



## wwPDB EM Validation Summary Report ⓘ

Nov 14, 2023 – 03:10 PM EST

PDB ID : 8UH4  
EMDB ID : EMD-42246  
Title : Cryo-EM structure of Maize Streak Virus (MSV) - single head Geminivirus  
Authors : Bennett, A.B.; McKenna, R.; Mietzsch, M.; Hull, J.A.  
Deposited on : 2023-10-06  
Resolution : 3.72 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](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:

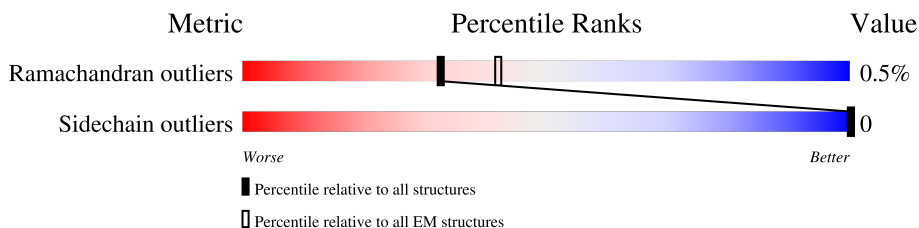
EMDB validation analysis : 0.0.1.dev70  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:  
*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.72 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)
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	1	243	87% 12%
1	2	243	87% 12%
1	3	243	87% 12%
1	4	243	87% 12%
1	5	243	87% 12%
1	6	243	87% 12%
1	7	243	87% 12%
1	8	243	87% 12%
1	A	243	87% 12%














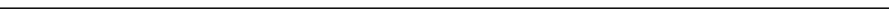











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Mol	Chain	Length	Quality of chain	
1	B	243		87% 12%
1	C	243		87% 12%
1	D	243		87% 12%
1	E	243		87% 12%
1	F	243		87% 12%
1	G	243		87% 12%
1	H	243		87% 12%
1	I	243		87% 12%
1	J	243		87% 12%
1	K	243		87% 12%
1	L	243		87% 12%
1	M	243		87% 12%
1	N	243		87% 12%
1	O	243		87% 12%
1	P	243		87% 12%
1	Q	243		87% 12%
1	R	243		87% 12%
1	S	243		87% 12%
1	T	243		87% 12%
1	U	243		87% 12%
1	V	243		87% 12%
1	W	243		87% 12%
1	X	243		87% 12%
1	Y	243		87% 12%
1	Z	243		87% 12%


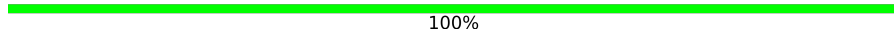
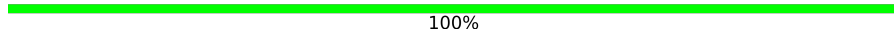

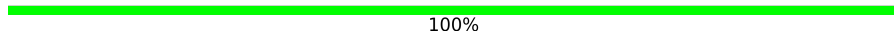
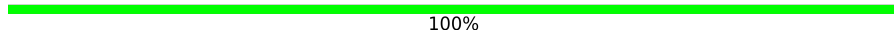
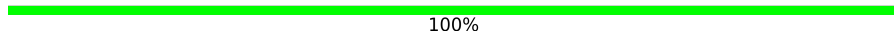
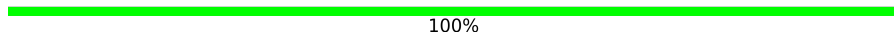
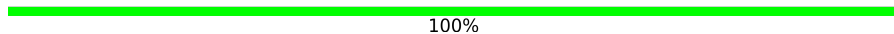
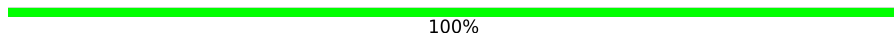
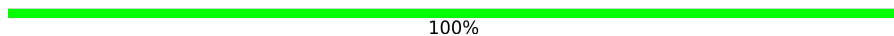
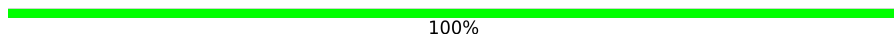

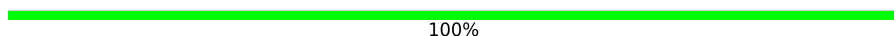
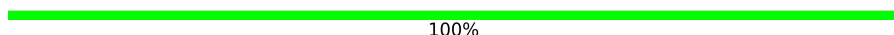
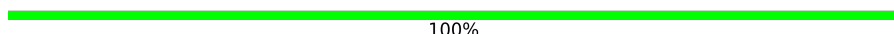
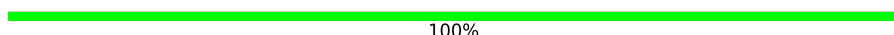
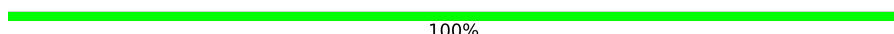
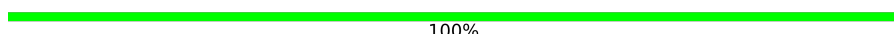
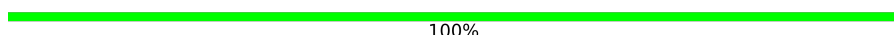
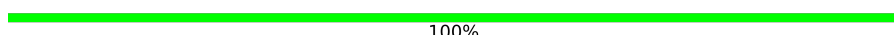
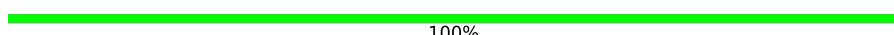
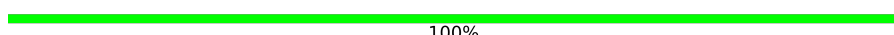
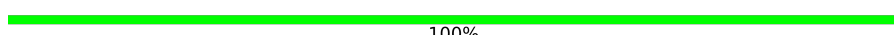
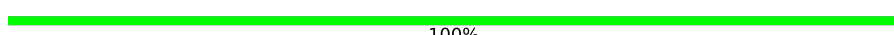
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Mol	Chain	Length	Quality of chain	
1	a	243		87% 12%
1	b	243		87% 12%
1	c	243		87% 12%
1	d	243		87% 12%
1	e	243		87% 12%
1	f	243		87% 12%
1	g	243		87% 12%
1	h	243		87% 12%
1	i	243		87% 12%
1	j	243		87% 12%
1	k	243		87% 12%
1	l	243		87% 12%
1	m	243		87% 12%
1	n	243		87% 12%
1	o	243		87% 12%
1	p	243		87% 12%
1	q	243		87% 12%
1	r	243		87% 12%
1	s	243		87% 12%
1	t	243		87% 12%
1	u	243		87% 12%
1	v	243		87% 12%
1	w	243		87% 12%
1	x	243		87% 12%
1	y	243		87% 12%

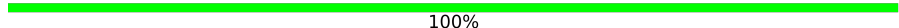
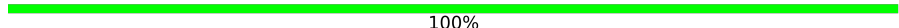

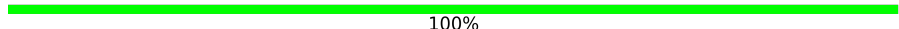
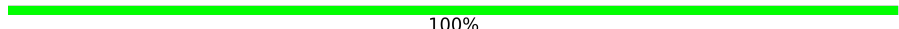
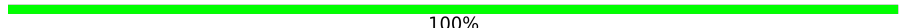
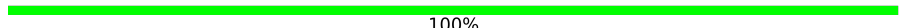
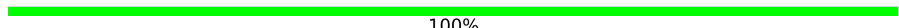
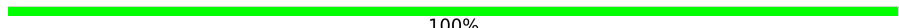
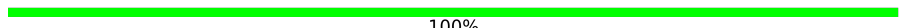
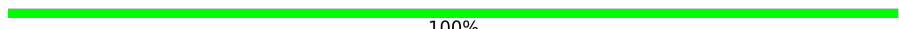
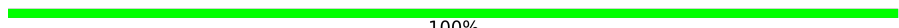
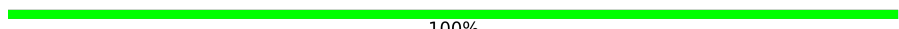
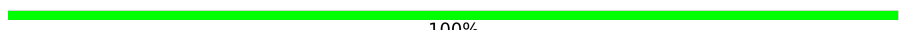
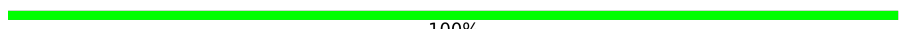
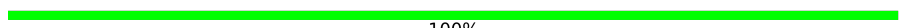
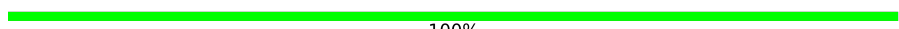
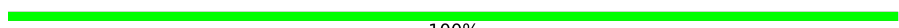
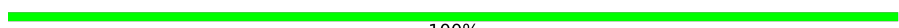
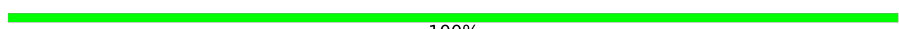
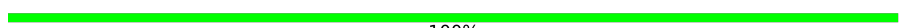

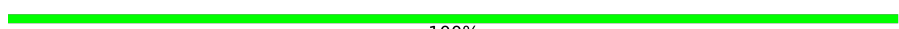


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Mol	Chain	Length	Quality of chain
1	z	243	 87% 12%
2	A1	9	 100%
2	A2	9	 100%
2	A3	9	 100%
2	A4	9	 100%
2	A5	9	 100%
2	A6	9	 100%
2	A7	9	 100%
2	A8	9	 100%
2	AA	9	 100%
2	AB	9	 100%
2	AC	9	 100%
2	AD	9	 100%
2	AE	9	 100%
2	AF	9	 100%
2	AG	9	 100%
2	AH	9	 100%
2	AI	9	 100%
2	AJ	9	 100%
2	AK	9	 100%
2	AL	9	 100%
2	AM	9	 100%
2	AN	9	 100%
2	AO	9	 100%
2	AP	9	 100%

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Mol	Chain	Length	Quality of chain
2	AQ	9	 100%
2	AR	9	 100%
2	AS	9	 100%
2	AT	9	 100%
2	AU	9	 100%
2	AV	9	 100%
2	AW	9	 100%
2	AX	9	 100%
2	AY	9	 100%
2	AZ	9	 100%
2	Aa	9	 100%
2	Ab	9	 100%
2	Ac	9	 100%
2	Ad	9	 100%
2	Ae	9	 100%
2	Af	9	 100%
2	Ag	9	 100%
2	Ah	9	 100%
2	Ai	9	 100%
2	Aj	9	 100%
2	Ak	9	 100%
2	Al	9	 100%
2	Am	9	 100%
2	An	9	 100%
2	Ao	9	 100%

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Mol	Chain	Length	Quality of chain
2	Ap	9	 100%
2	Aq	9	 100%
2	Ar	9	 100%
2	As	9	 100%
2	At	9	 100%
2	Au	9	 100%
2	Av	9	 100%
2	Aw	9	 100%
2	Ax	9	 100%
2	Ay	9	 100%
2	Az	9	 100%

## 2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 110100 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 Capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	213	1653	1045	297	303	8	0	0
1	B	213	1653	1045	297	303	8	0	0
1	C	213	1653	1045	297	303	8	0	0
1	D	213	1653	1045	297	303	8	0	0
1	E	213	1653	1045	297	303	8	0	0
1	F	213	1653	1045	297	303	8	0	0
1	G	213	1653	1045	297	303	8	0	0
1	H	213	1653	1045	297	303	8	0	0
1	I	213	1653	1045	297	303	8	0	0
1	J	213	1653	1045	297	303	8	0	0
1	K	213	1653	1045	297	303	8	0	0
1	L	213	1653	1045	297	303	8	0	0
1	M	213	1653	1045	297	303	8	0	0
1	N	213	1653	1045	297	303	8	0	0
1	O	213	1653	1045	297	303	8	0	0
1	P	213	1653	1045	297	303	8	0	0
1	Q	213	1653	1045	297	303	8	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	S	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	T	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	U	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	V	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	W	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	X	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	Y	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	Z	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	a	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	b	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	c	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	d	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	e	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	f	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	g	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	h	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	i	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	j	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	k	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	l	213	Total 1653	C 1045	N 297	O 303	S 8	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	m	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	n	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	o	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	p	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	q	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	r	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	s	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	t	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	u	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	v	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	w	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	x	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	y	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	z	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	1	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	2	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	3	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	4	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	5	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	6	213	Total 1653	C 1045	N 297	O 303	S 8	0	0
1	7	213	Total 1653	C 1045	N 297	O 303	S 8	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	8	213	1653	1045	297	303	8	0	0

- Molecule 2 is a protein called genomic DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	AA	9	182	87	36	50	9	0	0
2	AB	9	182	87	36	50	9	0	0
2	AC	9	182	87	36	50	9	0	0
2	AD	9	182	87	36	50	9	0	0
2	AE	9	182	87	36	50	9	0	0
2	AF	9	182	87	36	50	9	0	0
2	AG	9	182	87	36	50	9	0	0
2	AH	9	182	87	36	50	9	0	0
2	AI	9	182	87	36	50	9	0	0
2	AJ	9	182	87	36	50	9	0	0
2	AK	9	182	87	36	50	9	0	0
2	AL	9	182	87	36	50	9	0	0
2	AM	9	182	87	36	50	9	0	0
2	AN	9	182	87	36	50	9	0	0
2	AO	9	182	87	36	50	9	0	0
2	AP	9	182	87	36	50	9	0	0
2	AQ	9	182	87	36	50	9	0	0
2	AR	9	182	87	36	50	9	0	0

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*Continued from previous page...*

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	AS	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	AT	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	AU	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	AV	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	AW	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	AX	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	AY	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	AZ	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	Aa	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	Ab	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	Ac	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	Ad	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	Ae	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	Af	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	Ag	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	Ah	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	Ai	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	Aj	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	Ak	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	Al	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	Am	9	Total 182	C 87	N 36	O 50	P 9	0	0

*Continued on next page...*


*Continued from previous page...*

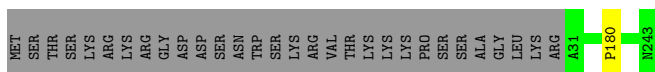
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
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2	Ao	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	Ap	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	Aq	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	Ar	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	As	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	At	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	Au	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	Av	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	Aw	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	Ax	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	Ay	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	Az	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	A1	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	A2	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	A3	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	A4	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	A5	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	A6	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	A7	9	Total 182	C 87	N 36	O 50	P 9	0	0
2	A8	9	Total 182	C 87	N 36	O 50	P 9	0	0

### 3 Residue-property plots [i](#)


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.

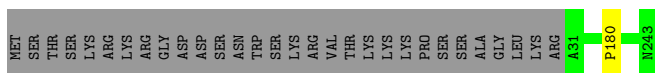
- Molecule 1: Capsid protein

Chain A: 




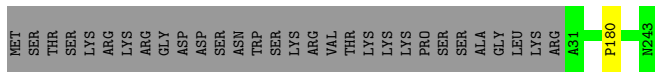
- Molecule 1: Capsid protein

Chain B: 




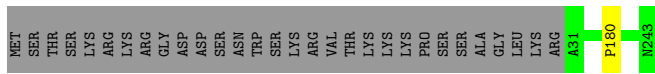
- Molecule 1: Capsid protein

Chain C: 




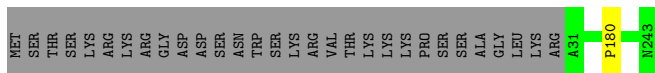
- Molecule 1: Capsid protein

Chain D: 




- Molecule 1: Capsid protein

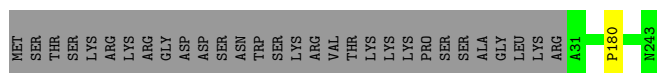
Chain E: 




- Molecule 1: Capsid protein

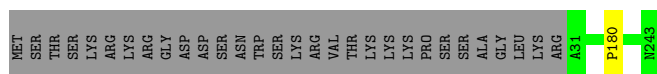


Chain M:  87% 12%




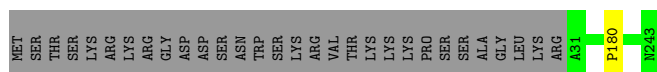
● Molecule 1: Capsid protein

Chain N:  87% 12%




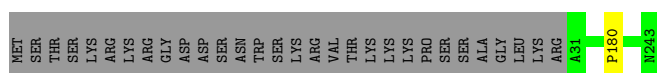
● Molecule 1: Capsid protein

Chain O:  87% 12%




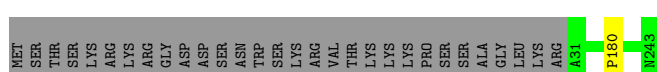
● Molecule 1: Capsid protein

Chain P:  87% 12%




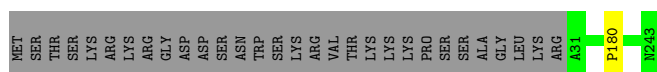
● Molecule 1: Capsid protein

Chain Q:  87% 12%




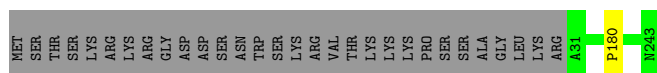
● Molecule 1: Capsid protein

Chain R:  87% 12%



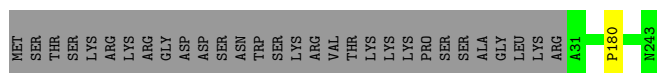
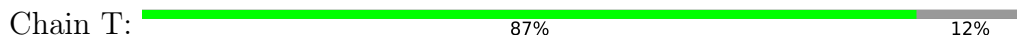
● Molecule 1: Capsid protein

Chain S:  87% 12%

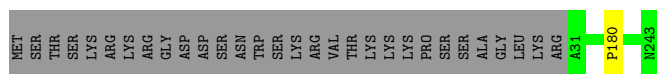
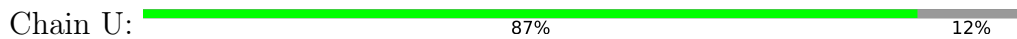


● Molecule 1: Capsid protein

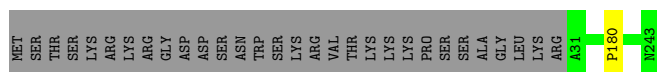
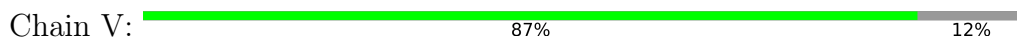




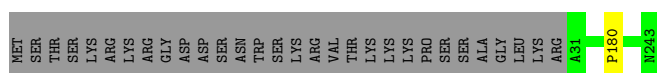
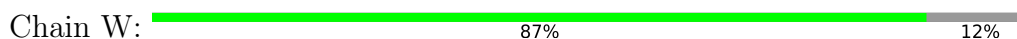
● Molecule 1: Capsid protein



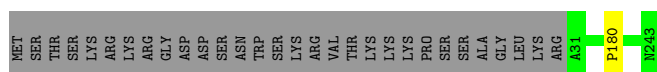
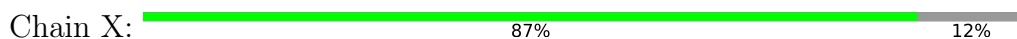
● Molecule 1: Capsid protein



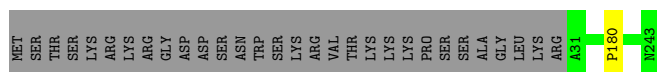
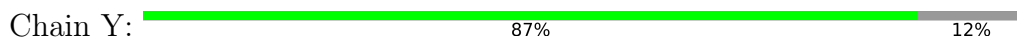
● Molecule 1: Capsid protein



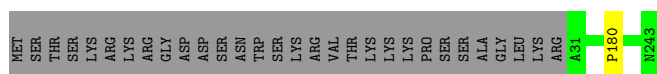
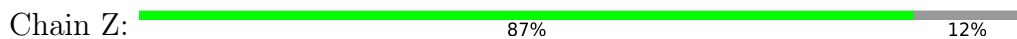
● Molecule 1: Capsid protein




● Molecule 1: Capsid protein

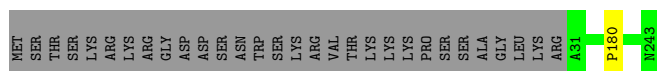


● Molecule 1: Capsid protein




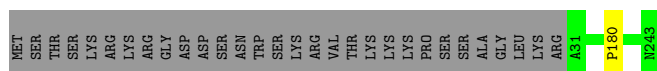
● Molecule 1: Capsid protein

Chain a:  87% 12%




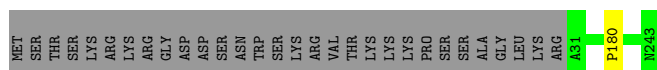
● Molecule 1: Capsid protein

Chain b:  87% 12%



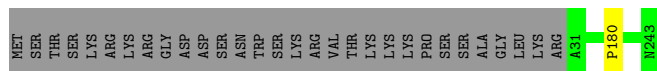
● Molecule 1: Capsid protein

Chain c:  87% 12%




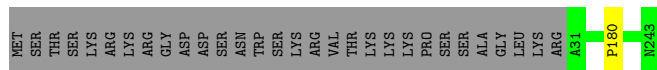
● Molecule 1: Capsid protein

Chain d:  87% 12%




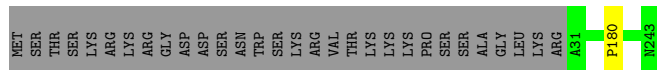
● Molecule 1: Capsid protein

Chain e:  87% 12%




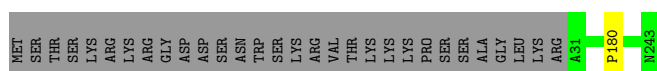
● Molecule 1: Capsid protein

Chain f:  87% 12%

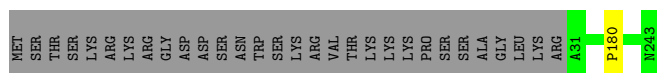
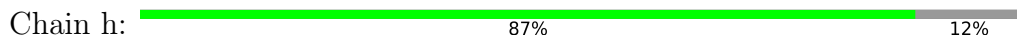


● Molecule 1: Capsid protein

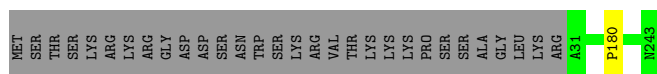
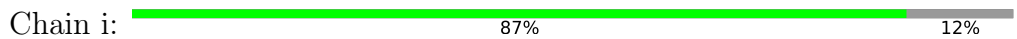
Chain g:  87% 12%



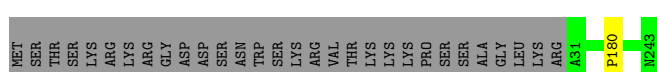
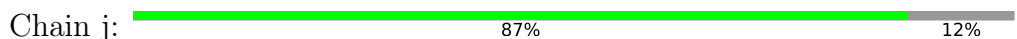
● Molecule 1: Capsid protein



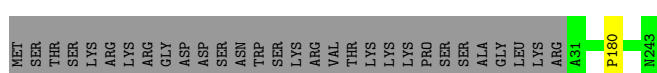
● Molecule 1: Capsid protein



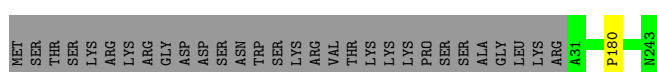
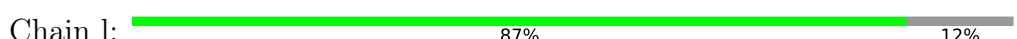
● Molecule 1: Capsid protein



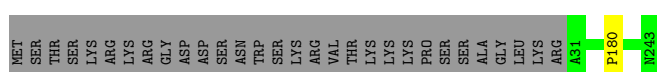
● Molecule 1: Capsid protein



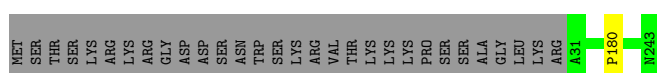
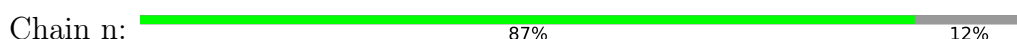
● Molecule 1: Capsid protein




● Molecule 1: Capsid protein

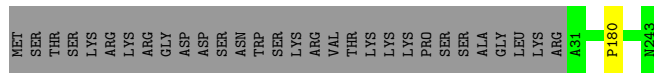


● Molecule 1: Capsid protein




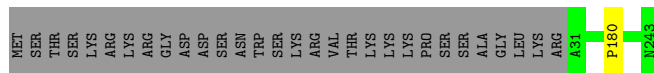
● Molecule 1: Capsid protein

Chain o:  87% 12%




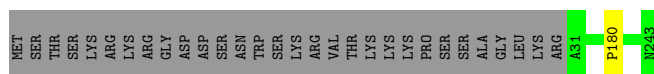
● Molecule 1: Capsid protein

Chain p:  87% 12%




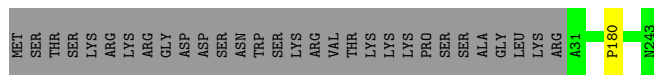
● Molecule 1: Capsid protein

Chain q:  87% 12%




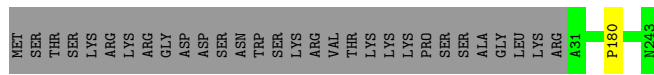
● Molecule 1: Capsid protein

Chain r:  87% 12%




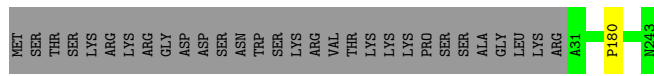
● Molecule 1: Capsid protein

Chain s:  87% 12%




● Molecule 1: Capsid protein

Chain t:  87% 12%

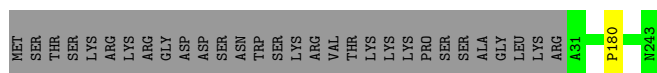
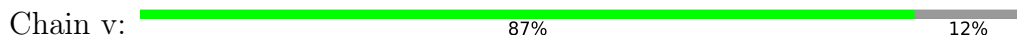


● Molecule 1: Capsid protein

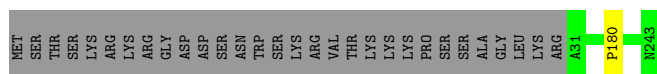
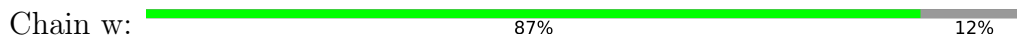
Chain u:  87% 12%



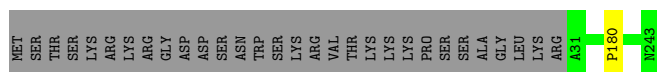
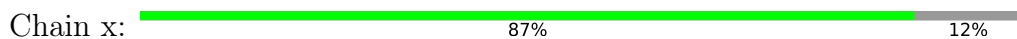
● Molecule 1: Capsid protein



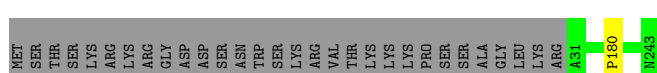
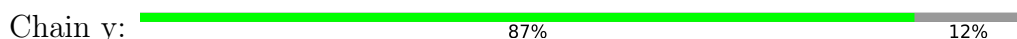
● Molecule 1: Capsid protein



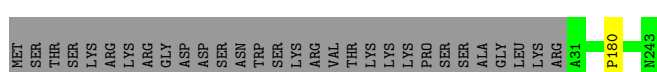
● Molecule 1: Capsid protein



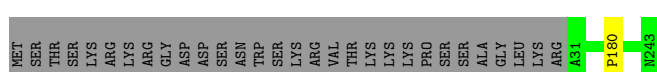
● Molecule 1: Capsid protein



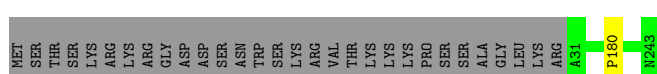
● Molecule 1: Capsid protein




● Molecule 1: Capsid protein

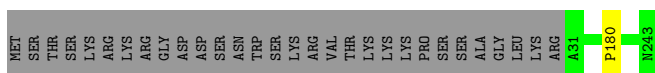


● Molecule 1: Capsid protein




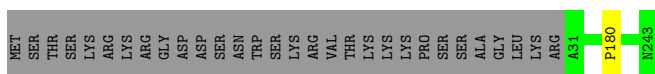
● Molecule 1: Capsid protein

Chain 3:  87% 12%




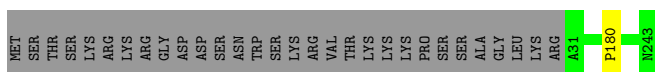
- Molecule 1: Capsid protein

Chain 4:  87% 12%




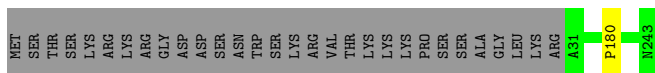
- Molecule 1: Capsid protein

Chain 5:  87% 12%




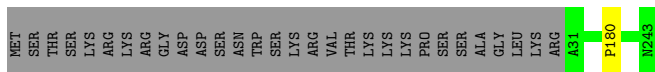
- Molecule 1: Capsid protein

Chain 6:  87% 12%




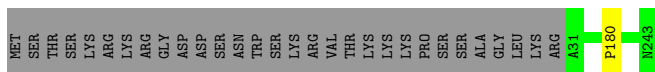
- Molecule 1: Capsid protein

Chain 7:  87% 12%



- Molecule 1: Capsid protein

Chain 8:  87% 12%



- Molecule 2: genomic DNA

Chain AA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain AB:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain AC:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain AD:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain AE:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain AF:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain AG:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain AH:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain AI:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain AJ:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain AK:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain AL:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain AM:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain AN:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain AO:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain AP:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain AQ:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain AR:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain AS:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain AT:  100%



There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain AU:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain AV:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain AW:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain AX:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain AY:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain AZ:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain Aa:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain Ab:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain Ac:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain Ad:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain Ae:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain Af:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain Ag:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain Ah:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain Ai:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain Aj:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain Ak:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain Al:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain Am:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain An:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain Ao:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain Ap:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain Aq:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain Ar:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain As:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain At:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain Au:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain Av:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain Aw:  100%

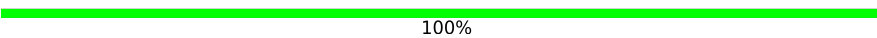
There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain Ax:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain Ay:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain Az:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain A1:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain A2:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain A3:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain A4:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain A5:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain A6:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain A7:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: genomic DNA

Chain A8:  100%

There are no outlier residues recorded for this chain.

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	43111	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 ( $e^-/\text{\AA}^2$ )	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	DIRECT ELECTRON DE-64 (8k x 8k)	Depositor
Maximum map value	17.267	Depositor
Minimum map value	-7.634	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1.0	Depositor
Map size (Å)	378.75, 378.75, 378.75	wwPDB
Map dimensions	375, 375, 375	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.01, 1.01, 1.01	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	1	0.46	0/1698	0.53	0/2309
1	2	0.46	0/1698	0.53	0/2309
1	3	0.46	0/1698	0.53	0/2309
1	4	0.46	0/1698	0.53	0/2309
1	5	0.46	0/1698	0.53	0/2309
1	6	0.46	0/1698	0.53	0/2309
1	7	0.46	0/1698	0.53	0/2309
1	8	0.46	0/1698	0.53	0/2309
1	A	0.46	0/1698	0.53	0/2309
1	B	0.46	0/1698	0.53	0/2309
1	C	0.46	0/1698	0.53	0/2309
1	D	0.46	0/1698	0.53	0/2309
1	E	0.46	0/1698	0.53	0/2309
1	F	0.46	0/1698	0.53	0/2309
1	G	0.46	0/1698	0.53	0/2309
1	H	0.46	0/1698	0.53	0/2309
1	I	0.46	0/1698	0.53	0/2309
1	J	0.46	0/1698	0.53	0/2309
1	K	0.46	0/1698	0.53	0/2309
1	L	0.46	0/1698	0.53	0/2309
1	M	0.46	0/1698	0.53	0/2309
1	N	0.46	0/1698	0.53	0/2309
1	O	0.46	0/1698	0.53	0/2309
1	P	0.46	0/1698	0.53	0/2309
1	Q	0.46	0/1698	0.53	0/2309
1	R	0.46	0/1698	0.53	0/2309
1	S	0.46	0/1698	0.53	0/2309
1	T	0.46	0/1698	0.53	0/2309
1	U	0.46	0/1698	0.53	0/2309
1	V	0.46	0/1698	0.53	0/2309
1	W	0.46	0/1698	0.53	0/2309
1	X	0.46	0/1698	0.53	0/2309
1	Y	0.46	0/1698	0.53	0/2309
1	Z	0.46	0/1698	0.53	0/2309

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	a	0.46	0/1698	0.53	0/2309
1	b	0.46	0/1698	0.53	0/2309
1	c	0.46	0/1698	0.53	0/2309
1	d	0.46	0/1698	0.53	0/2309
1	e	0.46	0/1698	0.53	0/2309
1	f	0.46	0/1698	0.53	0/2309
1	g	0.46	0/1698	0.53	0/2309
1	h	0.46	0/1698	0.53	0/2309
1	i	0.46	0/1698	0.53	0/2309
1	j	0.46	0/1698	0.53	0/2309
1	k	0.46	0/1698	0.53	0/2309
1	l	0.46	0/1698	0.53	0/2309
1	m	0.46	0/1698	0.53	0/2309
1	n	0.46	0/1698	0.53	0/2309
1	o	0.46	0/1698	0.53	0/2309
1	p	0.46	0/1698	0.53	0/2309
1	q	0.46	0/1698	0.53	0/2309
1	r	0.46	0/1698	0.53	0/2309
1	s	0.46	0/1698	0.53	0/2309
1	t	0.46	0/1698	0.53	0/2309
1	u	0.46	0/1698	0.53	0/2309
1	v	0.46	0/1698	0.53	0/2309
1	w	0.46	0/1698	0.53	0/2309
1	x	0.46	0/1698	0.53	0/2309
1	y	0.46	0/1698	0.53	0/2309
1	z	0.46	0/1698	0.53	0/2309
2	A1	0.60	0/204	0.81	0/311
2	A2	0.59	0/204	0.80	0/311
2	A3	0.59	0/204	0.80	0/311
2	A4	0.59	0/204	0.80	0/311
2	A5	0.59	0/204	0.81	0/311
2	A6	0.59	0/204	0.80	0/311
2	A7	0.60	0/204	0.80	0/311
2	A8	0.59	0/204	0.80	0/311
2	AA	0.59	0/204	0.80	0/311
2	AB	0.59	0/204	0.80	0/311
2	AC	0.59	0/204	0.80	0/311
2	AD	0.59	0/204	0.80	0/311
2	AE	0.59	0/204	0.80	0/311
2	AF	0.59	0/204	0.80	0/311
2	AG	0.59	0/204	0.80	0/311
2	AH	0.59	0/204	0.80	0/311
2	AI	0.59	0/204	0.80	0/311



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
2	AJ	0.59	0/204	0.80	0/311
2	AK	0.59	0/204	0.80	0/311
2	AL	0.59	0/204	0.80	0/311
2	AM	0.59	0/204	0.81	0/311
2	AN	0.59	0/204	0.80	0/311
2	AO	0.59	0/204	0.80	0/311
2	AP	0.60	0/204	0.80	0/311
2	AQ	0.59	0/204	0.80	0/311
2	AR	0.59	0/204	0.80	0/311
2	AS	0.60	0/204	0.80	0/311
2	AT	0.60	0/204	0.80	0/311
2	AU	0.59	0/204	0.80	0/311
2	AV	0.60	0/204	0.80	0/311
2	AW	0.59	0/204	0.80	0/311
2	AX	0.59	0/204	0.80	0/311
2	AY	0.59	0/204	0.80	0/311
2	AZ	0.60	0/204	0.80	0/311
2	Aa	0.59	0/204	0.80	0/311
2	Ab	0.59	0/204	0.80	0/311
2	Ac	0.59	0/204	0.80	0/311
2	Ad	0.59	0/204	0.80	0/311
2	Ae	0.59	0/204	0.80	0/311
2	Af	0.59	0/204	0.80	0/311
2	Ag	0.59	0/204	0.80	0/311
2	Ah	0.59	0/204	0.80	0/311
2	Ai	0.59	0/204	0.80	0/311
2	Aj	0.59	0/204	0.80	0/311
2	Ak	0.59	0/204	0.80	0/311
2	Al	0.59	0/204	0.80	0/311
2	Am	0.59	0/204	0.80	0/311
2	An	0.60	0/204	0.80	0/311
2	Ao	0.59	0/204	0.80	0/311
2	Ap	0.59	0/204	0.80	0/311
2	Aq	0.59	0/204	0.81	0/311
2	Ar	0.60	0/204	0.80	0/311
2	As	0.59	0/204	0.80	0/311
2	At	0.59	0/204	0.80	0/311
2	Au	0.60	0/204	0.80	0/311
2	Av	0.59	0/204	0.80	0/311
2	Aw	0.59	0/204	0.80	0/311
2	Ax	0.59	0/204	0.80	0/311
2	Ay	0.60	0/204	0.80	0/311
2	Az	0.59	0/204	0.80	0/311

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
All	All	0.47	0/114120	0.57	0/157200

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](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 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	1	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	2	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	3	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	4	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	5	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	6	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	7	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	8	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	A	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	B	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	C	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	D	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	F	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	G	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	H	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	I	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	J	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	K	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	L	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	M	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	N	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	O	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	P	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	Q	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	R	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	S	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	T	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	U	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	V	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	W	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	X	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	Y	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	Z	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	a	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	b	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	c	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	d	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	e	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	f	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	g	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	h	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	i	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	j	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	k	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	l	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	m	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	n	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	o	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	p	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	q	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	r	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	s	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	t	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	u	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	v	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	w	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	x	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	y	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
1	z	211/243 (87%)	205 (97%)	5 (2%)	1 (0%)	29	65
All	All	12660/14580 (87%)	12300 (97%)	300 (2%)	60 (0%)	32	65

5 of 60 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	M	180	PRO
1	A	180	PRO
1	B	180	PRO
1	C	180	PRO
1	D	180	PRO

### 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	1	173/200 (86%)	173 (100%)	0	100	100
1	2	173/200 (86%)	173 (100%)	0	100	100
1	3	173/200 (86%)	173 (100%)	0	100	100
1	4	173/200 (86%)	173 (100%)	0	100	100
1	5	173/200 (86%)	173 (100%)	0	100	100
1	6	173/200 (86%)	173 (100%)	0	100	100
1	7	173/200 (86%)	173 (100%)	0	100	100
1	8	173/200 (86%)	173 (100%)	0	100	100
1	A	173/200 (86%)	173 (100%)	0	100	100
1	B	173/200 (86%)	173 (100%)	0	100	100
1	C	173/200 (86%)	173 (100%)	0	100	100
1	D	173/200 (86%)	173 (100%)	0	100	100
1	E	173/200 (86%)	173 (100%)	0	100	100
1	F	173/200 (86%)	173 (100%)	0	100	100
1	G	173/200 (86%)	173 (100%)	0	100	100
1	H	173/200 (86%)	173 (100%)	0	100	100
1	I	173/200 (86%)	173 (100%)	0	100	100
1	J	173/200 (86%)	173 (100%)	0	100	100
1	K	173/200 (86%)	173 (100%)	0	100	100
1	L	173/200 (86%)	173 (100%)	0	100	100
1	M	173/200 (86%)	173 (100%)	0	100	100
1	N	173/200 (86%)	173 (100%)	0	100	100
1	O	173/200 (86%)	173 (100%)	0	100	100
1	P	173/200 (86%)	173 (100%)	0	100	100
1	Q	173/200 (86%)	173 (100%)	0	100	100
1	R	173/200 (86%)	173 (100%)	0	100	100
1	S	173/200 (86%)	173 (100%)	0	100	100
1	T	173/200 (86%)	173 (100%)	0	100	100
1	U	173/200 (86%)	173 (100%)	0	100	100
1	V	173/200 (86%)	173 (100%)	0	100	100
1	W	173/200 (86%)	173 (100%)	0	100	100
1	X	173/200 (86%)	173 (100%)	0	100	100

Continued on next page...

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Y	173/200 (86%)	173 (100%)	0	100	100
1	Z	173/200 (86%)	173 (100%)	0	100	100
1	a	173/200 (86%)	173 (100%)	0	100	100
1	b	173/200 (86%)	173 (100%)	0	100	100
1	c	173/200 (86%)	173 (100%)	0	100	100
1	d	173/200 (86%)	173 (100%)	0	100	100
1	e	173/200 (86%)	173 (100%)	0	100	100
1	f	173/200 (86%)	173 (100%)	0	100	100
1	g	173/200 (86%)	173 (100%)	0	100	100
1	h	173/200 (86%)	173 (100%)	0	100	100
1	i	173/200 (86%)	173 (100%)	0	100	100
1	j	173/200 (86%)	173 (100%)	0	100	100
1	k	173/200 (86%)	173 (100%)	0	100	100
1	l	173/200 (86%)	173 (100%)	0	100	100
1	m	173/200 (86%)	173 (100%)	0	100	100
1	n	173/200 (86%)	173 (100%)	0	100	100
1	o	173/200 (86%)	173 (100%)	0	100	100
1	p	173/200 (86%)	173 (100%)	0	100	100
1	q	173/200 (86%)	173 (100%)	0	100	100
1	r	173/200 (86%)	173 (100%)	0	100	100
1	s	173/200 (86%)	173 (100%)	0	100	100
1	t	173/200 (86%)	173 (100%)	0	100	100
1	u	173/200 (86%)	173 (100%)	0	100	100
1	v	173/200 (86%)	173 (100%)	0	100	100
1	w	173/200 (86%)	173 (100%)	0	100	100
1	x	173/200 (86%)	173 (100%)	0	100	100
1	y	173/200 (86%)	173 (100%)	0	100	100
1	z	173/200 (86%)	173 (100%)	0	100	100
All	All	10380/12000 (86%)	10380 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60

such sidechains are listed below:

Mol	Chain	Res	Type
1	c	47	HIS
1	4	47	HIS
1	j	47	HIS
1	3	47	HIS
1	8	47	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.

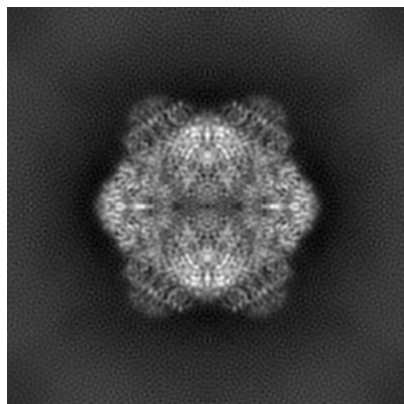
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42246. These allow visual inspection of the internal detail of the map and identification of artifacts.

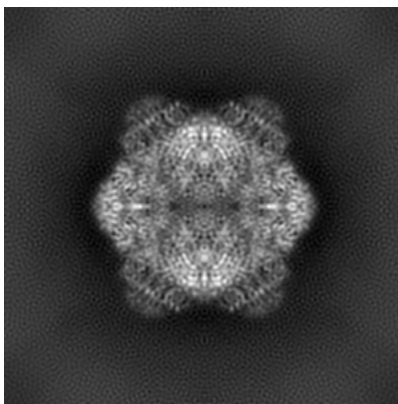
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

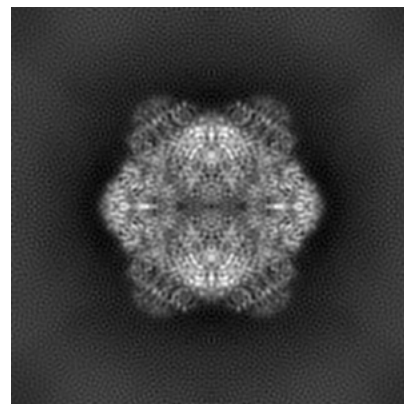
#### 6.1.1 Primary map



X

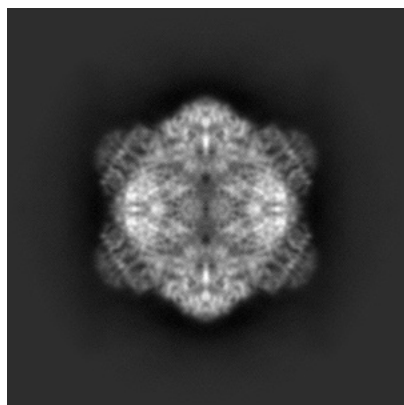


Y

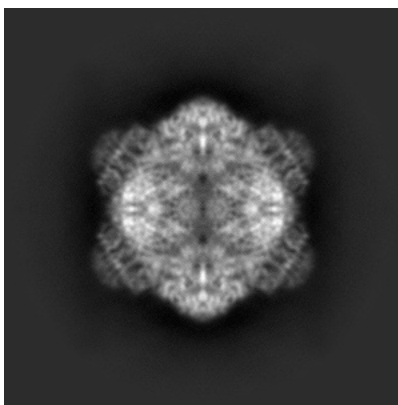


Z

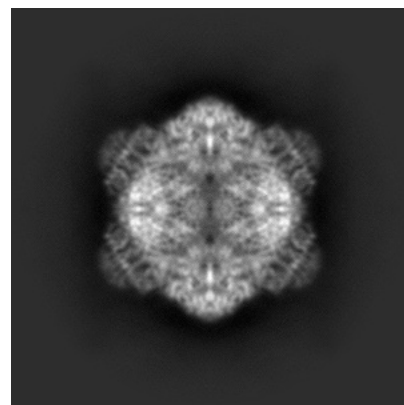
#### 6.1.2 Raw map



X



Y



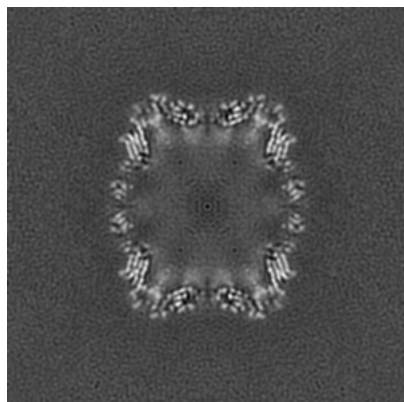
Z

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

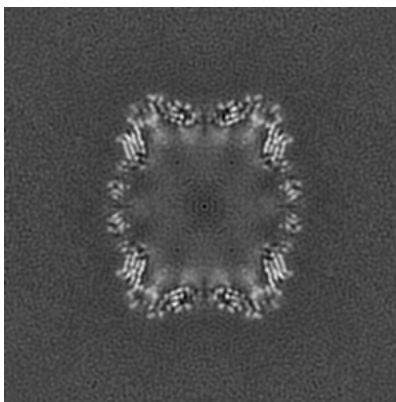


## 6.2 Central slices [i](#)

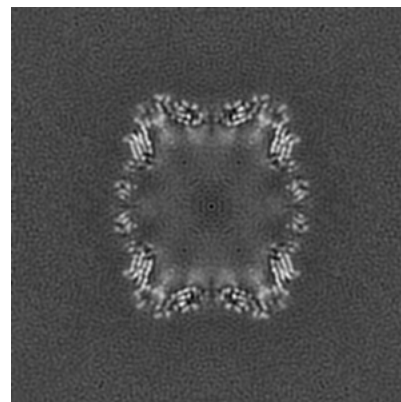
### 6.2.1 Primary map



X Index: 187

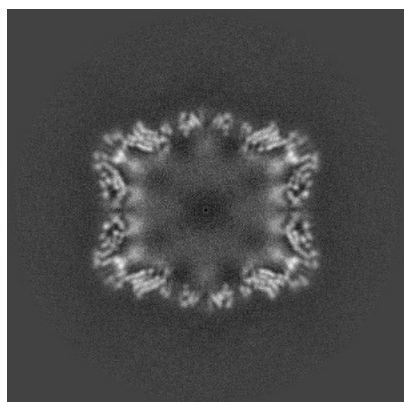


Y Index: 187

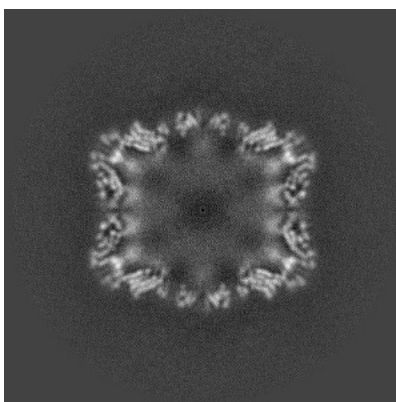


Z Index: 187

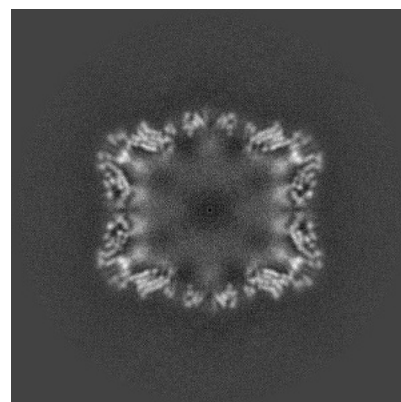
### 6.2.2 Raw map



X Index: 187



Y Index: 187

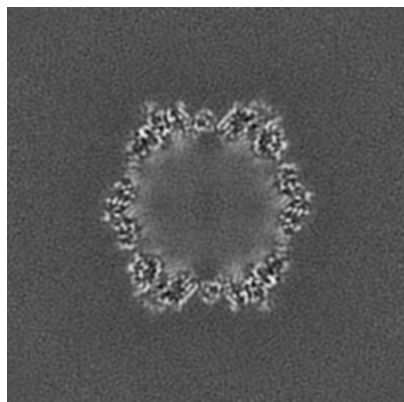


Z Index: 187

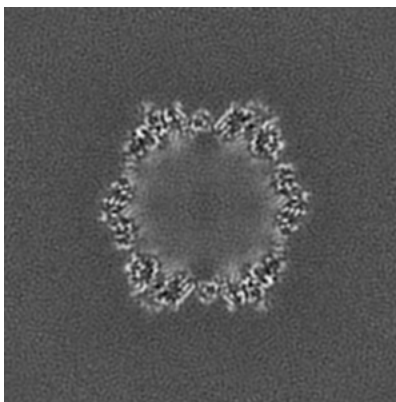
The images above show central slices of the map in three orthogonal directions.

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

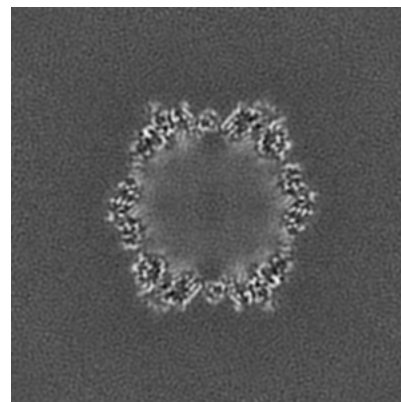
### 6.3.1 Primary map



X Index: 207

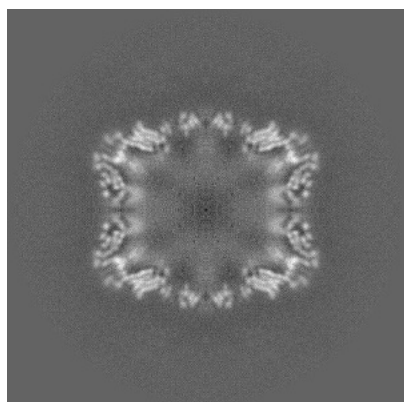


Y Index: 207

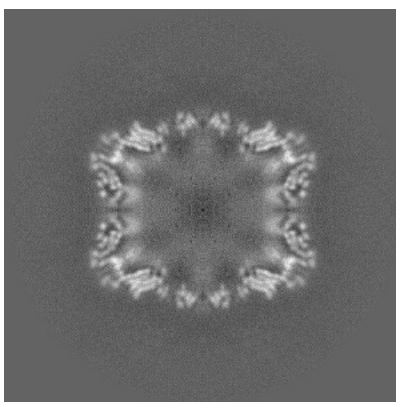


Z Index: 207

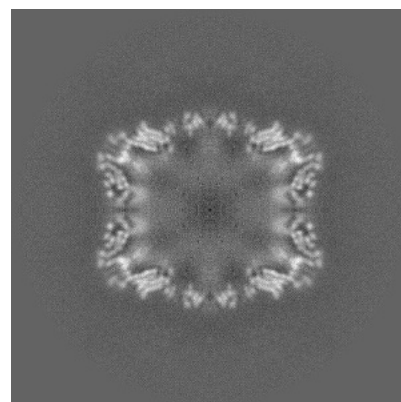
### 6.3.2 Raw map



X Index: 186



Y Index: 186

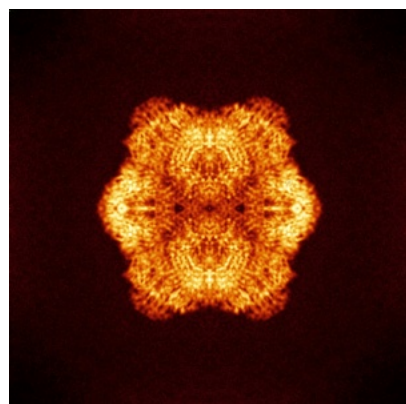


Z Index: 186

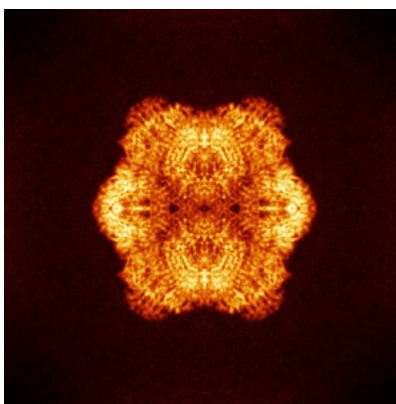
The images above show the largest variance slices of the map in three orthogonal directions.

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

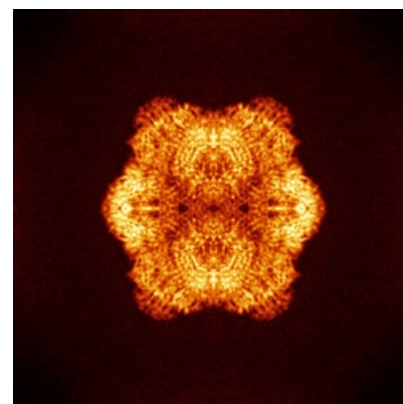
### 6.4.1 Primary map



X

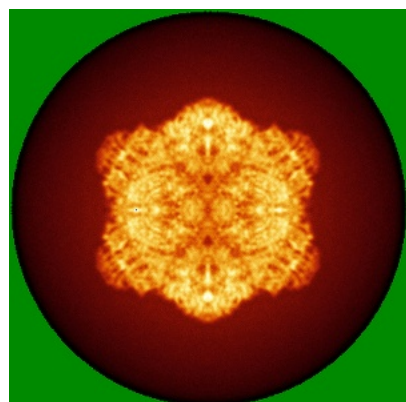


Y

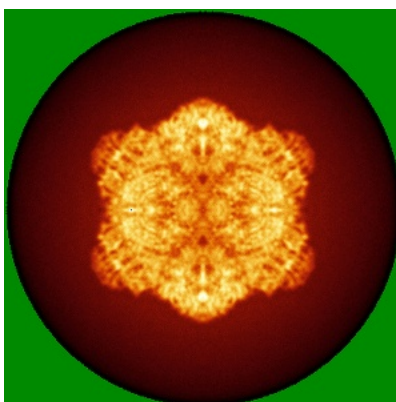


Z

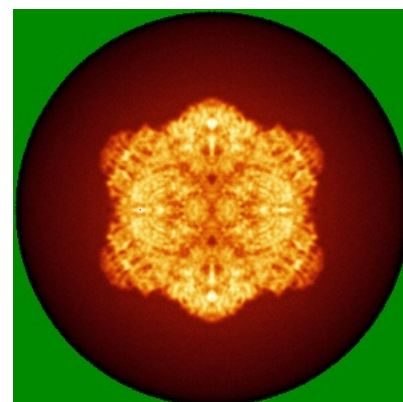
### 6.4.2 Raw map



X



Y

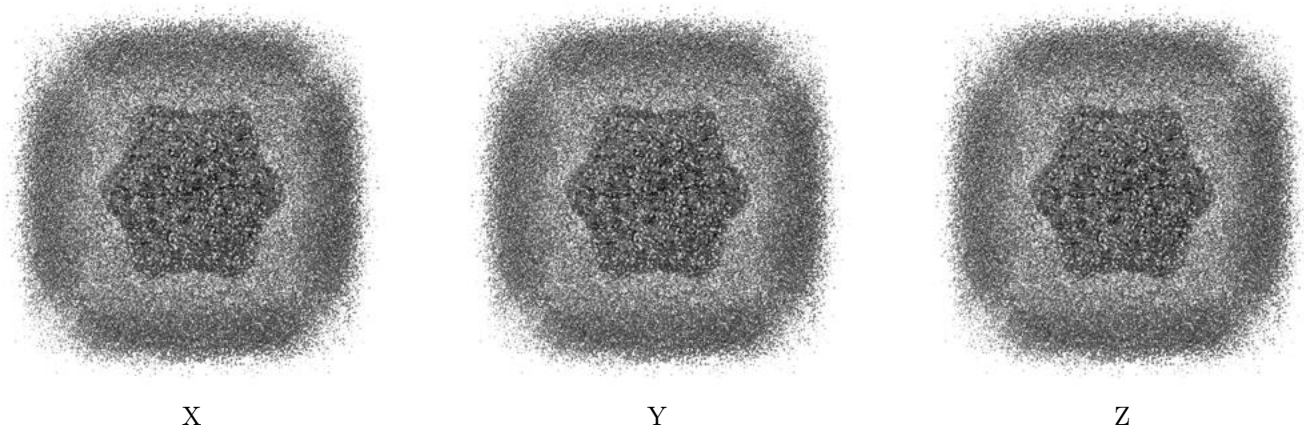


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

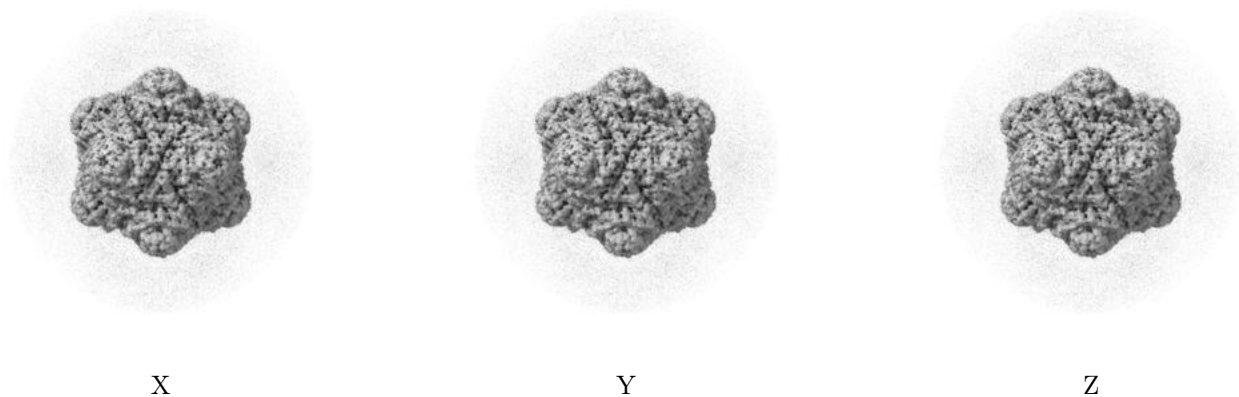
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

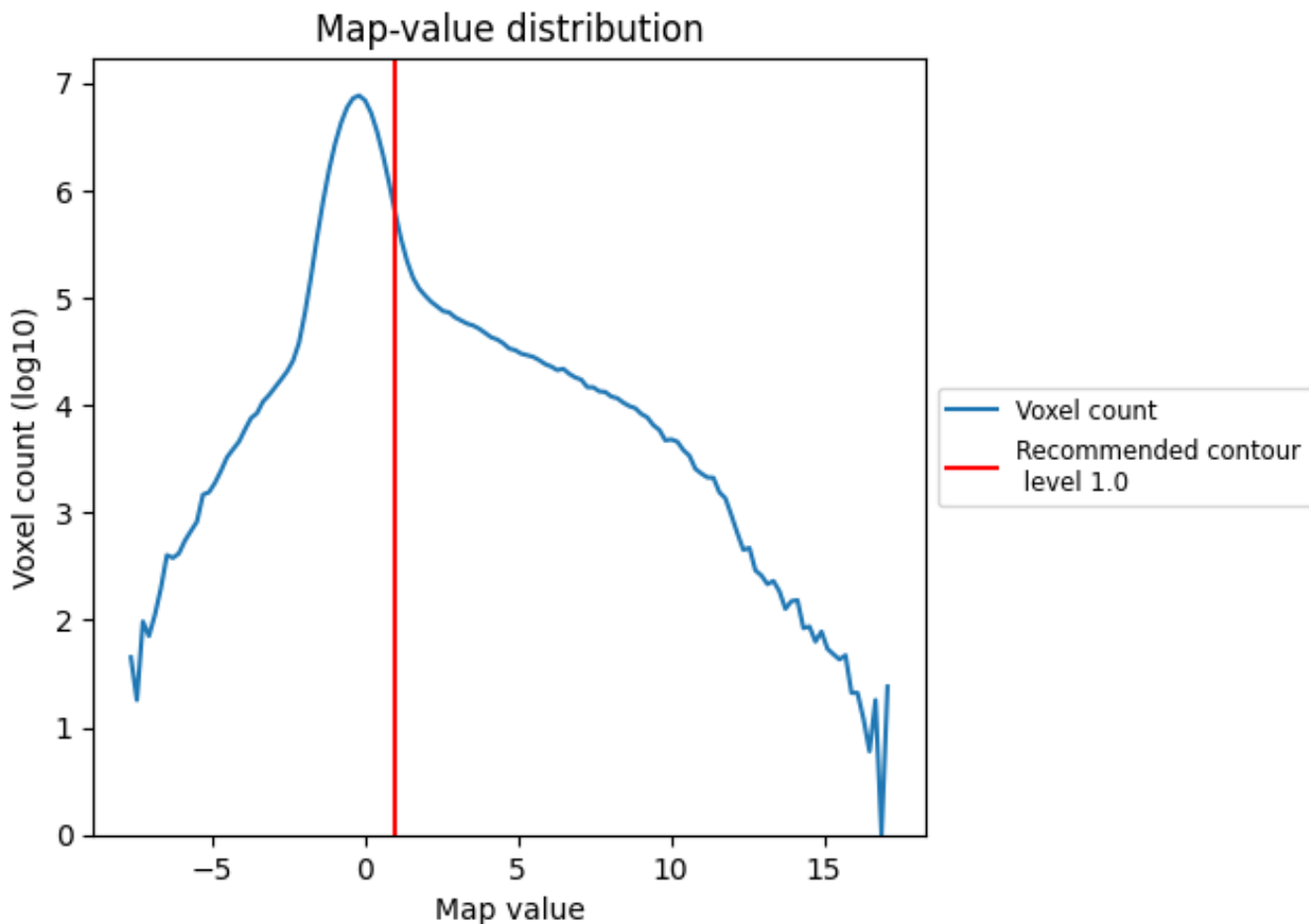
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

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

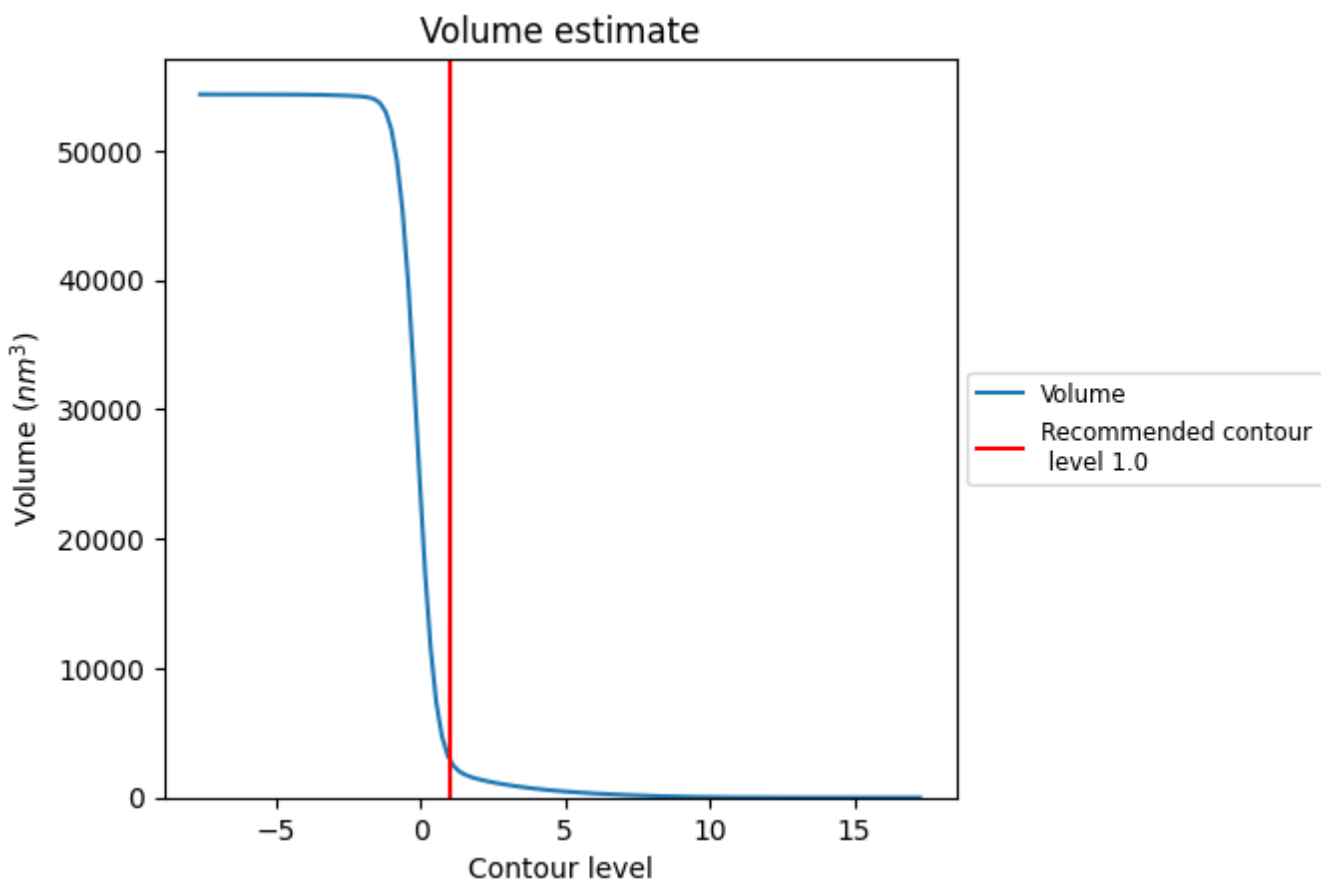
### 7.1 Map-value distribution [i](#)



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.



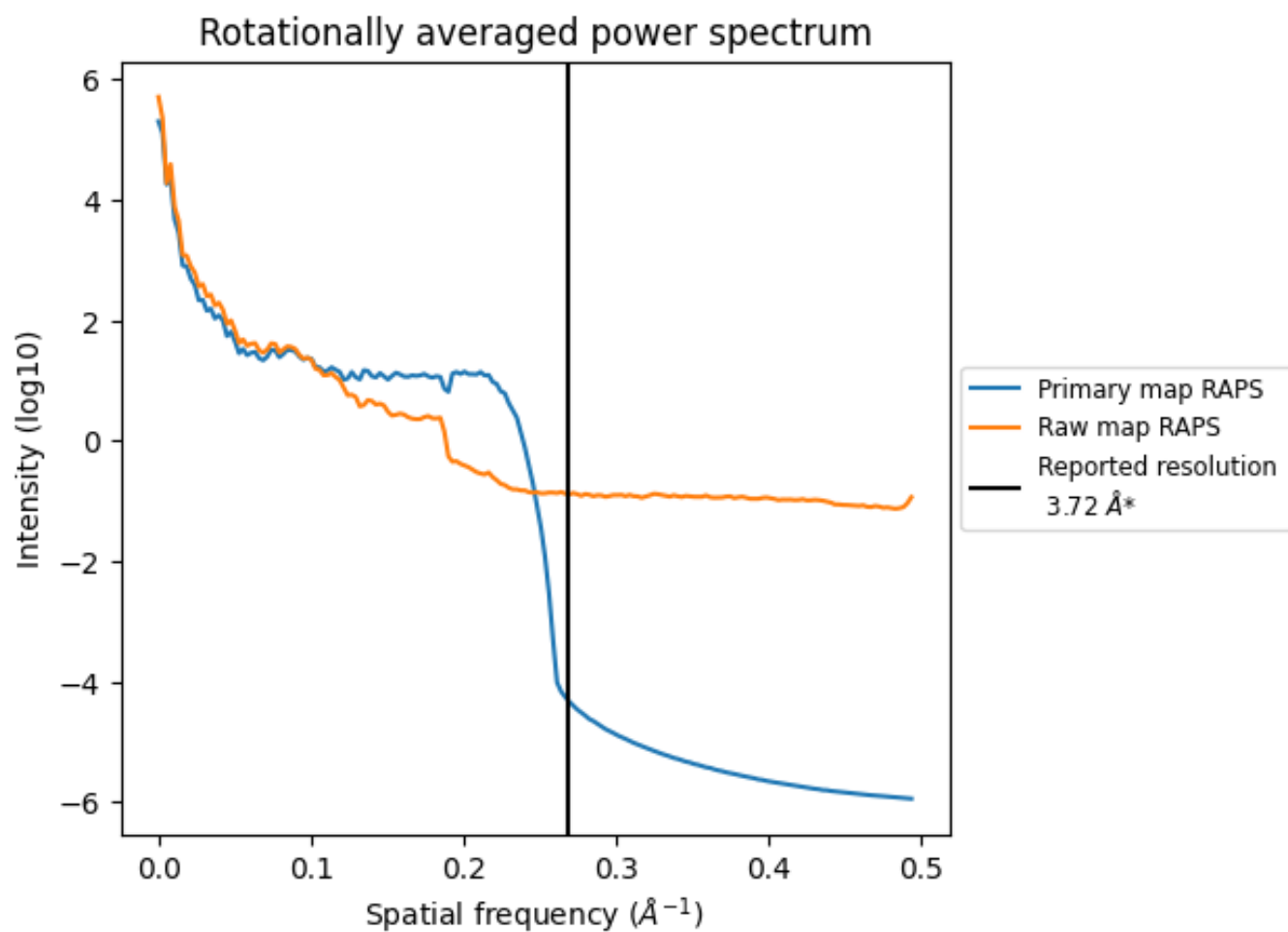
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2975  $\text{nm}^3$ ; this corresponds to an approximate mass of 2687 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

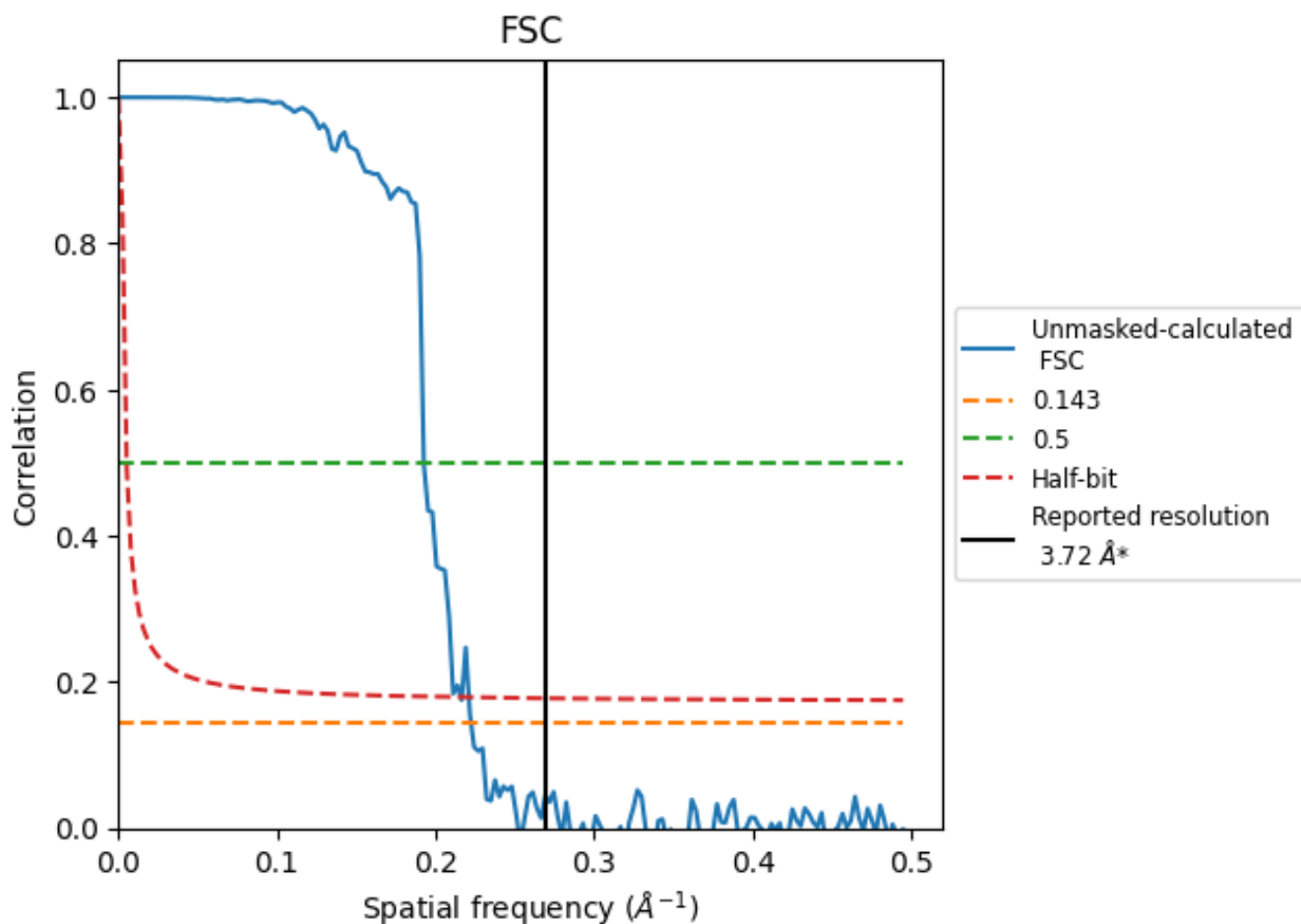


\*Reported resolution corresponds to spatial frequency of 0.269 Å<sup>-1</sup>

## 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 0.269 Å<sup>-1</sup>



## 8.2 Resolution estimates [i](#)

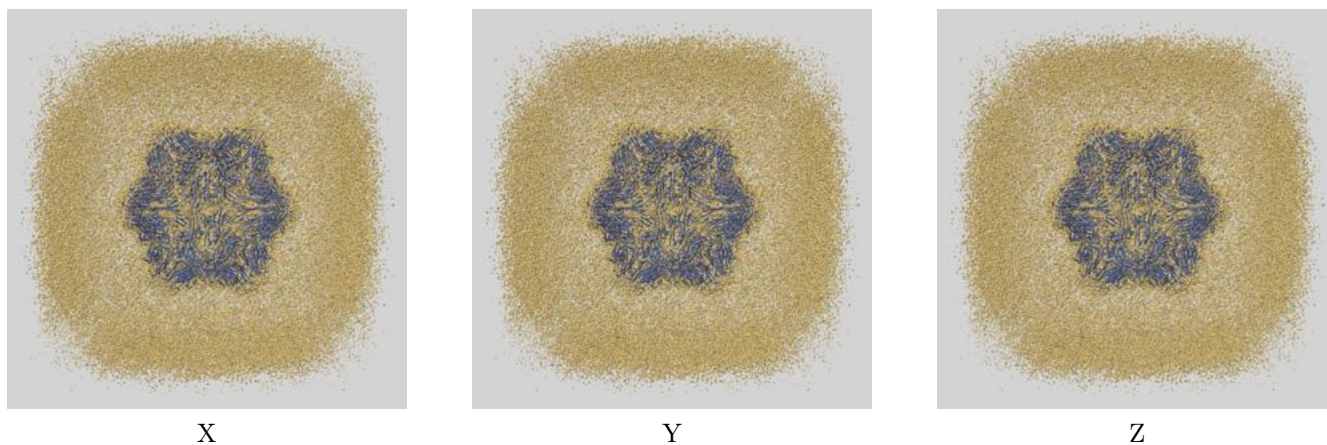
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.72	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.49	5.19	4.63

\*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 4.49 differs from the reported value 3.72 by more than 10 %

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

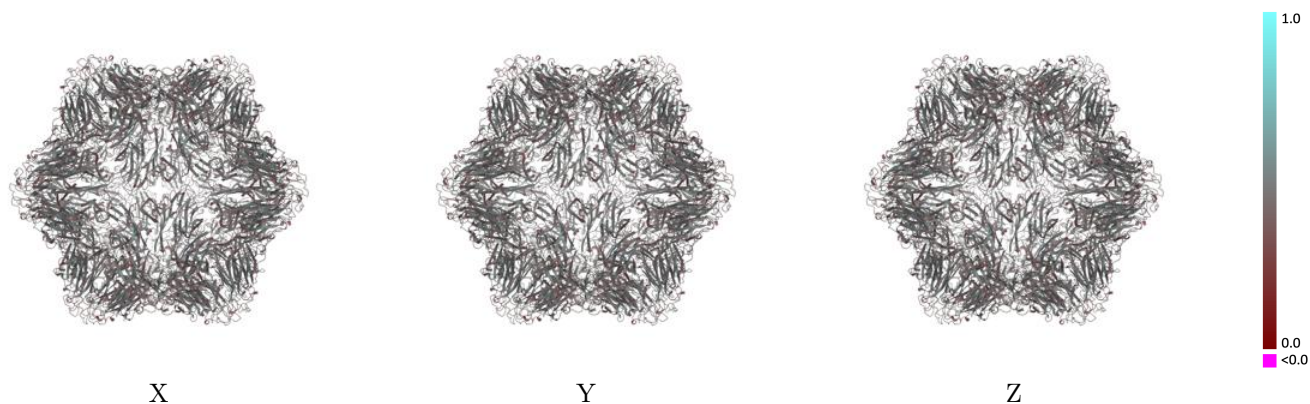
This section contains information regarding the fit between EMDB map EMD-42246 and PDB model 8UH4. Per-residue inclusion information can be found in section 3 on page 14.

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



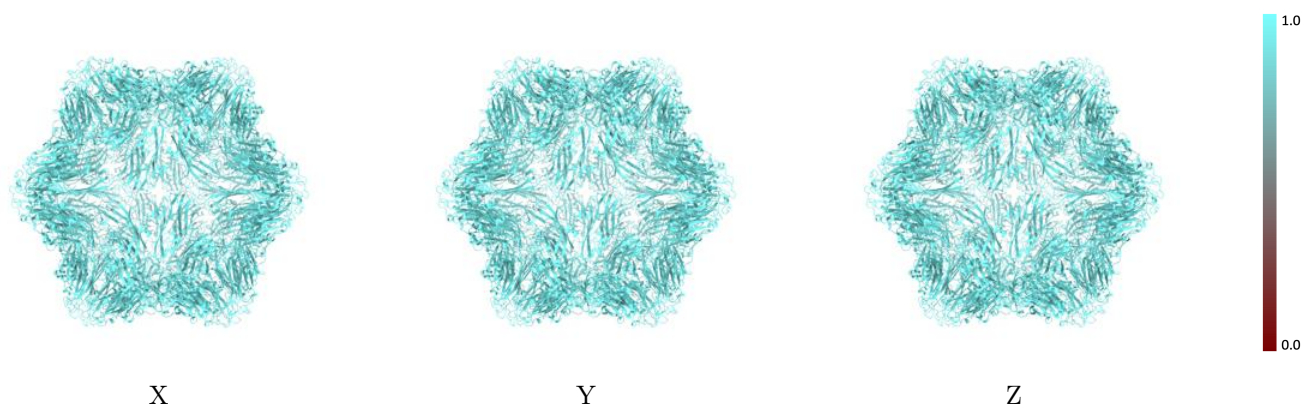
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



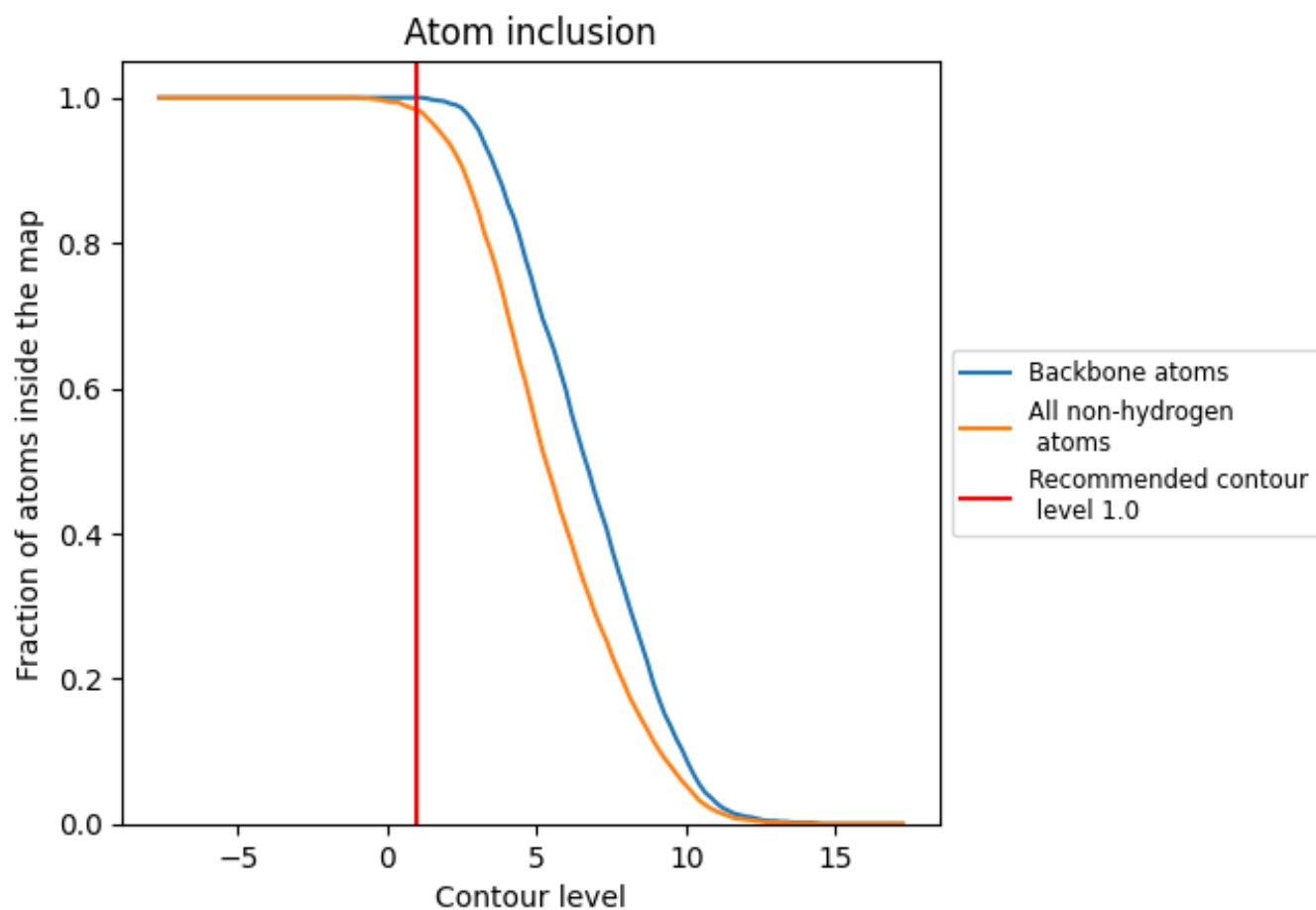
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (1.0).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 98% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary





















































































The table lists the average atom inclusion at the recommended contour level (1.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9830	 0.4500
1	 0.9800	 0.4530
2	 0.9800	 0.4540
3	 0.9810	 0.4560
4	 0.9820	 0.4540
5	 0.9810	 0.4550
6	 0.9810	 0.4530
7	 0.9810	 0.4530
8	 0.9810	 0.4560
A	 0.9810	 0.4540
A1	 0.9950	 0.4150
A2	 0.9950	 0.4140
A3	 0.9950	 0.4190
A4	 0.9950	 0.4140
A5	 0.9950	 0.4170
A6	 0.9950	 0.4210
A7	 0.9950	 0.4180
A8	 0.9950	 0.4140
AA	 0.9950	 0.4220
AB	 0.9950	 0.4230
AC	 0.9950	 0.4190
AD	 0.9950	 0.4200
AE	 0.9950	 0.4250
AF	 0.9950	 0.4240
AG	 0.9950	 0.4280
AH	 0.9950	 0.4220
AI	 0.9950	 0.4210
AJ	 0.9950	 0.4180
AK	 0.9950	 0.4160
AL	 0.9950	 0.4180
AM	 0.9950	 0.4150
AN	 0.9950	 0.4200
AO	 0.9950	 0.4190
AP	 0.9950	 0.4210
AQ	 0.9950	 0.4210























































































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Chain	Atom inclusion	Q-score
AR	 0.9950	 0.4160
AS	 0.9950	 0.4150
AT	 0.9950	 0.4160
AU	 0.9950	 0.4130
AV	 0.9950	 0.4180
AW	 0.9950	 0.4230
AX	 0.9950	 0.4190
AY	 0.9950	 0.4230
AZ	 0.9950	 0.4140
Aa	 0.9950	 0.4190
Ab	 0.9950	 0.4190
Ac	 0.9950	 0.4220
Ad	 0.9950	 0.4180
Ae	 0.9950	 0.4180
Af	 0.9950	 0.4150
Ag	 0.9950	 0.4180
Ah	 0.9950	 0.4190
Ai	 0.9950	 0.4190
Aj	 0.9950	 0.4230
Ak	 0.9950	 0.4220
Al	 0.9950	 0.4180
Am	 0.9950	 0.4190
An	 0.9950	 0.4180
Ao	 0.9950	 0.4200
Ap	 0.9950	 0.4160
Aq	 0.9950	 0.4200
Ar	 0.9950	 0.4160
As	 0.9950	 0.4180
At	 0.9950	 0.4210
Au	 0.9950	 0.4160
Av	 0.9950	 0.4230
Aw	 0.9950	 0.4270
Ax	 0.9950	 0.4260
Ay	 0.9950	 0.4240
Az	 0.9950	 0.4200
B	 0.9800	 0.4520
C	 0.9820	 0.4520
D	 0.9810	 0.4540
E	 0.9810	 0.4540
F	 0.9810	 0.4540
G	 0.9810	 0.4520
H	 0.9810	 0.4530





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Chain	Atom inclusion	Q-score
I	 0.9810	 0.4530
J	 0.9800	 0.4540
K	 0.9820	 0.4540
L	 0.9800	 0.4530
M	 0.9810	 0.4540
N	 0.9810	 0.4530
O	 0.9810	 0.4540
P	 0.9810	 0.4540
Q	 0.9820	 0.4550
R	 0.9800	 0.4530
S	 0.9800	 0.4540
T	 0.9820	 0.4550
U	 0.9800	 0.4530
V	 0.9820	 0.4520
W	 0.9810	 0.4530
X	 0.9810	 0.4540
Y	 0.9810	 0.4550
Z	 0.9810	 0.4530
a	 0.9810	 0.4540
b	 0.9810	 0.4550
c	 0.9810	 0.4540
d	 0.9810	 0.4550
e	 0.9810	 0.4570
f	 0.9810	 0.4550
g	 0.9820	 0.4530
h	 0.9810	 0.4530
i	 0.9810	 0.4530
j	 0.9810	 0.4540
k	 0.9810	 0.4530
l	 0.9810	 0.4520
m	 0.9820	 0.4550
n	 0.9810	 0.4530
o	 0.9810	 0.4550
p	 0.9820	 0.4530
q	 0.9800	 0.4520
r	 0.9800	 0.4530
s	 0.9800	 0.4540
t	 0.9810	 0.4530
u	 0.9810	 0.4540
v	 0.9810	 0.4530
w	 0.9810	 0.4530
x	 0.9810	 0.4530

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Chain	Atom inclusion	Q-score
y	 0.9810	 0.4540
z	 0.9810	 0.4540