



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 05:18 AM UTC

PDB ID : 6GYB / pdb_00006gyb
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 wwPDB EM Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

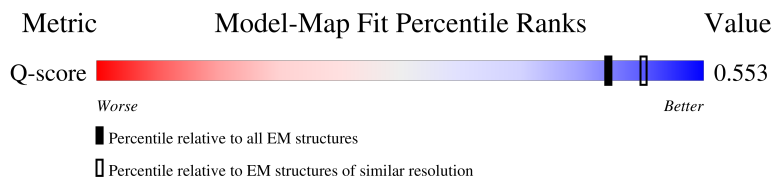
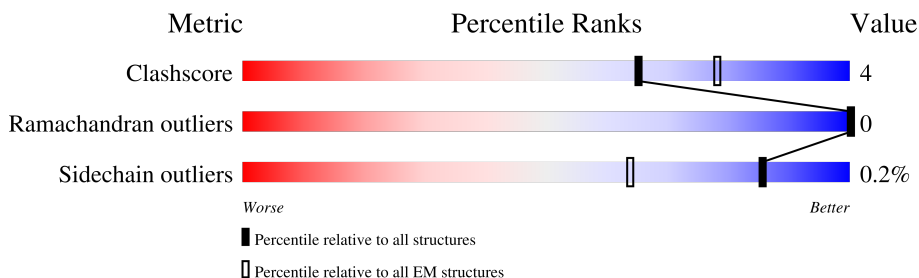
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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.



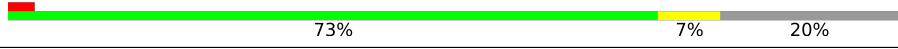
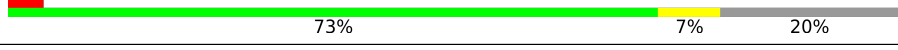
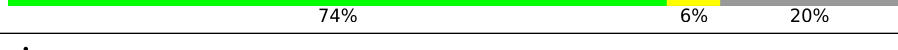
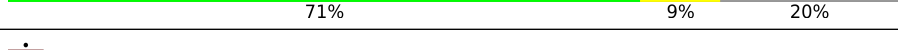
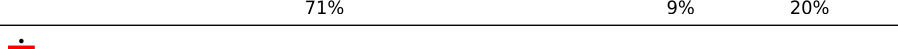
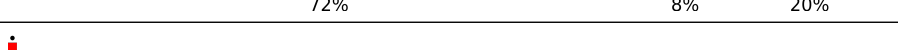
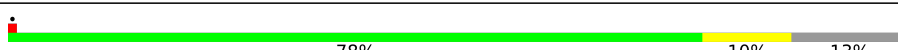
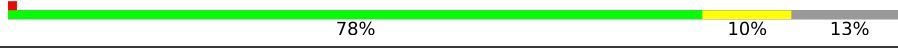
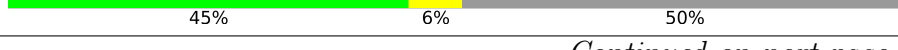
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14492 (2.78 - 3.78)

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	 73% 6% 20%
1	D	139	 72% 8% 20%
1	G	139	 72% 8% 20%
1	J	139	 73% 6% 20%

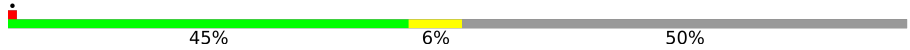
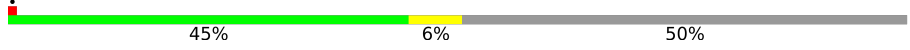
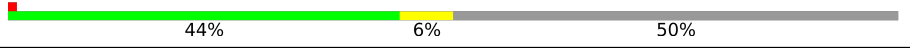
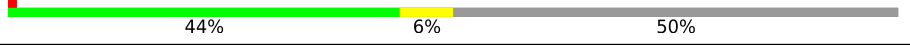
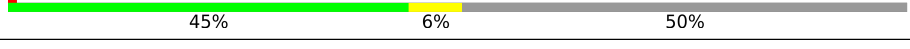
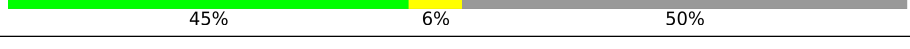
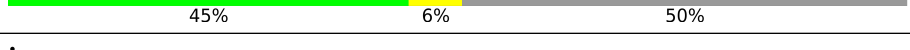
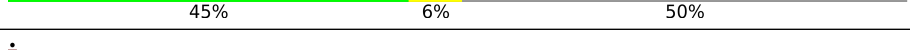
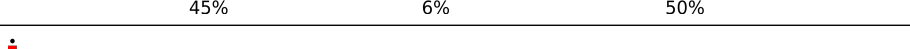
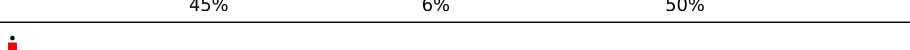
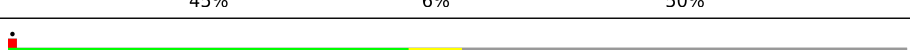
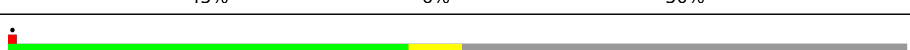
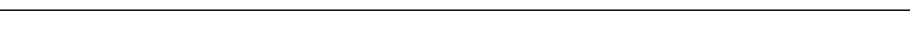
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Mol	Chain	Length	Quality of chain
1	M	139	
1	P	139	
1	S	139	
1	a	139	
1	d	139	
1	g	139	
1	j	139	
1	m	139	
1	p	139	
1	s	139	
2	B	255	
2	E	255	
2	H	255	
2	K	255	
2	N	255	
2	Q	255	
2	T	255	
2	b	255	
2	e	255	
2	h	255	
2	k	255	
2	n	255	
2	q	255	
2	t	255	
3	C	406	

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Mol	Chain	Length	Quality of chain
3	F	406	
3	I	406	
3	L	406	
3	O	406	
3	R	406	
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
1	a	111	Total	C	N	O	S	0	0
			842	534	137	167	4		
1	d	111	Total	C	N	O	S	0	0
			842	534	137	167	4		
1	g	111	Total	C	N	O	S	0	0
			842	534	137	167	4		
1	j	111	Total	C	N	O	S	0	0
			842	534	137	167	4		
1	m	111	Total	C	N	O	S	0	0
			842	534	137	167	4		
1	p	111	Total	C	N	O	S	0	0
			842	534	137	167	4		
1	s	111	Total	C	N	O	S	0	0
			842	534	137	167	4		
1	A	111	Total	C	N	O	S	0	0
			842	534	137	167	4		
1	D	111	Total	C	N	O	S	0	0
			842	534	137	167	4		
1	G	111	Total	C	N	O	S	0	0
			842	534	137	167	4		
1	J	111	Total	C	N	O	S	0	0
			842	534	137	167	4		
1	M	111	Total	C	N	O	S	0	0
			842	534	137	167	4		
1	P	111	Total	C	N	O	S	0	0
			842	534	137	167	4		
1	S	111	Total	C	N	O	S	0	0
			842	534	137	167	4		

- Molecule 2 is a protein called VirB9 protein.

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

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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
3	u	205	Total	C	N	O	S	0	0
			1555	985	268	297	5		
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		
3	U	205	Total	C	N	O	S	0	0
			1555	985	268	297	5		

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: 



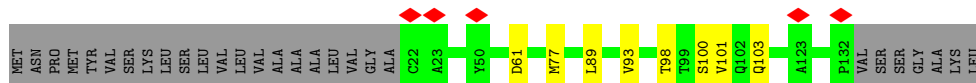
- Molecule 1: VirB7

Chain d: 



- Molecule 1: VirB7

Chain g: 



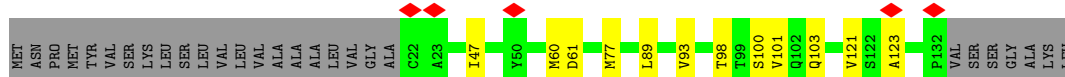
- Molecule 1: VirB7

Chain j: 

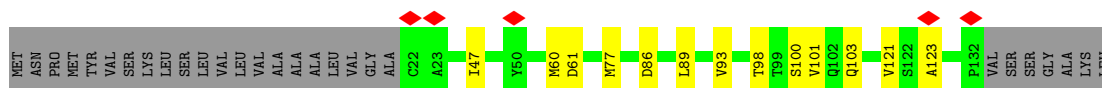


- Molecule 1: VirB7

Chain m: 



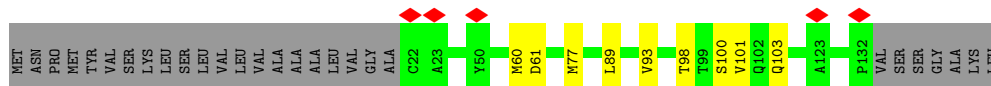
● Molecule 1: VirB7

Chain p:  71% 9% 20%

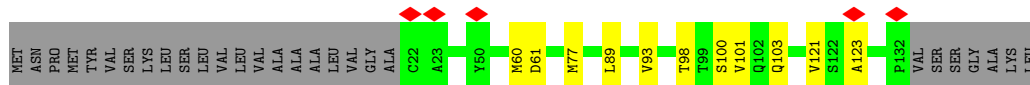
● Molecule 1: VirB7

Chain s:  72% 8% 20%

● Molecule 1: VirB7

Chain A:  73% 6% 20%

● Molecule 1: VirB7

Chain D:  72% 8% 20%

● Molecule 1: VirB7

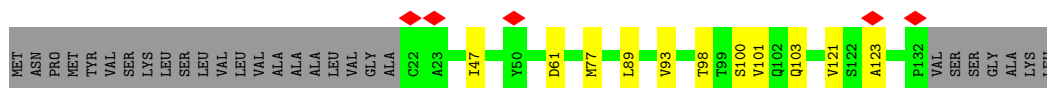
Chain G:  72% 8% 20%

● Molecule 1: VirB7

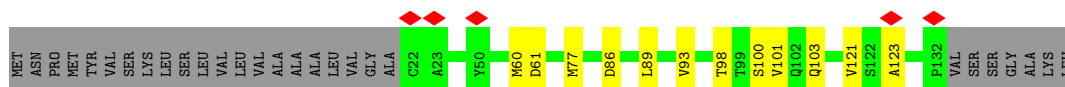
Chain J:  73% 6% 20%

● Molecule 1: VirB7

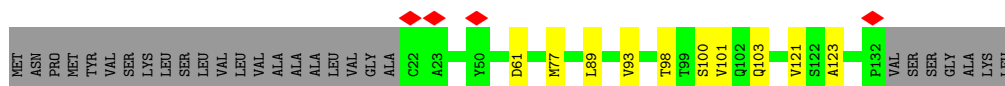
Chain M:  72% 8% 20%



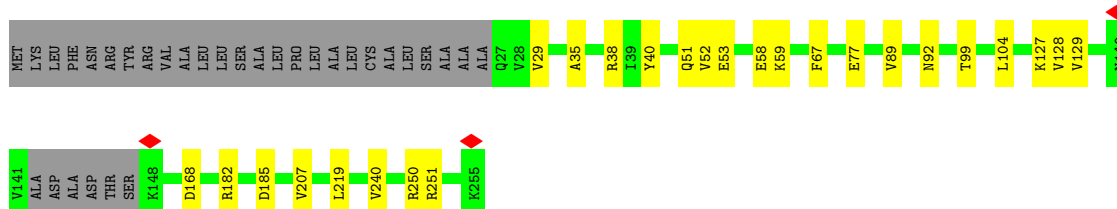
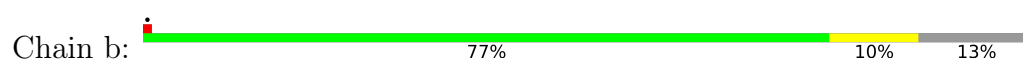
- Molecule 1: VirB7



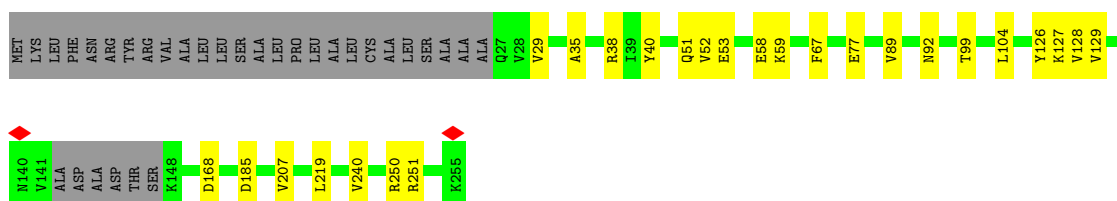
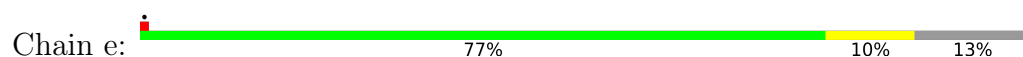
- Molecule 1: VirB7



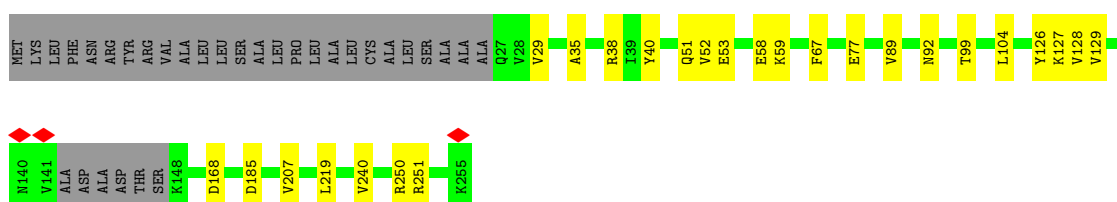
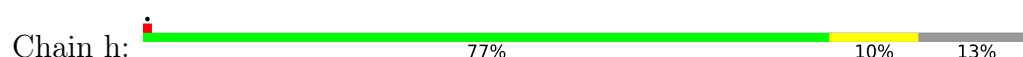
- Molecule 2: VirB9 protein



- Molecule 2: VirB9 protein

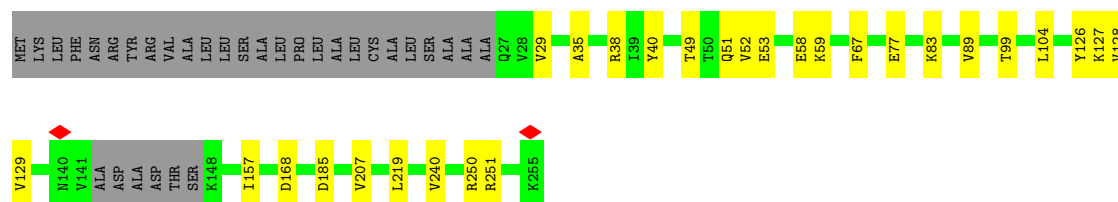


- Molecule 2: VirB9 protein



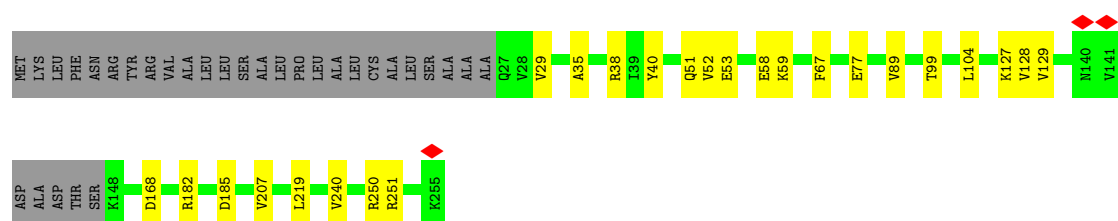
- Molecule 2: VirB9 protein

Chain k:  76% 11% 13%



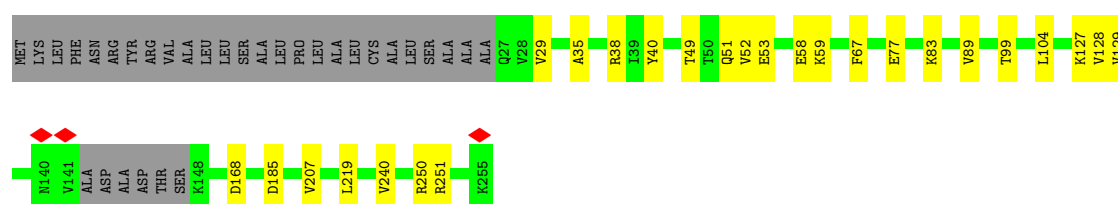
- Molecule 2: VirB9 protein

Chain n:  78% 10% 13%



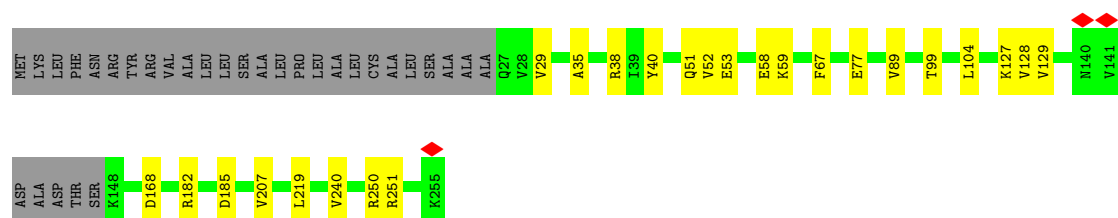
- Molecule 2: VirB9 protein

Chain q:  77% 10% 13%



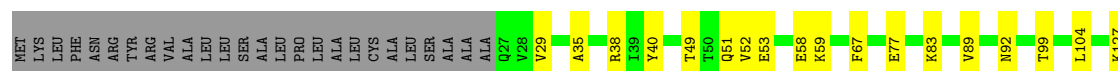
- Molecule 2: VirB9 protein

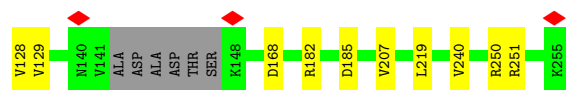
Chain t:  78% 10% 13%



- Molecule 2: VirB9 protein

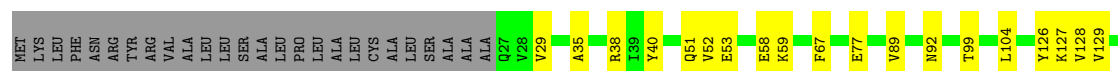
Chain B:  76% 11% 13%





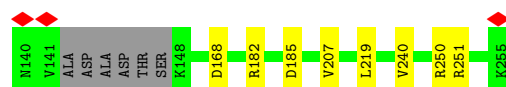
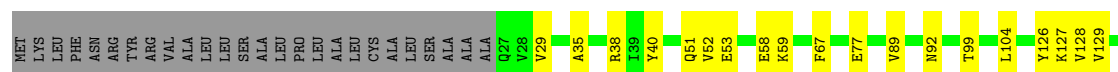
- Molecule 2: VirB9 protein

Chain E: 77% 11% 13%



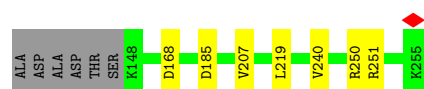
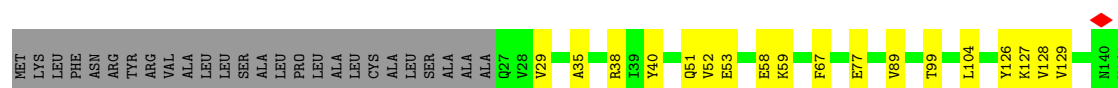
- Molecule 2: VirB9 protein

Chain H: 77% 11% 13%



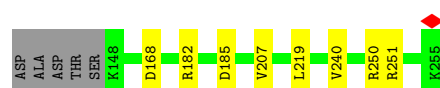
- Molecule 2: VirB9 protein

Chain K: 78% 10% 13%



- Molecule 2: VirB9 protein

Chain N: 78% 10% 13%



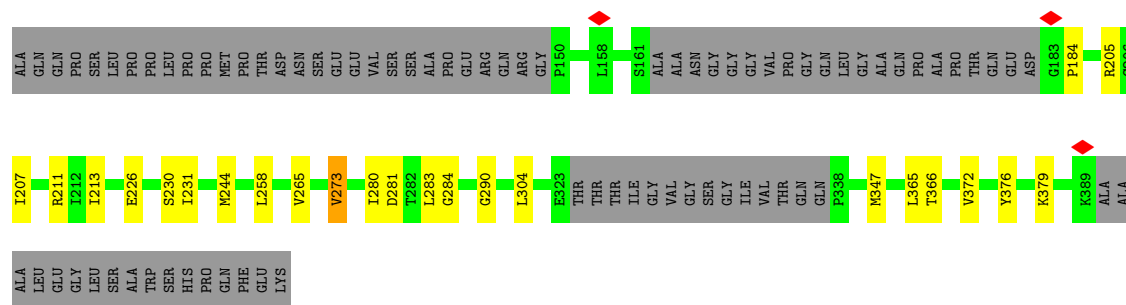
- Molecule 2: VirB9 protein

V141	ALA	ASP	ALA	ASP	THR	SER	K148	D168	D185	V207	L219	V240	R250	R251	K255
------	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------

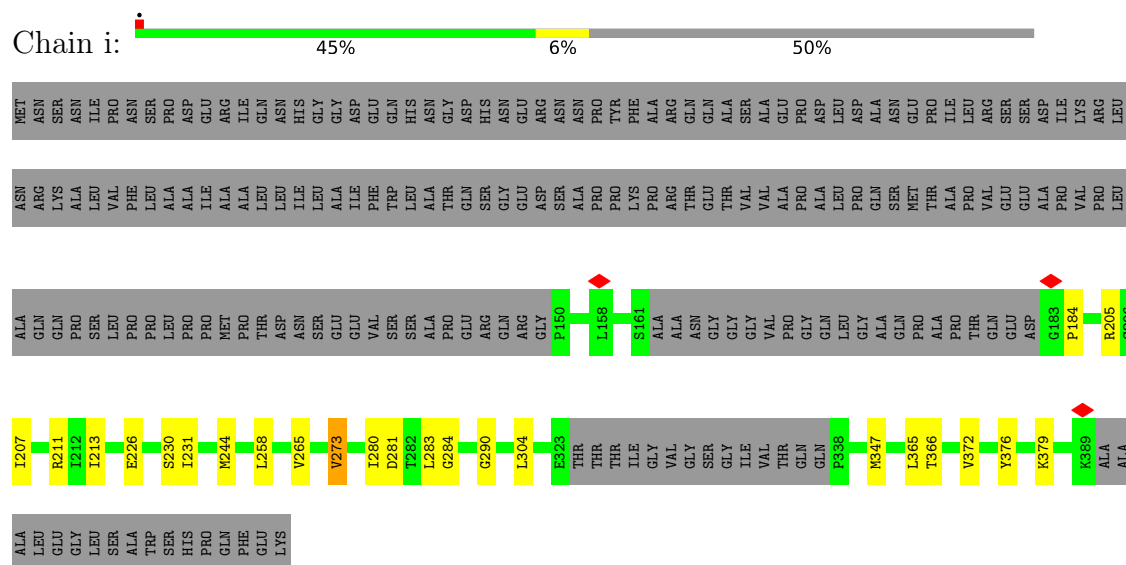
ALA	ASP	ALA	ASP	THR	SER	K148	D168	D185	V207	L219	V240	R250	R251	K255		ALA	ALA	ALA	SER	LEU	ALA	CYS	LEU	ALA	LEU	ALA	ALA	ALA	Q27	V28	V29	A35	R38	I39	Y40	Q51	V52	E53	E58	K59	F67	E77	V89	T99	L104	Y126	K127	V128	V129	N140
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ALA	T207	ALA	ASN	MET
LEU		GLN	ARG	
GLU	R211	GLN	LYS	ASN
GLY	T212	PRO	ALA	
LEU	T213	SER	LEU	ILE
SER		LEU	VAL	PRO
ALA	E226	PRO	PHE	ASN
ALA		PRO	LEU	SER
TRP	S230	LEU	ALA	PRO
SER		PRO	ASP	ASP
HIS	T231	PRO	ILE	GLU
PRO		PRO	ALA	ARG
GLN	R244	MET	ALA	
GLU		PRO	ILE	ILE
PHE	L258	THR	LEU	GLN
GLY		ASP	LEU	ASN
LYS		ASN	ILE	HIS
	V265	SER	LEU	GLY
		GLU	ALA	GLY
	V273	GLU	ILE	ASP
		VAL	PHE	GLU
T280		SER	TRP	GLN
D281		SER	LEU	HIS
T282		ALA	ALA	ASN
L283		PRO	THR	GLY
G284		GLU	GLN	ASP
		ARG	SER	HIS
	G290	GLN	GLY	ASN
		ARG	GLU	GLU
	L304	GLY	ASP	ARG
		P150	SER	ASN
	E323		ALA	ASN
THR			PRO	PRO
THR		L158	PRO	TYR
THR			LYS	PHE
ILE		S161	PRO	ALA
GLY		ALA	ARG	ARG
VAL		ALA	THR	GLN
GLY		ASN	GLU	GLN
SER		GLY	THR	ALA
GLY		GLY	VAL	SER
ILE		GLY	VAL	ALA
VAL		VAL	ALA	GLU
THR		PRO	PRO	PRO
GLN		GLY	ALA	ASP
GLN		GLN	LEU	LEU
	F338	GLY	PRO	ASP
		ALA	GLN	ASN
	R347	GLN	SER	ASN
		PRO	MET	GLU
L366		THR	THR	GLU
	T366	ALA	ALA	ILE
		PRO	PRO	LEU
	V372	THR	VAL	ARG
		GLN	GLU	SER
	Y376	GLU	GLU	SER
		ASP	ALA	ASP
	K379	G183	VAL	ILE
		P184	PRO	LYS
	K389		VAL	LYS
			LEU	ARG
ALA		R205	PRO	LEU
ALA			LEU	ARG

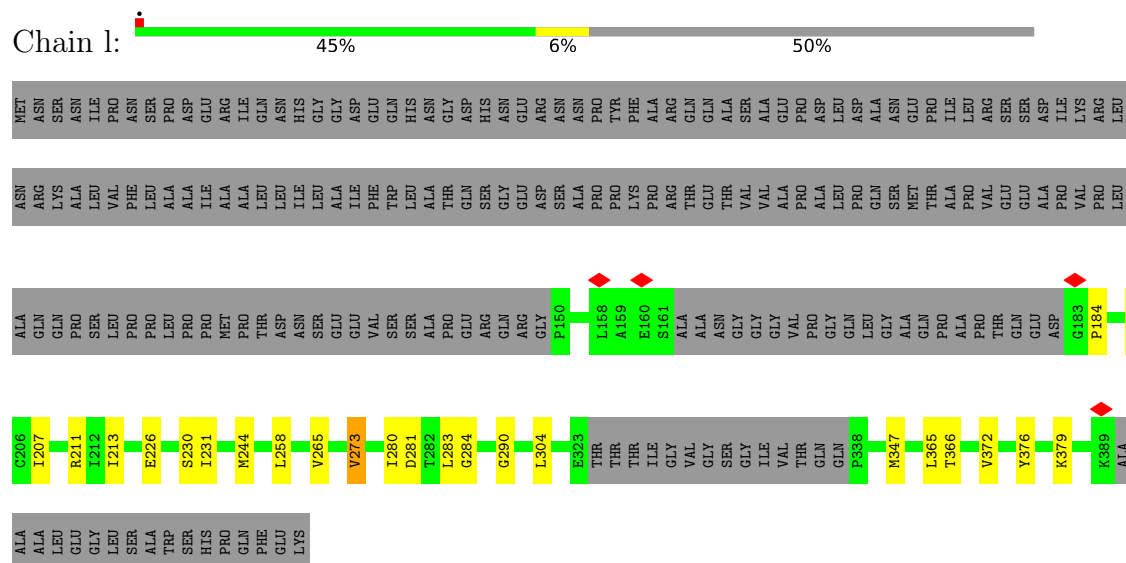
ASV	ARG	LVS	ALA	VAL	PHE	LEU	ALA	ALA	ILE	ALA	ALA	ILE	ALA	ILE	THR	GLN	GLY	ASP	GLY	GLN	ASP	ASN	HIS	GLU	ASP	ARG	ASN	ASN	PRO	PRO	THR	PHE	ALA	ARG	GLN	GLN	ALA	ALA	VAL	VAL	ALA	ALA	PRO	ALA	ALA	LEU	PRO	PRO	VAL	GLU	GLU	ALA	THR	THR	ALA	PRO	VAL	PRO	PRO	LEU
MET	ASN	SER	ASN	ILE	PRO	SER	ASP	GLU	ARG	ILE	GLN	HIS	GLY	GLY	THR	GLN	ASP	HIS	ASN	ARG	ASN	ASN	PRO	THR	ALA	ALA	ARG	GLN	GLN	ALA	ALA	SER	ALA	ALA	GLU	PRO	ASP	LEU	ASP	ASN	ASN	ILE	LEU	ARG	SER	SER	ASP	GLU	PRO	THR	ILE	LEU	ARG	LEU						



- Molecule 3: VirB10 protein



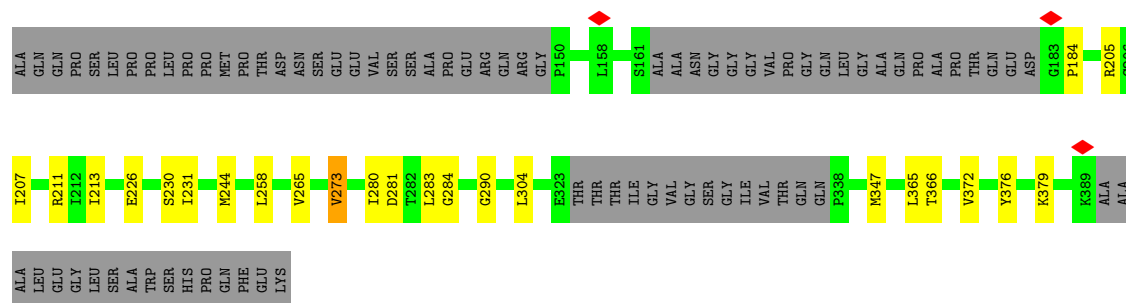
- Molecule 3: VirB10 protein



- Molecule 3: VirB10 protein

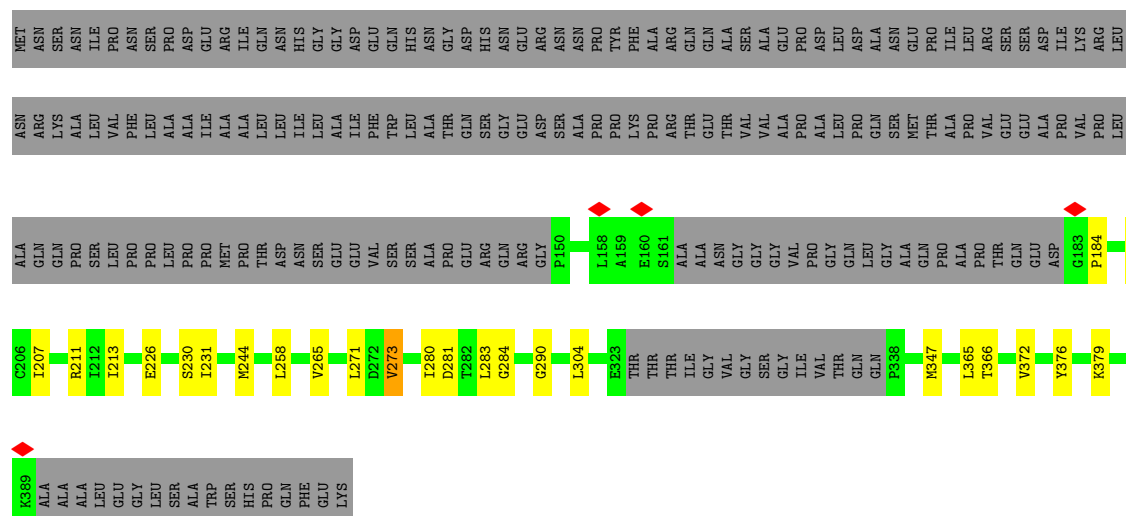


ASN	ARG	LYS	LEU	LEU	VAL	PHE	LEU	ALA	ALA	ILE	ALA	ALA	LEU	LEU	ILE	LEU	ALA	THR	GLN	SER	GLY	ASP	SER	ALA	PRO	PRO	LYS	PRO	ARG	THR	GLU	THR	VAL	VAL	ALA	ALA	ALA	LEU	PRO	GLN	SER	MET	THR	ALA	ALA	PRO	VAL	VAL	PRO	LEU	PRO	THR	GLU	GLU	ASN
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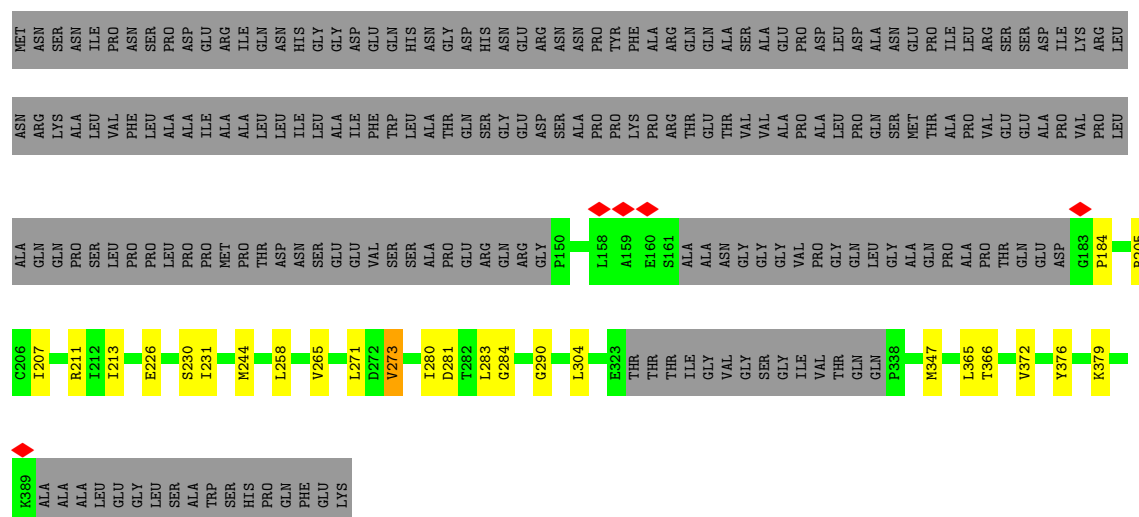
• Molecule 3: VirB10 protein

Chain L: 44% 6% 50%

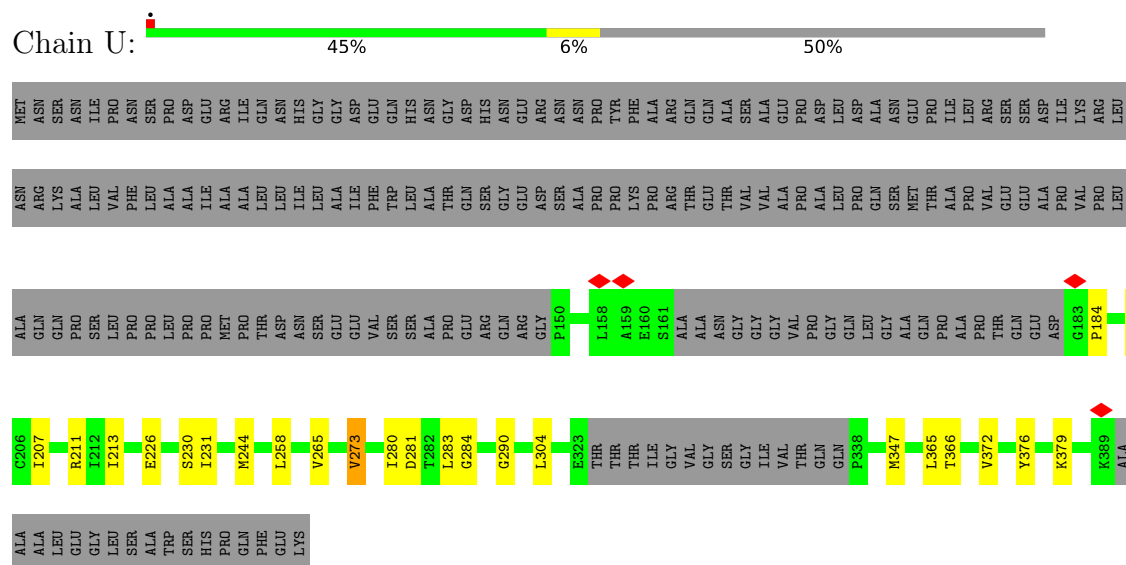


• Molecule 3: VirB10 protein

Chain O: 44% 6% 50%



• Molecule 3: VirB10 protein



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

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.21	0/864	0.44	0/1186
1	D	0.21	0/864	0.44	0/1186
1	G	0.21	0/864	0.44	0/1186
1	J	0.21	0/864	0.45	0/1186
1	M	0.21	0/864	0.44	0/1186
1	P	0.21	0/864	0.44	0/1186
1	S	0.21	0/864	0.45	0/1186
1	a	0.21	0/864	0.44	0/1186
1	d	0.21	0/864	0.44	0/1186
1	g	0.21	0/864	0.44	0/1186
1	j	0.21	0/864	0.44	0/1186
1	m	0.21	0/864	0.44	0/1186
1	p	0.21	0/864	0.44	0/1186
1	s	0.21	0/864	0.45	0/1186
2	B	0.35	0/1883	0.51	0/2554
2	E	0.35	0/1883	0.51	0/2554
2	H	0.35	0/1883	0.51	0/2554
2	K	0.35	0/1883	0.51	0/2554
2	N	0.34	0/1883	0.51	0/2554
2	Q	0.34	0/1883	0.51	0/2554
2	T	0.34	0/1883	0.51	0/2554
2	b	0.35	0/1883	0.51	0/2554
2	e	0.35	0/1883	0.51	0/2554
2	h	0.34	0/1883	0.51	0/2554
2	k	0.34	0/1883	0.51	0/2554
2	n	0.35	0/1883	0.51	0/2554
2	q	0.34	0/1883	0.51	0/2554
2	t	0.35	0/1883	0.51	0/2554
3	C	0.37	0/1587	0.53	0/2157
3	F	0.37	0/1587	0.53	0/2157
3	I	0.37	0/1587	0.53	0/2157
3	L	0.37	0/1587	0.53	0/2157
3	O	0.37	0/1587	0.53	0/2157
3	R	0.37	0/1587	0.53	0/2157

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	U	0.37	0/1587	0.53	0/2157
3	c	0.37	0/1587	0.53	0/2157
3	f	0.37	0/1587	0.53	0/2157
3	i	0.37	0/1587	0.53	0/2157
3	l	0.37	0/1587	0.53	0/2157
3	o	0.37	0/1587	0.52	0/2157
3	r	0.37	0/1587	0.53	0/2157
3	u	0.37	0/1587	0.53	0/2157
All	All	0.33	0/60676	0.50	0/82558

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

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	842	0	819	6	0
1	D	842	0	819	7	0
1	G	842	0	819	7	0
1	J	842	0	819	6	0
1	M	842	0	819	7	0
1	P	842	0	819	8	0
1	S	842	0	819	6	0
1	a	842	0	819	6	0
1	d	842	0	819	6	0
1	g	842	0	819	5	0
1	j	842	0	819	5	0
1	m	842	0	819	8	0
1	p	842	0	819	9	0
1	s	842	0	819	7	0
2	B	1840	0	1817	16	0
2	E	1840	0	1817	16	0
2	H	1840	0	1817	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	K	1840	0	1817	14	0
2	N	1840	0	1817	14	0
2	Q	1840	0	1817	14	0
2	T	1840	0	1817	14	0
2	b	1840	0	1817	15	0
2	e	1840	0	1817	15	0
2	h	1840	0	1817	15	0
2	k	1840	0	1817	16	0
2	n	1840	0	1817	14	0
2	q	1840	0	1817	14	0
2	t	1840	0	1817	14	0
3	C	1555	0	1559	18	0
3	F	1555	0	1559	18	0
3	I	1555	0	1559	17	0
3	L	1555	0	1559	18	0
3	O	1555	0	1559	19	0
3	R	1555	0	1559	19	0
3	U	1555	0	1559	18	0
3	c	1555	0	1559	18	0
3	f	1555	0	1559	19	0
3	i	1555	0	1559	18	0
3	l	1555	0	1559	18	0
3	o	1555	0	1559	17	0
3	r	1555	0	1559	17	0
3	u	1555	0	1559	17	0
All	All	59318	0	58730	477	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 477 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:379:LYS:NZ	3:O:184:PRO:O	2.30	0.64
1:S:98:THR:HG22	1:S:100:SER:H	1.65	0.62
1:a:98:THR:HG22	1:a:100:SER:H	1.65	0.62
1:d:98:THR:HG22	1:d:100:SER:H	1.65	0.62
1:P:98:THR:HG22	1:P:100:SER:H	1.65	0.62

There are no symmetry-related clashes.

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 ⓘ

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%)	169 (99%)	1 (1%)	78	82
3	F	170/331 (51%)	169 (99%)	1 (1%)	78	82
3	I	170/331 (51%)	169 (99%)	1 (1%)	78	82
3	L	170/331 (51%)	169 (99%)	1 (1%)	78	82
3	O	170/331 (51%)	169 (99%)	1 (1%)	78	82
3	R	170/331 (51%)	169 (99%)	1 (1%)	78	82
3	U	170/331 (51%)	169 (99%)	1 (1%)	78	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	c	170/331 (51%)	169 (99%)	1 (1%)	78	82
3	f	170/331 (51%)	169 (99%)	1 (1%)	78	82
3	i	170/331 (51%)	169 (99%)	1 (1%)	78	82
3	l	170/331 (51%)	169 (99%)	1 (1%)	78	82
3	o	170/331 (51%)	169 (99%)	1 (1%)	78	82
3	r	170/331 (51%)	169 (99%)	1 (1%)	78	82
3	u	170/331 (51%)	169 (99%)	1 (1%)	78	82
All	All	6482/9352 (69%)	6468 (100%)	14 (0%)	85	88

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	273	VAL
3	F	273	VAL
3	U	273	VAL
3	O	273	VAL
3	R	273	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
3	R	298	ASN
2	T	51	GLN
2	K	51	GLN
2	K	154	ASN
3	O	298	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

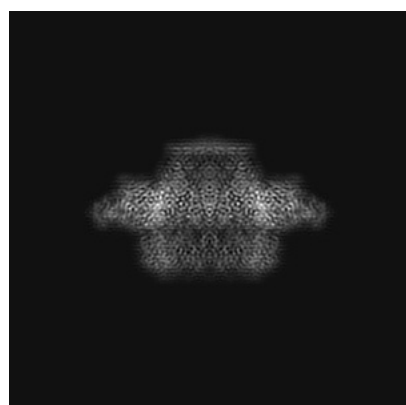
6 Map visualisation [i](#)

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

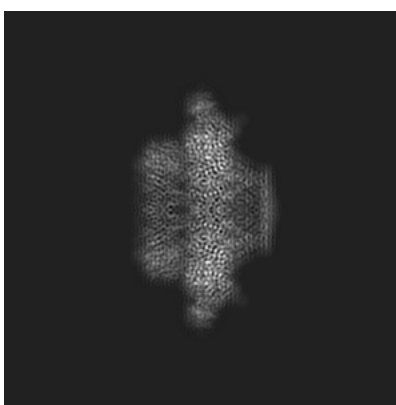
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

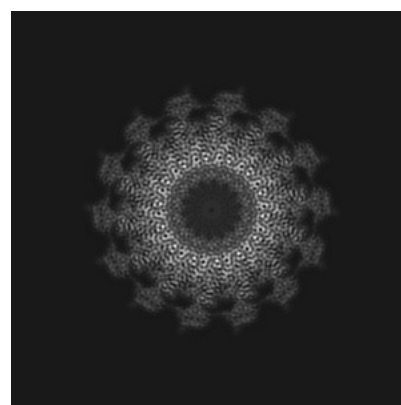
6.1.1 Primary map



X



Y

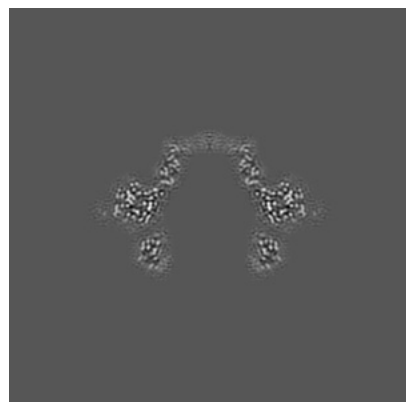


Z

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

6.2 Central slices [i](#)

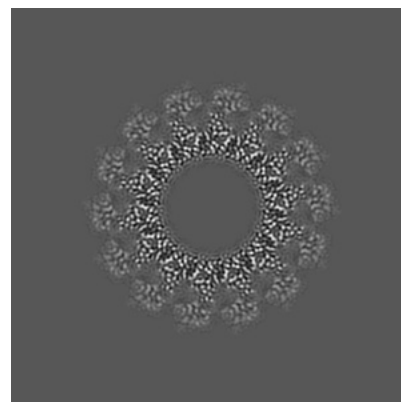
6.2.1 Primary map



X Index: 175



Y Index: 175

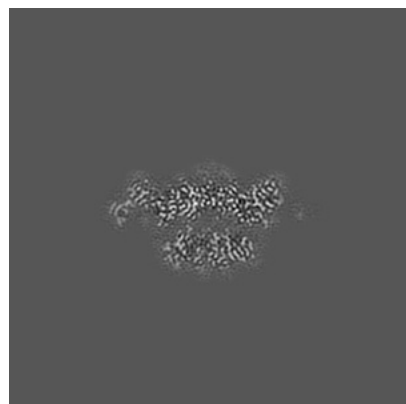


Z Index: 175

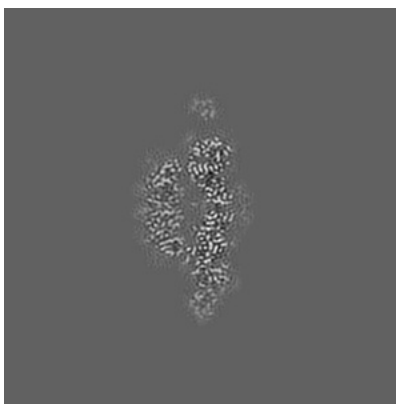
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

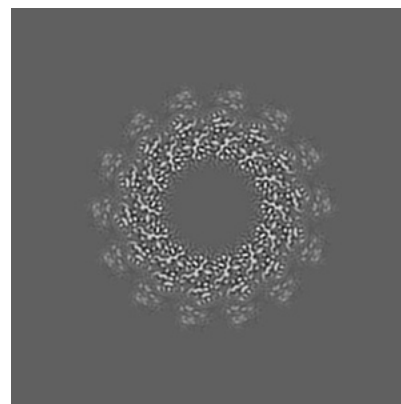
6.3.1 Primary map



X Index: 129



Y Index: 131

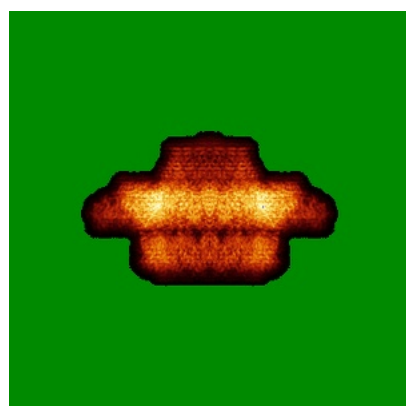


Z Index: 180

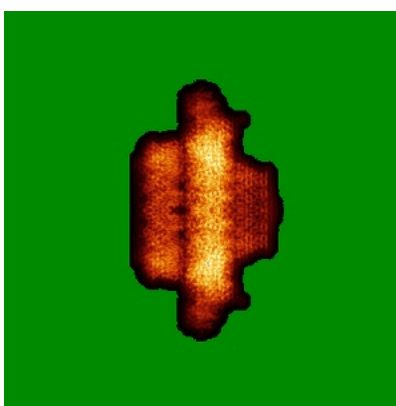
The images above show the largest variance slices of the map in three orthogonal directions.

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

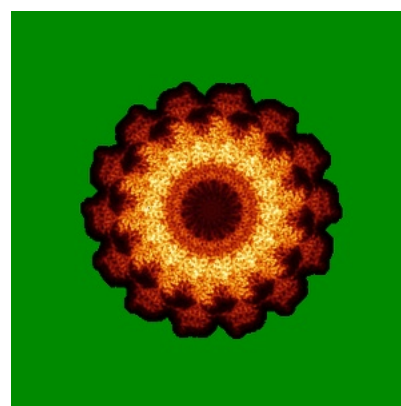
6.4.1 Primary map



X



Y

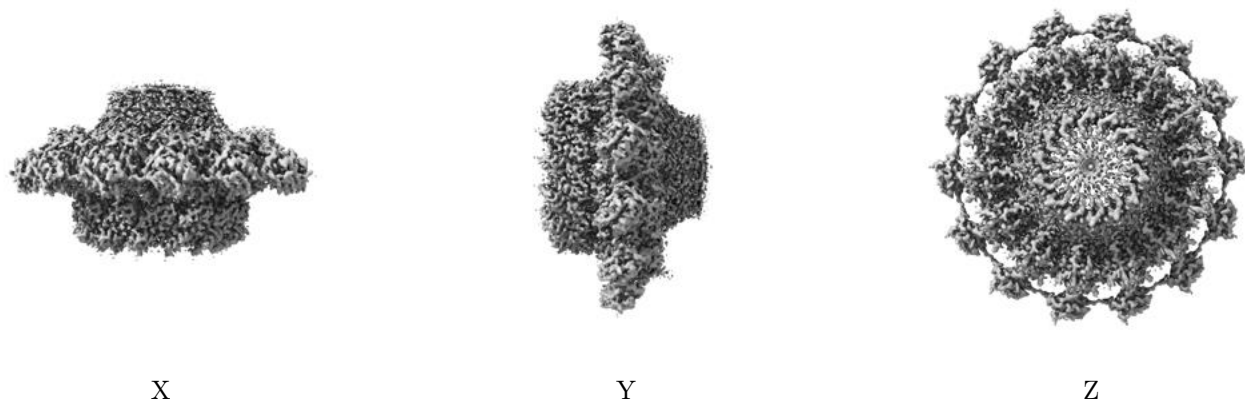


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

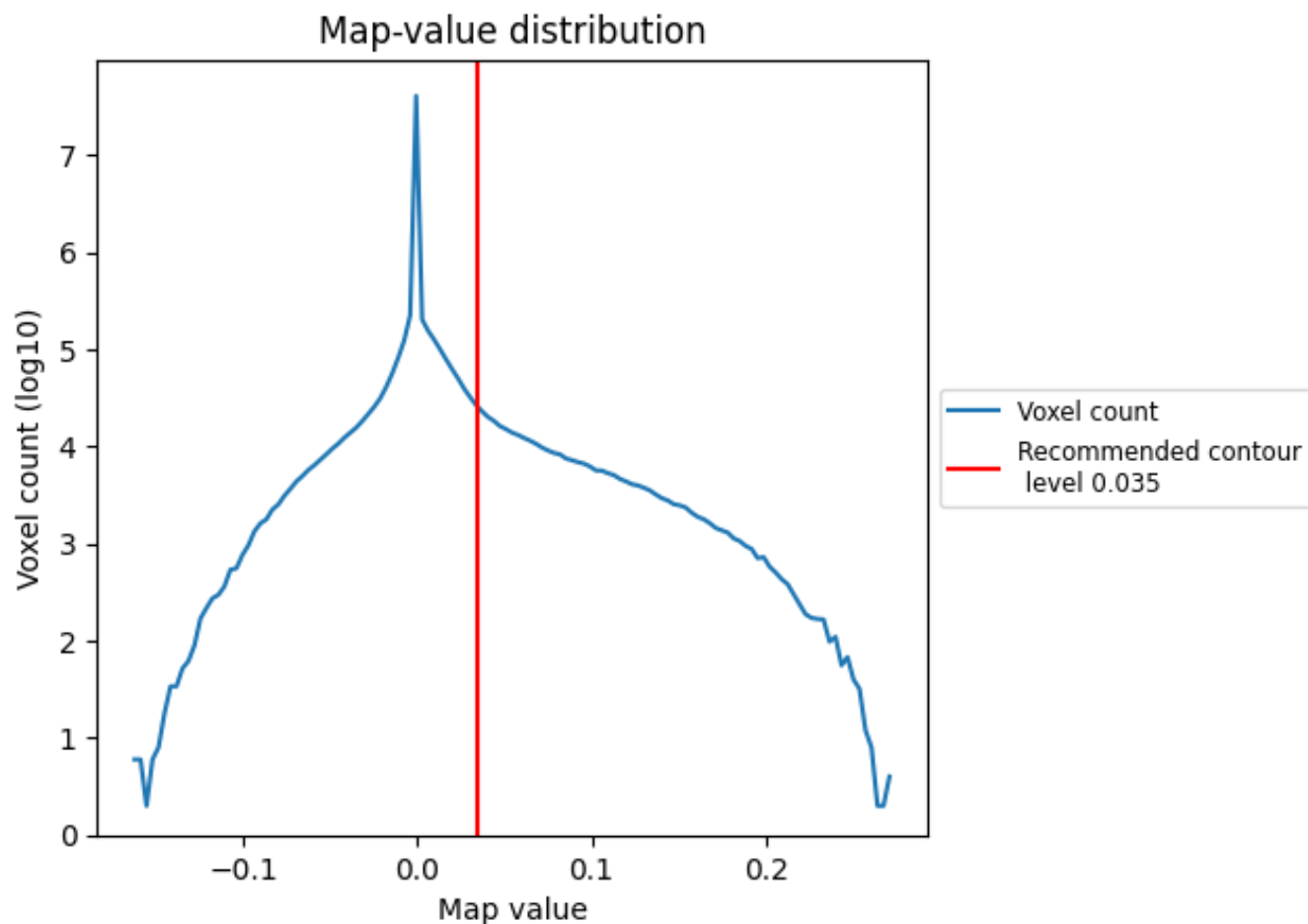
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

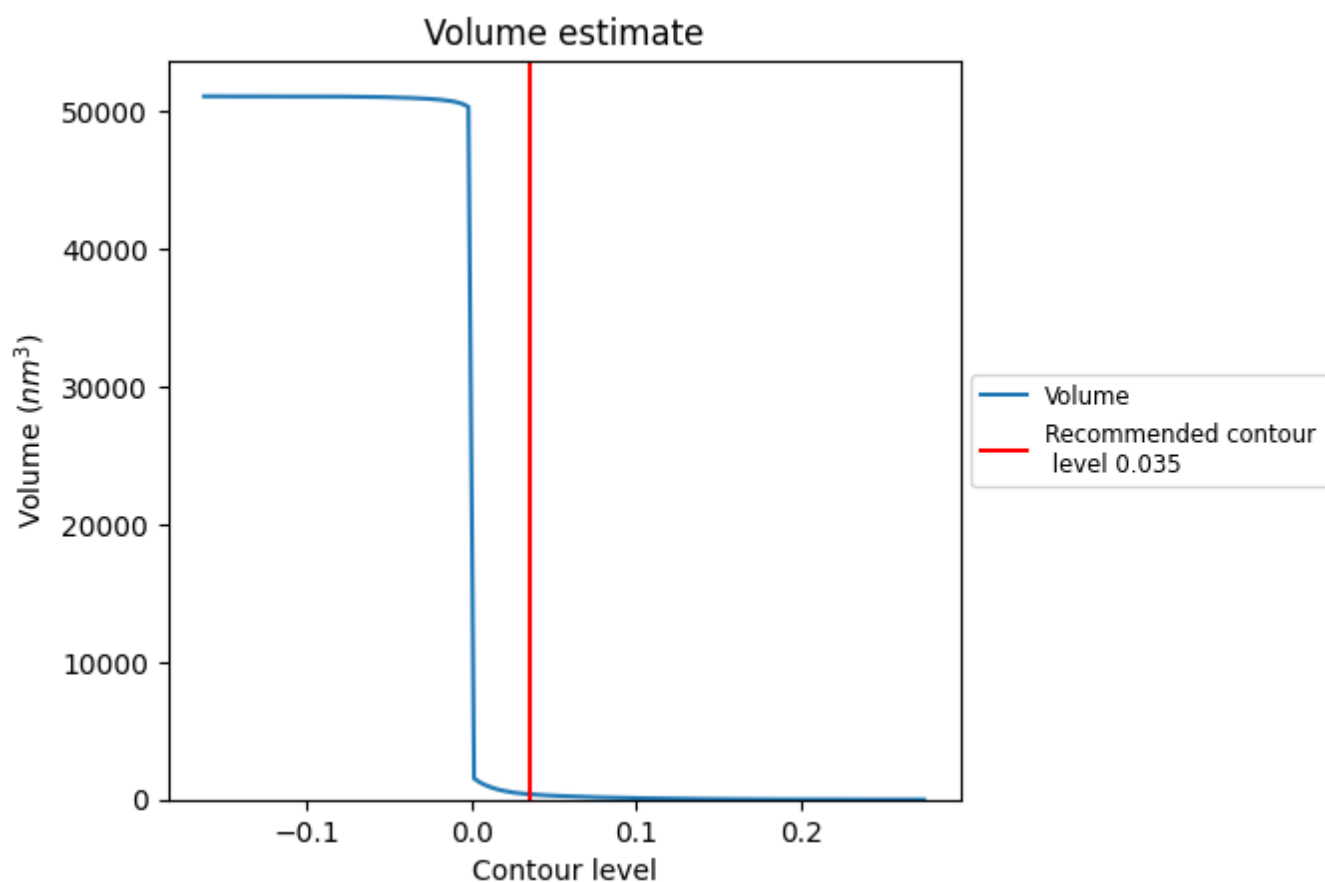
This section contains the results of statistical analysis of the map.

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.

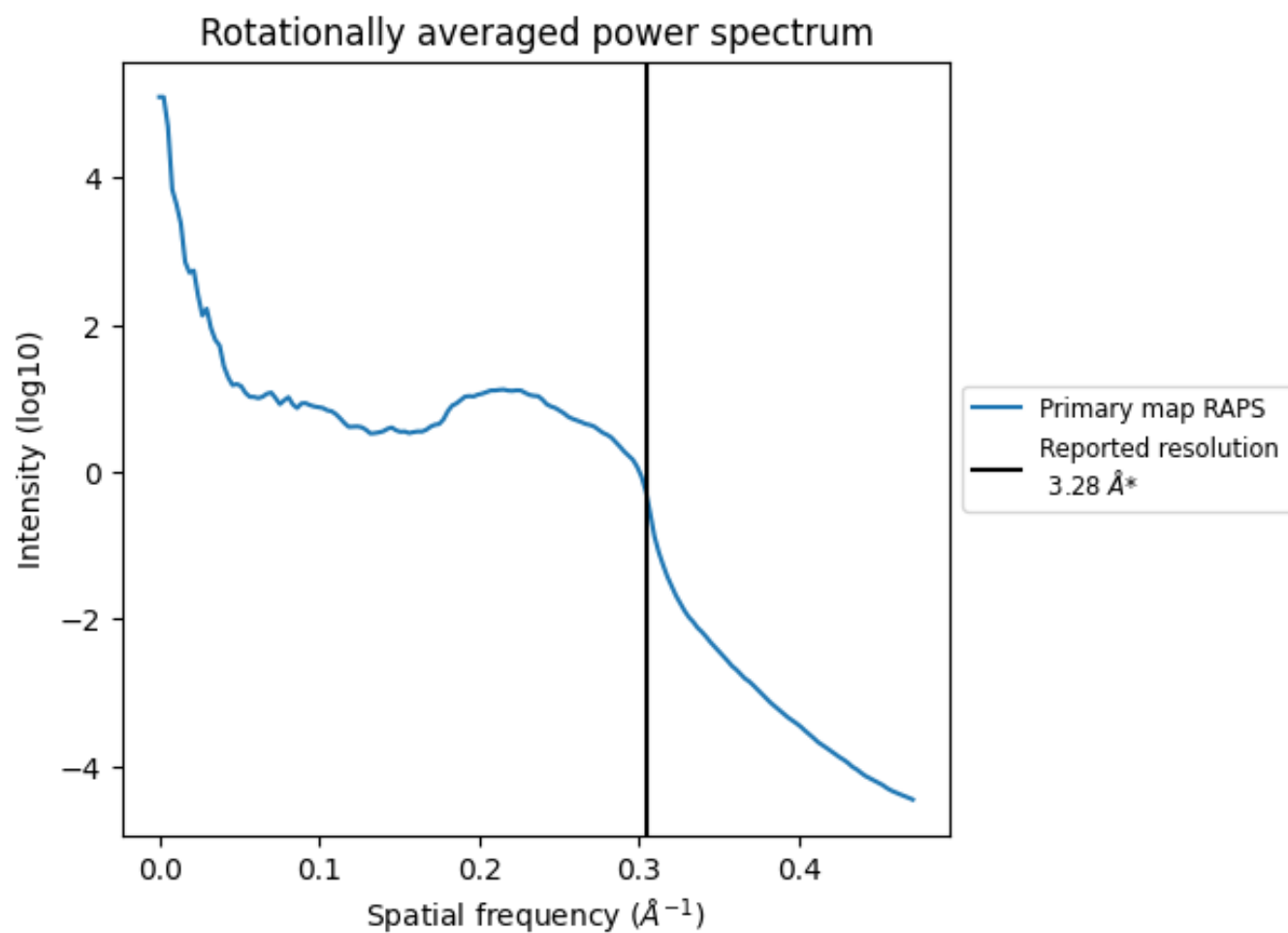
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 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 ⓘ

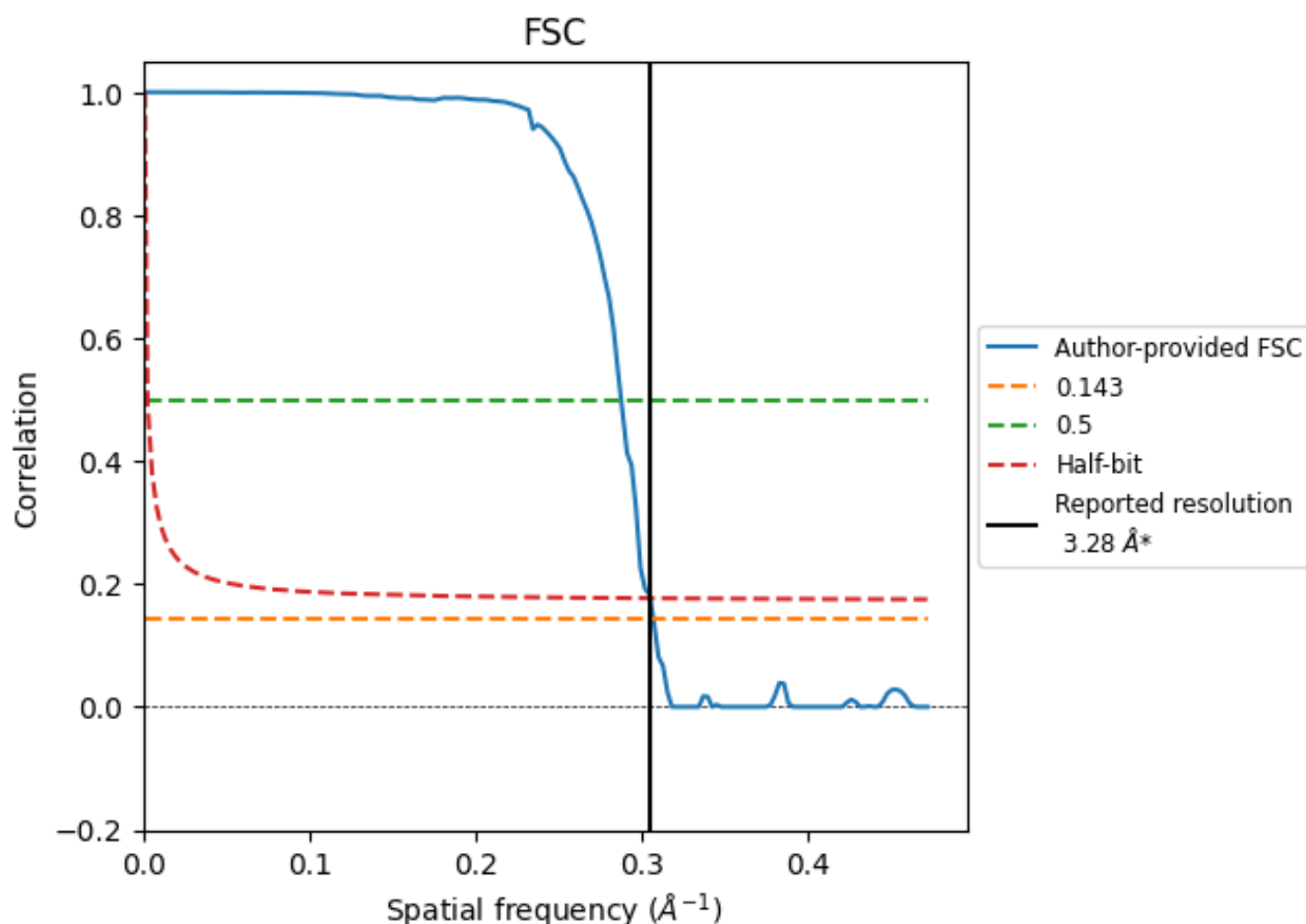


*Reported resolution corresponds to spatial frequency of 0.305 Å⁻¹

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](#)

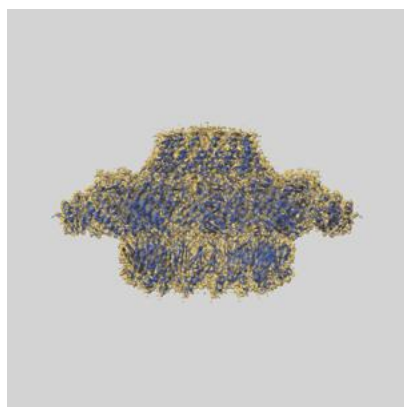
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.28	-	-
Author-provided FSC curve	3.26	3.48	3.28
Unmasked-calculated*	-	-	-

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

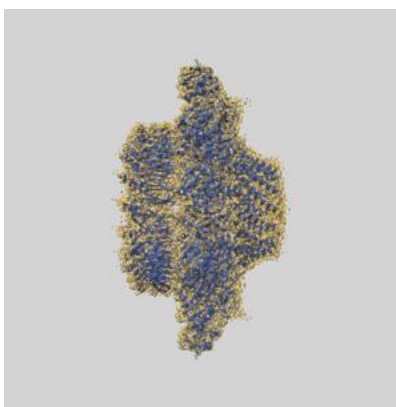
9 Map-model fit [i](#)

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](#).

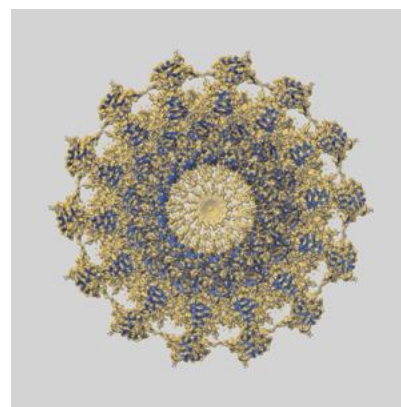
9.1 Map-model overlay [i](#)



X



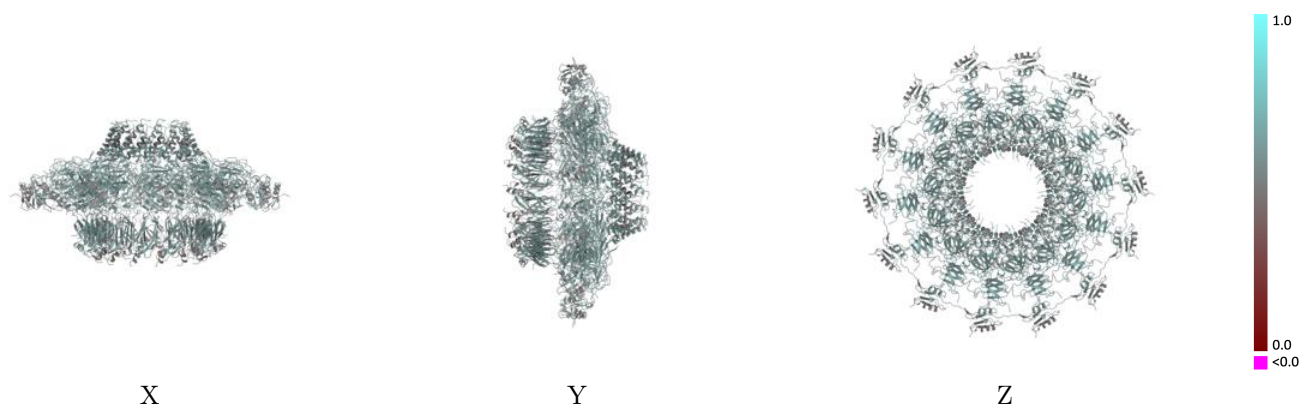
Y



Z

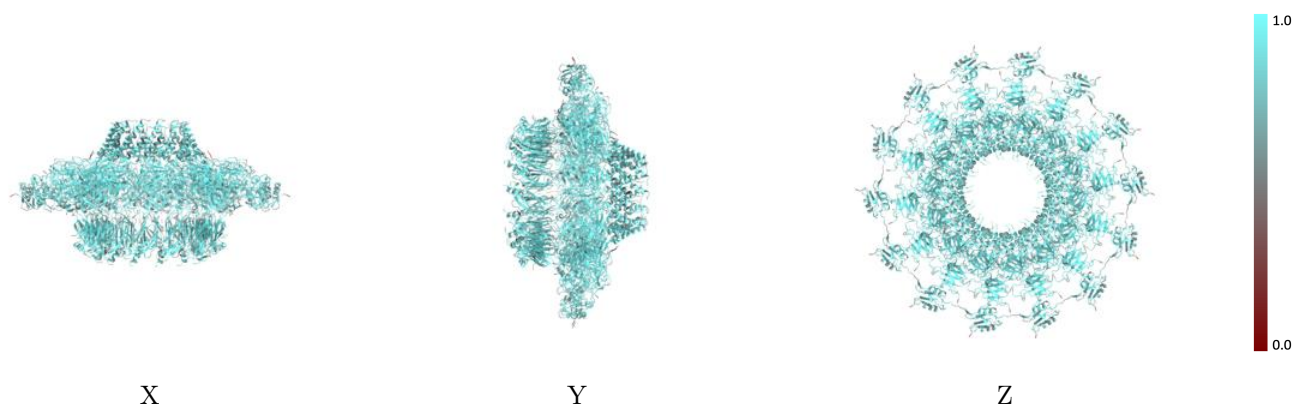
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



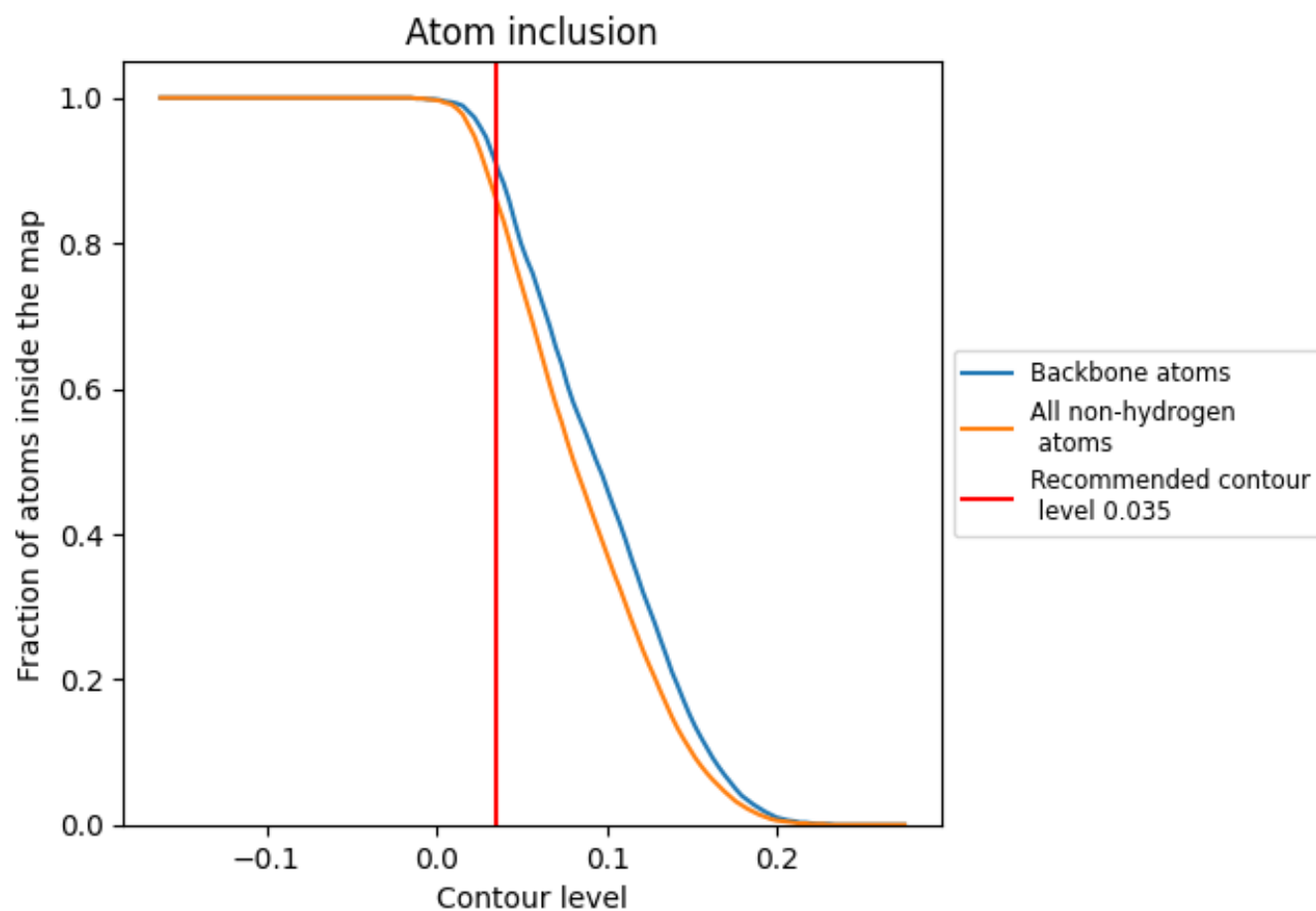
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.8580	 0.5530
A	 0.7690	 0.5250
B	 0.8720	 0.5600
C	 0.8890	 0.5590
D	 0.7700	 0.5210
E	 0.8730	 0.5580
F	 0.8930	 0.5600
G	 0.7700	 0.5210
H	 0.8740	 0.5590
I	 0.8900	 0.5610
J	 0.7670	 0.5210
K	 0.8750	 0.5590
L	 0.8870	 0.5590
M	 0.7650	 0.5220
N	 0.8720	 0.5600
O	 0.8870	 0.5610
P	 0.7670	 0.5200
Q	 0.8760	 0.5600
R	 0.8870	 0.5610
S	 0.7710	 0.5200
T	 0.8730	 0.5610
U	 0.8910	 0.5590
a	 0.7690	 0.5230
b	 0.8720	 0.5630
c	 0.8900	 0.5590
d	 0.7700	 0.5210
e	 0.8730	 0.5630
f	 0.8930	 0.5580
g	 0.7700	 0.5240
h	 0.8740	 0.5630
i	 0.8900	 0.5600
j	 0.7670	 0.5220
k	 0.8750	 0.5620
l	 0.8870	 0.5590
m	 0.7650	 0.5240



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Chain	Atom inclusion	Q-score
n	 0.8720	 0.5610
o	 0.8910	 0.5600
p	 0.7670	 0.5230
q	 0.8760	 0.5600
r	 0.8880	 0.5590
s	 0.7710	 0.5220
t	 0.8730	 0.5600
u	 0.8900	 0.5590