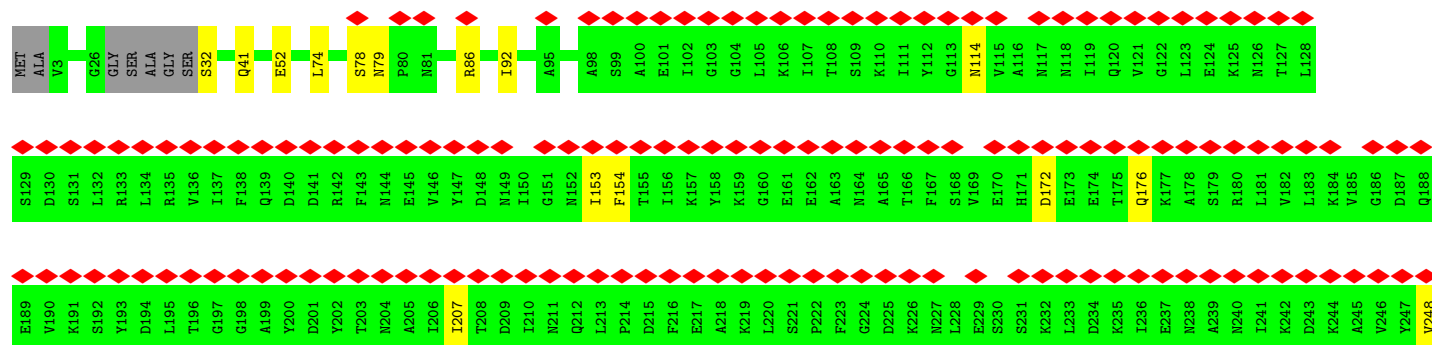
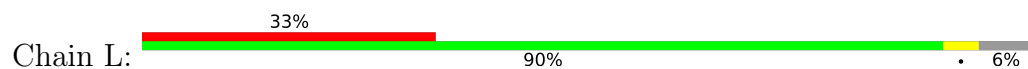


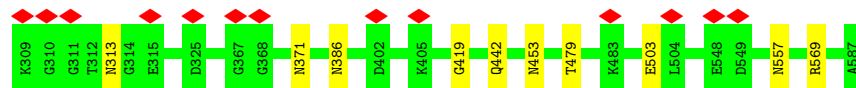
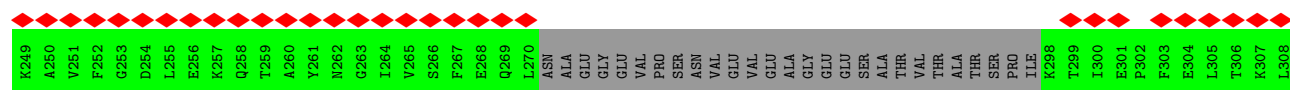


- Molecule 2: Major tail sheath protein

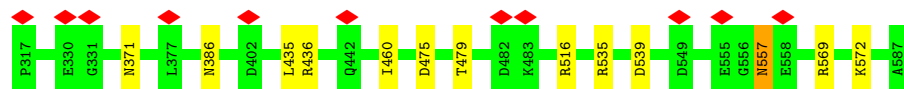
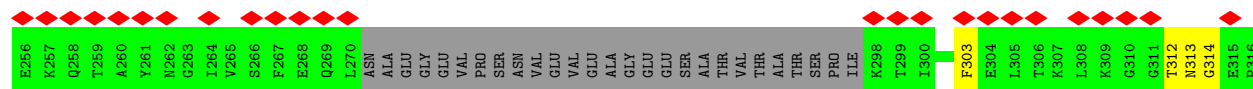
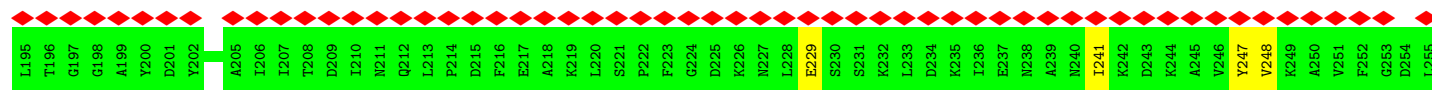
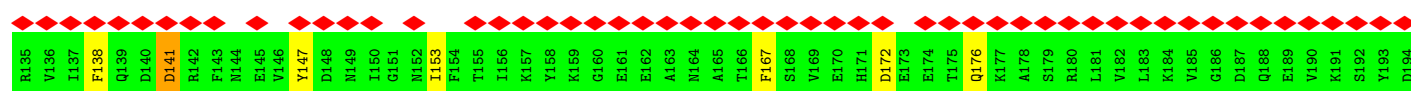
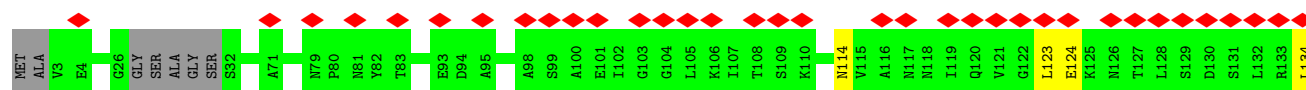
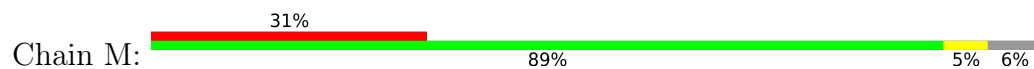


- Molecule 2: Major tail sheath protein

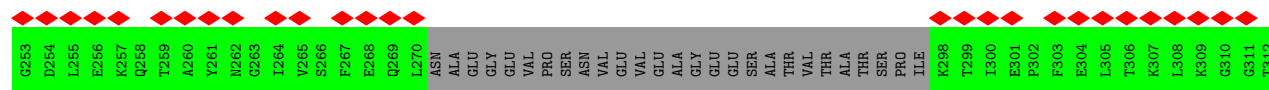
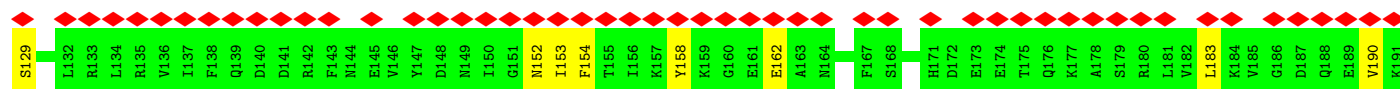
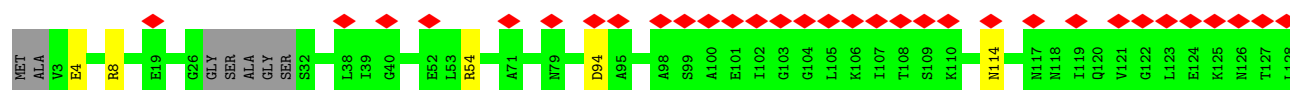
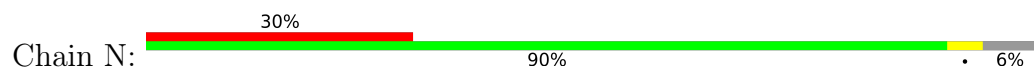




• Molecule 2: Major tail sheath protein



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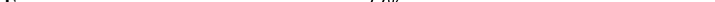
LYS VAL	SER	SER	ILE	SER	THR	LYS
	ASN	ILE	ILE	ILE	SER	ALA
VAL	PRO	TYR	LYS	TRP	LEU	SER
	ASN	GLU	ALA	ASN	LYS	THR
ASN	PHE	GLU	THR	VAL	ASN	PRO
	ASN	LEU	LEU	LYS	VAL	VAL
GLU	GLU	PRO	PHE	LEU	THR	VAL
	THR	ASN	ASN	GLY	LEU	PHE
PHE	THR	THR	VAL	GLU	TYR	PHE
	ILE	SER	GLY	LEU	TYR	ASN
TYR	ILE	ILE	ALA	ASN	SER	THR
	PRO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

- Molecule 6: DUF4815 domain-containing protein

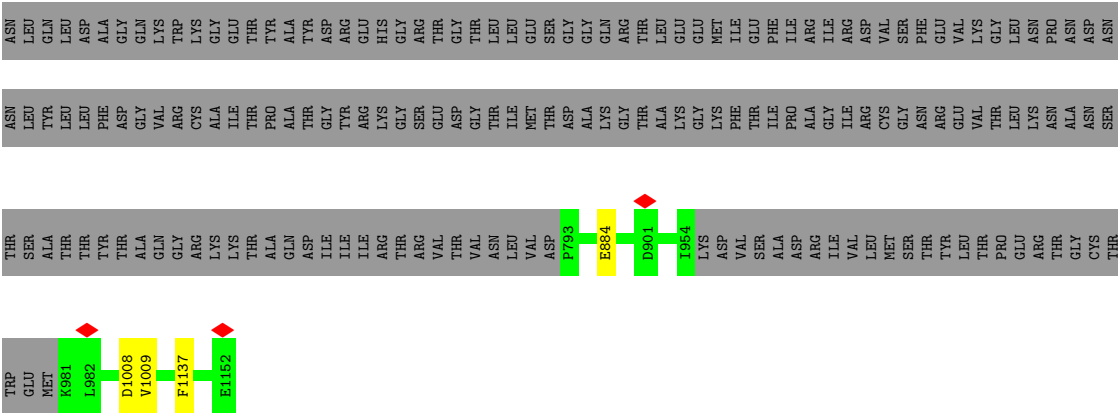
Chain E: 77% 21%

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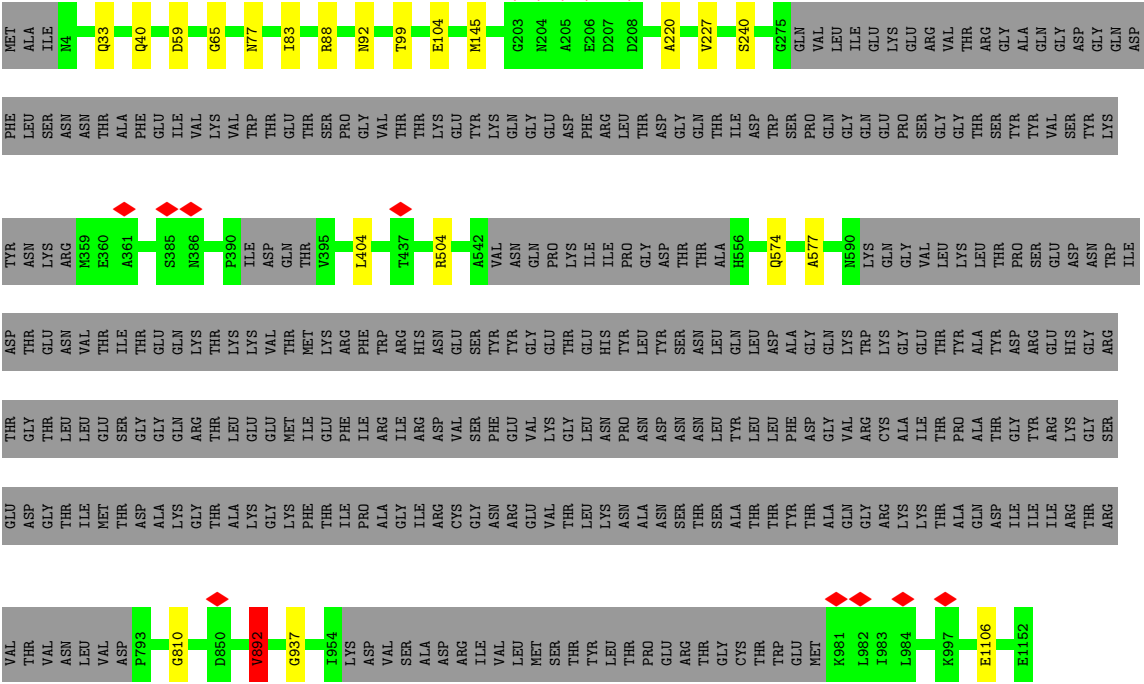
- Molecule 6: DUF4815 domain-containing protein

Chain F:  77% 21%

[illegible]



● Molecule 6: DUF4815 domain-containing protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C6	Depositor
Number of particles used	25203	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 ($e^-/\text{\AA}^2$)	42	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.048	Depositor
Minimum map value	-0.020	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	761.04004, 761.04004, 761.04004	wwPDB
Map dimensions	720, 720, 720	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.057, 1.057, 1.057	Depositor

5 Model quality

5.1 Standard geometry

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	H	0.36	0/1377	0.58	0/1872
2	I	0.36	0/4280	0.57	2/5777 (0.0%)
2	J	0.35	0/4392	0.55	0/5930
2	K	0.36	0/4392	0.54	0/5930
2	L	0.35	0/4392	0.55	0/5930
2	M	0.36	0/4392	0.56	0/5930
2	N	0.35	0/4392	0.56	0/5930
3	A	0.35	0/1902	0.54	0/2572
4	B	0.37	0/2803	0.56	0/3794
4	C	0.36	0/2795	0.55	0/3784
5	D	0.35	0/1580	0.54	0/2137
6	E	0.36	0/7308	0.56	0/9911
6	F	0.36	0/7308	0.59	0/9911
6	G	0.37	0/6594	0.58	1/8940 (0.0%)
All	All	0.36	0/57907	0.56	3/78348 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	K	0	1
4	B	0	1
6	E	0	1
All	All	0	3

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	444	TYR	CB-CG-CD2	-5.78	117.53	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	444	TYR	CB-CG-CD1	5.74	124.45	121.00
6	G	892	VAL	CA-CB-CG2	5.24	118.75	110.90

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	B	339	ARG	Sidechain
6	E	996	LEU	Mainchain
2	K	472	ARG	Sidechain

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	H	1349	0	1339	5	0
2	I	4213	0	4167	21	0
2	J	4321	0	4280	16	0
2	K	4321	0	4280	13	0
2	L	4321	0	4280	15	0
2	M	4321	0	4280	18	0
2	N	4321	0	4280	11	0
3	A	1871	0	1828	8	0
4	B	2760	0	2729	8	0
4	C	2752	0	2717	6	0
5	D	1547	0	1518	3	0
6	E	7166	0	6971	12	0
6	F	7166	0	6971	12	0
6	G	6469	0	6310	11	0
All	All	56898	0	55950	143	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.

The worst 5 of 143 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:B:191:ARG:NH1	4:C:187:GLU:OE1	2.16	0.78
2:N:129:SER:O	2:N:152:ASN:ND2	2.23	0.71
6:E:99:THR:OG1	6:E:104:GLU:OE2	2.08	0.71
5:D:33:ASN:OD1	5:D:37:ASN:ND2	2.24	0.70
2:L:32:SER:OG	2:L:503:GLU:OE2	2.09	0.69

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	H	170/194 (88%)	166 (98%)	3 (2%)	1 (1%)	22	58
2	I	534/587 (91%)	504 (94%)	29 (5%)	1 (0%)	44	76
2	J	547/587 (93%)	519 (95%)	28 (5%)	0	100	100
2	K	547/587 (93%)	521 (95%)	26 (5%)	0	100	100
2	L	547/587 (93%)	526 (96%)	21 (4%)	0	100	100
2	M	547/587 (93%)	521 (95%)	26 (5%)	0	100	100
2	N	547/587 (93%)	518 (95%)	29 (5%)	0	100	100
3	A	232/234 (99%)	222 (96%)	10 (4%)	0	100	100
4	B	346/348 (99%)	337 (97%)	9 (3%)	0	100	100
4	C	345/348 (99%)	339 (98%)	6 (2%)	0	100	100
5	D	187/1019 (18%)	180 (96%)	7 (4%)	0	100	100
6	E	900/1152 (78%)	860 (96%)	39 (4%)	1 (0%)	48	81
6	F	900/1152 (78%)	862 (96%)	38 (4%)	0	100	100
6	G	809/1152 (70%)	771 (95%)	37 (5%)	1 (0%)	48	81
All	All	7158/9121 (78%)	6846 (96%)	308 (4%)	4 (0%)	50	81

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	150	PHE
6	E	562	ILE
2	I	409	PRO
6	G	892	VAL

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	H	152/171 (89%)	152 (100%)	0	100	100
2	I	459/495 (93%)	456 (99%)	3 (1%)	81	86
2	J	471/495 (95%)	466 (99%)	5 (1%)	70	80
2	K	471/495 (95%)	466 (99%)	5 (1%)	70	80
2	L	471/495 (95%)	470 (100%)	1 (0%)	92	93
2	M	471/495 (95%)	464 (98%)	7 (2%)	60	75
2	N	471/495 (95%)	468 (99%)	3 (1%)	84	88
3	A	209/209 (100%)	208 (100%)	1 (0%)	86	89
4	B	311/311 (100%)	310 (100%)	1 (0%)	91	92
4	C	310/311 (100%)	310 (100%)	0	100	100
5	D	167/928 (18%)	167 (100%)	0	100	100
6	E	800/1010 (79%)	797 (100%)	3 (0%)	89	91
6	F	800/1010 (79%)	796 (100%)	4 (0%)	86	89
6	G	724/1010 (72%)	721 (100%)	3 (0%)	89	91
All	All	6287/7930 (79%)	6251 (99%)	36 (1%)	82	88

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	E	1134	GLU
6	G	574	GLN
6	F	57	ASP
6	F	1137	PHE

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Mol	Chain	Res	Type
2	K	481	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
2	L	507	GLN
3	A	80	ASN
6	G	77	ASN
3	A	106	ASN
2	K	126	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.

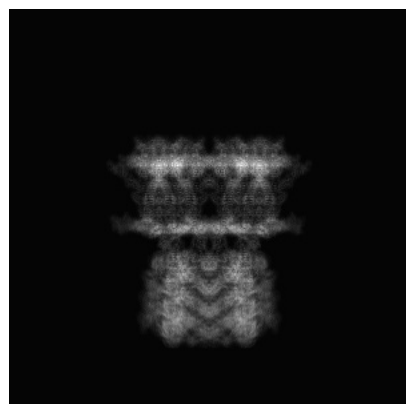
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19972. These allow visual inspection of the internal detail of the map and identification of artifacts.

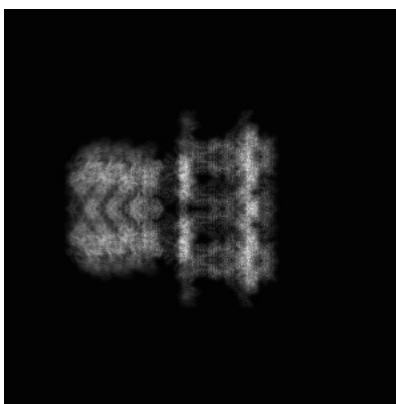
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

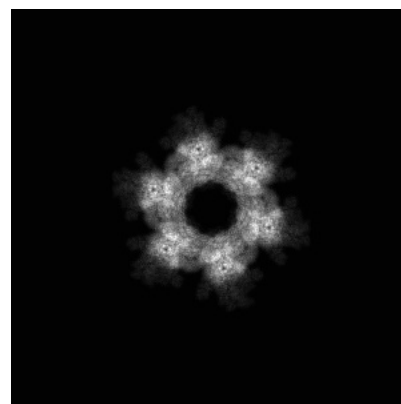
6.1.1 Primary map



X

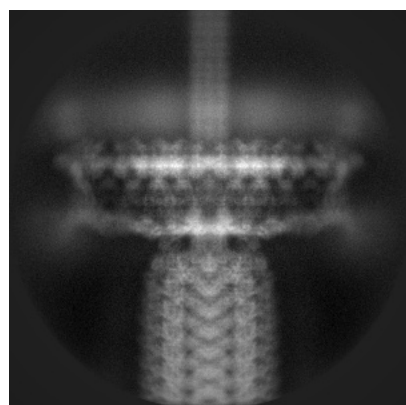


Y

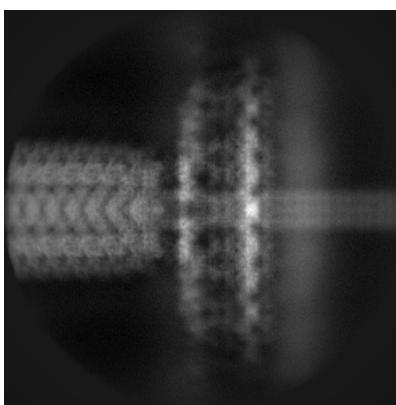


Z

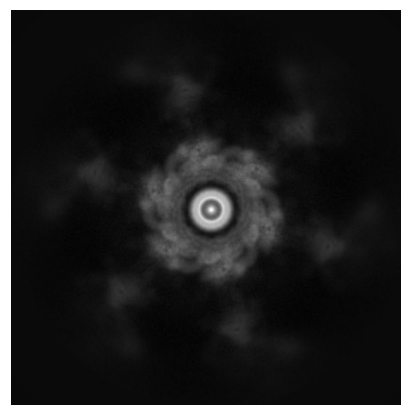
6.1.2 Raw map



X



Y

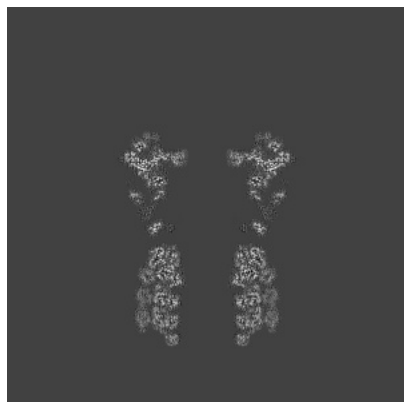


Z

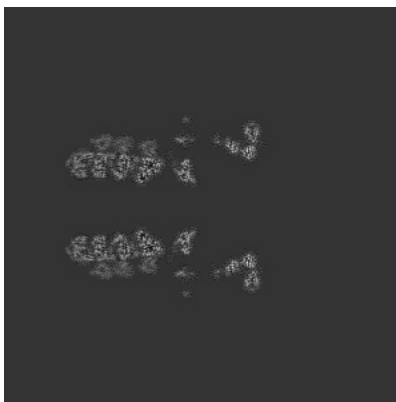
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

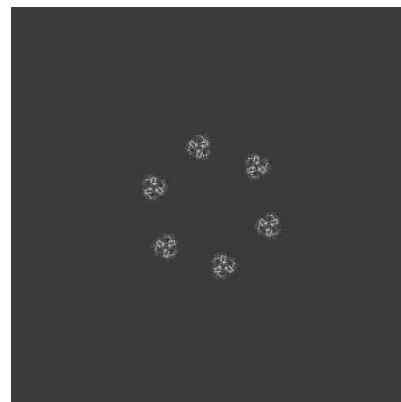
6.2.1 Primary map



X Index: 360

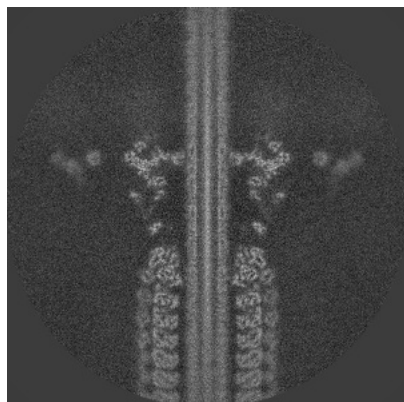


Y Index: 360

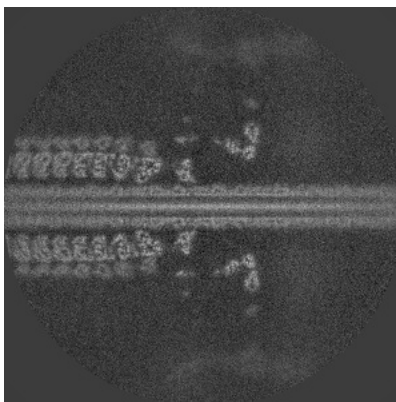


Z Index: 360

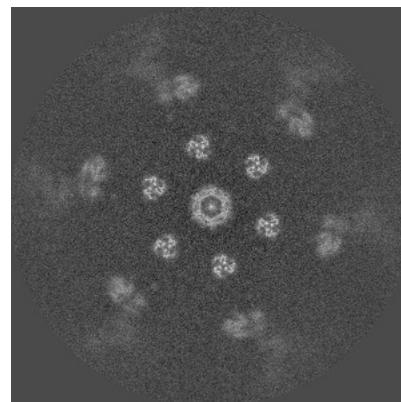
6.2.2 Raw map



X Index: 360



Y Index: 360

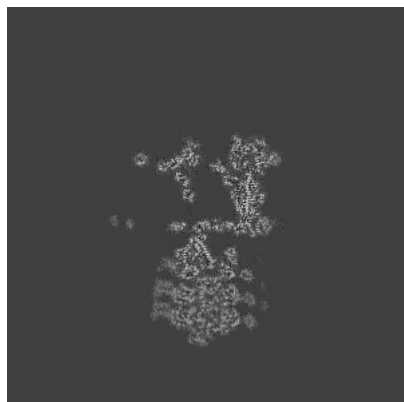


Z Index: 360

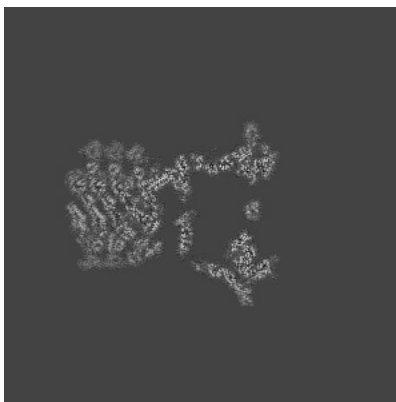
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

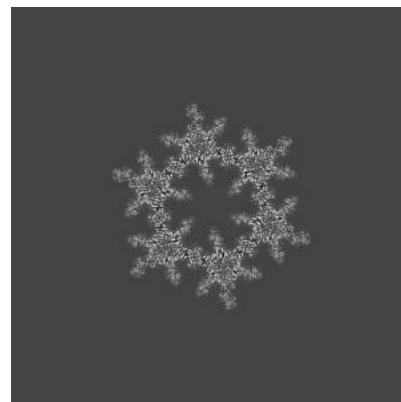
6.3.1 Primary map



X Index: 435

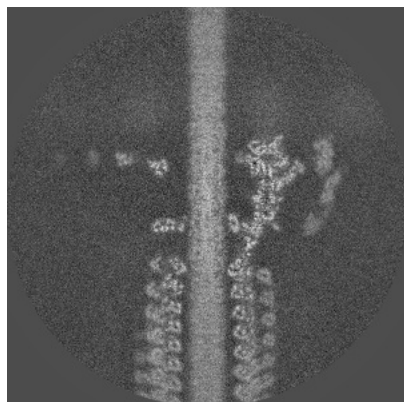


Y Index: 416

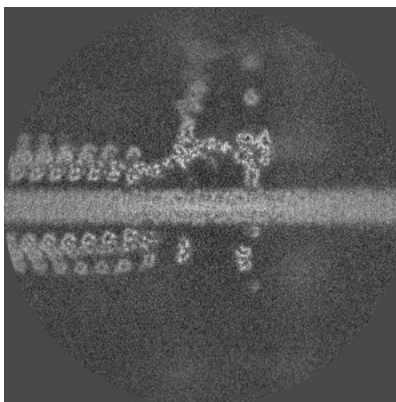


Z Index: 438

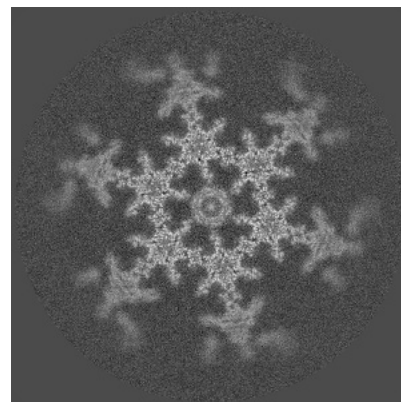
6.3.2 Raw map



X Index: 339



Y Index: 338

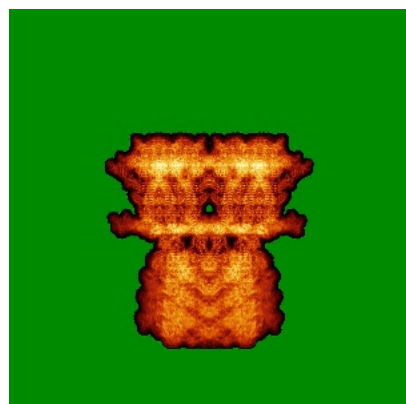


Z Index: 438

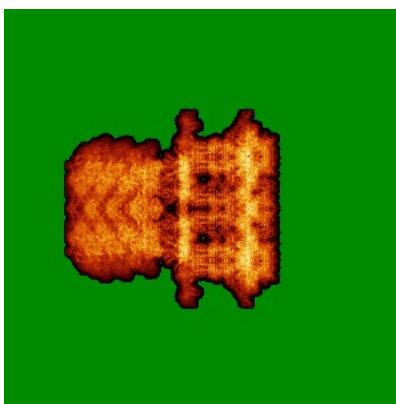
The images above show the largest variance slices of the map in three orthogonal directions.

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

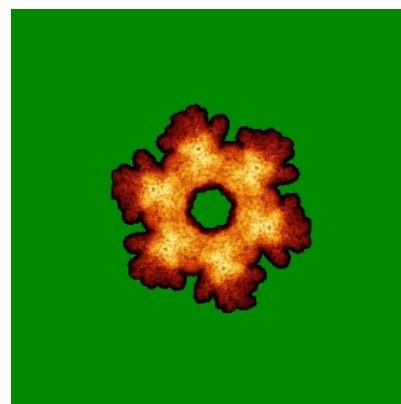
6.4.1 Primary map



X

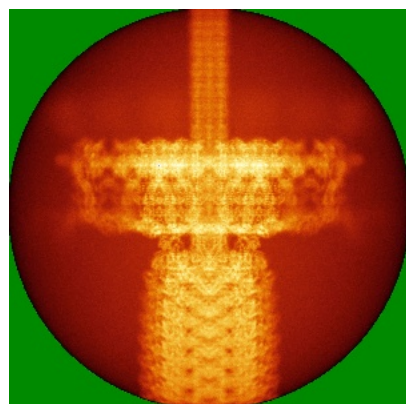


Y

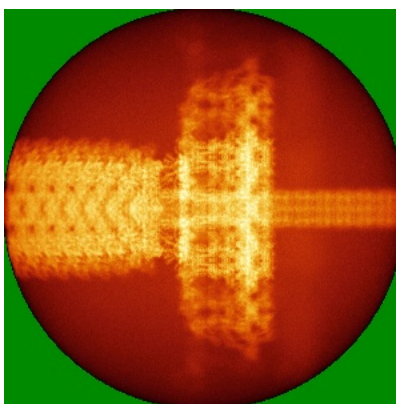


Z

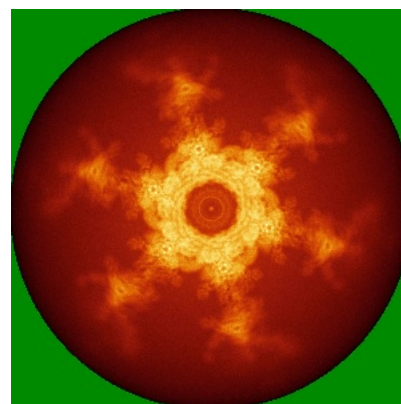
6.4.2 Raw map



X



Y

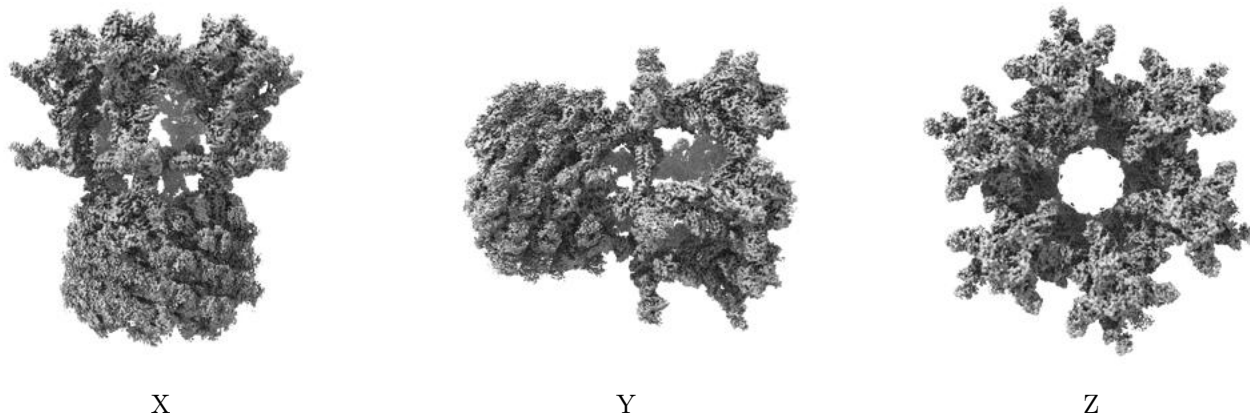


Z

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.

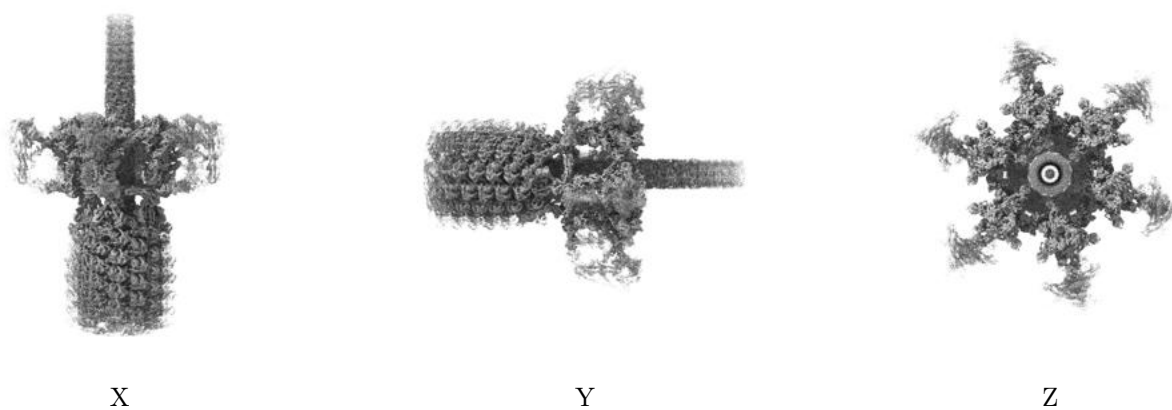
6.5 Orthogonal surface views [i](#)

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.

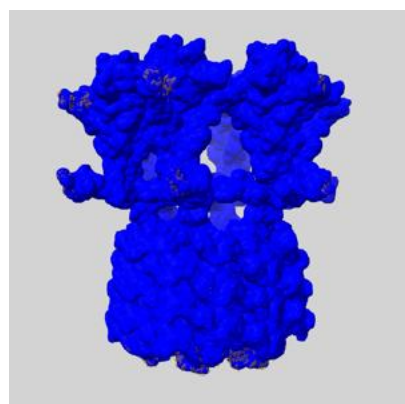
6.6 Mask visualisation [i](#)

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

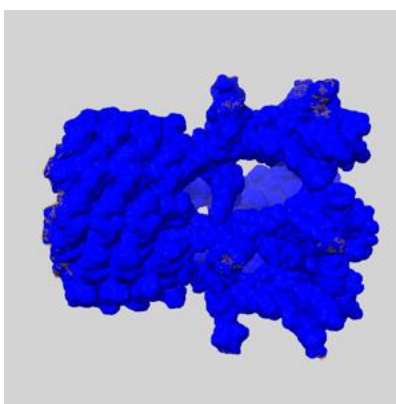
A mask typically either:

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

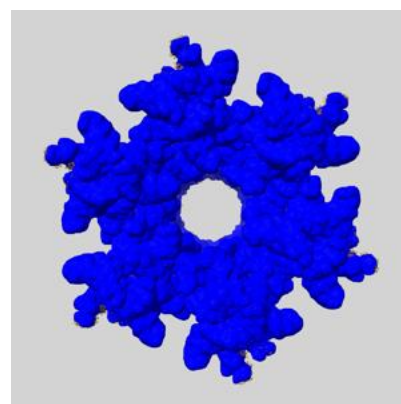
6.6.1 emd_19972_msk_1.map [i](#)



X



Y

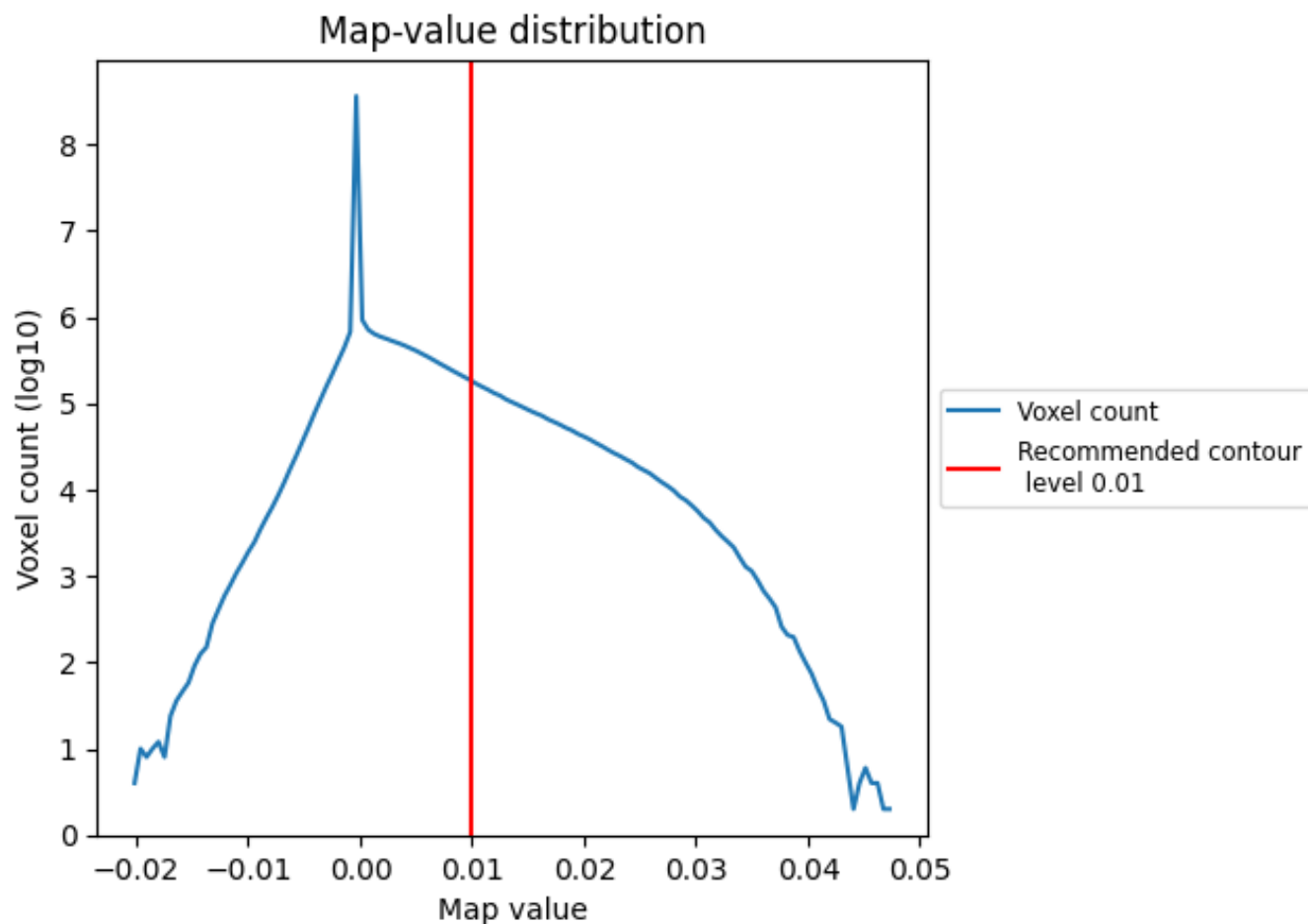


Z

7 Map analysis [i](#)

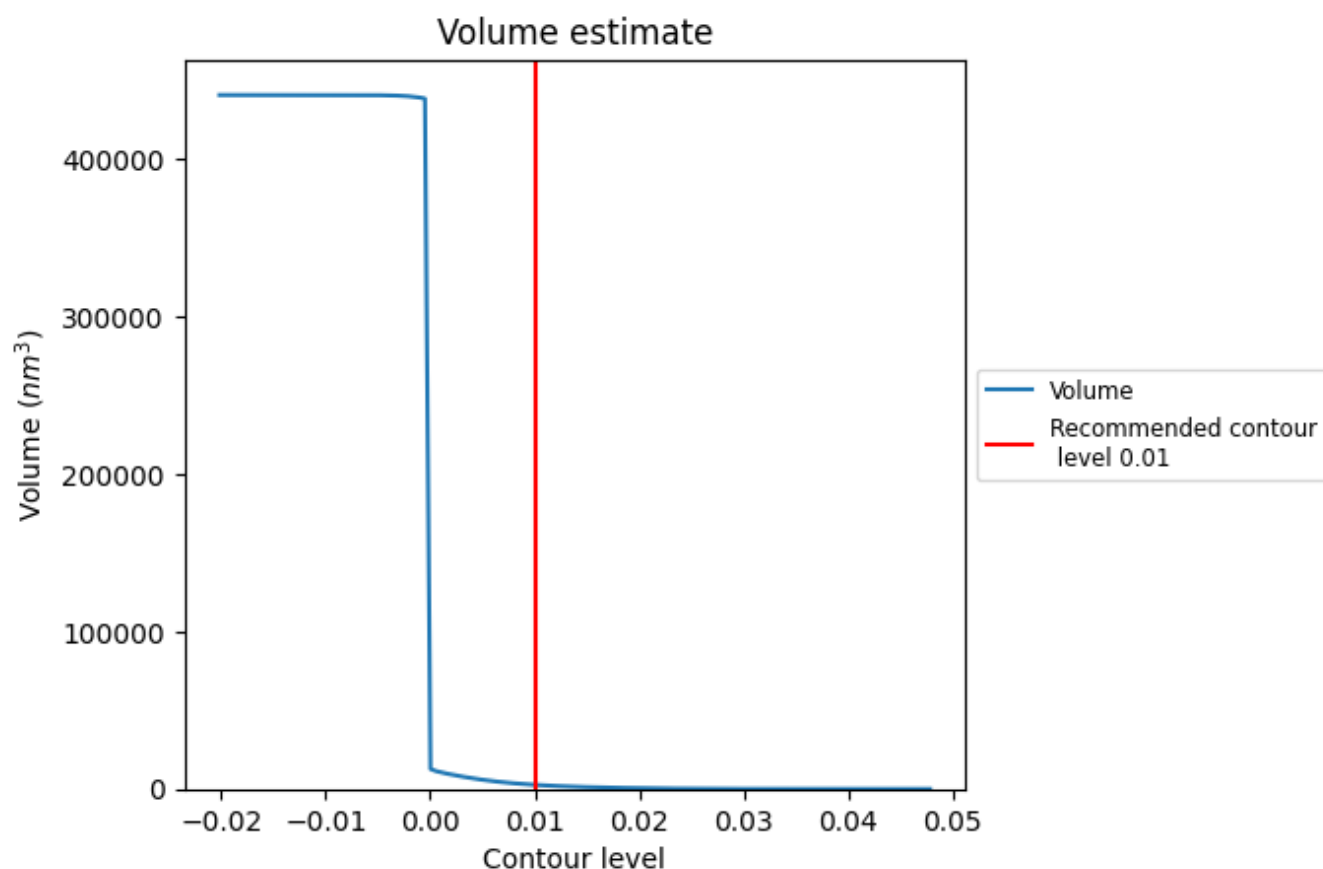
This section contains the results of statistical analysis of the map.

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.

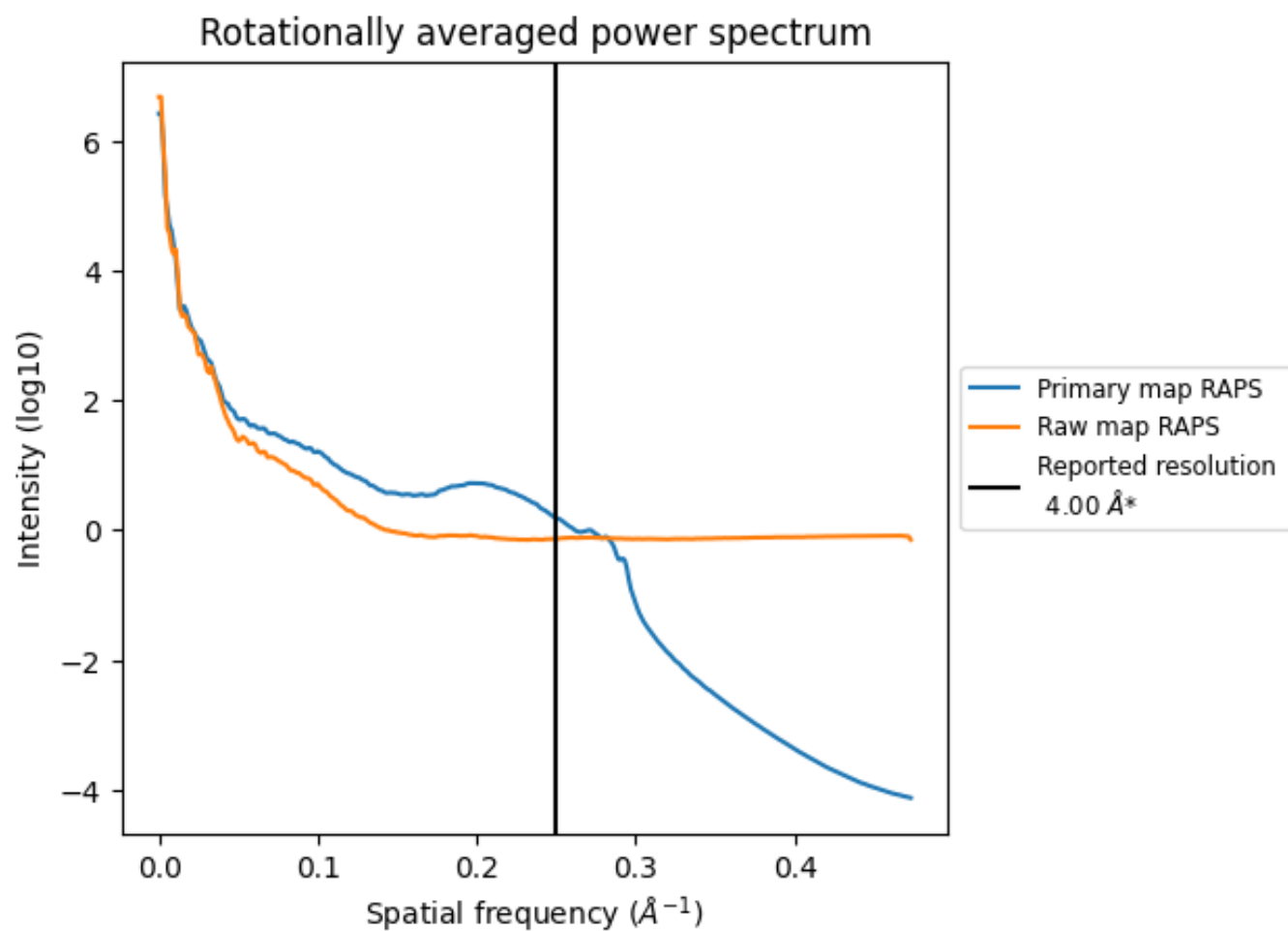
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2625 nm³; this corresponds to an approximate mass of 2371 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 ⓘ

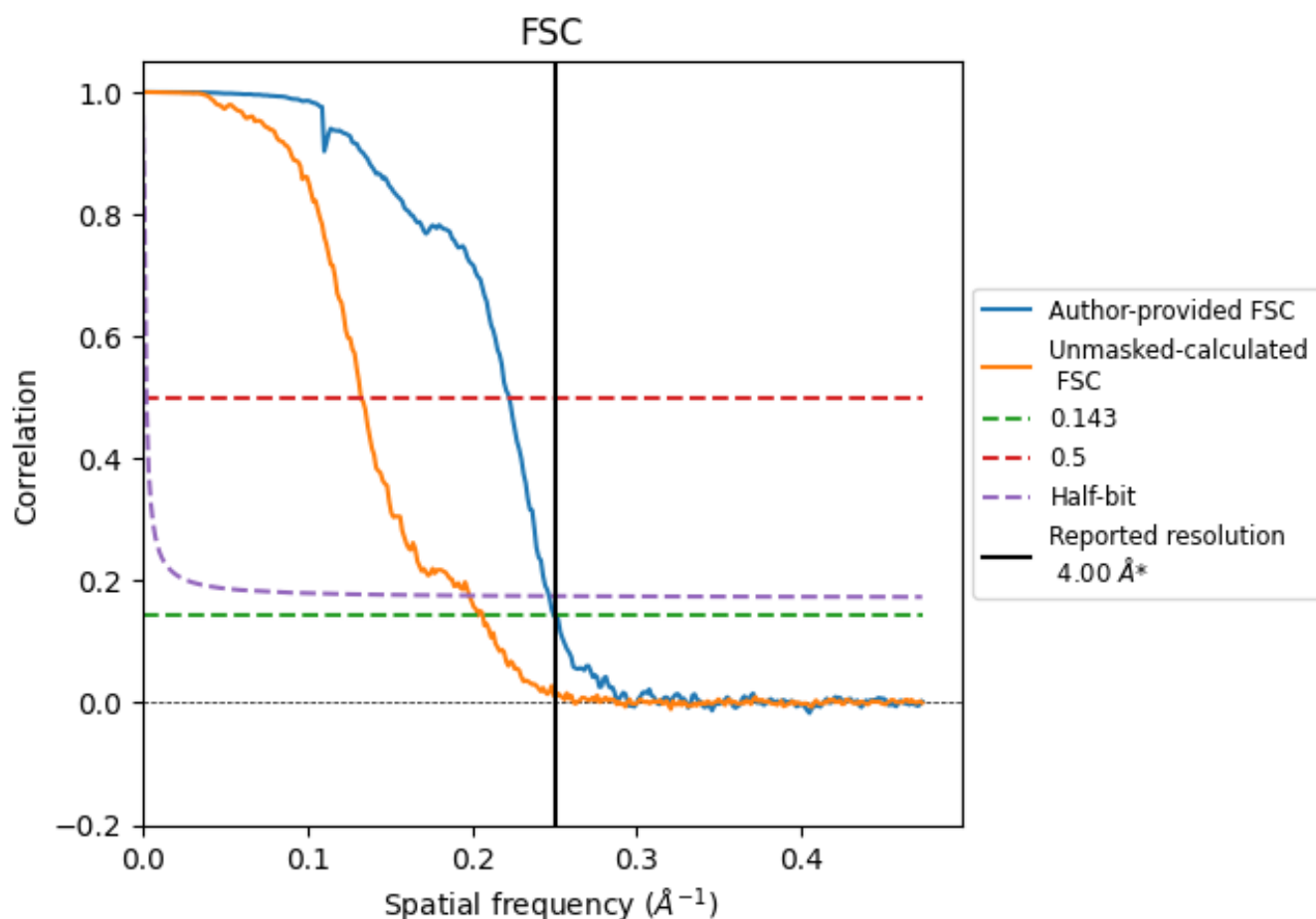


*Reported resolution corresponds to spatial frequency of 0.250 Å⁻¹

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 0.250 \AA^{-1}

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	4.01	4.50	4.05
Unmasked-calculated*	4.91	7.54	5.04

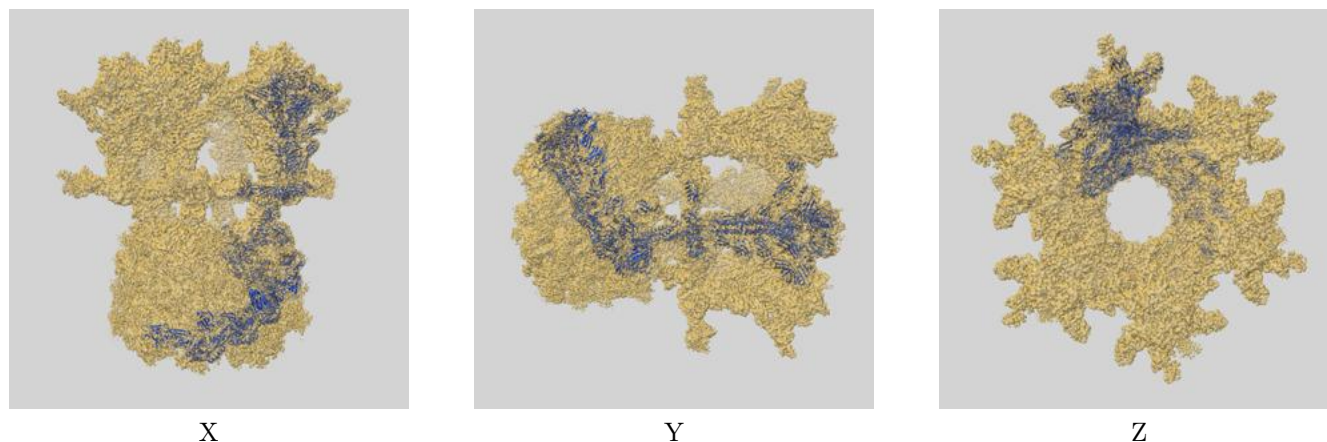
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.91 differs from the reported value 4.0 by more than 10 %

9 Map-model fit [i](#)

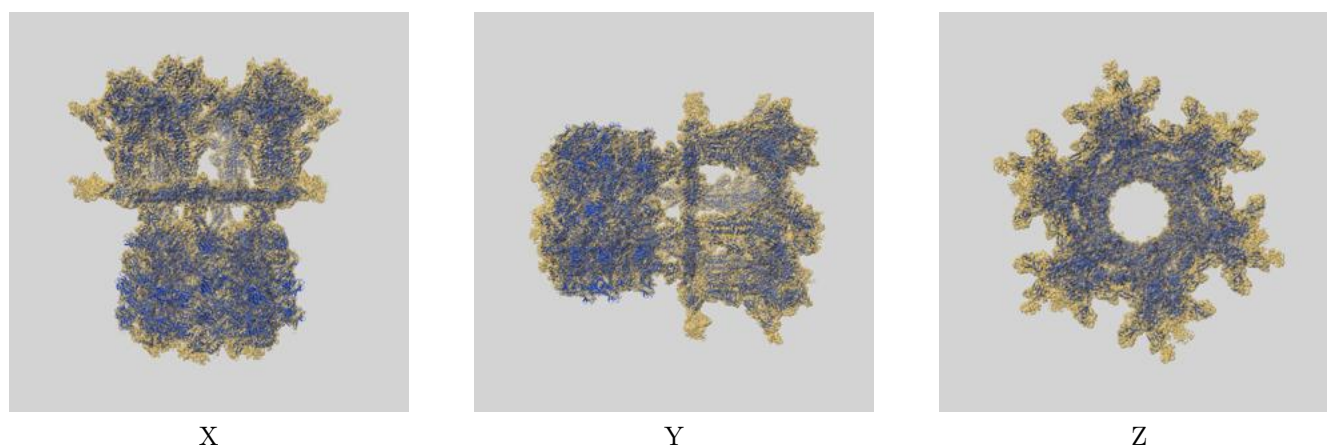
This section contains information regarding the fit between EMDB map EMD-19972 and PDB model 9EUJ. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)

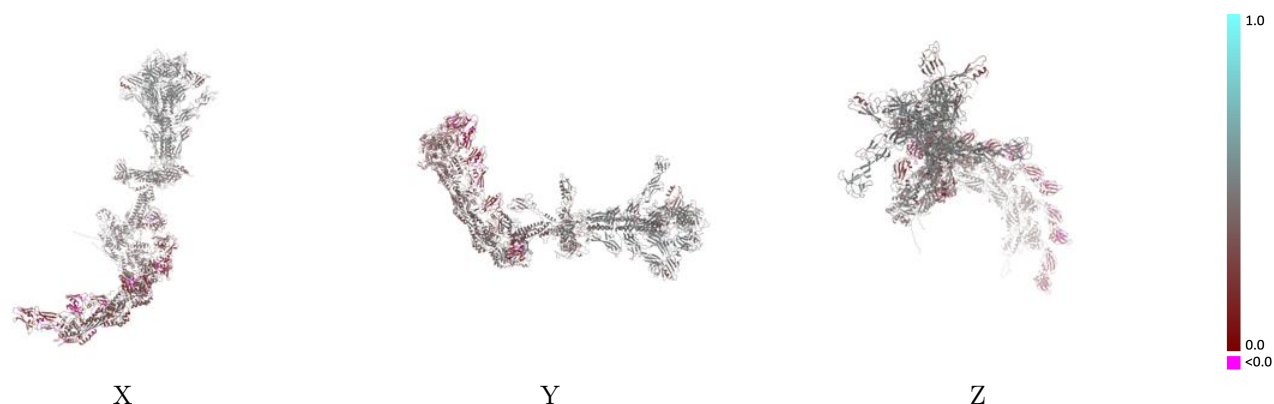


9.1.2 Map-model assembly overlay [i](#)



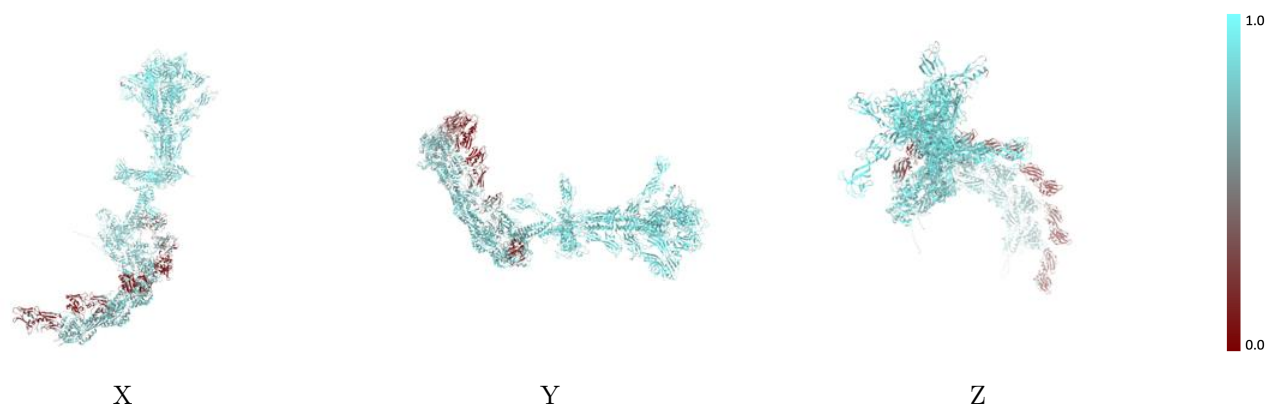
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



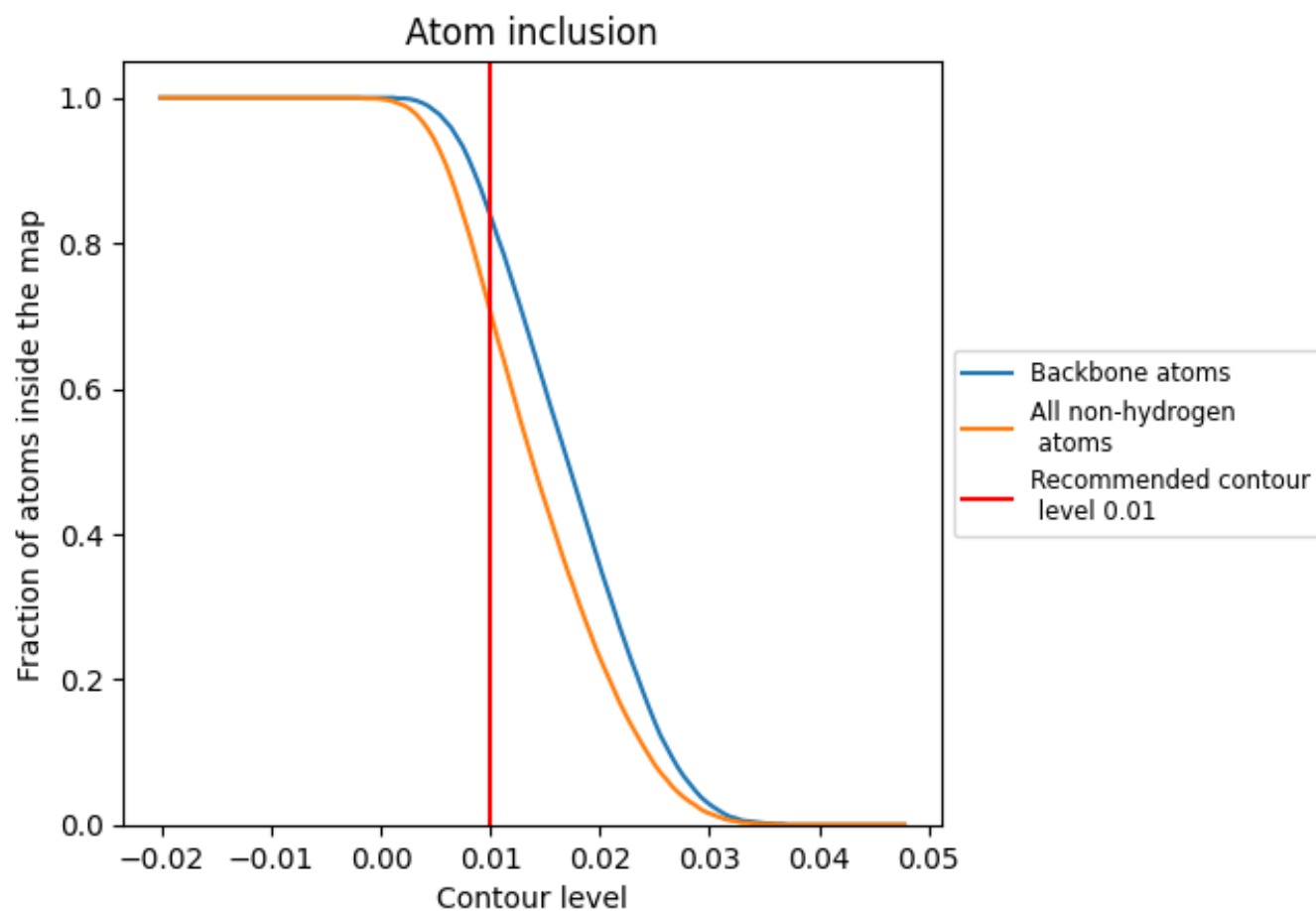
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 84% of all backbone atoms, 70% 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	 0.7050	 0.3870
A	 0.7870	 0.4270
B	 0.8110	 0.4180
C	 0.8160	 0.4230
D	 0.8390	 0.4370
E	 0.8330	 0.4480
F	 0.8420	 0.4580
G	 0.8190	 0.4400
H	 0.7920	 0.3970
I	 0.6080	 0.3640
J	 0.6620	 0.3640
K	 0.5540	 0.3220
L	 0.5050	 0.3100
M	 0.5160	 0.2980
N	 0.5180	 0.2810

