



## wwPDB EM Validation Summary Report ⓘ

Dec 22, 2022 – 04:45 AM EST

PDB ID : 7U6R  
EMDB ID : EMD-26378  
Title : Cryo-EM structure of PDF-2180 Spike glycoprotein  
Authors : Tortorici, M.A.; Veesler, D.; Seattle Structural Genomics Center for Infectious Disease (SSGCID)  
Deposited on : 2022-03-05  
Resolution : 2.50 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev43  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

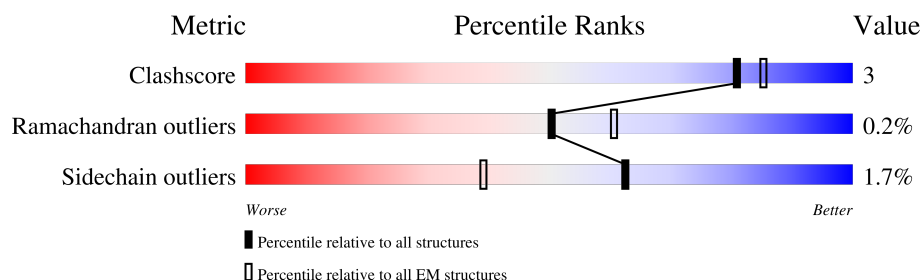
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.50 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\geq 3$ , 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	1337	
1	B	1337	
1	C	1337	
2	D	2	
2	E	2	
2	F	2	
2	G	2	
2	H	2	

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Mol	Chain	Length	Quality of chain
2	I	2	<div> <div style="width: 50%;"></div> <div>50%</div> <div>100%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 25561 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 PDF-2180 Spike glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1097	Total	C	N	O	S	0	0
			8282	5342	1388	1506	46		
1	B	1097	Total	C	N	O	S	0	0
			8283	5342	1388	1507	46		
1	C	1097	Total	C	N	O	S	0	0
			8282	5342	1388	1506	46		

There are 153 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1287	GLY	-	expression tag	UNP A0A1W6ASU7
A	1288	SER	-	expression tag	UNP A0A1W6ASU7
A	1289	GLY	-	expression tag	UNP A0A1W6ASU7
A	1290	ARG	-	expression tag	UNP A0A1W6ASU7
A	1291	GLU	-	expression tag	UNP A0A1W6ASU7
A	1292	ASN	-	expression tag	UNP A0A1W6ASU7
A	1293	LEU	-	expression tag	UNP A0A1W6ASU7
A	1294	TYR	-	expression tag	UNP A0A1W6ASU7
A	1295	PHE	-	expression tag	UNP A0A1W6ASU7
A	1296	GLN	-	expression tag	UNP A0A1W6ASU7
A	1297	GLY	-	expression tag	UNP A0A1W6ASU7
A	1298	GLY	-	expression tag	UNP A0A1W6ASU7
A	1299	GLY	-	expression tag	UNP A0A1W6ASU7
A	1300	GLY	-	expression tag	UNP A0A1W6ASU7
A	1301	SER	-	expression tag	UNP A0A1W6ASU7
A	1302	GLY	-	expression tag	UNP A0A1W6ASU7
A	1303	TYR	-	expression tag	UNP A0A1W6ASU7
A	1304	ILE	-	expression tag	UNP A0A1W6ASU7
A	1305	PRO	-	expression tag	UNP A0A1W6ASU7
A	1306	GLU	-	expression tag	UNP A0A1W6ASU7
A	1307	ALA	-	expression tag	UNP A0A1W6ASU7
A	1308	PRO	-	expression tag	UNP A0A1W6ASU7
A	1309	ARG	-	expression tag	UNP A0A1W6ASU7
A	1310	ASP	-	expression tag	UNP A0A1W6ASU7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1311	GLY	-	expression tag	UNP A0A1W6ASU7
A	1312	GLN	-	expression tag	UNP A0A1W6ASU7
A	1313	ALA	-	expression tag	UNP A0A1W6ASU7
A	1314	TYR	-	expression tag	UNP A0A1W6ASU7
A	1315	VAL	-	expression tag	UNP A0A1W6ASU7
A	1316	ARG	-	expression tag	UNP A0A1W6ASU7
A	1317	LYS	-	expression tag	UNP A0A1W6ASU7
A	1318	ASP	-	expression tag	UNP A0A1W6ASU7
A	1319	GLY	-	expression tag	UNP A0A1W6ASU7
A	1320	GLU	-	expression tag	UNP A0A1W6ASU7
A	1321	TRP	-	expression tag	UNP A0A1W6ASU7
A	1322	VAL	-	expression tag	UNP A0A1W6ASU7
A	1323	LEU	-	expression tag	UNP A0A1W6ASU7
A	1324	LEU	-	expression tag	UNP A0A1W6ASU7
A	1325	SER	-	expression tag	UNP A0A1W6ASU7
A	1326	THR	-	expression tag	UNP A0A1W6ASU7
A	1327	PHE	-	expression tag	UNP A0A1W6ASU7
A	1328	LEU	-	expression tag	UNP A0A1W6ASU7
A	1329	GLY	-	expression tag	UNP A0A1W6ASU7
A	1330	HIS	-	expression tag	UNP A0A1W6ASU7
A	1331	HIS	-	expression tag	UNP A0A1W6ASU7
A	1332	HIS	-	expression tag	UNP A0A1W6ASU7
A	1333	HIS	-	expression tag	UNP A0A1W6ASU7
A	1334	HIS	-	expression tag	UNP A0A1W6ASU7
A	1335	HIS	-	expression tag	UNP A0A1W6ASU7
A	1336	HIS	-	expression tag	UNP A0A1W6ASU7
A	1337	HIS	-	expression tag	UNP A0A1W6ASU7
B	1287	GLY	-	expression tag	UNP A0A1W6ASU7
B	1288	SER	-	expression tag	UNP A0A1W6ASU7
B	1289	GLY	-	expression tag	UNP A0A1W6ASU7
B	1290	ARG	-	expression tag	UNP A0A1W6ASU7
B	1291	GLU	-	expression tag	UNP A0A1W6ASU7
B	1292	ASN	-	expression tag	UNP A0A1W6ASU7
B	1293	LEU	-	expression tag	UNP A0A1W6ASU7
B	1294	TYR	-	expression tag	UNP A0A1W6ASU7
B	1295	PHE	-	expression tag	UNP A0A1W6ASU7
B	1296	GLN	-	expression tag	UNP A0A1W6ASU7
B	1297	GLY	-	expression tag	UNP A0A1W6ASU7
B	1298	GLY	-	expression tag	UNP A0A1W6ASU7
B	1299	GLY	-	expression tag	UNP A0A1W6ASU7
B	1300	GLY	-	expression tag	UNP A0A1W6ASU7
B	1301	SER	-	expression tag	UNP A0A1W6ASU7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1302	GLY	-	expression tag	UNP A0A1W6ASU7
B	1303	TYR	-	expression tag	UNP A0A1W6ASU7
B	1304	ILE	-	expression tag	UNP A0A1W6ASU7
B	1305	PRO	-	expression tag	UNP A0A1W6ASU7
B	1306	GLU	-	expression tag	UNP A0A1W6ASU7
B	1307	ALA	-	expression tag	UNP A0A1W6ASU7
B	1308	PRO	-	expression tag	UNP A0A1W6ASU7
B	1309	ARG	-	expression tag	UNP A0A1W6ASU7
B	1310	ASP	-	expression tag	UNP A0A1W6ASU7
B	1311	GLY	-	expression tag	UNP A0A1W6ASU7
B	1312	GLN	-	expression tag	UNP A0A1W6ASU7
B	1313	ALA	-	expression tag	UNP A0A1W6ASU7
B	1314	TYR	-	expression tag	UNP A0A1W6ASU7
B	1315	VAL	-	expression tag	UNP A0A1W6ASU7
B	1316	ARG	-	expression tag	UNP A0A1W6ASU7
B	1317	LYS	-	expression tag	UNP A0A1W6ASU7
B	1318	ASP	-	expression tag	UNP A0A1W6ASU7
B	1319	GLY	-	expression tag	UNP A0A1W6ASU7
B	1320	GLU	-	expression tag	UNP A0A1W6ASU7
B	1321	TRP	-	expression tag	UNP A0A1W6ASU7
B	1322	VAL	-	expression tag	UNP A0A1W6ASU7
B	1323	LEU	-	expression tag	UNP A0A1W6ASU7
B	1324	LEU	-	expression tag	UNP A0A1W6ASU7
B	1325	SER	-	expression tag	UNP A0A1W6ASU7
B	1326	THR	-	expression tag	UNP A0A1W6ASU7
B	1327	PHE	-	expression tag	UNP A0A1W6ASU7
B	1328	LEU	-	expression tag	UNP A0A1W6ASU7
B	1329	GLY	-	expression tag	UNP A0A1W6ASU7
B	1330	HIS	-	expression tag	UNP A0A1W6ASU7
B	1331	HIS	-	expression tag	UNP A0A1W6ASU7
B	1332	HIS	-	expression tag	UNP A0A1W6ASU7
B	1333	HIS	-	expression tag	UNP A0A1W6ASU7
B	1334	HIS	-	expression tag	UNP A0A1W6ASU7
B	1335	HIS	-	expression tag	UNP A0A1W6ASU7
B	1336	HIS	-	expression tag	UNP A0A1W6ASU7
B	1337	HIS	-	expression tag	UNP A0A1W6ASU7
C	1287	GLY	-	expression tag	UNP A0A1W6ASU7
C	1288	SER	-	expression tag	UNP A0A1W6ASU7
C	1289	GLY	-	expression tag	UNP A0A1W6ASU7
C	1290	ARG	-	expression tag	UNP A0A1W6ASU7
C	1291	GLU	-	expression tag	UNP A0A1W6ASU7
C	1292	ASN	-	expression tag	UNP A0A1W6ASU7

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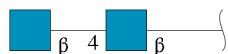
Chain	Residue	Modelled	Actual	Comment	Reference
C	1293	LEU	-	expression tag	UNP A0A1W6ASU7
C	1294	TYR	-	expression tag	UNP A0A1W6ASU7
C	1295	PHE	-	expression tag	UNP A0A1W6ASU7
C	1296	GLN	-	expression tag	UNP A0A1W6ASU7
C	1297	GLY	-	expression tag	UNP A0A1W6ASU7
C	1298	GLY	-	expression tag	UNP A0A1W6ASU7
C	1299	GLY	-	expression tag	UNP A0A1W6ASU7
C	1300	GLY	-	expression tag	UNP A0A1W6ASU7
C	1301	SER	-	expression tag	UNP A0A1W6ASU7
C	1302	GLY	-	expression tag	UNP A0A1W6ASU7
C	1303	TYR	-	expression tag	UNP A0A1W6ASU7
C	1304	ILE	-	expression tag	UNP A0A1W6ASU7
C	1305	PRO	-	expression tag	UNP A0A1W6ASU7
C	1306	GLU	-	expression tag	UNP A0A1W6ASU7
C	1307	ALA	-	expression tag	UNP A0A1W6ASU7
C	1308	PRO	-	expression tag	UNP A0A1W6ASU7
C	1309	ARG	-	expression tag	UNP A0A1W6ASU7
C	1310	ASP	-	expression tag	UNP A0A1W6ASU7
C	1311	GLY	-	expression tag	UNP A0A1W6ASU7
C	1312	GLN	-	expression tag	UNP A0A1W6ASU7
C	1313	ALA	-	expression tag	UNP A0A1W6ASU7
C	1314	TYR	-	expression tag	UNP A0A1W6ASU7
C	1315	VAL	-	expression tag	UNP A0A1W6ASU7
C	1316	ARG	-	expression tag	UNP A0A1W6ASU7
C	1317	LYS	-	expression tag	UNP A0A1W6ASU7
C	1318	ASP	-	expression tag	UNP A0A1W6ASU7
C	1319	GLY	-	expression tag	UNP A0A1W6ASU7
C	1320	GLU	-	expression tag	UNP A0A1W6ASU7
C	1321	TRP	-	expression tag	UNP A0A1W6ASU7
C	1322	VAL	-	expression tag	UNP A0A1W6ASU7
C	1323	LEU	-	expression tag	UNP A0A1W6ASU7
C	1324	LEU	-	expression tag	UNP A0A1W6ASU7
C	1325	SER	-	expression tag	UNP A0A1W6ASU7
C	1326	THR	-	expression tag	UNP A0A1W6ASU7
C	1327	PHE	-	expression tag	UNP A0A1W6ASU7
C	1328	LEU	-	expression tag	UNP A0A1W6ASU7
C	1329	GLY	-	expression tag	UNP A0A1W6ASU7
C	1330	HIS	-	expression tag	UNP A0A1W6ASU7
C	1331	HIS	-	expression tag	UNP A0A1W6ASU7
C	1332	HIS	-	expression tag	UNP A0A1W6ASU7
C	1333	HIS	-	expression tag	UNP A0A1W6ASU7
C	1334	HIS	-	expression tag	UNP A0A1W6ASU7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1335	HIS	-	expression tag	UNP A0A1W6ASU7
C	1336	HIS	-	expression tag	UNP A0A1W6ASU7
C	1337	HIS	-	expression tag	UNP A0A1W6ASU7

- 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	D	2	Total	C	N	O	0	0
			28	16	2	10		
2	E	2	Total	C	N	O	0	0
			28	16	2	10		
2	F	2	Total	C	N	O	0	0
			28	16	2	10		
2	G	2	Total	C	N	O	0	0
			28	16	2	10		
2	H	2	Total	C	N	O	0	0
			28	16	2	10		
2	I	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).





Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	C	N	O	0
			182	104	13	65	
3	A	1	Total	C	N	O	0
			182	104	13	65	
3	A	1	Total	C	N	O	0
			182	104	13	65	
3	A	1	Total	C	N	O	0
			182	104	13	65	
3	A	1	Total	C	N	O	0
			182	104	13	65	
3	A	1	Total	C	N	O	0
			182	104	13	65	
3	A	1	Total	C	N	O	0
			182	104	13	65	
3	A	1	Total	C	N	O	0
			182	104	13	65	
3	A	1	Total	C	N	O	0
			182	104	13	65	
3	A	1	Total	C	N	O	0
			182	104	13	65	
3	B	1	Total	C	N	O	0
			182	104	13	65	

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Mol	Chain	Residues	Atoms				AltConf
3	B	1	Total	C	N	O	0
			182	104	13	65	
3	B	1	Total	C	N	O	0
			182	104	13	65	
3	B	1	Total	C	N	O	0
			182	104	13	65	
3	B	1	Total	C	N	O	0
			182	104	13	65	
3	B	1	Total	C	N	O	0
			182	104	13	65	
3	B	1	Total	C	N	O	0
			182	104	13	65	
3	B	1	Total	C	N	O	0
			182	104	13	65	
3	B	1	Total	C	N	O	0
			182	104	13	65	
3	B	1	Total	C	N	O	0
			182	104	13	65	
3	B	1	Total	C	N	O	0
			182	104	13	65	
3	C	1	Total	C	N	O	0
			182	104	13	65	
3	C	1	Total	C	N	O	0
			182	104	13	65	
3	C	1	Total	C	N	O	0
			182	104	13	65	
3	C	1	Total	C	N	O	0
			182	104	13	65	
3	C	1	Total	C	N	O	0
			182	104	13	65	
3	C	1	Total	C	N	O	0
			182	104	13	65	
3	C	1	Total	C	N	O	0
			182	104	13	65	
3	C	1	Total	C	N	O	0
			182	104	13	65	

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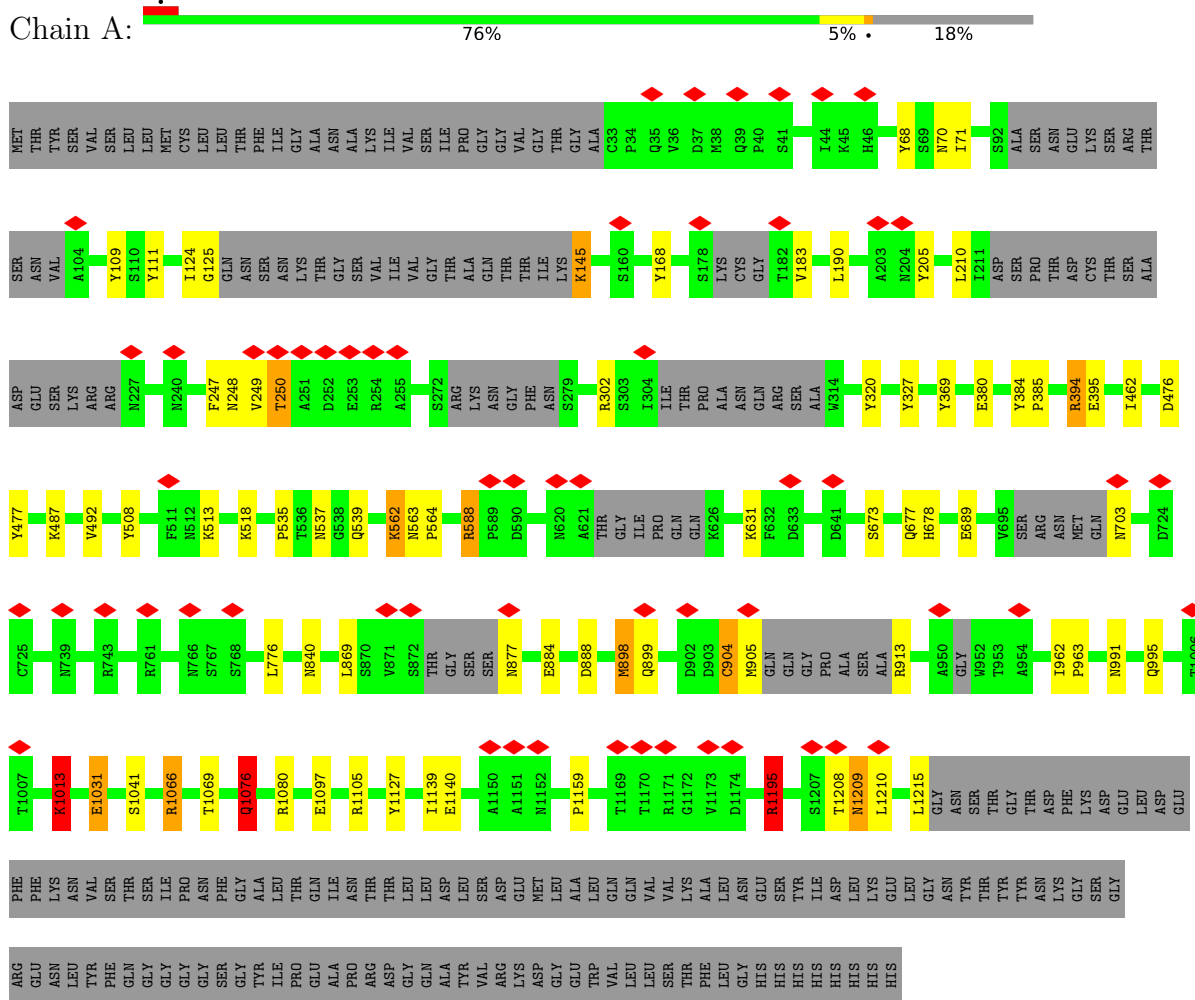
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Mol	Chain	Residues	Atoms				AltConf
3	C	1	Total	C	N	O	0
			182	104	13	65	
3	C	1	Total	C	N	O	0
			182	104	13	65	
3	C	1	Total	C	N	O	0
			182	104	13	65	
3	C	1	Total	C	N	O	0
			182	104	13	65	

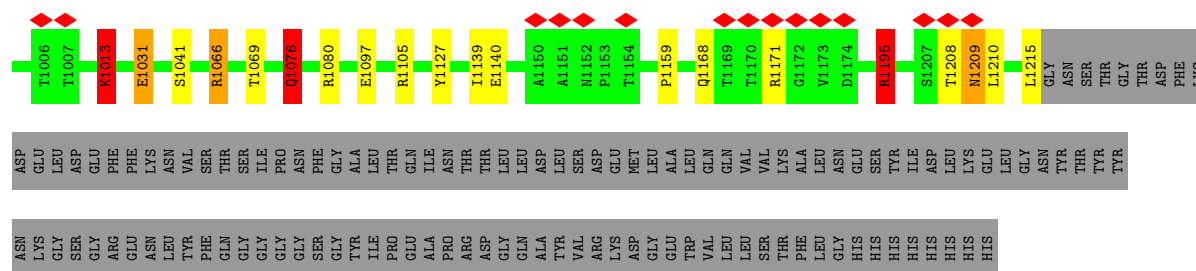
### 3 Residue-property plots [i](#)

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: PDF-2180 Spike glycoprotein







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



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



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



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



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





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



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	47094	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 ( $e^-/\text{\AA}^2$ )	70	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	8.747	Depositor
Minimum map value	-5.011	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.191	Depositor
Recommended contour level	1.5	Depositor
Map size (Å)	419.99997, 419.99997, 419.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	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	0.76	8/8480 (0.1%)	0.82	18/11580 (0.2%)
1	B	0.76	8/8481 (0.1%)	0.82	18/11581 (0.2%)
1	C	0.76	8/8480 (0.1%)	0.82	18/11580 (0.2%)
All	All	0.76	24/25441 (0.1%)	0.82	54/34741 (0.2%)

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	5
1	B	0	5
1	C	0	5
All	All	0	15

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	487	LYS	C-O	-5.93	1.12	1.23
1	B	487	LYS	C-O	-5.90	1.12	1.23
1	A	487	LYS	C-O	-5.90	1.12	1.23
1	A	1195	ARG	C-O	-5.78	1.12	1.23
1	C	1195	ARG	C-O	-5.73	1.12	1.23

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	327	TYR	CB-CG-CD1	-9.14	115.51	121.00
1	B	327	TYR	CB-CG-CD1	-9.09	115.55	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	327	TYR	CB-CG-CD1	-9.06	115.56	121.00
1	A	588	ARG	CB-CA-C	7.02	124.44	110.40
1	C	588	ARG	CB-CA-C	7.01	124.42	110.40

There are no chirality outliers.

5 of 15 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1080	ARG	Sidechain
1	A	1195	ARG	Sidechain
1	A	394	ARG	Sidechain
1	A	904	CYS	Mainchain
1	A	913	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	8282	0	7650	44	0
1	B	8283	0	7653	46	0
1	C	8282	0	7650	45	0
2	D	28	0	25	0	0
2	E	28	0	25	0	0
2	F	28	0	25	0	0
2	G	28	0	25	0	0
2	H	28	0	25	0	0
2	I	28	0	25	0	0
3	A	182	0	169	3	0
3	B	182	0	169	3	0
3	C	182	0	169	3	0
All	All	25561	0	23610	123	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 3.

The worst 5 of 123 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:678:HIS:CE1	1:C:905:MET:SD	2.69	0.85
1:A:905:MET:SD	1:B:678:HIS:CE1	2.69	0.85
1:B:905:MET:SD	1:C:678:HIS:CE1	2.69	0.85
1:A:68:TYR:HB3	1:A:71:ILE:HD11	1.64	0.80
1:C:68:TYR:HB3	1:C:71:ILE:HD11	1.64	0.79

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	1073/1337 (80%)	1054 (98%)	17 (2%)	2 (0%)	47	68
1	B	1073/1337 (80%)	1054 (98%)	17 (2%)	2 (0%)	47	68
1	C	1073/1337 (80%)	1054 (98%)	17 (2%)	2 (0%)	47	68
All	All	3219/4011 (80%)	3162 (98%)	51 (2%)	6 (0%)	50	68

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	250	THR
1	B	250	THR
1	C	250	THR
1	A	898	MET
1	B	898	MET

### 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	809/1142 (71%)	795 (98%)	14 (2%)	60	82
1	B	810/1142 (71%)	796 (98%)	14 (2%)	60	82
1	C	809/1142 (71%)	795 (98%)	14 (2%)	60	82
All	All	2428/3426 (71%)	2386 (98%)	42 (2%)	62	82

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	70	ASN
1	C	631	LYS
1	C	145	LYS
1	C	518	LYS
1	C	888	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	1161	ASN
1	C	877	ASN
1	B	1161	ASN
1	B	678	HIS
1	C	678	HIS

### 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 ⓘ

12 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	D	1	1,2	14,14,15	1.45	1 (7%)	17,19,21	1.09	1 (5%)
2	NAG	D	2	2	14,14,15	1.44	2 (14%)	17,19,21	0.87	1 (5%)
2	NAG	E	1	1,2	14,14,15	1.52	1 (7%)	17,19,21	1.11	3 (17%)
2	NAG	E	2	2	14,14,15	1.46	2 (14%)	17,19,21	0.91	1 (5%)
2	NAG	F	1	1,2	14,14,15	1.46	1 (7%)	17,19,21	1.09	1 (5%)
2	NAG	F	2	2	14,14,15	1.44	2 (14%)	17,19,21	0.87	1 (5%)
2	NAG	G	1	1,2	14,14,15	1.52	1 (7%)	17,19,21	1.11	3 (17%)
2	NAG	G	2	2	14,14,15	1.46	2 (14%)	17,19,21	0.91	1 (5%)
2	NAG	H	1	1,2	14,14,15	1.46	1 (7%)	17,19,21	1.09	1 (5%)
2	NAG	H	2	2	14,14,15	1.44	2 (14%)	17,19,21	0.87	1 (5%)
2	NAG	I	1	1,2	14,14,15	1.52	1 (7%)	17,19,21	1.11	3 (17%)
2	NAG	I	2	2	14,14,15	1.46	2 (14%)	17,19,21	0.91	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	D	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	D	2	2	-	0/6/23/26	0/1/1/1
2	NAG	E	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	E	2	2	-	0/6/23/26	0/1/1/1
2	NAG	F	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	F	2	2	-	0/6/23/26	0/1/1/1
2	NAG	G	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	G	2	2	-	0/6/23/26	0/1/1/1
2	NAG	H	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	H	2	2	-	0/6/23/26	0/1/1/1
2	NAG	I	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	I	2	2	-	0/6/23/26	0/1/1/1

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	1	NAG	C1-C2	4.40	1.58	1.52
2	I	1	NAG	C1-C2	4.39	1.58	1.52
2	E	1	NAG	C1-C2	4.38	1.58	1.52
2	H	2	NAG	C1-C2	3.82	1.58	1.52
2	D	2	NAG	C1-C2	3.81	1.58	1.52

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	2	NAG	C8-C7-N2	2.49	120.32	116.10
2	D	2	NAG	C8-C7-N2	2.49	120.32	116.10
2	H	2	NAG	C8-C7-N2	2.49	120.31	116.10
2	F	2	NAG	C8-C7-N2	2.49	120.31	116.10
2	G	2	NAG	C8-C7-N2	2.47	120.28	116.10

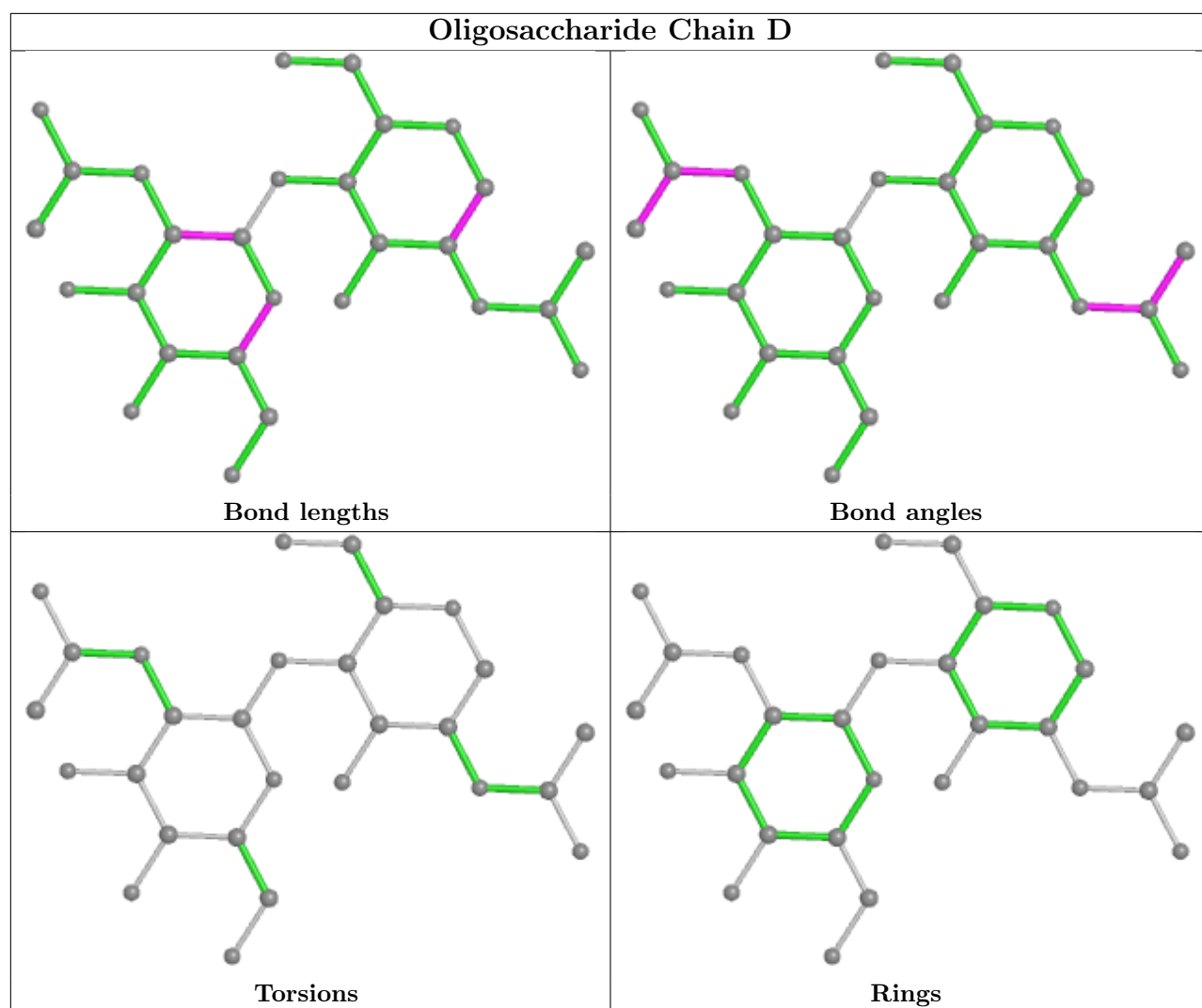
There are no chirality outliers.

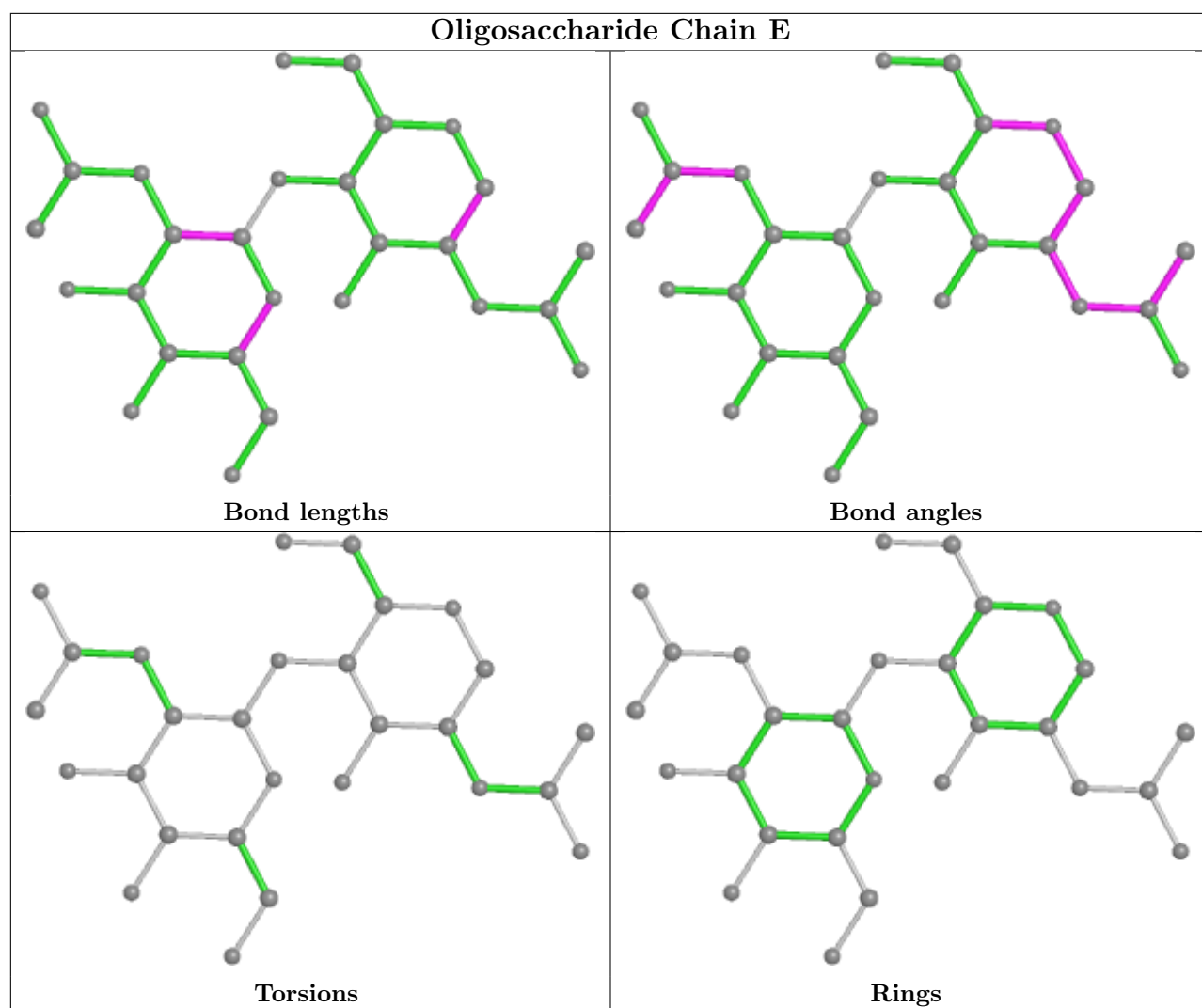
There are no torsion outliers.

There are no ring outliers.

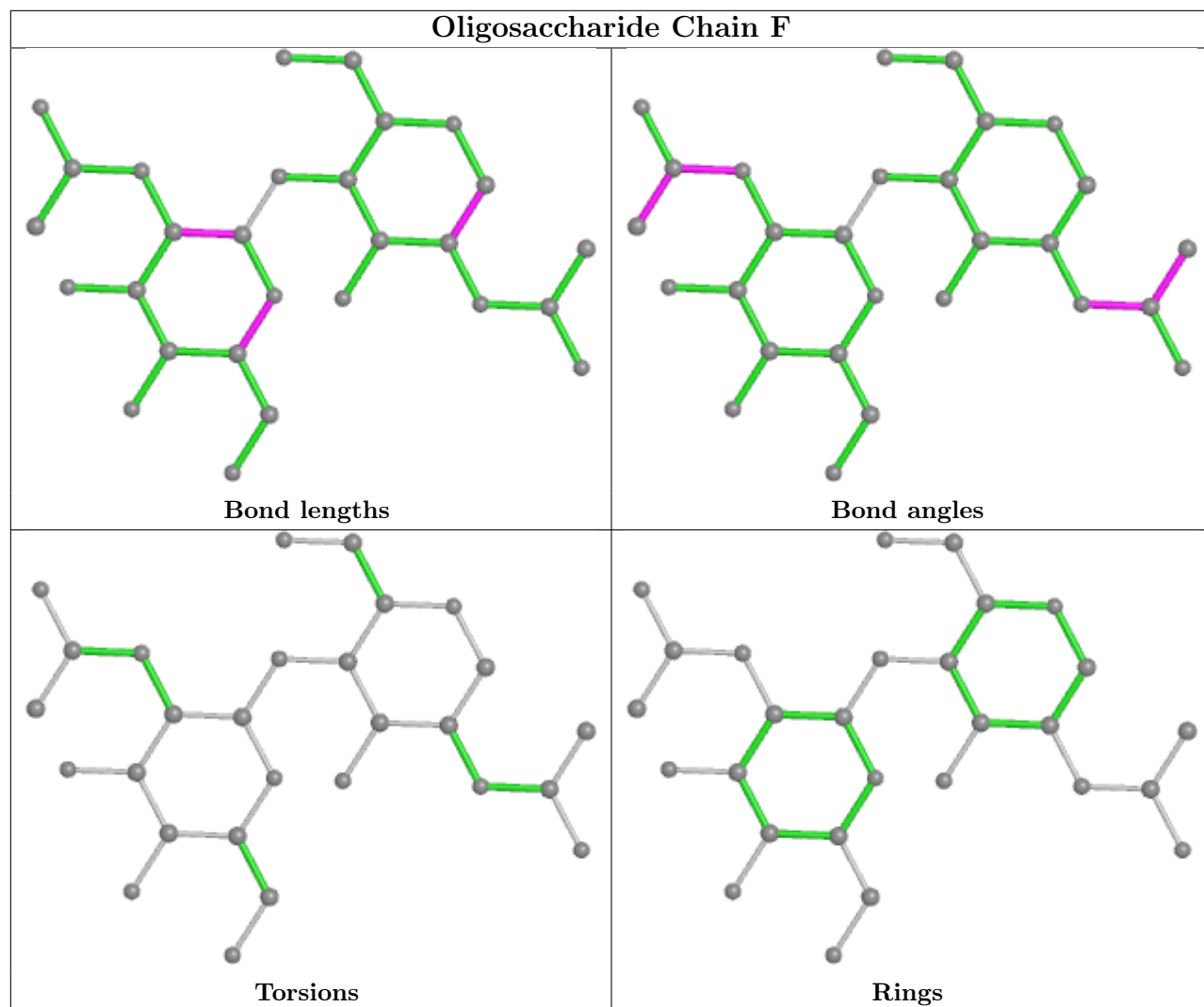
No monomer is involved in short contacts.

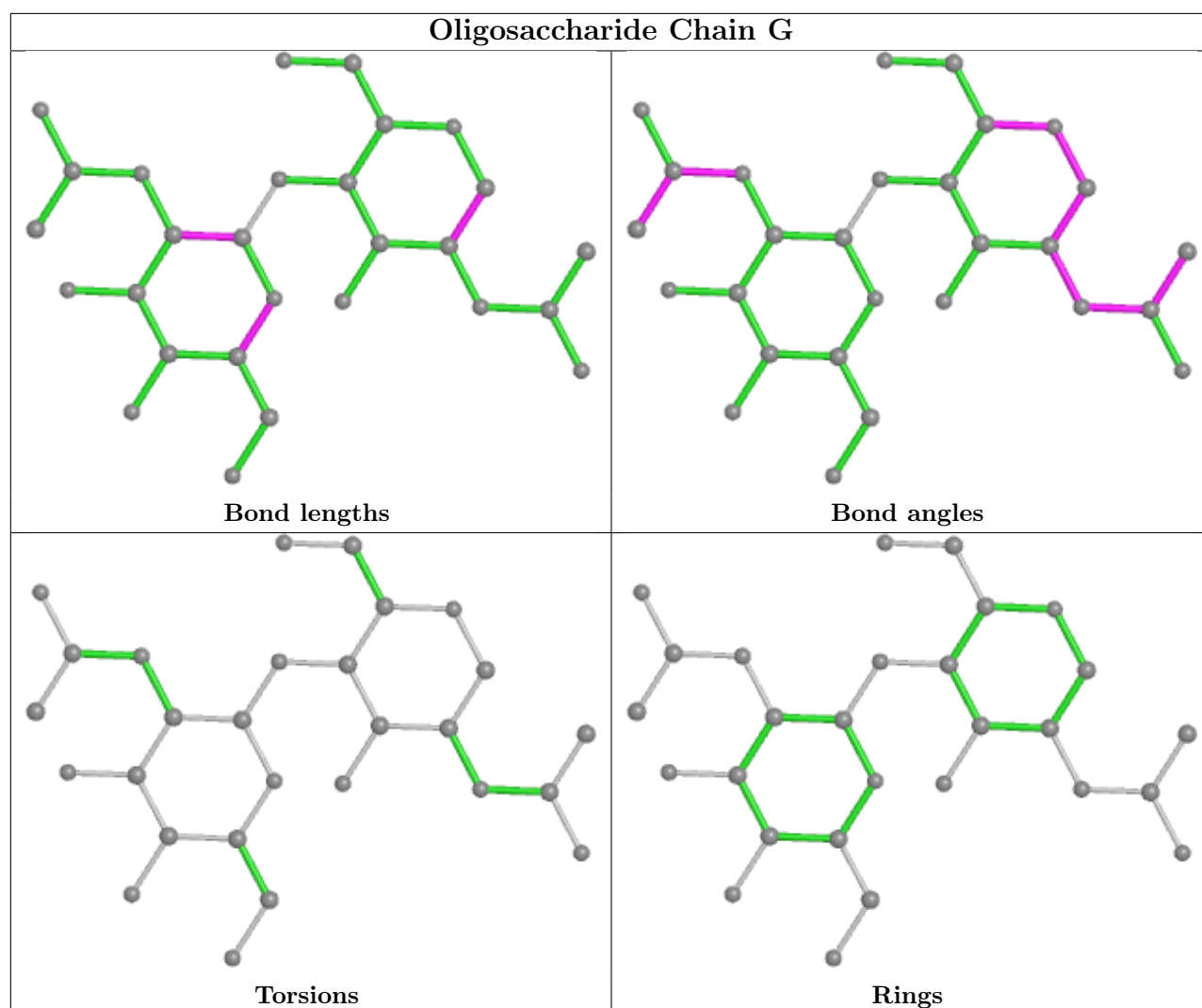
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

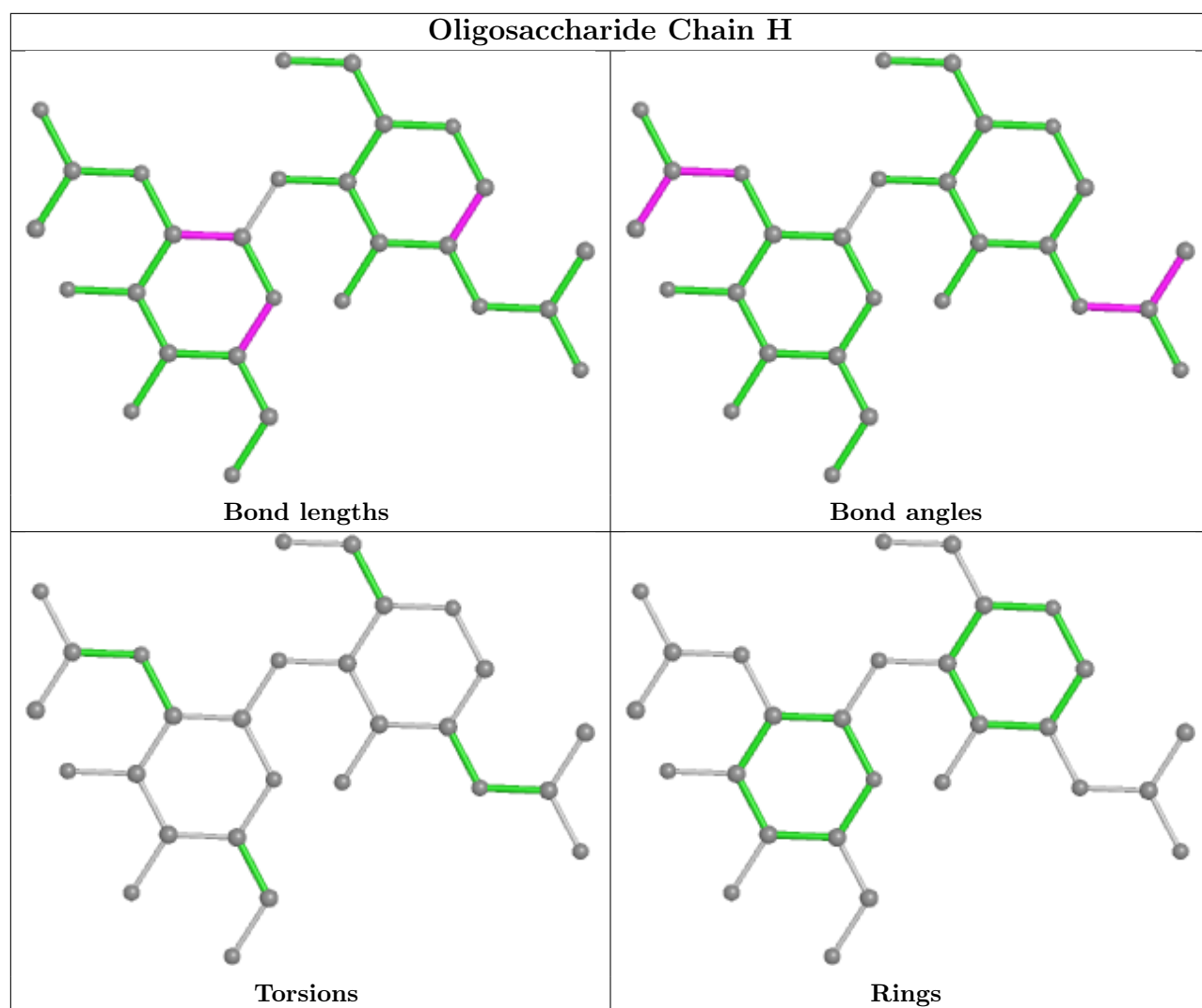


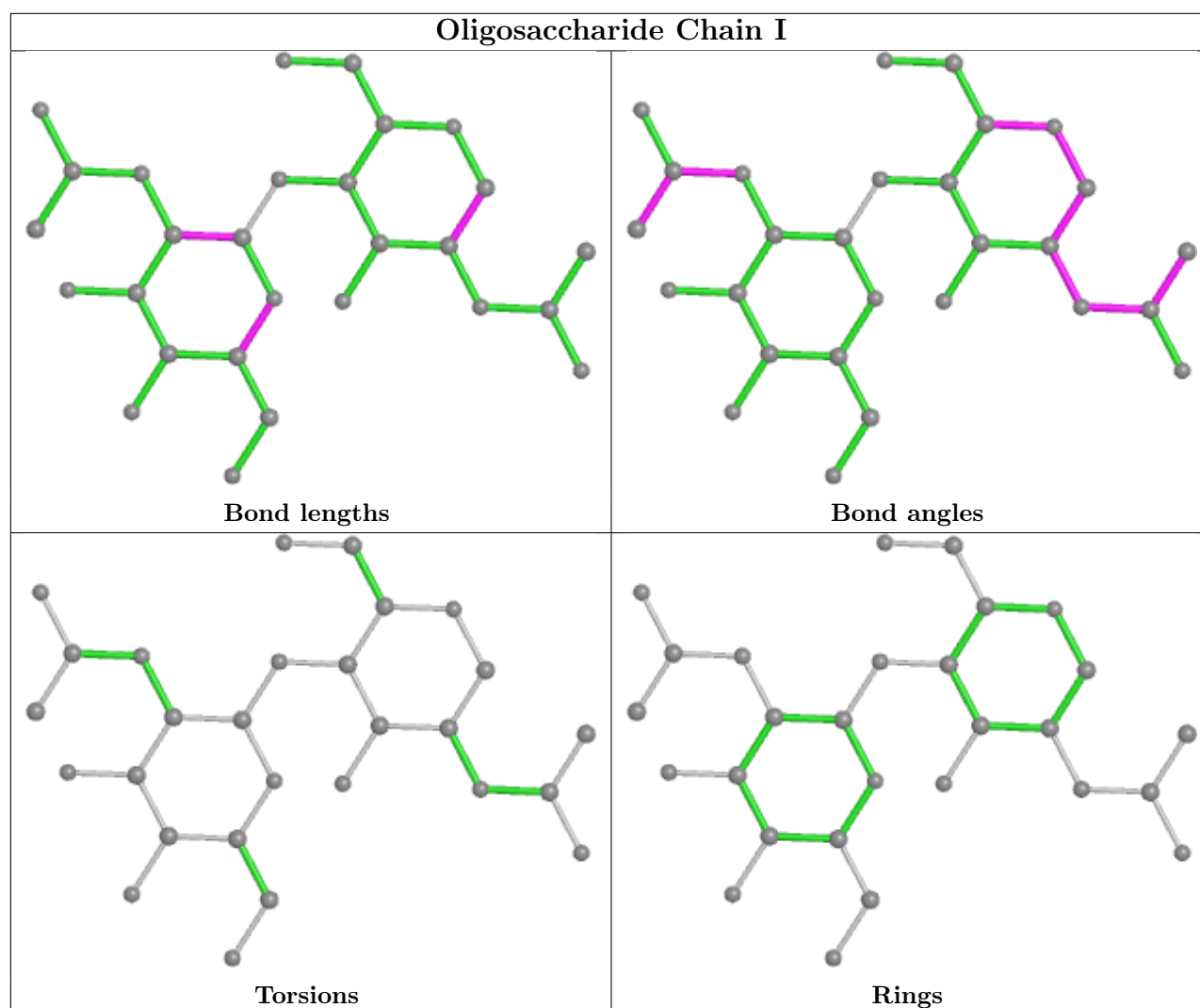












## 5.6 Ligand geometry [i](#)

39 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	NAG	C	1412	1	14,14,15	0.28	0	17,19,21	0.61	0
3	NAG	C	1402	1	14,14,15	1.46	2 (14%)	17,19,21	0.97	1 (5%)
3	NAG	C	1403	1	14,14,15	1.57	2 (14%)	17,19,21	1.02	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	NAG	A	1407	1	14,14,15	1.58	2 (14%)	17,19,21	0.94	1 (5%)
3	NAG	B	1404	1	14,14,15	1.44	2 (14%)	17,19,21	0.93	1 (5%)
3	NAG	B	1413	1	14,14,15	0.40	0	17,19,21	0.82	0
3	NAG	C	1410	1	14,14,15	0.28	0	17,19,21	0.76	0
3	NAG	A	1410	1	14,14,15	0.28	0	17,19,21	0.75	0
3	NAG	B	1408	1	14,14,15	1.70	3 (21%)	17,19,21	1.23	2 (11%)
3	NAG	A	1411	1	14,14,15	0.38	0	17,19,21	0.82	0
3	NAG	B	1409	1	14,14,15	0.26	0	17,19,21	0.56	0
3	NAG	C	1401	1	14,14,15	1.67	2 (14%)	17,19,21	0.86	1 (5%)
3	NAG	C	1405	1	14,14,15	1.53	2 (14%)	17,19,21	0.88	0
3	NAG	A	1401	1	14,14,15	1.66	2 (14%)	17,19,21	0.85	0
3	NAG	A	1404	1	14,14,15	1.45	2 (14%)	17,19,21	0.93	1 (5%)
3	NAG	C	1406	1	14,14,15	1.52	2 (14%)	17,19,21	0.86	1 (5%)
3	NAG	C	1411	1	14,14,15	0.39	0	17,19,21	0.82	0
3	NAG	C	1404	1	14,14,15	1.45	2 (14%)	17,19,21	0.94	1 (5%)
3	NAG	B	1402	1	14,14,15	1.45	2 (14%)	17,19,21	0.97	1 (5%)
3	NAG	A	1408	1	14,14,15	1.70	3 (21%)	17,19,21	1.23	2 (11%)
3	NAG	B	1412	1	14,14,15	0.28	0	17,19,21	0.61	0
3	NAG	C	1409	1	14,14,15	0.26	0	17,19,21	0.56	0
3	NAG	C	1407	1	14,14,15	1.59	2 (14%)	17,19,21	0.94	1 (5%)
3	NAG	B	1406	1	14,14,15	1.53	2 (14%)	17,19,21	0.86	1 (5%)
3	NAG	A	1409	1	14,14,15	0.25	0	17,19,21	0.56	0
3	NAG	A	1412	1	14,14,15	0.28	0	17,19,21	0.61	0
3	NAG	A	1402	1	14,14,15	1.46	2 (14%)	17,19,21	0.97	1 (5%)
3	NAG	B	1401	1	14,14,15	1.66	2 (14%)	17,19,21	0.85	0
3	NAG	B	1405	1	14,14,15	1.52	2 (14%)	17,19,21	0.88	0
3	NAG	C	1413	1	14,14,15	0.42	0	17,19,21	0.82	0
3	NAG	B	1411	1	14,14,15	0.38	0	17,19,21	0.82	0
3	NAG	B	1407	1	14,14,15	1.58	2 (14%)	17,19,21	0.94	1 (5%)
3	NAG	C	1408	1	14,14,15	1.70	3 (21%)	17,19,21	1.23	2 (11%)
3	NAG	A	1403	1	14,14,15	1.57	2 (14%)	17,19,21	1.02	1 (5%)
3	NAG	B	1403	1	14,14,15	1.58	2 (14%)	17,19,21	1.02	1 (5%)
3	NAG	A	1413	1	14,14,15	0.41	0	17,19,21	0.81	0
3	NAG	A	1405	1	14,14,15	1.52	2 (14%)	17,19,21	0.88	0
3	NAG	B	1410	1	14,14,15	0.28	0	17,19,21	0.75	0
3	NAG	A	1406	1	14,14,15	1.53	2 (14%)	17,19,21	0.86	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
3	NAG	C	1412	1	-	1/6/23/26	0/1/1/1
3	NAG	C	1402	1	-	2/6/23/26	0/1/1/1
3	NAG	C	1403	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1407	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1404	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1413	1	-	0/6/23/26	0/1/1/1
3	NAG	C	1410	1	-	2/6/23/26	0/1/1/1
3	NAG	A	1410	1	-	2/6/23/26	0/1/1/1
3	NAG	B	1408	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1411	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1409	1	-	2/6/23/26	0/1/1/1
3	NAG	C	1401	1	-	0/6/23/26	0/1/1/1
3	NAG	C	1405	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1401	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1404	1	-	0/6/23/26	0/1/1/1
3	NAG	C	1406	1	-	0/6/23/26	0/1/1/1
3	NAG	C	1411	1	-	0/6/23/26	0/1/1/1
3	NAG	C	1404	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1402	1	-	2/6/23/26	0/1/1/1
3	NAG	A	1408	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1412	1	-	1/6/23/26	0/1/1/1
3	NAG	C	1409	1	-	2/6/23/26	0/1/1/1
3	NAG	C	1407	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1406	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1409	1	-	2/6/23/26	0/1/1/1
3	NAG	A	1412	1	-	1/6/23/26	0/1/1/1
3	NAG	A	1402	1	-	2/6/23/26	0/1/1/1
3	NAG	B	1401	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1405	1	-	0/6/23/26	0/1/1/1
3	NAG	C	1413	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1411	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1407	1	-	0/6/23/26	0/1/1/1
3	NAG	C	1408	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1403	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1403	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1413	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1405	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1410	1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	A	1406	1	-	0/6/23/26	0/1/1/1

The worst 5 of 51 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1401	NAG	C1-C2	4.59	1.59	1.52
3	B	1401	NAG	C1-C2	4.56	1.59	1.52
3	A	1401	NAG	C1-C2	4.56	1.59	1.52
3	B	1408	NAG	C1-C2	4.49	1.59	1.52
3	C	1408	NAG	C1-C2	4.48	1.59	1.52

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1408	NAG	C8-C7-N2	3.35	121.78	116.10
3	B	1408	NAG	C8-C7-N2	3.35	121.77	116.10
3	C	1408	NAG	C8-C7-N2	3.34	121.75	116.10
3	B	1408	NAG	O7-C7-C8	-2.63	117.18	122.06
3	C	1408	NAG	O7-C7-C8	-2.63	117.18	122.06

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1402	NAG	C4-C5-C6-O6
3	B	1402	NAG	C4-C5-C6-O6
3	C	1402	NAG	C4-C5-C6-O6
3	A	1402	NAG	O5-C5-C6-O6
3	B	1402	NAG	O5-C5-C6-O6

There are no ring outliers.

3 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1408	NAG	3	0
3	A	1408	NAG	3	0
3	C	1408	NAG	3	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.



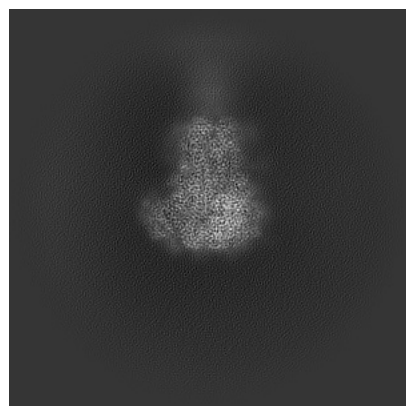
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26378. These allow visual inspection of the internal detail of the map and identification of artifacts.

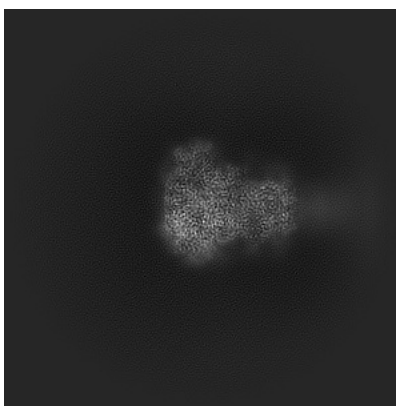
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

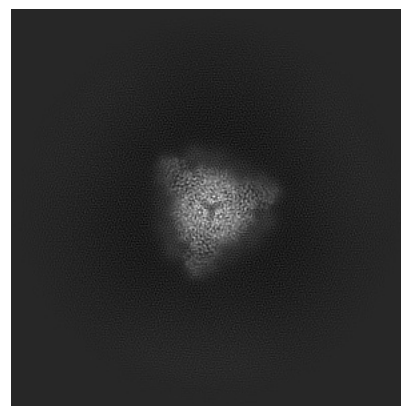
#### 6.1.1 Primary map



X

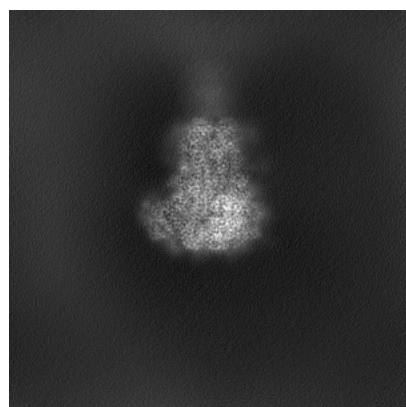


Y

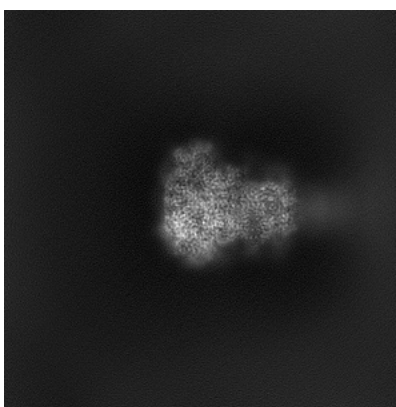


Z

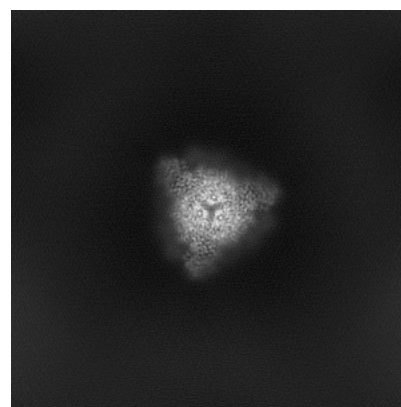
#### 6.1.2 Raw map



X



Y

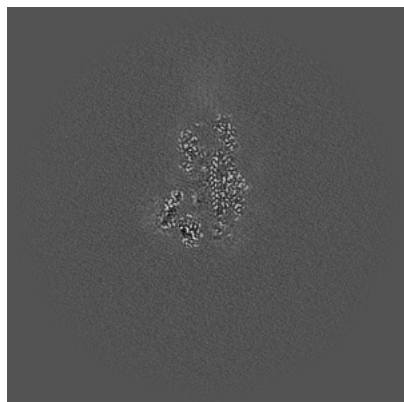


Z

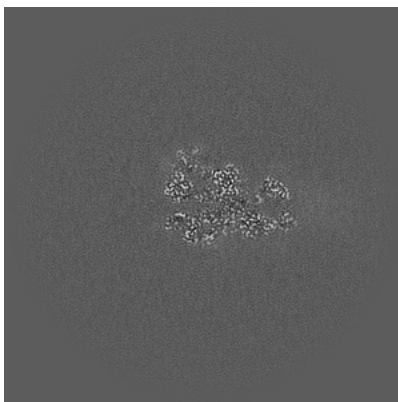
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

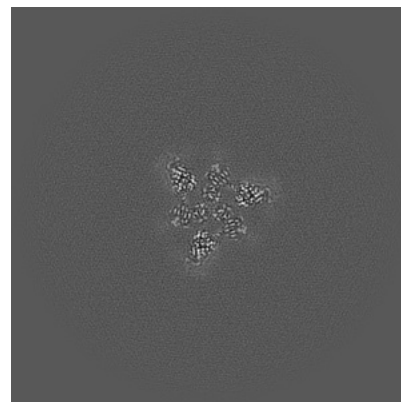
### 6.2.1 Primary map



X Index: 200

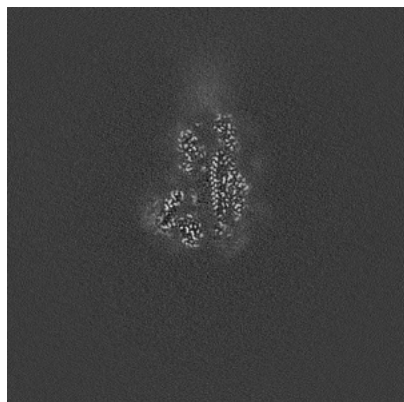


Y Index: 200

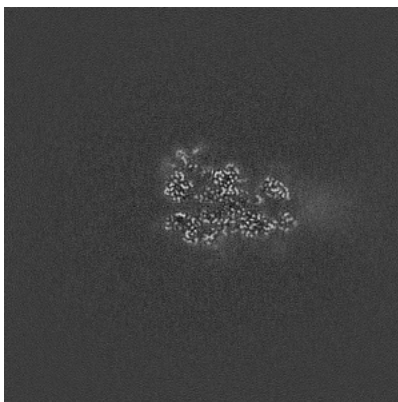


Z Index: 200

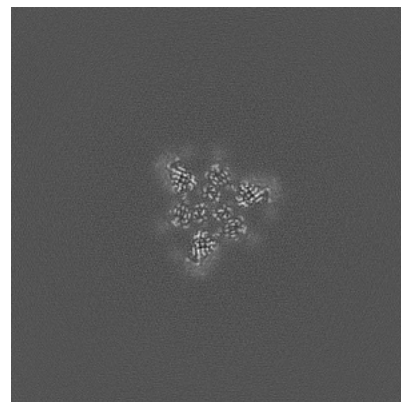
### 6.2.2 Raw map



X Index: 200



Y Index: 200

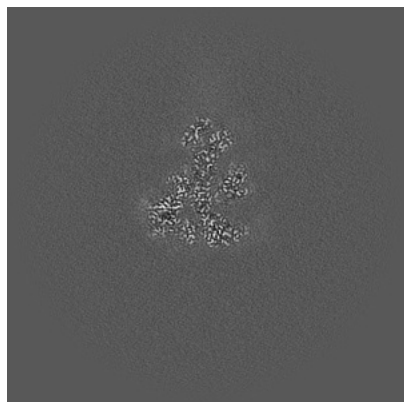


Z Index: 200

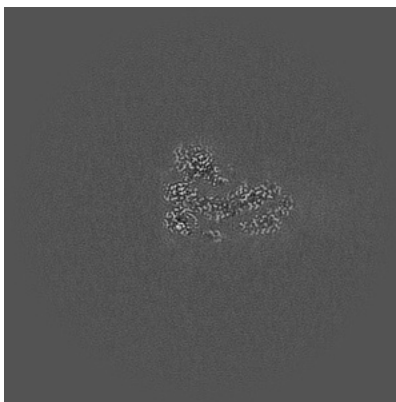
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

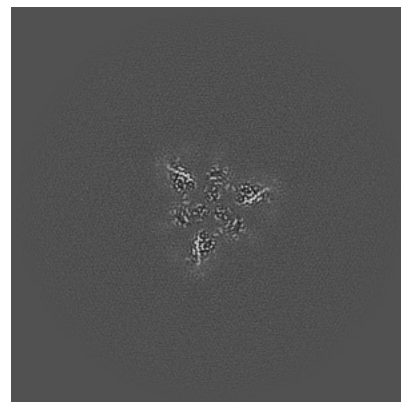
### 6.3.1 Primary map



X Index: 187

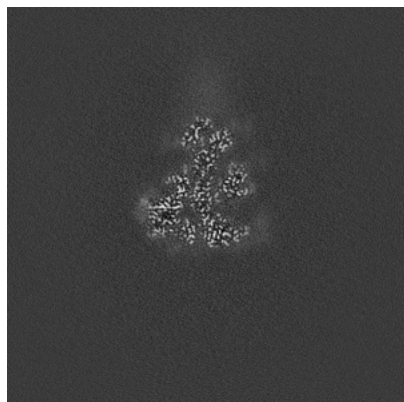


Y Index: 210

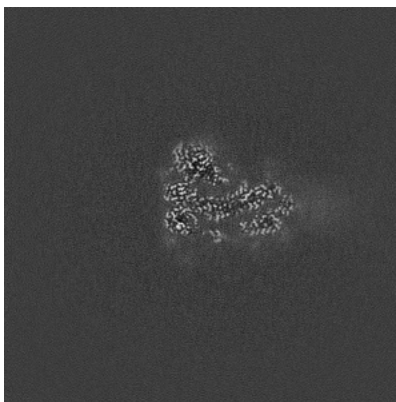


Z Index: 199

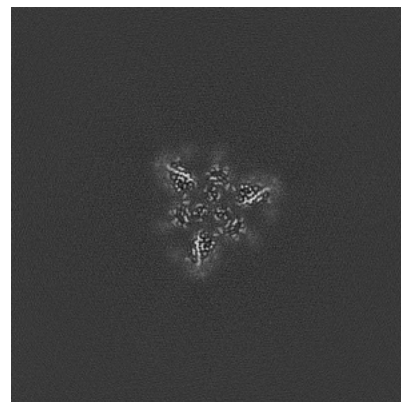
### 6.3.2 Raw map



X Index: 187



Y Index: 210

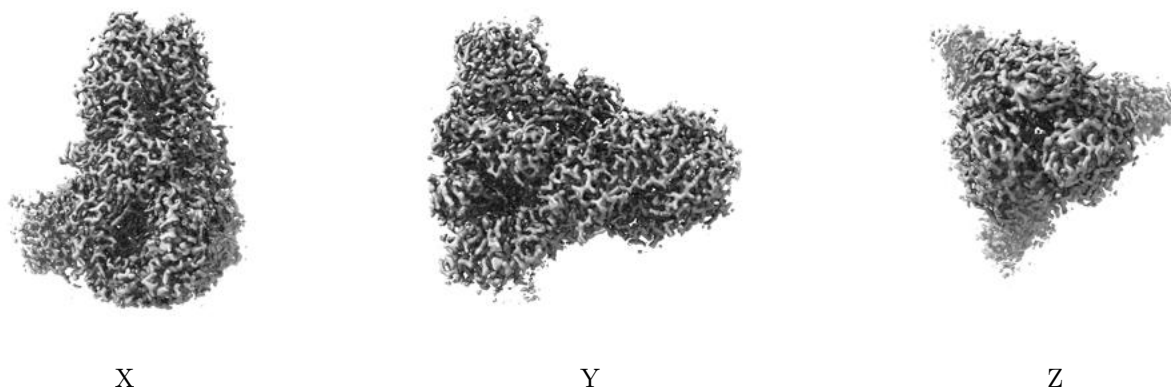


Z Index: 199

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

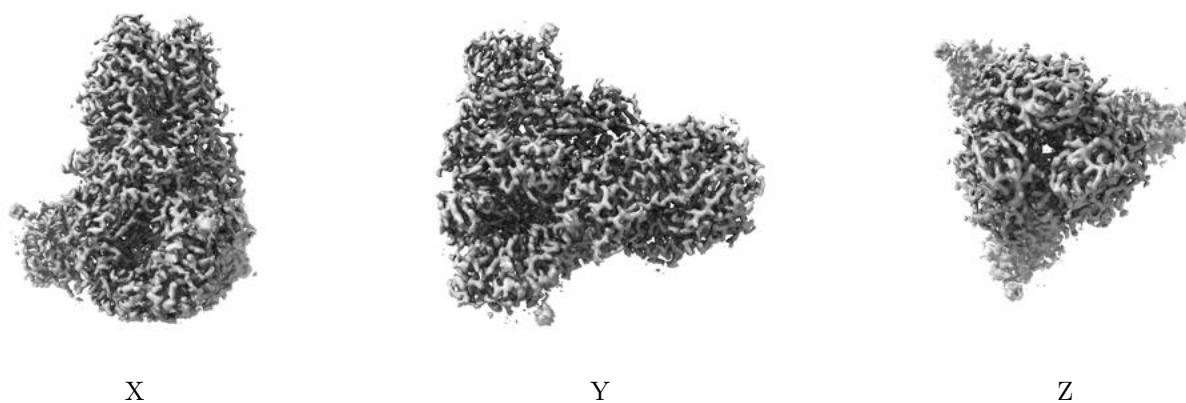
## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.4.2 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.

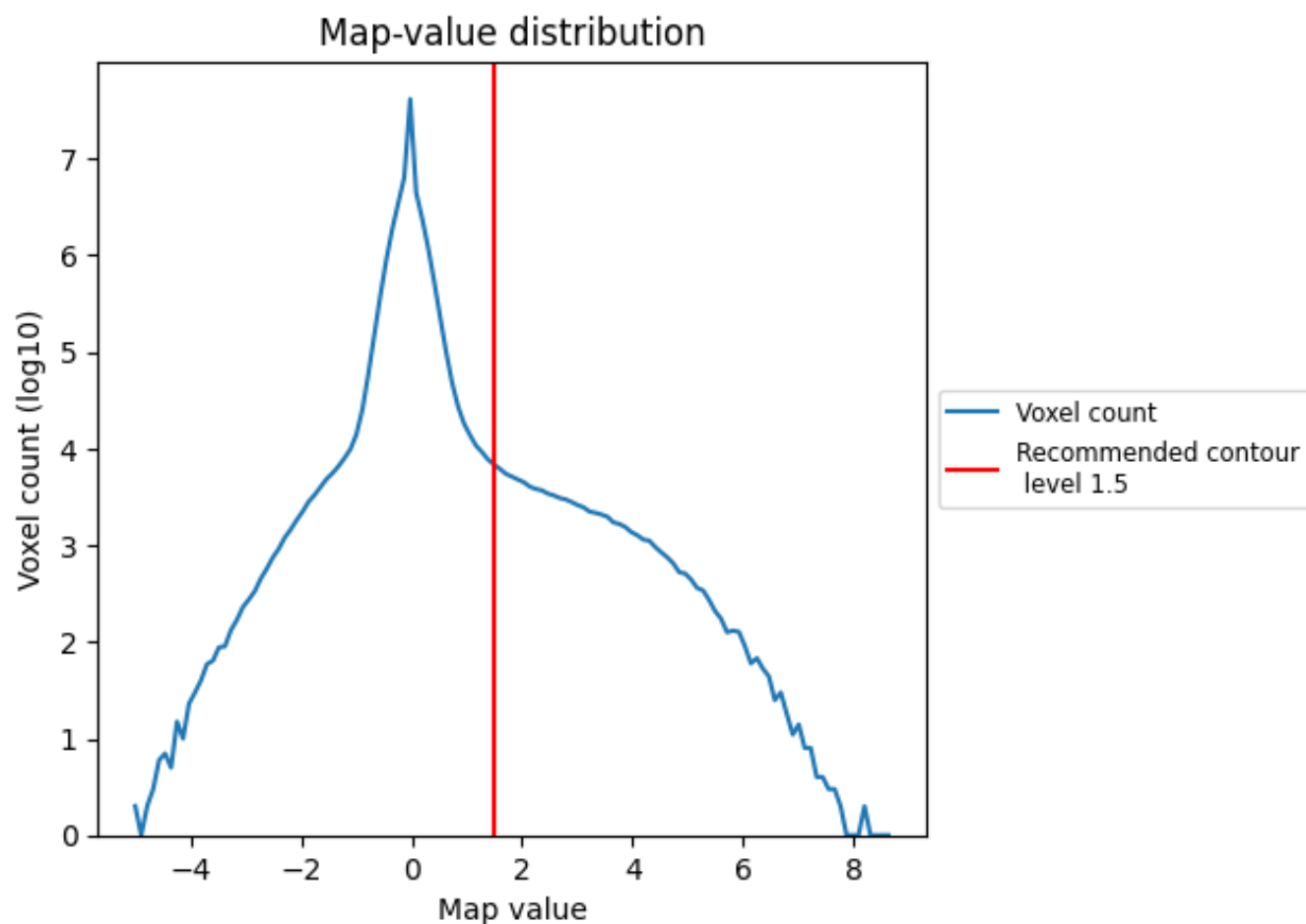
## 6.5 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

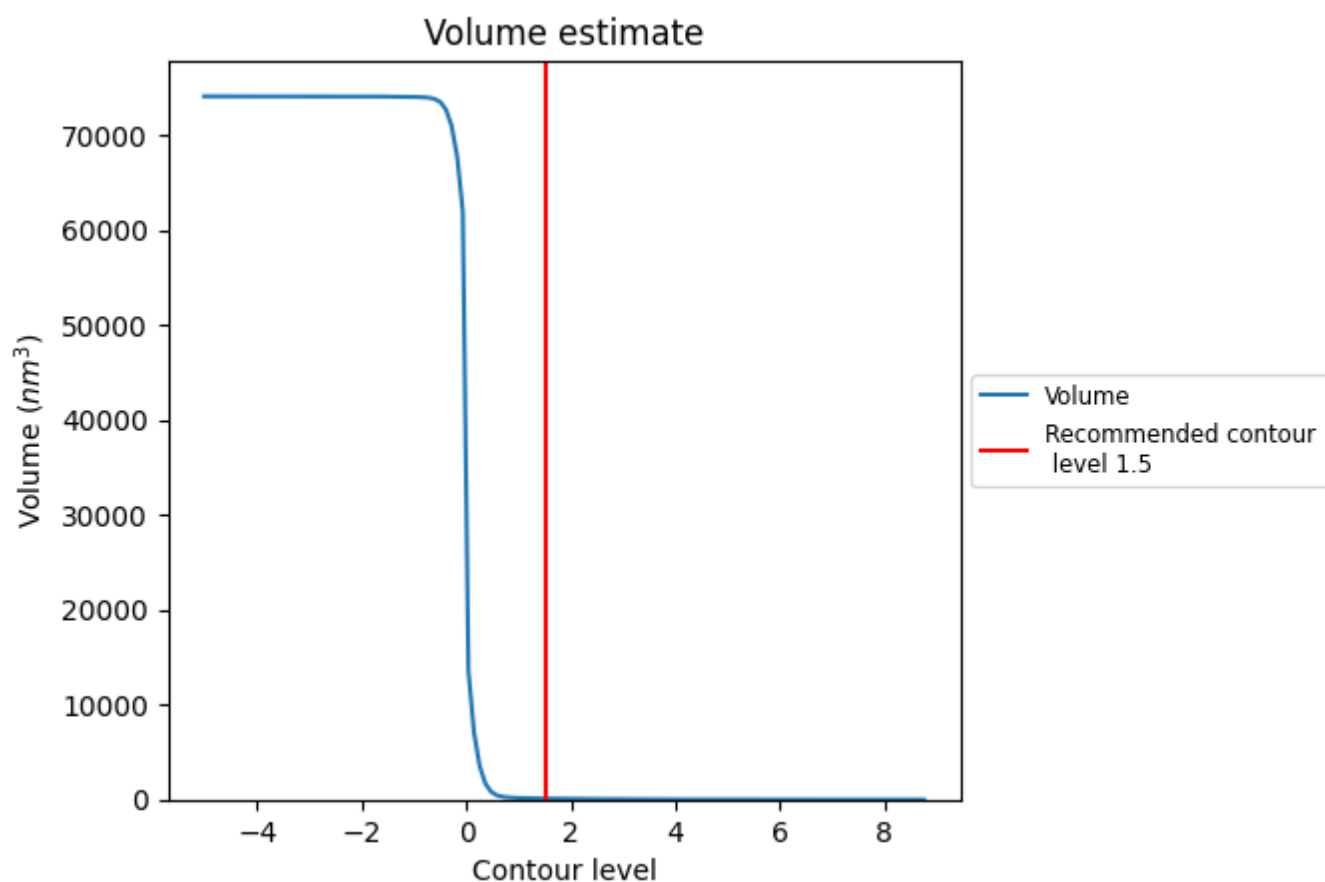
This section contains the results of statistical analysis of the map.

### 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](#)

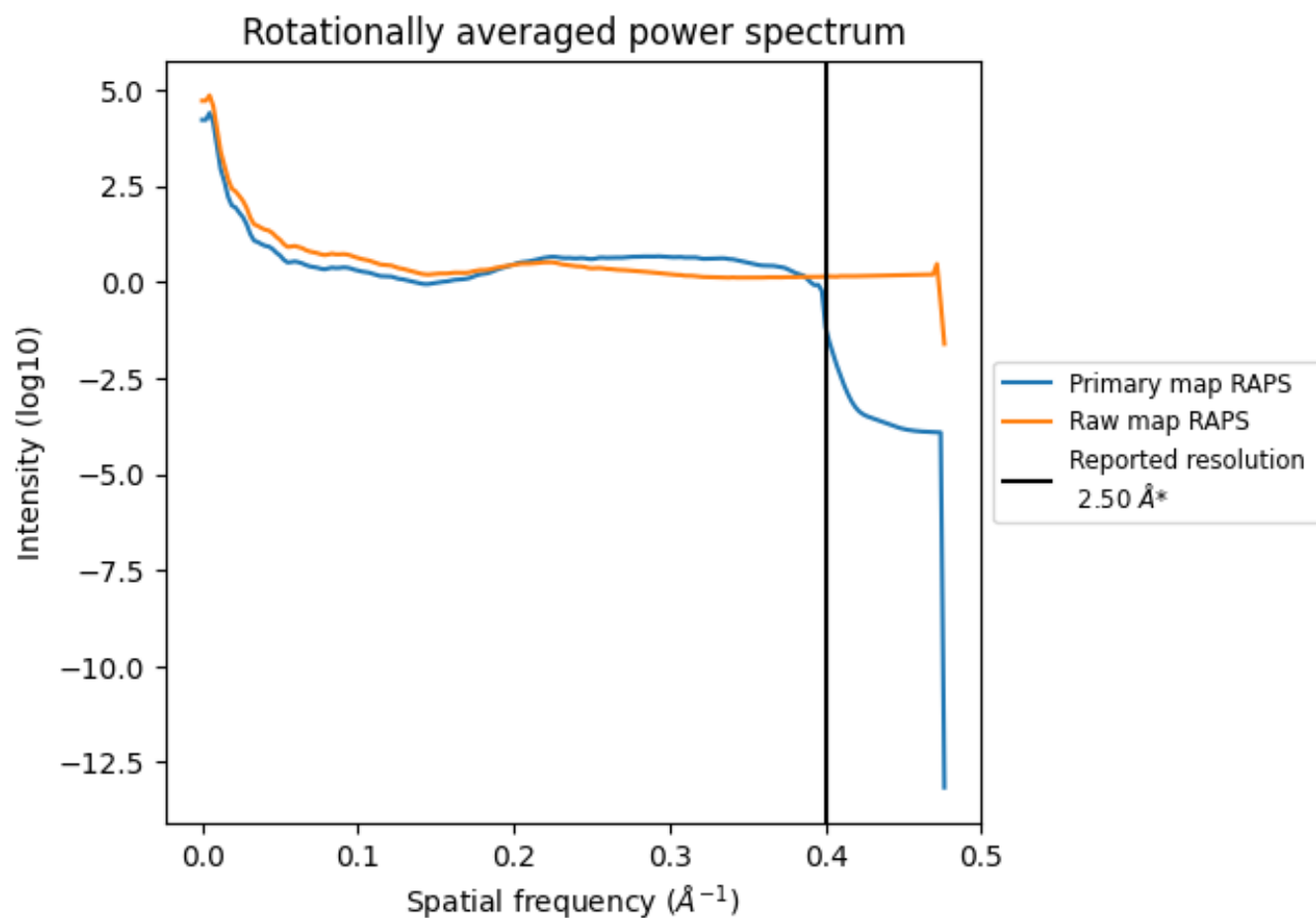


The volume at the recommended contour level is 104 nm<sup>3</sup>; this corresponds to an approximate mass of 94 kDa.

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 ⓘ

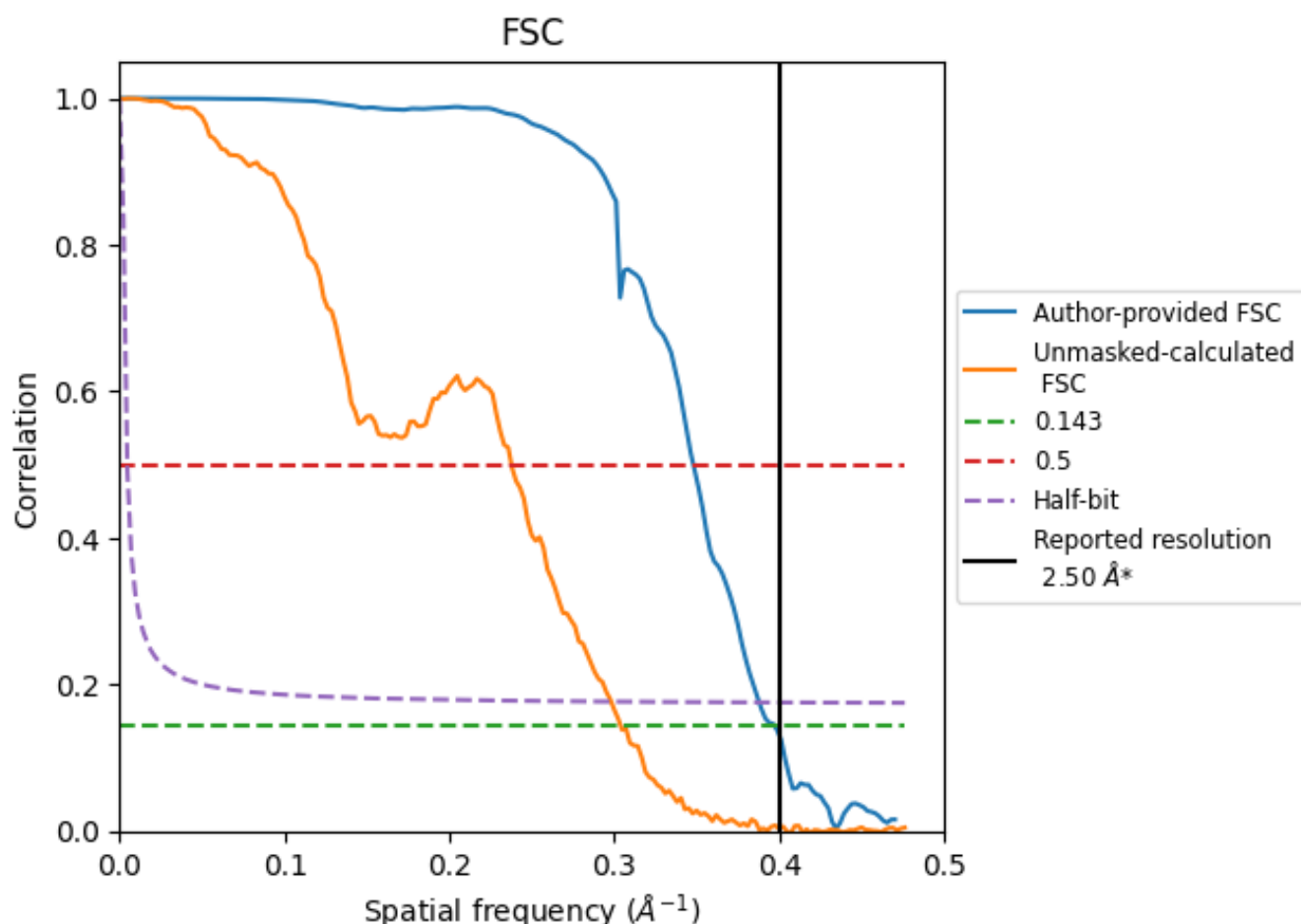


\*Reported resolution corresponds to spatial frequency of 0.400 Å<sup>-1</sup>

## 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 0.400  $\text{\AA}^{-1}$



## 8.2 Resolution estimates [i](#)

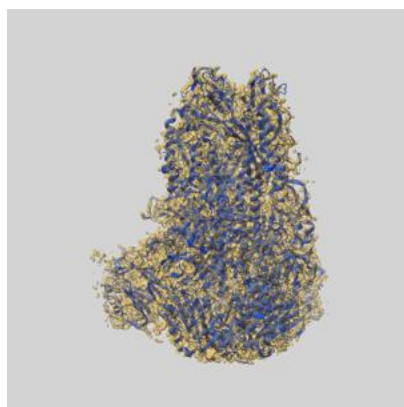
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.50	-	-
Author-provided FSC curve	2.52	2.87	2.58
Unmasked-calculated*	3.29	4.21	3.35

\*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 3.29 differs from the reported value 2.5 by more than 10 %

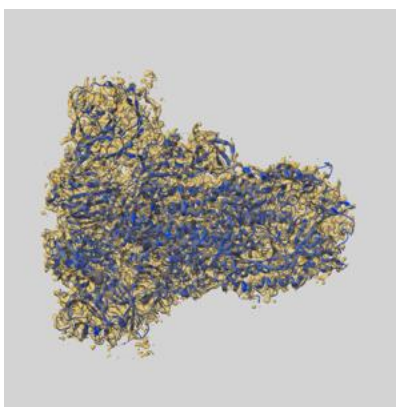
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-26378 and PDB model 7U6R. Per-residue inclusion information can be found in section [3](#) on page [12](#).

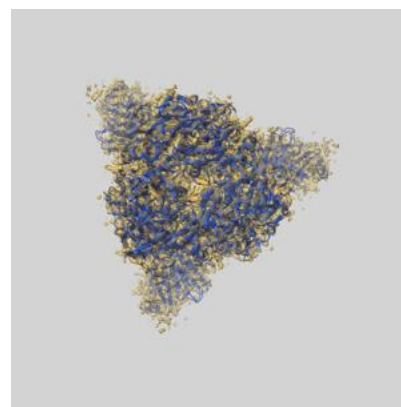
### 9.1 Map-model overlay [i](#)



X



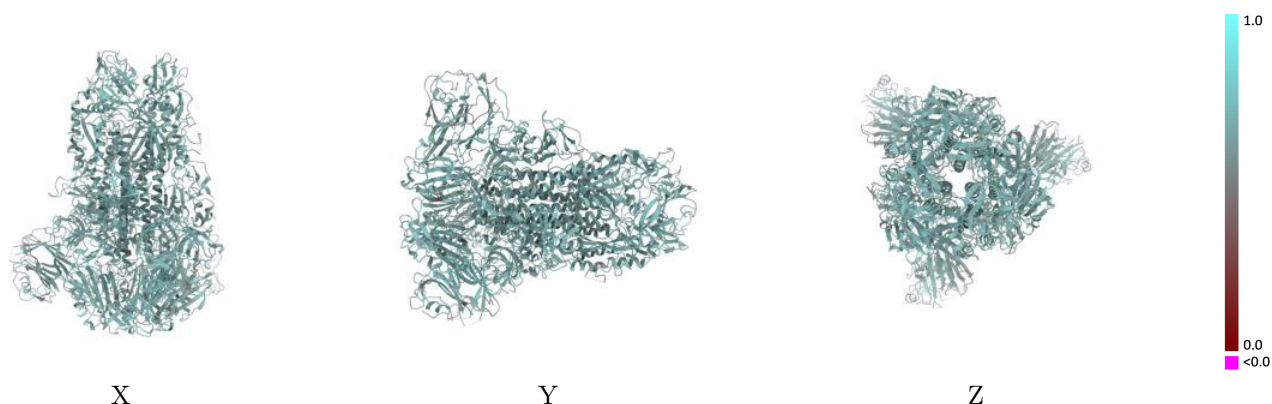
Y



Z

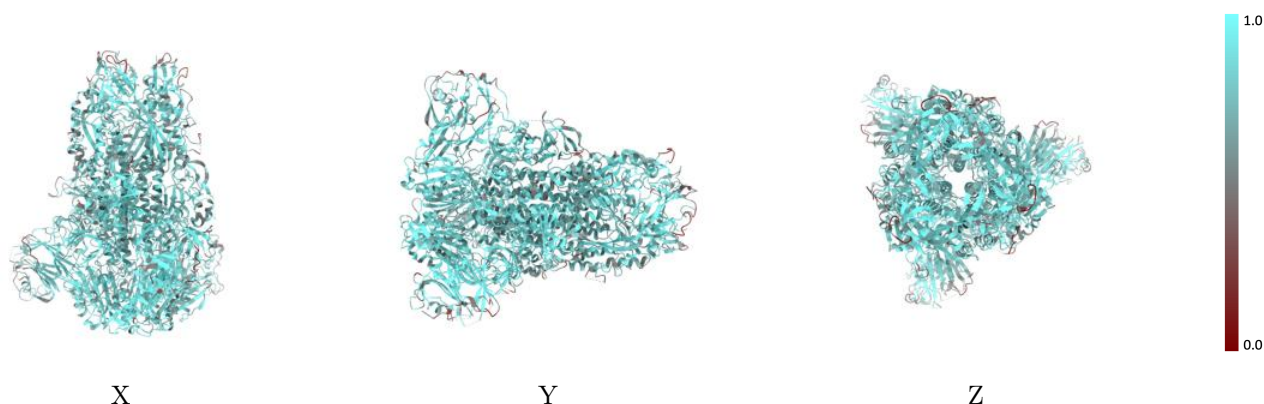
The images above show the 3D surface view of the map at the recommended contour level 1.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



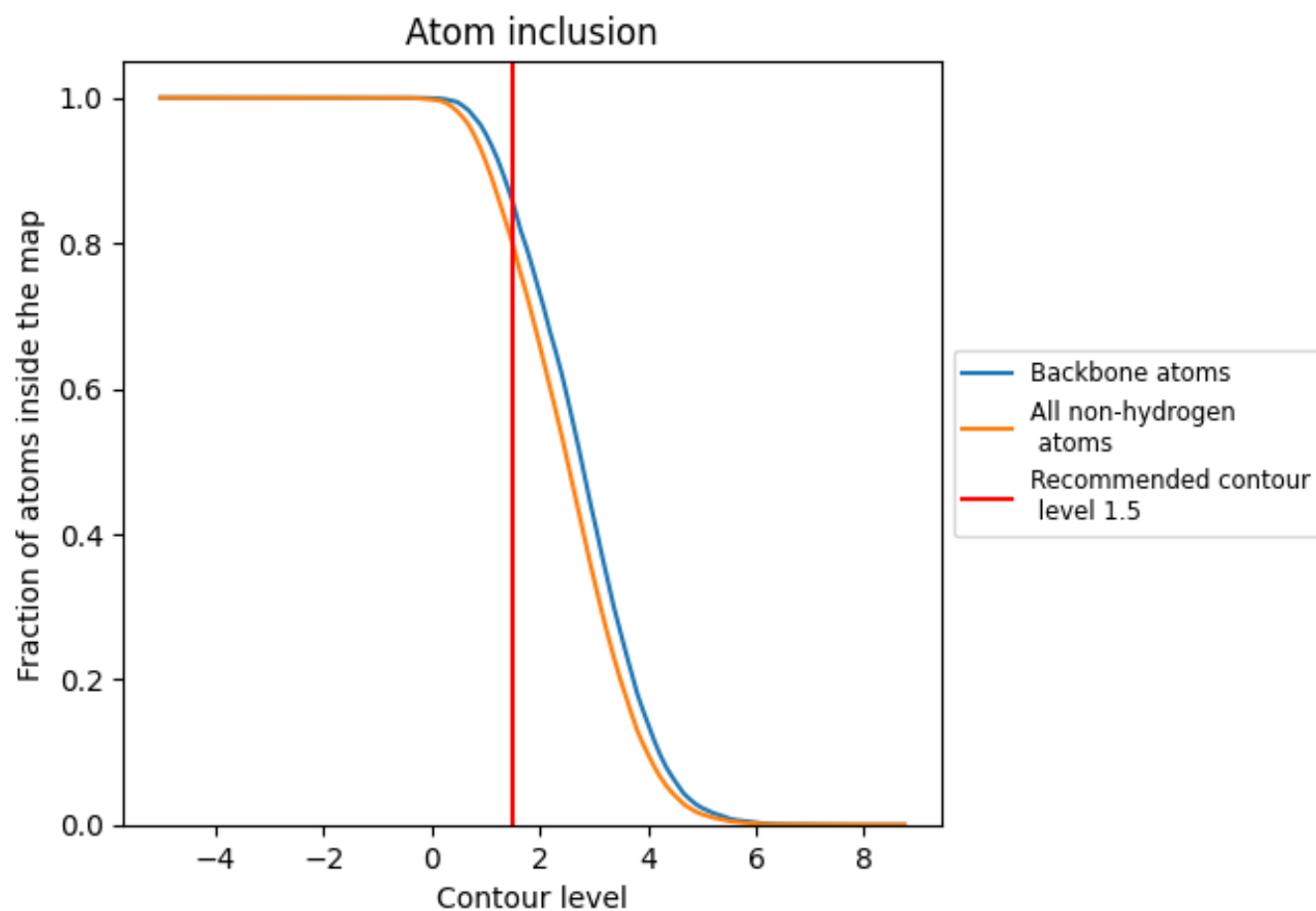
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.5).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 80% 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 (1.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7997	<div></div> 0.6300
A	<div></div> 0.8020	<div></div> 0.6310
B	<div></div> 0.8025	<div></div> 0.6300
C	<div></div> 0.8018	<div></div> 0.6310
D	<div></div> 0.4643	<div></div> 0.5520
E	<div></div> 0.4286	<div></div> 0.5590
F	<div></div> 0.3929	<div></div> 0.5400
G	<div></div> 0.4643	<div></div> 0.5500
H	<div></div> 0.4286	<div></div> 0.5500
I	<div></div> 0.4643	<div></div> 0.5480

1.0

0.0

<0.0