



wwPDB EM Validation Summary Report ⓘ

May 16, 2026 – 12:31 PM EDT

PDB ID : 9O8T / pdb_00009o8t
EMDB ID : EMD-70236
Title : Cryo-EM structure of NI04359_d30_240 Fab in complex with influenza virus hemagglutinin from A/Michigan/45/2015 (H1N1)
Authors : Jo, G.; Ward, A.B.
Deposited on : 2025-04-16
Resolution : 3.12 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:

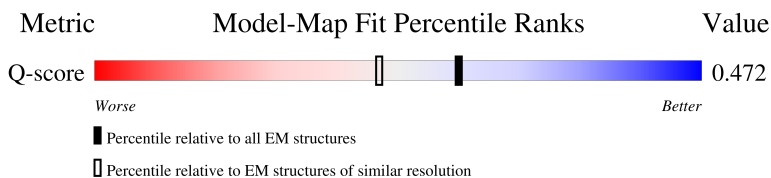
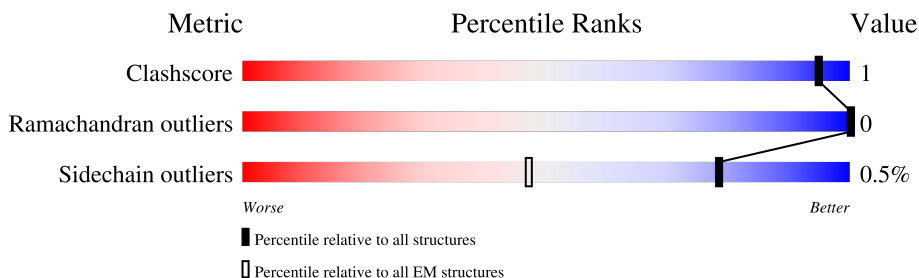
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 3.12 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	14478 (2.62 - 3.62)

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	344	
1	C	344	
1	D	344	
2	B	233	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	E	233	71% 28%
2	F	233	71% 28%
3	G	130	22% 92% 6%
3	H	130	24% 92% 6%
3	I	130	23% 92% 6%
4	J	107	21% 94%
4	K	107	21% 94%
4	L	107	21% 94%
5	M	2	50% 100%
5	N	2	50% 100%
5	O	2	50% 100%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 17142 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	323	Total	C	N	O	S	0	0
			2528	1594	437	486	11		
1	C	323	Total	C	N	O	S	0	0
			2528	1594	437	486	11		
1	D	323	Total	C	N	O	S	0	0
			2528	1594	437	486	11		

- Molecule 2 is a protein called Hemagglutinin HA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	167	Total	C	N	O	S	0	0
			1355	849	232	268	6		
2	E	167	Total	C	N	O	S	0	0
			1355	849	232	268	6		
2	F	167	Total	C	N	O	S	0	0
			1355	849	232	268	6		

There are 177 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	175	GLY	-	expression tag	UNP A0A1J0CXU0
B	176	GLY	-	expression tag	UNP A0A1J0CXU0
B	177	TYR	-	expression tag	UNP A0A1J0CXU0
B	178	ILE	-	expression tag	UNP A0A1J0CXU0
B	179	PRO	-	expression tag	UNP A0A1J0CXU0
B	180	GLU	-	expression tag	UNP A0A1J0CXU0
B	181	ALA	-	expression tag	UNP A0A1J0CXU0
B	182	PRO	-	expression tag	UNP A0A1J0CXU0
B	183	ARG	-	expression tag	UNP A0A1J0CXU0
B	184	ASP	-	expression tag	UNP A0A1J0CXU0
B	185	GLY	-	expression tag	UNP A0A1J0CXU0
B	186	GLN	-	expression tag	UNP A0A1J0CXU0
B	187	ALA	-	expression tag	UNP A0A1J0CXU0

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	188	TYR	-	expression tag	UNP A0A1J0CXU0
B	189	VAL	-	expression tag	UNP A0A1J0CXU0
B	190	ARG	-	expression tag	UNP A0A1J0CXU0
B	191	LYS	-	expression tag	UNP A0A1J0CXU0
B	192	ASP	-	expression tag	UNP A0A1J0CXU0
B	193	GLY	-	expression tag	UNP A0A1J0CXU0
B	194	GLU	-	expression tag	UNP A0A1J0CXU0
B	195	TRP	-	expression tag	UNP A0A1J0CXU0
B	196	VAL	-	expression tag	UNP A0A1J0CXU0
B	197	LEU	-	expression tag	UNP A0A1J0CXU0
B	198	LEU	-	expression tag	UNP A0A1J0CXU0
B	199	SER	-	expression tag	UNP A0A1J0CXU0
B	200	THR	-	expression tag	UNP A0A1J0CXU0
B	201	PHE	-	expression tag	UNP A0A1J0CXU0
B	202	LEU	-	expression tag	UNP A0A1J0CXU0
B	203	GLY	-	expression tag	UNP A0A1J0CXU0
B	204	SER	-	expression tag	UNP A0A1J0CXU0
B	205	GLU	-	expression tag	UNP A0A1J0CXU0
B	206	ASN	-	expression tag	UNP A0A1J0CXU0
B	207	LEU	-	expression tag	UNP A0A1J0CXU0
B	208	TYR	-	expression tag	UNP A0A1J0CXU0
B	209	PHE	-	expression tag	UNP A0A1J0CXU0
B	210	GLN	-	expression tag	UNP A0A1J0CXU0
B	211	GLY	-	expression tag	UNP A0A1J0CXU0
B	212	SER	-	expression tag	UNP A0A1J0CXU0
B	213	HIS	-	expression tag	UNP A0A1J0CXU0
B	214	HIS	-	expression tag	UNP A0A1J0CXU0
B	215	HIS	-	expression tag	UNP A0A1J0CXU0
B	216	HIS	-	expression tag	UNP A0A1J0CXU0
B	217	HIS	-	expression tag	UNP A0A1J0CXU0
B	218	HIS	-	expression tag	UNP A0A1J0CXU0
B	219	GLY	-	expression tag	UNP A0A1J0CXU0
B	220	LEU	-	expression tag	UNP A0A1J0CXU0
B	221	ASN	-	expression tag	UNP A0A1J0CXU0
B	222	ASP	-	expression tag	UNP A0A1J0CXU0
B	223	ILE	-	expression tag	UNP A0A1J0CXU0
B	224	PHE	-	expression tag	UNP A0A1J0CXU0
B	225	GLU	-	expression tag	UNP A0A1J0CXU0
B	226	ALA	-	expression tag	UNP A0A1J0CXU0
B	227	GLN	-	expression tag	UNP A0A1J0CXU0
B	228	LYS	-	expression tag	UNP A0A1J0CXU0
B	229	ILE	-	expression tag	UNP A0A1J0CXU0

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	230	GLU	-	expression tag	UNP A0A1J0CXU0
B	231	TRP	-	expression tag	UNP A0A1J0CXU0
B	232	HIS	-	expression tag	UNP A0A1J0CXU0
B	233	GLU	-	expression tag	UNP A0A1J0CXU0
E	175	GLY	-	expression tag	UNP A0A1J0CXU0
E	176	GLY	-	expression tag	UNP A0A1J0CXU0
E	177	TYR	-	expression tag	UNP A0A1J0CXU0
E	178	ILE	-	expression tag	UNP A0A1J0CXU0
E	179	PRO	-	expression tag	UNP A0A1J0CXU0
E	180	GLU	-	expression tag	UNP A0A1J0CXU0
E	181	ALA	-	expression tag	UNP A0A1J0CXU0
E	182	PRO	-	expression tag	UNP A0A1J0CXU0
E	183	ARG	-	expression tag	UNP A0A1J0CXU0
E	184	ASP	-	expression tag	UNP A0A1J0CXU0
E	185	GLY	-	expression tag	UNP A0A1J0CXU0
E	186	GLN	-	expression tag	UNP A0A1J0CXU0
E	187	ALA	-	expression tag	UNP A0A1J0CXU0
E	188	TYR	-	expression tag	UNP A0A1J0CXU0
E	189	VAL	-	expression tag	UNP A0A1J0CXU0
E	190	ARG	-	expression tag	UNP A0A1J0CXU0
E	191	LYS	-	expression tag	UNP A0A1J0CXU0
E	192	ASP	-	expression tag	UNP A0A1J0CXU0
E	193	GLY	-	expression tag	UNP A0A1J0CXU0
E	194	GLU	-	expression tag	UNP A0A1J0CXU0
E	195	TRP	-	expression tag	UNP A0A1J0CXU0
E	196	VAL	-	expression tag	UNP A0A1J0CXU0
E	197	LEU	-	expression tag	UNP A0A1J0CXU0
E	198	LEU	-	expression tag	UNP A0A1J0CXU0
E	199	SER	-	expression tag	UNP A0A1J0CXU0
E	200	THR	-	expression tag	UNP A0A1J0CXU0
E	201	PHE	-	expression tag	UNP A0A1J0CXU0
E	202	LEU	-	expression tag	UNP A0A1J0CXU0
E	203	GLY	-	expression tag	UNP A0A1J0CXU0
E	204	SER	-	expression tag	UNP A0A1J0CXU0
E	205	GLU	-	expression tag	UNP A0A1J0CXU0
E	206	ASN	-	expression tag	UNP A0A1J0CXU0
E	207	LEU	-	expression tag	UNP A0A1J0CXU0
E	208	TYR	-	expression tag	UNP A0A1J0CXU0
E	209	PHE	-	expression tag	UNP A0A1J0CXU0
E	210	GLN	-	expression tag	UNP A0A1J0CXU0
E	211	GLY	-	expression tag	UNP A0A1J0CXU0
E	212	SER	-	expression tag	UNP A0A1J0CXU0

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
E	213	HIS	-	expression tag	UNP A0A1J0CXU0
E	214	HIS	-	expression tag	UNP A0A1J0CXU0
E	215	HIS	-	expression tag	UNP A0A1J0CXU0
E	216	HIS	-	expression tag	UNP A0A1J0CXU0
E	217	HIS	-	expression tag	UNP A0A1J0CXU0
E	218	HIS	-	expression tag	UNP A0A1J0CXU0
E	219	GLY	-	expression tag	UNP A0A1J0CXU0
E	220	LEU	-	expression tag	UNP A0A1J0CXU0
E	221	ASN	-	expression tag	UNP A0A1J0CXU0
E	222	ASP	-	expression tag	UNP A0A1J0CXU0
E	223	ILE	-	expression tag	UNP A0A1J0CXU0
E	224	PHE	-	expression tag	UNP A0A1J0CXU0
E	225	GLU	-	expression tag	UNP A0A1J0CXU0
E	226	ALA	-	expression tag	UNP A0A1J0CXU0
E	227	GLN	-	expression tag	UNP A0A1J0CXU0
E	228	LYS	-	expression tag	UNP A0A1J0CXU0
E	229	ILE	-	expression tag	UNP A0A1J0CXU0
E	230	GLU	-	expression tag	UNP A0A1J0CXU0
E	231	TRP	-	expression tag	UNP A0A1J0CXU0
E	232	HIS	-	expression tag	UNP A0A1J0CXU0
E	233	GLU	-	expression tag	UNP A0A1J0CXU0
F	175	GLY	-	expression tag	UNP A0A1J0CXU0
F	176	GLY	-	expression tag	UNP A0A1J0CXU0
F	177	TYR	-	expression tag	UNP A0A1J0CXU0
F	178	ILE	-	expression tag	UNP A0A1J0CXU0
F	179	PRO	-	expression tag	UNP A0A1J0CXU0
F	180	GLU	-	expression tag	UNP A0A1J0CXU0
F	181	ALA	-	expression tag	UNP A0A1J0CXU0
F	182	PRO	-	expression tag	UNP A0A1J0CXU0
F	183	ARG	-	expression tag	UNP A0A1J0CXU0
F	184	ASP	-	expression tag	UNP A0A1J0CXU0
F	185	GLY	-	expression tag	UNP A0A1J0CXU0
F	186	GLN	-	expression tag	UNP A0A1J0CXU0
F	187	ALA	-	expression tag	UNP A0A1J0CXU0
F	188	TYR	-	expression tag	UNP A0A1J0CXU0
F	189	VAL	-	expression tag	UNP A0A1J0CXU0
F	190	ARG	-	expression tag	UNP A0A1J0CXU0
F	191	LYS	-	expression tag	UNP A0A1J0CXU0
F	192	ASP	-	expression tag	UNP A0A1J0CXU0
F	193	GLY	-	expression tag	UNP A0A1J0CXU0
F	194	GLU	-	expression tag	UNP A0A1J0CXU0
F	195	TRP	-	expression tag	UNP A0A1J0CXU0

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
F	196	VAL	-	expression tag	UNP A0A1J0CXU0
F	197	LEU	-	expression tag	UNP A0A1J0CXU0
F	198	LEU	-	expression tag	UNP A0A1J0CXU0
F	199	SER	-	expression tag	UNP A0A1J0CXU0
F	200	THR	-	expression tag	UNP A0A1J0CXU0
F	201	PHE	-	expression tag	UNP A0A1J0CXU0
F	202	LEU	-	expression tag	UNP A0A1J0CXU0
F	203	GLY	-	expression tag	UNP A0A1J0CXU0
F	204	SER	-	expression tag	UNP A0A1J0CXU0
F	205	GLU	-	expression tag	UNP A0A1J0CXU0
F	206	ASN	-	expression tag	UNP A0A1J0CXU0
F	207	LEU	-	expression tag	UNP A0A1J0CXU0
F	208	TYR	-	expression tag	UNP A0A1J0CXU0
F	209	PHE	-	expression tag	UNP A0A1J0CXU0
F	210	GLN	-	expression tag	UNP A0A1J0CXU0
F	211	GLY	-	expression tag	UNP A0A1J0CXU0
F	212	SER	-	expression tag	UNP A0A1J0CXU0
F	213	HIS	-	expression tag	UNP A0A1J0CXU0
F	214	HIS	-	expression tag	UNP A0A1J0CXU0
F	215	HIS	-	expression tag	UNP A0A1J0CXU0
F	216	HIS	-	expression tag	UNP A0A1J0CXU0
F	217	HIS	-	expression tag	UNP A0A1J0CXU0
F	218	HIS	-	expression tag	UNP A0A1J0CXU0
F	219	GLY	-	expression tag	UNP A0A1J0CXU0
F	220	LEU	-	expression tag	UNP A0A1J0CXU0
F	221	ASN	-	expression tag	UNP A0A1J0CXU0
F	222	ASP	-	expression tag	UNP A0A1J0CXU0
F	223	ILE	-	expression tag	UNP A0A1J0CXU0
F	224	PHE	-	expression tag	UNP A0A1J0CXU0
F	225	GLU	-	expression tag	UNP A0A1J0CXU0
F	226	ALA	-	expression tag	UNP A0A1J0CXU0
F	227	GLN	-	expression tag	UNP A0A1J0CXU0
F	228	LYS	-	expression tag	UNP A0A1J0CXU0
F	229	ILE	-	expression tag	UNP A0A1J0CXU0
F	230	GLU	-	expression tag	UNP A0A1J0CXU0
F	231	TRP	-	expression tag	UNP A0A1J0CXU0
F	232	HIS	-	expression tag	UNP A0A1J0CXU0
F	233	GLU	-	expression tag	UNP A0A1J0CXU0

- Molecule 3 is a protein called NI04359_d30_240 Fab heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	128	Total	C	N	O	S	0	0
			971	608	167	189	7		
3	G	128	Total	C	N	O	S	0	0
			971	608	167	189	7		
3	I	128	Total	C	N	O	S	0	0
			971	608	167	189	7		

- Molecule 4 is a protein called NI04359_d30_240 Fab light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L	105	Total	C	N	O	S	0	0
			790	492	129	166	3		
4	J	105	Total	C	N	O	S	0	0
			790	492	129	166	3		
4	K	105	Total	C	N	O	S	0	0
			790	492	129	166	3		

- Molecule 5 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
5	M	2	Total	C	N	O	0	0
			28	16	2	10		
5	N	2	Total	C	N	O	0	0
			28	16	2	10		
5	O	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



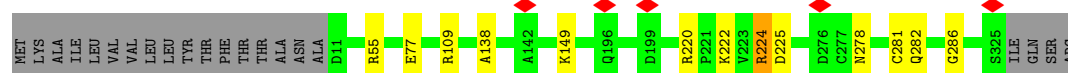
Mol	Chain	Residues	Atoms				AltConf
6	A	1	Total	C	N	O	0
			14	8	1	5	
6	A	1	Total	C	N	O	0
			14	8	1	5	
6	B	1	Total	C	N	O	0
			14	8	1	5	
6	C	1	Total	C	N	O	0
			14	8	1	5	
6	C	1	Total	C	N	O	0
			14	8	1	5	
6	E	1	Total	C	N	O	0
			14	8	1	5	
6	D	1	Total	C	N	O	0
			14	8	1	5	
6	D	1	Total	C	N	O	0
			14	8	1	5	
6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

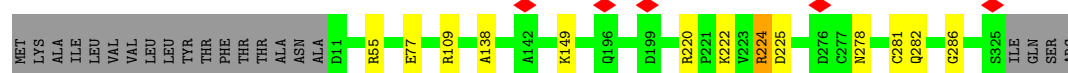
- Molecule 1: Hemagglutinin HA1

Chain A: 



- Molecule 1: Hemagglutinin HA1

Chain C: 



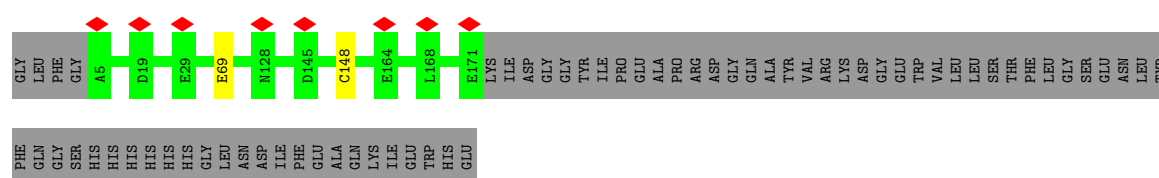
- Molecule 1: Hemagglutinin HA1

Chain D: 



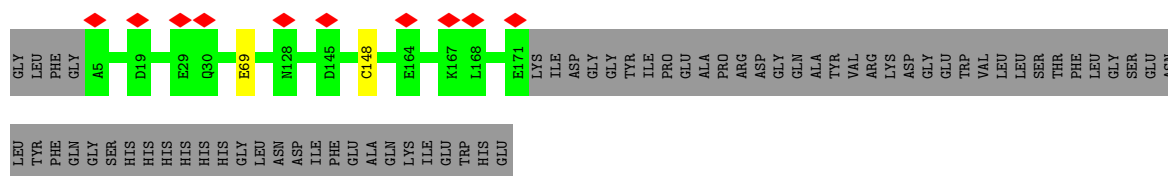
- Molecule 2: Hemagglutinin HA2

Chain B: 

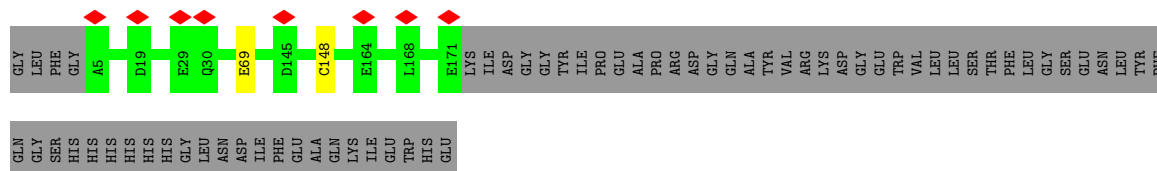


- Molecule 2: Hemagglutinin HA2

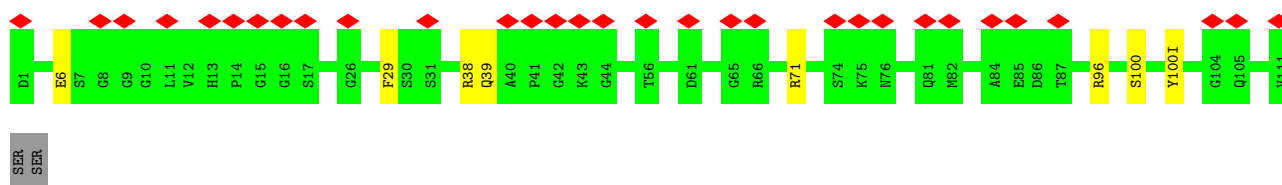
Chain E: 



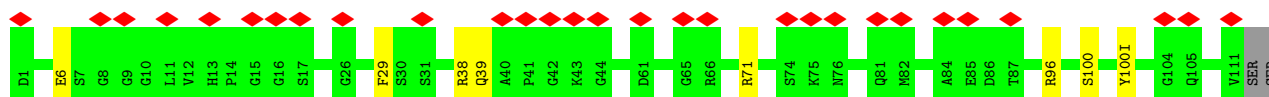
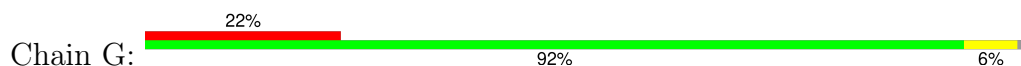
• Molecule 2: Hemagglutinin HA2



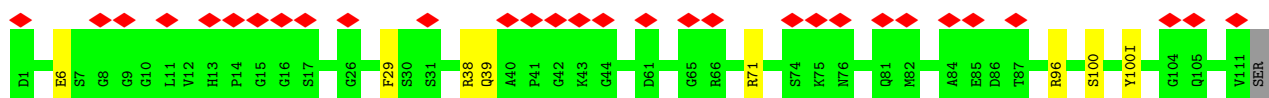
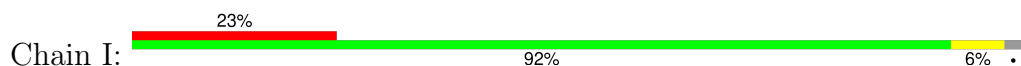
• Molecule 3: NI04359_d30_240 Fab heavy chain



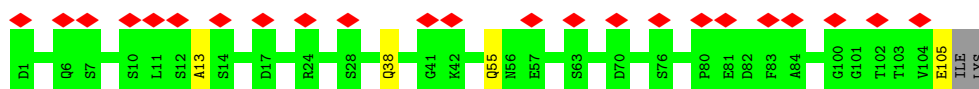
• Molecule 3: NI04359_d30_240 Fab heavy chain



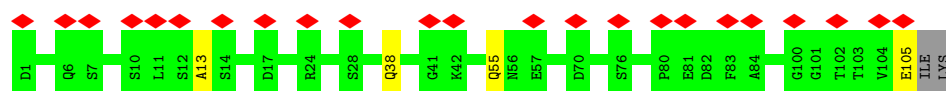
• Molecule 3: NI04359_d30_240 Fab heavy chain



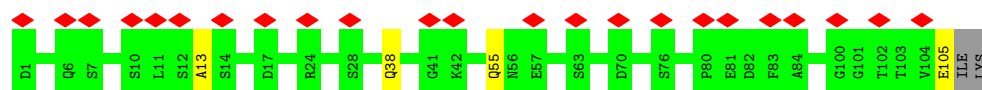
• Molecule 4: NI04359_d30_240 Fab light chain



• Molecule 4: NI04359_d30_240 Fab light chain



- Molecule 4: NI04359_d30_240 Fab light chain



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



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



- Molecule 5: 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	84345	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	44.87	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1400	Depositor
Magnification	190000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.869	Depositor
Minimum map value	-0.717	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.11	Depositor
Map size (Å)	319.0, 319.0, 319.0	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.725, 0.725, 0.725	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

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	0.22	0/2591	0.45	0/3525
1	C	0.22	0/2591	0.45	0/3525
1	D	0.22	0/2591	0.45	0/3525
2	B	0.20	0/1382	0.39	0/1862
2	E	0.20	0/1382	0.39	0/1862
2	F	0.20	0/1382	0.39	0/1862
3	G	0.21	0/993	0.54	1/1343 (0.1%)
3	H	0.21	0/993	0.54	1/1343 (0.1%)
3	I	0.21	0/993	0.54	1/1343 (0.1%)
4	J	0.20	0/807	0.41	0/1097
4	K	0.20	0/807	0.41	0/1097
4	L	0.20	0/807	0.40	0/1097
All	All	0.21	0/17319	0.45	3/23481 (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	A	0	2
1	C	0	2
1	D	0	2
3	G	0	1
3	H	0	1
3	I	0	1
All	All	0	9

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	100(I)	TYR	CA-CB-CG	8.16	128.59	113.90
3	I	100(I)	TYR	CA-CB-CG	8.15	128.56	113.90
3	G	100(I)	TYR	CA-CB-CG	8.14	128.55	113.90

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	224	ARG	Sidechain
1	A	55	ARG	Sidechain
1	C	224	ARG	Sidechain
1	C	55	ARG	Sidechain
3	H	38	ARG	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	2528	0	2461	6	0
1	C	2528	0	2461	6	0
1	D	2528	0	2461	6	0
2	B	1355	0	1281	1	0
2	E	1355	0	1281	1	0
2	F	1355	0	1281	1	0
3	G	971	0	919	5	0
3	H	971	0	919	5	0
3	I	971	0	919	5	0
4	J	790	0	756	3	0
4	K	790	0	756	3	0
4	L	790	0	756	3	0
5	M	28	0	25	0	0
5	N	28	0	25	0	0
5	O	28	0	25	0	0
6	A	28	0	26	0	0
6	B	14	0	13	0	0
6	C	28	0	26	0	0
6	D	28	0	26	0	0
6	E	14	0	13	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	F	14	0	13	0	0
All	All	17142	0	16443	36	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.

The worst 5 of 36 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:282:GLN:NE2	1:A:286:GLY:O	2.15	0.79
1:C:282:GLN:NE2	1:C:286:GLY:O	2.15	0.79
1:D:282:GLN:NE2	1:D:286:GLY:O	2.15	0.79
3:I:29:PHE:O	3:I:71:ARG:NH2	2.19	0.76
3:H:29:PHE:O	3:H:71:ARG:NH2	2.19	0.76

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	321/344 (93%)	306 (95%)	15 (5%)	0	100	100
1	C	321/344 (93%)	307 (96%)	14 (4%)	0	100	100
1	D	321/344 (93%)	306 (95%)	15 (5%)	0	100	100
2	B	165/233 (71%)	161 (98%)	4 (2%)	0	100	100
2	E	165/233 (71%)	161 (98%)	4 (2%)	0	100	100
2	F	165/233 (71%)	161 (98%)	4 (2%)	0	100	100
3	G	126/130 (97%)	123 (98%)	3 (2%)	0	100	100
3	H	126/130 (97%)	123 (98%)	3 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	I	126/130 (97%)	123 (98%)	3 (2%)	0	100	100
4	J	103/107 (96%)	95 (92%)	8 (8%)	0	100	100
4	K	103/107 (96%)	95 (92%)	8 (8%)	0	100	100
4	L	103/107 (96%)	95 (92%)	8 (8%)	0	100	100
All	All	2145/2442 (88%)	2056 (96%)	89 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	284/302 (94%)	282 (99%)	2 (1%)	76	80
1	C	284/302 (94%)	282 (99%)	2 (1%)	76	80
1	D	284/302 (94%)	282 (99%)	2 (1%)	76	80
2	B	145/199 (73%)	144 (99%)	1 (1%)	76	80
2	E	145/199 (73%)	144 (99%)	1 (1%)	76	80
2	F	145/199 (73%)	144 (99%)	1 (1%)	76	80
3	G	102/104 (98%)	102 (100%)	0	100	100
3	H	102/104 (98%)	102 (100%)	0	100	100
3	I	102/104 (98%)	102 (100%)	0	100	100
4	J	91/93 (98%)	91 (100%)	0	100	100
4	K	91/93 (98%)	91 (100%)	0	100	100
4	L	91/93 (98%)	91 (100%)	0	100	100
All	All	1866/2094 (89%)	1857 (100%)	9 (0%)	78	83

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	278	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	F	148	CYS
1	C	220	ARG
1	C	278	ASN
2	E	148	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	166	GLN
1	D	170	ASN
3	G	100(B)	ASN
3	I	100(B)	ASN
1	D	133	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 ⓘ

6 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	0.25	0	17,19,21	0.53	0
5	NAG	M	2	5	14,14,15	0.21	0	17,19,21	0.43	0
5	NAG	N	1	1,5	14,14,15	0.26	0	17,19,21	0.52	0
5	NAG	N	2	5	14,14,15	0.21	0	17,19,21	0.43	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	O	1	1,5	14,14,15	0.25	0	17,19,21	0.52	0
5	NAG	O	2	5	14,14,15	0.22	0	17,19,21	0.44	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	M	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	M	2	5	-	2/6/23/26	0/1/1/1
5	NAG	N	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	N	2	5	-	2/6/23/26	0/1/1/1
5	NAG	O	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	O	2	5	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

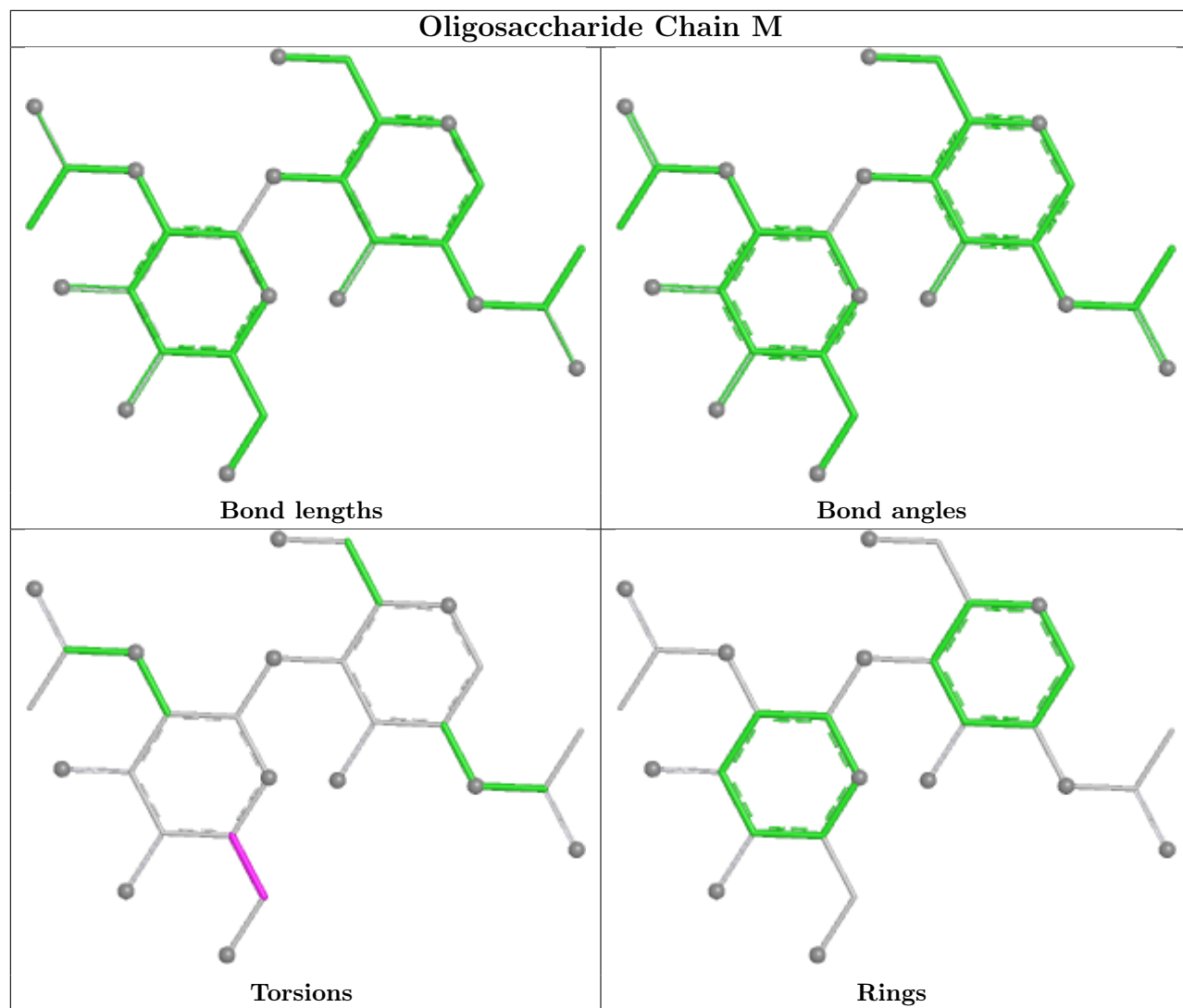
5 of 6 torsion outliers are listed below:

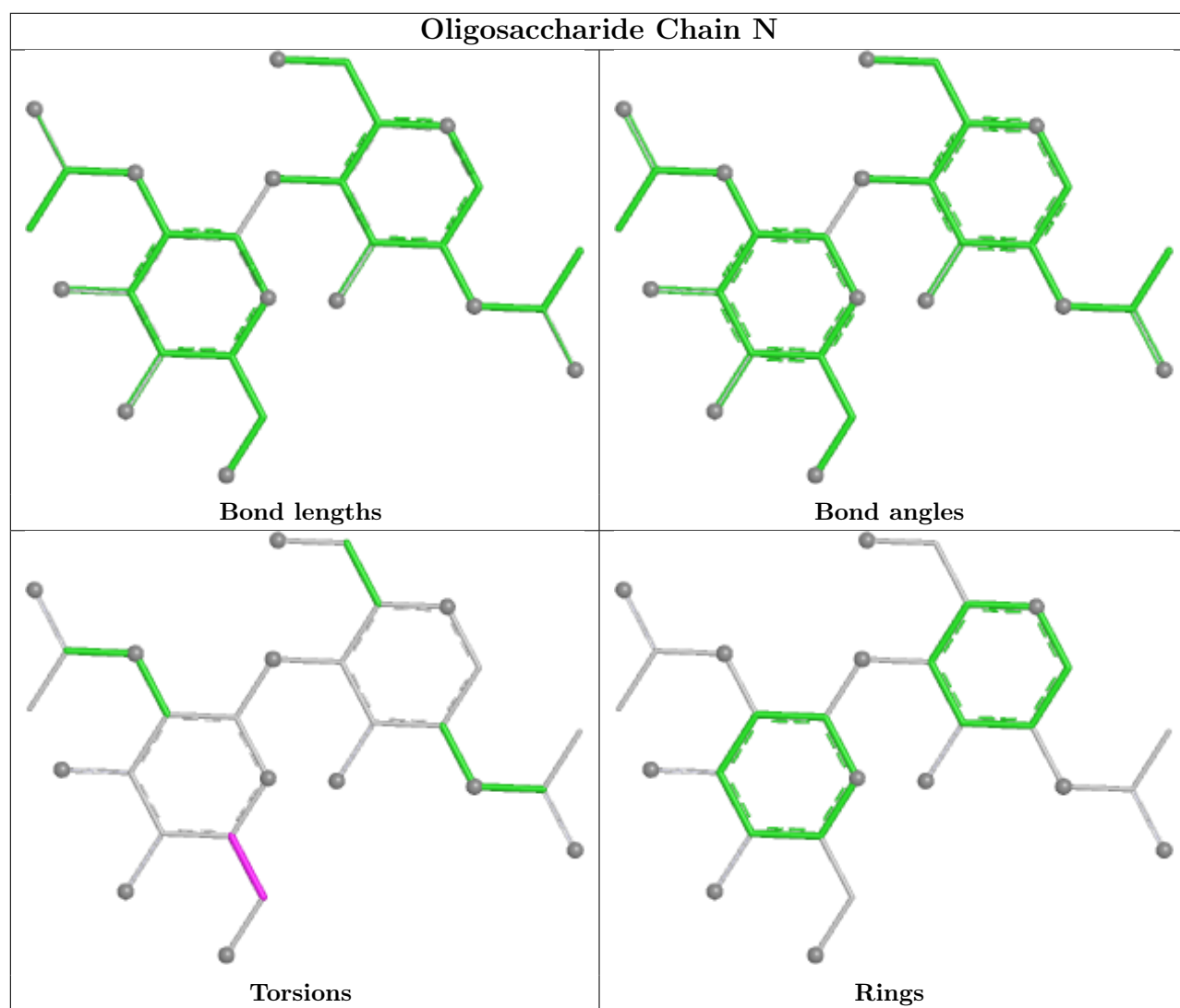
Mol	Chain	Res	Type	Atoms
5	O	2	NAG	O5-C5-C6-O6
5	M	2	NAG	O5-C5-C6-O6
5	N	2	NAG	O5-C5-C6-O6
5	M	2	NAG	C4-C5-C6-O6
5	N	2	NAG	C4-C5-C6-O6

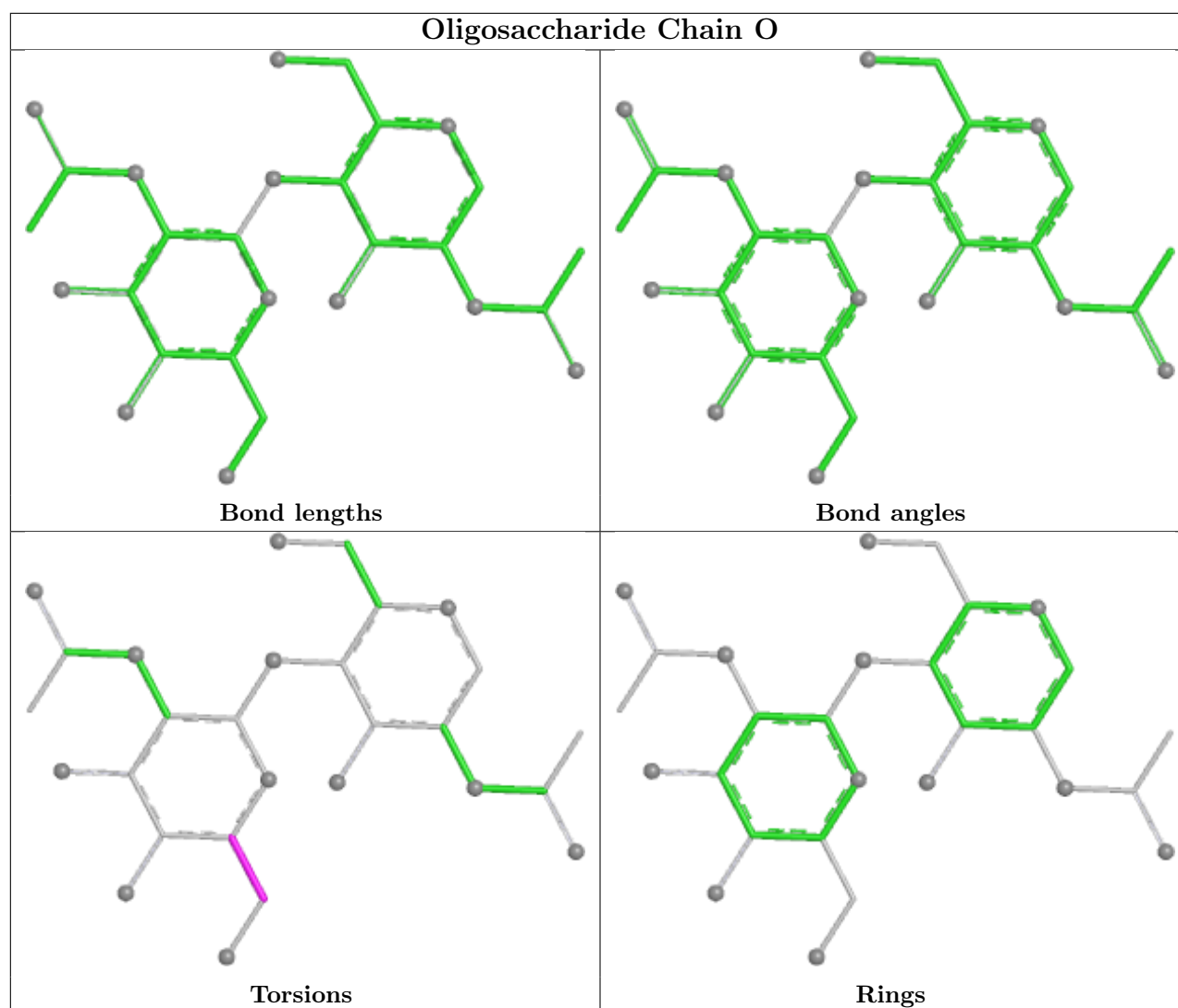
There are no ring outliers.

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](#)

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	E	301	2	14,14,15	0.32	0	17,19,21	0.56	0
6	NAG	D	402	1	14,14,15	0.46	0	17,19,21	0.66	1 (5%)
6	NAG	A	401	1	14,14,15	0.45	0	17,19,21	0.61	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NAG	A	402	1	14,14,15	0.47	0	17,19,21	0.66	1 (5%)
6	NAG	C	401	1	14,14,15	0.46	0	17,19,21	0.61	1 (5%)
6	NAG	D	401	1	14,14,15	0.45	0	17,19,21	0.61	1 (5%)
6	NAG	F	301	2	14,14,15	0.32	0	17,19,21	0.56	0
6	NAG	C	402	1	14,14,15	0.45	0	17,19,21	0.65	1 (5%)
6	NAG	B	301	2	14,14,15	0.32	0	17,19,21	0.55	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	E	301	2	-	0/6/23/26	0/1/1/1
6	NAG	D	402	1	-	0/6/23/26	0/1/1/1
6	NAG	A	401	1	-	1/6/23/26	0/1/1/1
6	NAG	A	402	1	-	0/6/23/26	0/1/1/1
6	NAG	C	401	1	-	2/6/23/26	0/1/1/1
6	NAG	D	401	1	-	1/6/23/26	0/1/1/1
6	NAG	F	301	2	-	0/6/23/26	0/1/1/1
6	NAG	C	402	1	-	0/6/23/26	0/1/1/1
6	NAG	B	301	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	D	402	NAG	C1-O5-C5	2.41	115.42	112.19
6	A	402	NAG	C1-O5-C5	2.40	115.40	112.19
6	C	402	NAG	C1-O5-C5	2.39	115.39	112.19
6	C	401	NAG	C1-O5-C5	2.11	115.01	112.19
6	D	401	NAG	C1-O5-C5	2.07	114.96	112.19

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	401	NAG	C4-C5-C6-O6
6	C	401	NAG	C4-C5-C6-O6
6	D	401	NAG	C4-C5-C6-O6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
6	C	401	NAG	C1-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

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.

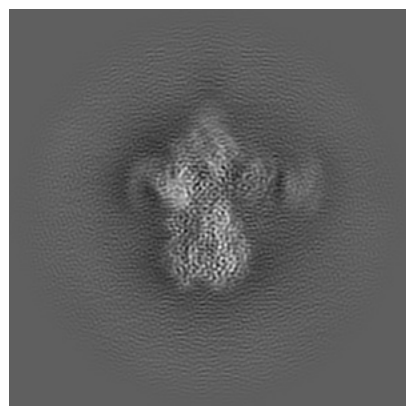
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-70236. These allow visual inspection of the internal detail of the map and identification of artifacts.

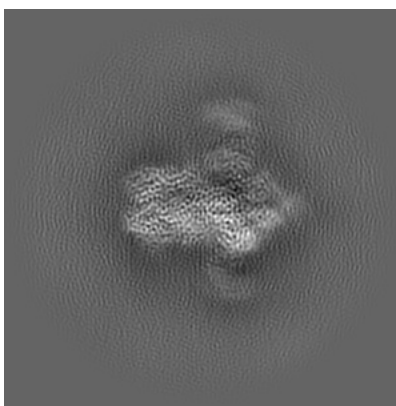
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

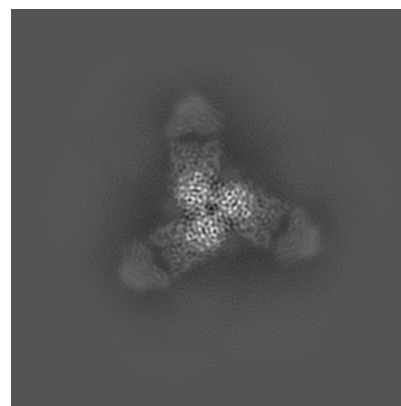
6.1.1 Primary map



X

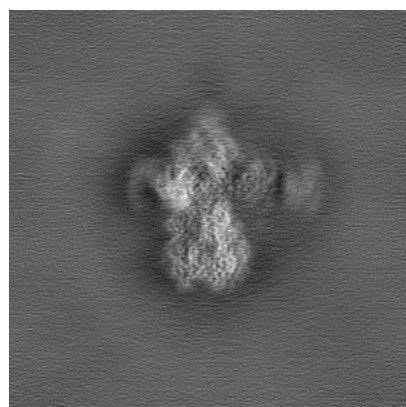


Y

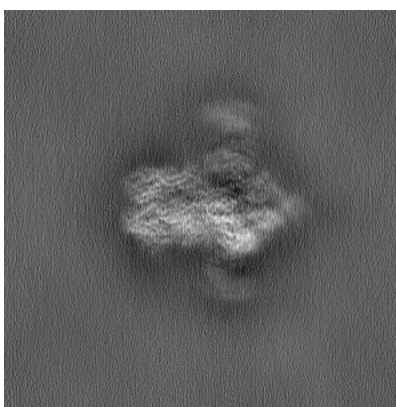


Z

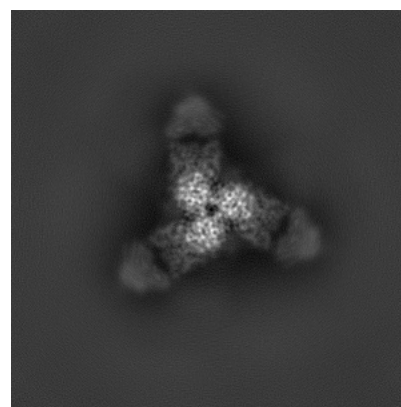
6.1.2 Raw map



X



Y

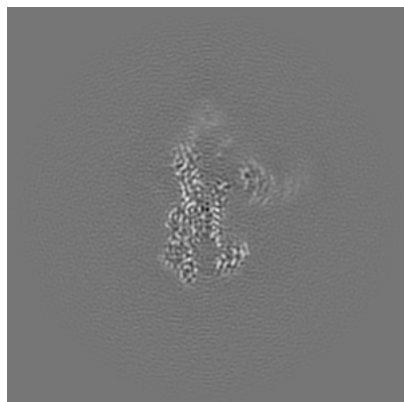


Z

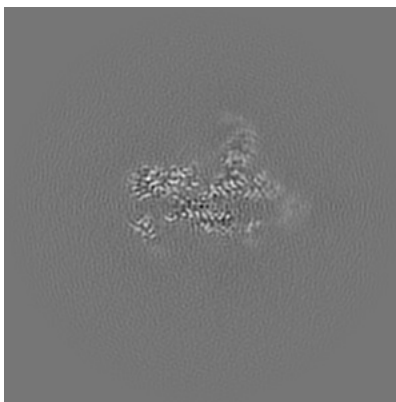
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

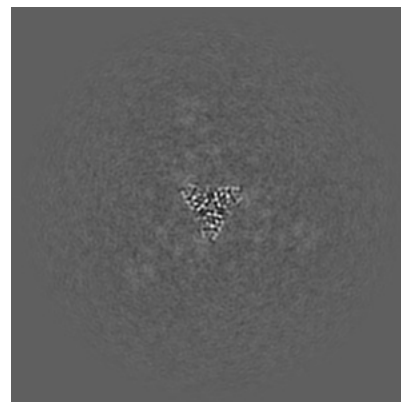
6.2.1 Primary map



X Index: 220

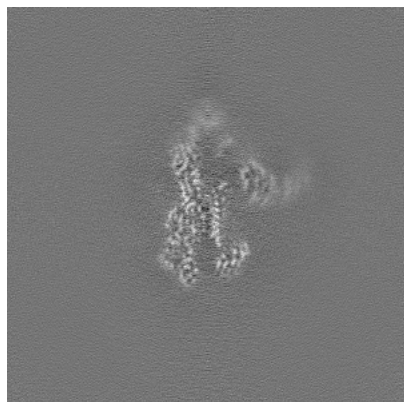


Y Index: 220

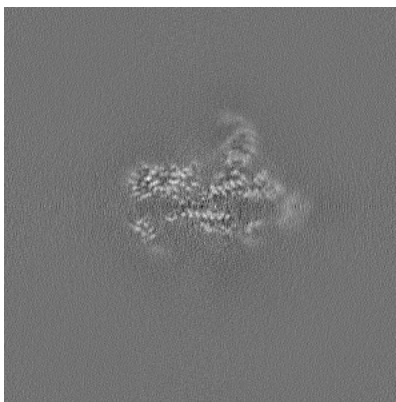


Z Index: 220

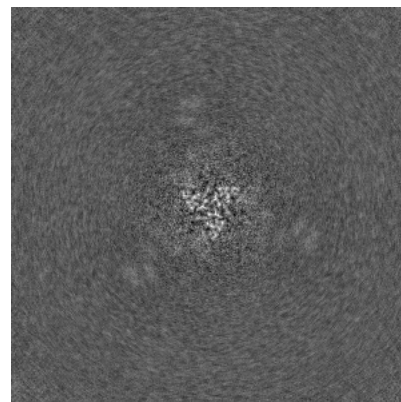
6.2.2 Raw map



X Index: 220



Y Index: 220

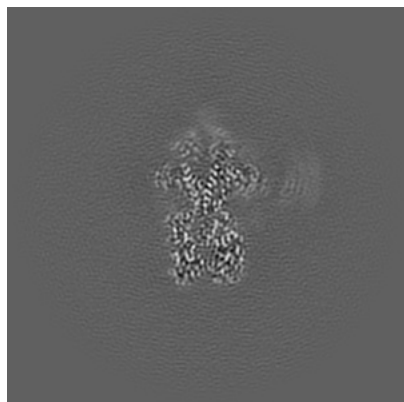


Z Index: 220

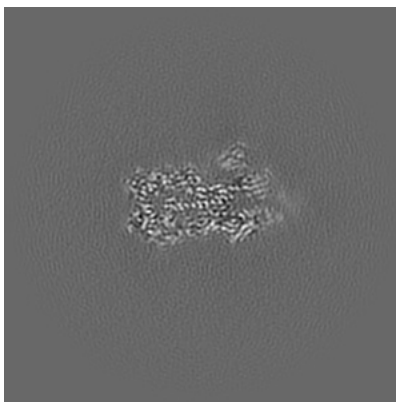
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

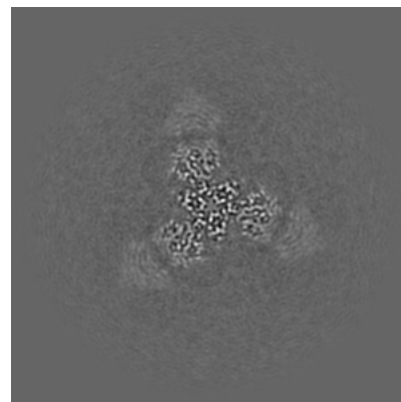
6.3.1 Primary map



X Index: 207

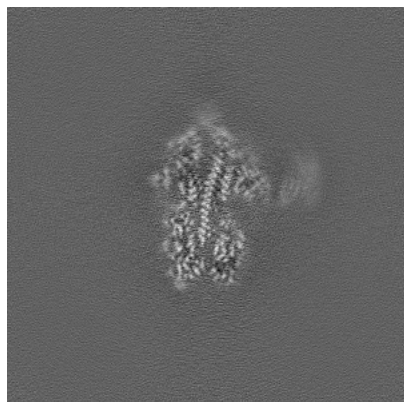


Y Index: 232

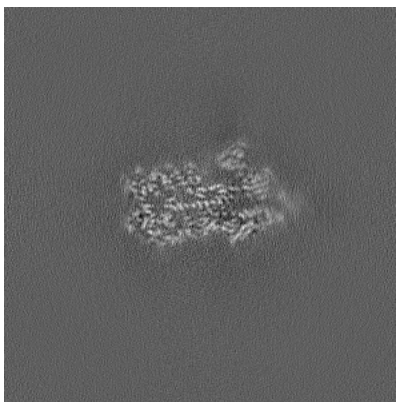


Z Index: 247

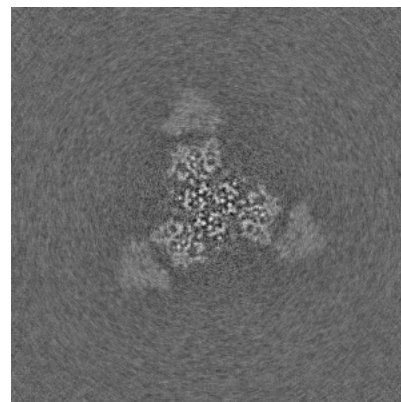
6.3.2 Raw map



X Index: 210



Y Index: 232

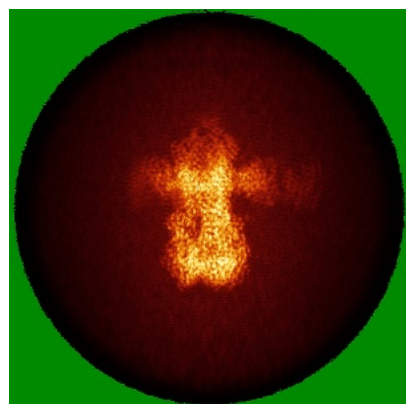


Z Index: 247

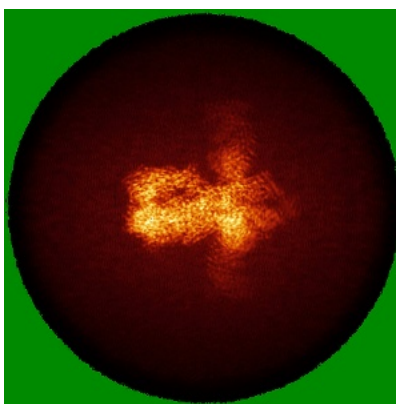
The images above show the largest variance slices of the map in three orthogonal directions.

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

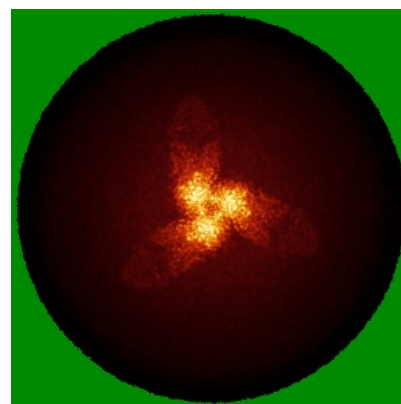
6.4.1 Primary map



X

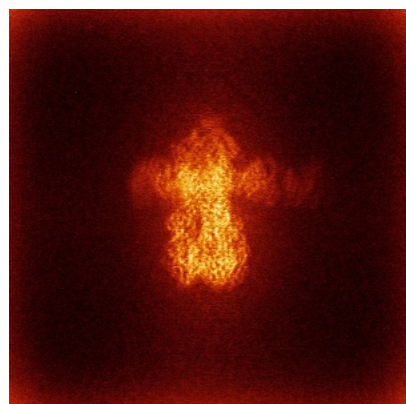


Y

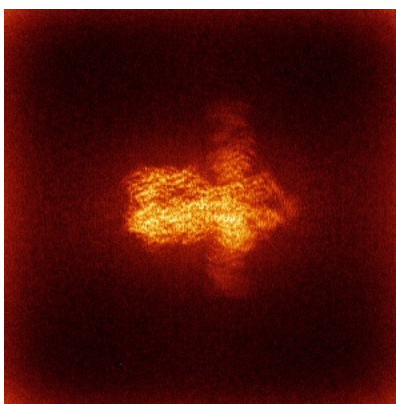


Z

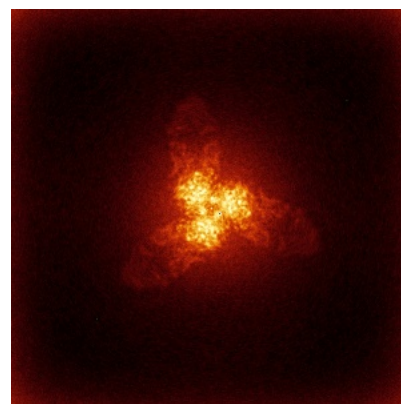
6.4.2 Raw map



X



Y

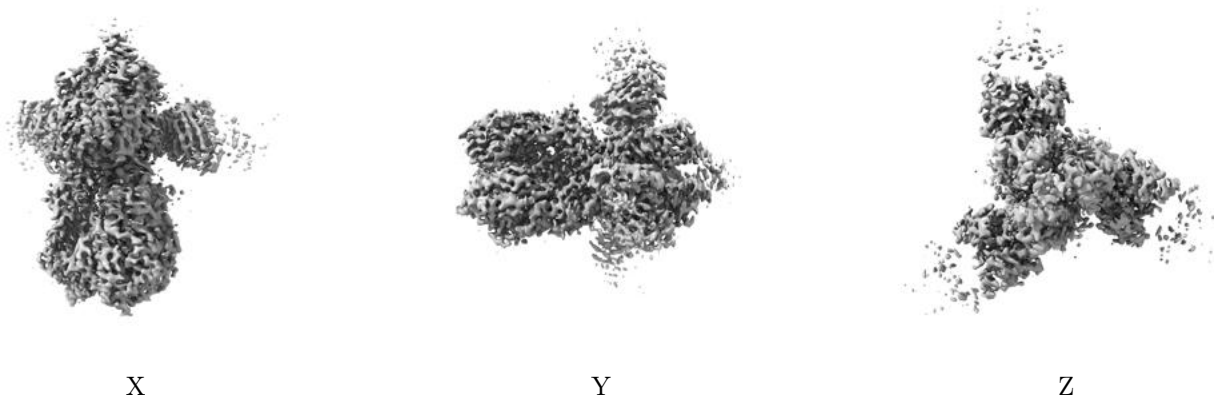


Z

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.

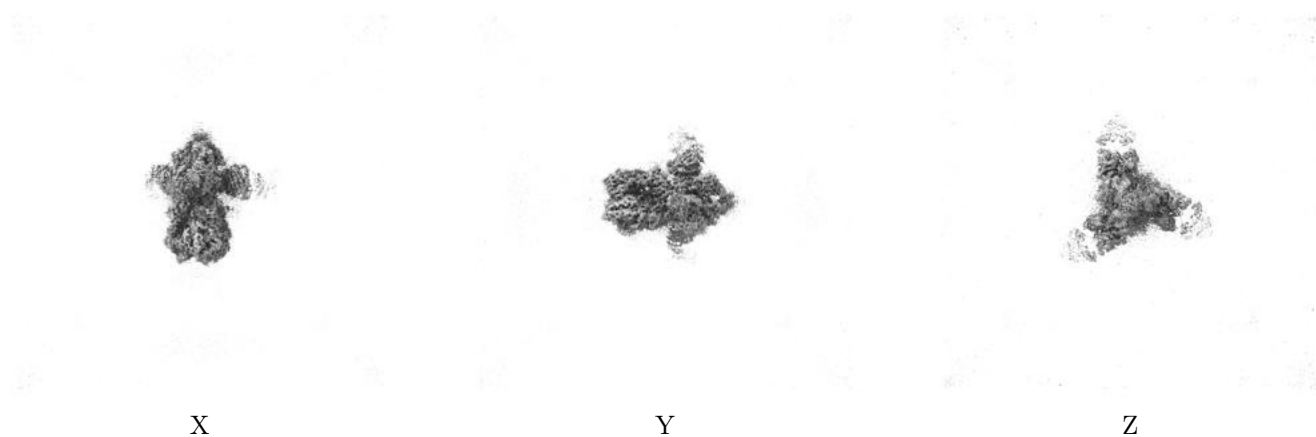
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.11. 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.

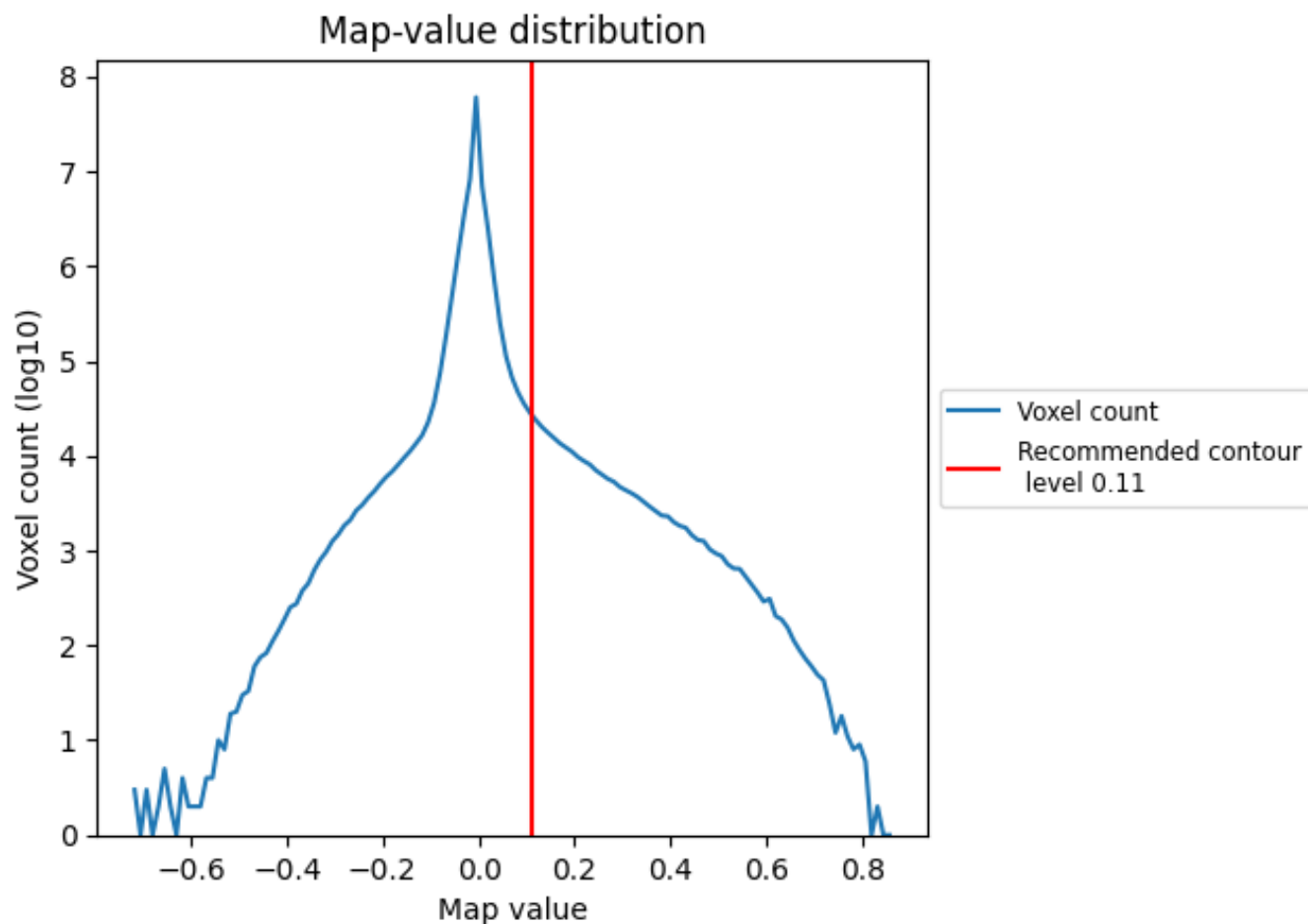
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

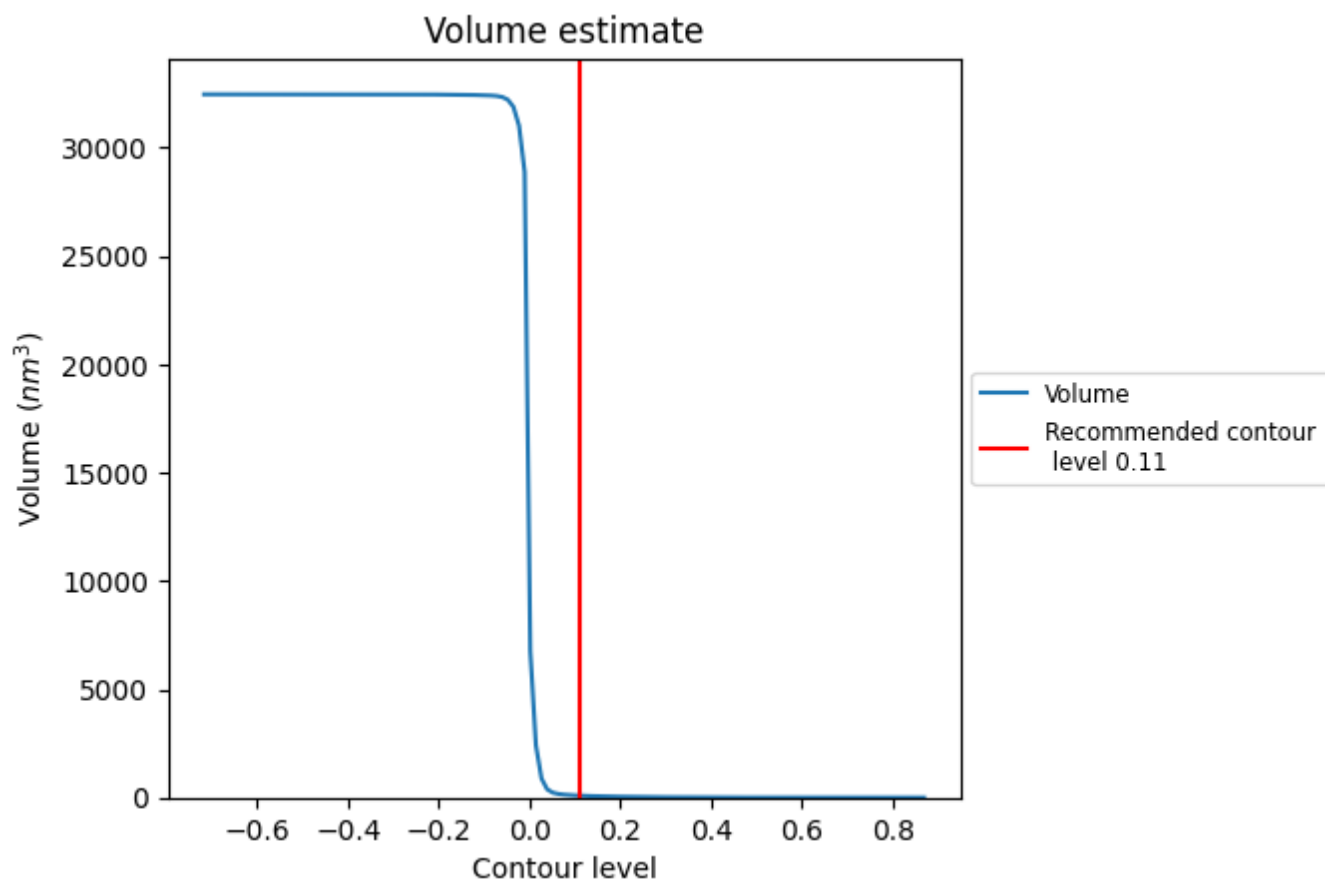
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

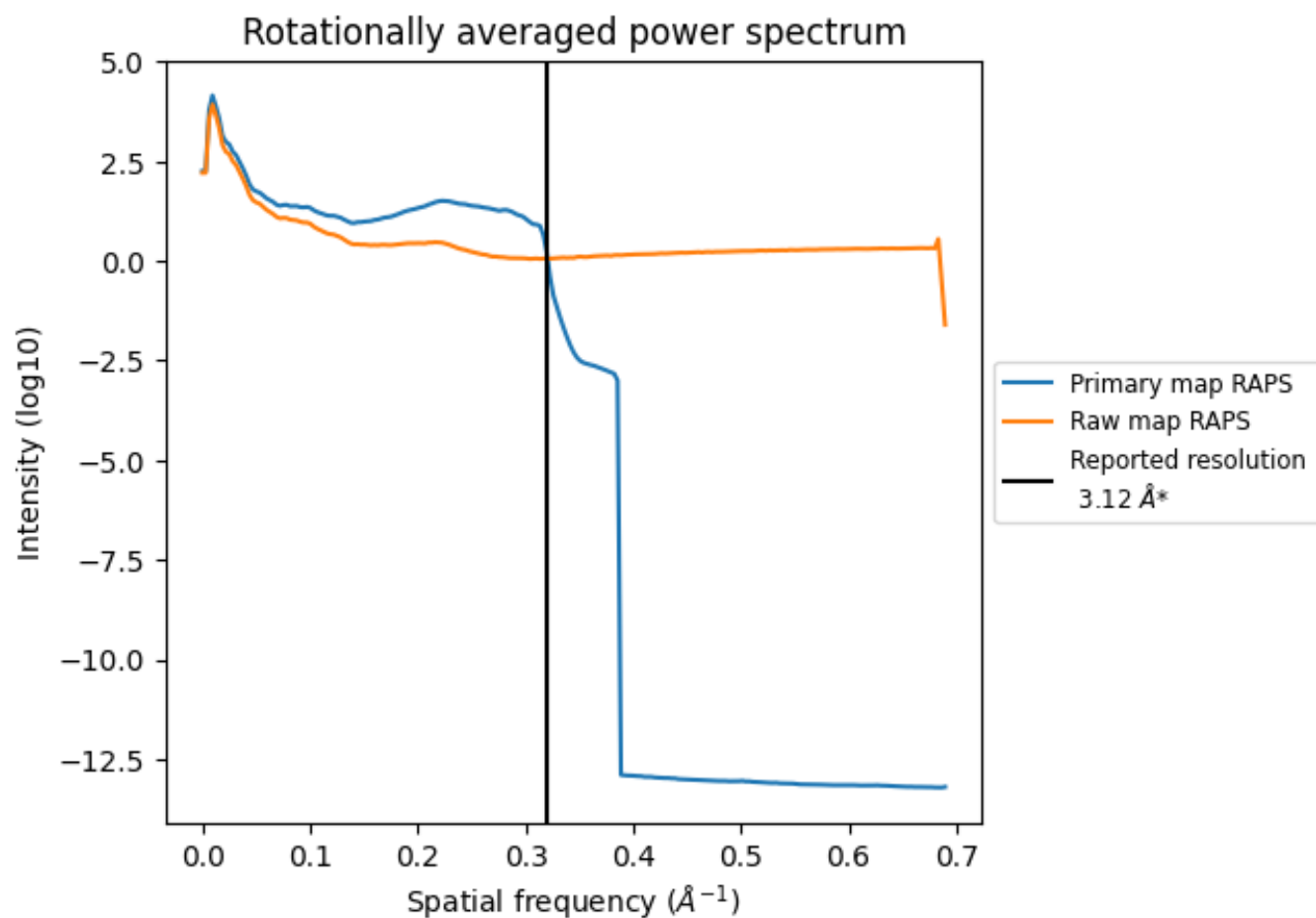
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 89 nm^3 ; this corresponds to an approximate mass of 80 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 ⓘ

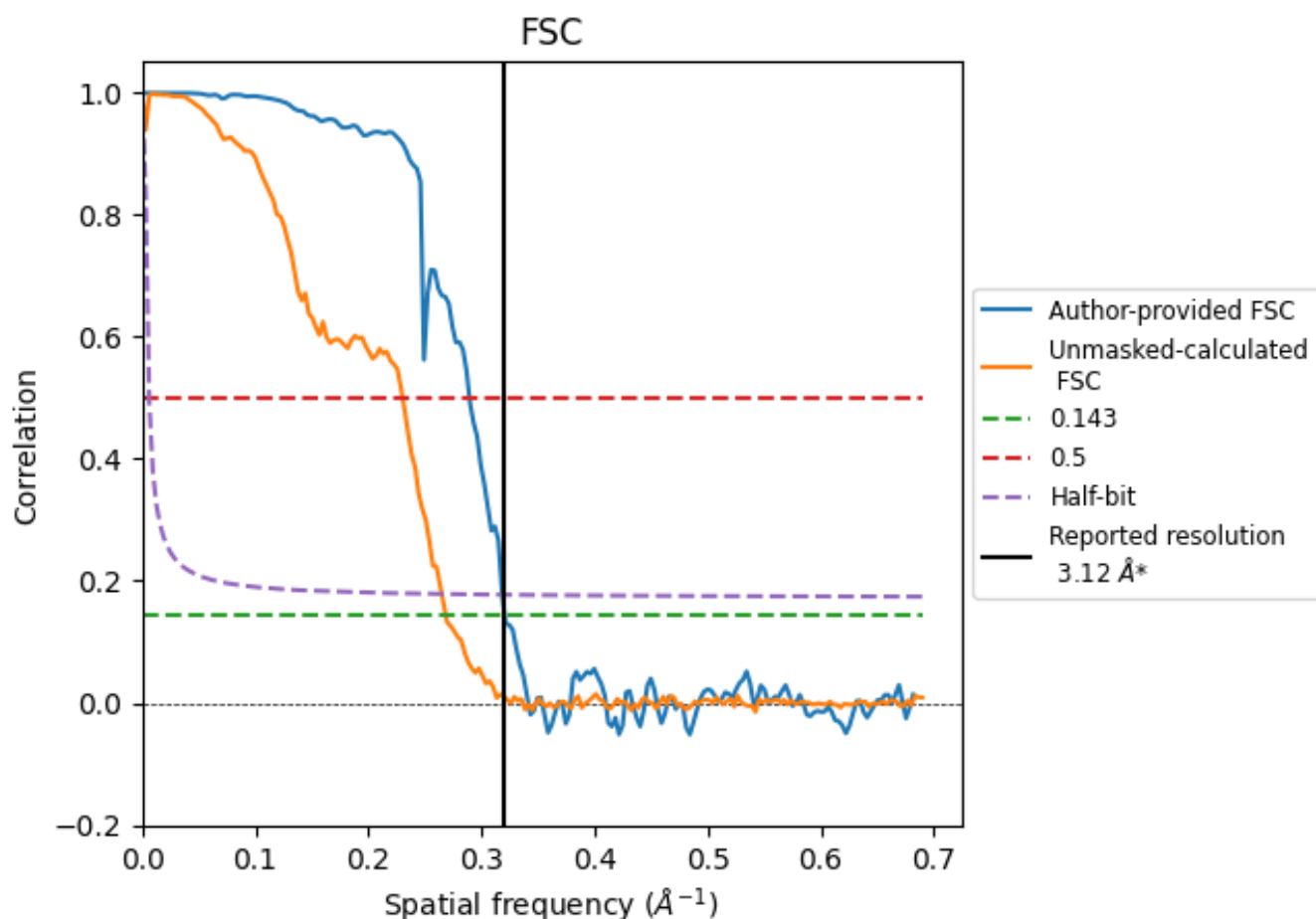


*Reported resolution corresponds to spatial frequency of 0.321 Å⁻¹

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 0.321 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

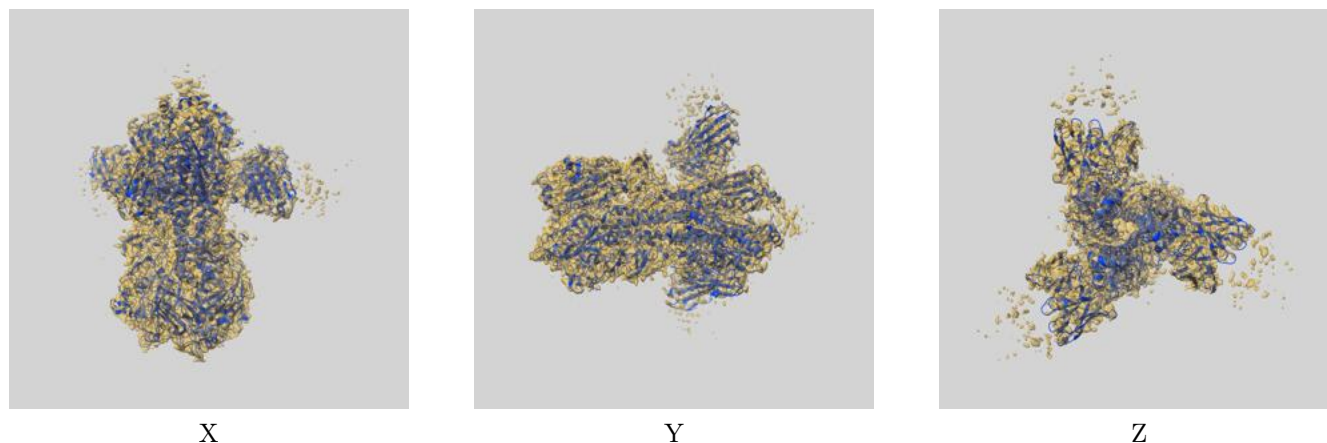
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.12	-	-
Author-provided FSC curve	3.12	3.46	3.14
Unmasked-calculated*	3.72	4.34	3.78

*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 3.72 differs from the reported value 3.12 by more than 10 %

9 Map-model fit [i](#)

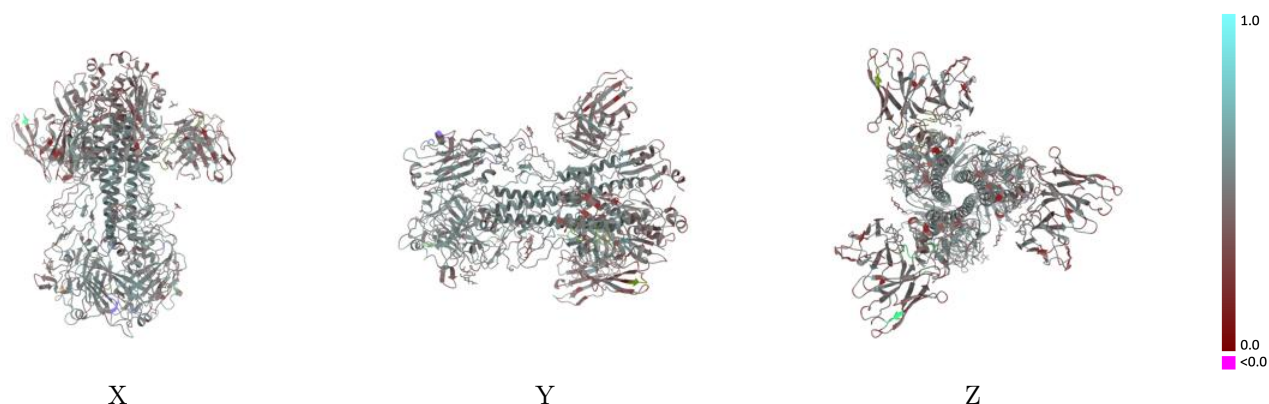
This section contains information regarding the fit between EMDB map EMD-70236 and PDB model 9O8T. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

9.1 Map-model overlay [i](#)



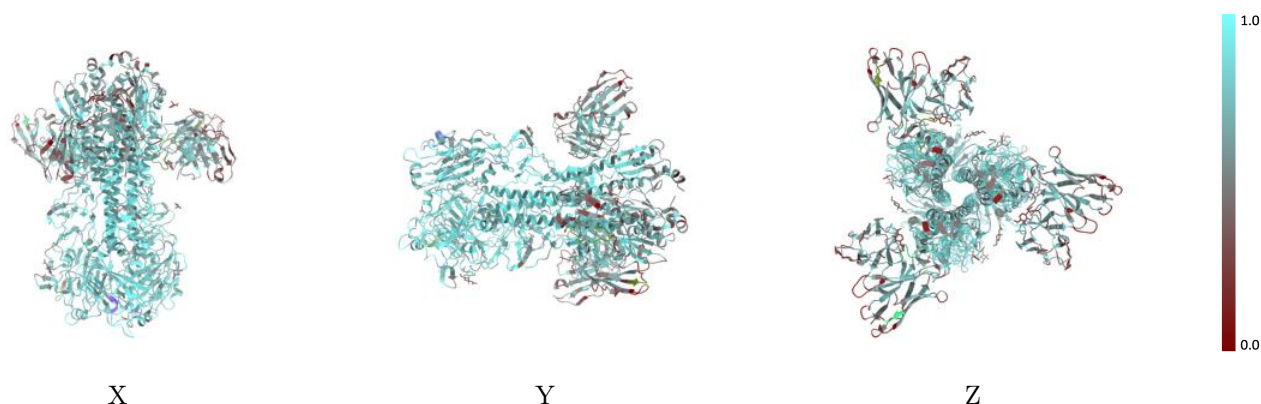
The images above show the 3D surface view of the map at the recommended contour level 0.11 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



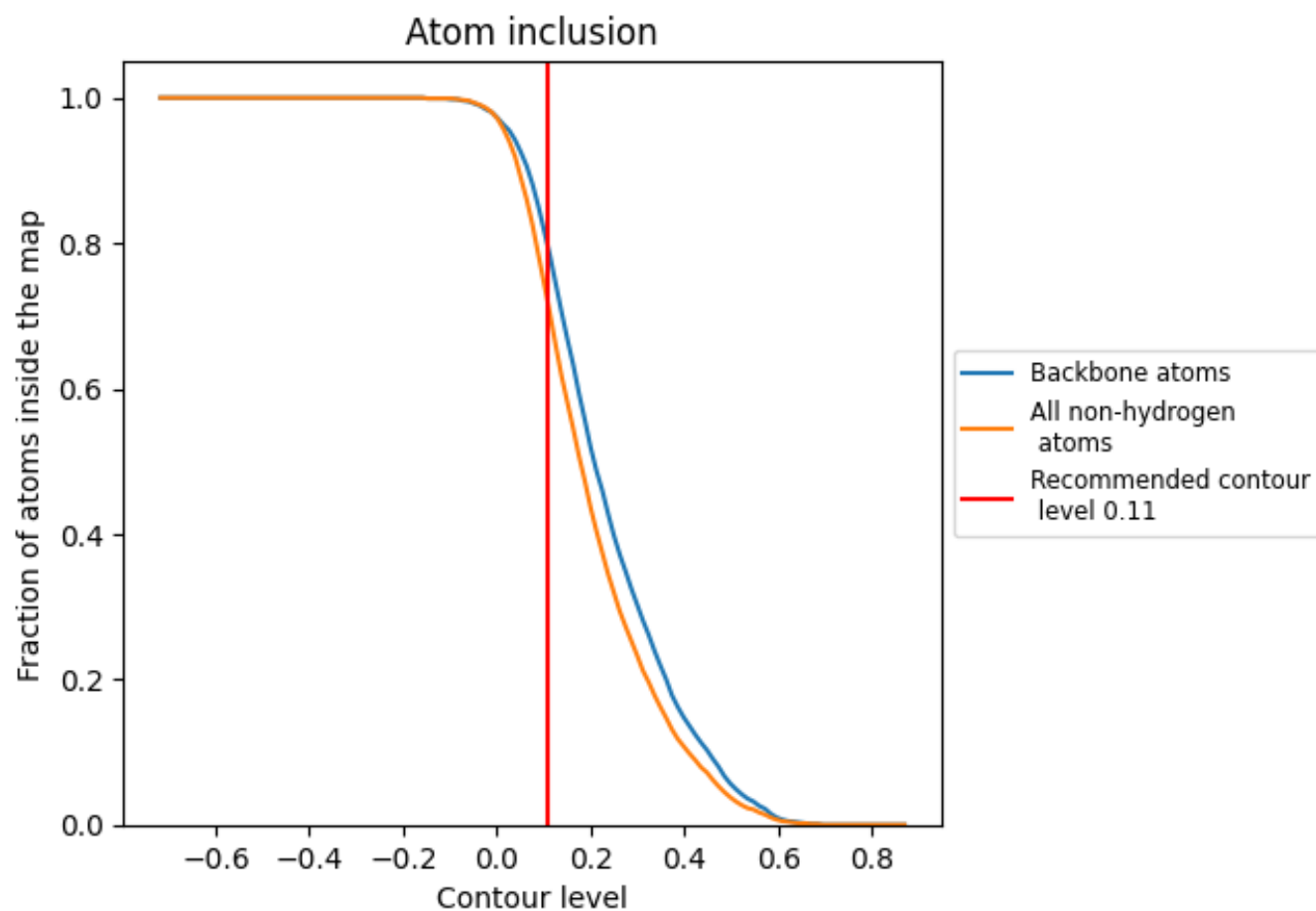
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.11).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% 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 (0.11) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7130	0.4720
A	0.7990	0.4990
B	0.7370	0.4900
C	0.7980	0.5000
D	0.7990	0.5000
E	0.7360	0.4910
F	0.7370	0.4890
G	0.5760	0.4220
H	0.5740	0.4190
I	0.5710	0.4240
J	0.5710	0.4130
K	0.5710	0.4150
L	0.5710	0.4140
M	0.5000	0.4230
N	0.5000	0.4250
O	0.5000	0.4180

1.0

0.0

<0.0