



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:56 PM UTC

PDB ID : 7UMT / pdb_00007umt
EMDB ID : EMD-26609
Title : Structure of the VP5*/VP8* assembly from the human rotavirus strain CDC-9
- Reversed conformation
Authors : Jenni, S.; Zongli, L.; Wang, Y.; Bessey, T.; Salgado, E.N.; Schmidt, A.G.;
Greenberg, H.B.; Jiang, B.; Harrison, S.C.
Deposited on : 2022-04-07
Resolution : 3.40 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:

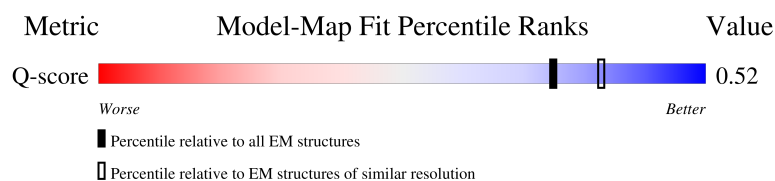
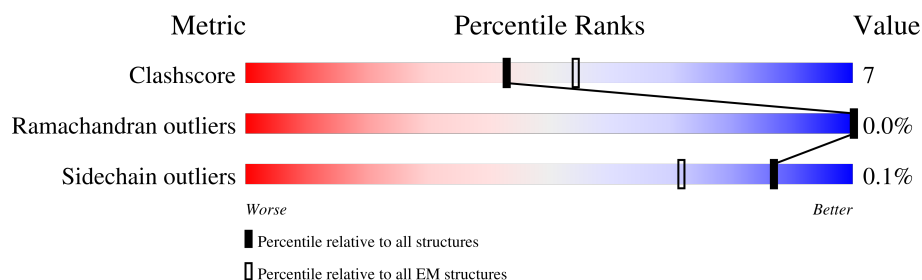
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 3.40 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.



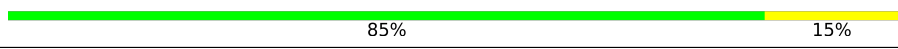
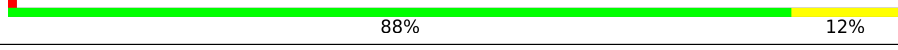
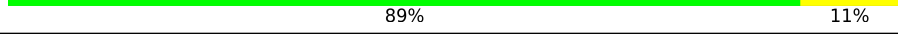
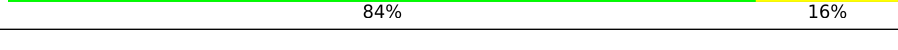
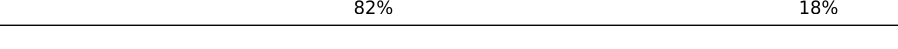
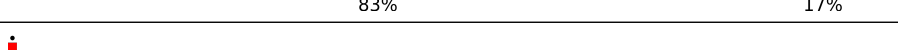
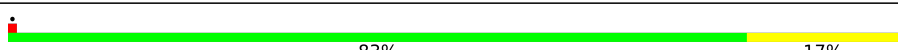
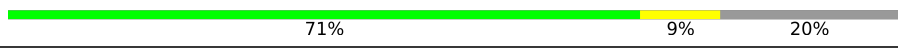
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	1	529	5% 42% 9% 49%
1	2	529	5% 42% 9% 49%
1	3	529	5% 40% 11% 49%
2	A	397	86% 14%

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Mol	Chain	Length	Quality of chain
2	B	397	
2	C	397	
2	D	397	
2	E	397	
2	F	397	
2	G	397	
2	H	397	
2	I	397	
2	J	397	
2	K	397	
2	L	397	
2	M	397	
2	N	397	
2	O	397	
2	P	397	
2	Q	397	
2	R	397	
3	a	326	
3	b	326	
3	c	326	
3	d	326	
3	e	326	
3	f	326	
3	g	326	
3	h	326	

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Mol	Chain	Length	Quality of chain
3	i	326	71% 13% 15%
3	j	326	71% 13% 16%
3	k	326	69% 16% 15%
3	l	326	71% 13% 15%
3	m	326	71% 13% 16%
3	n	326	70% 14% 15%
3	o	326	71% 13% 15%
3	p	326	71% 13% 16%
3	q	326	68% 14% 17%
3	r	326	69% 15% 16%
4	S	3	33% 33% 33%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 204779 atoms, of which 101341 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 Outer capsid protein VP5*.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	1	270	Total	C	H	N	O	S	0	0
			4248	1376	2086	366	414	6		
1	2	270	Total	C	H	N	O	S	0	0
			4248	1376	2086	366	414	6		
1	3	270	Total	C	H	N	O	S	0	0
			4248	1376	2086	366	414	6		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	250	ASP	ASN	conflict	UNP X4YMN0
1	331	PHE	SER	conflict	UNP X4YMN0
1	364	ILE	MET	conflict	UNP X4YMN0
1	378	ARG	LYS	conflict	UNP X4YMN0
1	385	HIS	ASP	conflict	UNP X4YMN0
1	388	LEU	ILE	conflict	UNP X4YMN0
1	499	ASN	ASP	conflict	UNP X4YMN0
1	605	ASN	SER	conflict	UNP X4YMN0
2	250	ASP	ASN	conflict	UNP X4YMN0
2	331	PHE	SER	conflict	UNP X4YMN0
2	364	ILE	MET	conflict	UNP X4YMN0
2	378	ARG	LYS	conflict	UNP X4YMN0
2	385	HIS	ASP	conflict	UNP X4YMN0
2	388	LEU	ILE	conflict	UNP X4YMN0
2	499	ASN	ASP	conflict	UNP X4YMN0
2	605	ASN	SER	conflict	UNP X4YMN0
3	250	ASP	ASN	conflict	UNP X4YMN0
3	331	PHE	SER	conflict	UNP X4YMN0
3	364	ILE	MET	conflict	UNP X4YMN0
3	378	ARG	LYS	conflict	UNP X4YMN0
3	385	HIS	ASP	conflict	UNP X4YMN0
3	388	LEU	ILE	conflict	UNP X4YMN0
3	499	ASN	ASP	conflict	UNP X4YMN0
3	605	ASN	SER	conflict	UNP X4YMN0

- Molecule 2 is a protein called Intermediate capsid protein VP6.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	A	397	Total 6295	C 2012	H 3127	N 552	O 589	S 15	0	0
2	B	397	Total 6295	C 2012	H 3127	N 552	O 589	S 15	0	0
2	C	397	Total 6296	C 2012	H 3128	N 552	O 589	S 15	0	0
2	D	397	Total 6295	C 2012	H 3127	N 552	O 589	S 15	0	0
2	E	397	Total 6295	C 2012	H 3127	N 552	O 589	S 15	0	0
2	F	397	Total 6295	C 2012	H 3127	N 552	O 589	S 15	0	0
2	G	397	Total 6295	C 2012	H 3127	N 552	O 589	S 15	0	0
2	H	397	Total 6295	C 2012	H 3127	N 552	O 589	S 15	0	0
2	I	397	Total 6295	C 2012	H 3127	N 552	O 589	S 15	0	0
2	J	397	Total 6295	C 2012	H 3127	N 552	O 589	S 15	0	0
2	K	397	Total 6295	C 2012	H 3127	N 552	O 589	S 15	0	0
2	L	397	Total 6296	C 2012	H 3128	N 552	O 589	S 15	0	0
2	M	397	Total 6295	C 2012	H 3127	N 552	O 589	S 15	0	0
2	N	397	Total 6295	C 2012	H 3127	N 552	O 589	S 15	0	0
2	O	397	Total 6295	C 2012	H 3127	N 552	O 589	S 15	0	0
2	P	397	Total 6296	C 2012	H 3128	N 552	O 589	S 15	0	0
2	Q	397	Total 6295	C 2012	H 3127	N 552	O 589	S 15	0	0
2	R	397	Total 6295	C 2012	H 3127	N 552	O 589	S 15	0	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	281	VAL	ILE	conflict	UNP A0A223GHC7
B	281	VAL	ILE	conflict	UNP A0A223GHC7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	281	VAL	ILE	conflict	UNP A0A223GHC7
D	281	VAL	ILE	conflict	UNP A0A223GHC7
E	281	VAL	ILE	conflict	UNP A0A223GHC7
F	281	VAL	ILE	conflict	UNP A0A223GHC7
G	281	VAL	ILE	conflict	UNP A0A223GHC7
H	281	VAL	ILE	conflict	UNP A0A223GHC7
I	281	VAL	ILE	conflict	UNP A0A223GHC7
J	281	VAL	ILE	conflict	UNP A0A223GHC7
K	281	VAL	ILE	conflict	UNP A0A223GHC7
L	281	VAL	ILE	conflict	UNP A0A223GHC7
M	281	VAL	ILE	conflict	UNP A0A223GHC7
N	281	VAL	ILE	conflict	UNP A0A223GHC7
O	281	VAL	ILE	conflict	UNP A0A223GHC7
P	281	VAL	ILE	conflict	UNP A0A223GHC7
Q	281	VAL	ILE	conflict	UNP A0A223GHC7
R	281	VAL	ILE	conflict	UNP A0A223GHC7

- Molecule 3 is a protein called Outer capsid glycoprotein VP7.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	a	271	Total	C	H	N	O	S	0	0
			4279	1374	2111	351	426	17		
3	b	276	Total	C	H	N	O	S	0	0
			4357	1400	2148	358	434	17		
3	c	260	Total	C	H	N	O	S	0	0
			4096	1314	2023	333	409	17		
3	d	276	Total	C	H	N	O	S	0	0
			4357	1400	2148	358	434	17		
3	e	261	Total	C	H	N	O	S	0	0
			4103	1316	2026	334	410	17		
3	f	276	Total	C	H	N	O	S	0	0
			4357	1400	2148	358	434	17		
3	g	276	Total	C	H	N	O	S	0	0
			4357	1400	2148	358	434	17		
3	h	271	Total	C	H	N	O	S	0	0
			4279	1374	2111	351	426	17		
3	i	276	Total	C	H	N	O	S	0	0
			4357	1400	2148	358	434	17		
3	j	274	Total	C	H	N	O	S	0	0
			4326	1391	2134	354	430	17		
3	k	276	Total	C	H	N	O	S	0	0
			4357	1400	2148	358	434	17		

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Mol	Chain	Residues	Atoms						AltConf	Trace
3	l	276	Total	C	H	N	O	S	0	0
			4357	1400	2148	358	434	17		
3	m	275	Total	C	H	N	O	S	0	0
			4340	1395	2140	356	432	17		
3	n	276	Total	C	H	N	O	S	0	0
			4357	1400	2148	358	434	17		
3	o	276	Total	C	H	N	O	S	0	0
			4357	1400	2148	358	434	17		
3	p	275	Total	C	H	N	O	S	0	0
			4340	1395	2140	356	432	17		
3	q	271	Total	C	H	N	O	S	0	0
			4279	1374	2111	351	426	17		
3	r	275	Total	C	H	N	O	S	0	0
			4340	1395	2140	356	432	17		

There are 36 discrepancies between the modelled and reference sequences:

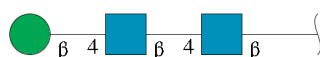
Chain	Residue	Modelled	Actual	Comment	Reference
a	108	ILE	THR	conflict	UNP B1NP55
a	147	SER	ASN	conflict	UNP B1NP55
b	108	ILE	THR	conflict	UNP B1NP55
b	147	SER	ASN	conflict	UNP B1NP55
c	108	ILE	THR	conflict	UNP B1NP55
c	147	SER	ASN	conflict	UNP B1NP55
d	108	ILE	THR	conflict	UNP B1NP55
d	147	SER	ASN	conflict	UNP B1NP55
e	108	ILE	THR	conflict	UNP B1NP55
e	147	SER	ASN	conflict	UNP B1NP55
f	108	ILE	THR	conflict	UNP B1NP55
f	147	SER	ASN	conflict	UNP B1NP55
g	108	ILE	THR	conflict	UNP B1NP55
g	147	SER	ASN	conflict	UNP B1NP55
h	108	ILE	THR	conflict	UNP B1NP55
h	147	SER	ASN	conflict	UNP B1NP55
i	108	ILE	THR	conflict	UNP B1NP55
i	147	SER	ASN	conflict	UNP B1NP55
j	108	ILE	THR	conflict	UNP B1NP55
j	147	SER	ASN	conflict	UNP B1NP55
k	108	ILE	THR	conflict	UNP B1NP55
k	147	SER	ASN	conflict	UNP B1NP55
l	108	ILE	THR	conflict	UNP B1NP55
l	147	SER	ASN	conflict	UNP B1NP55
m	108	ILE	THR	conflict	UNP B1NP55

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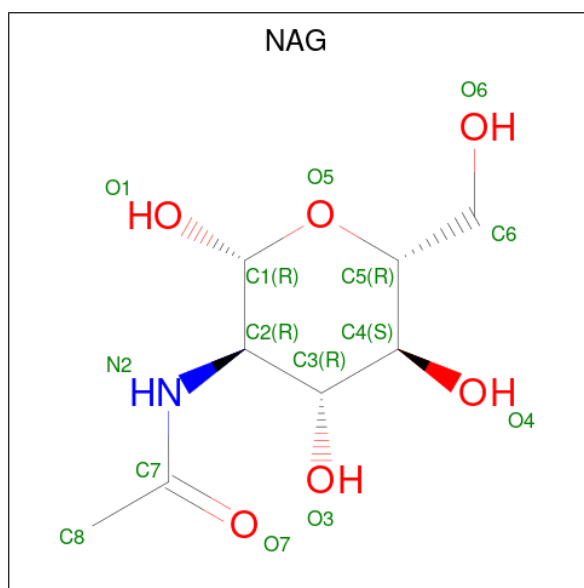
Chain	Residue	Modelled	Actual	Comment	Reference
m	147	SER	ASN	conflict	UNP B1NP55
n	108	ILE	THR	conflict	UNP B1NP55
n	147	SER	ASN	conflict	UNP B1NP55
o	108	ILE	THR	conflict	UNP B1NP55
o	147	SER	ASN	conflict	UNP B1NP55
p	108	ILE	THR	conflict	UNP B1NP55
p	147	SER	ASN	conflict	UNP B1NP55
q	108	ILE	THR	conflict	UNP B1NP55
q	147	SER	ASN	conflict	UNP B1NP55
r	108	ILE	THR	conflict	UNP B1NP55
r	147	SER	ASN	conflict	UNP B1NP55

- Molecule 4 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms					AltConf	Trace
4	S	3	Total	C	H	N	O	0	0
			76	22	37	2	15		

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms					AltConf
5	a	1	Total	C	H	N	O	0
			27	8	13	1	5	
5	b	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	b	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	c	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	c	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	d	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	d	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	e	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	e	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	f	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	f	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	g	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	g	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	h	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	h	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	i	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	i	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	j	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	j	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	k	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	k	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	l	1	Total	C	H	N	O	0
			28	8	14	1	5	

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Mol	Chain	Residues	Atoms					AltConf
5	l	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	m	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	m	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	n	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	n	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	o	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	o	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	p	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	p	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	q	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	q	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	r	1	Total	C	H	N	O	0
			28	8	14	1	5	
5	r	1	Total	C	H	N	O	0
			28	8	14	1	5	

- Molecule 6 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
6	a	4	Total	Ca	0
			4	4	
6	b	4	Total	Ca	0
			4	4	
6	c	4	Total	Ca	0
			4	4	
6	d	4	Total	Ca	0
			4	4	
6	e	4	Total	Ca	0
			4	4	
6	f	4	Total	Ca	0
			4	4	

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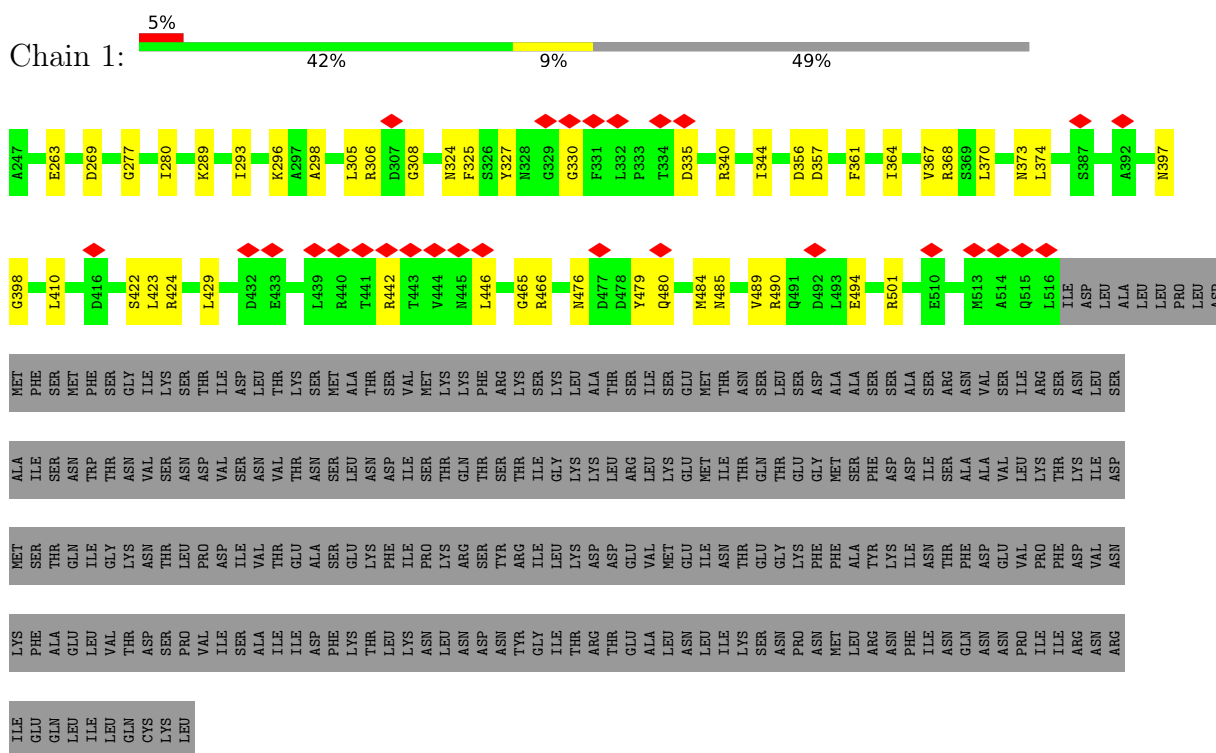
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Mol	Chain	Residues	Atoms		AltConf
6	g	4	Total 4	Ca 4	0
6	h	4	Total 4	Ca 4	0
6	i	4	Total 4	Ca 4	0
6	j	4	Total 4	Ca 4	0
6	k	4	Total 4	Ca 4	0
6	l	4	Total 4	Ca 4	0
6	m	4	Total 4	Ca 4	0
6	n	4	Total 4	Ca 4	0
6	o	4	Total 4	Ca 4	0
6	p	4	Total 4	Ca 4	0
6	q	4	Total 4	Ca 4	0
6	r	4	Total 4	Ca 4	0

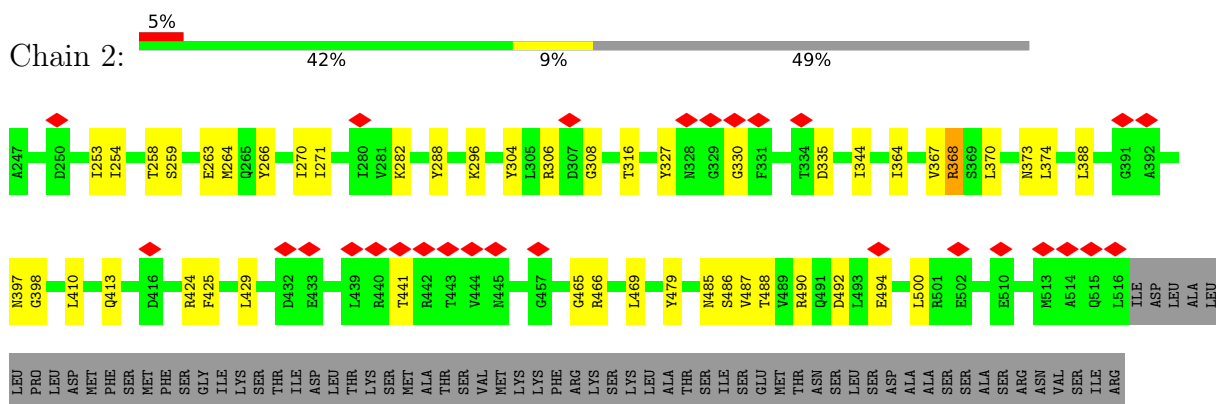
3 Residue-property plots

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

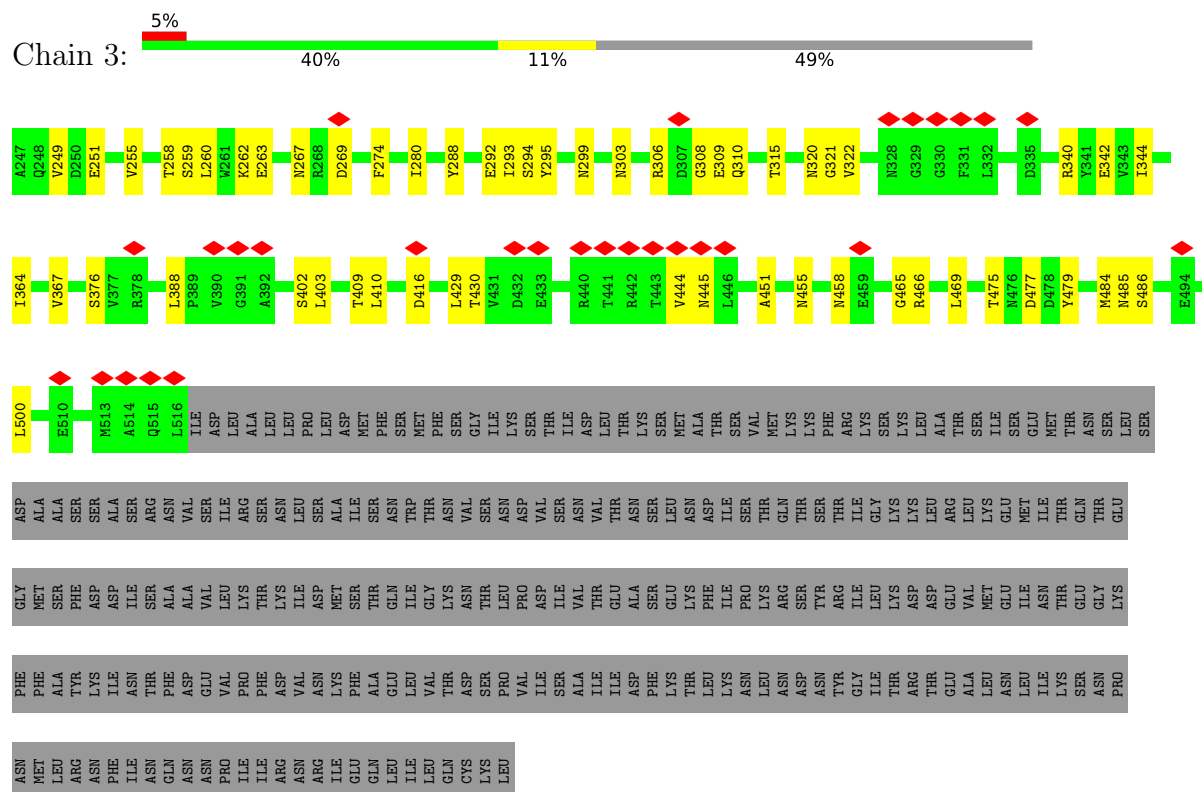
• Molecule 1: Outer capsid protein VP5*



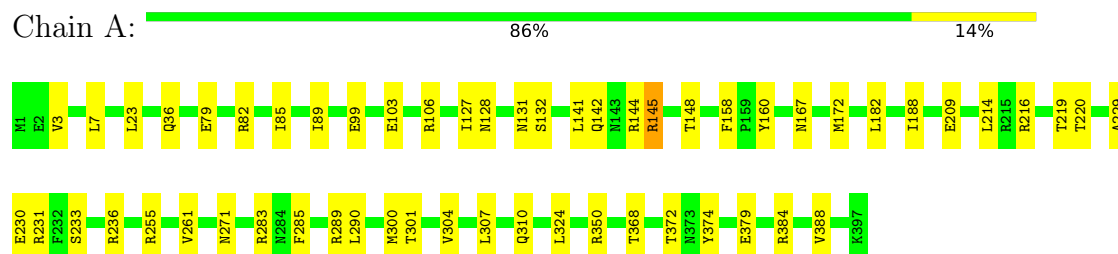
• Molecule 1: Outer capsid protein VP5*



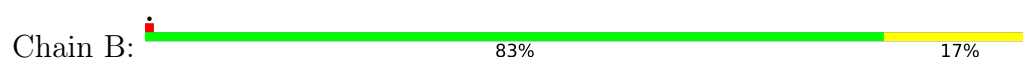
- Molecule 1: Outer capsid protein VP5*



- Molecule 2: Intermediate capsid protein VP6

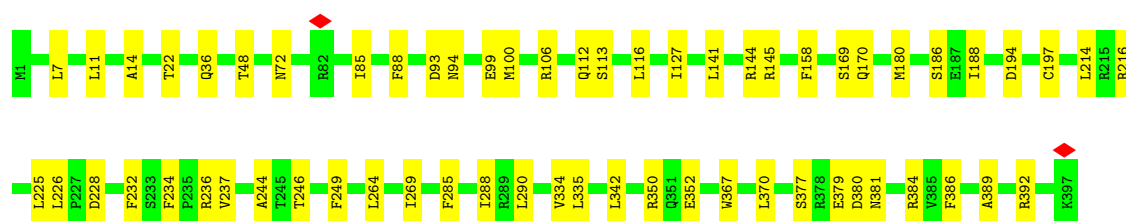
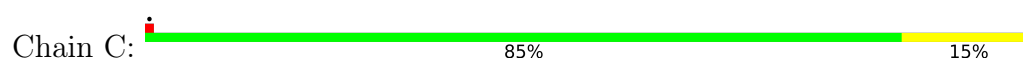


- Molecule 2: Intermediate capsid protein VP6

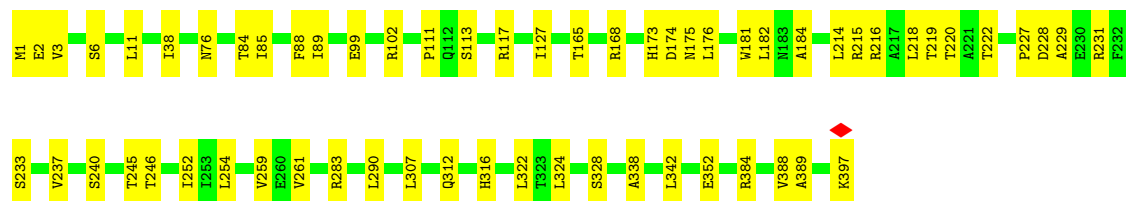
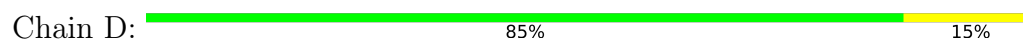




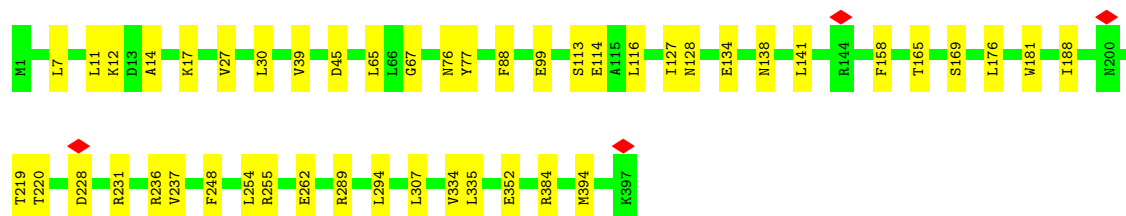
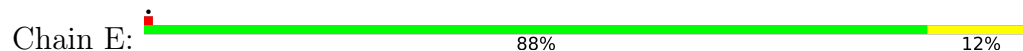
- Molecule 2: Intermediate capsid protein VP6



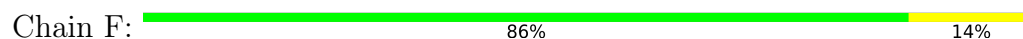
- Molecule 2: Intermediate capsid protein VP6



- Molecule 2: Intermediate capsid protein VP6



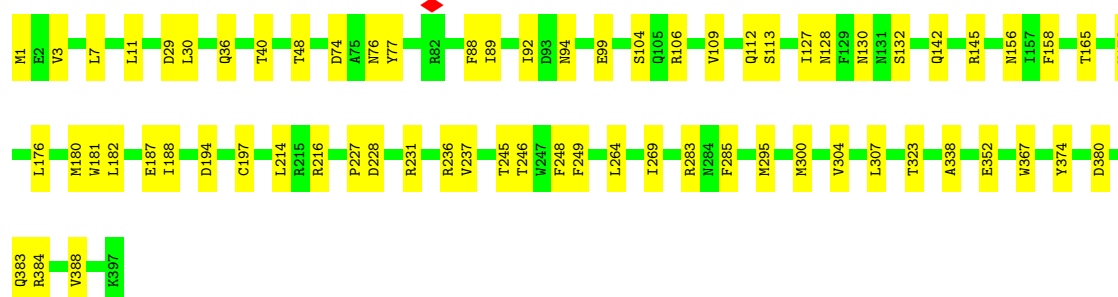
- Molecule 2: Intermediate capsid protein VP6





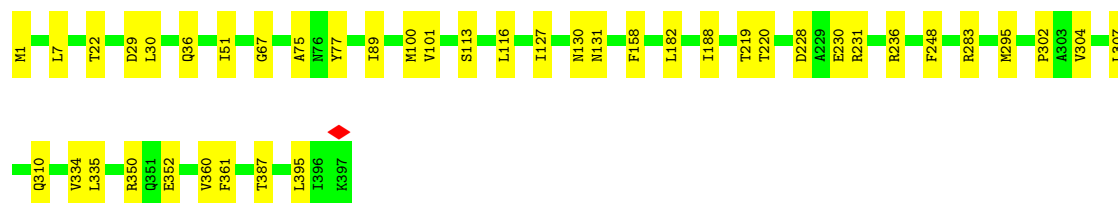
• Molecule 2: Intermediate capsid protein VP6

Chain G: 83% 17%



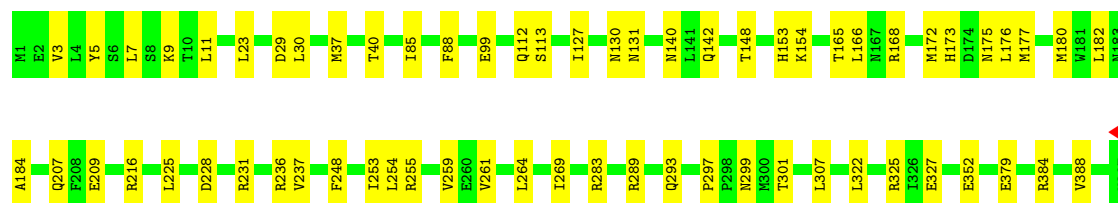
• Molecule 2: Intermediate capsid protein VP6

Chain H: 89% 11%



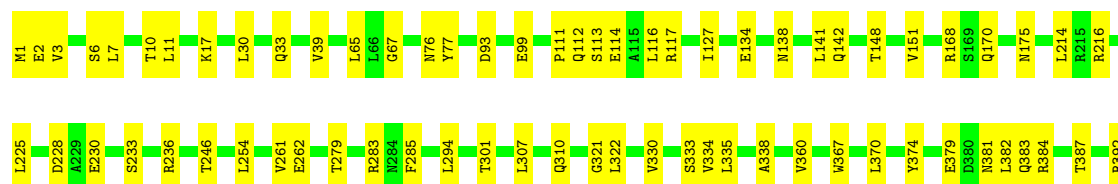
• Molecule 2: Intermediate capsid protein VP6

Chain I: 84% 16%



• Molecule 2: Intermediate capsid protein VP6

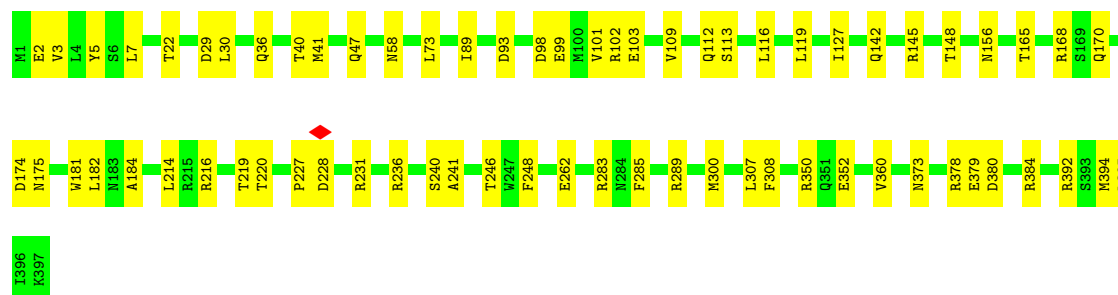
Chain J: 82% 18%





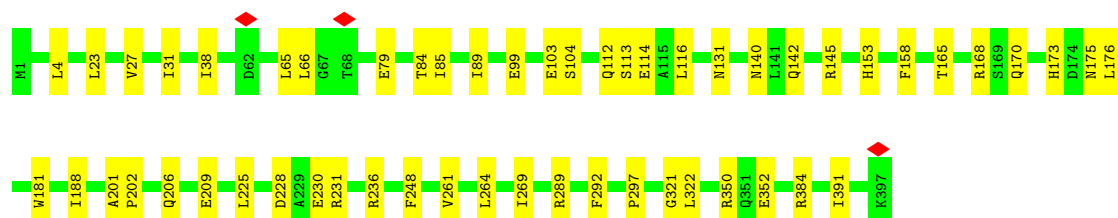
• Molecule 2: Intermediate capsid protein VP6

Chain K: 83% 17%



• Molecule 2: Intermediate capsid protein VP6

Chain L: 86% 14%



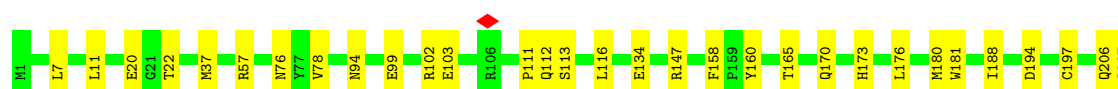
• Molecule 2: Intermediate capsid protein VP6

Chain M: 83% 17%



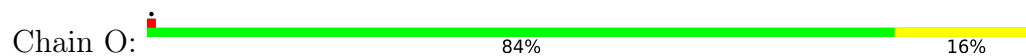
• Molecule 2: Intermediate capsid protein VP6

Chain N: 86% 14%

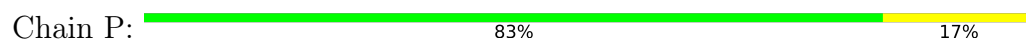




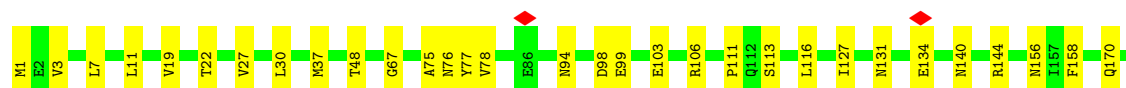
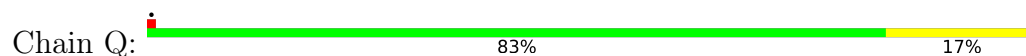
• Molecule 2: Intermediate capsid protein VP6



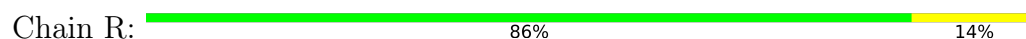
• Molecule 2: Intermediate capsid protein VP6

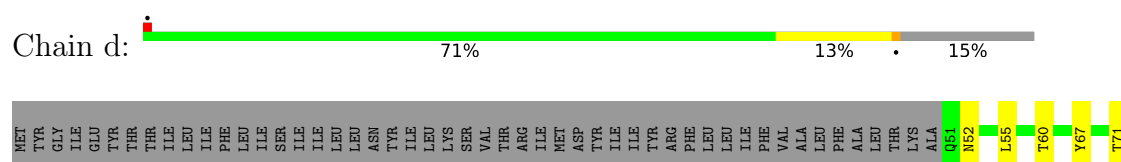


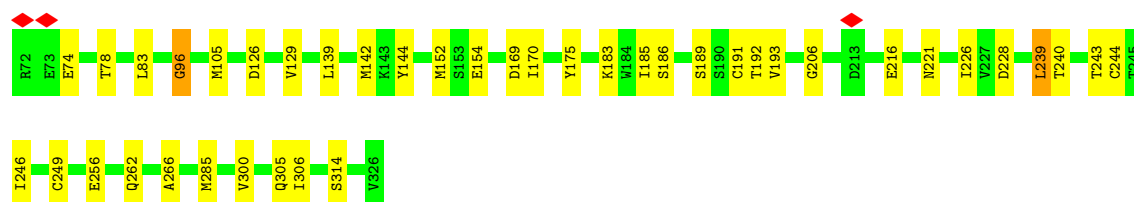
• Molecule 2: Intermediate capsid protein VP6



• Molecule 2: Intermediate capsid protein VP6

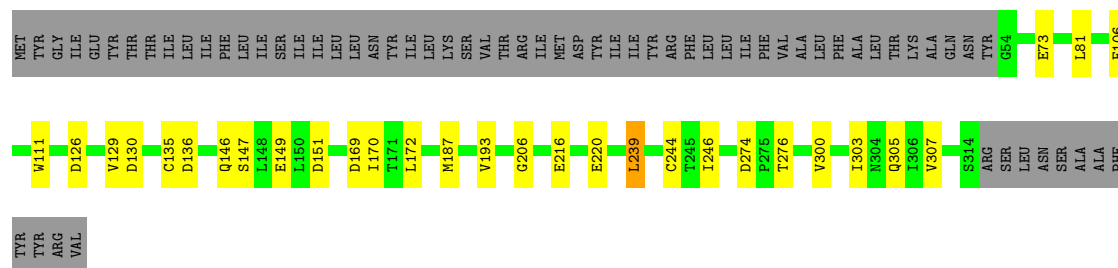






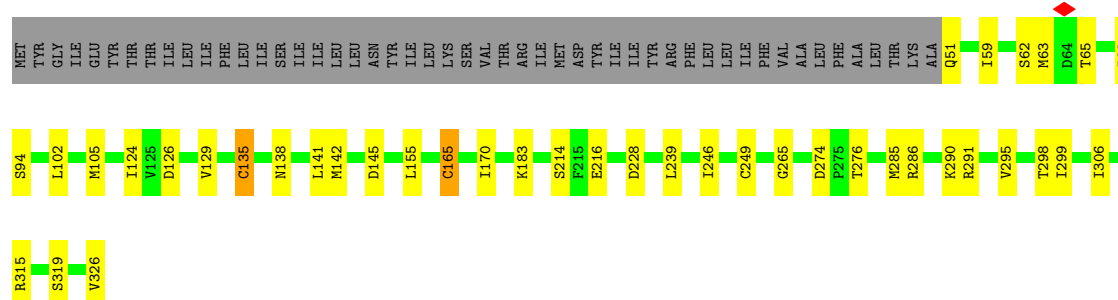
• Molecule 3: Outer capsid glycoprotein VP7

Chain e:



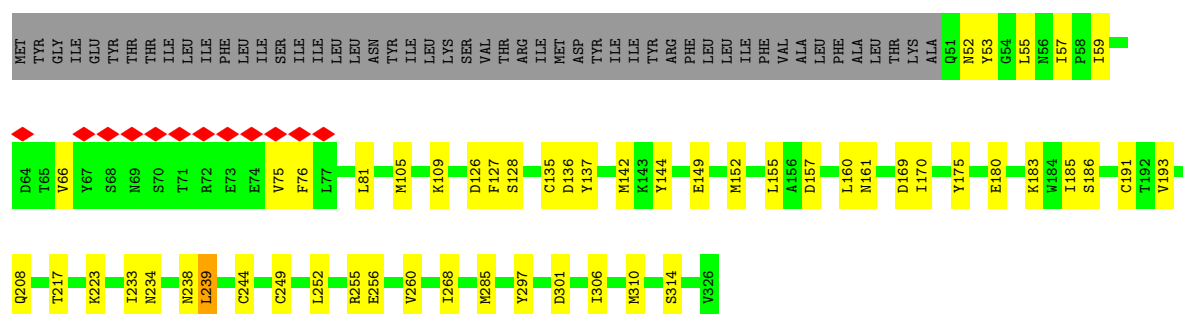
• Molecule 3: Outer capsid glycoprotein VP7

Chain f:



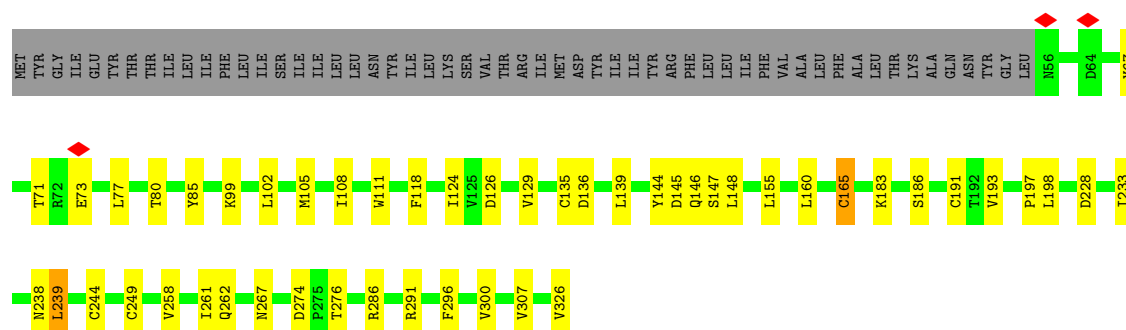
• Molecule 3: Outer capsid glycoprotein VP7

Chain g:

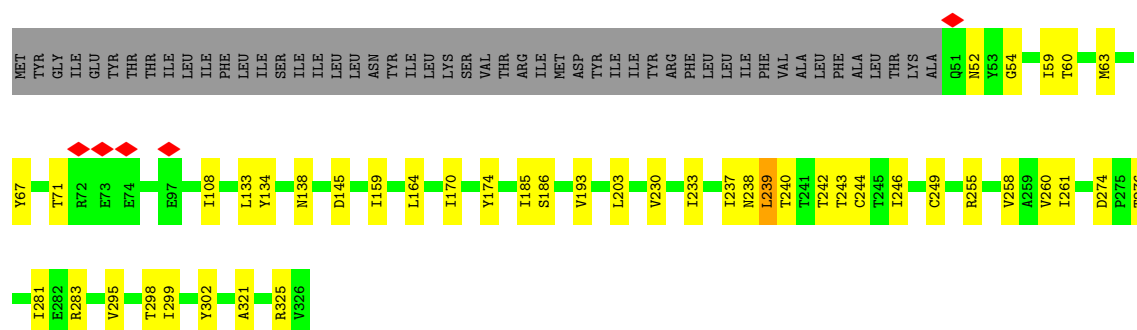


• Molecule 3: Outer capsid glycoprotein VP7

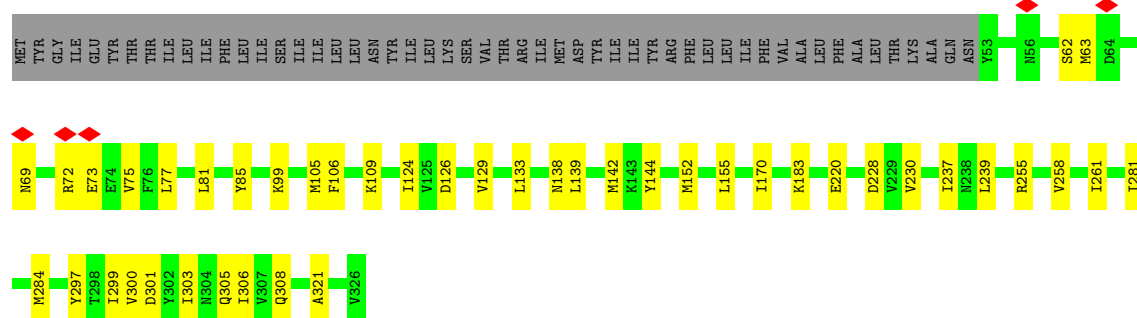
Chain h:



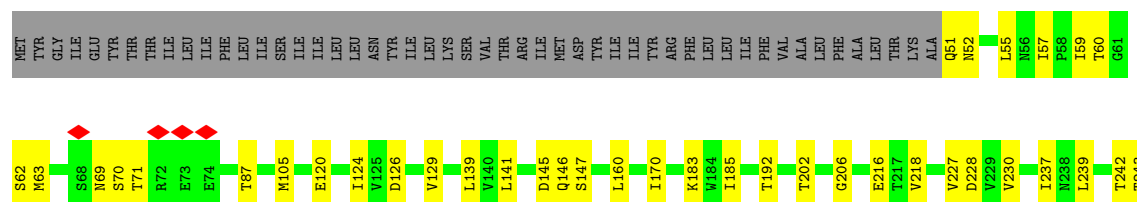
• Molecule 3: Outer capsid glycoprotein VP7



• Molecule 3: Outer capsid glycoprotein VP7



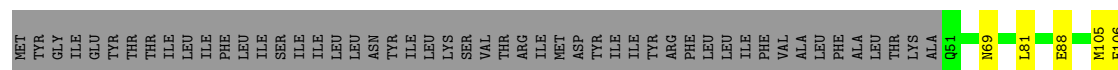
• Molecule 3: Outer capsid glycoprotein VP7





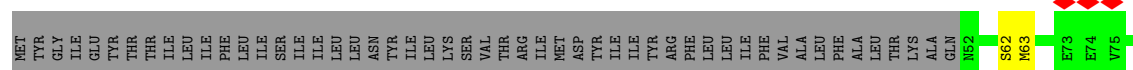
• Molecule 3: Outer capsid glycoprotein VP7

Chain l: 71% 13% 15%



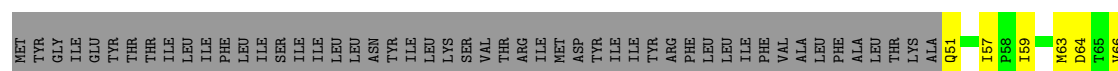
• Molecule 3: Outer capsid glycoprotein VP7

Chain m: 71% 13% 16%



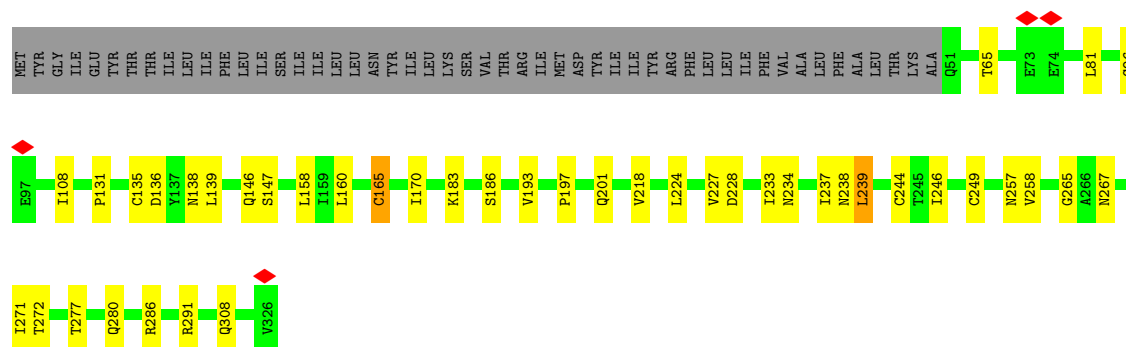
• Molecule 3: Outer capsid glycoprotein VP7

Chain n: 70% 14% 15%

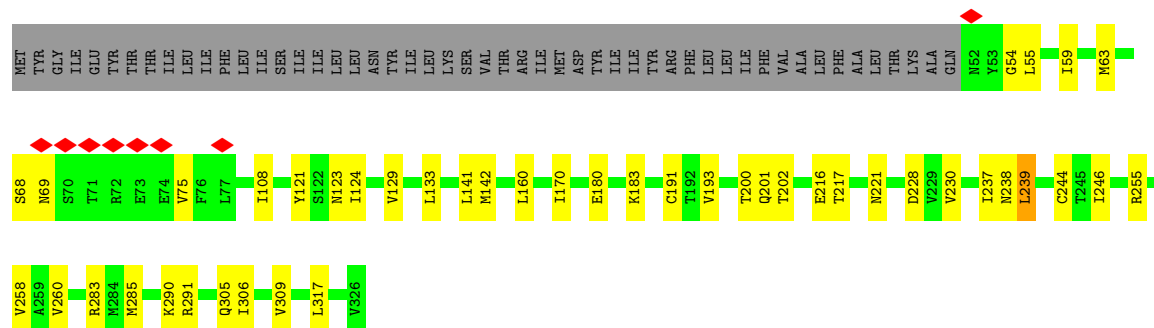


• Molecule 3: Outer capsid glycoprotein VP7

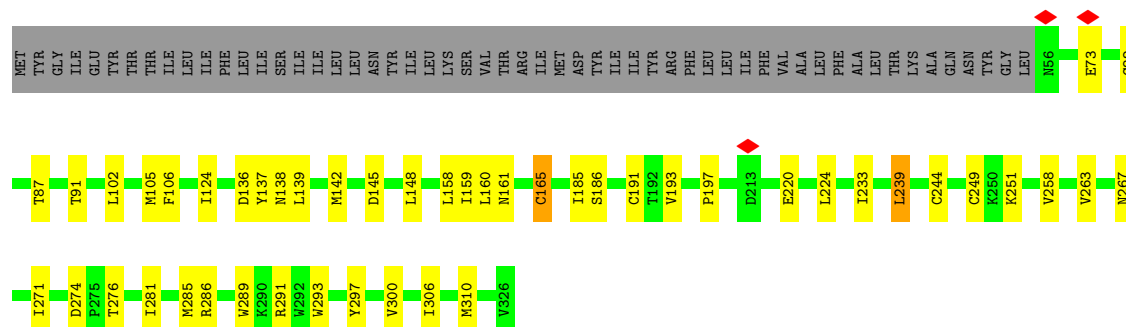
Chain o: 71% 13% 15%



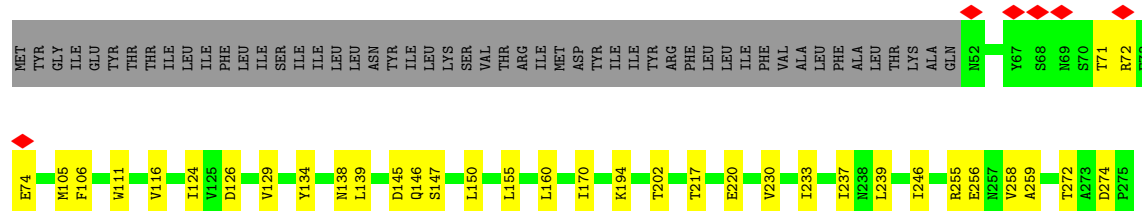
• Molecule 3: Outer capsid glycoprotein VP7



• Molecule 3: Outer capsid glycoprotein VP7



• Molecule 3: Outer capsid glycoprotein VP7





● Molecule 4: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	359970	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60.0	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.094	Depositor
Minimum map value	-0.049	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.015	Depositor
Map size ($\text{\AA}$)	393.91998, 393.91998, 393.91998	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.231, 1.231, 1.231	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, BMA, CA

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.24	0/2213	0.39	0/3008
1	2	0.25	0/2213	0.36	0/3008
1	3	0.24	0/2213	0.36	0/3008
2	A	0.34	0/3238	0.42	0/4404
2	B	0.34	0/3238	0.43	0/4404
2	C	0.34	0/3238	0.44	0/4404
2	D	0.33	0/3238	0.42	0/4404
2	E	0.34	0/3238	0.43	0/4404
2	F	0.34	0/3238	0.43	0/4404
2	G	0.33	0/3238	0.44	0/4404
2	H	0.32	0/3238	0.42	0/4404
2	I	0.34	0/3238	0.45	0/4404
2	J	0.32	0/3238	0.42	0/4404
2	K	0.32	0/3238	0.43	0/4404
2	L	0.32	0/3238	0.41	0/4404
2	M	0.33	0/3238	0.42	0/4404
2	N	0.32	0/3238	0.43	0/4404
2	O	0.32	0/3238	0.42	0/4404
2	P	0.33	0/3238	0.44	0/4404
2	Q	0.33	0/3238	0.44	0/4404
2	R	0.32	0/3238	0.43	0/4404
3	a	0.29	0/2213	0.40	0/3013
3	b	0.33	0/2255	0.46	0/3070
3	c	0.30	0/2115	0.41	0/2882
3	d	0.31	0/2255	0.43	0/3070
3	e	0.28	0/2119	0.39	0/2887
3	f	0.32	0/2255	0.47	1/3070 (0.0%)
3	g	0.30	0/2255	0.43	0/3070
3	h	0.30	0/2213	0.46	1/3013 (0.0%)
3	i	0.32	0/2255	0.45	0/3070
3	j	0.29	0/2238	0.42	0/3047
3	k	0.30	0/2255	0.43	0/3070

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	l	0.31	0/2255	0.46	1/3070 (0.0%)
3	m	0.31	0/2246	0.43	0/3058
3	n	0.28	0/2255	0.39	0/3070
3	o	0.31	0/2255	0.46	1/3070 (0.0%)
3	p	0.31	0/2246	0.45	0/3058
3	q	0.30	0/2213	0.47	1/3013 (0.0%)
3	r	0.30	0/2246	0.41	0/3058
All	All	0.32	0/105067	0.43	5/142955 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	1	0	1
1	2	0	1
2	A	0	1
2	C	0	1
2	P	0	1
2	Q	0	1
3	a	0	1
3	b	0	3
3	c	0	2
3	d	0	2
3	e	0	1
3	f	0	2
3	g	0	2
3	h	0	1
3	i	0	2
3	j	0	1
3	k	0	1
3	l	0	1
3	m	0	2
3	n	0	1
3	o	0	2
3	p	0	1
3	q	0	1
3	r	0	2
All	All	0	34

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	l	165	CYS	CA-CB-SG	8.32	133.54	114.40
3	f	165	CYS	CA-CB-SG	8.07	132.97	114.40
3	o	165	CYS	CA-CB-SG	7.97	132.72	114.40
3	h	165	CYS	CA-CB-SG	7.91	132.60	114.40
3	q	165	CYS	CA-CB-SG	7.72	132.15	114.40

There are no chirality outliers.

5 of 34 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1	368	ARG	Peptide
1	2	368	ARG	Peptide
2	A	145	ARG	Peptide
2	C	144	ARG	Peptide
2	P	144	ARG	Peptide

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	1	2162	2086	2086	37	0
1	2	2162	2086	2086	37	0
1	3	2162	2086	2086	39	0
2	A	3168	3127	3127	43	0
2	B	3168	3127	3127	50	0
2	C	3168	3128	3127	42	0
2	D	3168	3127	3127	48	0
2	E	3168	3127	3127	34	0
2	F	3168	3127	3127	42	0
2	G	3168	3127	3127	60	0
2	H	3168	3127	3127	34	0
2	I	3168	3127	3127	53	0
2	J	3168	3127	3127	49	0
2	K	3168	3127	3127	44	0
2	L	3168	3128	3127	41	0
2	M	3168	3127	3127	53	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	N	3168	3127	3127	43	0
2	O	3168	3127	3127	43	0
2	P	3168	3128	3127	47	0
2	Q	3168	3127	3127	47	0
2	R	3168	3127	3127	42	0
3	a	2168	2111	2111	37	0
3	b	2209	2148	2148	35	0
3	c	2073	2023	2023	38	0
3	d	2209	2148	2148	30	0
3	e	2077	2026	2026	21	0
3	f	2209	2148	2148	31	0
3	g	2209	2148	2148	39	0
3	h	2168	2111	2111	36	0
3	i	2209	2148	2148	30	0
3	j	2192	2134	2134	32	0
3	k	2209	2148	2148	43	0
3	l	2209	2148	2148	30	0
3	m	2200	2140	2140	30	0
3	n	2209	2148	2148	42	0
3	o	2209	2148	2148	32	0
3	p	2200	2140	2140	38	0
3	q	2168	2111	2111	35	0
3	r	2200	2140	2140	36	0
4	S	39	37	34	1	0
5	a	14	13	13	0	0
5	b	28	28	26	0	0
5	c	28	28	26	0	0
5	d	28	28	26	0	0
5	e	28	28	26	0	0
5	f	28	28	26	0	0
5	g	28	28	26	0	0
5	h	28	28	26	0	0
5	i	28	28	26	0	0
5	j	28	28	26	0	0
5	k	28	28	26	0	0
5	l	28	28	26	1	0
5	m	28	28	26	0	0
5	n	28	28	26	0	0
5	o	28	28	26	1	0
5	p	28	28	26	1	0
5	q	28	28	26	0	0
5	r	28	28	26	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	a	4	0	0	0	0
6	b	4	0	0	0	0
6	c	4	0	0	0	0
6	d	4	0	0	0	0
6	e	4	0	0	0	0
6	f	4	0	0	0	0
6	g	4	0	0	0	0
6	h	4	0	0	0	0
6	i	4	0	0	0	0
6	j	4	0	0	0	0
6	k	4	0	0	0	0
6	l	4	0	0	0	0
6	m	4	0	0	0	0
6	n	4	0	0	0	0
6	o	4	0	0	0	0
6	p	4	0	0	0	0
6	q	4	0	0	0	0
6	r	4	0	0	0	0
All	All	103438	101341	101301	1351	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 7.

The worst 5 of 1351 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:d:206:GLY:O	3:d:216:GLU:OE2	1.88	0.92
2:J:1:MET:HE1	2:J:387:THR:HG23	1.50	0.90
3:g:193:VAL:HG22	3:g:239:LEU:HD12	1.54	0.89
3:f:141:LEU:HD21	3:f:299:ILE:HD11	1.58	0.84
2:K:216:ARG:NE	2:K:379:GLU:OE2	2.11	0.82

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	268/529 (51%)	247 (92%)	21 (8%)	0	100	100
1	2	268/529 (51%)	253 (94%)	15 (6%)	0	100	100
1	3	268/529 (51%)	252 (94%)	16 (6%)	0	100	100
2	A	395/397 (100%)	374 (95%)	21 (5%)	0	100	100
2	B	395/397 (100%)	372 (94%)	23 (6%)	0	100	100
2	C	395/397 (100%)	369 (93%)	26 (7%)	0	100	100
2	D	395/397 (100%)	371 (94%)	24 (6%)	0	100	100
2	E	395/397 (100%)	366 (93%)	29 (7%)	0	100	100
2	F	395/397 (100%)	367 (93%)	28 (7%)	0	100	100
2	G	395/397 (100%)	364 (92%)	31 (8%)	0	100	100
2	H	395/397 (100%)	369 (93%)	26 (7%)	0	100	100
2	I	395/397 (100%)	371 (94%)	24 (6%)	0	100	100
2	J	395/397 (100%)	363 (92%)	32 (8%)	0	100	100
2	K	395/397 (100%)	376 (95%)	19 (5%)	0	100	100
2	L	395/397 (100%)	378 (96%)	17 (4%)	0	100	100
2	M	395/397 (100%)	372 (94%)	23 (6%)	0	100	100
2	N	395/397 (100%)	371 (94%)	24 (6%)	0	100	100
2	O	395/397 (100%)	370 (94%)	25 (6%)	0	100	100
2	P	395/397 (100%)	368 (93%)	27 (7%)	0	100	100
2	Q	395/397 (100%)	366 (93%)	29 (7%)	0	100	100
2	R	395/397 (100%)	365 (92%)	30 (8%)	0	100	100
3	a	269/326 (82%)	249 (93%)	20 (7%)	0	100	100
3	b	274/326 (84%)	246 (90%)	28 (10%)	0	100	100
3	c	258/326 (79%)	239 (93%)	19 (7%)	0	100	100
3	d	274/326 (84%)	248 (90%)	25 (9%)	1 (0%)	30	59
3	e	259/326 (79%)	240 (93%)	19 (7%)	0	100	100
3	f	274/326 (84%)	252 (92%)	22 (8%)	0	100	100
3	g	274/326 (84%)	253 (92%)	21 (8%)	0	100	100
3	h	269/326 (82%)	248 (92%)	21 (8%)	0	100	100
3	i	274/326 (84%)	249 (91%)	25 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	j	272/326 (83%)	259 (95%)	13 (5%)	0	100	100
3	k	274/326 (84%)	248 (90%)	26 (10%)	0	100	100
3	l	274/326 (84%)	250 (91%)	24 (9%)	0	100	100
3	m	273/326 (84%)	252 (92%)	21 (8%)	0	100	100
3	n	274/326 (84%)	254 (93%)	20 (7%)	0	100	100
3	o	274/326 (84%)	249 (91%)	25 (9%)	0	100	100
3	p	273/326 (84%)	252 (92%)	21 (8%)	0	100	100
3	q	269/326 (82%)	250 (93%)	19 (7%)	0	100	100
3	r	273/326 (84%)	243 (89%)	30 (11%)	0	100	100
All	All	12795/14601 (88%)	11885 (93%)	909 (7%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	d	96	GLY

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	1	238/477 (50%)	238 (100%)	0	100	100
1	2	238/477 (50%)	238 (100%)	0	100	100
1	3	238/477 (50%)	238 (100%)	0	100	100
2	A	348/348 (100%)	348 (100%)	0	100	100
2	B	348/348 (100%)	348 (100%)	0	100	100
2	C	348/348 (100%)	348 (100%)	0	100	100
2	D	348/348 (100%)	348 (100%)	0	100	100
2	E	348/348 (100%)	348 (100%)	0	100	100
2	F	348/348 (100%)	348 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	G	348/348 (100%)	348 (100%)	0	100	100
2	H	348/348 (100%)	348 (100%)	0	100	100
2	I	348/348 (100%)	348 (100%)	0	100	100
2	J	348/348 (100%)	348 (100%)	0	100	100
2	K	348/348 (100%)	348 (100%)	0	100	100
2	L	348/348 (100%)	348 (100%)	0	100	100
2	M	348/348 (100%)	348 (100%)	0	100	100
2	N	348/348 (100%)	348 (100%)	0	100	100
2	O	348/348 (100%)	348 (100%)	0	100	100
2	P	348/348 (100%)	348 (100%)	0	100	100
2	Q	348/348 (100%)	348 (100%)	0	100	100
2	R	348/348 (100%)	348 (100%)	0	100	100
3	a	250/300 (83%)	250 (100%)	0	100	100
3	b	254/300 (85%)	253 (100%)	1 (0%)	84	83
3	c	241/300 (80%)	241 (100%)	0	100	100
3	d	254/300 (85%)	254 (100%)	0	100	100
3	e	241/300 (80%)	241 (100%)	0	100	100
3	f	254/300 (85%)	254 (100%)	0	100	100
3	g	254/300 (85%)	253 (100%)	1 (0%)	84	83
3	h	250/300 (83%)	249 (100%)	1 (0%)	84	83
3	i	254/300 (85%)	253 (100%)	1 (0%)	84	83
3	j	252/300 (84%)	251 (100%)	1 (0%)	84	83
3	k	254/300 (85%)	254 (100%)	0	100	100
3	l	254/300 (85%)	253 (100%)	1 (0%)	84	83
3	m	253/300 (84%)	253 (100%)	0	100	100
3	n	254/300 (85%)	253 (100%)	1 (0%)	84	83
3	o	254/300 (85%)	254 (100%)	0	100	100
3	p	253/300 (84%)	252 (100%)	1 (0%)	84	83
3	q	250/300 (83%)	250 (100%)	0	100	100
3	r	253/300 (84%)	253 (100%)	0	100	100
All	All	11507/13095 (88%)	11499 (100%)	8 (0%)	87	89

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	p	238	ASN
3	n	238	ASN
3	j	69	ASN
3	i	238	ASN
3	l	238	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 78 such sidechains are listed below:

Mol	Chain	Res	Type
2	R	183	ASN
3	l	56	ASN
3	b	166	ASN
3	h	294	GLN
3	p	234	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 ⓘ

3 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	S	1	4,3	14,14,15	0.48	0	17,19,21	1.03	1 (5%)
4	NAG	S	2	4	14,14,15	0.22	0	17,19,21	0.46	0
4	BMA	S	3	4	11,11,12	0.68	0	15,15,17	0.75	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	S	1	4,3	-	2/6/23/26	0/1/1/1
4	NAG	S	2	4	-	2/6/23/26	0/1/1/1
4	BMA	S	3	4	-	2/2/19/22	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	S	1	NAG	C1-O5-C5	3.44	116.80	112.19

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

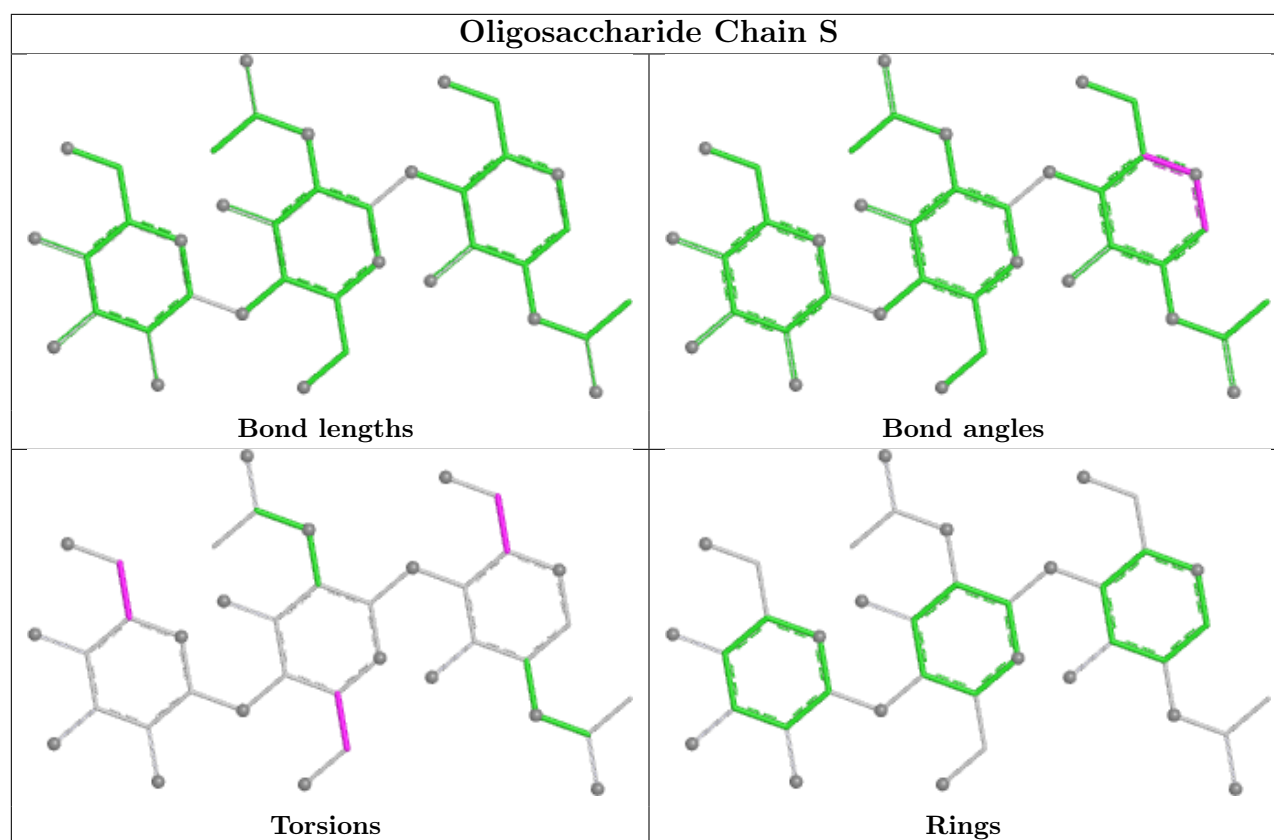
Mol	Chain	Res	Type	Atoms
4	S	1	NAG	C4-C5-C6-O6
4	S	1	NAG	O5-C5-C6-O6
4	S	3	BMA	O5-C5-C6-O6
4	S	3	BMA	C4-C5-C6-O6
4	S	2	NAG	C4-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	S	1	NAG	1	0
4	S	2	NAG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



5.6 Ligand geometry [i](#)

Of 107 ligands modelled in this entry, 72 are monoatomic - leaving 35 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	NAG	n	401	3	14,14,15	0.22	0	17,19,21	0.52	0
5	NAG	h	401	3	14,14,15	0.35	0	17,19,21	0.46	0
5	NAG	j	401	3	14,14,15	0.27	0	17,19,21	0.39	0
5	NAG	p	402	3	14,14,15	0.28	0	17,19,21	0.40	0
5	NAG	b	401	3	14,14,15	0.21	0	17,19,21	0.39	0
5	NAG	i	504	3	14,14,15	0.25	0	17,19,21	0.35	0
5	NAG	m	402	3	14,14,15	0.22	0	17,19,21	0.50	0
5	NAG	f	504	3	14,14,15	0.30	0	17,19,21	0.48	0
5	NAG	d	402	3	14,14,15	0.36	0	17,19,21	0.50	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	p	401	3	14,14,15	0.44	0	17,19,21	0.62	0
5	NAG	m	401	3	14,14,15	0.22	0	17,19,21	0.40	0
5	NAG	j	402	3	14,14,15	0.30	0	17,19,21	0.47	0
5	NAG	c	504	3	14,14,15	0.31	0	17,19,21	0.42	0
5	NAG	b	402	3	14,14,15	0.27	0	17,19,21	0.38	0
5	NAG	q	401	3	14,14,15	0.16	0	17,19,21	0.50	0
5	NAG	n	402	3	14,14,15	0.24	0	17,19,21	0.41	0
5	NAG	i	503	3	14,14,15	0.20	0	17,19,21	0.42	0
5	NAG	r	503	3	14,14,15	0.41	0	17,19,21	0.42	0
5	NAG	f	503	3	14,14,15	0.20	0	17,19,21	0.44	0
5	NAG	l	503	3	14,14,15	0.30	0	17,19,21	0.52	0
5	NAG	o	504	3	14,14,15	0.34	0	17,19,21	0.47	0
5	NAG	e	401	3	14,14,15	0.24	0	17,19,21	0.43	0
5	NAG	r	504	3	14,14,15	0.40	0	17,19,21	0.50	0
5	NAG	a	401	3	14,14,15	0.31	0	17,19,21	0.53	0
5	NAG	k	402	3	14,14,15	0.26	0	17,19,21	0.53	0
5	NAG	q	402	3	14,14,15	0.28	0	17,19,21	0.53	0
5	NAG	g	402	3	14,14,15	0.36	0	17,19,21	0.42	0
5	NAG	l	504	3	14,14,15	0.24	0	17,19,21	0.43	0
5	NAG	d	401	3	14,14,15	0.21	0	17,19,21	0.57	0
5	NAG	c	503	3	14,14,15	0.37	0	17,19,21	0.42	0
5	NAG	k	401	3	14,14,15	0.41	0	17,19,21	0.62	0
5	NAG	o	503	3	14,14,15	0.45	0	17,19,21	0.50	0
5	NAG	g	401	3	14,14,15	0.35	0	17,19,21	1.56	2 (11%)
5	NAG	h	402	3	14,14,15	0.29	0	17,19,21	0.41	0
5	NAG	e	402	3	14,14,15	0.41	0	17,19,21	0.38	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	n	401	3	-	2/6/23/26	0/1/1/1
5	NAG	h	401	3	-	3/6/23/26	0/1/1/1
5	NAG	j	401	3	-	2/6/23/26	0/1/1/1
5	NAG	p	402	3	-	0/6/23/26	0/1/1/1
5	NAG	b	401	3	-	2/6/23/26	0/1/1/1
5	NAG	i	504	3	-	2/6/23/26	0/1/1/1
5	NAG	m	402	3	-	0/6/23/26	0/1/1/1
5	NAG	f	504	3	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	d	402	3	-	2/6/23/26	0/1/1/1
5	NAG	p	401	3	-	2/6/23/26	0/1/1/1
5	NAG	m	401	3	-	0/6/23/26	0/1/1/1
5	NAG	j	402	3	-	2/6/23/26	0/1/1/1
5	NAG	c	504	3	-	1/6/23/26	0/1/1/1
5	NAG	b	402	3	-	0/6/23/26	0/1/1/1
5	NAG	q	401	3	-	2/6/23/26	0/1/1/1
5	NAG	n	402	3	-	2/6/23/26	0/1/1/1
5	NAG	i	503	3	-	2/6/23/26	0/1/1/1
5	NAG	r	503	3	-	3/6/23/26	0/1/1/1
5	NAG	f	503	3	-	2/6/23/26	0/1/1/1
5	NAG	l	503	3	-	1/6/23/26	0/1/1/1
5	NAG	o	504	3	-	0/6/23/26	0/1/1/1
5	NAG	e	401	3	-	2/6/23/26	0/1/1/1
5	NAG	r	504	3	-	0/6/23/26	0/1/1/1
5	NAG	a	401	3	-	0/6/23/26	0/1/1/1
5	NAG	k	402	3	-	2/6/23/26	0/1/1/1
5	NAG	q	402	3	-	0/6/23/26	0/1/1/1
5	NAG	g	402	3	-	0/6/23/26	0/1/1/1
5	NAG	l	504	3	-	0/6/23/26	0/1/1/1
5	NAG	d	401	3	-	2/6/23/26	0/1/1/1
5	NAG	c	503	3	-	0/6/23/26	0/1/1/1
5	NAG	k	401	3	-	2/6/23/26	0/1/1/1
5	NAG	o	503	3	-	3/6/23/26	0/1/1/1
5	NAG	g	401	3	-	5/6/23/26	0/1/1/1
5	NAG	h	402	3	-	1/6/23/26	0/1/1/1
5	NAG	e	402	3	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	g	401	NAG	C2-N2-C7	4.97	129.57	122.90
5	g	401	NAG	C1-C2-N2	3.22	115.51	110.43

There are no chirality outliers.

5 of 47 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	g	401	NAG	C1-C2-N2-C7
5	f	503	NAG	O5-C5-C6-O6
5	e	401	NAG	O5-C5-C6-O6
5	h	401	NAG	O5-C5-C6-O6
5	n	402	NAG	C4-C5-C6-O6

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	p	401	NAG	1	0
5	r	503	NAG	1	0
5	l	503	NAG	1	0
5	o	504	NAG	1	0

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.

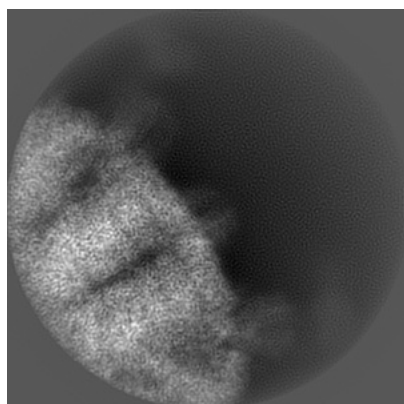
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26609. These allow visual inspection of the internal detail of the map and identification of artifacts.

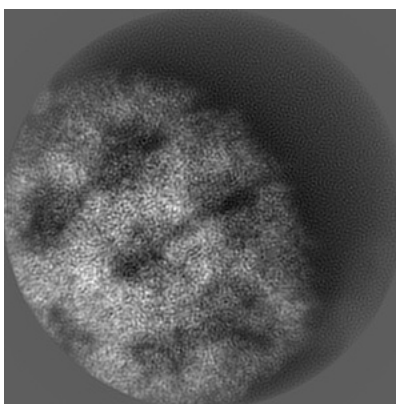
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

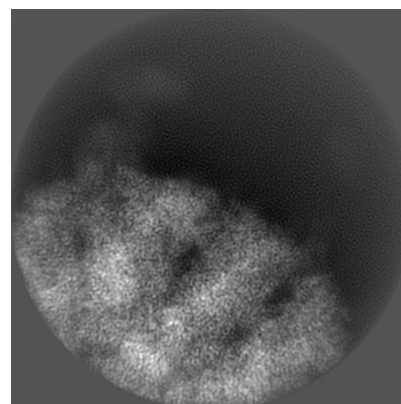
6.1.1 Primary map



X

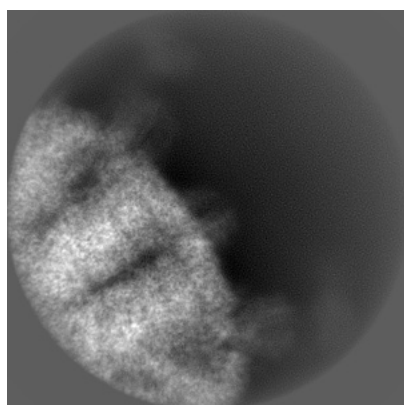


Y

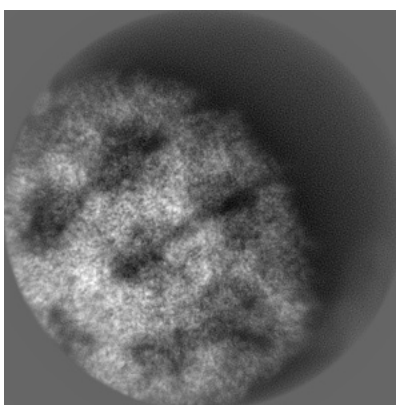


Z

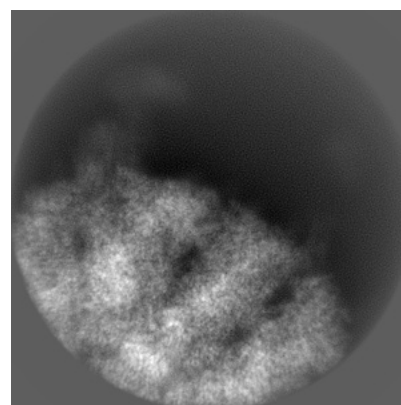
6.1.2 Raw map



X



Y

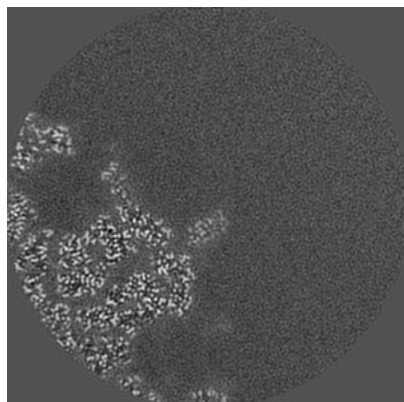


Z

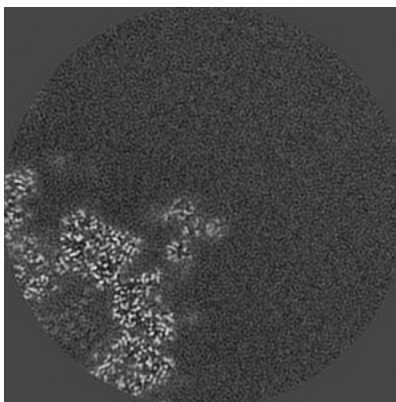
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

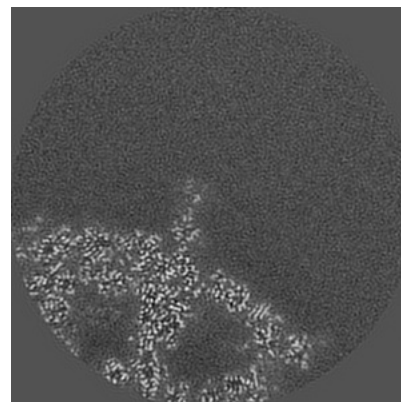
6.2.1 Primary map



X Index: 160

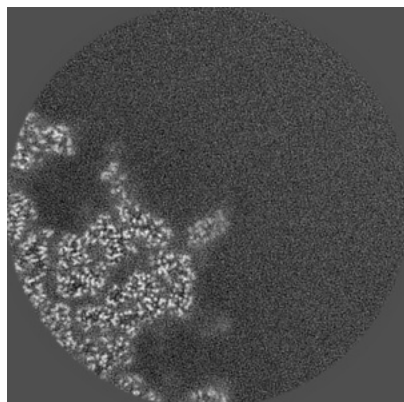


Y Index: 160

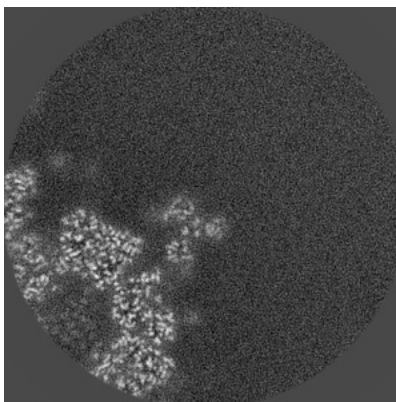


Z Index: 160

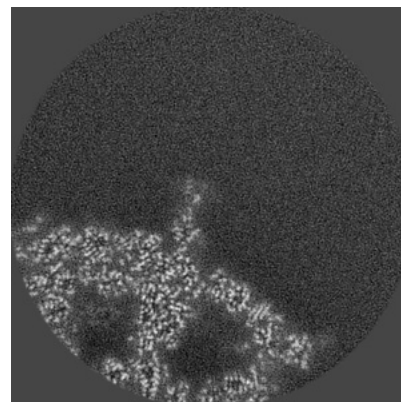
6.2.2 Raw map



X Index: 160



Y Index: 160

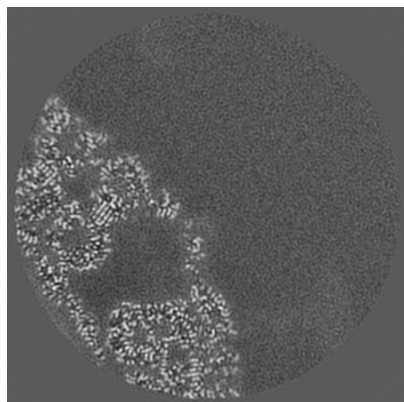


Z Index: 160

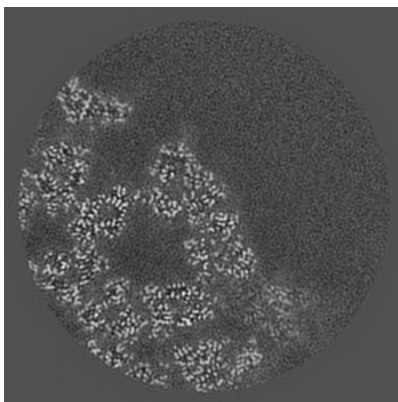
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

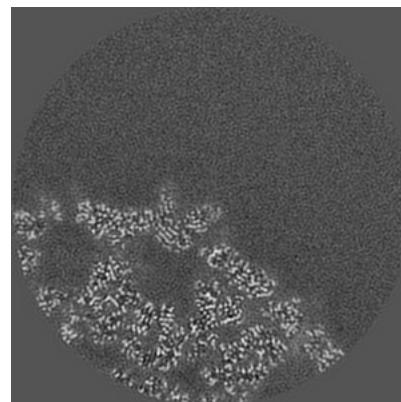
6.3.1 Primary map



X Index: 112

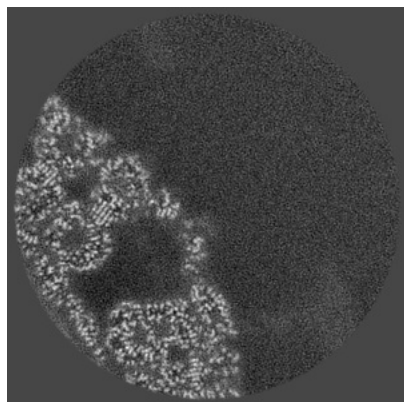


Y Index: 96

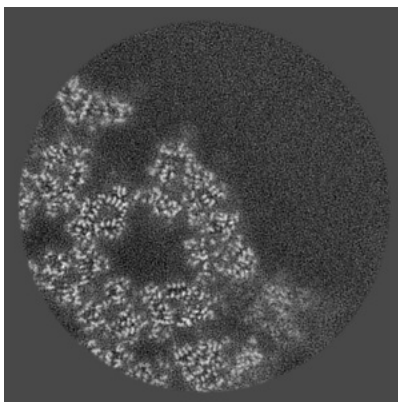


Z Index: 133

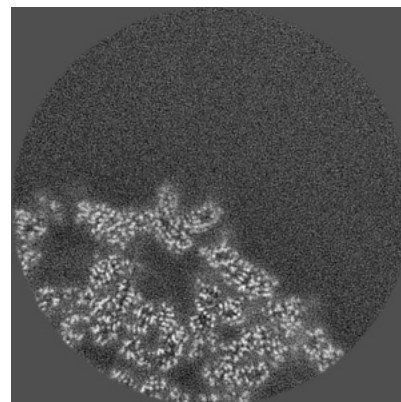
6.3.2 Raw map



X Index: 112



Y Index: 96

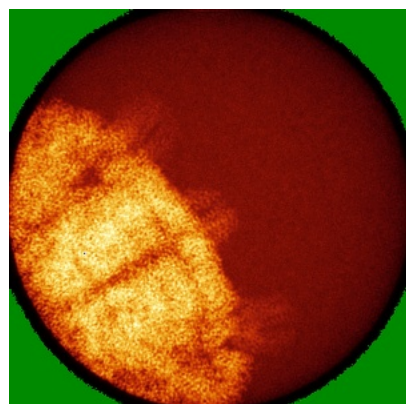


Z Index: 134

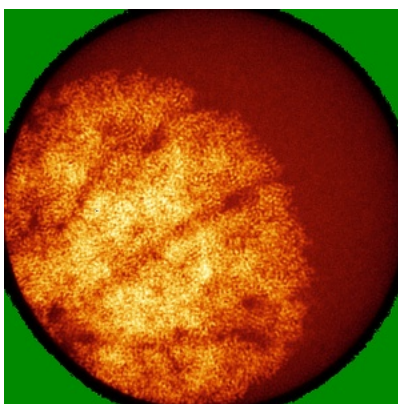
The images above show the largest variance slices of the map in three orthogonal directions.

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

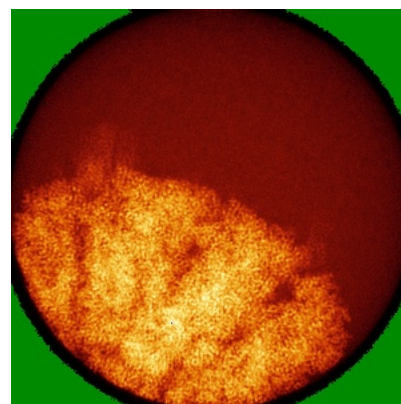
6.4.1 Primary map



X

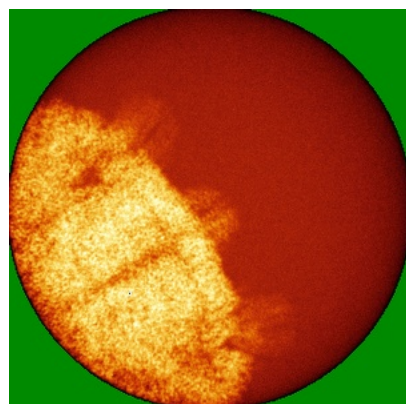


Y

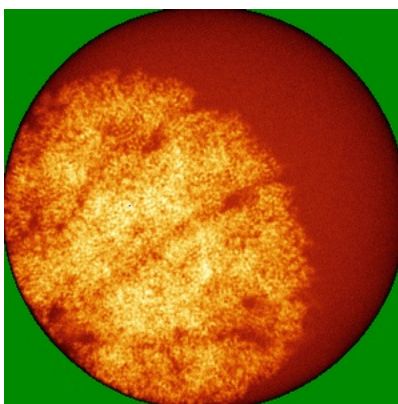


Z

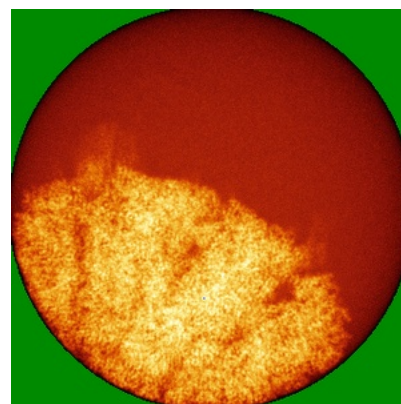
6.4.2 Raw map



X



Y

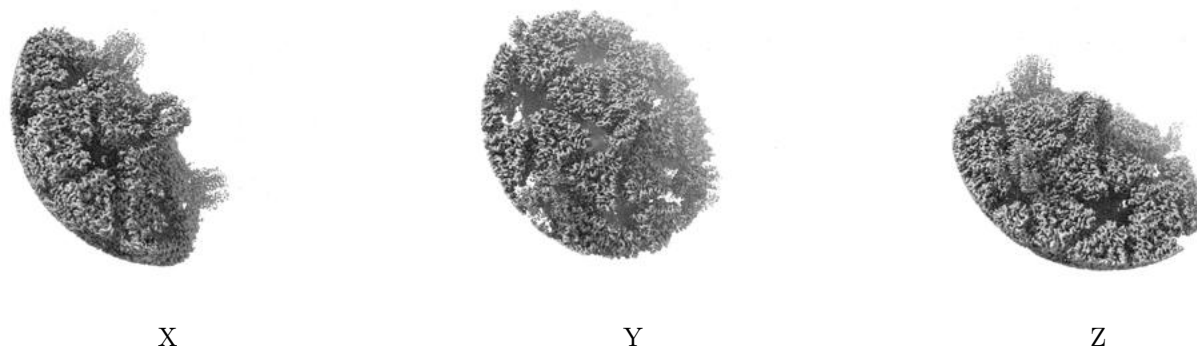


Z

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

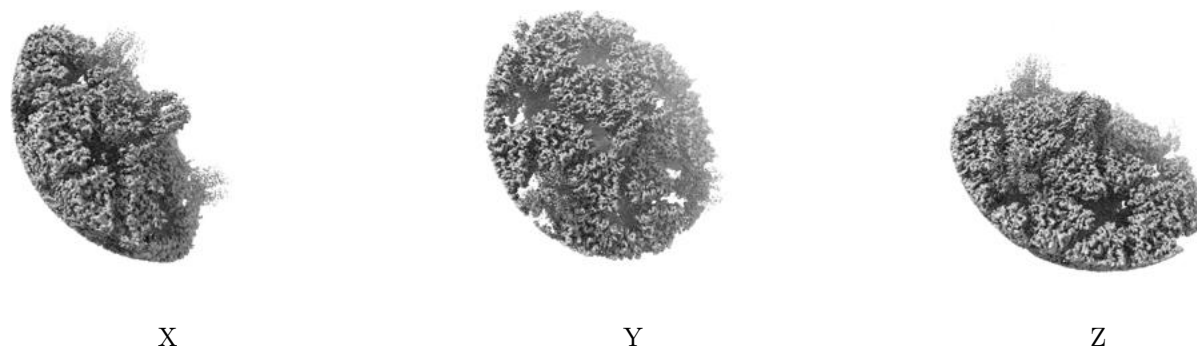
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

6.6 Mask visualisation [i](#)

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

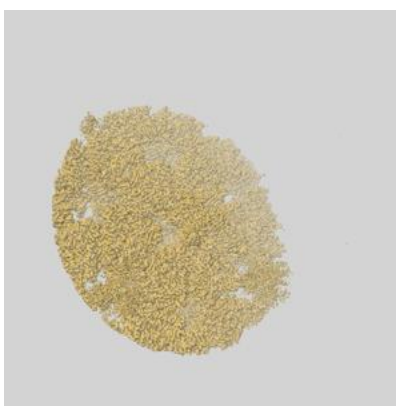
A mask typically either:

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

6.6.1 emd_26609_msk_1.map [i](#)



X



Y

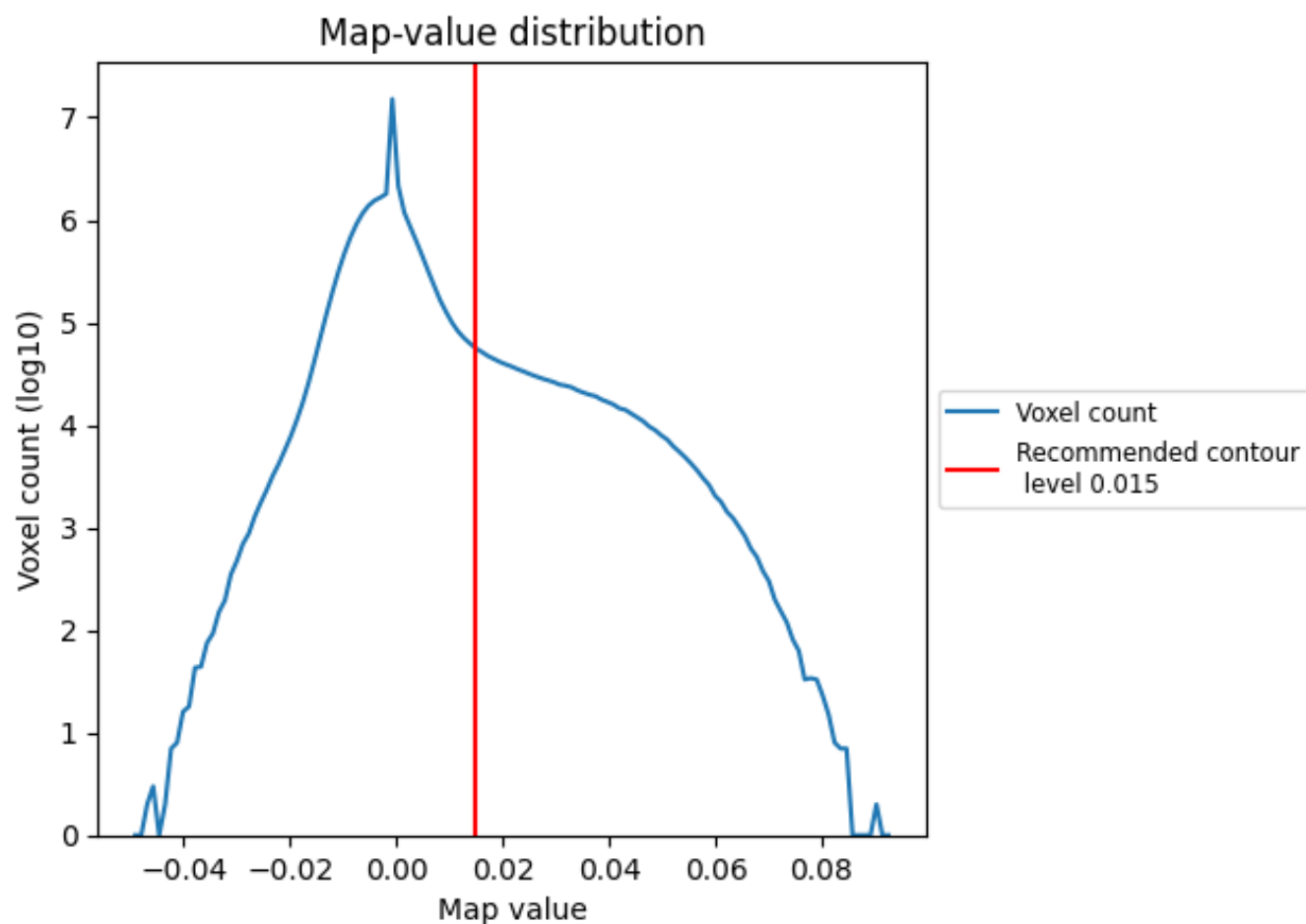


Z

7 Map analysis [i](#)

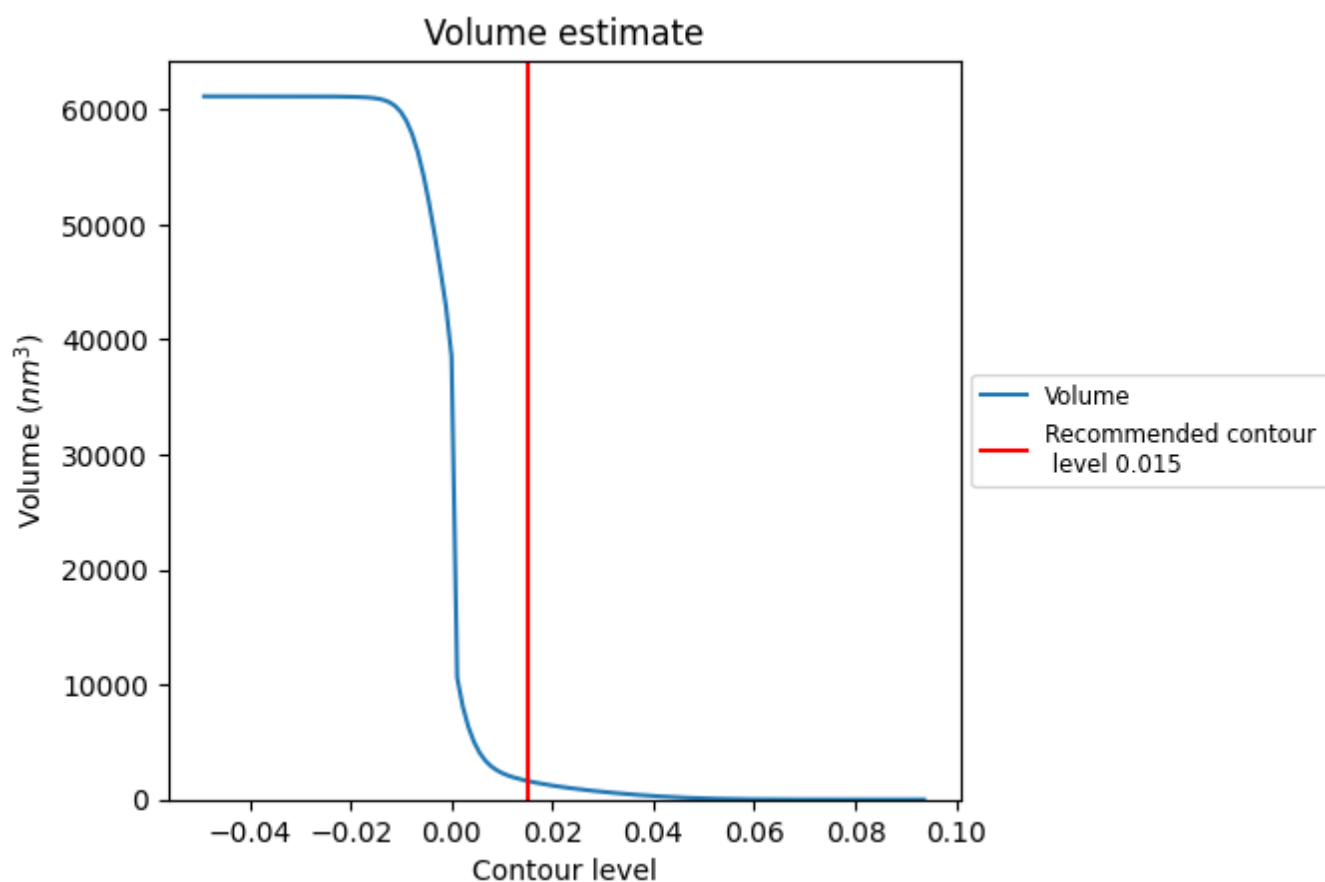
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

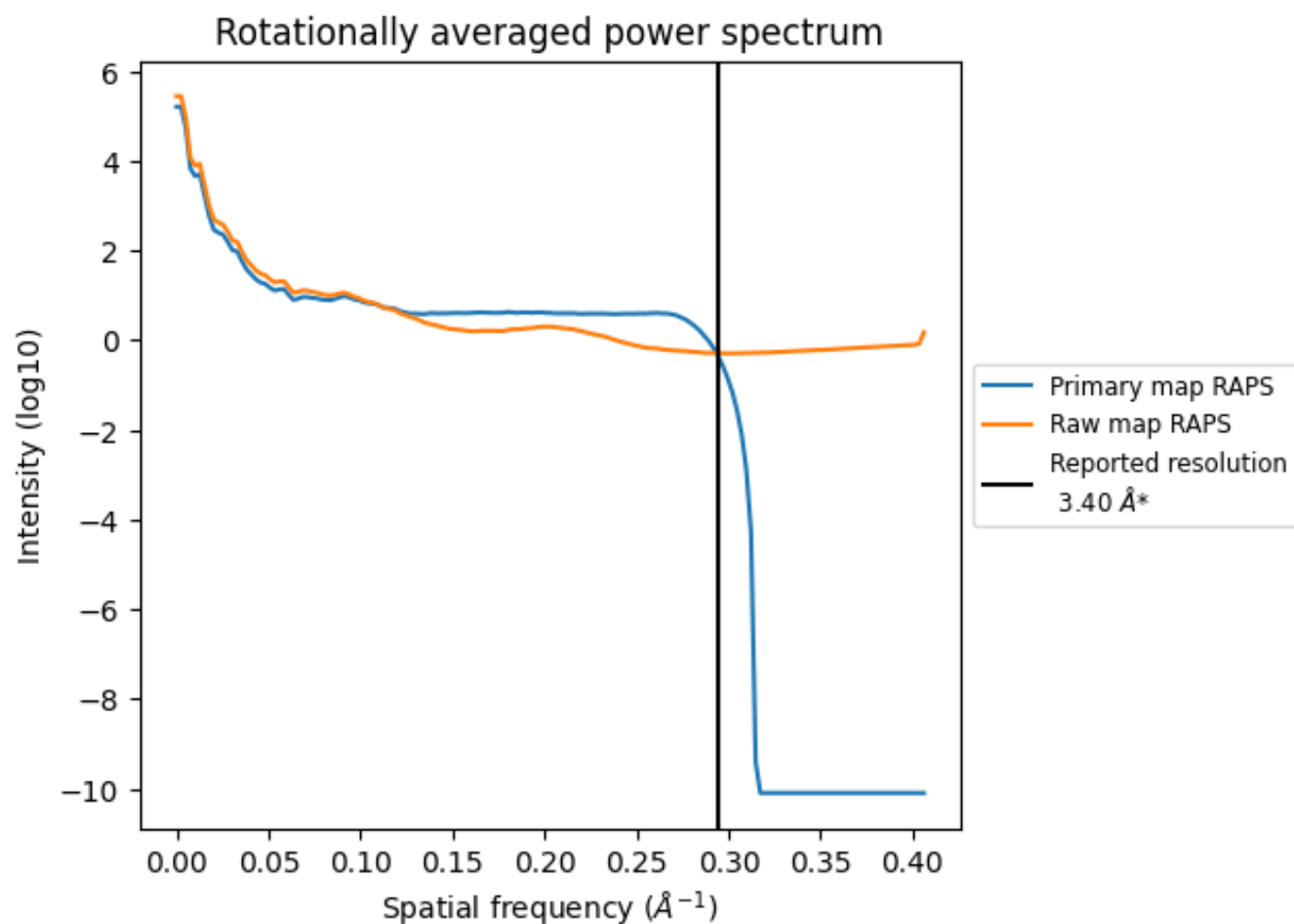
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1624 nm³; this corresponds to an approximate mass of 1467 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 ⓘ

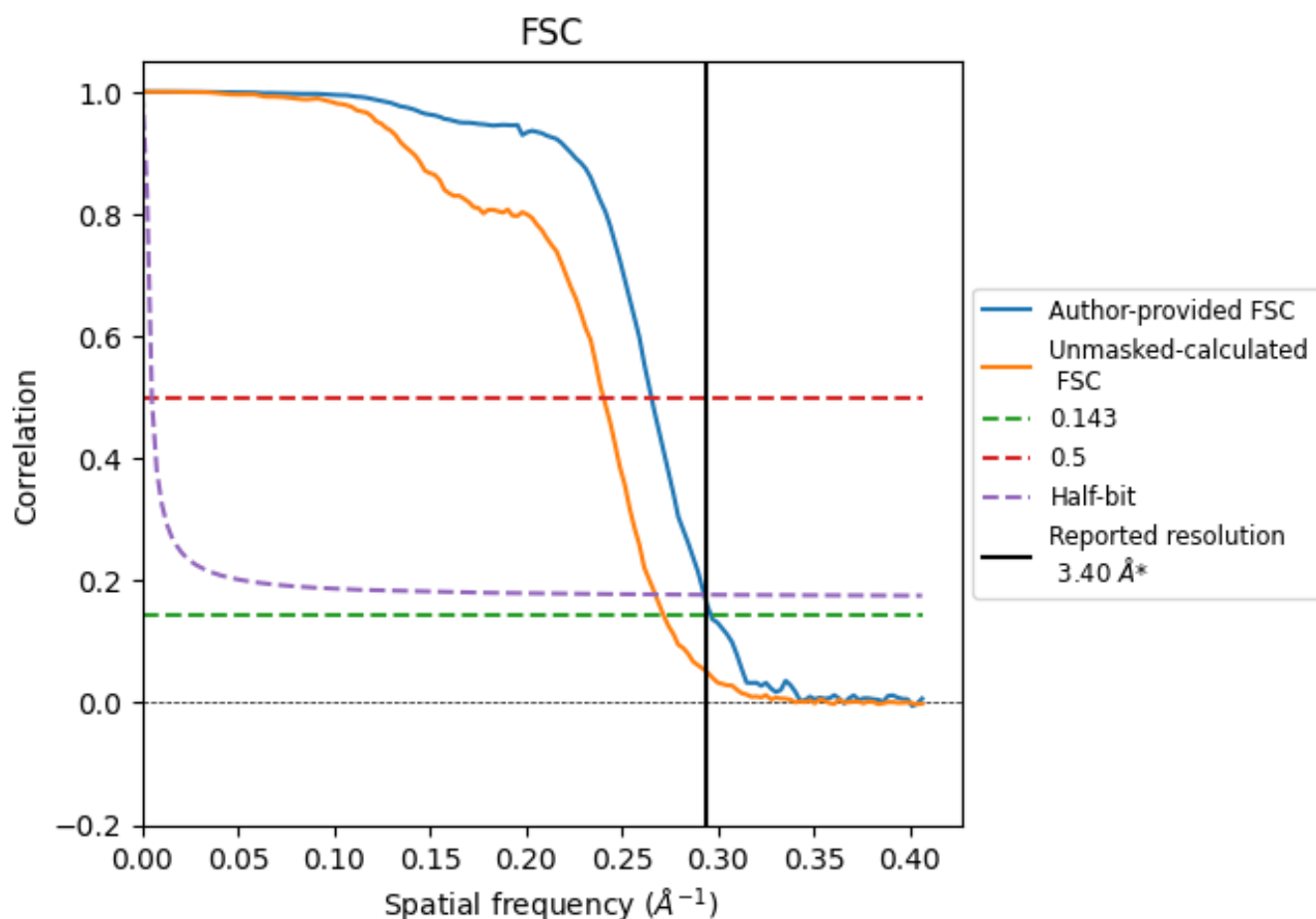


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

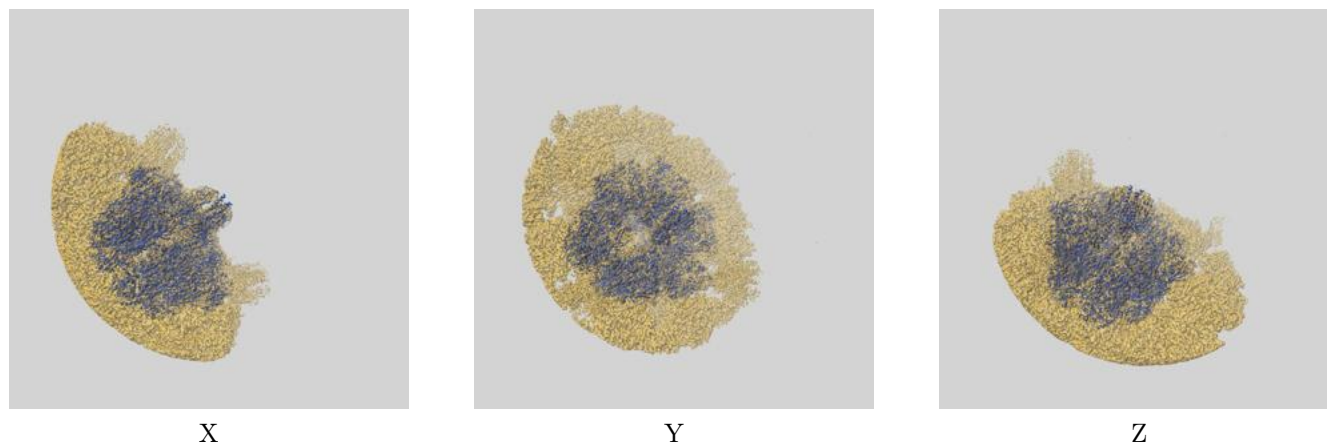
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.38	3.77	3.42
Unmasked-calculated*	3.68	4.16	3.74

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

9 Map-model fit [i](#)

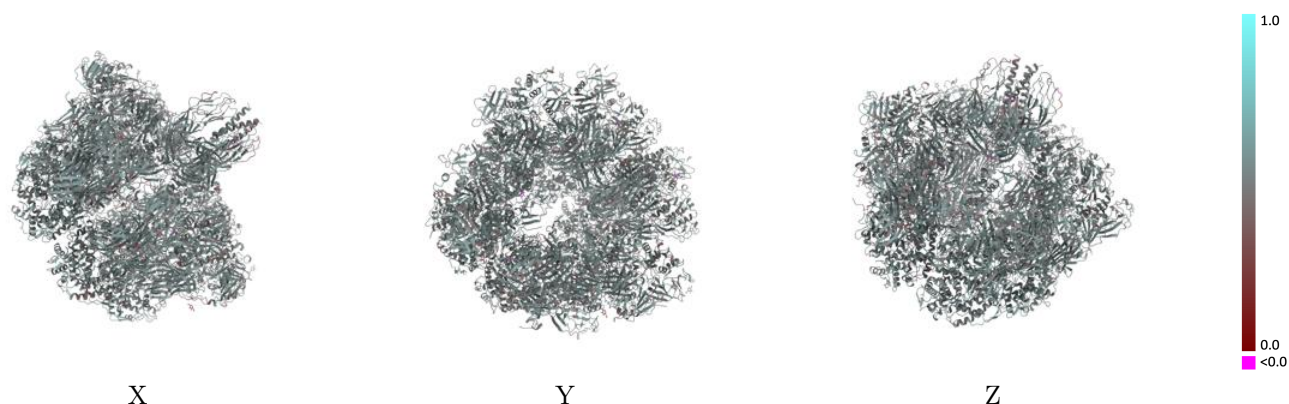
This section contains information regarding the fit between EMDB map EMD-26609 and PDB model 7UMT. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



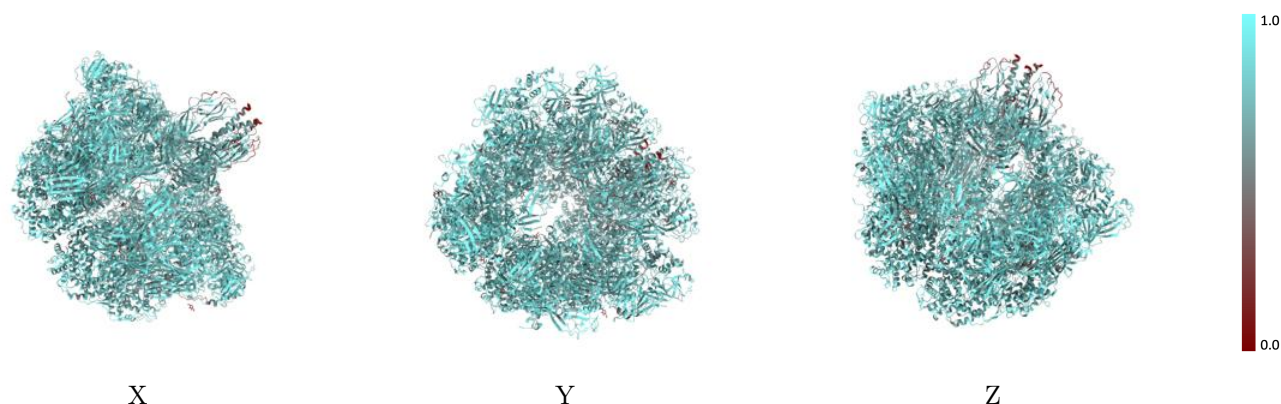
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



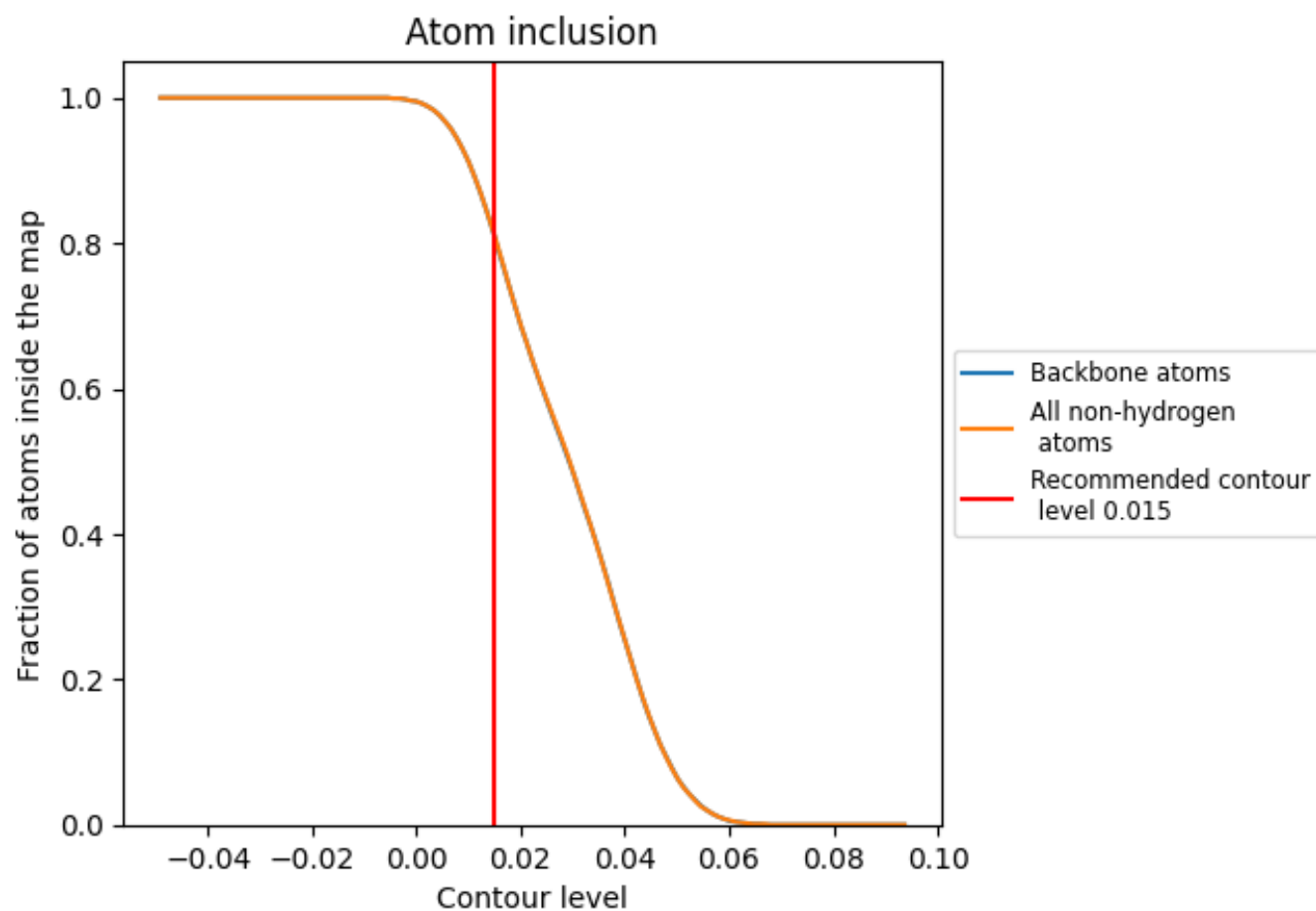
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.015).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 81% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8110	 0.5200
1	 0.6850	 0.5100
2	 0.7060	 0.5110
3	 0.7000	 0.5150
A	 0.8510	 0.5330
B	 0.8380	 0.5270
C	 0.8540	 0.5280
D	 0.8410	 0.5330
E	 0.8450	 0.5320
F	 0.8450	 0.5350
G	 0.8450	 0.5310
H	 0.8330	 0.5300
I	 0.8380	 0.5330
J	 0.8270	 0.5290
K	 0.8400	 0.5300
L	 0.8310	 0.5240
M	 0.8220	 0.5270
N	 0.8310	 0.5270
O	 0.8250	 0.5200
P	 0.8360	 0.5280
Q	 0.8310	 0.5290
R	 0.8280	 0.5220
S	 0.4620	 0.3860
a	 0.8310	 0.5150
b	 0.7900	 0.5010
c	 0.8190	 0.5110
d	 0.8260	 0.5150
e	 0.8280	 0.5110
f	 0.8270	 0.5160
g	 0.7970	 0.5020
h	 0.8220	 0.5130
i	 0.8310	 0.5180
j	 0.8180	 0.5060
k	 0.8100	 0.5060
l	 0.8120	 0.5130



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Chain	Atom inclusion	Q-score
m	 0.8230	 0.5170
n	 0.8080	 0.5080
o	 0.8110	 0.5060
p	 0.8000	 0.5000
q	 0.8110	 0.5070
r	 0.8010	 0.5000