



wwPDB EM Validation Summary Report ⓘ

Mar 23, 2026 – 03:12 AM UTC

PDB ID : 9BU8 / pdb_00009bu8
EMDB ID : EMD-44903
Title : Vaccine elicited Fab c115.131 with influenza H10 JD13 HA trimer
Authors : Gorman, J.; Kwong, P.D.
Deposited on : 2024-05-16
Resolution : 3.96 Å(reported)
Based on initial model : .

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:

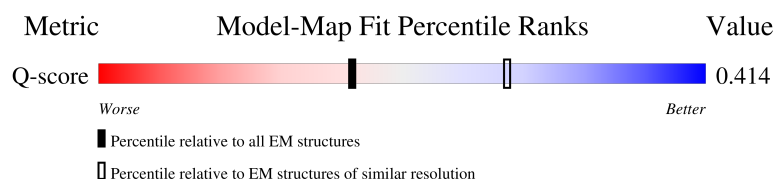
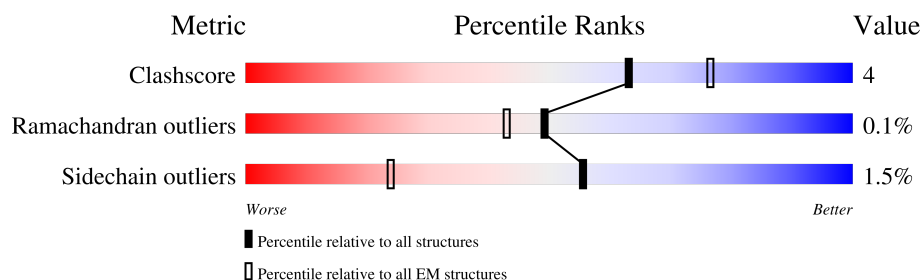
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
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 3.96 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.



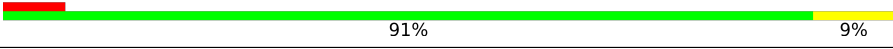
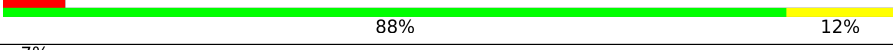
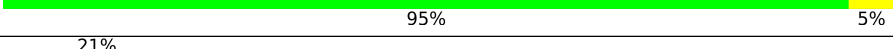
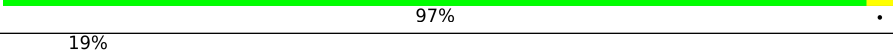
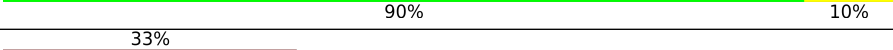
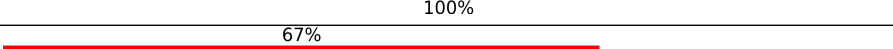
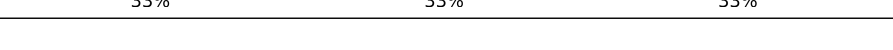
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	7646 (3.46 - 4.46)

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	325	
1	E	325	
1	J	325	
2	B	230	

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Mol	Chain	Length	Quality of chain
2	G	230	
2	L	230	
3	C	121	
3	F	121	
3	I	121	
4	D	107	
4	H	107	
4	K	107	
5	M	3	
5	N	3	
5	O	3	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 17109 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Hemagglutinin HA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	325	Total	C	N	O	S	0	0
			2489	1539	460	473	17		
1	E	325	Total	C	N	O	S	0	0
			2489	1539	460	473	17		
1	J	325	Total	C	N	O	S	0	0
			2489	1539	460	473	17		

- Molecule 2 is a protein called Hemagglutinin HA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	172	Total	C	N	O	S	0	0
			1386	856	240	282	8		
2	G	172	Total	C	N	O	S	0	0
			1386	856	240	282	8		
2	L	172	Total	C	N	O	S	0	0
			1386	856	240	282	8		

There are 159 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	178	GLY	-	expression tag	UNP A0A0B4UV34
B	179	SER	-	expression tag	UNP A0A0B4UV34
B	180	GLY	-	expression tag	UNP A0A0B4UV34
B	181	TYR	-	expression tag	UNP A0A0B4UV34
B	182	ILE	-	expression tag	UNP A0A0B4UV34
B	183	PRO	-	expression tag	UNP A0A0B4UV34
B	184	GLU	-	expression tag	UNP A0A0B4UV34
B	185	ALA	-	expression tag	UNP A0A0B4UV34
B	186	PRO	-	expression tag	UNP A0A0B4UV34
B	187	ARG	-	expression tag	UNP A0A0B4UV34
B	188	ASP	-	expression tag	UNP A0A0B4UV34
B	189	GLY	-	expression tag	UNP A0A0B4UV34
B	190	GLN	-	expression tag	UNP A0A0B4UV34

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Chain	Residue	Modelled	Actual	Comment	Reference
B	191	ALA	-	expression tag	UNP A0A0B4UV34
B	192	TYR	-	expression tag	UNP A0A0B4UV34
B	193	VAL	-	expression tag	UNP A0A0B4UV34
B	194	ARG	-	expression tag	UNP A0A0B4UV34
B	195	LYS	-	expression tag	UNP A0A0B4UV34
B	196	ASP	-	expression tag	UNP A0A0B4UV34
B	197	GLY	-	expression tag	UNP A0A0B4UV34
B	198	GLU	-	expression tag	UNP A0A0B4UV34
B	199	TRP	-	expression tag	UNP A0A0B4UV34
B	200	VAL	-	expression tag	UNP A0A0B4UV34
B	201	LEU	-	expression tag	UNP A0A0B4UV34
B	202	LEU	-	expression tag	UNP A0A0B4UV34
B	203	SER	-	expression tag	UNP A0A0B4UV34
B	204	THR	-	expression tag	UNP A0A0B4UV34
B	205	PHE	-	expression tag	UNP A0A0B4UV34
B	206	LEU	-	expression tag	UNP A0A0B4UV34
B	207	GLY	-	expression tag	UNP A0A0B4UV34
B	208	SER	-	expression tag	UNP A0A0B4UV34
B	209	GLY	-	expression tag	UNP A0A0B4UV34
B	210	LEU	-	expression tag	UNP A0A0B4UV34
B	211	ASN	-	expression tag	UNP A0A0B4UV34
B	212	ASP	-	expression tag	UNP A0A0B4UV34
B	213	ILE	-	expression tag	UNP A0A0B4UV34
B	214	PHE	-	expression tag	UNP A0A0B4UV34
B	215	GLU	-	expression tag	UNP A0A0B4UV34
B	216	ALA	-	expression tag	UNP A0A0B4UV34
B	217	GLN	-	expression tag	UNP A0A0B4UV34
B	218	LYS	-	expression tag	UNP A0A0B4UV34
B	219	ILE	-	expression tag	UNP A0A0B4UV34
B	220	GLU	-	expression tag	UNP A0A0B4UV34
B	221	TRP	-	expression tag	UNP A0A0B4UV34
B	222	HIS	-	expression tag	UNP A0A0B4UV34
B	223	GLU	-	expression tag	UNP A0A0B4UV34
B	224	GLY	-	expression tag	UNP A0A0B4UV34
B	225	HIS	-	expression tag	UNP A0A0B4UV34
B	226	HIS	-	expression tag	UNP A0A0B4UV34
B	227	HIS	-	expression tag	UNP A0A0B4UV34
B	228	HIS	-	expression tag	UNP A0A0B4UV34
B	229	HIS	-	expression tag	UNP A0A0B4UV34
B	230	HIS	-	expression tag	UNP A0A0B4UV34
G	178	GLY	-	expression tag	UNP A0A0B4UV34
G	179	SER	-	expression tag	UNP A0A0B4UV34

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Chain	Residue	Modelled	Actual	Comment	Reference
G	180	GLY	-	expression tag	UNP A0A0B4UV34
G	181	TYR	-	expression tag	UNP A0A0B4UV34
G	182	ILE	-	expression tag	UNP A0A0B4UV34
G	183	PRO	-	expression tag	UNP A0A0B4UV34
G	184	GLU	-	expression tag	UNP A0A0B4UV34
G	185	ALA	-	expression tag	UNP A0A0B4UV34
G	186	PRO	-	expression tag	UNP A0A0B4UV34
G	187	ARG	-	expression tag	UNP A0A0B4UV34
G	188	ASP	-	expression tag	UNP A0A0B4UV34
G	189	GLY	-	expression tag	UNP A0A0B4UV34
G	190	GLN	-	expression tag	UNP A0A0B4UV34
G	191	ALA	-	expression tag	UNP A0A0B4UV34
G	192	TYR	-	expression tag	UNP A0A0B4UV34
G	193	VAL	-	expression tag	UNP A0A0B4UV34
G	194	ARG	-	expression tag	UNP A0A0B4UV34
G	195	LYS	-	expression tag	UNP A0A0B4UV34
G	196	ASP	-	expression tag	UNP A0A0B4UV34
G	197	GLY	-	expression tag	UNP A0A0B4UV34
G	198	GLU	-	expression tag	UNP A0A0B4UV34
G	199	TRP	-	expression tag	UNP A0A0B4UV34
G	200	VAL	-	expression tag	UNP A0A0B4UV34
G	201	LEU	-	expression tag	UNP A0A0B4UV34
G	202	LEU	-	expression tag	UNP A0A0B4UV34
G	203	SER	-	expression tag	UNP A0A0B4UV34
G	204	THR	-	expression tag	UNP A0A0B4UV34
G	205	PHE	-	expression tag	UNP A0A0B4UV34
G	206	LEU	-	expression tag	UNP A0A0B4UV34
G	207	GLY	-	expression tag	UNP A0A0B4UV34
G	208	SER	-	expression tag	UNP A0A0B4UV34
G	209	GLY	-	expression tag	UNP A0A0B4UV34
G	210	LEU	-	expression tag	UNP A0A0B4UV34
G	211	ASN	-	expression tag	UNP A0A0B4UV34
G	212	ASP	-	expression tag	UNP A0A0B4UV34
G	213	ILE	-	expression tag	UNP A0A0B4UV34
G	214	PHE	-	expression tag	UNP A0A0B4UV34
G	215	GLU	-	expression tag	UNP A0A0B4UV34
G	216	ALA	-	expression tag	UNP A0A0B4UV34
G	217	GLN	-	expression tag	UNP A0A0B4UV34
G	218	LYS	-	expression tag	UNP A0A0B4UV34
G	219	ILE	-	expression tag	UNP A0A0B4UV34
G	220	GLU	-	expression tag	UNP A0A0B4UV34
G	221	TRP	-	expression tag	UNP A0A0B4UV34

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Chain	Residue	Modelled	Actual	Comment	Reference
G	222	HIS	-	expression tag	UNP A0A0B4UV34
G	223	GLU	-	expression tag	UNP A0A0B4UV34
G	224	GLY	-	expression tag	UNP A0A0B4UV34
G	225	HIS	-	expression tag	UNP A0A0B4UV34
G	226	HIS	-	expression tag	UNP A0A0B4UV34
G	227	HIS	-	expression tag	UNP A0A0B4UV34
G	228	HIS	-	expression tag	UNP A0A0B4UV34
G	229	HIS	-	expression tag	UNP A0A0B4UV34
G	230	HIS	-	expression tag	UNP A0A0B4UV34
L	178	GLY	-	expression tag	UNP A0A0B4UV34
L	179	SER	-	expression tag	UNP A0A0B4UV34
L	180	GLY	-	expression tag	UNP A0A0B4UV34
L	181	TYR	-	expression tag	UNP A0A0B4UV34
L	182	ILE	-	expression tag	UNP A0A0B4UV34
L	183	PRO	-	expression tag	UNP A0A0B4UV34
L	184	GLU	-	expression tag	UNP A0A0B4UV34
L	185	ALA	-	expression tag	UNP A0A0B4UV34
L	186	PRO	-	expression tag	UNP A0A0B4UV34
L	187	ARG	-	expression tag	UNP A0A0B4UV34
L	188	ASP	-	expression tag	UNP A0A0B4UV34
L	189	GLY	-	expression tag	UNP A0A0B4UV34
L	190	GLN	-	expression tag	UNP A0A0B4UV34
L	191	ALA	-	expression tag	UNP A0A0B4UV34
L	192	TYR	-	expression tag	UNP A0A0B4UV34
L	193	VAL	-	expression tag	UNP A0A0B4UV34
L	194	ARG	-	expression tag	UNP A0A0B4UV34
L	195	LYS	-	expression tag	UNP A0A0B4UV34
L	196	ASP	-	expression tag	UNP A0A0B4UV34
L	197	GLY	-	expression tag	UNP A0A0B4UV34
L	198	GLU	-	expression tag	UNP A0A0B4UV34
L	199	TRP	-	expression tag	UNP A0A0B4UV34
L	200	VAL	-	expression tag	UNP A0A0B4UV34
L	201	LEU	-	expression tag	UNP A0A0B4UV34
L	202	LEU	-	expression tag	UNP A0A0B4UV34
L	203	SER	-	expression tag	UNP A0A0B4UV34
L	204	THR	-	expression tag	UNP A0A0B4UV34
L	205	PHE	-	expression tag	UNP A0A0B4UV34
L	206	LEU	-	expression tag	UNP A0A0B4UV34
L	207	GLY	-	expression tag	UNP A0A0B4UV34
L	208	SER	-	expression tag	UNP A0A0B4UV34
L	209	GLY	-	expression tag	UNP A0A0B4UV34
L	210	LEU	-	expression tag	UNP A0A0B4UV34

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Chain	Residue	Modelled	Actual	Comment	Reference
L	211	ASN	-	expression tag	UNP A0A0B4UV34
L	212	ASP	-	expression tag	UNP A0A0B4UV34
L	213	ILE	-	expression tag	UNP A0A0B4UV34
L	214	PHE	-	expression tag	UNP A0A0B4UV34
L	215	GLU	-	expression tag	UNP A0A0B4UV34
L	216	ALA	-	expression tag	UNP A0A0B4UV34
L	217	GLN	-	expression tag	UNP A0A0B4UV34
L	218	LYS	-	expression tag	UNP A0A0B4UV34
L	219	ILE	-	expression tag	UNP A0A0B4UV34
L	220	GLU	-	expression tag	UNP A0A0B4UV34
L	221	TRP	-	expression tag	UNP A0A0B4UV34
L	222	HIS	-	expression tag	UNP A0A0B4UV34
L	223	GLU	-	expression tag	UNP A0A0B4UV34
L	224	GLY	-	expression tag	UNP A0A0B4UV34
L	225	HIS	-	expression tag	UNP A0A0B4UV34
L	226	HIS	-	expression tag	UNP A0A0B4UV34
L	227	HIS	-	expression tag	UNP A0A0B4UV34
L	228	HIS	-	expression tag	UNP A0A0B4UV34
L	229	HIS	-	expression tag	UNP A0A0B4UV34
L	230	HIS	-	expression tag	UNP A0A0B4UV34

- Molecule 3 is a protein called Fab c115.131 heavy chain.

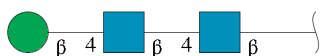
Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	121	Total 929	C 584	N 159	O 182	S 4	0	0
3	F	121	Total 929	C 584	N 159	O 182	S 4	0	0
3	I	121	Total 929	C 584	N 159	O 182	S 4	0	0

- Molecule 4 is a protein called Fab c115.131 light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	107	Total 818	C 512	N 141	O 162	S 3	0	0
4	H	107	Total 818	C 512	N 141	O 162	S 3	0	0
4	K	107	Total 818	C 512	N 141	O 162	S 3	0	0

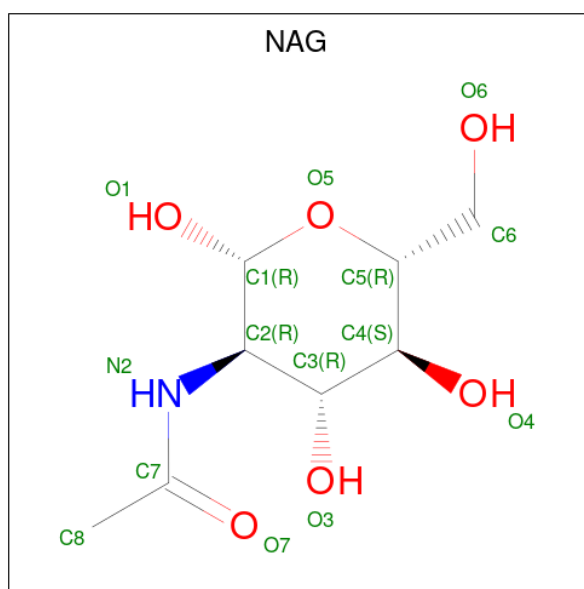
- Molecule 5 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-b

eta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
5	M	3	Total	C	N	O	0	0
			39	22	2	15		
5	N	3	Total	C	N	O	0	0
			39	22	2	15		
5	O	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				AltConf
6	A	1	Total	C	N	O	0
			14	8	1	5	
6	B	1	Total	C	N	O	0
			14	8	1	5	
6	B	1	Total	C	N	O	0
			14	8	1	5	
6	E	1	Total	C	N	O	0
			14	8	1	5	
6	G	1	Total	C	N	O	0
			14	8	1	5	

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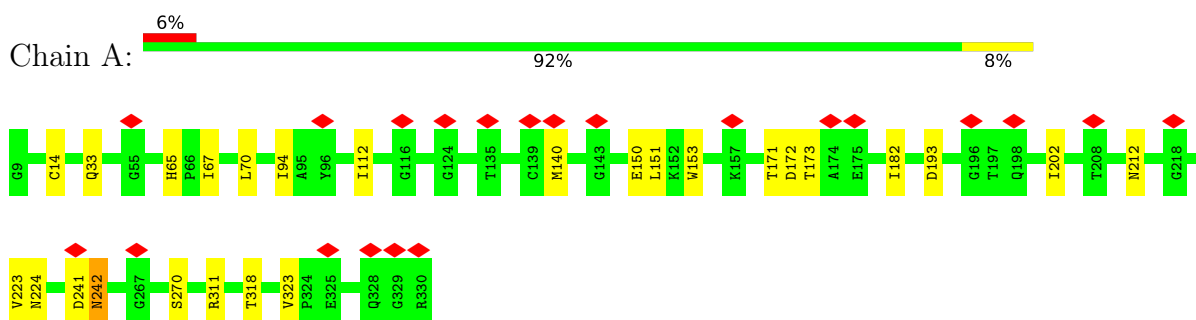
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Mol	Chain	Residues	Atoms				AltConf
6	G	1	Total	C	N	O	0
			14	8	1	5	
6	J	1	Total	C	N	O	0
			14	8	1	5	
6	L	1	Total	C	N	O	0
			14	8	1	5	
6	L	1	Total	C	N	O	0
			14	8	1	5	

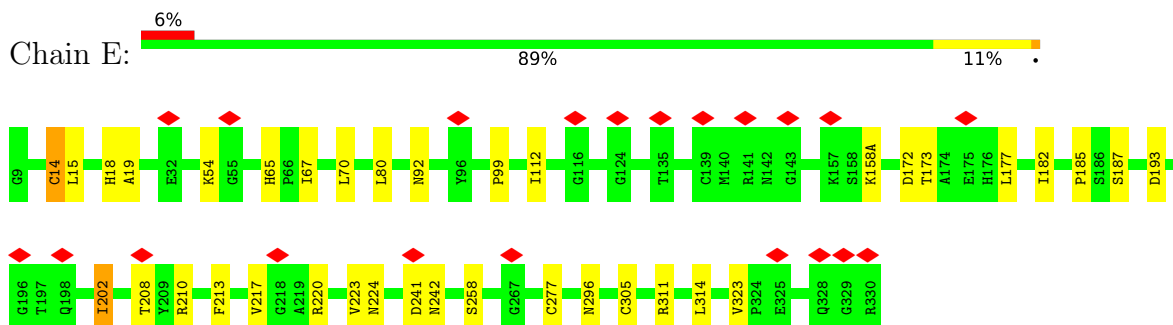
3 Residue-property plots [i](#)

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

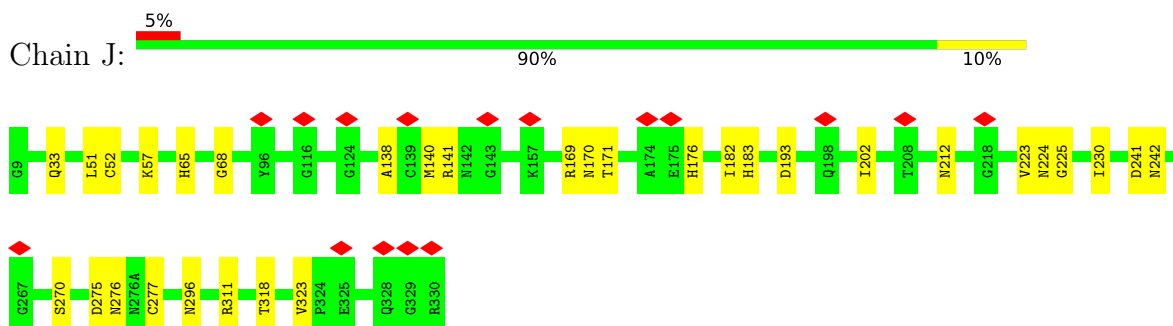
- Molecule 1: Hemagglutinin HA1



- Molecule 1: Hemagglutinin HA1

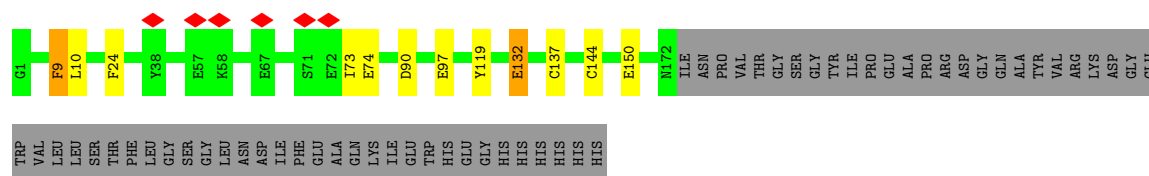


- Molecule 1: Hemagglutinin HA1



- Molecule 2: Hemagglutinin HA2





- Molecule 2: Hemagglutinin HA2



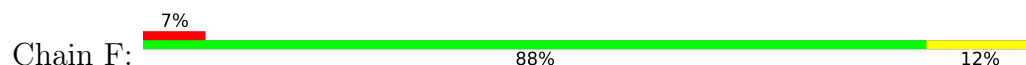
- Molecule 2: Hemagglutinin HA2



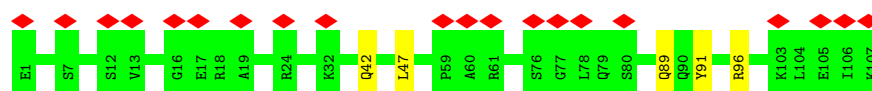
- Molecule 3: Fab c115.131 heavy chain



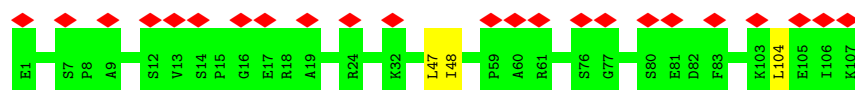
- Molecule 3: Fab c115.131 heavy chain



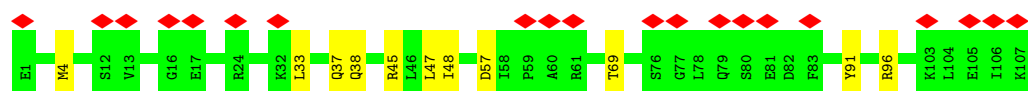
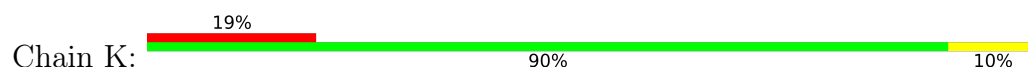
- Molecule 4: Fab c115.131 light chain



- Molecule 4: Fab c115.131 light chain



- Molecule 4: Fab c115.131 light chain



- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 5: 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, C3	Depositor
Number of particles used	98574	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	52.75	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.550	Depositor
Minimum map value	-0.760	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.030	Depositor
Recommended contour level	0.22	Depositor
Map size ($\text{\AA}$)	344.32, 344.32, 344.32	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.076, 1.076, 1.076	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, 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	0.15	0/2538	0.36	0/3437
1	E	0.14	0/2538	0.35	0/3437
1	J	0.15	0/2538	0.35	0/3437
2	B	0.14	0/1411	0.36	0/1904
2	G	0.15	0/1411	0.37	0/1904
2	L	0.15	0/1411	0.39	0/1904
3	C	0.13	0/952	0.30	0/1293
3	F	0.12	0/952	0.33	0/1293
3	I	0.13	0/952	0.34	0/1293
4	D	0.13	0/836	0.32	0/1136
4	H	0.14	0/836	0.33	0/1136
4	K	0.12	0/836	0.34	0/1136
All	All	0.14	0/17211	0.35	0/23310

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	E	0	1
2	B	0	1
2	L	0	1
All	All	0	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	144	CYS	Peptide
1	E	14	CYS	Peptide
2	L	70	PHE	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	A	2489	0	2445	25	0
1	E	2489	0	2445	25	0
1	J	2489	0	2445	26	0
2	B	1386	0	1283	8	0
2	G	1386	0	1283	17	0
2	L	1386	0	1283	10	0
3	C	929	0	879	6	0
3	F	929	0	879	8	0
3	I	929	0	879	7	0
4	D	818	0	797	2	0
4	H	818	0	797	3	0
4	K	818	0	797	8	0
5	M	39	0	34	0	0
5	N	39	0	34	1	0
5	O	39	0	34	1	0
6	A	14	0	13	4	0
6	B	28	0	26	0	0
6	E	14	0	13	1	0
6	G	28	0	26	2	0
6	J	14	0	13	5	0
6	L	28	0	26	0	0
All	All	17109	0	16431	140	0

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

The worst 5 of 140 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:J:296:ASN:ND2	1:J:311:ARG:O	2.10	0.85
1:E:172:ASP:OD2	1:E:173:THR:N	2.21	0.73
4:K:45:ARG:NH2	4:K:57:ASP:OD1	2.20	0.73
4:H:47:LEU:C	4:H:48:ILE:HD13	2.15	0.72
6:G:302:NAG:H83	6:G:302:NAG:H3	1.74	0.68

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	323/325 (99%)	309 (96%)	14 (4%)	0	100	100
1	E	323/325 (99%)	310 (96%)	13 (4%)	0	100	100
1	J	323/325 (99%)	304 (94%)	19 (6%)	0	100	100
2	B	170/230 (74%)	159 (94%)	11 (6%)	0	100	100
2	G	170/230 (74%)	160 (94%)	9 (5%)	1 (1%)	21	56
2	L	170/230 (74%)	158 (93%)	11 (6%)	1 (1%)	21	56
3	C	119/121 (98%)	111 (93%)	8 (7%)	0	100	100
3	F	119/121 (98%)	112 (94%)	7 (6%)	0	100	100
3	I	119/121 (98%)	112 (94%)	7 (6%)	0	100	100
4	D	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
4	H	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
4	K	105/107 (98%)	97 (92%)	8 (8%)	0	100	100
All	All	2151/2349 (92%)	2030 (94%)	119 (6%)	2 (0%)	49	81

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	L	73	ILE
2	G	127	ARG

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	274/274 (100%)	271 (99%)	3 (1%)	65	74
1	E	274/274 (100%)	268 (98%)	6 (2%)	45	64
1	J	274/274 (100%)	272 (99%)	2 (1%)	76	79
2	B	146/194 (75%)	143 (98%)	3 (2%)	47	65
2	G	146/194 (75%)	141 (97%)	5 (3%)	32	55
2	L	146/194 (75%)	144 (99%)	2 (1%)	59	71
3	C	98/98 (100%)	97 (99%)	1 (1%)	68	76
3	F	98/98 (100%)	98 (100%)	0	100	100
3	I	98/98 (100%)	96 (98%)	2 (2%)	48	66
4	D	89/89 (100%)	87 (98%)	2 (2%)	45	64
4	H	89/89 (100%)	88 (99%)	1 (1%)	65	74
4	K	89/89 (100%)	88 (99%)	1 (1%)	65	74
All	All	1821/1965 (93%)	1793 (98%)	28 (2%)	55	70

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	305	CYS
2	L	167	LEU
2	G	132	GLU
1	J	270	SER
2	G	24	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
1	J	247	HIS
1	J	296	ASN
2	L	75	HIS
4	D	38	GLN
4	D	27	GLN

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 ⓘ

9 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	$\# Z > 2$
5	NAG	M	1	1,5	14,14,15	0.72	0	17,19,21	1.34	1 (5%)
5	NAG	M	2	5	14,14,15	0.68	0	17,19,21	0.91	1 (5%)
5	BMA	M	3	5	11,11,12	0.84	0	15,15,17	2.37	5 (33%)
5	NAG	N	1	1,5	14,14,15	0.77	0	17,19,21	1.89	5 (29%)
5	NAG	N	2	5	14,14,15	0.71	0	17,19,21	1.01	2 (11%)
5	BMA	N	3	5	11,11,12	0.85	0	15,15,17	2.52	5 (33%)
5	NAG	O	1	1,5	14,14,15	0.71	0	17,19,21	0.96	0
5	NAG	O	2	5	14,14,15	0.66	0	17,19,21	1.87	4 (23%)
5	BMA	O	3	5	11,11,12	0.85	0	15,15,17	2.57	6 (40%)

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	M	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	M	2	5	-	1/6/23/26	0/1/1/1
5	BMA	M	3	5	-	1/2/19/22	0/1/1/1
5	NAG	N	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	N	2	5	-	0/6/23/26	0/1/1/1
5	BMA	N	3	5	-	1/2/19/22	0/1/1/1
5	NAG	O	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	O	2	5	-	5/6/23/26	0/1/1/1
5	BMA	O	3	5	-	1/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	O	3	BMA	C1-O5-C5	7.53	122.28	112.19
5	N	3	BMA	C1-O5-C5	7.52	122.27	112.19
5	M	3	BMA	C1-O5-C5	6.91	121.45	112.19
5	O	2	NAG	C2-N2-C7	5.57	130.36	122.90
5	N	1	NAG	O5-C1-C2	-4.13	104.90	111.29

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

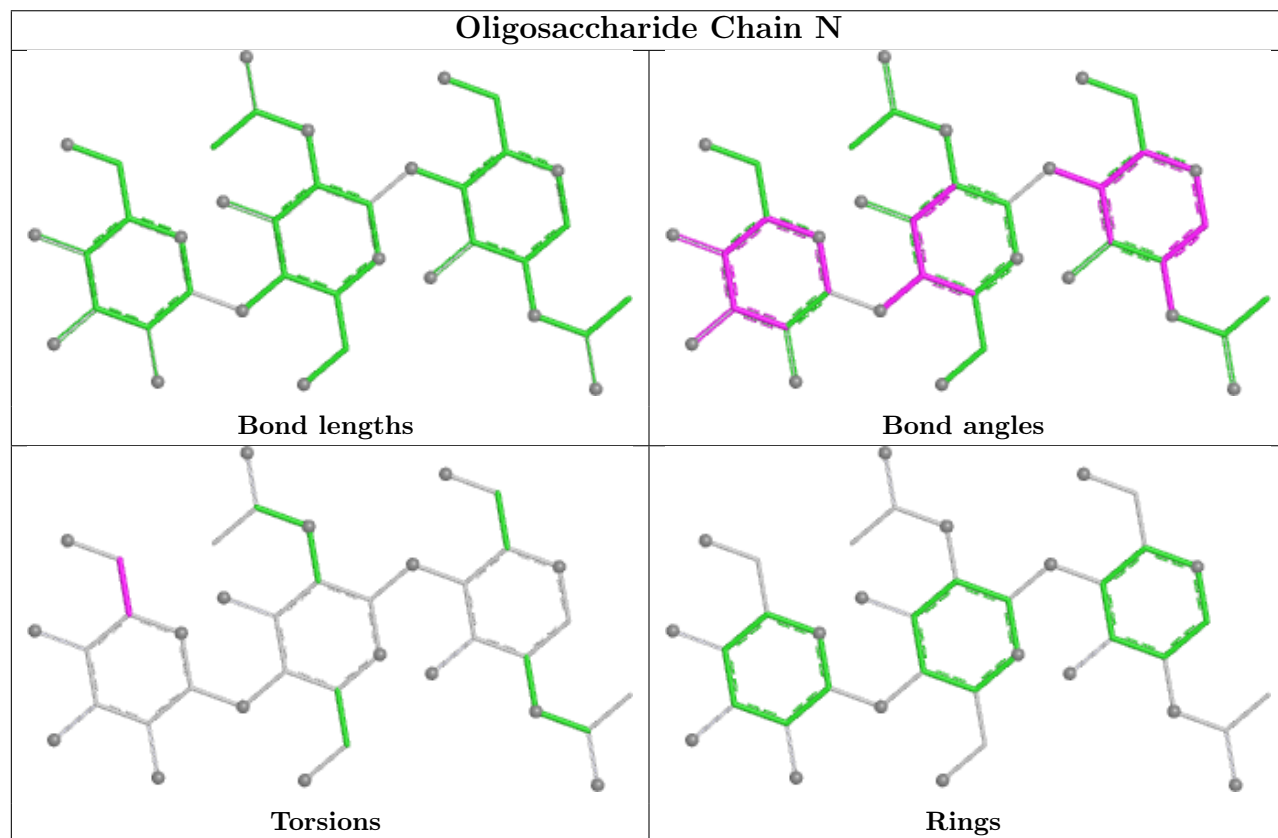
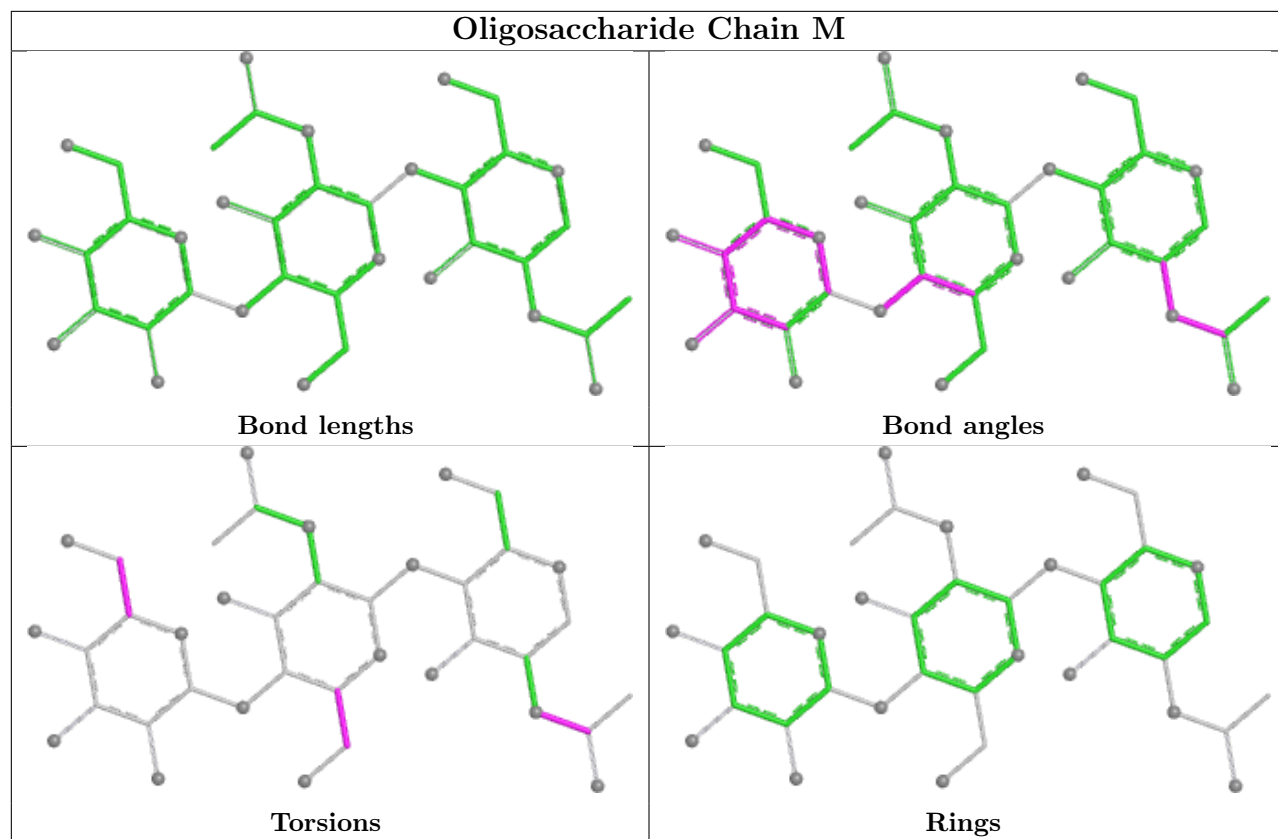
Mol	Chain	Res	Type	Atoms
5	O	2	NAG	O5-C5-C6-O6
5	M	1	NAG	C8-C7-N2-C2
5	M	1	NAG	O7-C7-N2-C2
5	O	2	NAG	C8-C7-N2-C2
5	O	2	NAG	O7-C7-N2-C2

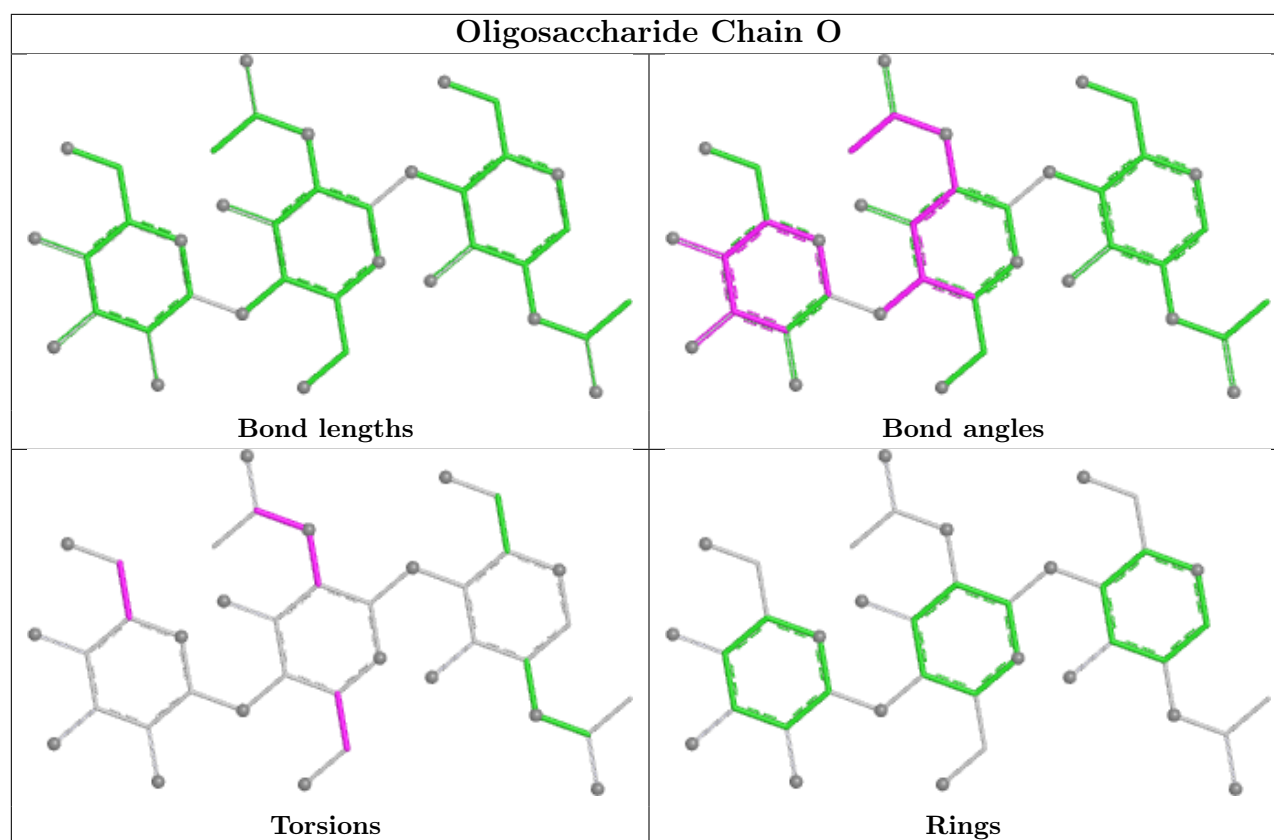
There are no ring outliers.

3 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	N	3	BMA	1	0
5	O	2	NAG	1	0
5	N	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](#)

9 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$
6	NAG	G	301	2	14,14,15	0.69	0	17,19,21	1.04	2 (11%)
6	NAG	L	302	2	14,14,15	0.73	0	17,19,21	0.81	0
6	NAG	G	302	2	14,14,15	0.72	0	17,19,21	1.20	1 (5%)
6	NAG	B	301	2	14,14,15	0.68	0	17,19,21	1.03	1 (5%)
6	NAG	J	401	1	14,14,15	0.74	0	17,19,21	0.96	2 (11%)
6	NAG	E	401	1	14,14,15	0.72	0	17,19,21	0.84	0
6	NAG	L	301	2	14,14,15	0.71	0	17,19,21	0.84	0
6	NAG	A	401	1	14,14,15	0.78	0	17,19,21	1.01	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NAG	B	302	2	14,14,15	0.73	0	17,19,21	0.82	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
6	NAG	G	301	2	-	2/6/23/26	0/1/1/1
6	NAG	L	302	2	-	2/6/23/26	0/1/1/1
6	NAG	G	302	2	-	4/6/23/26	0/1/1/1
6	NAG	B	301	2	-	2/6/23/26	0/1/1/1
6	NAG	J	401	1	-	1/6/23/26	0/1/1/1
6	NAG	E	401	1	-	1/6/23/26	0/1/1/1
6	NAG	L	301	2	-	1/6/23/26	0/1/1/1
6	NAG	A	401	1	-	0/6/23/26	0/1/1/1
6	NAG	B	302	2	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	G	302	NAG	C2-N2-C7	3.70	127.86	122.90
6	A	401	NAG	C1-C2-N2	2.52	114.40	110.43
6	B	301	NAG	C2-N2-C7	2.51	126.26	122.90
6	G	301	NAG	C2-N2-C7	2.25	125.91	122.90
6	J	401	NAG	C1-C2-N2	2.16	113.84	110.43

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	G	301	NAG	C1-C2-N2-C7
6	B	302	NAG	C8-C7-N2-C2
6	B	302	NAG	O7-C7-N2-C2
6	G	302	NAG	C8-C7-N2-C2
6	G	302	NAG	O7-C7-N2-C2

There are no ring outliers.

4 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	G	302	NAG	2	0
6	J	401	NAG	5	0
6	E	401	NAG	1	0
6	A	401	NAG	4	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.

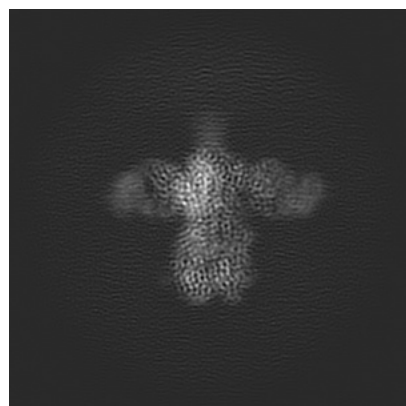
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44903. These allow visual inspection of the internal detail of the map and identification of artifacts.

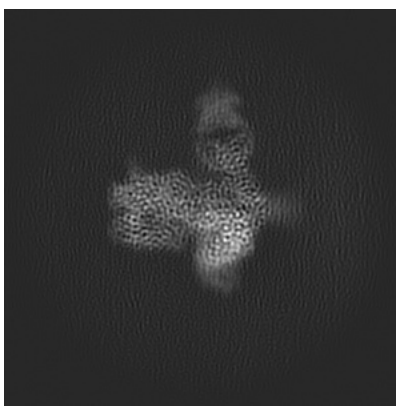
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

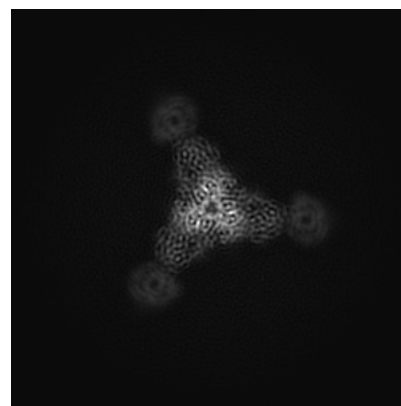
6.1.1 Primary map



X

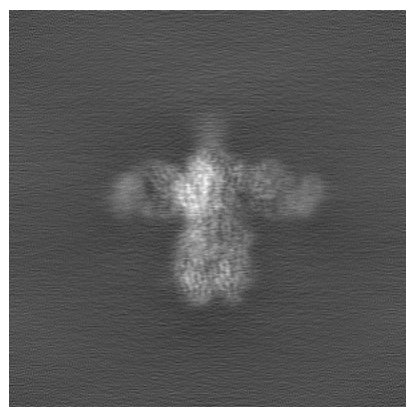


Y

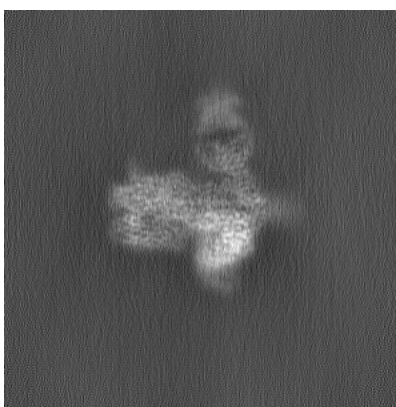


Z

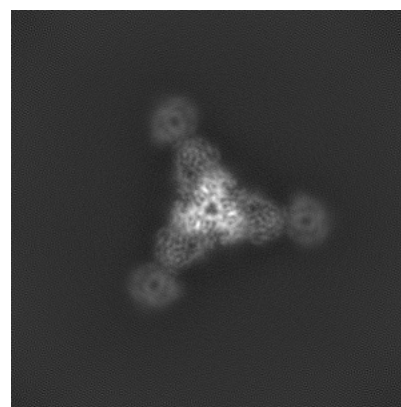
6.1.2 Raw map



X



Y

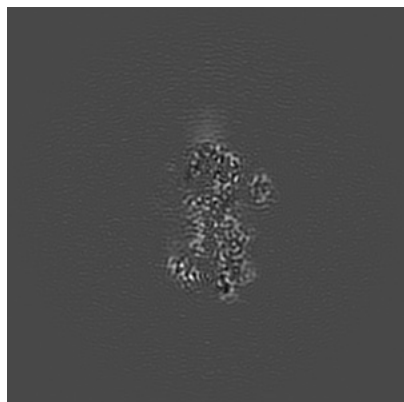


Z

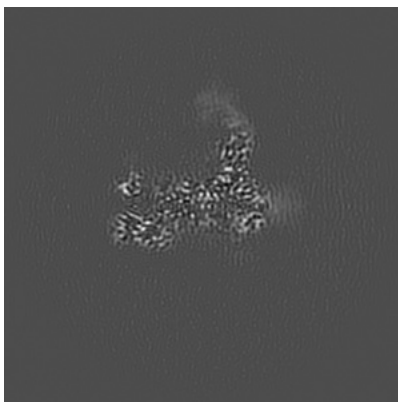
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

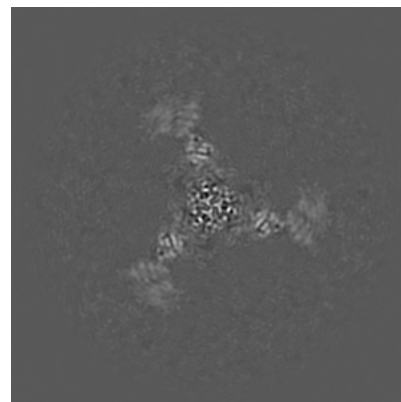
6.2.1 Primary map



X Index: 160

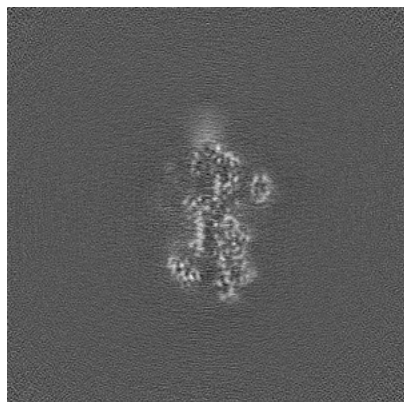


Y Index: 160

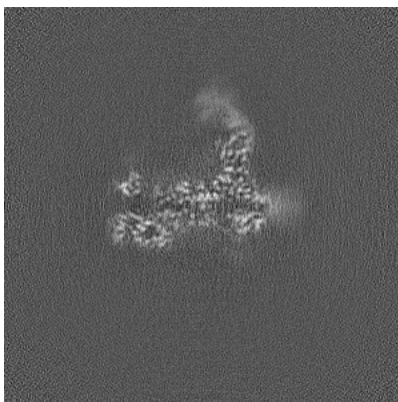


Z Index: 160

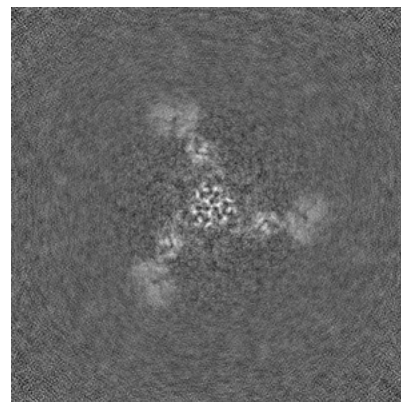
6.2.2 Raw map



X Index: 160



Y Index: 160

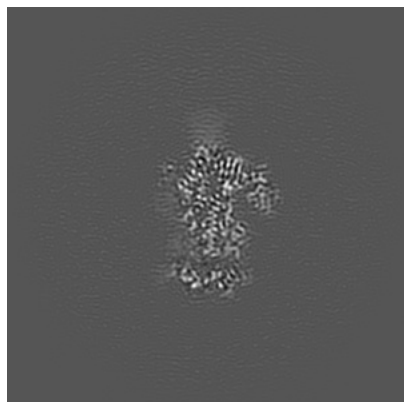


Z Index: 160

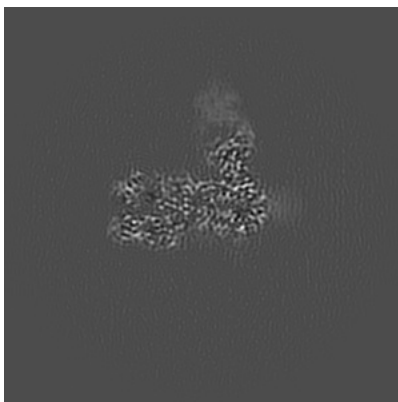
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

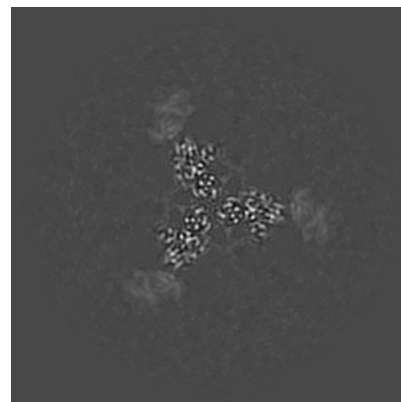
6.3.1 Primary map



X Index: 154

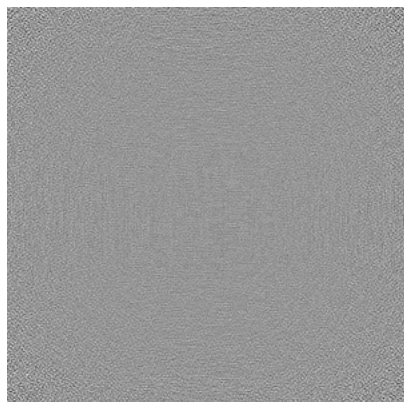


Y Index: 156

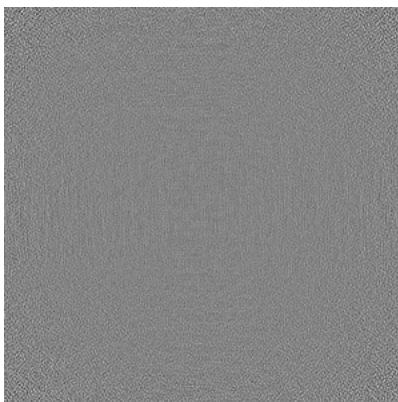


Z Index: 182

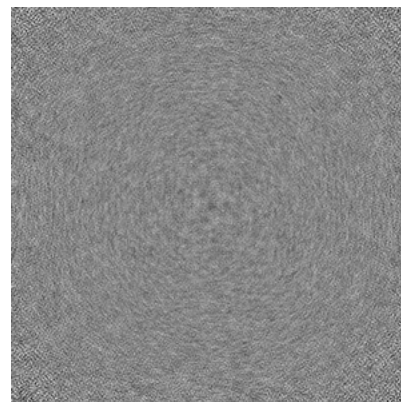
6.3.2 Raw map



X Index: 0



Y Index: 0

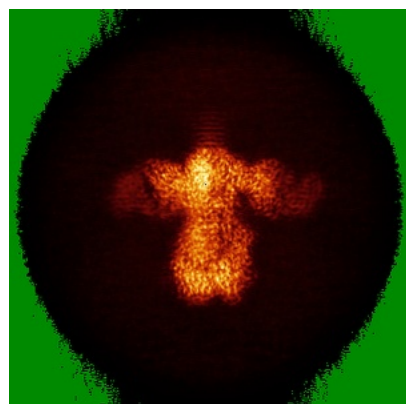


Z Index: 0

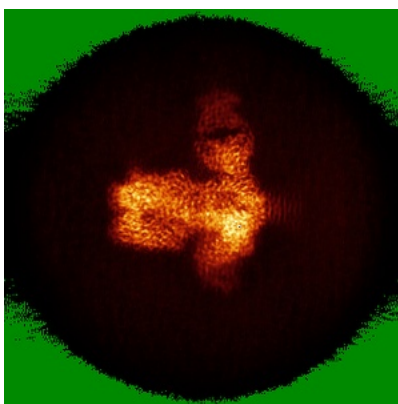
The images above show the largest variance slices of the map in three orthogonal directions.

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

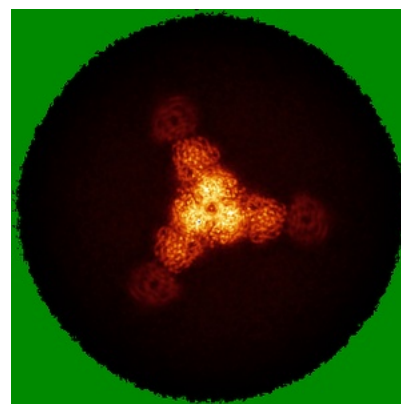
6.4.1 Primary map



X

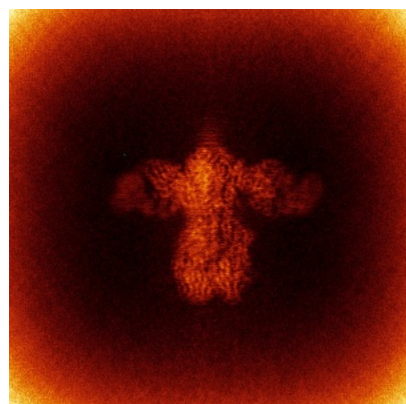


Y

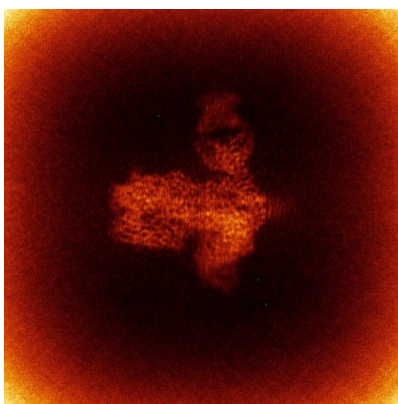


Z

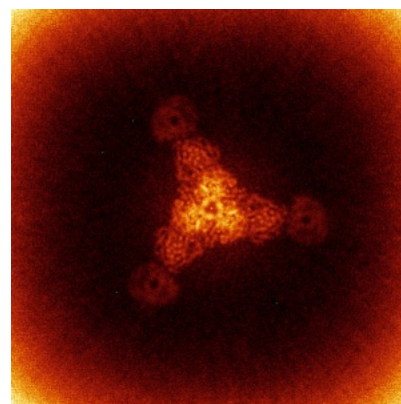
6.4.2 Raw map



X



Y

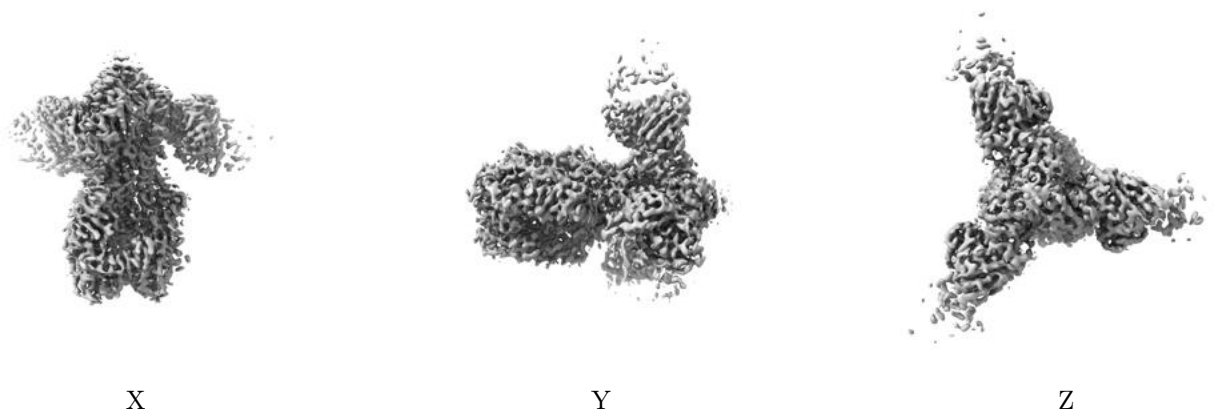


Z

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.

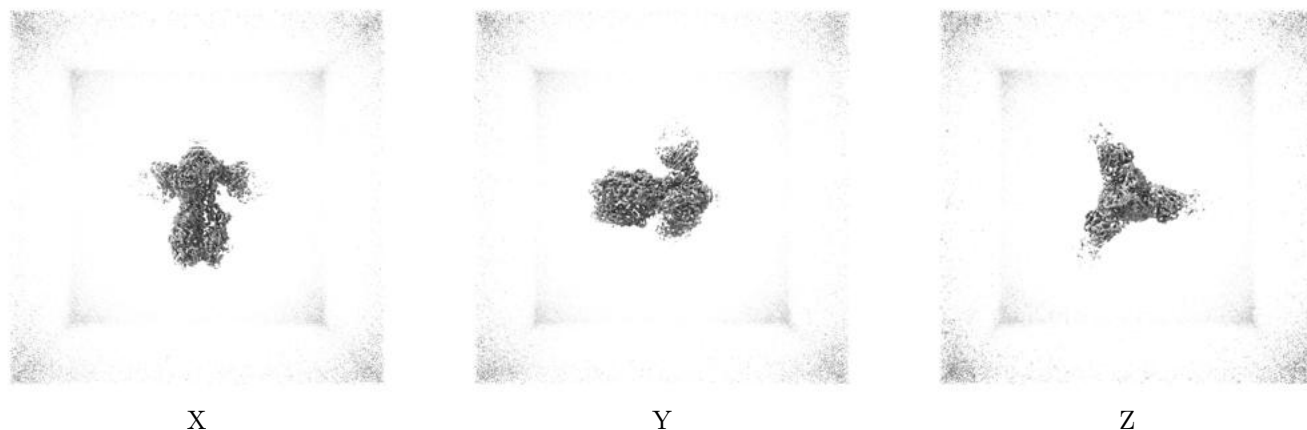
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.22. 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.

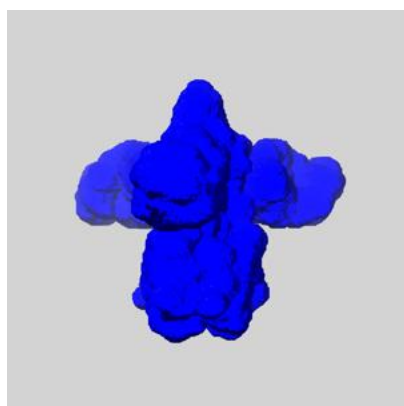
6.6 Mask visualisation [i](#)

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

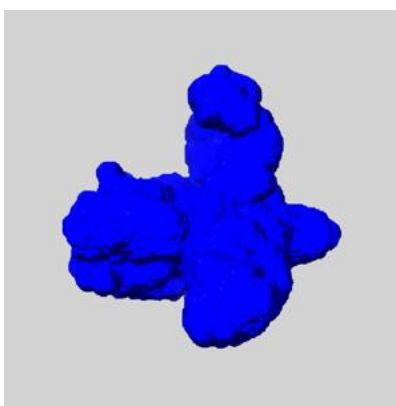
A mask typically either:

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

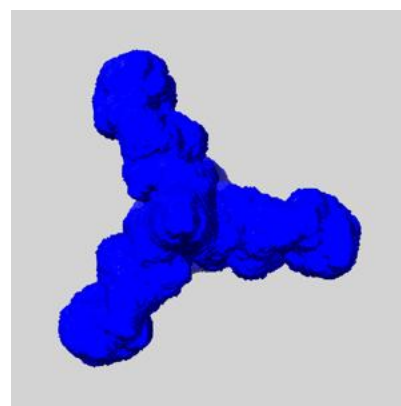
6.6.1 emd_44903_msk_1.map [i](#)



X



Y

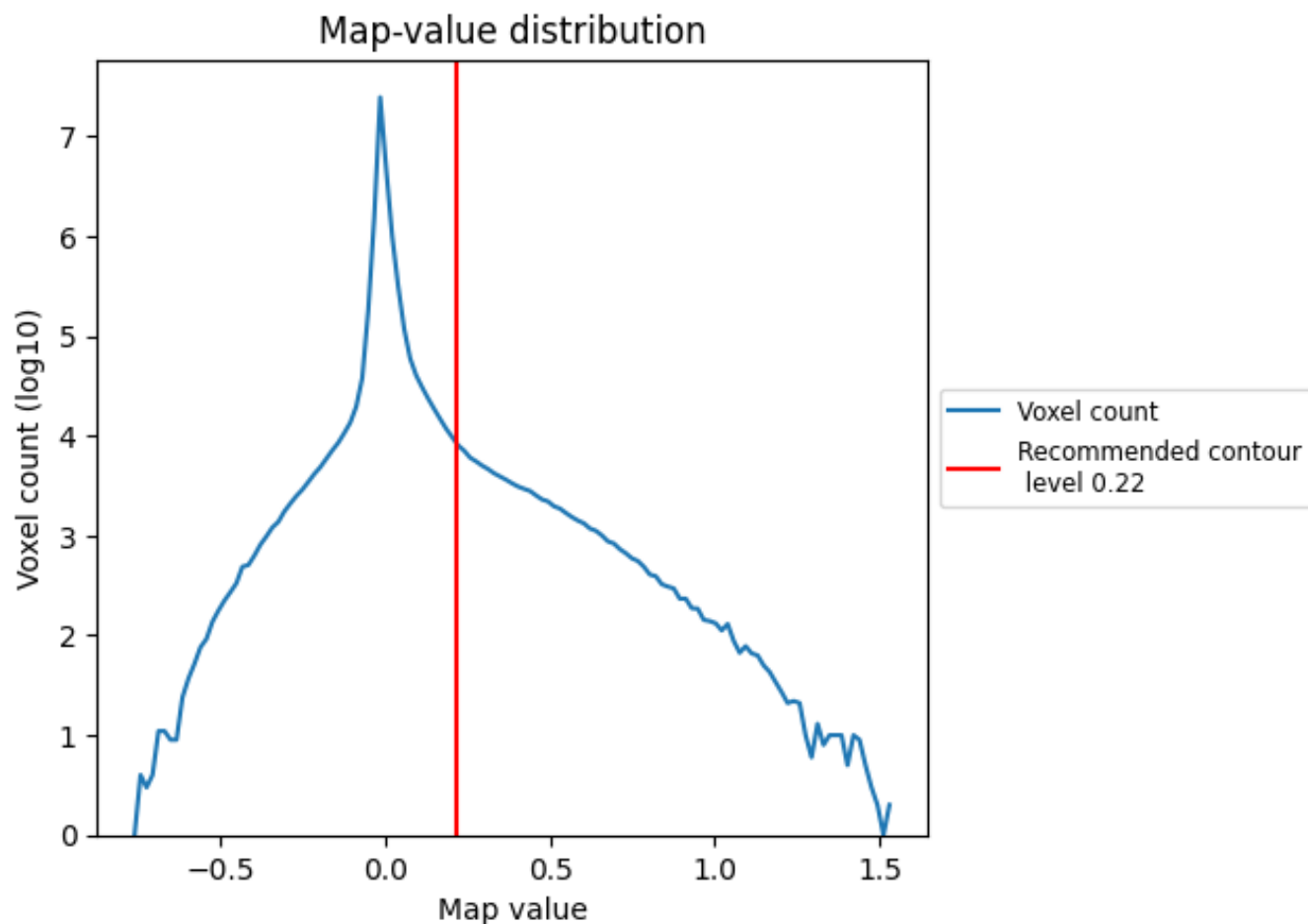


Z

7 Map analysis [i](#)

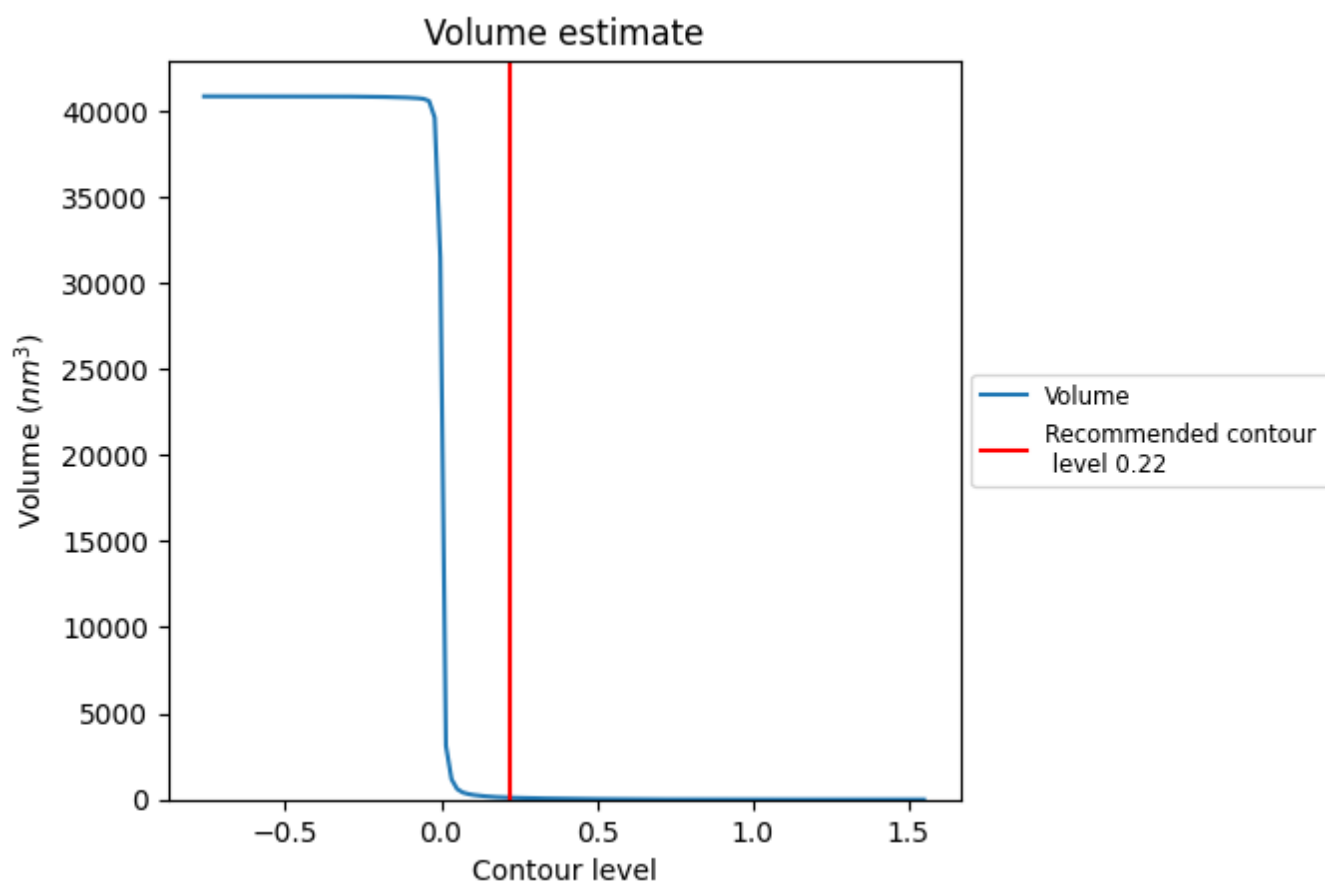
This section contains the results of statistical analysis of the map.

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.

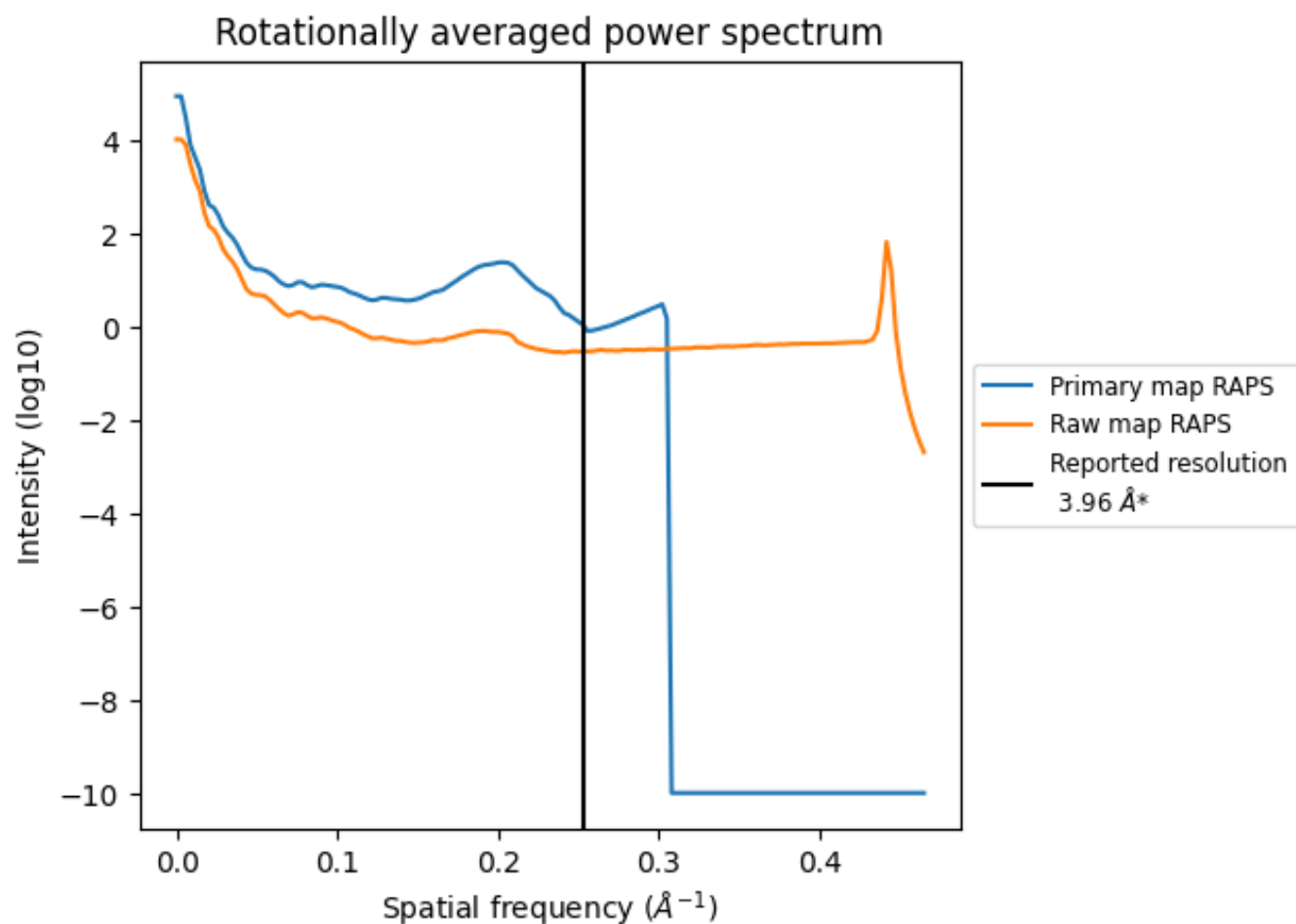
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 112 nm³; this corresponds to an approximate mass of 101 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 ⓘ

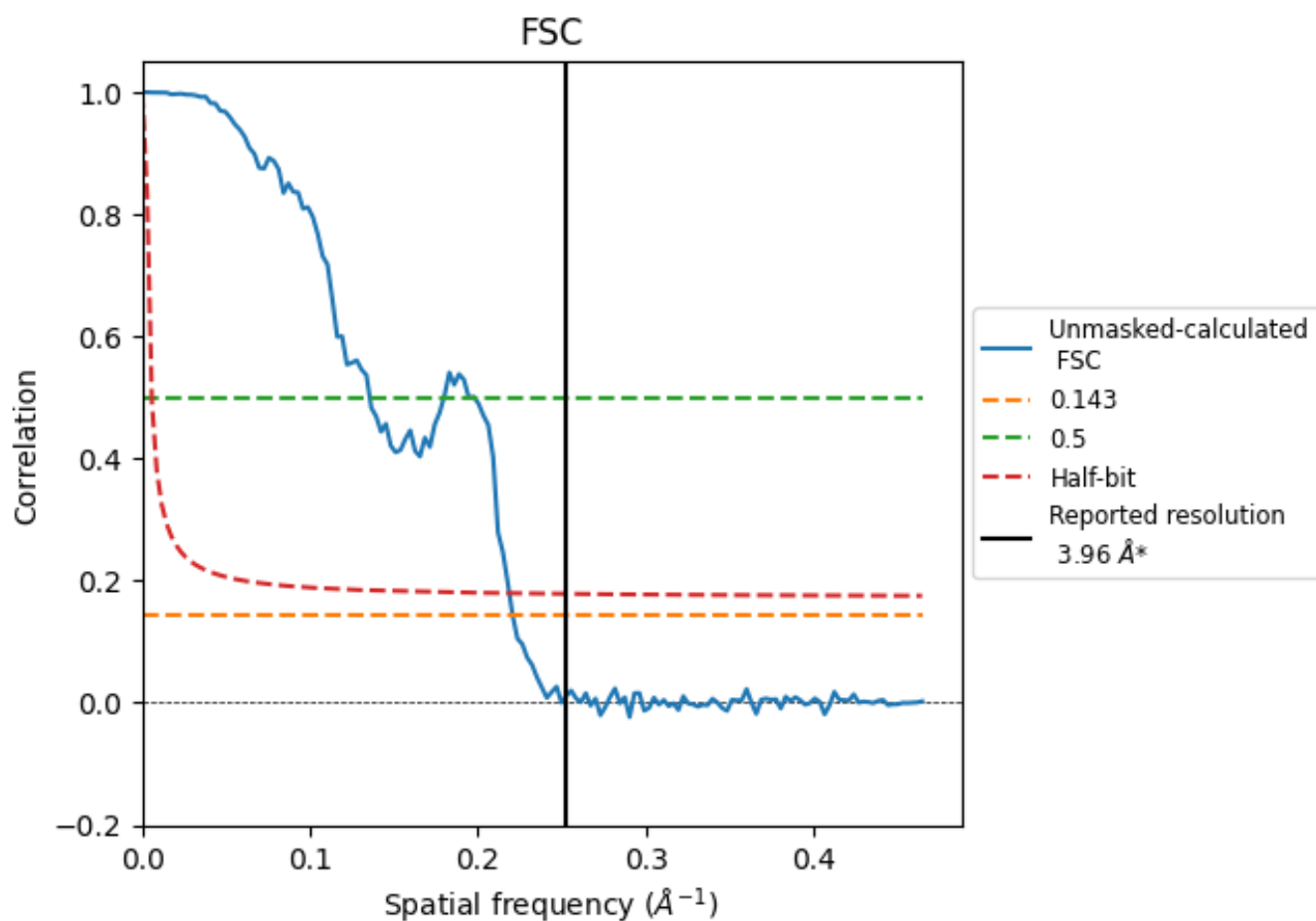


*Reported resolution corresponds to spatial frequency of 0.253 Å⁻¹

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 0.253 Å⁻¹

8.2 Resolution estimates [i](#)

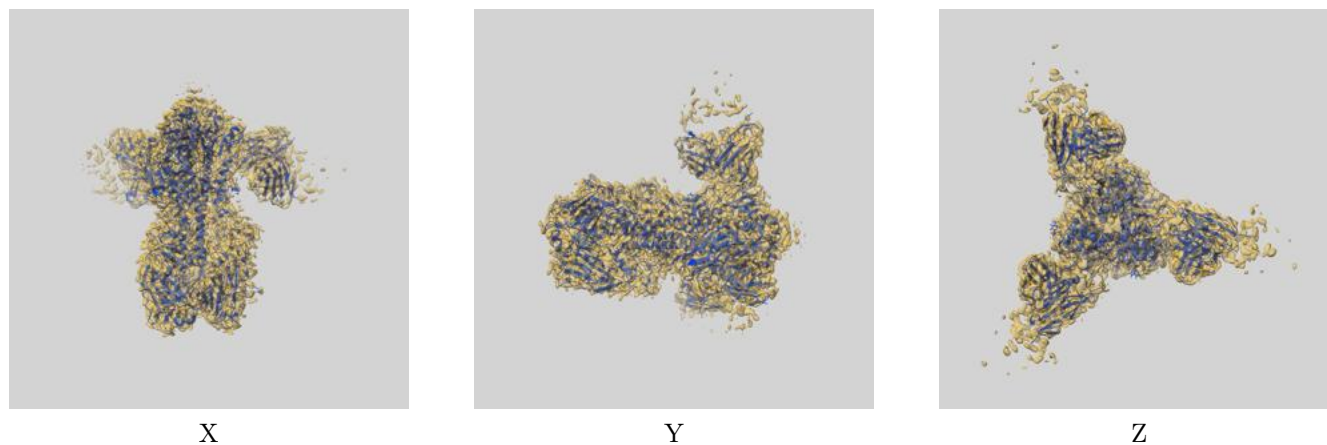
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.96	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.53	7.37	4.57

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.53 differs from the reported value 3.96 by more than 10 %

9 Map-model fit [i](#)

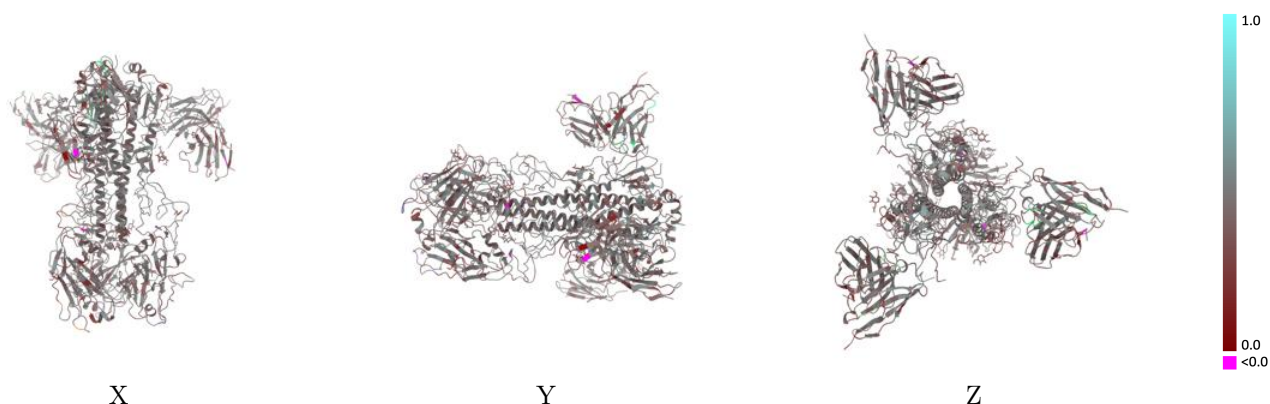
This section contains information regarding the fit between EMDB map EMD-44903 and PDB model 9BU8. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

9.1 Map-model overlay [i](#)



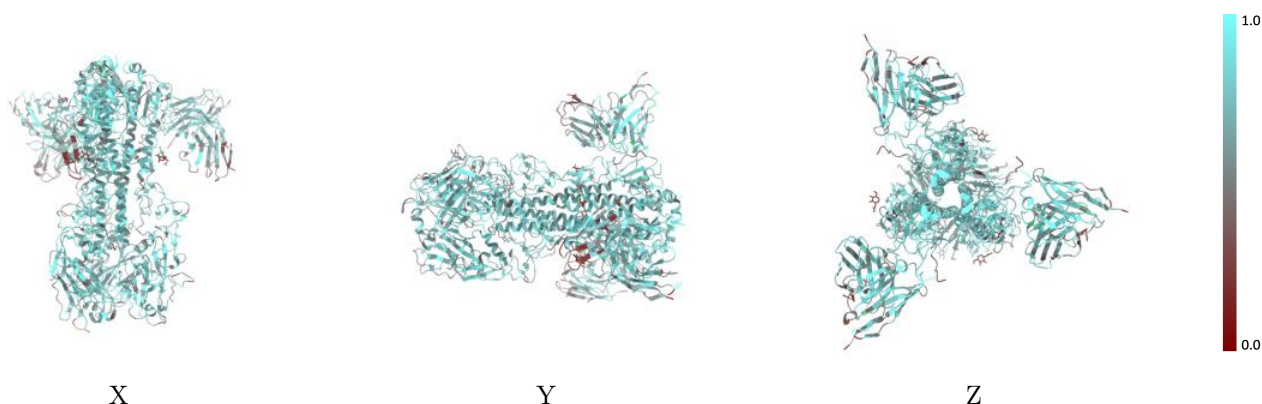
The images above show the 3D surface view of the map at the recommended contour level 0.22 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



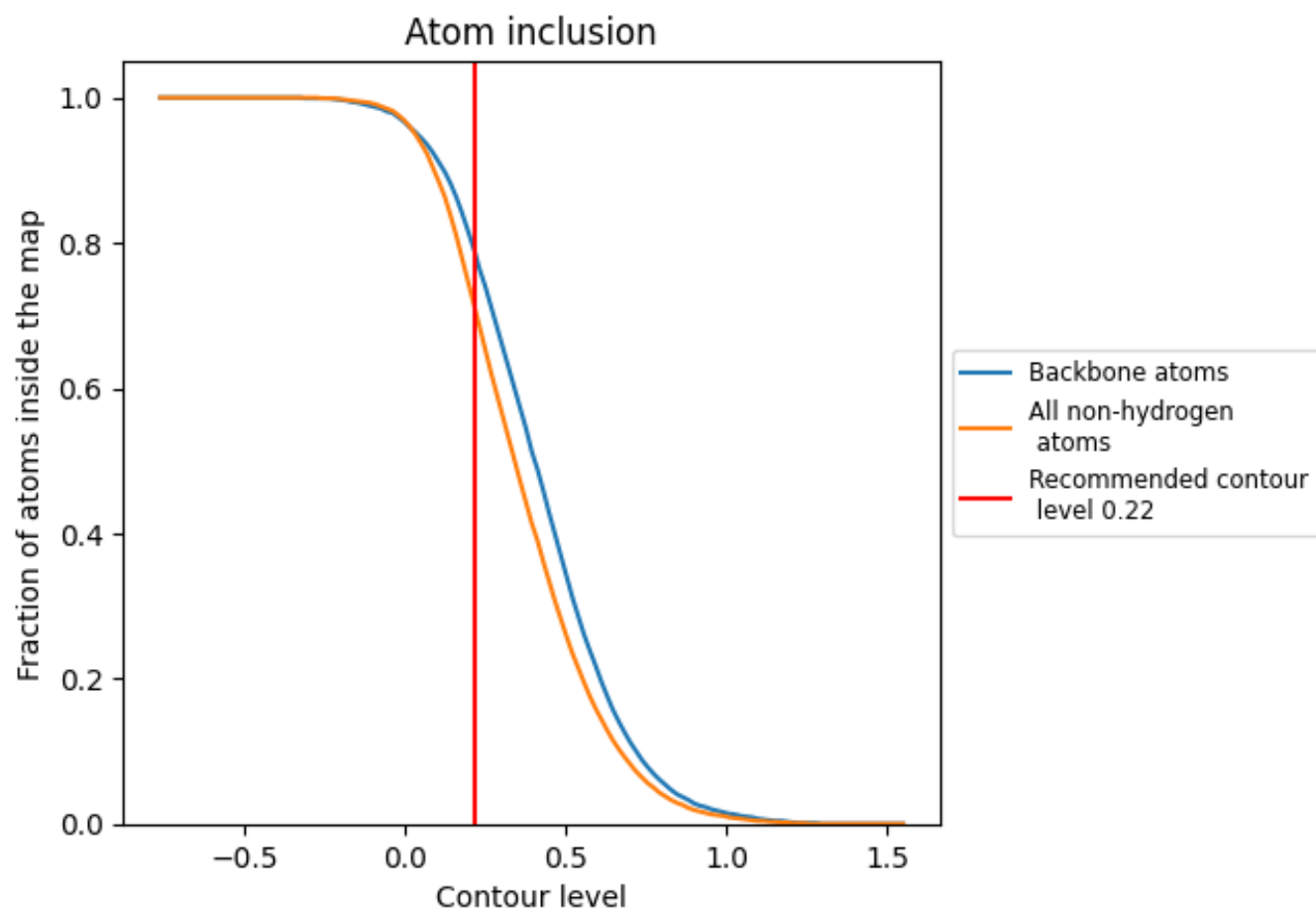
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.22).

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 71% 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 (0.22) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7070	0.4140
A	0.7190	0.4140
B	0.7390	0.4330
C	0.7120	0.4160
D	0.6230	0.3860
E	0.7270	0.4150
F	0.7090	0.4130
G	0.7380	0.4300
H	0.6080	0.3800
I	0.7150	0.4130
J	0.7180	0.4180
K	0.6200	0.3820
L	0.7400	0.4290
M	0.4100	0.2880
N	0.3080	0.2550
O	0.3850	0.3340

1.0

0.0

<0.0