



Full wwPDB EM Validation Report ⓘ

Nov 20, 2022 – 03:45 am GMT

PDB ID : 6GYB
EMDB ID : EMD-0089
Title : Cryo-EM structure of the bacteria-killing type IV secretion system core complex from *Xanthomonas citri*
Authors : Sgro, G.G.; Costa, T.R.D.; Farah, C.S.; Waksman, G.
Deposited on : 2018-06-28
Resolution : 3.28 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

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.dev43
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) : 2.31.2

1 Overall quality at a glance

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






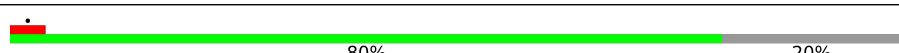
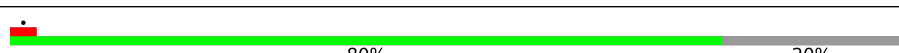
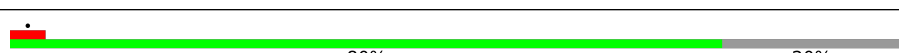

The reported resolution of this entry is 3.28 Å.

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	139	 80% 20%
1	D	139	 80% 20%
1	G	139	 80% 20%
1	J	139	 80% 20%
1	M	139	 80% 20%
1	P	139	 80% 20%
1	S	139	 80% 20%
1	a	139	 80% 20%
1	d	139	 80% 20%









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Mol	Chain	Length	Quality of chain	
1	g	139	80%	20%
1	j	139	80%	20%
1	m	139	80%	20%
1	p	139	80%	20%
1	s	139	80%	20%
2	B	255	87%	13%
2	E	255	87%	13%
2	H	255	87%	13%
2	K	255	87%	13%
2	N	255	87%	13%
2	Q	255	87%	13%
2	T	255	87%	13%
2	b	255	87%	13%
2	e	255	87%	13%
2	h	255	87%	13%
2	k	255	87%	13%
2	n	255	87%	13%
2	q	255	87%	13%
2	t	255	87%	13%
3	C	406	50%	50%
3	F	406	50%	50%
3	I	406	50%	50%
3	L	406	50%	50%
3	O	406	50%	50%
3	R	406	50%	50%

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Mol	Chain	Length	Quality of chain
3	U	406	
3	c	406	
3	f	406	
3	i	406	
3	l	406	
3	o	406	
3	r	406	
3	u	406	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 59318 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 VirB7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	a	111	842	534	137	167	4	0	0
1	d	111	842	534	137	167	4	0	0
1	g	111	842	534	137	167	4	0	0
1	j	111	842	534	137	167	4	0	0
1	m	111	842	534	137	167	4	0	0
1	p	111	842	534	137	167	4	0	0
1	s	111	842	534	137	167	4	0	0
1	A	111	842	534	137	167	4	0	0
1	D	111	842	534	137	167	4	0	0
1	G	111	842	534	137	167	4	0	0
1	J	111	842	534	137	167	4	0	0
1	M	111	842	534	137	167	4	0	0
1	P	111	842	534	137	167	4	0	0
1	S	111	842	534	137	167	4	0	0

- Molecule 2 is a protein called VirB9 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	b	223	1840	1178	318	341	3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	e	223	Total	C	N	O	S	0	0
			1840	1178	318	341	3		
2	h	223	Total	C	N	O	S	0	0
			1840	1178	318	341	3		
2	k	223	Total	C	N	O	S	0	0
			1840	1178	318	341	3		
2	n	223	Total	C	N	O	S	0	0
			1840	1178	318	341	3		
2	q	223	Total	C	N	O	S	0	0
			1840	1178	318	341	3		
2	t	223	Total	C	N	O	S	0	0
			1840	1178	318	341	3		
2	B	223	Total	C	N	O	S	0	0
			1840	1178	318	341	3		
2	E	223	Total	C	N	O	S	0	0
			1840	1178	318	341	3		
2	H	223	Total	C	N	O	S	0	0
			1840	1178	318	341	3		
2	K	223	Total	C	N	O	S	0	0
			1840	1178	318	341	3		
2	N	223	Total	C	N	O	S	0	0
			1840	1178	318	341	3		
2	Q	223	Total	C	N	O	S	0	0
			1840	1178	318	341	3		
2	T	223	Total	C	N	O	S	0	0
			1840	1178	318	341	3		

- Molecule 3 is a protein called VirB10 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	c	205	Total	C	N	O	S	0	0
			1555	985	268	297	5		
3	f	205	Total	C	N	O	S	0	0
			1555	985	268	297	5		
3	i	205	Total	C	N	O	S	0	0
			1555	985	268	297	5		
3	l	205	Total	C	N	O	S	0	0
			1555	985	268	297	5		
3	o	205	Total	C	N	O	S	0	0
			1555	985	268	297	5		
3	r	205	Total	C	N	O	S	0	0
			1555	985	268	297	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	u	205	1555	985	268	297	5	0	0
3	C	205	1555	985	268	297	5	0	0
3	F	205	1555	985	268	297	5	0	0
3	I	205	1555	985	268	297	5	0	0
3	L	205	1555	985	268	297	5	0	0
3	O	205	1555	985	268	297	5	0	0
3	R	205	1555	985	268	297	5	0	0
3	U	205	1555	985	268	297	5	0	0

There are 238 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
c	390	ALA	-	expression tag	UNP Q8PJB6
c	391	ALA	-	expression tag	UNP Q8PJB6
c	392	ALA	-	expression tag	UNP Q8PJB6
c	393	LEU	-	expression tag	UNP Q8PJB6
c	394	GLU	-	expression tag	UNP Q8PJB6
c	395	GLY	-	expression tag	UNP Q8PJB6
c	396	LEU	-	expression tag	UNP Q8PJB6
c	397	SER	-	expression tag	UNP Q8PJB6
c	398	ALA	-	expression tag	UNP Q8PJB6
c	399	TRP	-	expression tag	UNP Q8PJB6
c	400	SER	-	expression tag	UNP Q8PJB6
c	401	HIS	-	expression tag	UNP Q8PJB6
c	402	PRO	-	expression tag	UNP Q8PJB6
c	403	GLN	-	expression tag	UNP Q8PJB6
c	404	PHE	-	expression tag	UNP Q8PJB6
c	405	GLU	-	expression tag	UNP Q8PJB6
c	406	LYS	-	expression tag	UNP Q8PJB6
f	390	ALA	-	expression tag	UNP Q8PJB6
f	391	ALA	-	expression tag	UNP Q8PJB6
f	392	ALA	-	expression tag	UNP Q8PJB6
f	393	LEU	-	expression tag	UNP Q8PJB6
f	394	GLU	-	expression tag	UNP Q8PJB6
f	395	GLY	-	expression tag	UNP Q8PJB6

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Chain	Residue	Modelled	Actual	Comment	Reference
f	396	LEU	-	expression tag	UNP Q8PJB6
f	397	SER	-	expression tag	UNP Q8PJB6
f	398	ALA	-	expression tag	UNP Q8PJB6
f	399	TRP	-	expression tag	UNP Q8PJB6
f	400	SER	-	expression tag	UNP Q8PJB6
f	401	HIS	-	expression tag	UNP Q8PJB6
f	402	PRO	-	expression tag	UNP Q8PJB6
f	403	GLN	-	expression tag	UNP Q8PJB6
f	404	PHE	-	expression tag	UNP Q8PJB6
f	405	GLU	-	expression tag	UNP Q8PJB6
f	406	LYS	-	expression tag	UNP Q8PJB6
i	390	ALA	-	expression tag	UNP Q8PJB6
i	391	ALA	-	expression tag	UNP Q8PJB6
i	392	ALA	-	expression tag	UNP Q8PJB6
i	393	LEU	-	expression tag	UNP Q8PJB6
i	394	GLU	-	expression tag	UNP Q8PJB6
i	395	GLY	-	expression tag	UNP Q8PJB6
i	396	LEU	-	expression tag	UNP Q8PJB6
i	397	SER	-	expression tag	UNP Q8PJB6
i	398	ALA	-	expression tag	UNP Q8PJB6
i	399	TRP	-	expression tag	UNP Q8PJB6
i	400	SER	-	expression tag	UNP Q8PJB6
i	401	HIS	-	expression tag	UNP Q8PJB6
i	402	PRO	-	expression tag	UNP Q8PJB6
i	403	GLN	-	expression tag	UNP Q8PJB6
i	404	PHE	-	expression tag	UNP Q8PJB6
i	405	GLU	-	expression tag	UNP Q8PJB6
i	406	LYS	-	expression tag	UNP Q8PJB6
l	390	ALA	-	expression tag	UNP Q8PJB6
l	391	ALA	-	expression tag	UNP Q8PJB6
l	392	ALA	-	expression tag	UNP Q8PJB6
l	393	LEU	-	expression tag	UNP Q8PJB6
l	394	GLU	-	expression tag	UNP Q8PJB6
l	395	GLY	-	expression tag	UNP Q8PJB6
l	396	LEU	-	expression tag	UNP Q8PJB6
l	397	SER	-	expression tag	UNP Q8PJB6
l	398	ALA	-	expression tag	UNP Q8PJB6
l	399	TRP	-	expression tag	UNP Q8PJB6
l	400	SER	-	expression tag	UNP Q8PJB6
l	401	HIS	-	expression tag	UNP Q8PJB6
l	402	PRO	-	expression tag	UNP Q8PJB6
l	403	GLN	-	expression tag	UNP Q8PJB6

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Chain	Residue	Modelled	Actual	Comment	Reference
l	404	PHE	-	expression tag	UNP Q8PJB6
l	405	GLU	-	expression tag	UNP Q8PJB6
l	406	LYS	-	expression tag	UNP Q8PJB6
o	390	ALA	-	expression tag	UNP Q8PJB6
o	391	ALA	-	expression tag	UNP Q8PJB6
o	392	ALA	-	expression tag	UNP Q8PJB6
o	393	LEU	-	expression tag	UNP Q8PJB6
o	394	GLU	-	expression tag	UNP Q8PJB6
o	395	GLY	-	expression tag	UNP Q8PJB6
o	396	LEU	-	expression tag	UNP Q8PJB6
o	397	SER	-	expression tag	UNP Q8PJB6
o	398	ALA	-	expression tag	UNP Q8PJB6
o	399	TRP	-	expression tag	UNP Q8PJB6
o	400	SER	-	expression tag	UNP Q8PJB6
o	401	HIS	-	expression tag	UNP Q8PJB6
o	402	PRO	-	expression tag	UNP Q8PJB6
o	403	GLN	-	expression tag	UNP Q8PJB6
o	404	PHE	-	expression tag	UNP Q8PJB6
o	405	GLU	-	expression tag	UNP Q8PJB6
o	406	LYS	-	expression tag	UNP Q8PJB6
r	390	ALA	-	expression tag	UNP Q8PJB6
r	391	ALA	-	expression tag	UNP Q8PJB6
r	392	ALA	-	expression tag	UNP Q8PJB6
r	393	LEU	-	expression tag	UNP Q8PJB6
r	394	GLU	-	expression tag	UNP Q8PJB6
r	395	GLY	-	expression tag	UNP Q8PJB6
r	396	LEU	-	expression tag	UNP Q8PJB6
r	397	SER	-	expression tag	UNP Q8PJB6
r	398	ALA	-	expression tag	UNP Q8PJB6
r	399	TRP	-	expression tag	UNP Q8PJB6
r	400	SER	-	expression tag	UNP Q8PJB6
r	401	HIS	-	expression tag	UNP Q8PJB6
r	402	PRO	-	expression tag	UNP Q8PJB6
r	403	GLN	-	expression tag	UNP Q8PJB6
r	404	PHE	-	expression tag	UNP Q8PJB6
r	405	GLU	-	expression tag	UNP Q8PJB6
r	406	LYS	-	expression tag	UNP Q8PJB6
u	390	ALA	-	expression tag	UNP Q8PJB6
u	391	ALA	-	expression tag	UNP Q8PJB6
u	392	ALA	-	expression tag	UNP Q8PJB6
u	393	LEU	-	expression tag	UNP Q8PJB6
u	394	GLU	-	expression tag	UNP Q8PJB6

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Chain	Residue	Modelled	Actual	Comment	Reference
u	395	GLY	-	expression tag	UNP Q8PJB6
u	396	LEU	-	expression tag	UNP Q8PJB6
u	397	SER	-	expression tag	UNP Q8PJB6
u	398	ALA	-	expression tag	UNP Q8PJB6
u	399	TRP	-	expression tag	UNP Q8PJB6
u	400	SER	-	expression tag	UNP Q8PJB6
u	401	HIS	-	expression tag	UNP Q8PJB6
u	402	PRO	-	expression tag	UNP Q8PJB6
u	403	GLN	-	expression tag	UNP Q8PJB6
u	404	PHE	-	expression tag	UNP Q8PJB6
u	405	GLU	-	expression tag	UNP Q8PJB6
u	406	LYS	-	expression tag	UNP Q8PJB6
C	390	ALA	-	expression tag	UNP Q8PJB6
C	391	ALA	-	expression tag	UNP Q8PJB6
C	392	ALA	-	expression tag	UNP Q8PJB6
C	393	LEU	-	expression tag	UNP Q8PJB6
C	394	GLU	-	expression tag	UNP Q8PJB6
C	395	GLY	-	expression tag	UNP Q8PJB6
C	396	LEU	-	expression tag	UNP Q8PJB6
C	397	SER	-	expression tag	UNP Q8PJB6
C	398	ALA	-	expression tag	UNP Q8PJB6
C	399	TRP	-	expression tag	UNP Q8PJB6
C	400	SER	-	expression tag	UNP Q8PJB6
C	401	HIS	-	expression tag	UNP Q8PJB6
C	402	PRO	-	expression tag	UNP Q8PJB6
C	403	GLN	-	expression tag	UNP Q8PJB6
C	404	PHE	-	expression tag	UNP Q8PJB6
C	405	GLU	-	expression tag	UNP Q8PJB6
C	406	LYS	-	expression tag	UNP Q8PJB6
F	390	ALA	-	expression tag	UNP Q8PJB6
F	391	ALA	-	expression tag	UNP Q8PJB6
F	392	ALA	-	expression tag	UNP Q8PJB6
F	393	LEU	-	expression tag	UNP Q8PJB6
F	394	GLU	-	expression tag	UNP Q8PJB6
F	395	GLY	-	expression tag	UNP Q8PJB6
F	396	LEU	-	expression tag	UNP Q8PJB6
F	397	SER	-	expression tag	UNP Q8PJB6
F	398	ALA	-	expression tag	UNP Q8PJB6
F	399	TRP	-	expression tag	UNP Q8PJB6
F	400	SER	-	expression tag	UNP Q8PJB6
F	401	HIS	-	expression tag	UNP Q8PJB6
F	402	PRO	-	expression tag	UNP Q8PJB6

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Chain	Residue	Modelled	Actual	Comment	Reference
F	403	GLN	-	expression tag	UNP Q8PJB6
F	404	PHE	-	expression tag	UNP Q8PJB6
F	405	GLU	-	expression tag	UNP Q8PJB6
F	406	LYS	-	expression tag	UNP Q8PJB6
I	390	ALA	-	expression tag	UNP Q8PJB6
I	391	ALA	-	expression tag	UNP Q8PJB6
I	392	ALA	-	expression tag	UNP Q8PJB6
I	393	LEU	-	expression tag	UNP Q8PJB6
I	394	GLU	-	expression tag	UNP Q8PJB6
I	395	GLY	-	expression tag	UNP Q8PJB6
I	396	LEU	-	expression tag	UNP Q8PJB6
I	397	SER	-	expression tag	UNP Q8PJB6
I	398	ALA	-	expression tag	UNP Q8PJB6
I	399	TRP	-	expression tag	UNP Q8PJB6
I	400	SER	-	expression tag	UNP Q8PJB6
I	401	HIS	-	expression tag	UNP Q8PJB6
I	402	PRO	-	expression tag	UNP Q8PJB6
I	403	GLN	-	expression tag	UNP Q8PJB6
I	404	PHE	-	expression tag	UNP Q8PJB6
I	405	GLU	-	expression tag	UNP Q8PJB6
I	406	LYS	-	expression tag	UNP Q8PJB6
L	390	ALA	-	expression tag	UNP Q8PJB6
L	391	ALA	-	expression tag	UNP Q8PJB6
L	392	ALA	-	expression tag	UNP Q8PJB6
L	393	LEU	-	expression tag	UNP Q8PJB6
L	394	GLU	-	expression tag	UNP Q8PJB6
L	395	GLY	-	expression tag	UNP Q8PJB6
L	396	LEU	-	expression tag	UNP Q8PJB6
L	397	SER	-	expression tag	UNP Q8PJB6
L	398	ALA	-	expression tag	UNP Q8PJB6
L	399	TRP	-	expression tag	UNP Q8PJB6
L	400	SER	-	expression tag	UNP Q8PJB6
L	401	HIS	-	expression tag	UNP Q8PJB6
L	402	PRO	-	expression tag	UNP Q8PJB6
L	403	GLN	-	expression tag	UNP Q8PJB6
L	404	PHE	-	expression tag	UNP Q8PJB6
L	405	GLU	-	expression tag	UNP Q8PJB6
L	406	LYS	-	expression tag	UNP Q8PJB6
O	390	ALA	-	expression tag	UNP Q8PJB6
O	391	ALA	-	expression tag	UNP Q8PJB6
O	392	ALA	-	expression tag	UNP Q8PJB6
O	393	LEU	-	expression tag	UNP Q8PJB6

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Chain	Residue	Modelled	Actual	Comment	Reference
O	394	GLU	-	expression tag	UNP Q8PJB6
O	395	GLY	-	expression tag	UNP Q8PJB6
O	396	LEU	-	expression tag	UNP Q8PJB6
O	397	SER	-	expression tag	UNP Q8PJB6
O	398	ALA	-	expression tag	UNP Q8PJB6
O	399	TRP	-	expression tag	UNP Q8PJB6
O	400	SER	-	expression tag	UNP Q8PJB6
O	401	HIS	-	expression tag	UNP Q8PJB6
O	402	PRO	-	expression tag	UNP Q8PJB6
O	403	GLN	-	expression tag	UNP Q8PJB6
O	404	PHE	-	expression tag	UNP Q8PJB6
O	405	GLU	-	expression tag	UNP Q8PJB6
O	406	LYS	-	expression tag	UNP Q8PJB6
R	390	ALA	-	expression tag	UNP Q8PJB6
R	391	ALA	-	expression tag	UNP Q8PJB6
R	392	ALA	-	expression tag	UNP Q8PJB6
R	393	LEU	-	expression tag	UNP Q8PJB6
R	394	GLU	-	expression tag	UNP Q8PJB6
R	395	GLY	-	expression tag	UNP Q8PJB6
R	396	LEU	-	expression tag	UNP Q8PJB6
R	397	SER	-	expression tag	UNP Q8PJB6
R	398	ALA	-	expression tag	UNP Q8PJB6
R	399	TRP	-	expression tag	UNP Q8PJB6
R	400	SER	-	expression tag	UNP Q8PJB6
R	401	HIS	-	expression tag	UNP Q8PJB6
R	402	PRO	-	expression tag	UNP Q8PJB6
R	403	GLN	-	expression tag	UNP Q8PJB6
R	404	PHE	-	expression tag	UNP Q8PJB6
R	405	GLU	-	expression tag	UNP Q8PJB6
R	406	LYS	-	expression tag	UNP Q8PJB6
U	390	ALA	-	expression tag	UNP Q8PJB6
U	391	ALA	-	expression tag	UNP Q8PJB6
U	392	ALA	-	expression tag	UNP Q8PJB6
U	393	LEU	-	expression tag	UNP Q8PJB6
U	394	GLU	-	expression tag	UNP Q8PJB6
U	395	GLY	-	expression tag	UNP Q8PJB6
U	396	LEU	-	expression tag	UNP Q8PJB6
U	397	SER	-	expression tag	UNP Q8PJB6
U	398	ALA	-	expression tag	UNP Q8PJB6
U	399	TRP	-	expression tag	UNP Q8PJB6
U	400	SER	-	expression tag	UNP Q8PJB6
U	401	HIS	-	expression tag	UNP Q8PJB6

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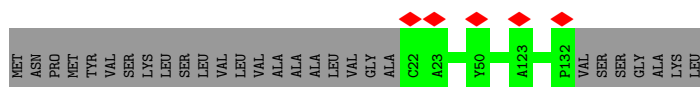
Chain	Residue	Modelled	Actual	Comment	Reference
U	402	PRO	-	expression tag	UNP Q8PJB6
U	403	GLN	-	expression tag	UNP Q8PJB6
U	404	PHE	-	expression tag	UNP Q8PJB6
U	405	GLU	-	expression tag	UNP Q8PJB6
U	406	LYS	-	expression tag	UNP Q8PJB6

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.

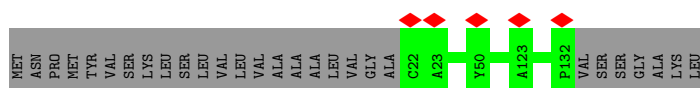
- Molecule 1: VirB7

Chain a: 




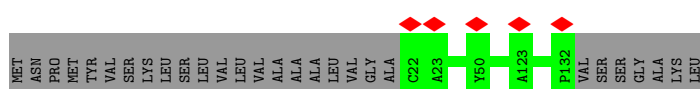
- Molecule 1: VirB7

Chain d: 




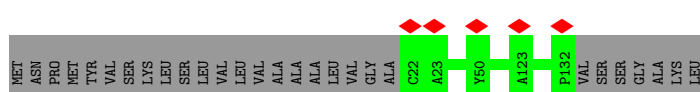
- Molecule 1: VirB7

Chain g: 




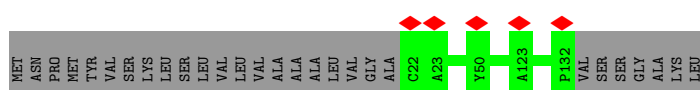
- Molecule 1: VirB7

Chain j: 

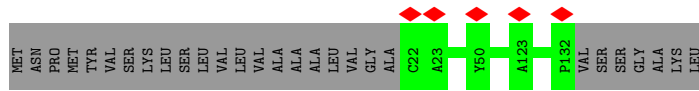
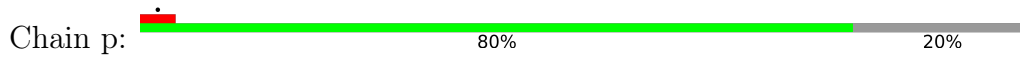


- Molecule 1: VirB7

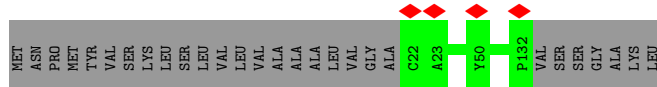
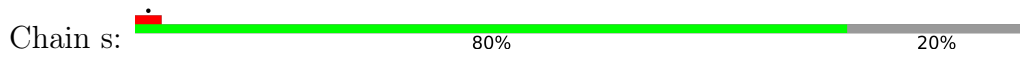
Chain m: 



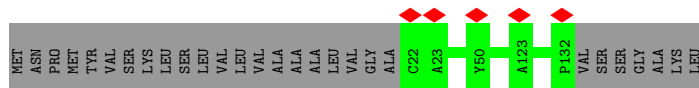
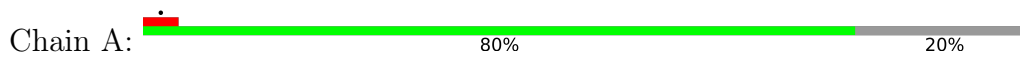
• Molecule 1: VirB7



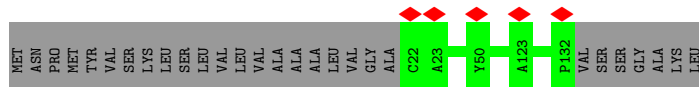
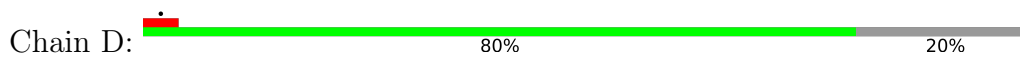
• Molecule 1: VirB7



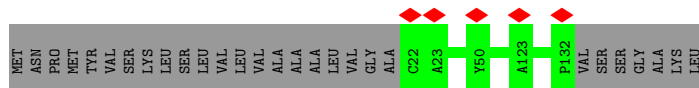
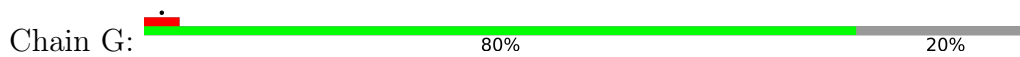
• Molecule 1: VirB7



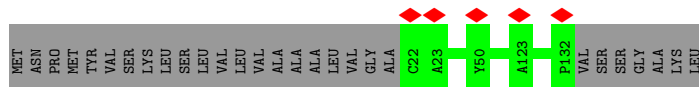
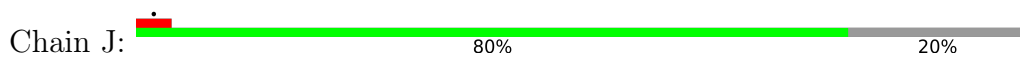
• Molecule 1: VirB7



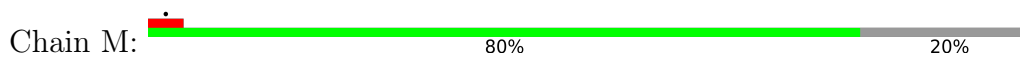
• Molecule 1: VirB7

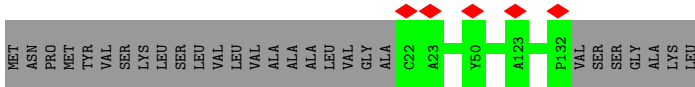


• Molecule 1: VirB7

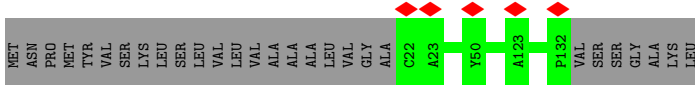
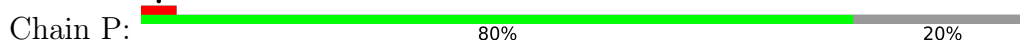


• Molecule 1: VirB7

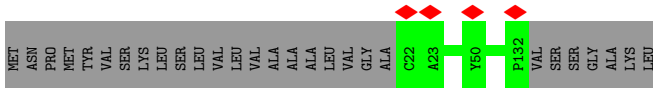
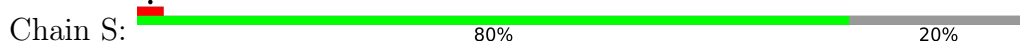




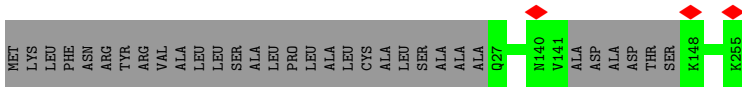
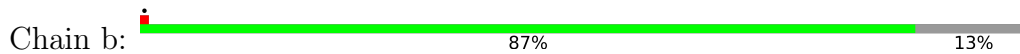
• Molecule 1: VirB7



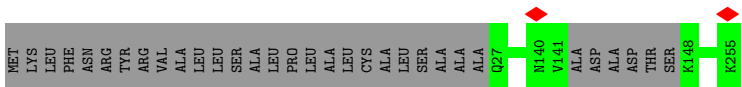
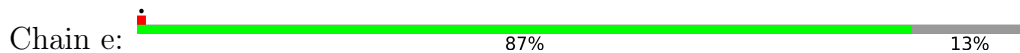
• Molecule 1: VirB7



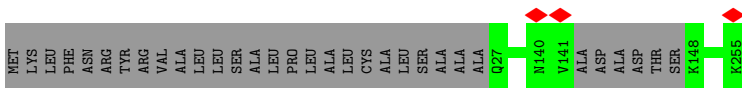
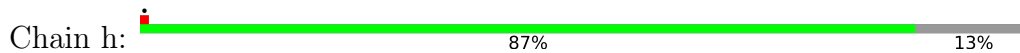
• Molecule 2: VirB9 protein



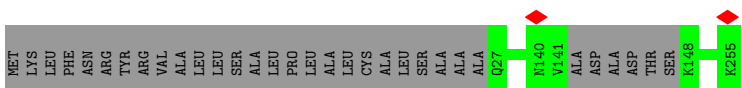
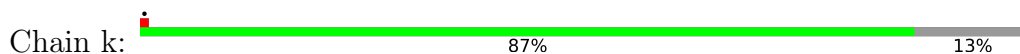
• Molecule 2: VirB9 protein



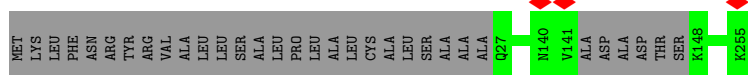
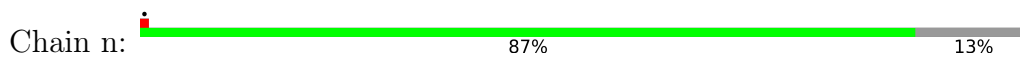
• Molecule 2: VirB9 protein



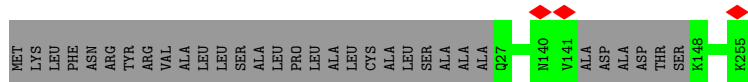
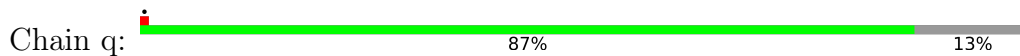
• Molecule 2: VirB9 protein



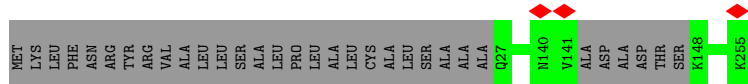
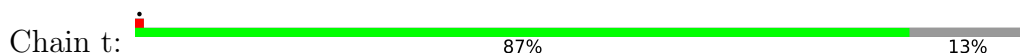
• Molecule 2: VirB9 protein



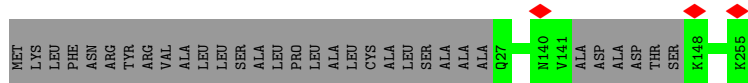
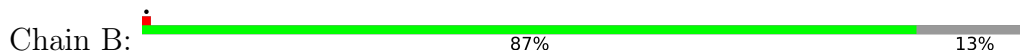
• Molecule 2: VirB9 protein



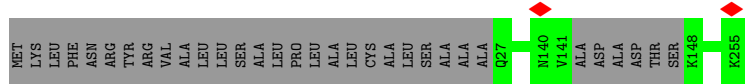
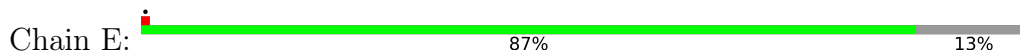
• Molecule 2: VirB9 protein



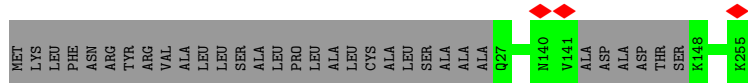
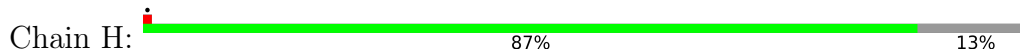
• Molecule 2: VirB9 protein



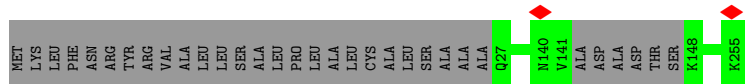
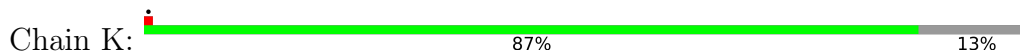
• Molecule 2: VirB9 protein

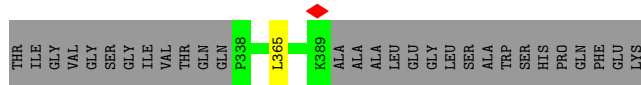


• Molecule 2: VirB9 protein

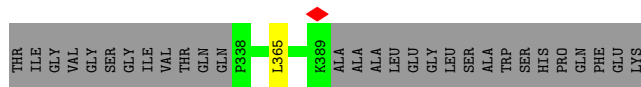
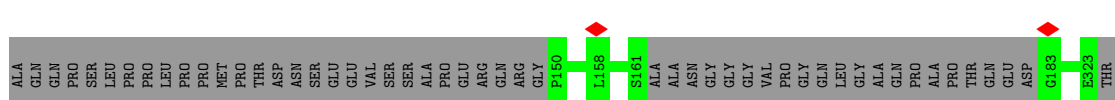


• Molecule 2: VirB9 protein

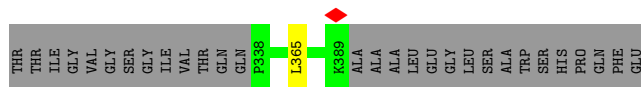
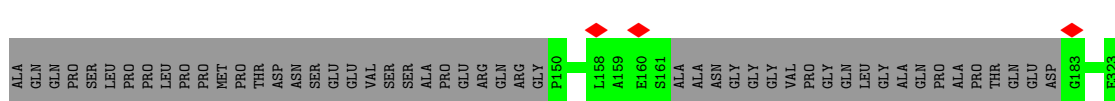




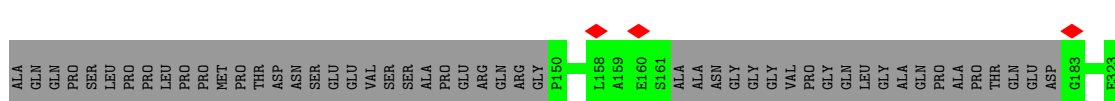
• Molecule 3: VirB10 protein

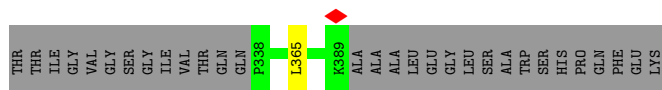


• Molecule 3: VirB10 protein

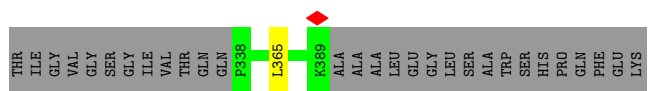
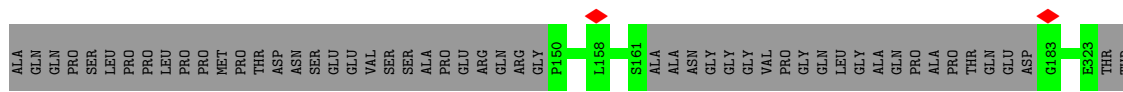
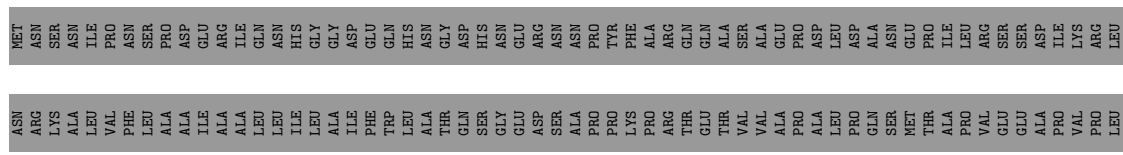


• Molecule 3: VirB10 protein

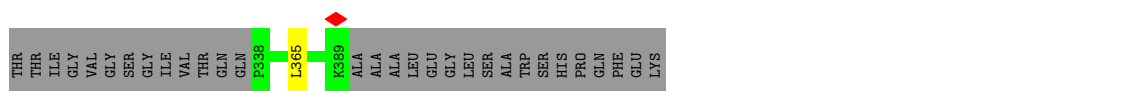
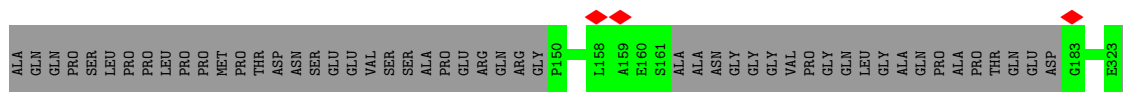
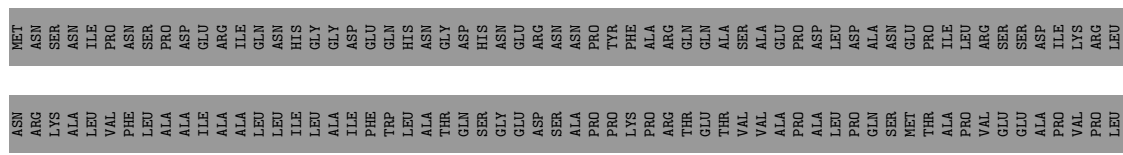




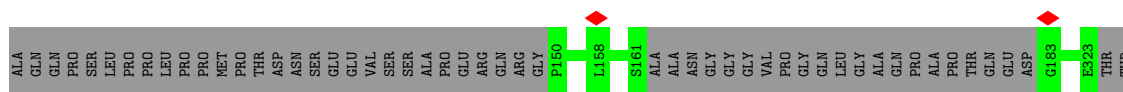
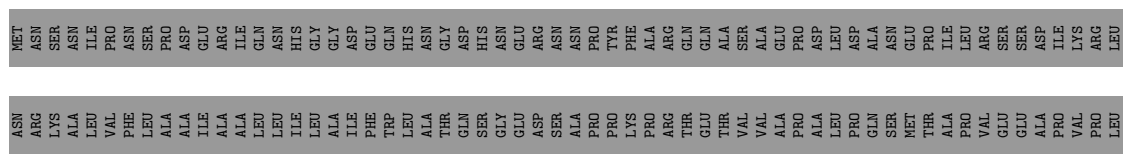
• Molecule 3: VirB10 protein



• Molecule 3: VirB10 protein



• Molecule 3: VirB10 protein



THR	THR	ILE	GLY	VAL	GLY	SER	GLY	ILE	VAL	THR	GLN	K368	L365	K369	ALA	ALA	ALA	LEU	GLU	GLY	LEU	SER	ALA	TRP	SER	HIS	PRO	GLN	PHE	GLU	LYS
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C14	Depositor
Number of particles used	142306	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)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.275	Depositor
Minimum map value	-0.162	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.035	Depositor
Map size (Å)	370.99997, 370.99997, 370.99997	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.31	0/864	0.50	0/1186
1	D	0.31	0/864	0.50	0/1186
1	G	0.31	0/864	0.50	0/1186
1	J	0.31	0/864	0.50	0/1186
1	M	0.31	0/864	0.50	0/1186
1	P	0.31	0/864	0.50	0/1186
1	S	0.31	0/864	0.50	0/1186
1	a	0.31	0/864	0.50	0/1186
1	d	0.31	0/864	0.50	0/1186
1	g	0.31	0/864	0.50	0/1186
1	j	0.31	0/864	0.50	0/1186
1	m	0.31	0/864	0.50	0/1186
1	p	0.31	0/864	0.50	0/1186
1	s	0.31	0/864	0.50	0/1186
2	B	0.45	0/1883	0.59	0/2554
2	E	0.45	0/1883	0.59	0/2554
2	H	0.45	0/1883	0.59	0/2554
2	K	0.45	0/1883	0.59	0/2554
2	N	0.45	0/1883	0.59	0/2554
2	Q	0.45	0/1883	0.59	0/2554
2	T	0.45	0/1883	0.59	0/2554
2	b	0.45	0/1883	0.59	0/2554
2	e	0.45	0/1883	0.59	0/2554
2	h	0.45	0/1883	0.59	0/2554
2	k	0.45	0/1883	0.59	0/2554
2	n	0.45	0/1883	0.59	0/2554
2	q	0.45	0/1883	0.59	0/2554
2	t	0.45	0/1883	0.59	0/2554
3	C	0.43	0/1587	0.60	1/2157 (0.0%)
3	F	0.43	0/1587	0.60	1/2157 (0.0%)
3	I	0.43	0/1587	0.60	1/2157 (0.0%)
3	L	0.43	0/1587	0.60	1/2157 (0.0%)
3	O	0.43	0/1587	0.60	1/2157 (0.0%)
3	R	0.43	0/1587	0.60	1/2157 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	U	0.43	0/1587	0.60	1/2157 (0.0%)
3	c	0.43	0/1587	0.60	1/2157 (0.0%)
3	f	0.43	0/1587	0.60	1/2157 (0.0%)
3	i	0.43	0/1587	0.60	1/2157 (0.0%)
3	l	0.43	0/1587	0.60	1/2157 (0.0%)
3	o	0.43	0/1587	0.60	1/2157 (0.0%)
3	r	0.43	0/1587	0.60	1/2157 (0.0%)
3	u	0.43	0/1587	0.60	1/2157 (0.0%)
All	All	0.42	0/60676	0.58	14/82558 (0.0%)

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	f	365	LEU	CA-CB-CG	5.99	129.07	115.30
3	F	365	LEU	CA-CB-CG	5.99	129.07	115.30
3	l	365	LEU	CA-CB-CG	5.98	129.05	115.30
3	L	365	LEU	CA-CB-CG	5.98	129.05	115.30
3	i	365	LEU	CA-CB-CG	5.97	129.03	115.30
3	I	365	LEU	CA-CB-CG	5.97	129.03	115.30
3	c	365	LEU	CA-CB-CG	5.97	129.03	115.30
3	C	365	LEU	CA-CB-CG	5.97	129.03	115.30
3	u	365	LEU	CA-CB-CG	5.96	129.01	115.30
3	U	365	LEU	CA-CB-CG	5.96	129.01	115.30
3	r	365	LEU	CA-CB-CG	5.96	129.00	115.30
3	R	365	LEU	CA-CB-CG	5.96	129.00	115.30
3	o	365	LEU	CA-CB-CG	5.95	128.99	115.30
3	O	365	LEU	CA-CB-CG	5.95	129.00	115.30

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

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	109/139 (78%)	98 (90%)	11 (10%)	0	100	100
1	D	109/139 (78%)	98 (90%)	11 (10%)	0	100	100
1	G	109/139 (78%)	98 (90%)	11 (10%)	0	100	100
1	J	109/139 (78%)	98 (90%)	11 (10%)	0	100	100
1	M	109/139 (78%)	98 (90%)	11 (10%)	0	100	100
1	P	109/139 (78%)	98 (90%)	11 (10%)	0	100	100
1	S	109/139 (78%)	98 (90%)	11 (10%)	0	100	100
1	a	109/139 (78%)	98 (90%)	11 (10%)	0	100	100
1	d	109/139 (78%)	98 (90%)	11 (10%)	0	100	100
1	g	109/139 (78%)	98 (90%)	11 (10%)	0	100	100
1	j	109/139 (78%)	98 (90%)	11 (10%)	0	100	100
1	m	109/139 (78%)	98 (90%)	11 (10%)	0	100	100
1	p	109/139 (78%)	98 (90%)	11 (10%)	0	100	100
1	s	109/139 (78%)	98 (90%)	11 (10%)	0	100	100
2	B	219/255 (86%)	206 (94%)	13 (6%)	0	100	100
2	E	219/255 (86%)	206 (94%)	13 (6%)	0	100	100
2	H	219/255 (86%)	206 (94%)	13 (6%)	0	100	100
2	K	219/255 (86%)	206 (94%)	13 (6%)	0	100	100
2	N	219/255 (86%)	206 (94%)	13 (6%)	0	100	100
2	Q	219/255 (86%)	206 (94%)	13 (6%)	0	100	100
2	T	219/255 (86%)	206 (94%)	13 (6%)	0	100	100
2	b	219/255 (86%)	206 (94%)	13 (6%)	0	100	100
2	e	219/255 (86%)	206 (94%)	13 (6%)	0	100	100
2	h	219/255 (86%)	206 (94%)	13 (6%)	0	100	100
2	k	219/255 (86%)	206 (94%)	13 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	n	219/255 (86%)	206 (94%)	13 (6%)	0	100	100
2	q	219/255 (86%)	206 (94%)	13 (6%)	0	100	100
2	t	219/255 (86%)	206 (94%)	13 (6%)	0	100	100
3	C	199/406 (49%)	188 (94%)	11 (6%)	0	100	100
3	F	199/406 (49%)	188 (94%)	11 (6%)	0	100	100
3	I	199/406 (49%)	188 (94%)	11 (6%)	0	100	100
3	L	199/406 (49%)	188 (94%)	11 (6%)	0	100	100
3	O	199/406 (49%)	188 (94%)	11 (6%)	0	100	100
3	R	199/406 (49%)	188 (94%)	11 (6%)	0	100	100
3	U	199/406 (49%)	188 (94%)	11 (6%)	0	100	100
3	c	199/406 (49%)	188 (94%)	11 (6%)	0	100	100
3	f	199/406 (49%)	188 (94%)	11 (6%)	0	100	100
3	i	199/406 (49%)	188 (94%)	11 (6%)	0	100	100
3	l	199/406 (49%)	188 (94%)	11 (6%)	0	100	100
3	o	199/406 (49%)	188 (94%)	11 (6%)	0	100	100
3	r	199/406 (49%)	188 (94%)	11 (6%)	0	100	100
3	u	199/406 (49%)	188 (94%)	11 (6%)	0	100	100
All	All	7378/11200 (66%)	6888 (93%)	490 (7%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	93/114 (82%)	93 (100%)	0	100	100
1	D	93/114 (82%)	93 (100%)	0	100	100
1	G	93/114 (82%)	93 (100%)	0	100	100
1	J	93/114 (82%)	93 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	M	93/114 (82%)	93 (100%)	0	100	100
1	P	93/114 (82%)	93 (100%)	0	100	100
1	S	93/114 (82%)	93 (100%)	0	100	100
1	a	93/114 (82%)	93 (100%)	0	100	100
1	d	93/114 (82%)	93 (100%)	0	100	100
1	g	93/114 (82%)	93 (100%)	0	100	100
1	j	93/114 (82%)	93 (100%)	0	100	100
1	m	93/114 (82%)	93 (100%)	0	100	100
1	p	93/114 (82%)	93 (100%)	0	100	100
1	s	93/114 (82%)	93 (100%)	0	100	100
2	B	200/223 (90%)	200 (100%)	0	100	100
2	E	200/223 (90%)	200 (100%)	0	100	100
2	H	200/223 (90%)	200 (100%)	0	100	100
2	K	200/223 (90%)	200 (100%)	0	100	100
2	N	200/223 (90%)	200 (100%)	0	100	100
2	Q	200/223 (90%)	200 (100%)	0	100	100
2	T	200/223 (90%)	200 (100%)	0	100	100
2	b	200/223 (90%)	200 (100%)	0	100	100
2	e	200/223 (90%)	200 (100%)	0	100	100
2	h	200/223 (90%)	200 (100%)	0	100	100
2	k	200/223 (90%)	200 (100%)	0	100	100
2	n	200/223 (90%)	200 (100%)	0	100	100
2	q	200/223 (90%)	200 (100%)	0	100	100
2	t	200/223 (90%)	200 (100%)	0	100	100
3	C	170/331 (51%)	170 (100%)	0	100	100
3	F	170/331 (51%)	170 (100%)	0	100	100
3	I	170/331 (51%)	170 (100%)	0	100	100
3	L	170/331 (51%)	170 (100%)	0	100	100
3	O	170/331 (51%)	170 (100%)	0	100	100
3	R	170/331 (51%)	170 (100%)	0	100	100
3	U	170/331 (51%)	170 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	c	170/331 (51%)	170 (100%)	0	100	100
3	f	170/331 (51%)	170 (100%)	0	100	100
3	i	170/331 (51%)	170 (100%)	0	100	100
3	l	170/331 (51%)	170 (100%)	0	100	100
3	o	170/331 (51%)	170 (100%)	0	100	100
3	r	170/331 (51%)	170 (100%)	0	100	100
3	u	170/331 (51%)	170 (100%)	0	100	100
All	All	6482/9352 (69%)	6482 (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. There are no such sidechains identified.

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.

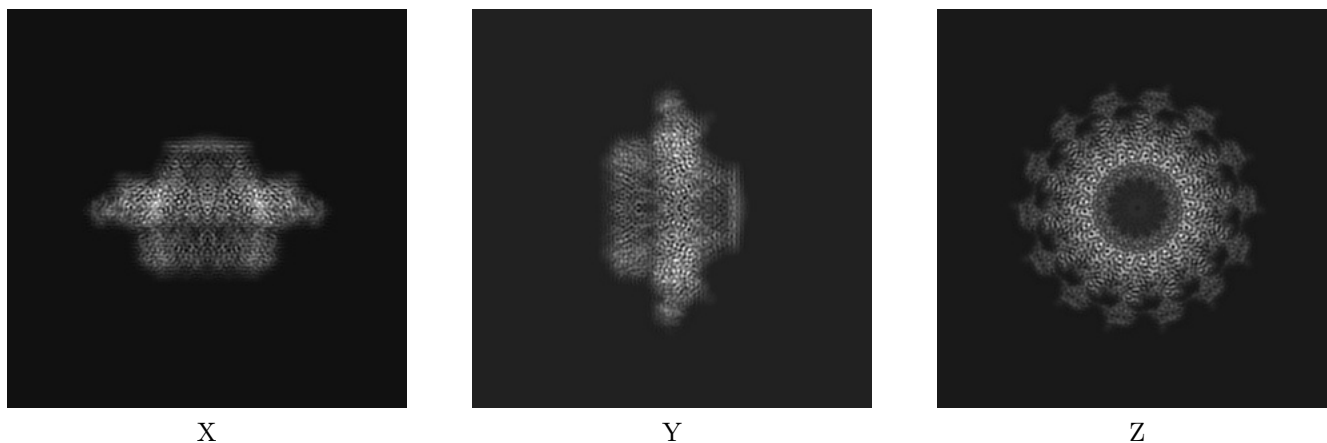
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0089. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

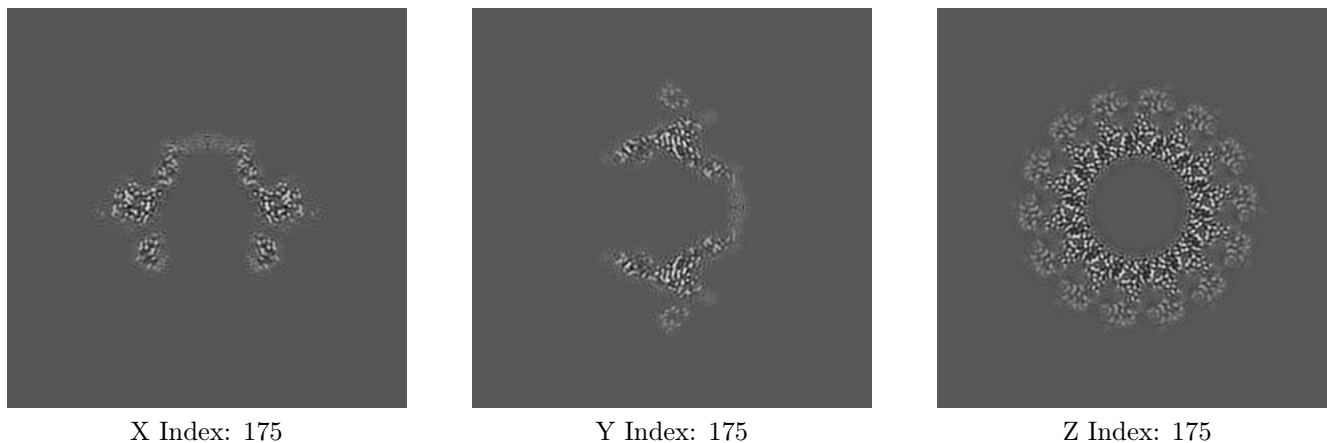
6.1.1 Primary map



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

6.2 Central slices [i](#)

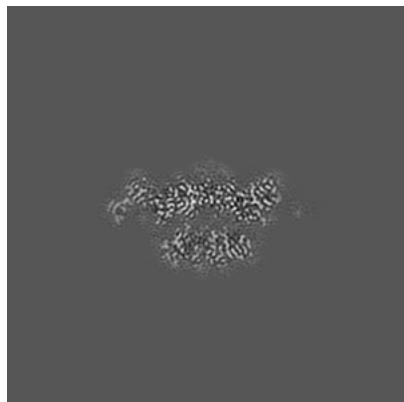
6.2.1 Primary map



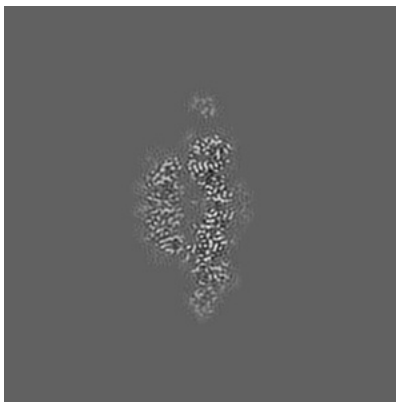
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

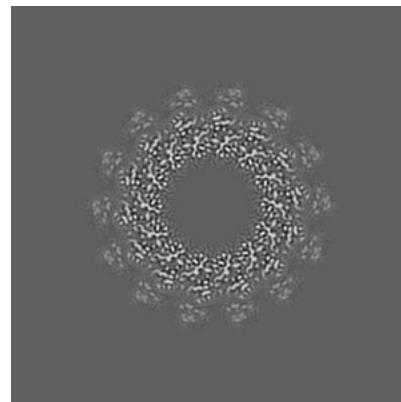
6.3.1 Primary map



X Index: 129



Y Index: 131

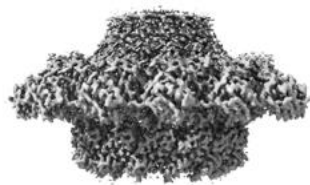


Z Index: 180

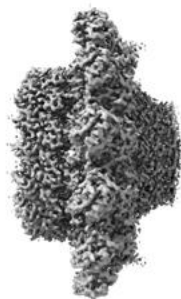
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

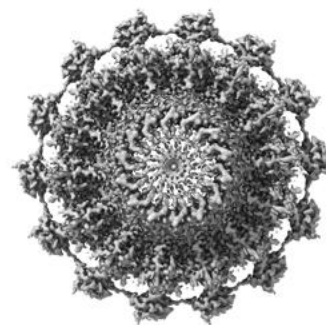
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.035. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

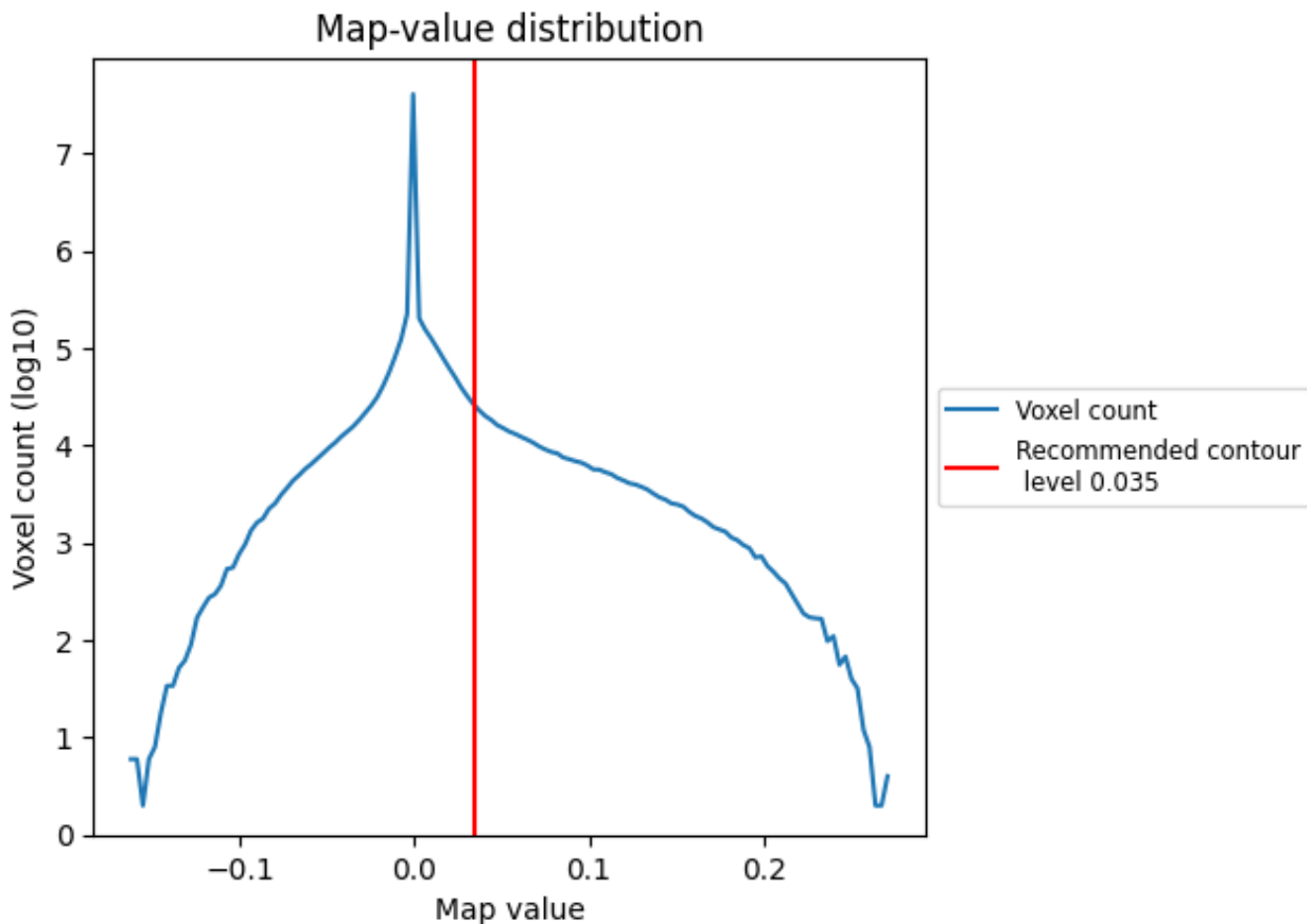
6.5 Mask visualisation

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

7 Map analysis [i](#)

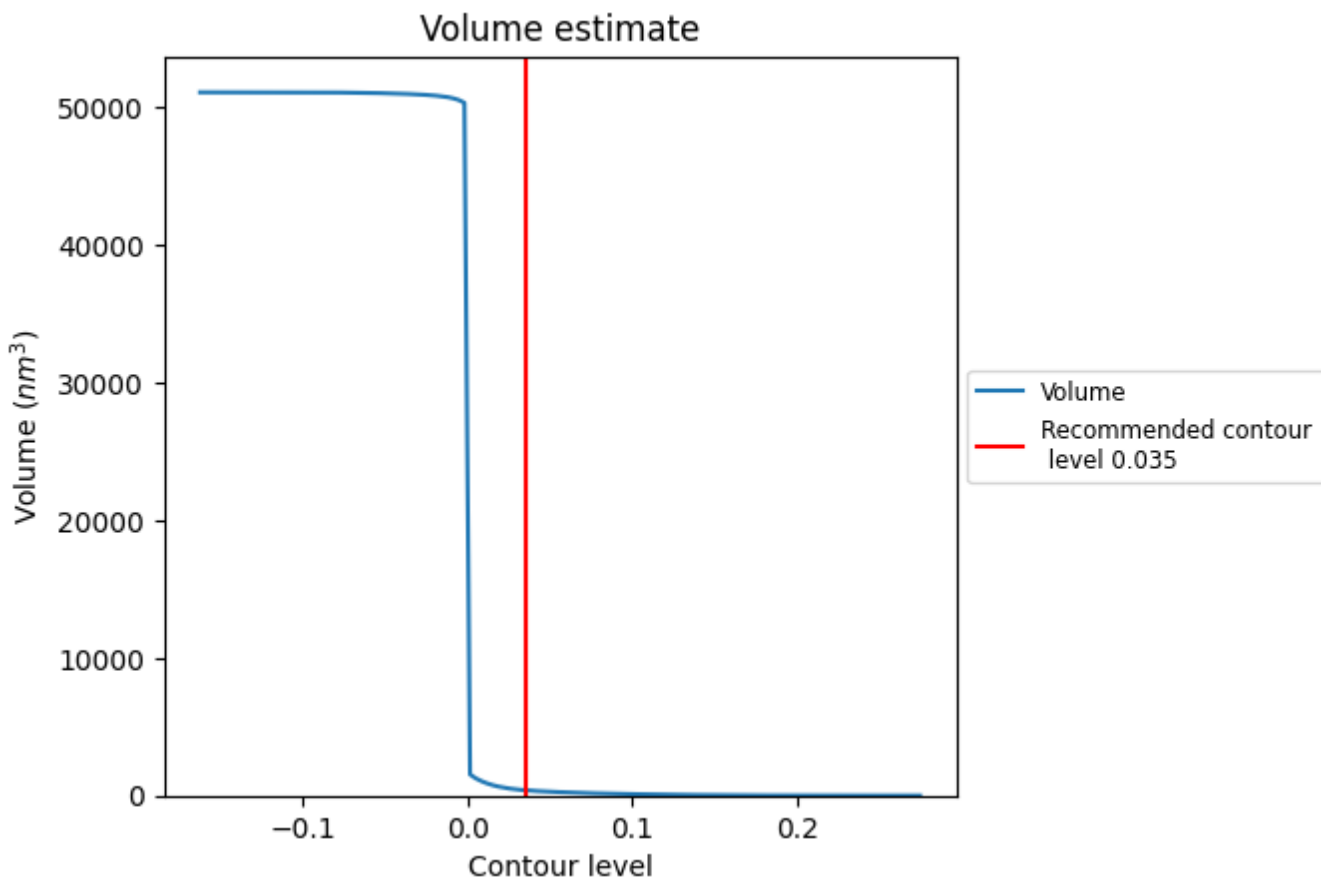
This section contains the results of statistical analysis of the map.

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.

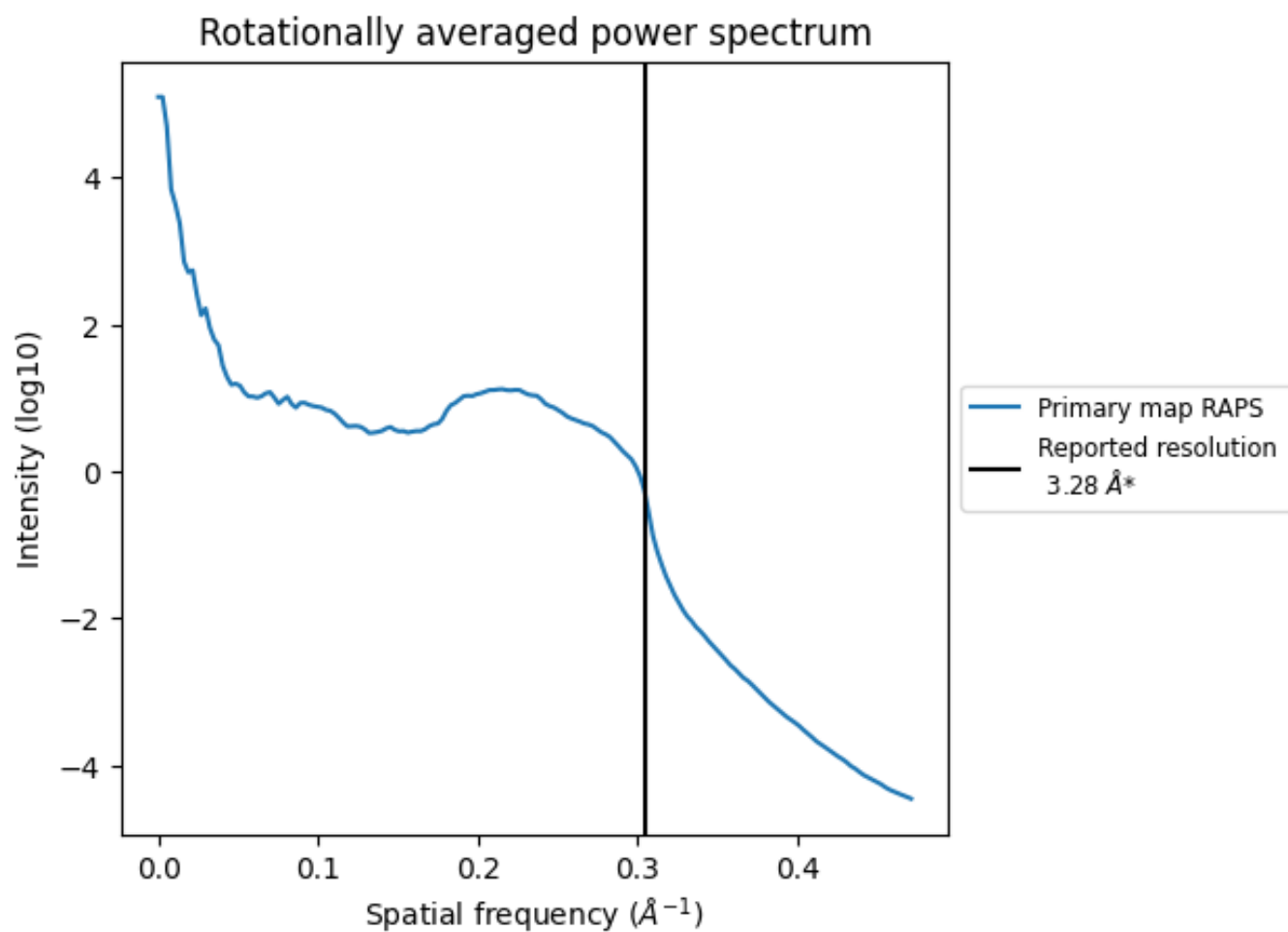
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 387 nm³; this corresponds to an approximate mass of 350 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](#)

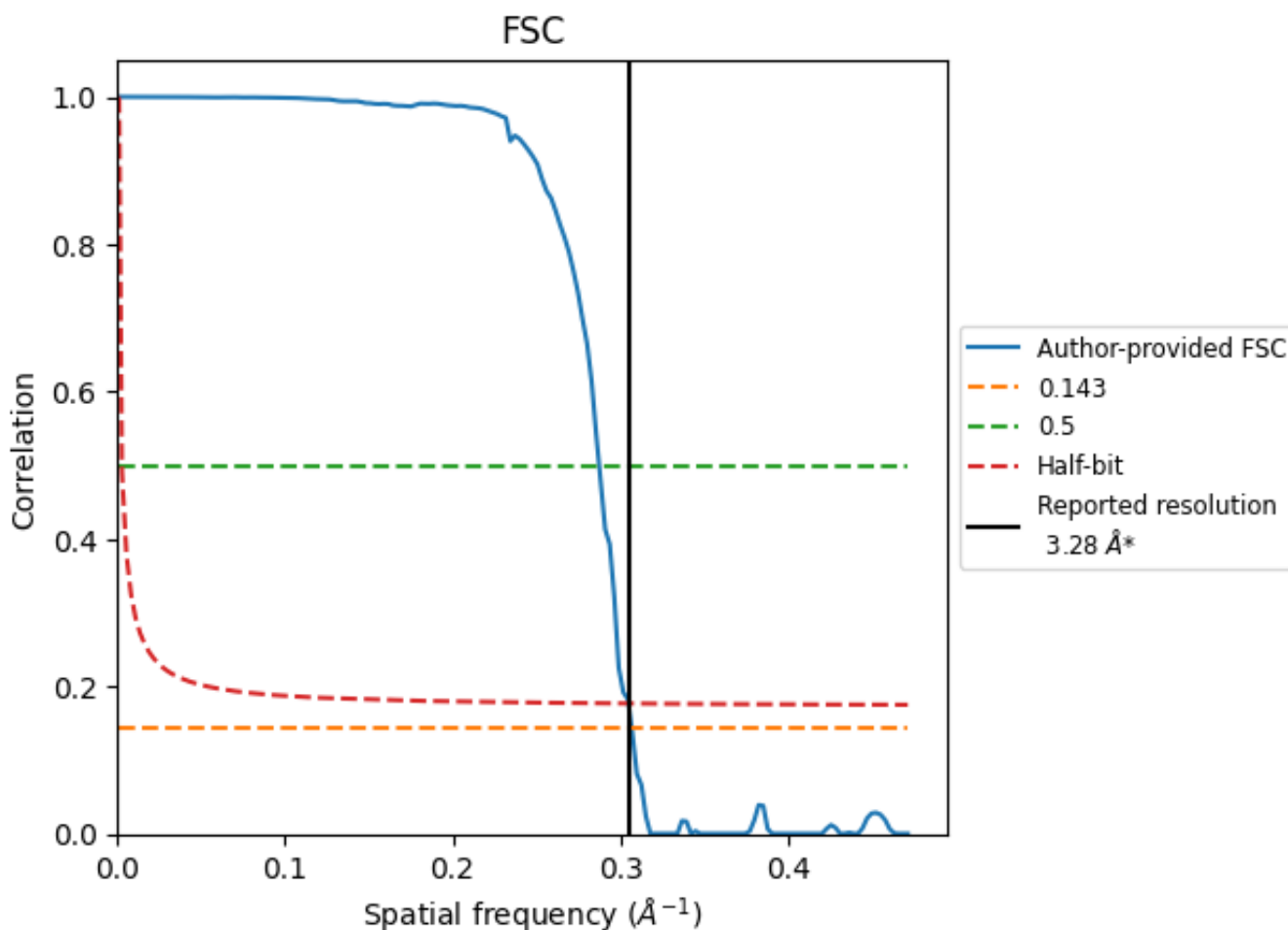


*Reported resolution corresponds to spatial frequency of 0.305 Å⁻¹

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 0.305 Å⁻¹

8.2 Resolution estimates [i](#)

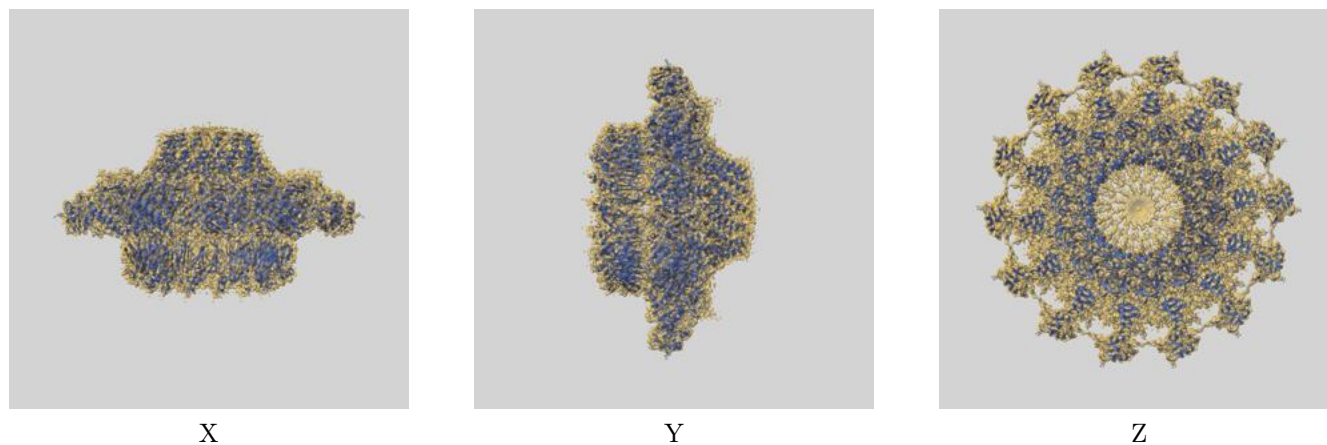
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.28	-	-
Author-provided FSC curve	3.26	3.48	3.28
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

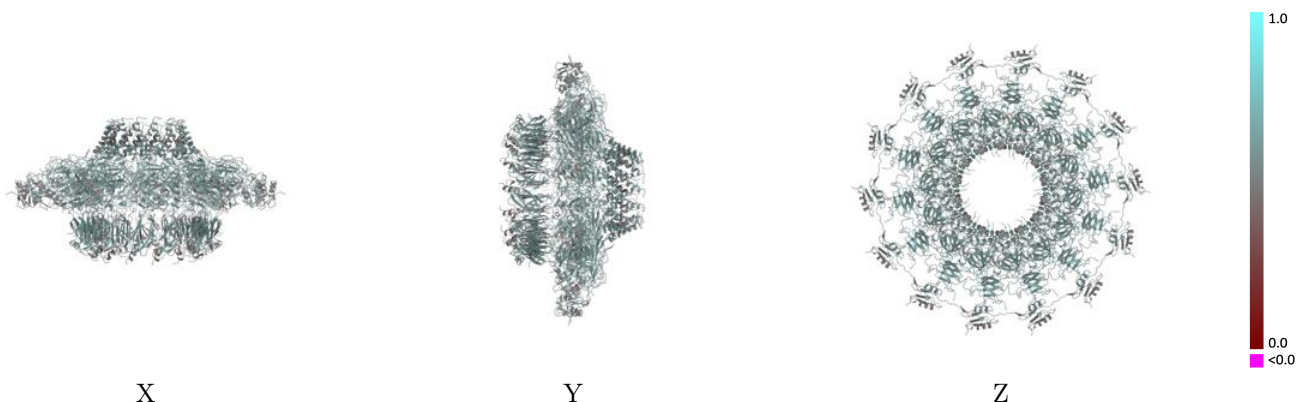
This section contains information regarding the fit between EMDB map EMD-0089 and PDB model 6GYB. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)



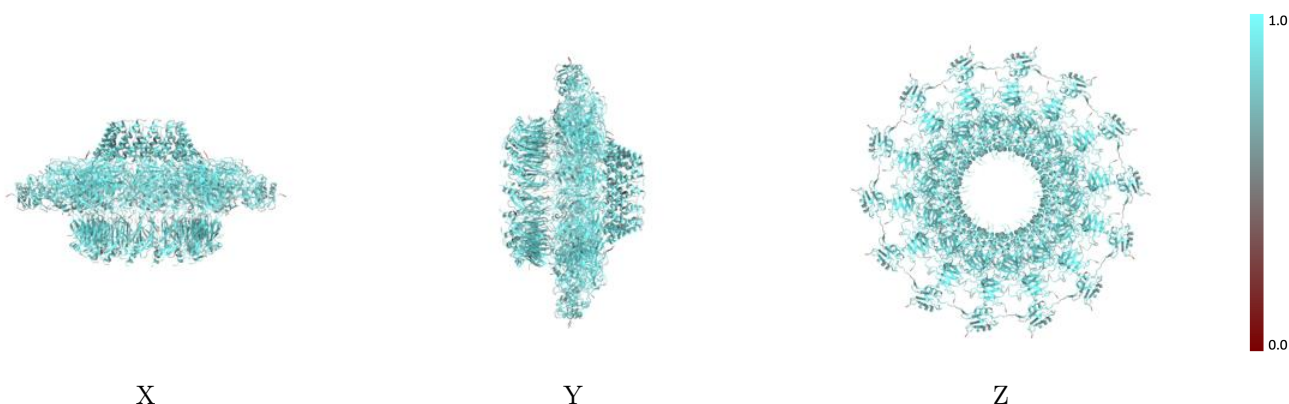
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



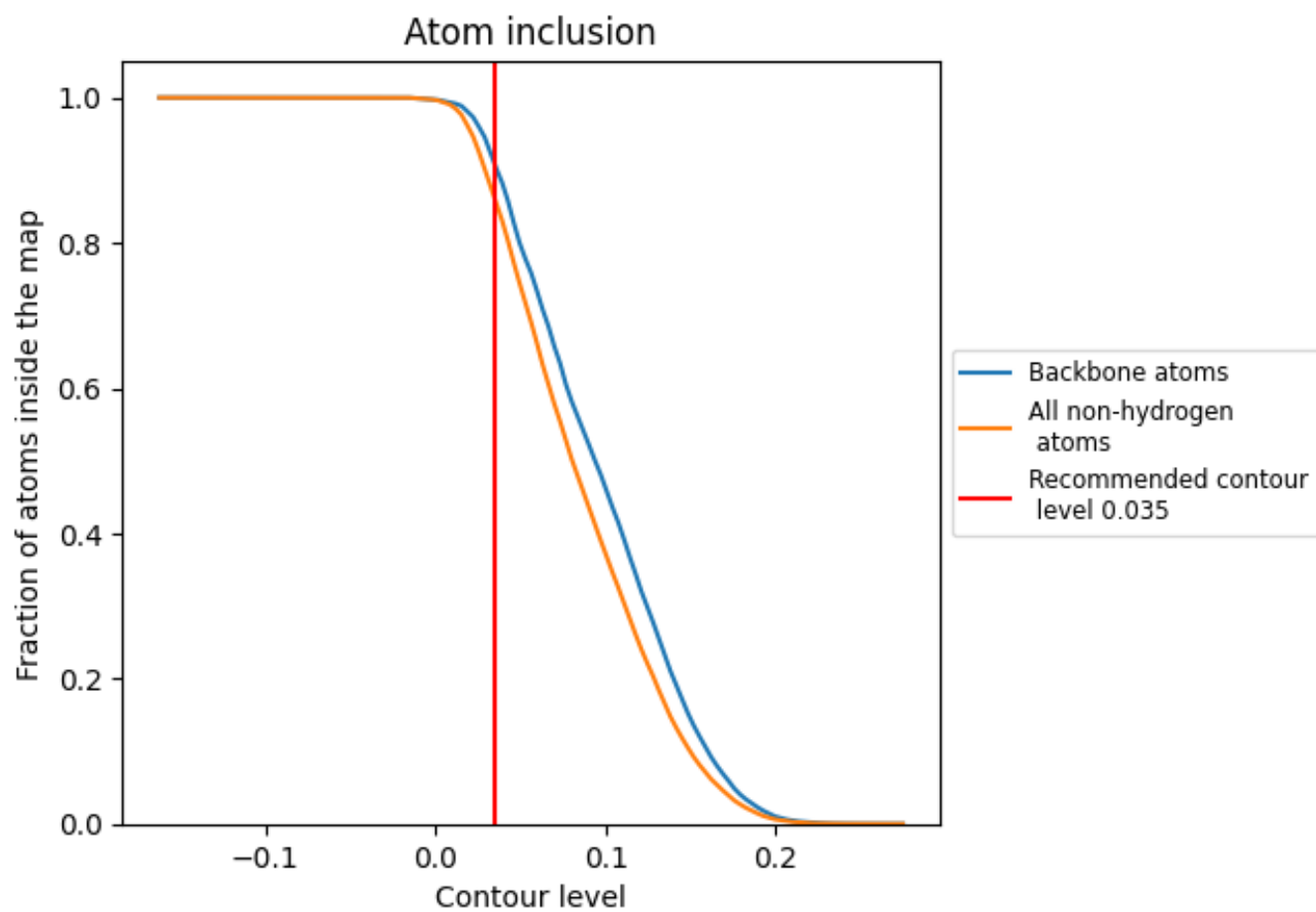
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.035).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 86% 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 (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8584	 0.5530
A	 0.7687	 0.5250
B	 0.8716	 0.5600
C	 0.8892	 0.5590
D	 0.7699	 0.5210
E	 0.8727	 0.5580
F	 0.8931	 0.5600
G	 0.7699	 0.5210
H	 0.8738	 0.5590
I	 0.8898	 0.5610
J	 0.7675	 0.5210
K	 0.8749	 0.5590
L	 0.8866	 0.5590
M	 0.7651	 0.5220
N	 0.8721	 0.5600
O	 0.8872	 0.5610
P	 0.7675	 0.5200
Q	 0.8760	 0.5600
R	 0.8872	 0.5610
S	 0.7711	 0.5200
T	 0.8733	 0.5610
U	 0.8911	 0.5590
a	 0.7687	 0.5230
b	 0.8716	 0.5630
c	 0.8898	 0.5590
d	 0.7699	 0.5210
e	 0.8727	 0.5630
f	 0.8931	 0.5580
g	 0.7699	 0.5240
h	 0.8738	 0.5630
i	 0.8898	 0.5600
j	 0.7675	 0.5210
k	 0.8749	 0.5620
l	 0.8866	 0.5590
m	 0.7651	 0.5240



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Chain	Atom inclusion	Q-score
n	 0.8721	 0.5610
o	 0.8911	 0.5600
p	 0.7675	 0.5230
q	 0.8760	 0.5600
r	 0.8879	 0.5590
s	 0.7711	 0.5220
t	 0.8733	 0.5600
u	 0.8905	 0.5590