



wwPDB EM Validation Summary Report ⓘ

Mar 26, 2026 – 12:55 PM UTC

PDB ID : 9N15 / pdb_00009n15
EMDB ID : EMD-48806
Title : Cryo-EM structure of HCoV-HKU1 glycoprotein D1 Domain in complex with 9OAc-GD3(mutant T31VPR34 to GGGG)
Authors : Jin, M.; Rini, J.M.
Deposited on : 2025-01-24
Resolution : 3.20 Å(reported)

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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

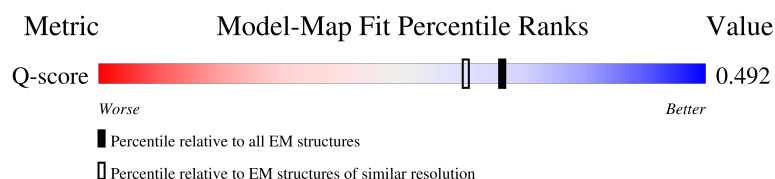
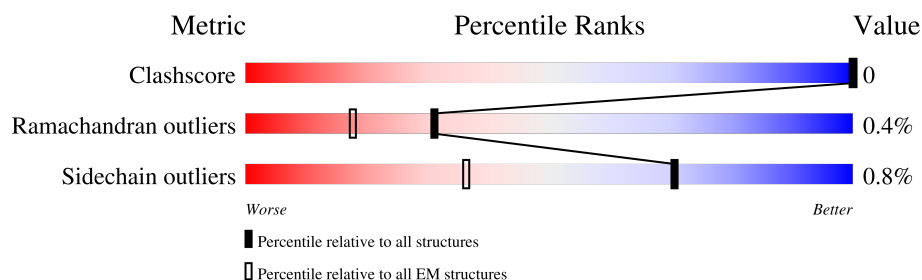
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

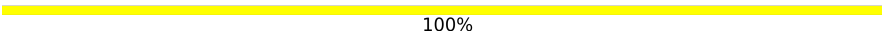
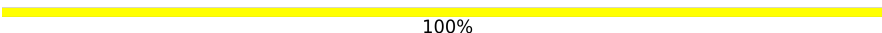
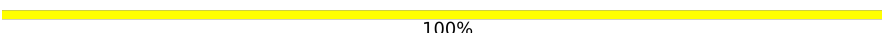
The reported resolution of this entry is 3.20 Å.

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	15020 (2.70 - 3.70)

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	1348	
2	B	2	
2	C	2	
2	F	2	

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Mol	Chain	Length	Quality of chain
3	D	5	 100%
4	E	3	 100%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4753 atoms, of which 2321 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	268	Total	C	H	N	O	S	0	0
			4258	1416	2082	343	409	8		

There are 70 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	31	GLY	THR	engineered mutation	UNP Q5MQD0
A	32	GLY	VAL	engineered mutation	UNP Q5MQD0
A	33	GLY	PRO	engineered mutation	UNP Q5MQD0
A	34	GLY	ARG	engineered mutation	UNP Q5MQD0
A	1026	PRO	THR	conflict	UNP Q5MQD0
A	1071	PRO	ALA	conflict	UNP Q5MQD0
A	1072	PRO	LEU	conflict	UNP Q5MQD0
A	1299	SER	-	expression tag	UNP Q5MQD0
A	1300	GLY	-	expression tag	UNP Q5MQD0
A	1301	GLY	-	expression tag	UNP Q5MQD0
A	1302	TYR	-	expression tag	UNP Q5MQD0
A	1303	ILE	-	expression tag	UNP Q5MQD0
A	1304	PRO	-	expression tag	UNP Q5MQD0
A	1305	GLU	-	expression tag	UNP Q5MQD0
A	1306	ALA	-	expression tag	UNP Q5MQD0
A	1307	PRO	-	expression tag	UNP Q5MQD0
A	1308	ARG	-	expression tag	UNP Q5MQD0
A	1309	ASP	-	expression tag	UNP Q5MQD0
A	1310	GLY	-	expression tag	UNP Q5MQD0
A	1311	GLN	-	expression tag	UNP Q5MQD0
A	1312	ALA	-	expression tag	UNP Q5MQD0
A	1313	TYR	-	expression tag	UNP Q5MQD0
A	1314	VAL	-	expression tag	UNP Q5MQD0
A	1315	ARG	-	expression tag	UNP Q5MQD0
A	1316	LYS	-	expression tag	UNP Q5MQD0
A	1317	ASP	-	expression tag	UNP Q5MQD0
A	1318	GLY	-	expression tag	UNP Q5MQD0
A	1319	GLU	-	expression tag	UNP Q5MQD0

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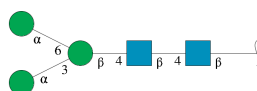
Chain	Residue	Modelled	Actual	Comment	Reference
A	1320	TRP	-	expression tag	UNP Q5MQD0
A	1321	VAL	-	expression tag	UNP Q5MQD0
A	1322	LEU	-	expression tag	UNP Q5MQD0
A	1323	LEU	-	expression tag	UNP Q5MQD0
A	1324	SER	-	expression tag	UNP Q5MQD0
A	1325	THR	-	expression tag	UNP Q5MQD0
A	1326	PHE	-	expression tag	UNP Q5MQD0
A	1327	LEU	-	expression tag	UNP Q5MQD0
A	1328	ASN	-	expression tag	UNP Q5MQD0
A	1329	SER	-	expression tag	UNP Q5MQD0
A	1330	GLY	-	expression tag	UNP Q5MQD0
A	1331	ARG	-	expression tag	UNP Q5MQD0
A	1332	ALA	-	expression tag	UNP Q5MQD0
A	1333	HIS	-	expression tag	UNP Q5MQD0
A	1334	HIS	-	expression tag	UNP Q5MQD0
A	1335	HIS	-	expression tag	UNP Q5MQD0
A	1336	HIS	-	expression tag	UNP Q5MQD0
A	1337	HIS	-	expression tag	UNP Q5MQD0
A	1338	HIS	-	expression tag	UNP Q5MQD0
A	1339	GLY	-	expression tag	UNP Q5MQD0
A	1340	ALA	-	expression tag	UNP Q5MQD0
A	1341	GLY	-	expression tag	UNP Q5MQD0
A	1342	GLY	-	expression tag	UNP Q5MQD0
A	1343	LEU	-	expression tag	UNP Q5MQD0
A	1344	ASN	-	expression tag	UNP Q5MQD0
A	1345	ASP	-	expression tag	UNP Q5MQD0
A	1346	ILE	-	expression tag	UNP Q5MQD0
A	1347	PHE	-	expression tag	UNP Q5MQD0
A	1348	GLU	-	expression tag	UNP Q5MQD0
A	1349	ALA	-	expression tag	UNP Q5MQD0
A	1350	GLN	-	expression tag	UNP Q5MQD0
A	1351	LYS	-	expression tag	UNP Q5MQD0
A	1352	ILE	-	expression tag	UNP Q5MQD0
A	1353	GLU	-	expression tag	UNP Q5MQD0
A	1354	TRP	-	expression tag	UNP Q5MQD0
A	1355	HIS	-	expression tag	UNP Q5MQD0
A	1356	GLU	-	expression tag	UNP Q5MQD0
A	1357	ASP	-	expression tag	UNP Q5MQD0
A	1358	THR	-	expression tag	UNP Q5MQD0
A	1359	ALA	-	expression tag	UNP Q5MQD0
A	1360	ALA	-	expression tag	UNP Q5MQD0
A	1361	ALA	-	expression tag	UNP Q5MQD0

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



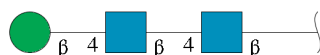
Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	2	Total	C	H	N	O	0	0
			55	16	27	2	10		
2	C	2	Total	C	H	N	O	0	0
			55	16	27	2	10		
2	F	2	Total	C	H	N	O	0	0
			55	16	27	2	10		

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	5	Total	C	H	N	O	0	0
			118	34	57	2	25		

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



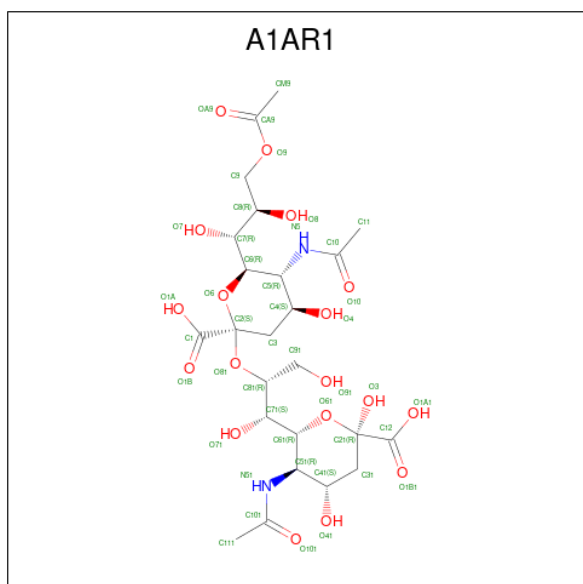
Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	3	Total	C	H	N	O	0	0
			76	22	37	2	15		

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 6 is 5-acetamido-8-O-(5-acetamido-9-O-acetyl-3,5-dideoxy-D-glycero- α -D-galacto-non-2-ulopyranonosyl)-3,5-dideoxy-D-glycero- α -D-galacto-non-2-ulopyranosonic acid (CCD ID: A1AR1) (formula: $C_{24}H_{38}N_2O_{18}$) (labeled as "Ligand of Interest" by depositor).

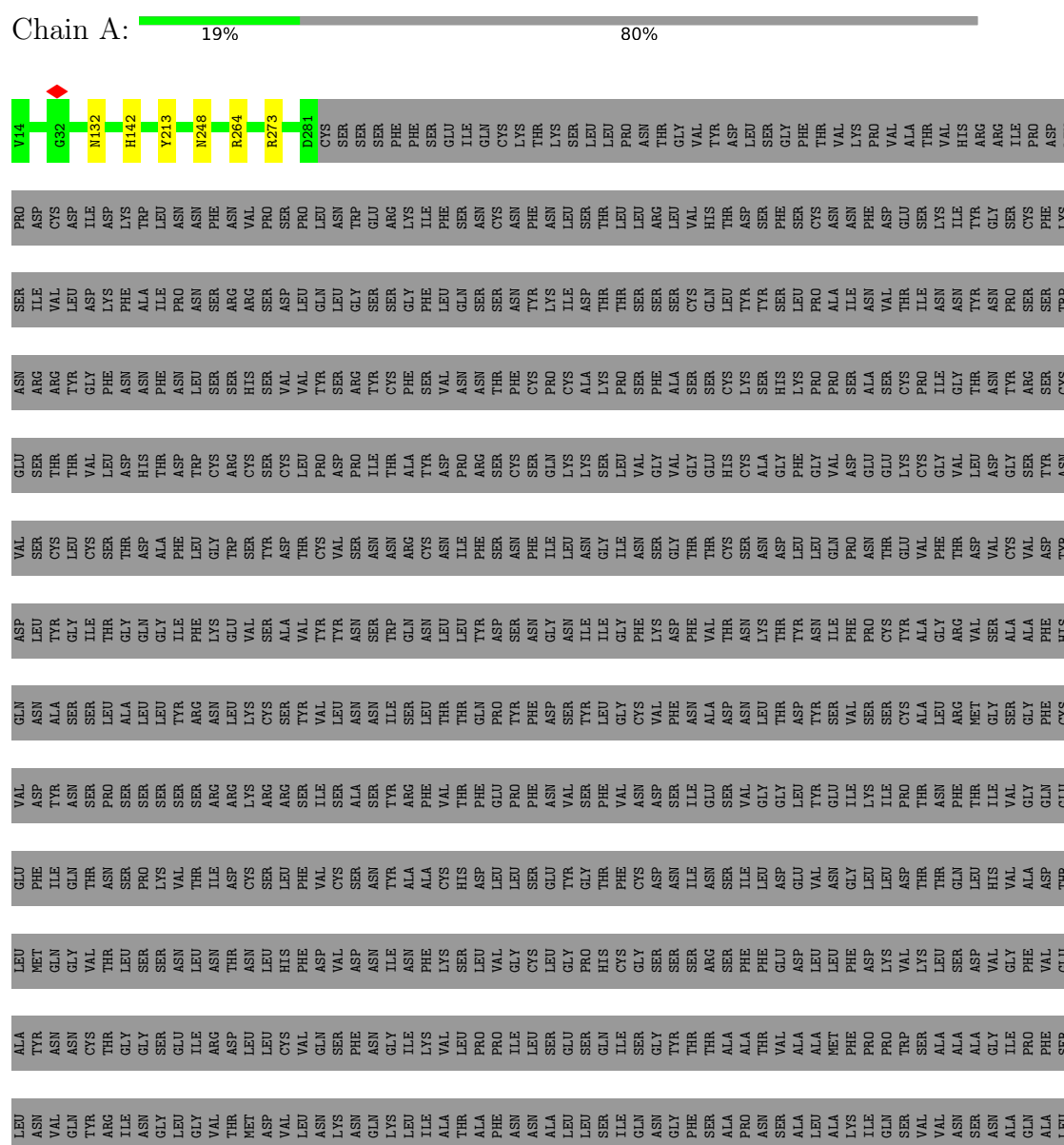


Mol	Chain	Residues	Atoms					AltConf
			Total	C	H	N	O	
6	A	1	80	24	36	2	18	0

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: Spike glycoprotein



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

● 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

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

Chain F: 100%

NAG1
NAG2

● Molecule 3: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D: 100%

NAG1
NAG2
BMA3
MAN4
MAN5

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

Chain E:  100%

MAG1
MAG2
BGA3

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	268011	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 ($e^-/\text{\AA}^2$)	36	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	92000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.567	Depositor
Minimum map value	-0.591	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.039	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	295.5, 295.5, 295.5	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1542969, 1.1542969, 1.1542969	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: MAN, NAG, BMA, A1AR1

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	0.66	0/2239	1.07	2/3050 (0.1%)

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	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	273	ARG	NE-CZ-NH2	5.80	124.42	119.20
1	A	142	HIS	CB-CG-CD2	-5.17	124.48	131.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	264	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	2176	2082	2079	0	0
2	B	28	27	25	0	0
2	C	28	27	25	0	0
2	F	28	27	25	0	0
3	D	61	57	52	0	0
4	E	39	37	34	0	0
5	A	28	28	26	0	0
6	A	44	36	0	0	0
All	All	2432	2321	2266	0	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 0.

There are no clashes within the asymmetric unit.

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	266/1348 (20%)	243 (91%)	22 (8%)	1 (0%)	30 62

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	132	ASN

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	243/1203 (20%)	241 (99%)	2 (1%)	73 82

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	213	TYR
1	A	248	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	234	HIS
1	A	243	ASN
1	A	248	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 ⓘ

14 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	1.24	1 (7%)	17,19,21	0.85	0
2	NAG	B	2	2	14,14,15	1.30	3 (21%)	17,19,21	0.87	0
2	NAG	C	1	2,1	14,14,15	1.25	2 (14%)	17,19,21	0.68	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	C	2	2	14,14,15	1.32	2 (14%)	17,19,21	0.80	1 (5%)
3	NAG	D	1	1,3	14,14,15	1.07	1 (7%)	17,19,21	0.67	0
3	NAG	D	2	3	14,14,15	1.29	2 (14%)	17,19,21	0.85	0
3	BMA	D	3	3	11,11,12	1.44	3 (27%)	15,15,17	0.96	1 (6%)
3	MAN	D	4	3	11,11,12	1.51	2 (18%)	15,15,17	1.00	1 (6%)
3	MAN	D	5	3	11,11,12	1.43	2 (18%)	15,15,17	0.81	1 (6%)
4	NAG	E	1	1,4	14,14,15	1.16	1 (7%)	17,19,21	0.79	0
4	NAG	E	2	4	14,14,15	1.35	3 (21%)	17,19,21	0.92	1 (5%)
4	BMA	E	3	4	11,11,12	1.31	2 (18%)	15,15,17	0.88	1 (6%)
2	NAG	F	1	2,1	14,14,15	1.22	2 (14%)	17,19,21	0.69	1 (5%)
2	NAG	F	2	2	14,14,15	1.30	2 (14%)	17,19,21	0.84	1 (5%)

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	-	3/6/23/26	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
3	NAG	D	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	0/6/23/26	0/1/1/1
3	BMA	D	3	3	-	0/2/19/22	0/1/1/1
3	MAN	D	4	3	-	0/2/19/22	0/1/1/1
3	MAN	D	5	3	-	0/2/19/22	0/1/1/1
4	NAG	E	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	E	2	4	-	2/6/23/26	0/1/1/1
4	BMA	E	3	4	-	0/2/19/22	0/1/1/1
2	NAG	F	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	F	2	2	-	0/6/23/26	0/1/1/1

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	4	MAN	O5-C5	3.11	1.49	1.43
2	C	2	NAG	O5-C5	2.94	1.49	1.43
3	D	5	MAN	O5-C5	2.90	1.49	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	2	NAG	O5-C5	2.85	1.49	1.43
4	E	3	BMA	O5-C5	2.71	1.48	1.43

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	4	MAN	C1-O5-C5	3.51	116.89	112.19
4	E	3	BMA	C1-O5-C5	2.97	116.17	112.19
3	D	5	MAN	C1-O5-C5	2.49	115.52	112.19
2	F	2	NAG	C1-O5-C5	2.40	115.40	112.19
2	F	1	NAG	C1-O5-C5	2.16	115.08	112.19

There are no chirality outliers.

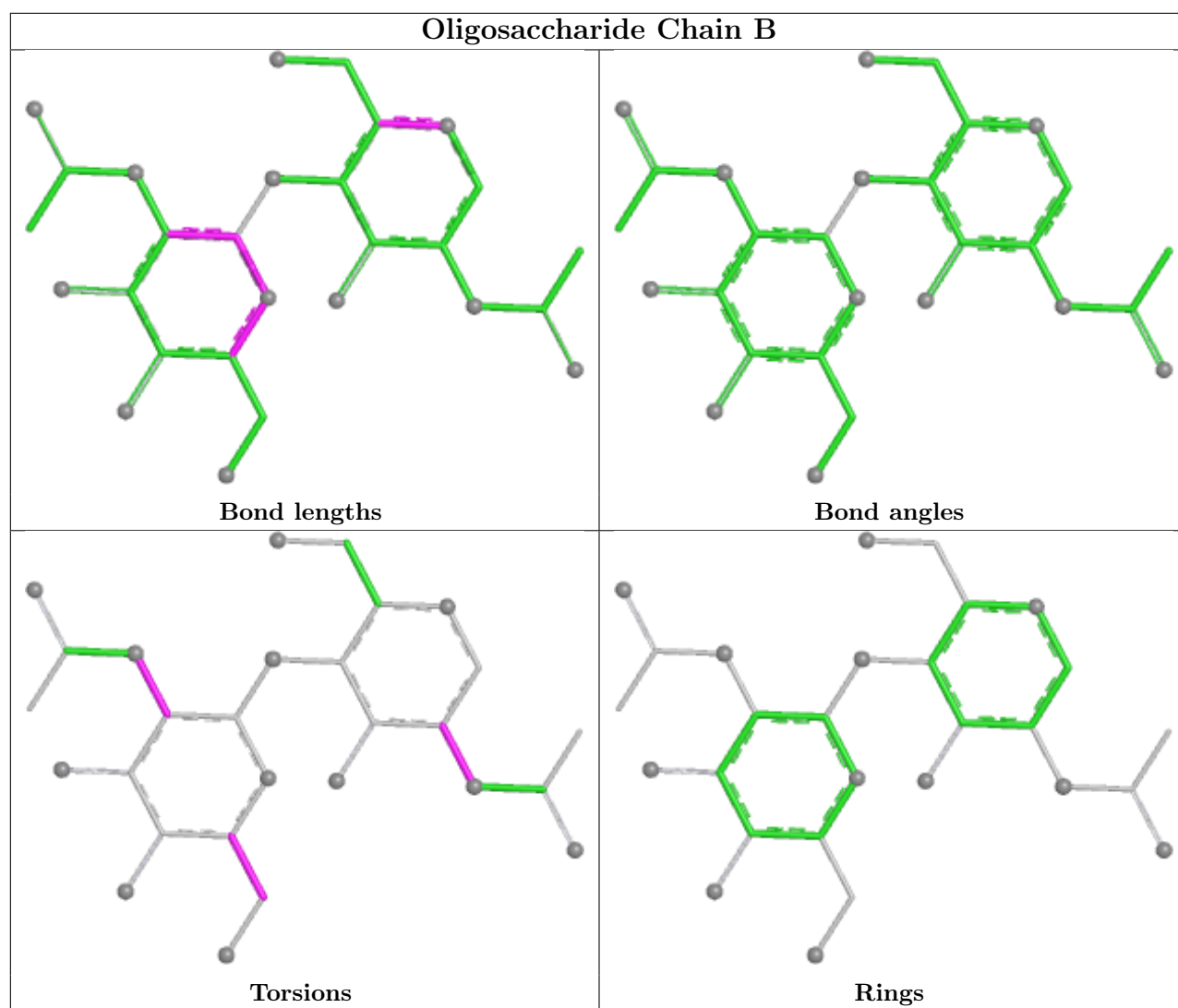
5 of 9 torsion outliers are listed below:

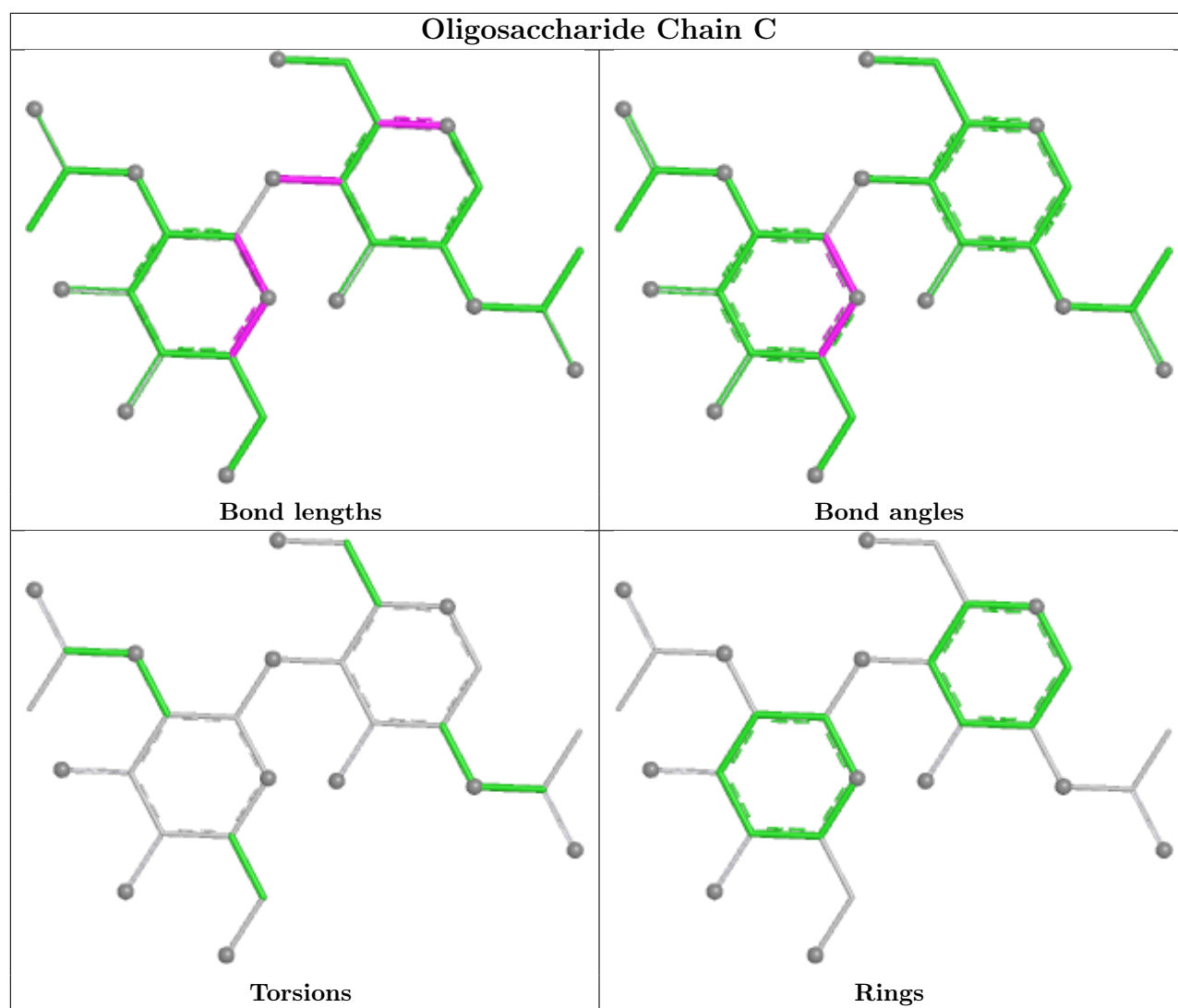
Mol	Chain	Res	Type	Atoms
2	B	2	NAG	O5-C5-C6-O6
2	B	1	NAG	C1-C2-N2-C7
2	B	2	NAG	C1-C2-N2-C7
4	E	1	NAG	C1-C2-N2-C7
4	E	2	NAG	C1-C2-N2-C7

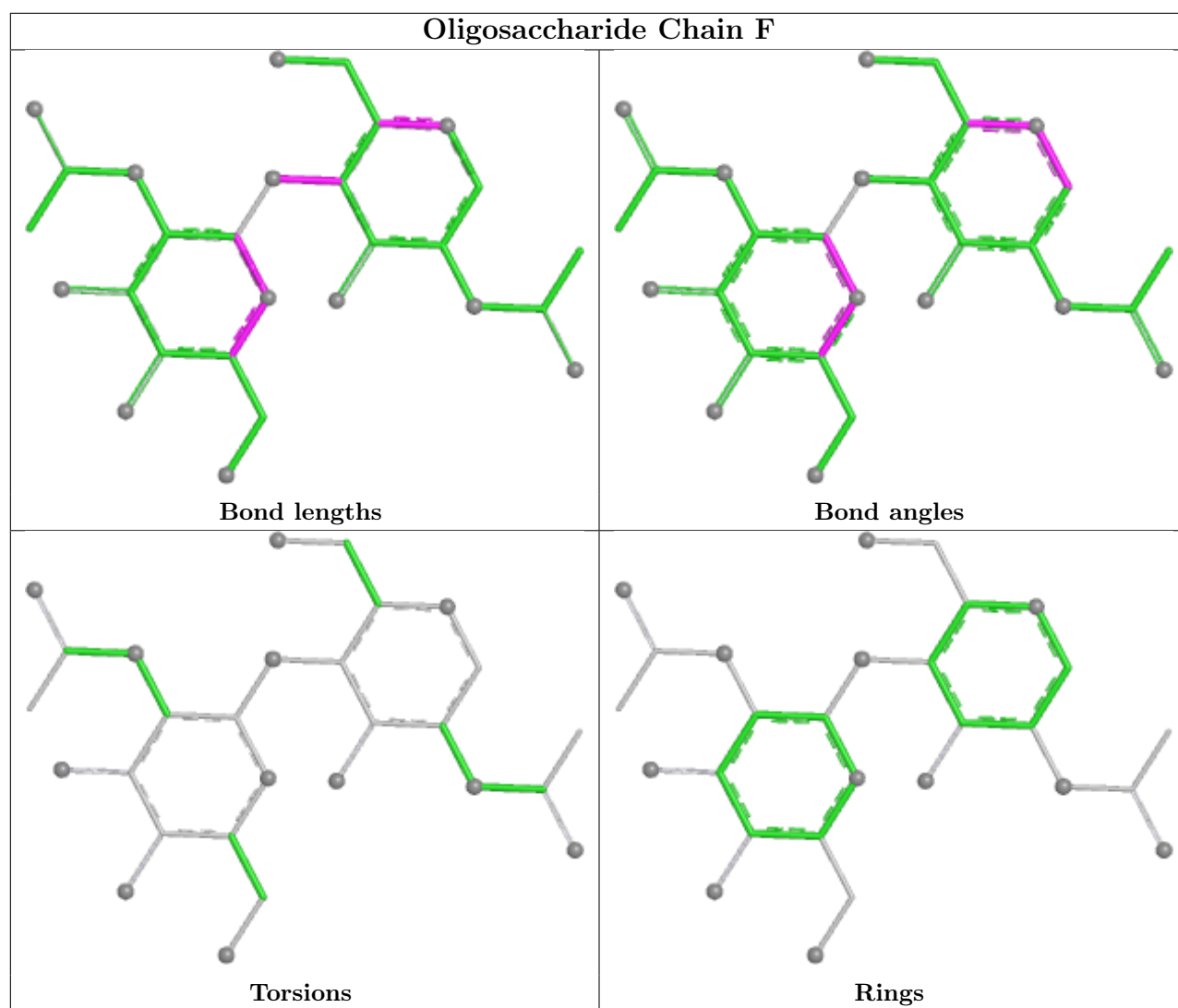
There are no ring outliers.

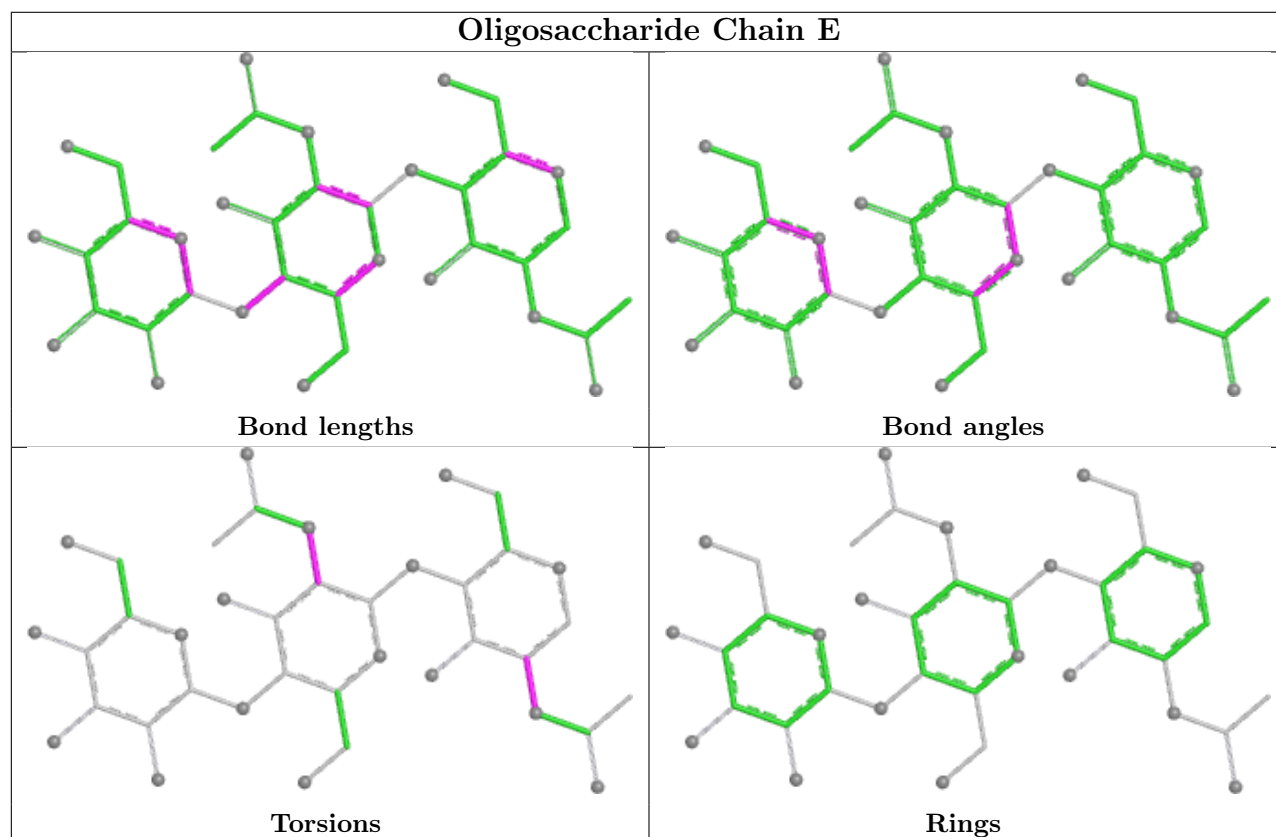
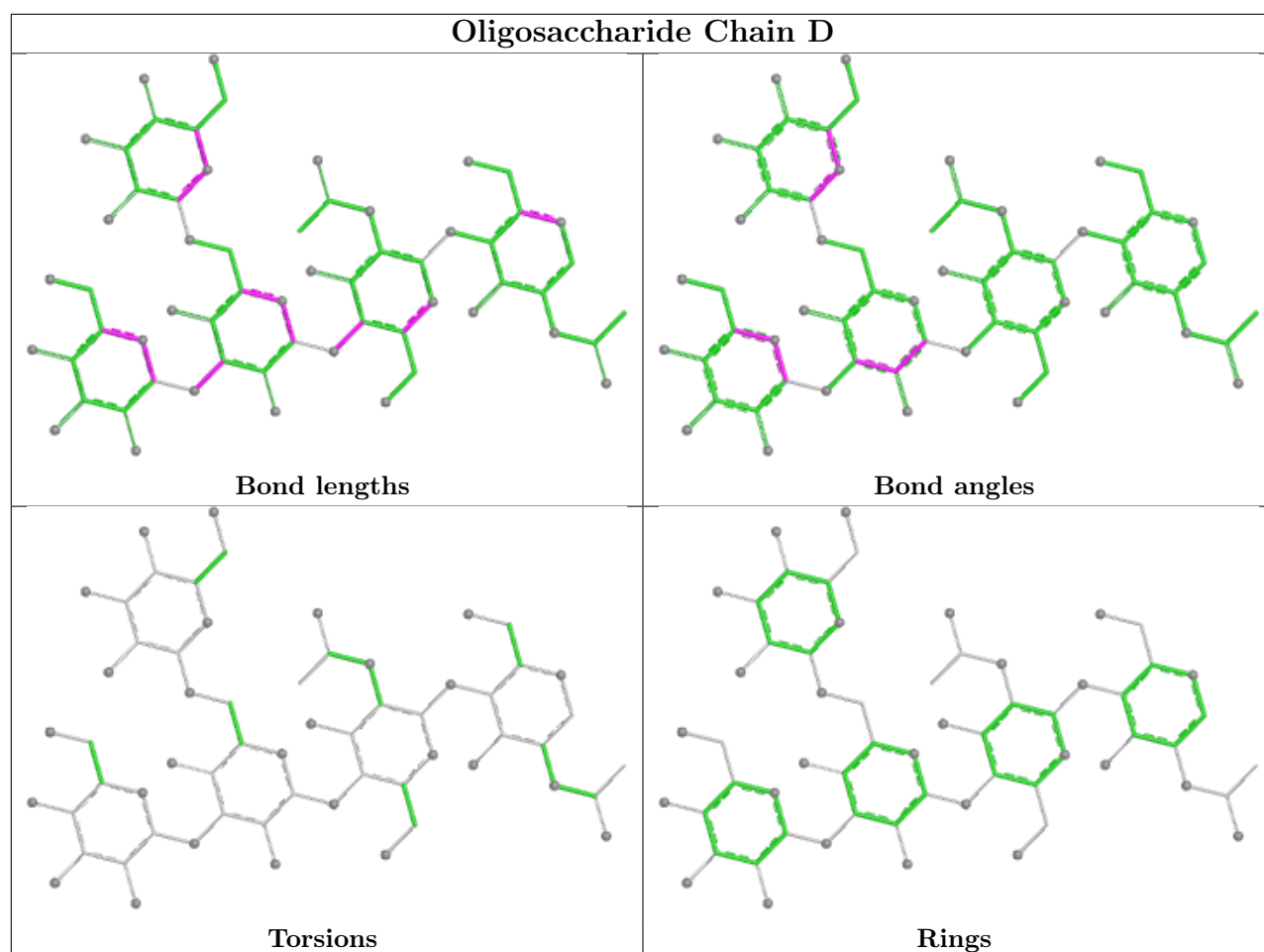
No monomer is involved in short contacts.

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

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	$\# Z > 2$
5	NAG	A	1402	1	14,14,15	1.30	1 (7%)	17,19,21	0.87	1 (5%)
5	NAG	A	1401	1	14,14,15	1.30	2 (14%)	17,19,21	0.78	1 (5%)
6	A1AR1	A	1403	-	44,45,45	1.58	9 (20%)	55,67,67	1.24	4 (7%)

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	A	1402	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1401	1	-	0/6/23/26	0/1/1/1
6	A1AR1	A	1403	-	-	9/47/84/84	0/2/2/2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	1403	A1AR1	C21-C12	4.75	1.60	1.53
6	A	1403	A1AR1	C31-C21	3.00	1.55	1.51
6	A	1403	A1AR1	C41-C51	3.00	1.55	1.53
5	A	1402	NAG	O5-C5	2.99	1.49	1.43
5	A	1401	NAG	O5-C5	2.76	1.48	1.43

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1403	A1AR1	O6-C2-C3	-3.30	106.91	111.35
6	A	1403	A1AR1	O1B1-C12-C21	-3.17	118.57	123.85
6	A	1403	A1AR1	C9-C8-C7	-2.71	107.11	112.22
6	A	1403	A1AR1	O6-C6-C5	-2.69	107.38	109.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1401	NAG	C1-O5-C5	2.29	115.26	112.19

There are no chirality outliers.

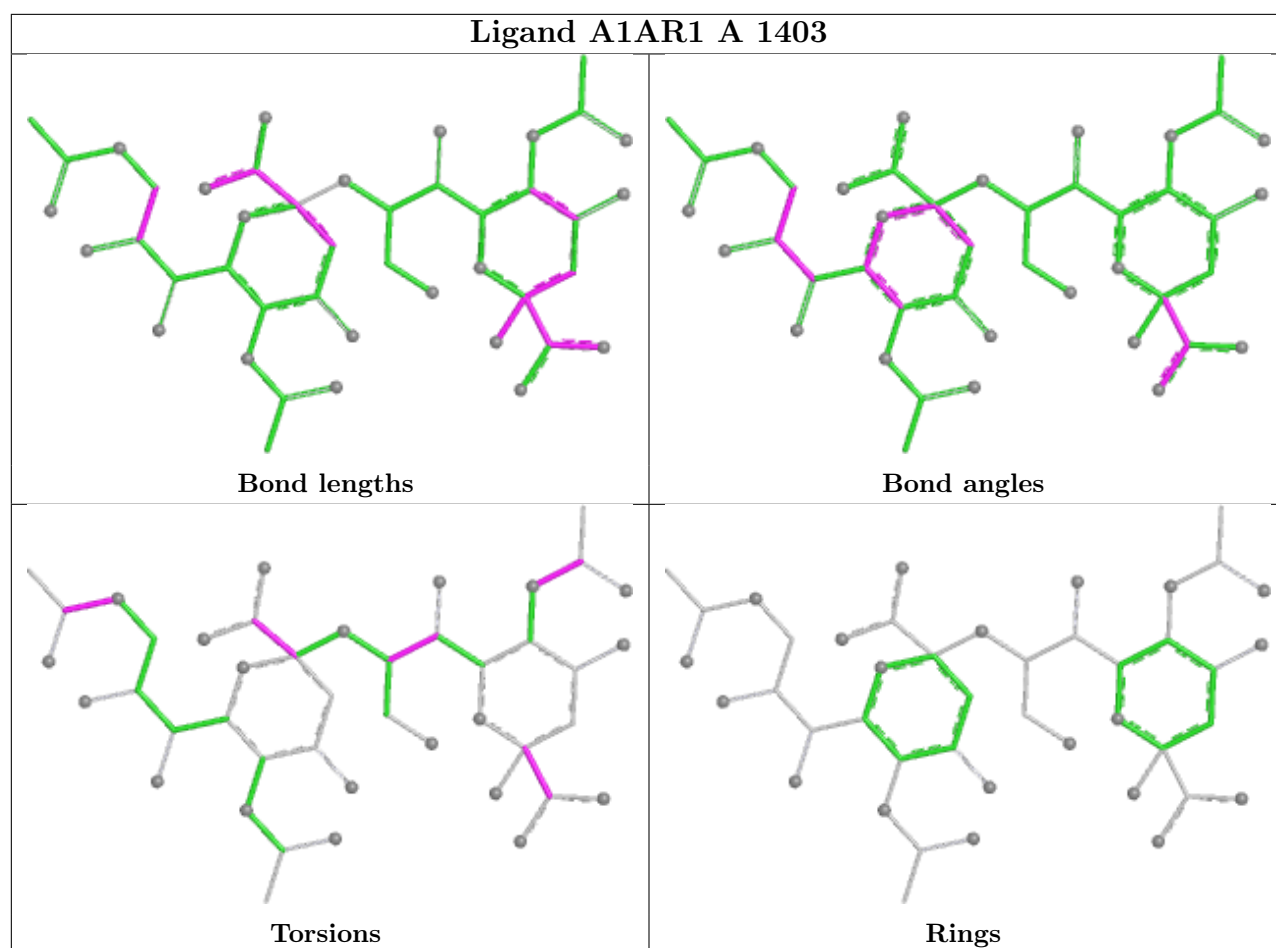
5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	1403	A1AR1	O1A-C1-C2-O81
6	A	1403	A1AR1	C111-C101-N51-C51
6	A	1403	A1AR1	O101-C101-N51-C51
6	A	1403	A1AR1	OA9-CA9-O9-C9
6	A	1403	A1AR1	CM9-CA9-O9-C9

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 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.

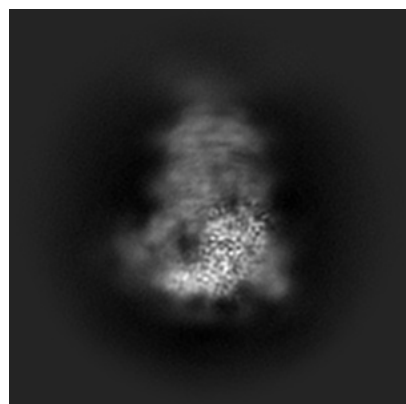
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-48806. These allow visual inspection of the internal detail of the map and identification of artifacts.

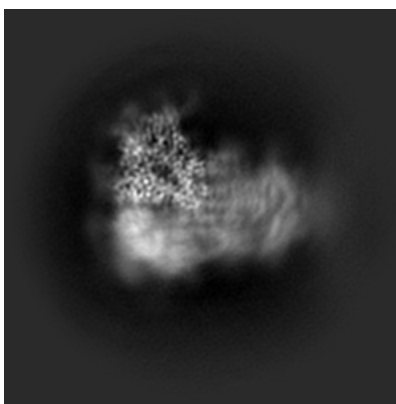
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

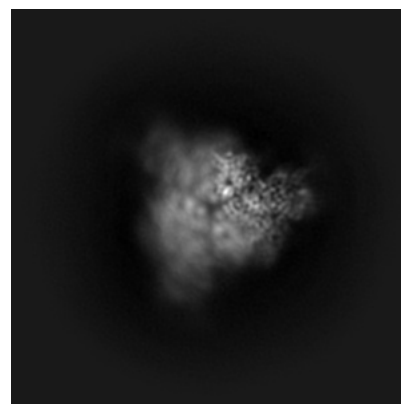
6.1.1 Primary map



X

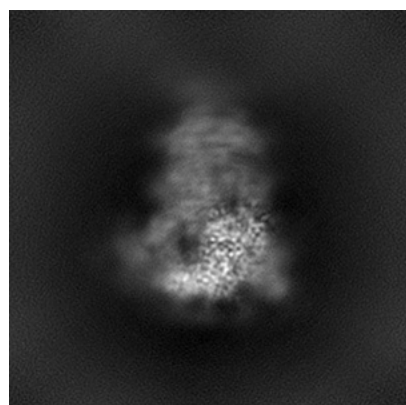


Y

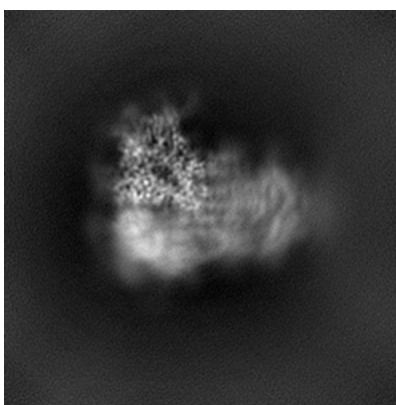


Z

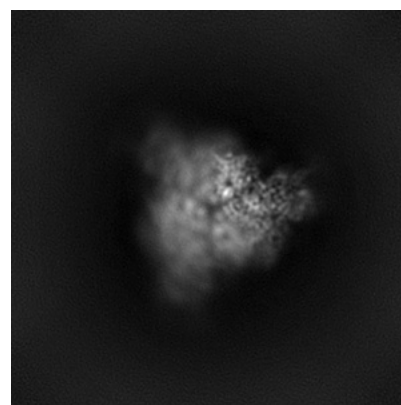
6.1.2 Raw map



X



Y

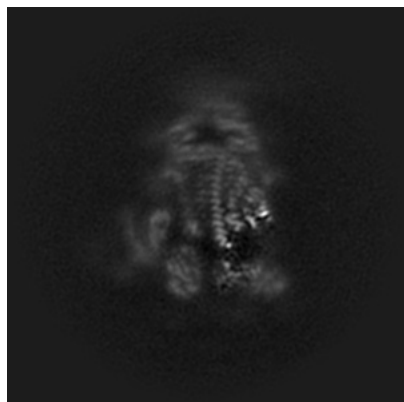


Z

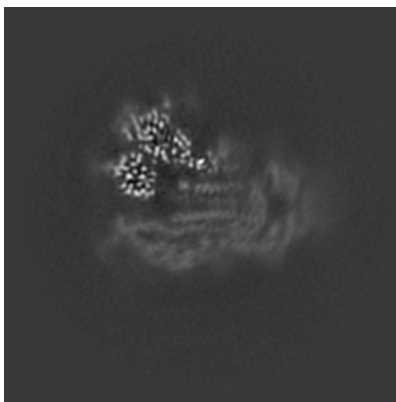
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

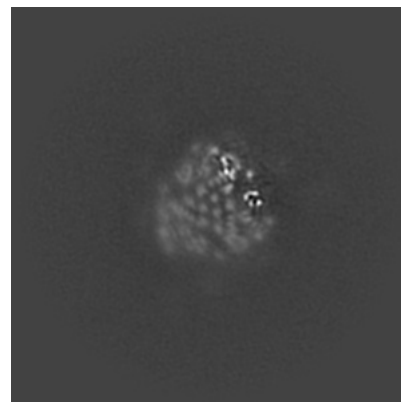
6.2.1 Primary map



X Index: 128

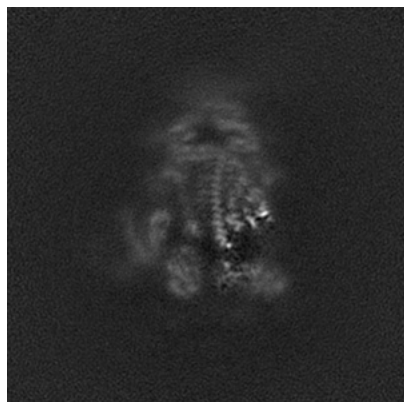


Y Index: 128

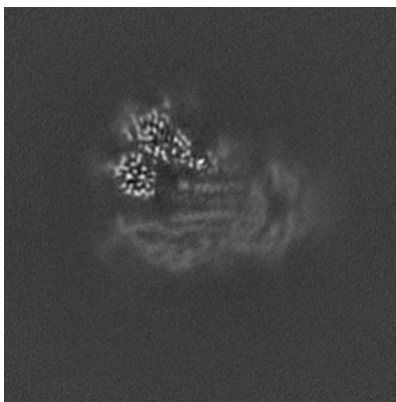


Z Index: 128

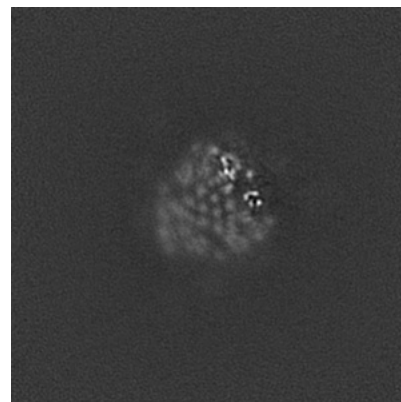
6.2.2 Raw map



X Index: 128



Y Index: 128

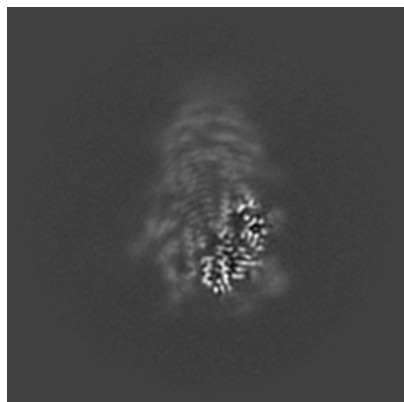


Z Index: 128

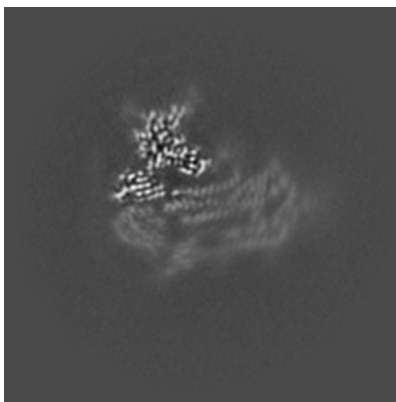
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

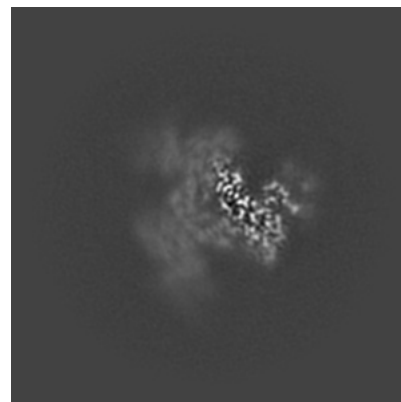
6.3.1 Primary map



X Index: 137

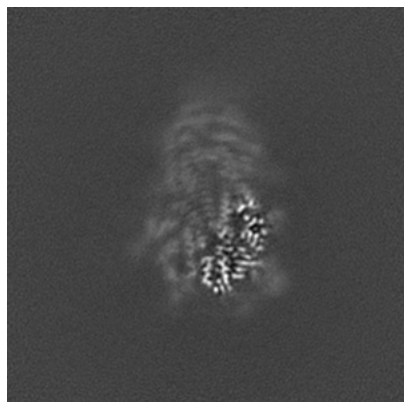


Y Index: 137

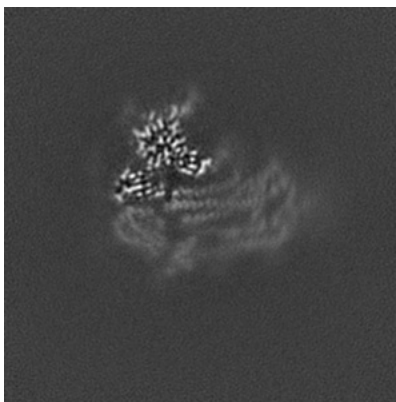


Z Index: 84

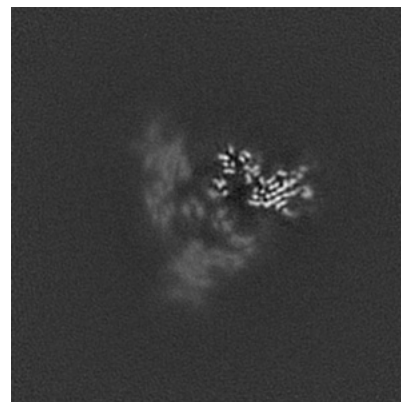
6.3.2 Raw map



X Index: 137



Y Index: 136

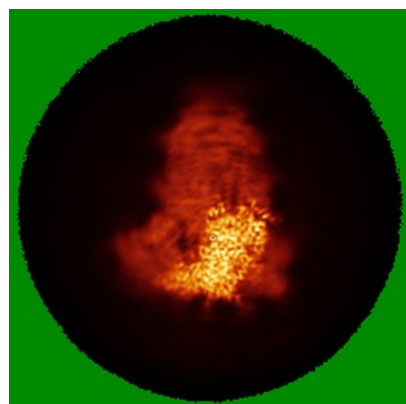


Z Index: 109

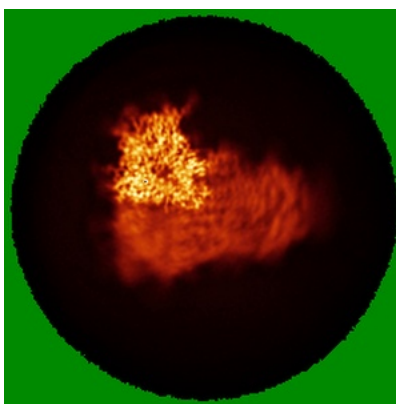
The images above show the largest variance slices of the map in three orthogonal directions.

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

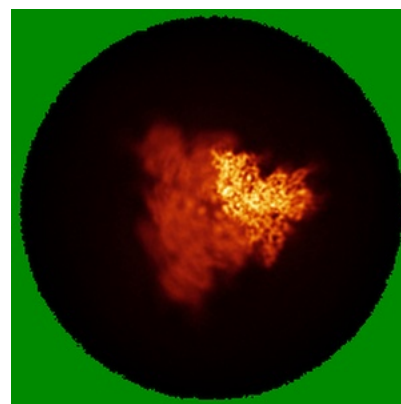
6.4.1 Primary map



X

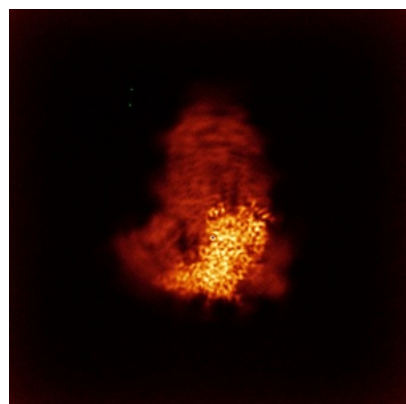


Y

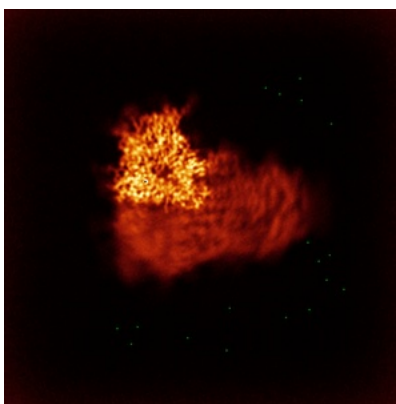


Z

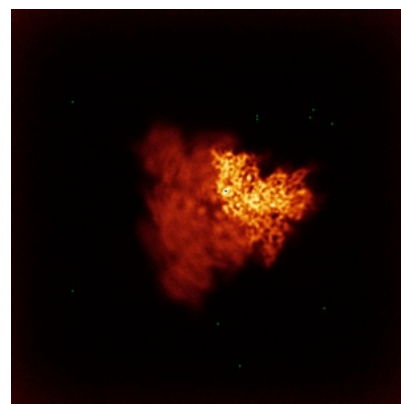
6.4.2 Raw map



X



Y

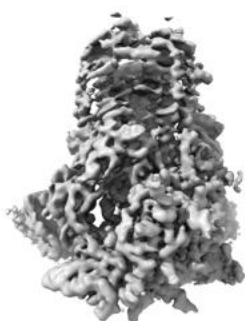


Z

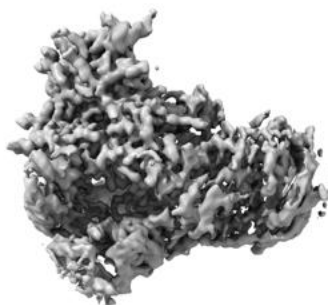
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

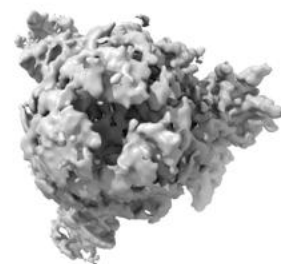
6.5.1 Primary map



X



Y



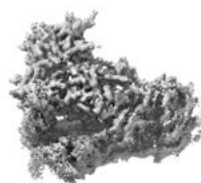
Z

The images above show the 3D surface view of the map at the recommended contour level 0.2. 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



X



Y



Z

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.

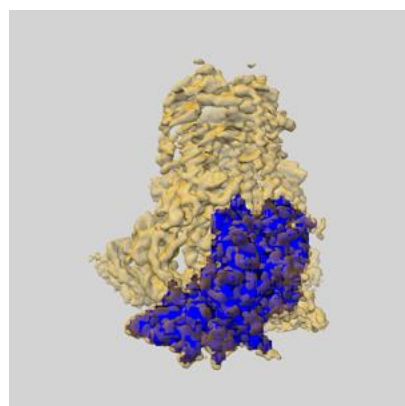
6.6 Mask visualisation [i](#)

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

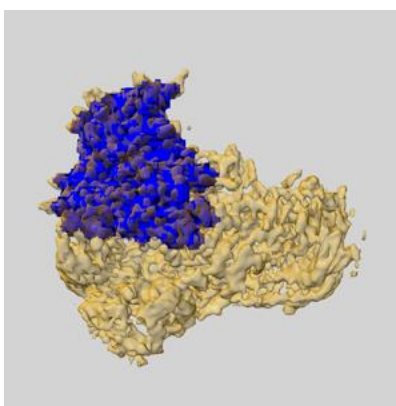
A mask typically either:

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

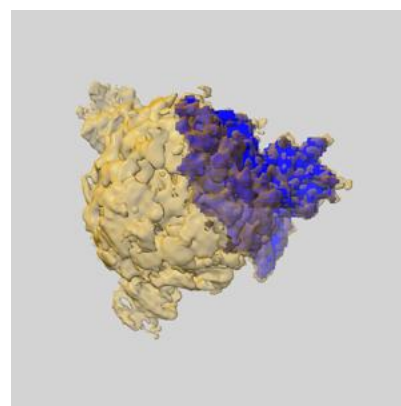
6.6.1 emd_48806_msk_1.map [i](#)



X



Y

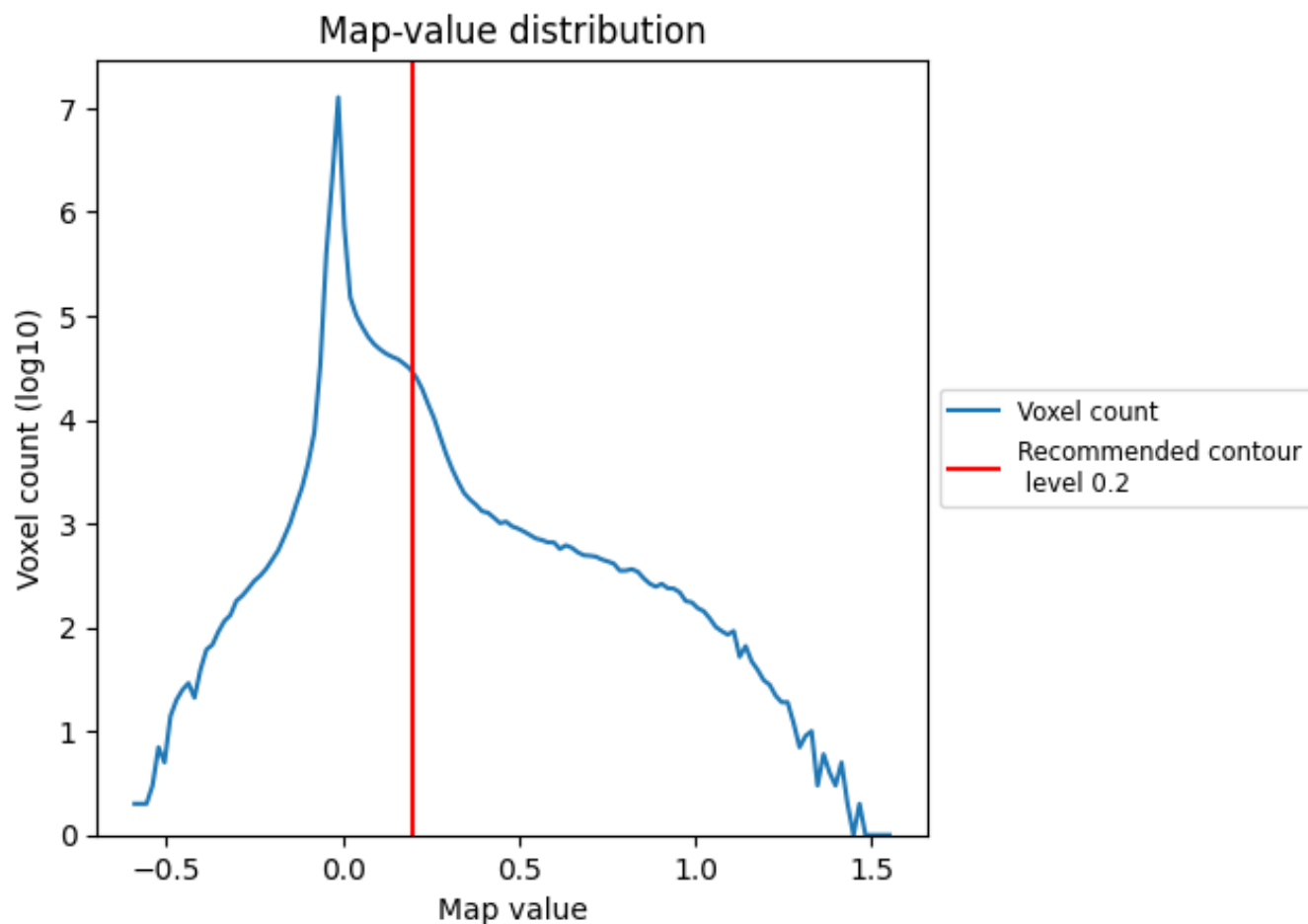


Z

7 Map analysis [i](#)

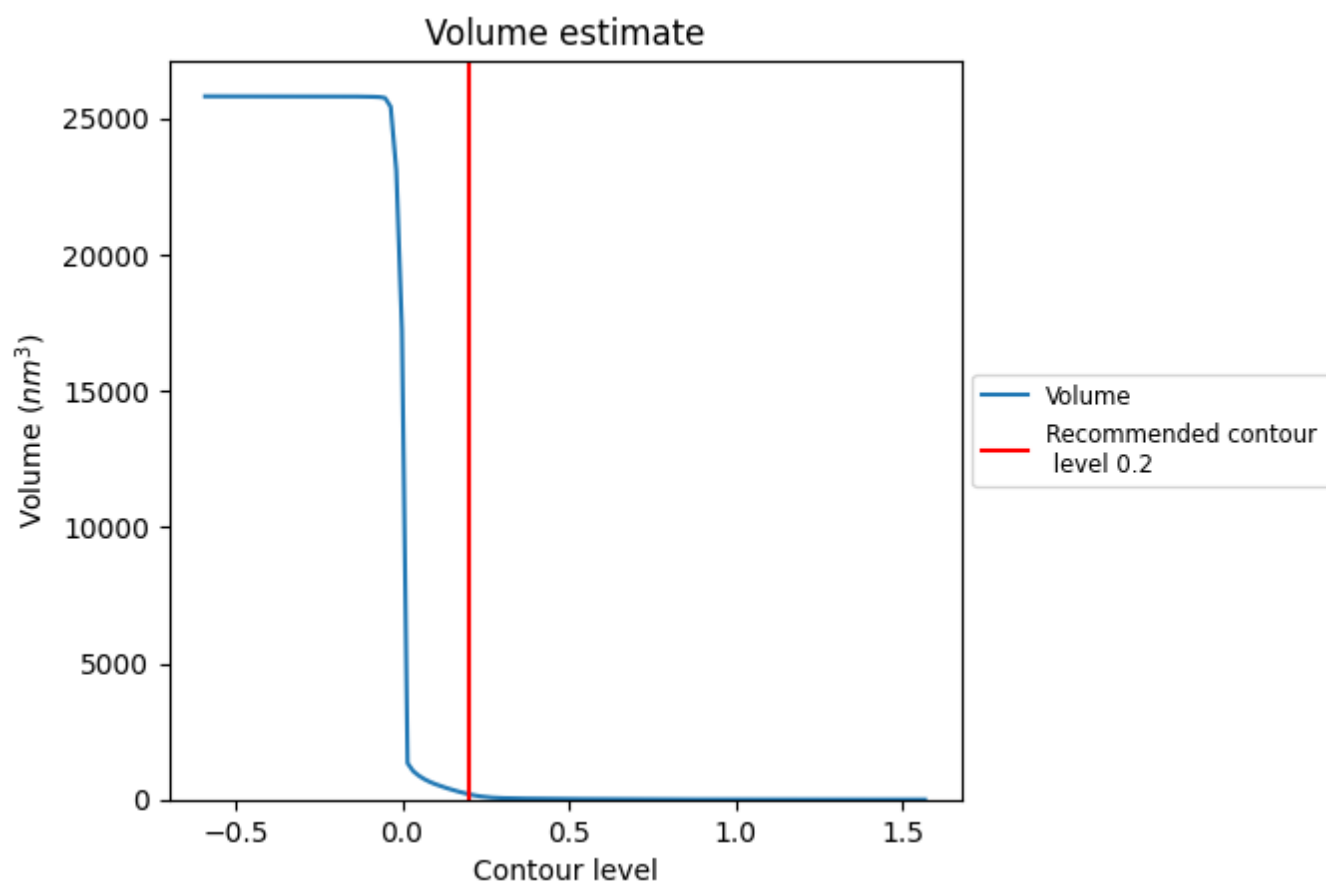
This section contains the results of statistical analysis of the map.

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.

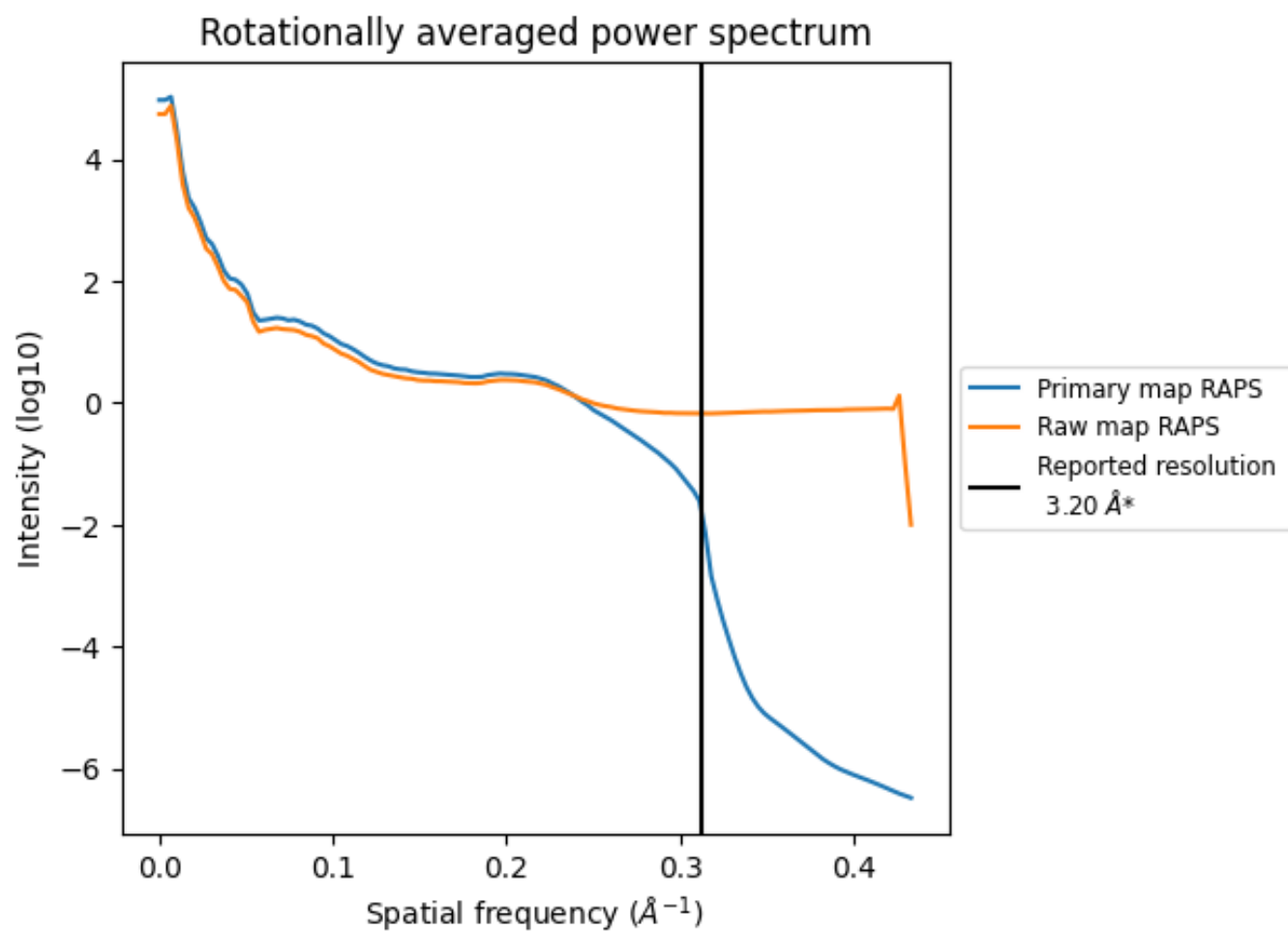
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 196 nm³; this corresponds to an approximate mass of 177 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 ⓘ

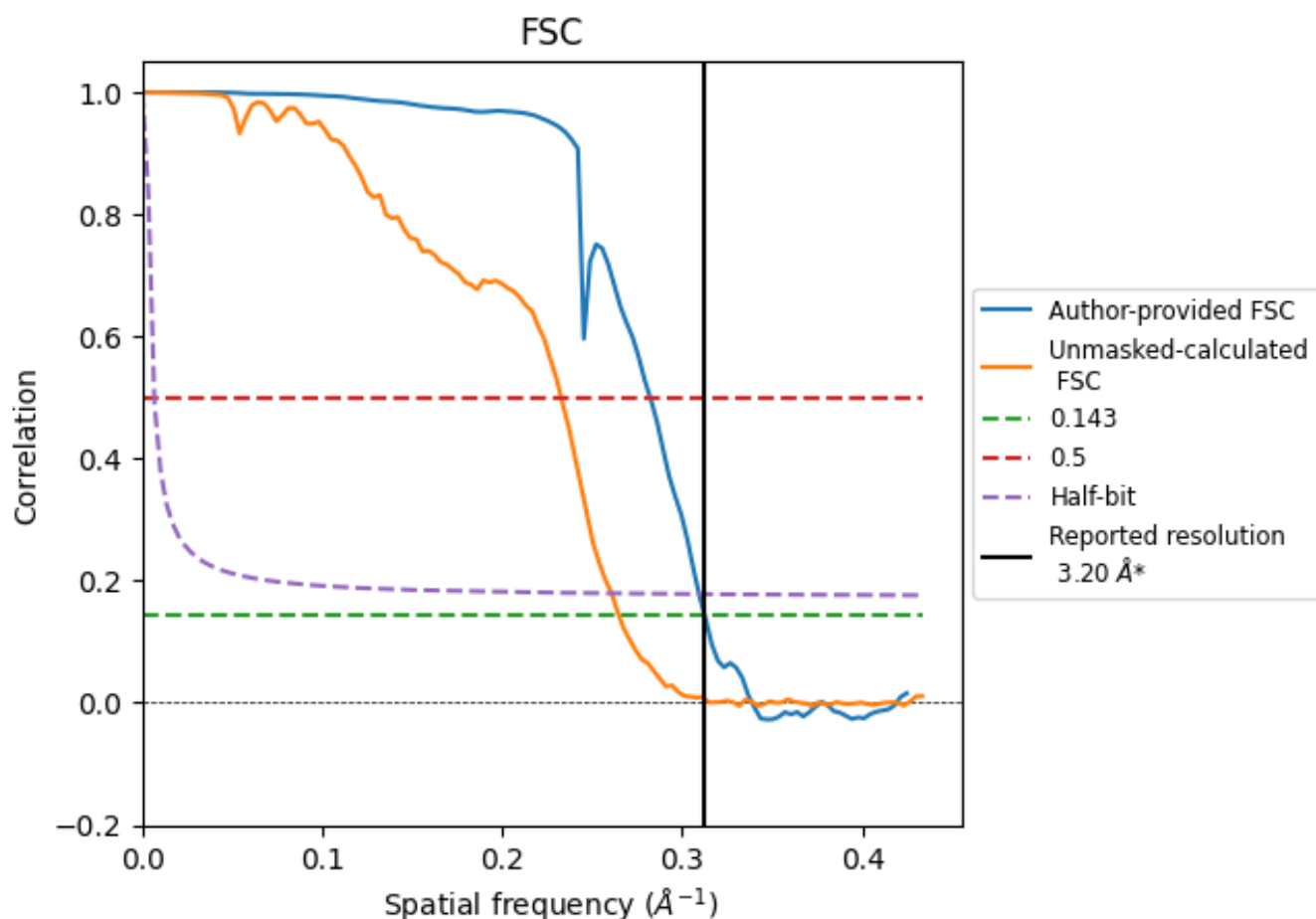


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

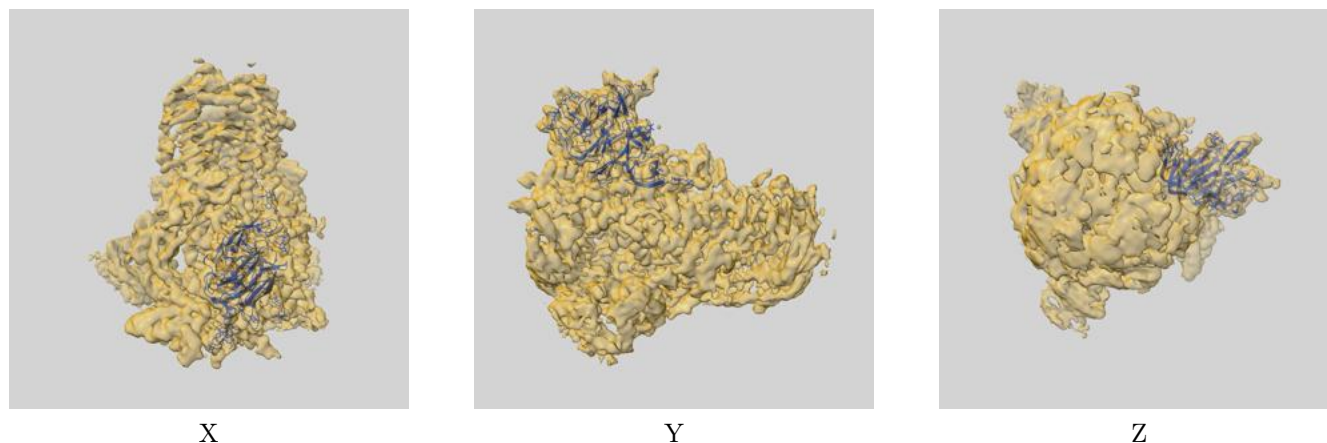
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.20	3.54	3.23
Unmasked-calculated*	3.78	4.30	3.84

*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 3.78 differs from the reported value 3.2 by more than 10 %

9 Map-model fit [i](#)

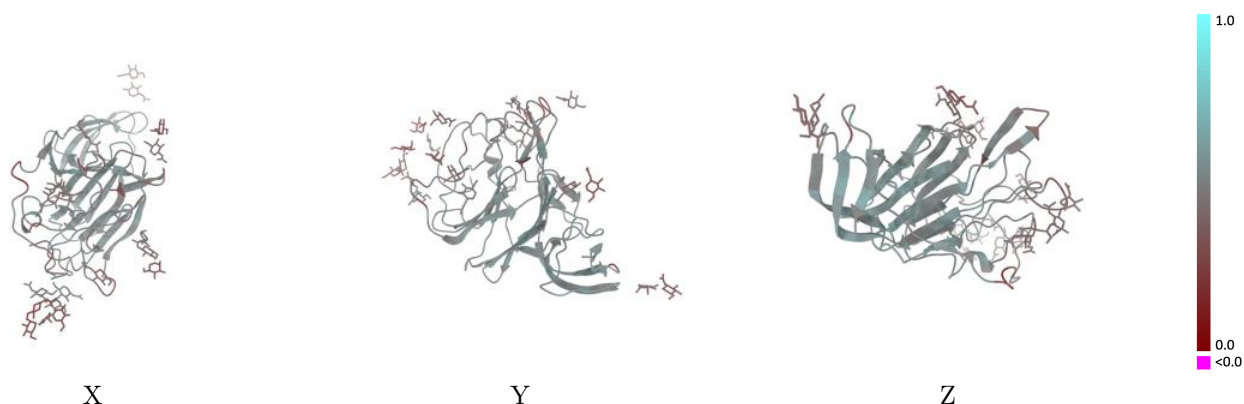
This section contains information regarding the fit between EMDB map EMD-48806 and PDB model 9N15. Per-residue inclusion information can be found in section [3](#) on page [9](#).

9.1 Map-model overlay [i](#)



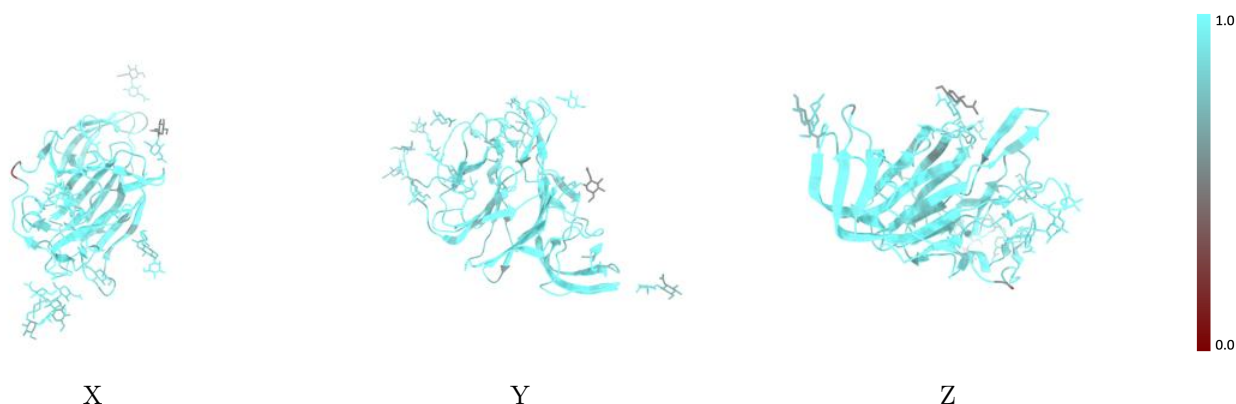
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



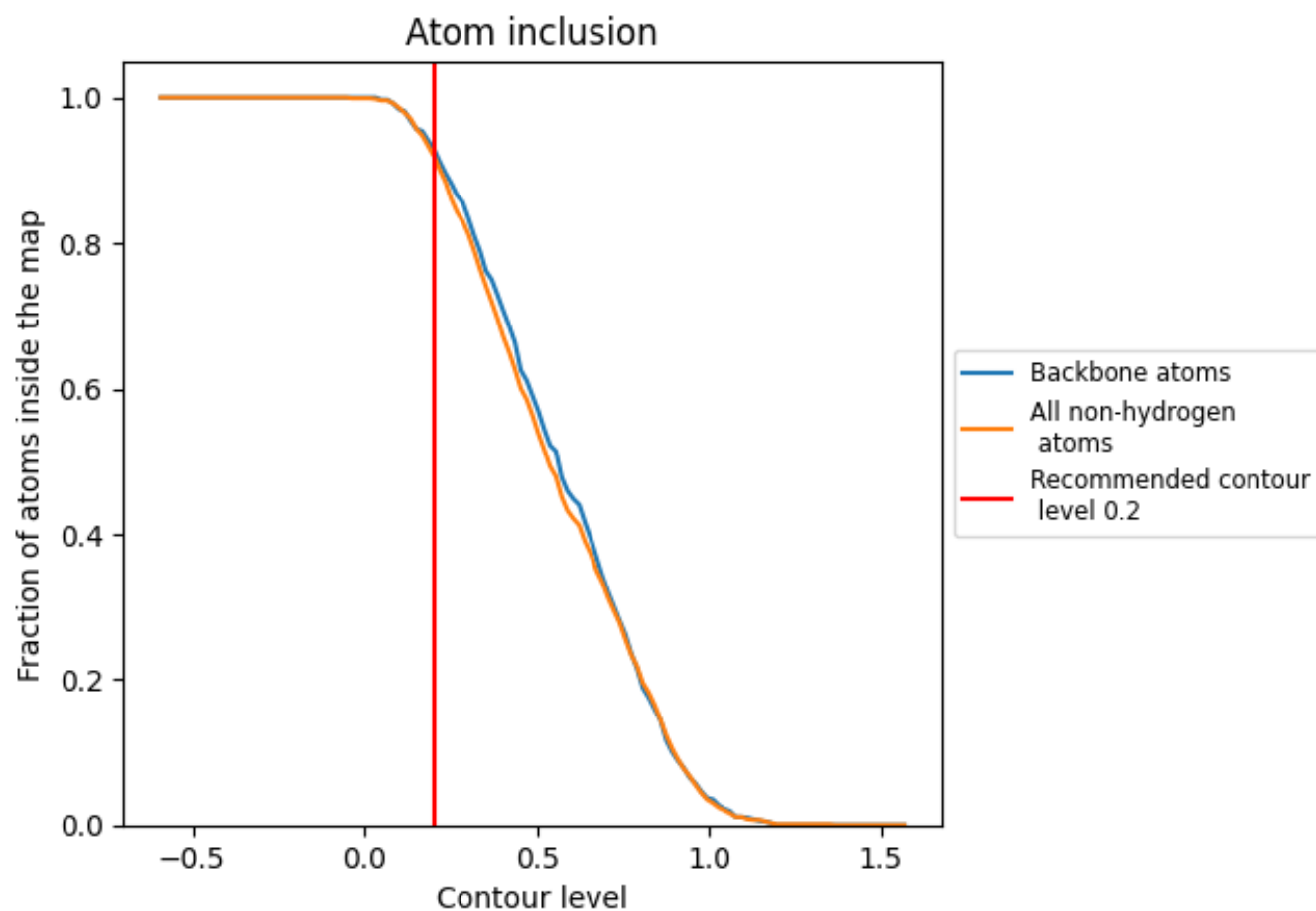
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).

9.4 Atom inclusion ⓘ



At the recommended contour level, 93% of all backbone atoms, 92% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9210	0.4920
A	0.9360	0.5000
B	0.8570	0.3740
C	0.7140	0.3850
D	0.8530	0.4070
E	0.8720	0.4030
F	0.6790	0.3610

1.0

0.0

<0.0