



wwPDB EM Validation Summary Report ⓘ

May 19, 2026 – 04:34 PM EDT

PDB ID : 9OVK / pdb_00009ovk
EMDB ID : EMD-70900
Title : Cryo-EM structure of HCoV-OC43-Lab Spike glycoprotein in complex with 9O-acetyl GD3 sialoglycan (D1 domain local refine)
Authors : Jin, M.; Rini, J.M.
Deposited on : 2025-05-30
Resolution : 1.70 Å(reported)

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

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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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

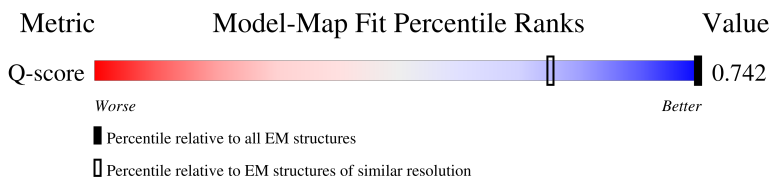
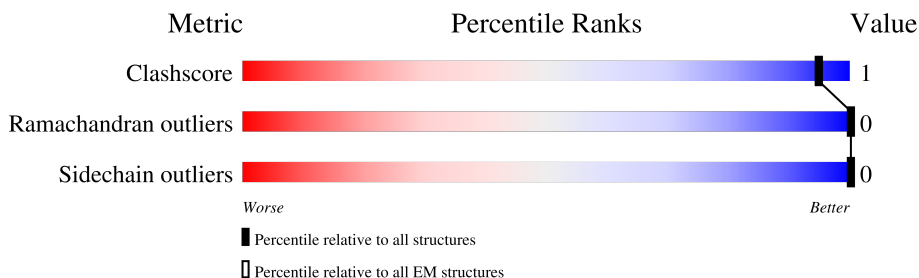
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY


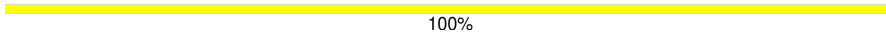
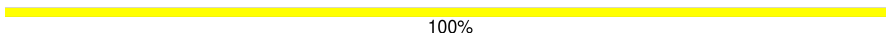
The reported resolution of this entry is 1.70 Å.

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	597 (1.20 - 2.20)

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	1344	 19% 79%
2	B	2	 100%
2	C	2	 100%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5008 atoms, of which 2303 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 Spike glycoprotein.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	279	Total	C	H	N	O	S	0	0
			4430	1457	2185	356	417	15		

There are 67 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	958	ILE	PHE	conflict	UNP Q696P8
A	1025	PRO	THR	conflict	UNP Q696P8
A	1070	PRO	ALA	conflict	UNP Q696P8
A	1071	PRO	LEU	conflict	UNP Q696P8
A	1296	SER	-	expression tag	UNP Q696P8
A	1297	GLY	-	expression tag	UNP Q696P8
A	1298	GLY	-	expression tag	UNP Q696P8
A	1299	TYR	-	expression tag	UNP Q696P8
A	1300	ILE	-	expression tag	UNP Q696P8
A	1301	PRO	-	expression tag	UNP Q696P8
A	1302	GLU	-	expression tag	UNP Q696P8
A	1303	ALA	-	expression tag	UNP Q696P8
A	1304	PRO	-	expression tag	UNP Q696P8
A	1305	ARG	-	expression tag	UNP Q696P8
A	1306	ASP	-	expression tag	UNP Q696P8
A	1307	GLY	-	expression tag	UNP Q696P8
A	1308	GLN	-	expression tag	UNP Q696P8
A	1309	ALA	-	expression tag	UNP Q696P8
A	1310	TYR	-	expression tag	UNP Q696P8
A	1311	VAL	-	expression tag	UNP Q696P8
A	1312	ARG	-	expression tag	UNP Q696P8
A	1313	LYS	-	expression tag	UNP Q696P8
A	1314	ASP	-	expression tag	UNP Q696P8
A	1315	GLY	-	expression tag	UNP Q696P8
A	1316	GLU	-	expression tag	UNP Q696P8
A	1317	TRP	-	expression tag	UNP Q696P8
A	1318	VAL	-	expression tag	UNP Q696P8
A	1319	LEU	-	expression tag	UNP Q696P8

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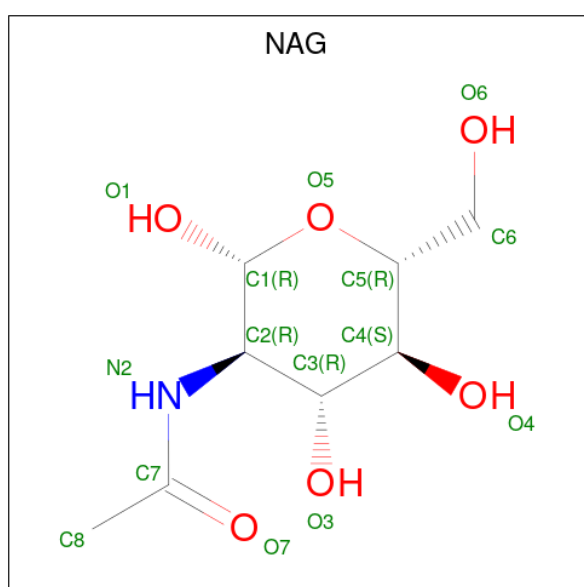
Chain	Residue	Modelled	Actual	Comment	Reference
A	1320	LEU	-	expression tag	UNP Q696P8
A	1321	SER	-	expression tag	UNP Q696P8
A	1322	THR	-	expression tag	UNP Q696P8
A	1323	PHE	-	expression tag	UNP Q696P8
A	1324	LEU	-	expression tag	UNP Q696P8
A	1325	ASN	-	expression tag	UNP Q696P8
A	1326	SER	-	expression tag	UNP Q696P8
A	1327	GLY	-	expression tag	UNP Q696P8
A	1328	ARG	-	expression tag	UNP Q696P8
A	1329	ALA	-	expression tag	UNP Q696P8
A	1330	HIS	-	expression tag	UNP Q696P8
A	1331	HIS	-	expression tag	UNP Q696P8
A	1332	HIS	-	expression tag	UNP Q696P8
A	1333	HIS	-	expression tag	UNP Q696P8
A	1334	HIS	-	expression tag	UNP Q696P8
A	1335	HIS	-	expression tag	UNP Q696P8
A	1336	GLY	-	expression tag	UNP Q696P8
A	1337	ALA	-	expression tag	UNP Q696P8
A	1338	GLY	-	expression tag	UNP Q696P8
A	1339	GLY	-	expression tag	UNP Q696P8
A	1340	LEU	-	expression tag	UNP Q696P8
A	1341	ASN	-	expression tag	UNP Q696P8
A	1342	ASP	-	expression tag	UNP Q696P8
A	1343	ILE	-	expression tag	UNP Q696P8
A	1344	PHE	-	expression tag	UNP Q696P8
A	1345	GLU	-	expression tag	UNP Q696P8
A	1346	ALA	-	expression tag	UNP Q696P8
A	1347	GLN	-	expression tag	UNP Q696P8
A	1348	LYS	-	expression tag	UNP Q696P8
A	1349	ILE	-	expression tag	UNP Q696P8
A	1350	GLU	-	expression tag	UNP Q696P8
A	1351	TRP	-	expression tag	UNP Q696P8
A	1352	HIS	-	expression tag	UNP Q696P8
A	1353	GLU	-	expression tag	UNP Q696P8
A	1354	ASP	-	expression tag	UNP Q696P8
A	1355	THR	-	expression tag	UNP Q696P8
A	1356	ALA	-	expression tag	UNP Q696P8
A	1357	ALA	-	expression tag	UNP Q696P8
A	1358	ALA	-	expression tag	UNP Q696P8

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



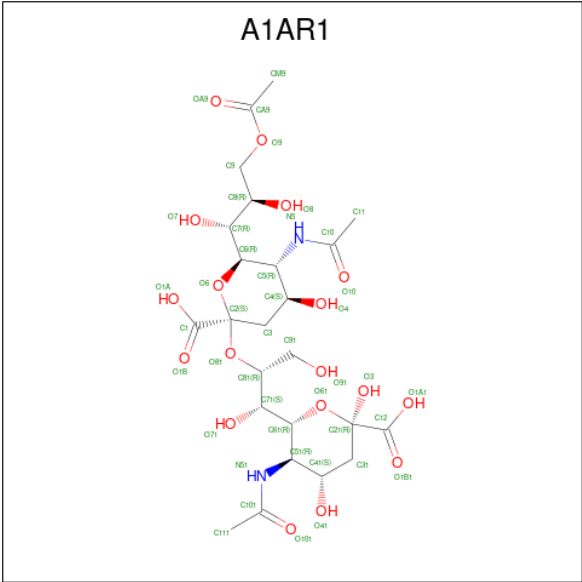
Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	2	Total	C	H	N	O	0	0
			55	16	27	2	10		
2	C	2	Total	C	H	N	O	0	0
			55	16	27	2	10		

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	H	N	O	0
			28	8	14	1	5	
3	A	1	Total	C	H	N	O	0
			28	8	14	1	5	

- Molecule 4 is 5-acetamido-8-O-(5-acetamido-9-O-acetyl-3,5-dideoxy-D-glycero-alpha-D-galacto-non-2-ulopyranonosyl)-3,5-dideoxy-D-glycero-alpha-D-galacto-non-2-ulopyranosonic acid (CCD ID: A1AR1) (formula: $C_{24}H_{38}N_2O_{18}$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	H	N	O	
4	A	1	80	24	36	2	18	0

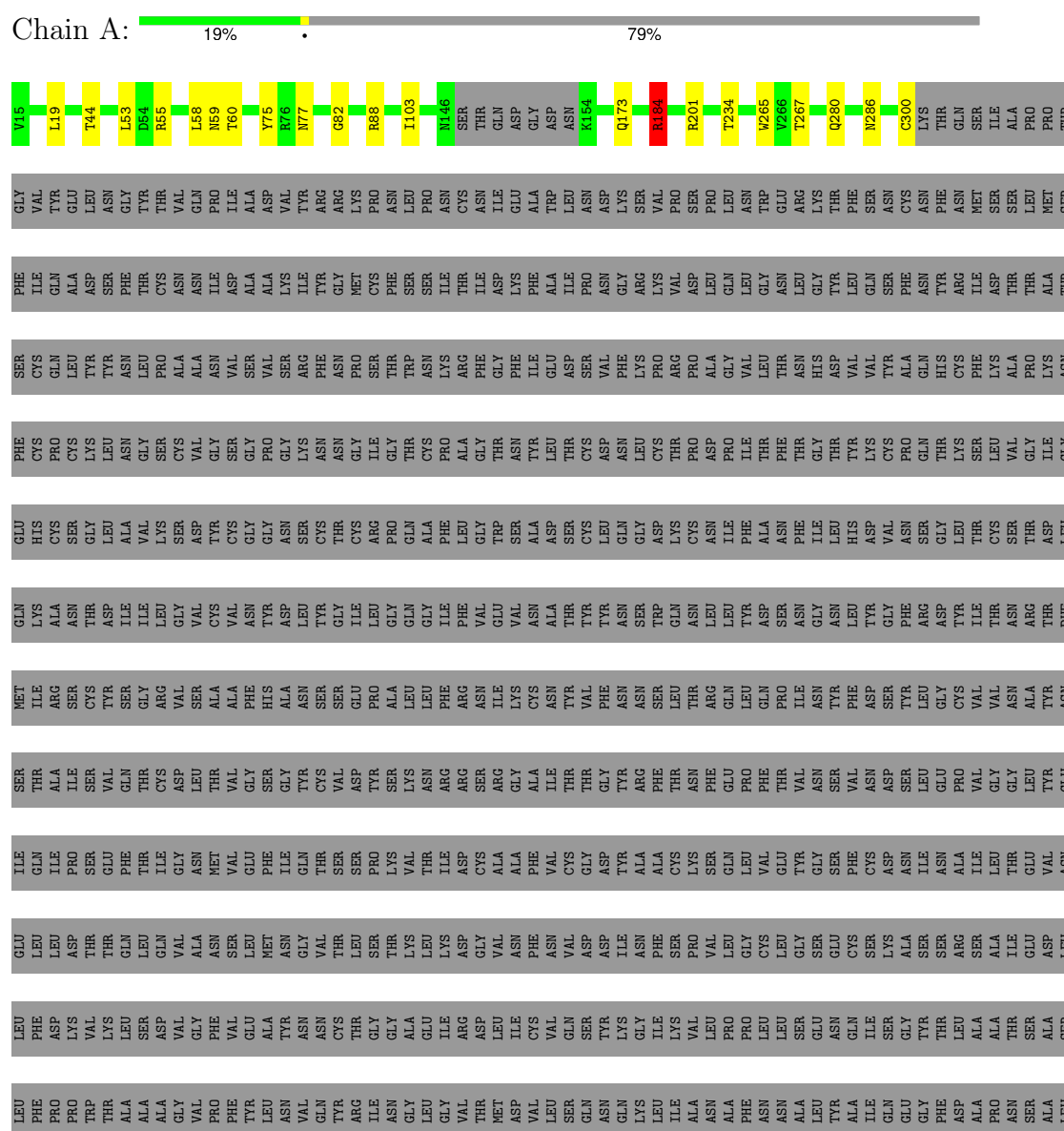
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		AltConf
5	A	332	Total	O	0
			332	332	

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: Spike glycoprotein



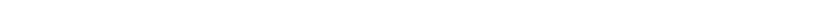
HIS	LEU	THR	SER	ALA	VAL
HIS	GLN	CYS	TYR	THR	LYS
HIS	GLU	ALA	VAL	VAL	ILE
HIS	ALA	VAL	PRO	THR	GLN
HIS	ILE	ASN	THR	GLN	VAL
HIS	LYS	TYR	LYS	GLN	VAL
GLY	VAL	THR	TYR	LEU	VAL
ALA	LEU	THR	VAL	SER	VAL
GLY	ALA	LYS	THR	ASP	ASN
GLY	ASN	ALA	THR	ASP	ASN
LEU	GLN	PRO	ALA	THR	ALA
LEU	SER	TYR	ARG	THR	GLU
ASN	TYR	VAL	VAL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

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

Chain B: 100%

NAG1
NAG2

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

Chain C:  100%

NAG1
NAG2

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	4195440	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	36	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	120000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	176.771	Depositor
Minimum map value	-59.664	Depositor
Average map value	-0.051	Depositor
Map value standard deviation	2.363	Depositor
Recommended contour level	25	Depositor
Map size (\AA)	345.6, 345.6, 345.6	wwPDB
Map dimensions	540, 540, 540	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.64, 0.64, 0.64	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: A1AR1, NAG

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	1.73	3/2305 (0.1%)	1.43	12/3139 (0.4%)

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	A	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	184	ARG	CD-NE	-6.17	1.37	1.46
1	A	103	ILE	C-O	-5.43	1.18	1.23
1	A	234	THR	CB-OG1	-5.23	1.35	1.43

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	184	ARG	NE-CZ-NH2	11.47	129.52	119.20
1	A	184	ARG	NE-CZ-NH1	-10.32	111.18	121.50
1	A	300	CYS	CA-C-O	-6.57	109.63	120.80
1	A	55	ARG	NE-CZ-NH2	6.27	124.84	119.20
1	A	60	THR	CA-CB-CG2	6.00	120.70	110.50

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	184	ARG	Sidechain
1	A	75	TYR	Sidechain

5.2 Too-close contacts [i](#)

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	2245	2185	2181	5	0
2	B	28	27	25	0	0
2	C	28	27	25	0	0
3	A	28	28	26	1	0
4	A	44	36	0	0	0
5	A	332	0	0	0	0
All	All	2705	2303	2257	5	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

All (5) 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)
1:A:173:GLN:OE1	1:A:184:ARG:HD3	2.16	0.46
1:A:58:LEU:HD12	3:A:1401:NAG:H82	2.01	0.42
1:A:19:LEU:HD12	1:A:19:LEU:HA	1.90	0.42
1:A:77:ASN:HB2	1:A:265:TRP:CZ3	2.55	0.41
1:A:44:THR:O	1:A:286:ASN:HA	2.21	0.40

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	A	275/1344 (20%)	267 (97%)	8 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	254/1166 (22%)	254 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	183	HIS
1	A	248	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

4 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
2	NAG	B	1	2,1	14,14,15	0.84	0	17,19,21	1.45	3 (17%)
2	NAG	B	2	2	14,14,15	1.07	1 (7%)	17,19,21	1.13	1 (5%)
2	NAG	C	1	2,1	14,14,15	0.69	0	17,19,21	0.90	1 (5%)
2	NAG	C	2	2	14,14,15	0.90	1 (7%)	17,19,21	1.59	3 (17%)

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
2	NAG	B	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	B	2	2	-	0/6/23/26	0/1/1/1
2	NAG	C	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	C	2	2	-	0/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	2	NAG	O5-C5	2.64	1.48	1.43
2	B	2	NAG	O5-C5	2.63	1.48	1.43

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	NAG	C1-O5-C5	4.78	118.59	112.19
2	B	1	NAG	C1-C2-N2	-3.44	105.02	110.43
2	C	2	NAG	C2-N2-C7	2.64	126.44	122.90
2	B	2	NAG	O5-C1-C2	-2.39	107.59	111.29
2	B	1	NAG	C6-C5-C4	2.22	118.47	113.02

There are no chirality outliers.

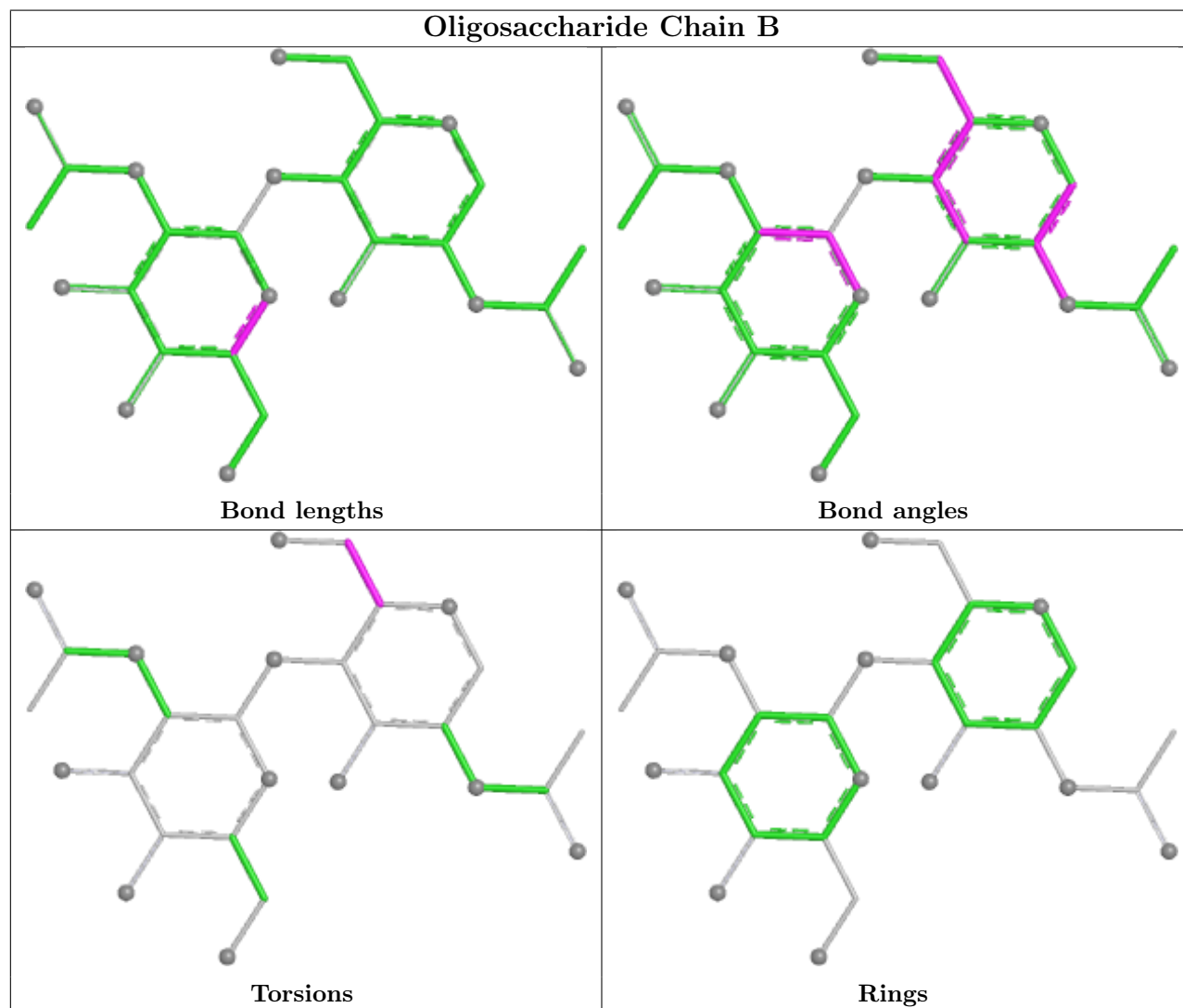
All (2) torsion outliers are listed below:

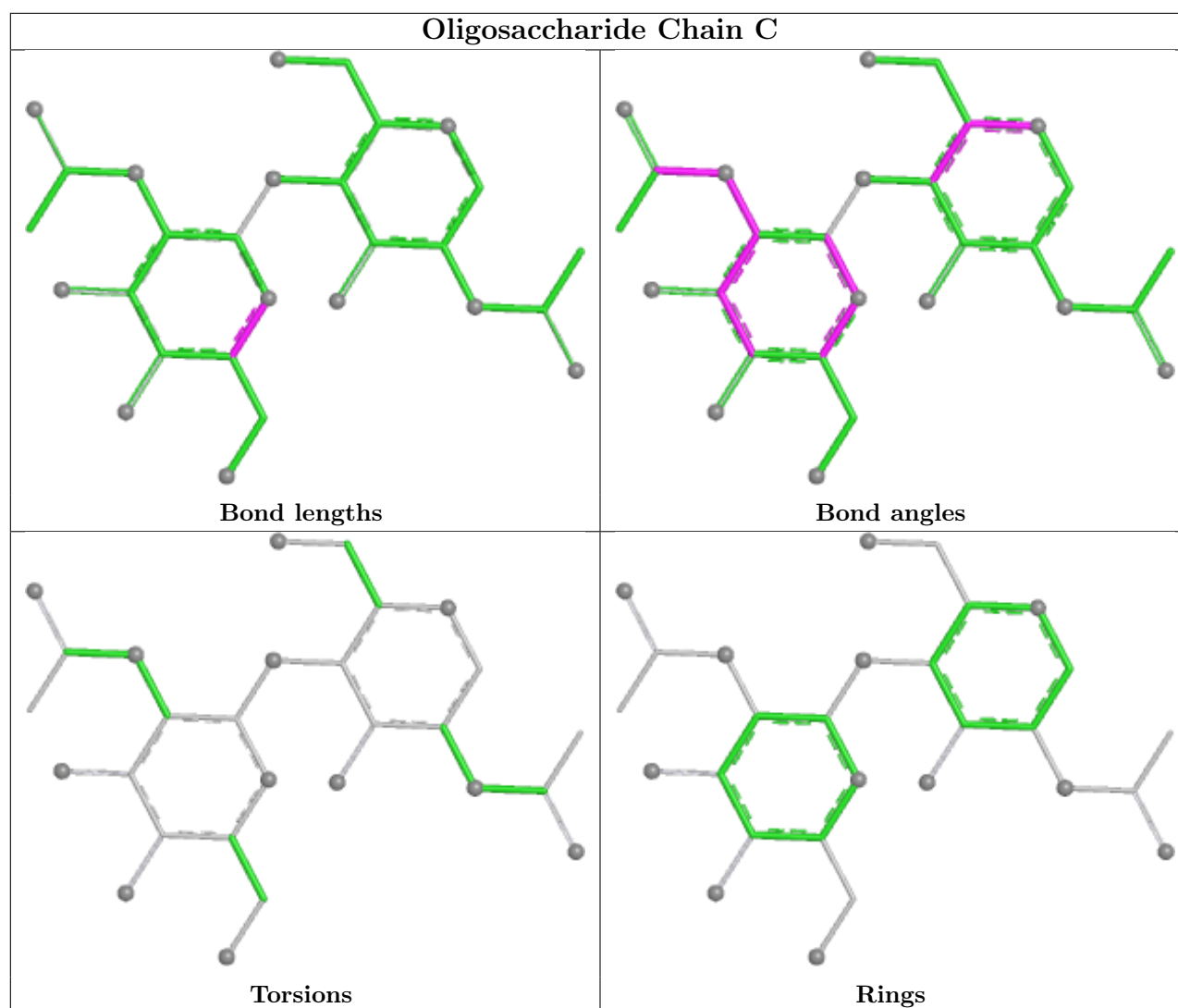
Mol	Chain	Res	Type	Atoms
2	B	1	NAG	C4-C5-C6-O6
2	B	1	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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](#)

3 ligands 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	$\# Z > 2$
3	NAG	A	1402	1	14,14,15	1.12	1 (7%)	17,19,21	0.82	0
3	NAG	A	1401	1	14,14,15	1.00	1 (7%)	17,19,21	1.30	1 (5%)
4	A1AR1	A	1403	-	44,45,45	1.42	7 (15%)	55,67,67	1.33	6 (10%)

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
3	NAG	A	1402	1	-	2/6/23/26	0/1/1/1
3	NAG	A	1401	1	-	0/6/23/26	0/1/1/1
4	A1AR1	A	1403	-	-	11/47/84/84	0/2/2/2

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1403	A1AR1	C21-C12	3.71	1.59	1.53
4	A	1403	A1AR1	C2-C1	3.34	1.62	1.54
4	A	1403	A1AR1	O3-C21	3.08	1.44	1.39
3	A	1402	NAG	O5-C5	3.01	1.49	1.43
3	A	1401	NAG	C8-C7	2.73	1.56	1.50

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1403	A1AR1	O6-C2-C3	-4.57	105.21	111.35
4	A	1403	A1AR1	O1B1-C12-C21	-3.57	117.89	123.85
4	A	1403	A1AR1	O6-C6-C5	-3.07	107.03	109.84
3	A	1401	NAG	O5-C1-C2	-2.72	107.08	111.29
4	A	1403	A1AR1	C31-C21-C12	-2.54	108.12	112.84

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

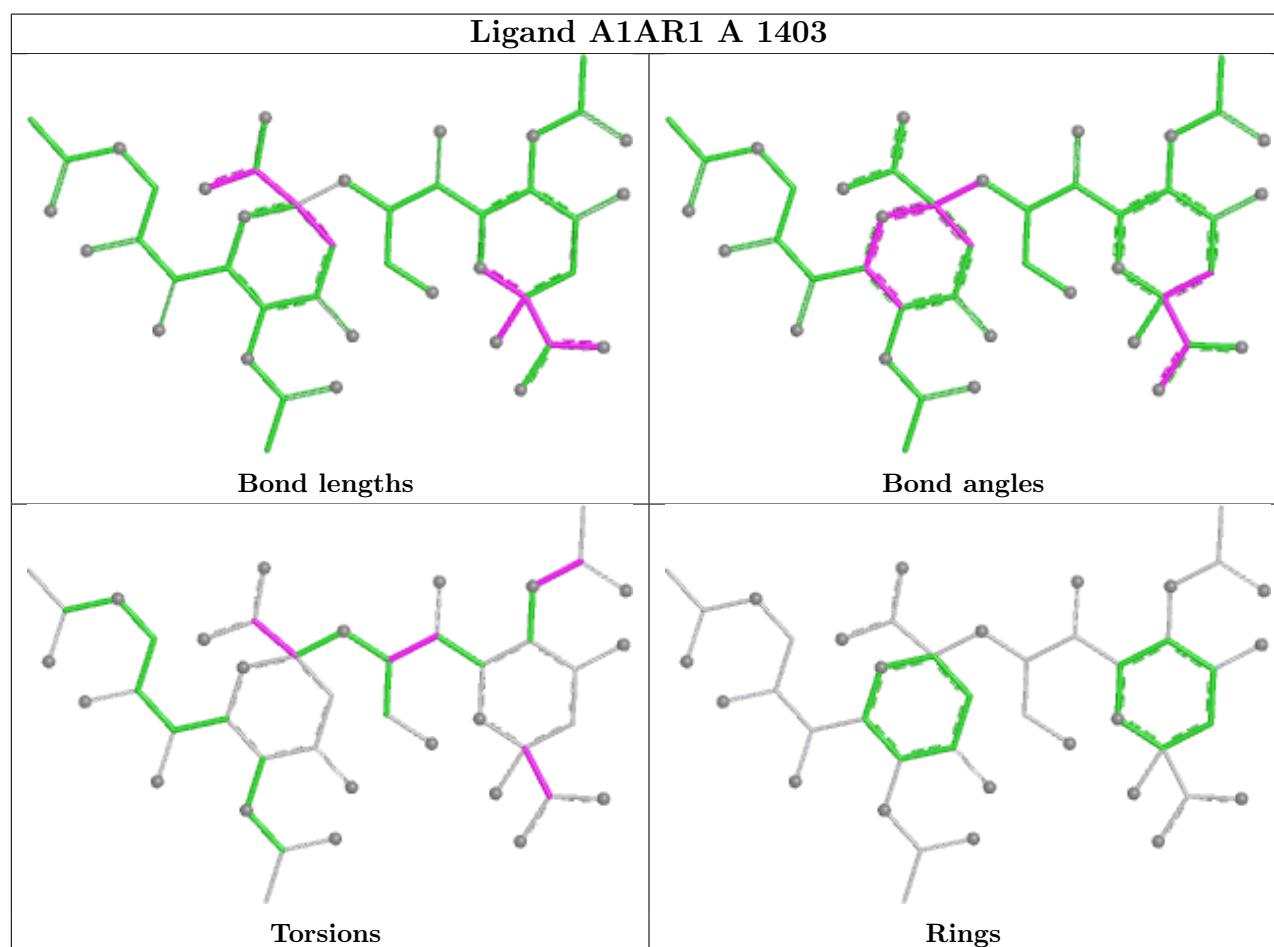
Mol	Chain	Res	Type	Atoms
4	A	1403	A1AR1	O1A1-C12-C21-O3
4	A	1403	A1AR1	O1B1-C12-C21-O3
4	A	1403	A1AR1	O1A1-C12-C21-O61
4	A	1403	A1AR1	O1A-C1-C2-O81
4	A	1403	A1AR1	C111-C101-N51-C51

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1401	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 all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

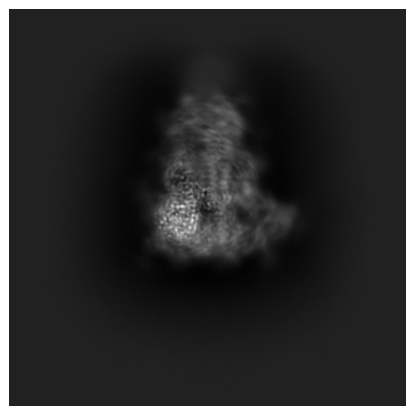
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-70900. These allow visual inspection of the internal detail of the map and identification of artifacts.

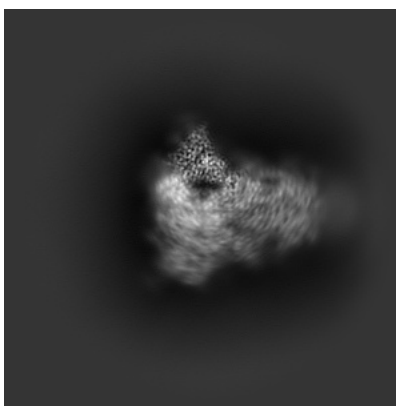
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

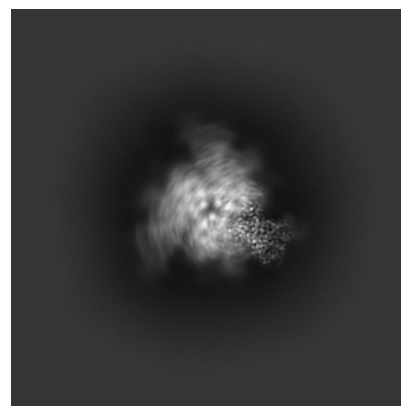
6.1.1 Primary map



X

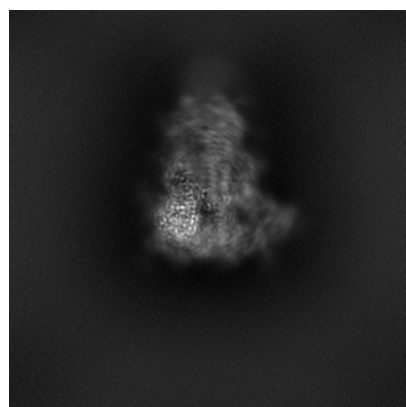


Y

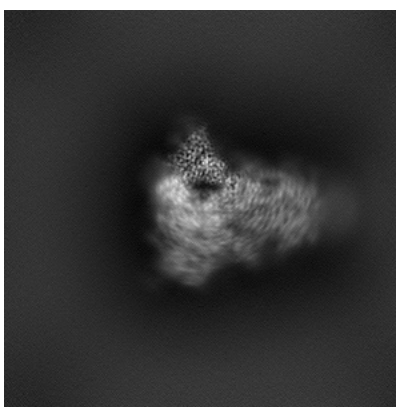


Z

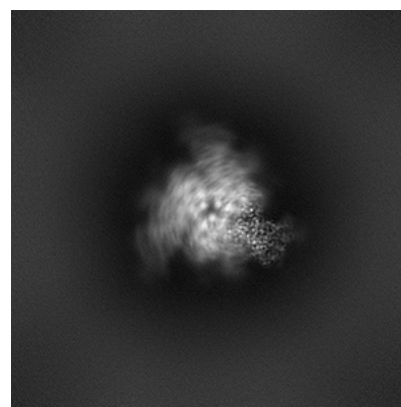
6.1.2 Raw map



X



Y

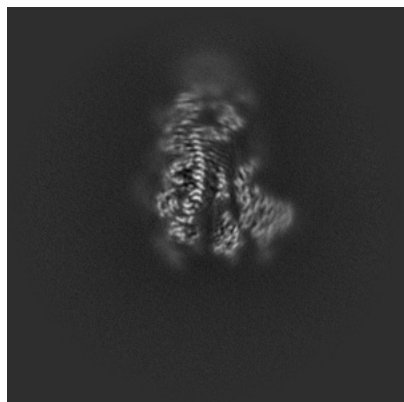


Z

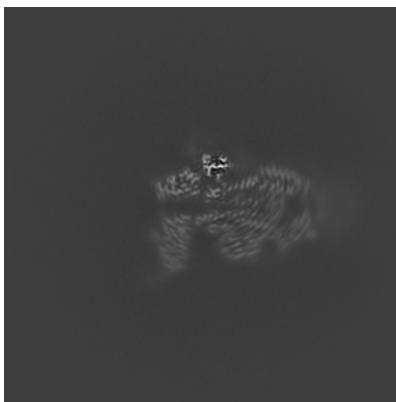
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 270



Y Index: 270

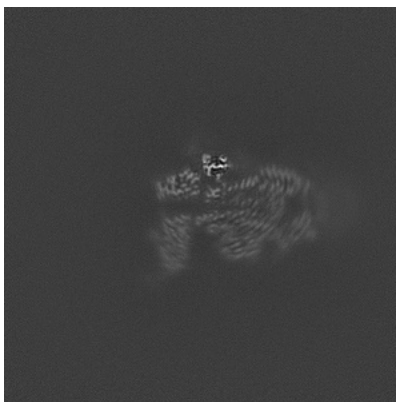


Z Index: 270

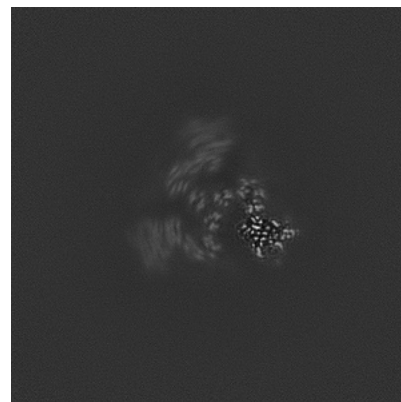
6.2.2 Raw map



X Index: 270



Y Index: 270

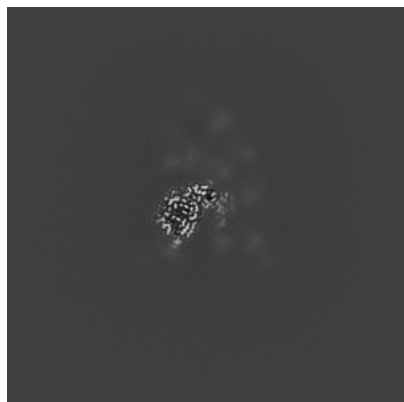


Z Index: 270

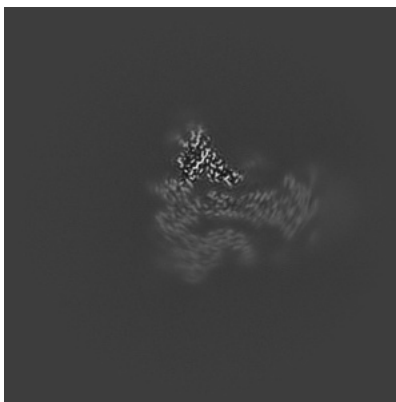
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 331

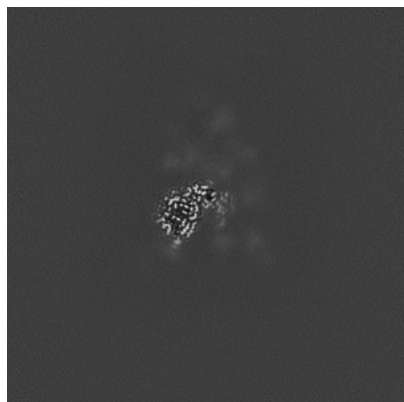


Y Index: 248

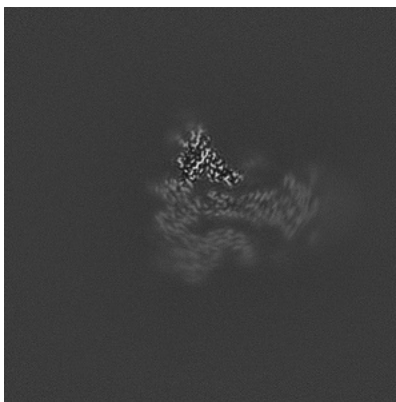


Z Index: 256

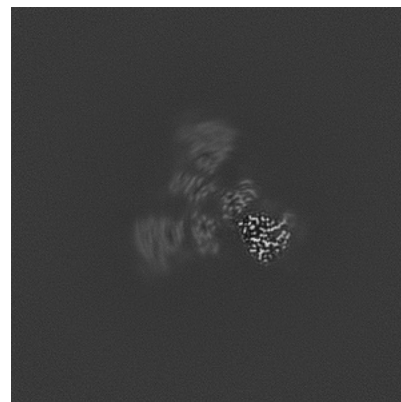
6.3.2 Raw map



X Index: 331



Y Index: 248

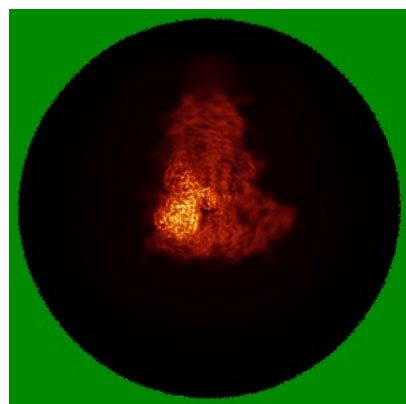


Z Index: 256

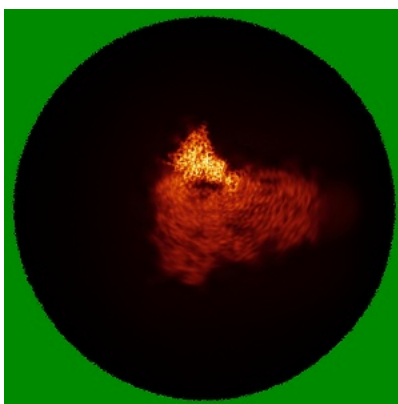
The images above show the largest variance slices of the map in three orthogonal directions.

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

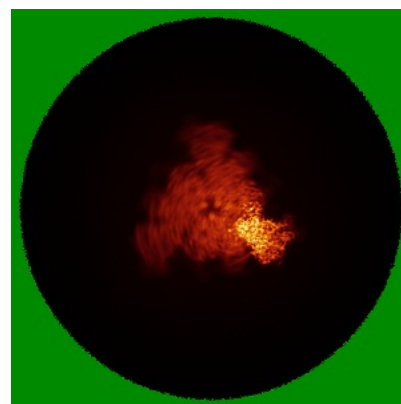
6.4.1 Primary map



X

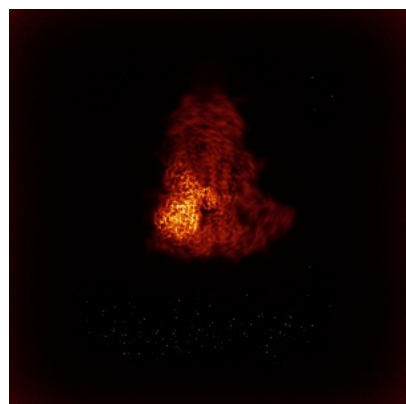


Y

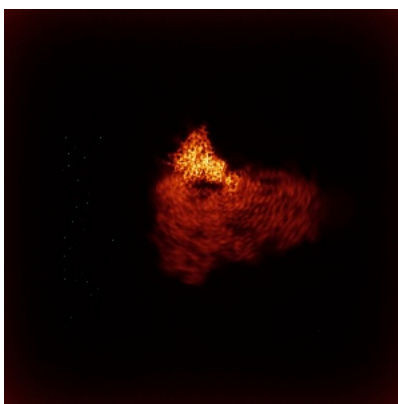


Z

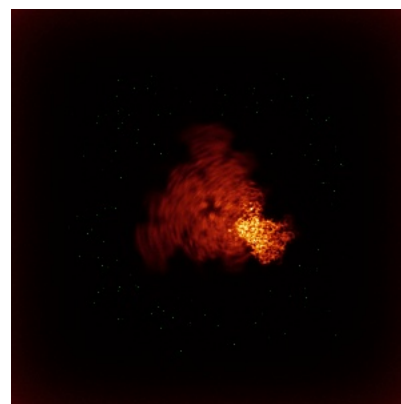
6.4.2 Raw map



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 25.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

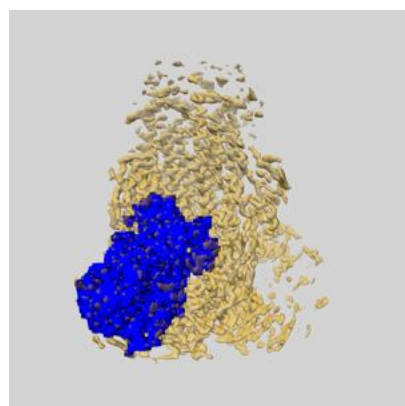
6.6 Mask visualisation [i](#)

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

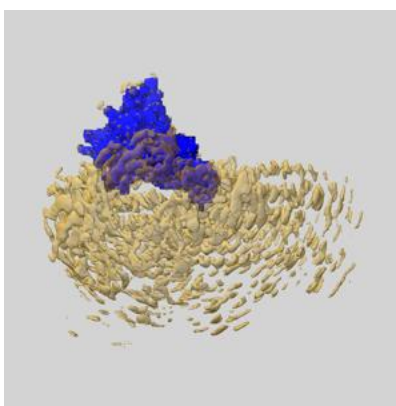
A mask typically either:

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

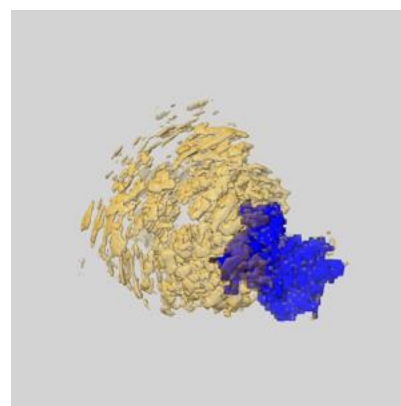
6.6.1 emd_70900_msk_1.map [i](#)



X



Y

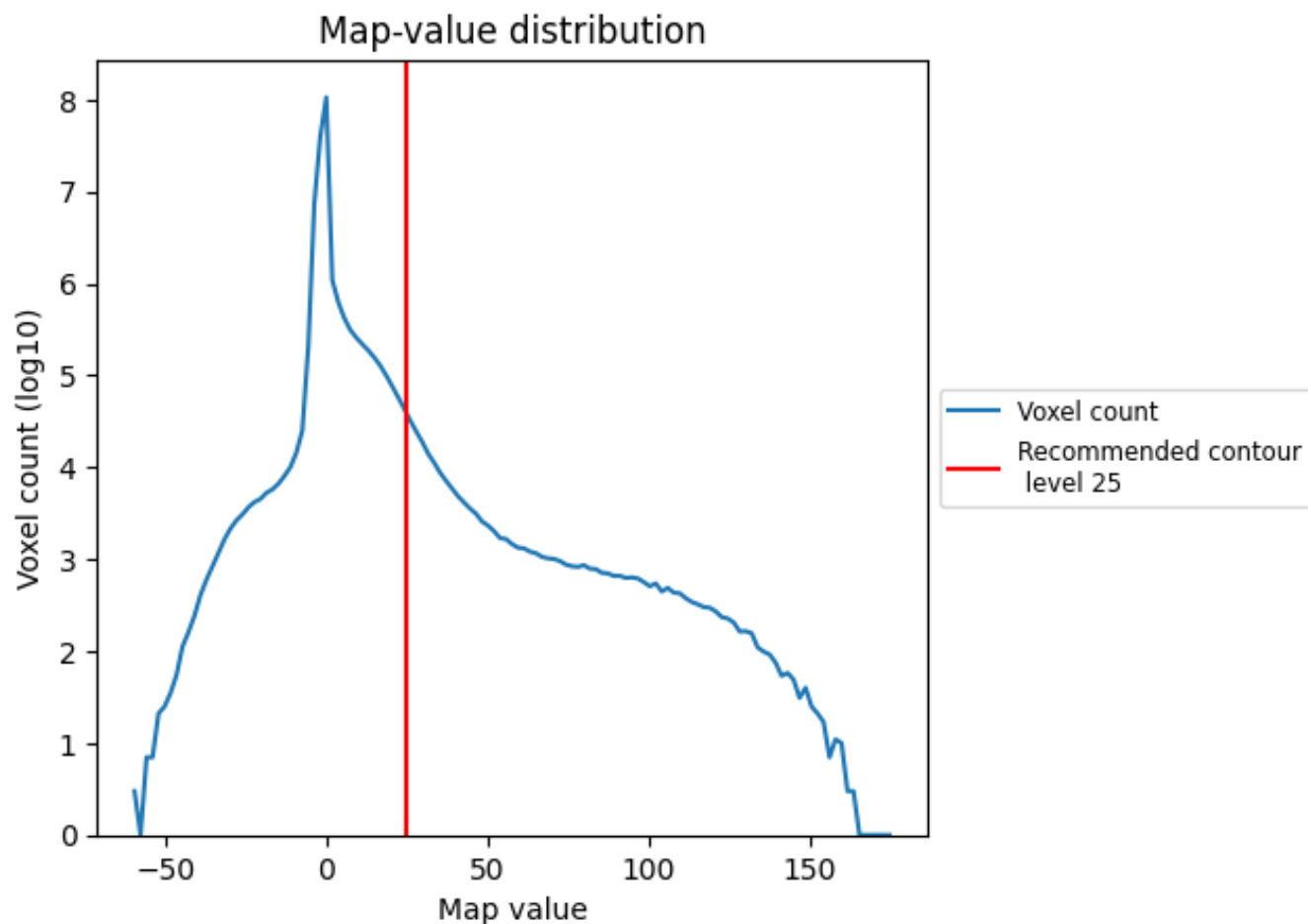


Z

7 Map analysis [i](#)

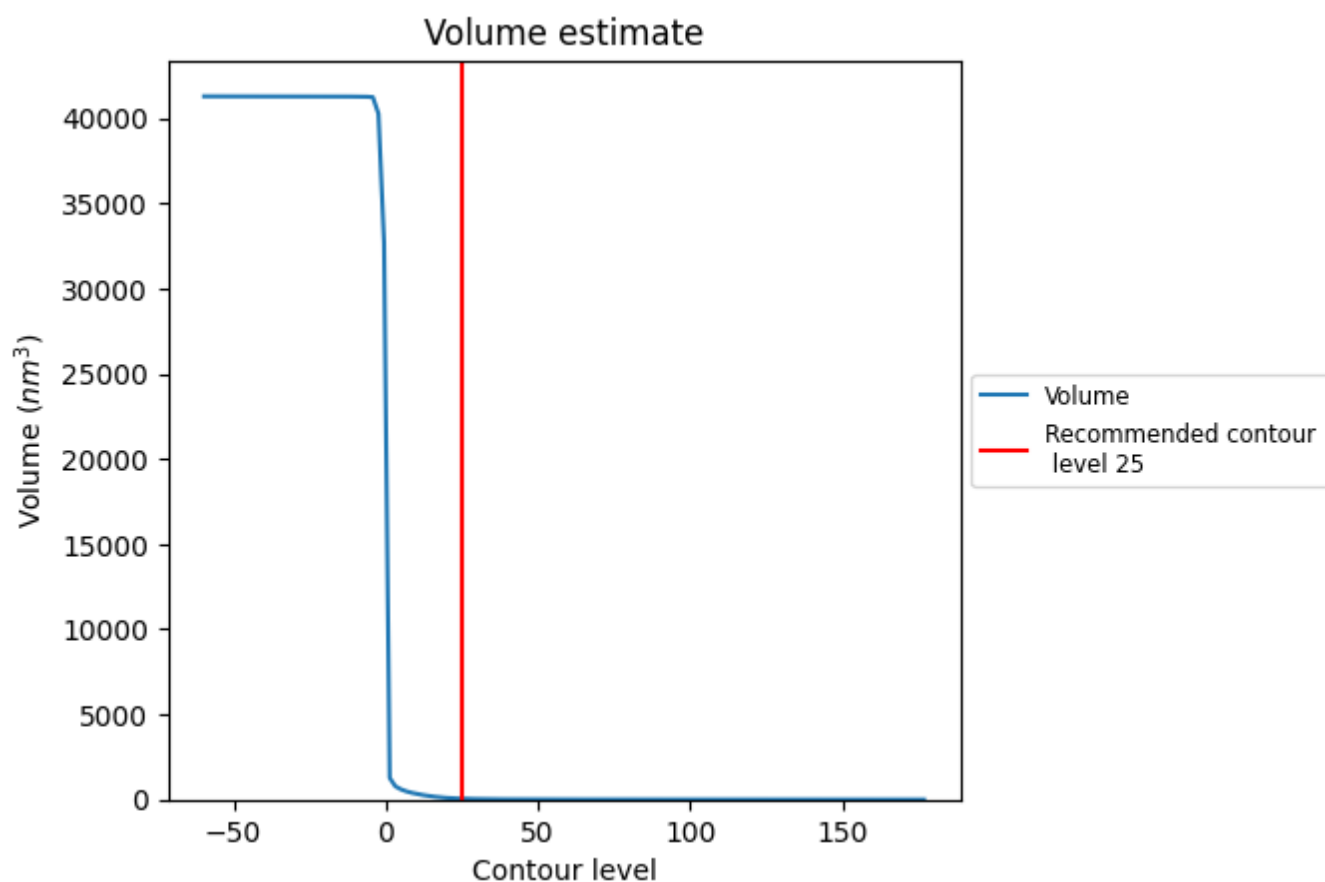
This section contains the results of statistical analysis of the map.

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.

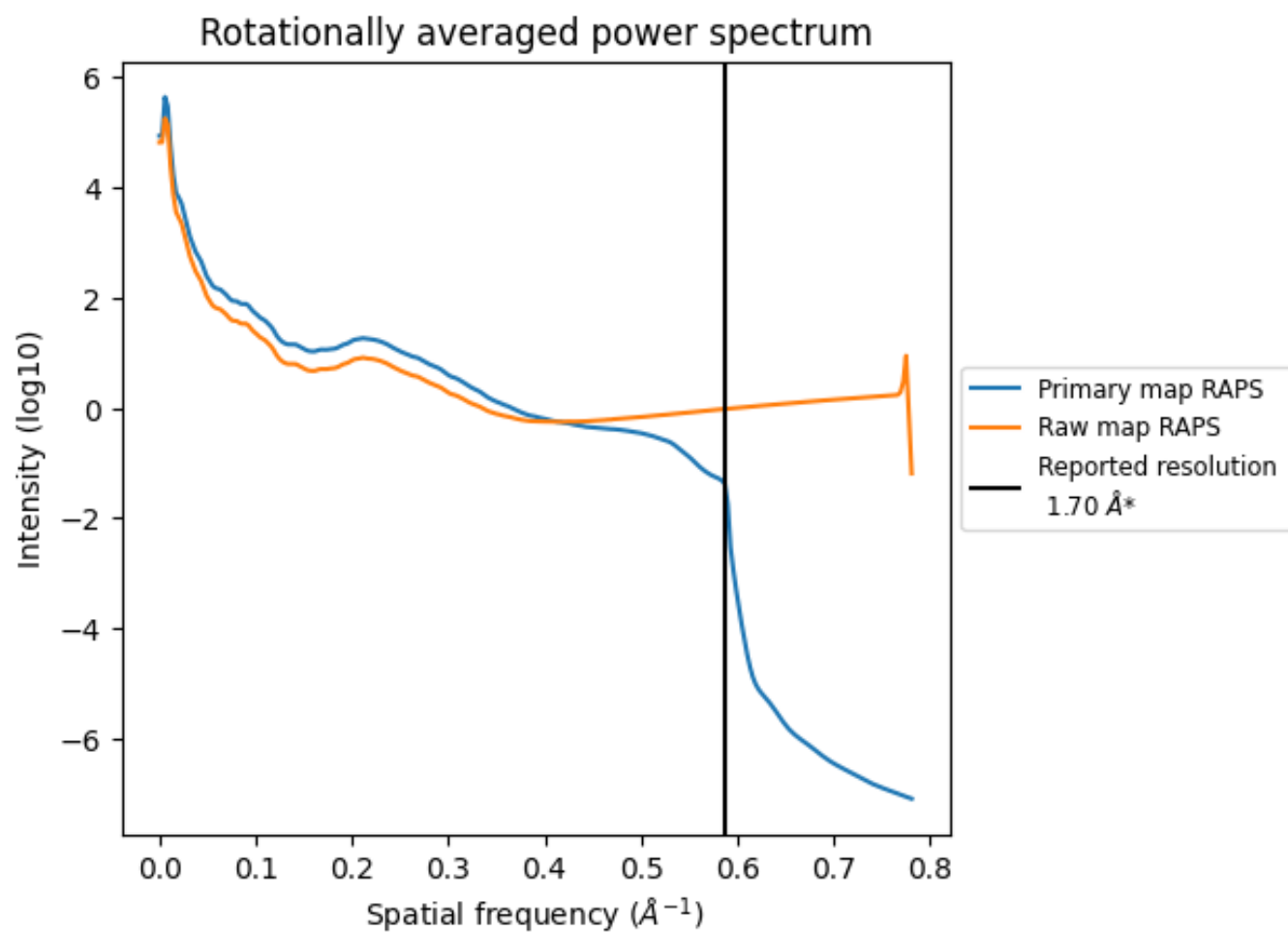
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 52 nm^3 ; this corresponds to an approximate mass of 47 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 ⓘ

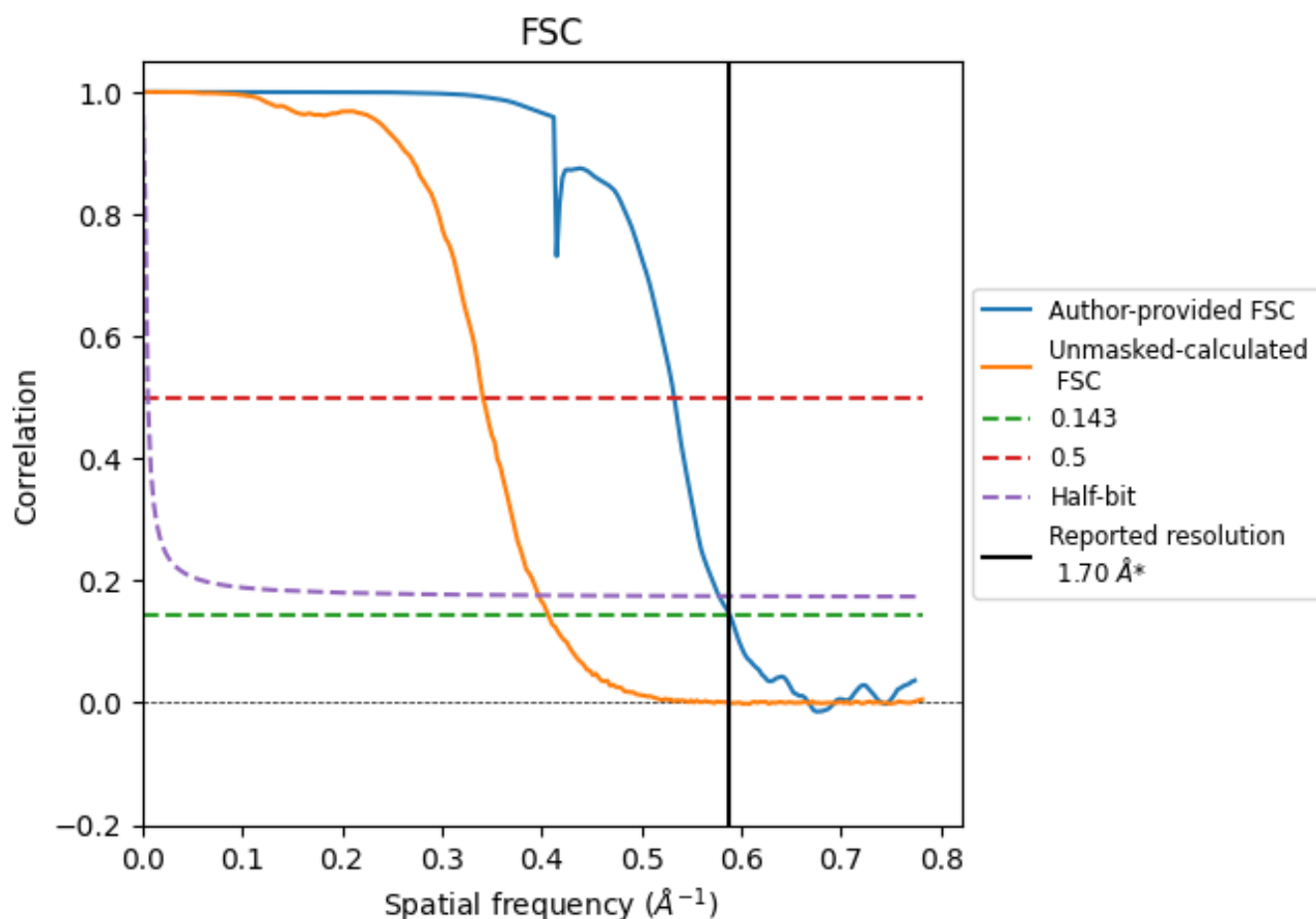


*Reported resolution corresponds to spatial frequency of 0.588 \AA^{-1}

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 0.588 \AA^{-1}

8.2 Resolution estimates [i](#)

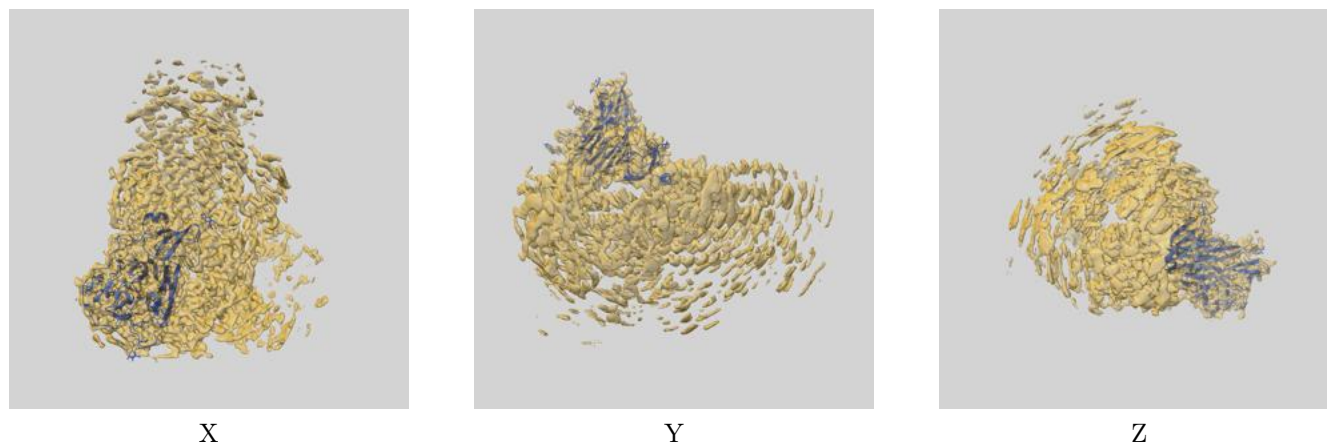
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	1.70	-	-
Author-provided FSC curve	1.70	1.88	1.73
Unmasked-calculated*	2.46	2.93	2.52

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.46 differs from the reported value 1.7 by more than 10 %

9 Map-model fit [i](#)

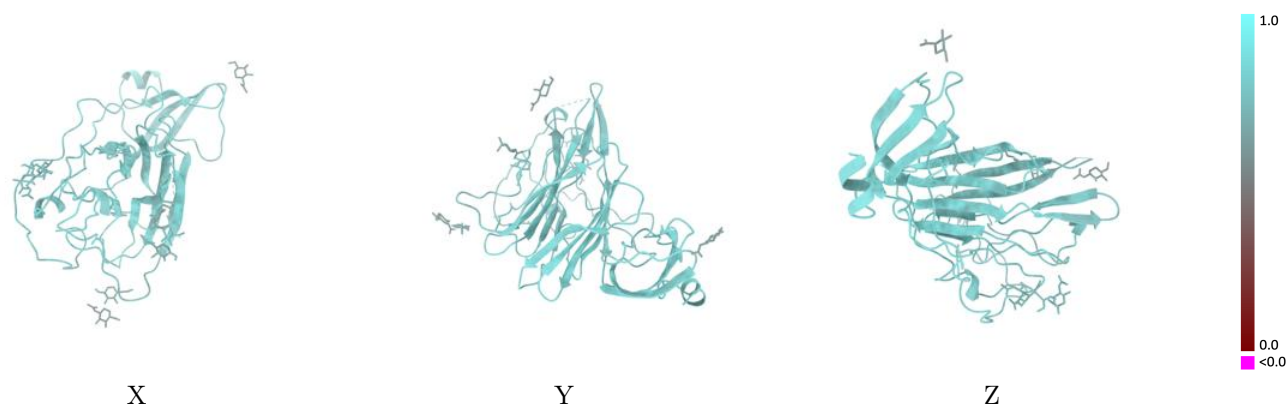
This section contains information regarding the fit between EMDB map EMD-70900 and PDB model 9OVK. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

9.1 Map-model overlay [i](#)



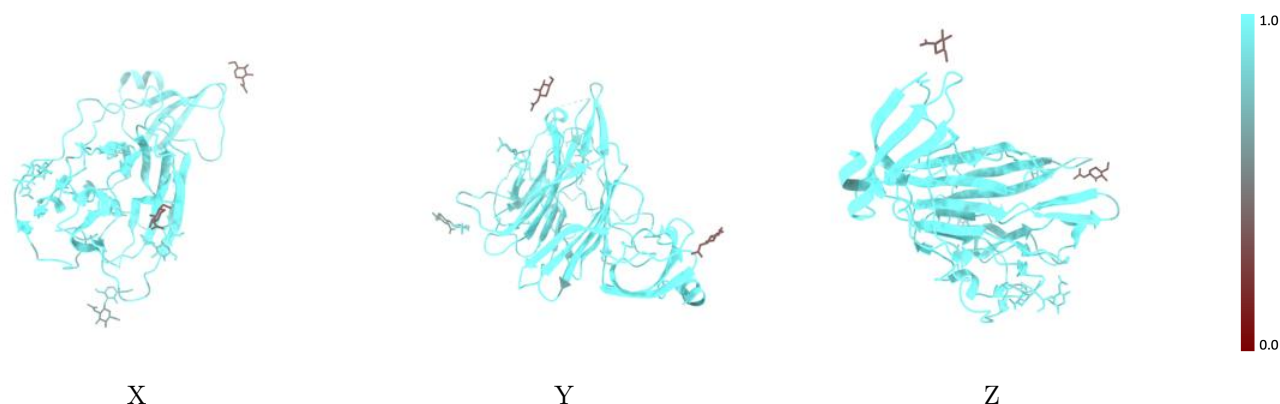
The images above show the 3D surface view of the map at the recommended contour level 25.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



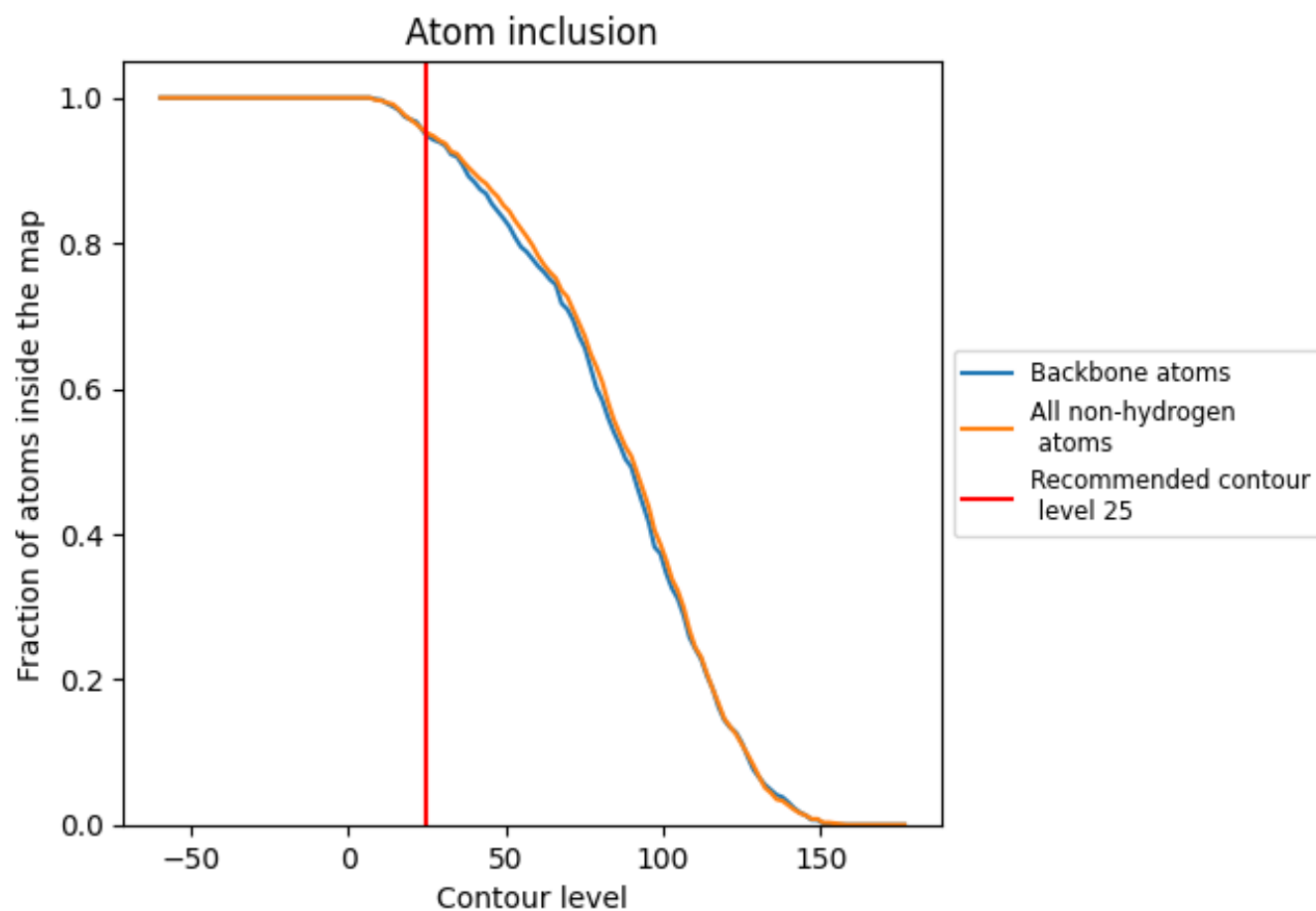
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (25).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 95% 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 (25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.9510	<div></div> 0.7420
A	<div></div> 0.9650	<div></div> 0.7450
B	<div></div> 0.6790	<div></div> 0.5800
C	<div></div> 0.8930	<div></div> 0.6620

