



# wwPDB EM Validation Summary Report ⓘ

Oct 13, 2024 – 03:23 am BST

PDB ID : 7PNM  
EMDB ID : EMD-13549  
Title : Human coronavirus OC43 spike glycoprotein ectodomain in complex with the 46C12 antibody Fab fragment  
Authors : Hurdiss, D.L.  
Deposited on : 2021-09-07  
Resolution : 3.70 Å(reported)  
Based on initial model : 6NZK

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.dev113  
Mogul : 1.8.4, CSD as541be (2020)  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

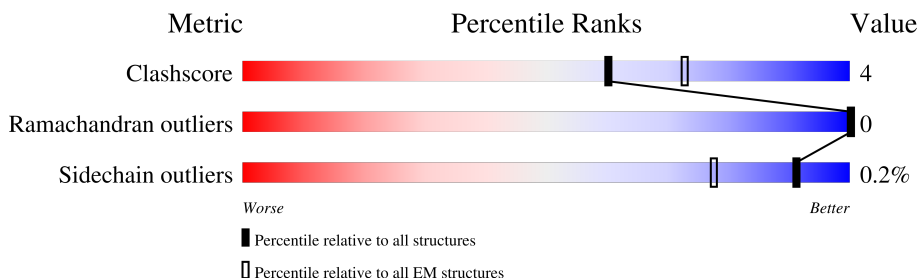
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	1322	<div> <div>17%</div> <div>79%</div> <div>10%</div> <div>11%</div> </div>
1	B	1322	<div> <div>17%</div> <div>80%</div> <div>9%</div> <div>11%</div> </div>
1	C	1322	<div> <div>17%</div> <div>79%</div> <div>10%</div> <div>11%</div> </div>
2	D	112	<div> <div>46%</div> <div>89%</div> <div>11%</div> </div>
2	E	112	<div> <div>43%</div> <div>88%</div> <div>12%</div> </div>
2	L	112	<div> <div>38%</div> <div>88%</div> <div>12%</div> </div>
3	G	121	<div> <div>45%</div> <div>82%</div> <div>18%</div> </div>
3	H	121	<div> <div>40%</div> <div>81%</div> <div>19%</div> </div>

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Mol	Chain	Length	Quality of chain
3	I	121	<div> <div>48%</div> <div>79%</div> <div>21%</div> </div>
4	F	2	<div> <div>50%</div> <div>100%</div> </div>
4	J	2	<div> <div>50%</div> <div>50%</div> </div>
4	K	2	<div> <div>50%</div> <div>100%</div> </div>
4	M	2	<div> <div>100%</div> <div>100%</div> </div>
4	N	2	<div> <div>50%</div> <div>100%</div> </div>
4	O	2	<div> <div>50%</div> <div>100%</div> </div>
4	P	2	<div> <div>50%</div> <div>100%</div> </div>
4	Q	2	<div> <div>100%</div> <div>100%</div> </div>
4	R	2	<div> <div>50%</div> <div>100%</div> </div>
4	S	2	<div> <div>100%</div> </div>
4	T	2	<div> <div>50%</div> <div>100%</div> </div>
4	U	2	<div> <div>100%</div> <div>100%</div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 33540 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 Spike glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1175	Total	C	N	O	S	0	0
			9150	5832	1506	1751	61		
1	B	1175	Total	C	N	O	S	0	0
			9150	5832	1506	1751	61		
1	C	1175	Total	C	N	O	S	0	0
			9150	5832	1506	1751	61		

There are 216 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-9	MET	-	initiating methionine	UNP Q696P8
A	-8	PRO	-	expression tag	UNP Q696P8
A	-7	MET	-	expression tag	UNP Q696P8
A	-6	GLY	-	expression tag	UNP Q696P8
A	-5	SER	-	expression tag	UNP Q696P8
A	-4	LEU	-	expression tag	UNP Q696P8
A	-3	GLN	-	expression tag	UNP Q696P8
A	-2	PRO	-	expression tag	UNP Q696P8
A	-1	LEU	-	expression tag	UNP Q696P8
A	0	ALA	-	expression tag	UNP Q696P8
A	1	THR	-	expression tag	UNP Q696P8
A	2	LEU	-	expression tag	UNP Q696P8
A	3	TYR	-	expression tag	UNP Q696P8
A	4	LEU	-	expression tag	UNP Q696P8
A	5	LEU	-	expression tag	UNP Q696P8
A	6	GLY	-	expression tag	UNP Q696P8
A	7	MET	-	expression tag	UNP Q696P8
A	8	LEU	-	expression tag	UNP Q696P8
A	9	VAL	-	expression tag	UNP Q696P8
A	10	ALA	-	expression tag	UNP Q696P8
A	11	SER	-	expression tag	UNP Q696P8
A	12	VAL	-	expression tag	UNP Q696P8
A	13	LEU	-	expression tag	UNP Q696P8
A	1266	LEU	-	expression tag	UNP Q696P8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1267	ILE	-	expression tag	UNP Q696P8
A	1268	LYS	-	expression tag	UNP Q696P8
A	1269	ARG	-	expression tag	UNP Q696P8
A	1270	MET	-	expression tag	UNP Q696P8
A	1271	LYS	-	expression tag	UNP Q696P8
A	1272	GLN	-	expression tag	UNP Q696P8
A	1273	ILE	-	expression tag	UNP Q696P8
A	1274	GLU	-	expression tag	UNP Q696P8
A	1275	ASP	-	expression tag	UNP Q696P8
A	1276	LYS	-	expression tag	UNP Q696P8
A	1277	ILE	-	expression tag	UNP Q696P8
A	1278	GLU	-	expression tag	UNP Q696P8
A	1279	GLU	-	expression tag	UNP Q696P8
A	1280	ILE	-	expression tag	UNP Q696P8
A	1281	GLU	-	expression tag	UNP Q696P8
A	1282	SER	-	expression tag	UNP Q696P8
A	1283	LYS	-	expression tag	UNP Q696P8
A	1284	GLN	-	expression tag	UNP Q696P8
A	1285	LYS	-	expression tag	UNP Q696P8
A	1286	LYS	-	expression tag	UNP Q696P8
A	1287	ILE	-	expression tag	UNP Q696P8
A	1288	GLU	-	expression tag	UNP Q696P8
A	1289	ASN	-	expression tag	UNP Q696P8
A	1290	GLU	-	expression tag	UNP Q696P8
A	1291	ILE	-	expression tag	UNP Q696P8
A	1292	ALA	-	expression tag	UNP Q696P8
A	1293	ARG	-	expression tag	UNP Q696P8
A	1294	ILE	-	expression tag	UNP Q696P8
A	1295	LYS	-	expression tag	UNP Q696P8
A	1296	LYS	-	expression tag	UNP Q696P8
A	1297	ILE	-	expression tag	UNP Q696P8
A	1298	LYS	-	expression tag	UNP Q696P8
A	1299	LEU	-	expression tag	UNP Q696P8
A	1300	VAL	-	expression tag	UNP Q696P8
A	1301	PRO	-	expression tag	UNP Q696P8
A	1302	ARG	-	expression tag	UNP Q696P8
A	1303	GLY	-	expression tag	UNP Q696P8
A	1304	SER	-	expression tag	UNP Q696P8
A	1305	LEU	-	expression tag	UNP Q696P8
A	1306	GLU	-	expression tag	UNP Q696P8
A	1307	TRP	-	expression tag	UNP Q696P8
A	1308	SER	-	expression tag	UNP Q696P8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1309	HIS	-	expression tag	UNP Q696P8
A	1310	PRO	-	expression tag	UNP Q696P8
A	1311	GLN	-	expression tag	UNP Q696P8
A	1312	PHE	-	expression tag	UNP Q696P8
A	1313	GLU	-	expression tag	UNP Q696P8
A	1314	LYS	-	expression tag	UNP Q696P8
B	-9	MET	-	initiating methionine	UNP Q696P8
B	-8	PRO	-	expression tag	UNP Q696P8
B	-7	MET	-	expression tag	UNP Q696P8
B	-6	GLY	-	expression tag	UNP Q696P8
B	-5	SER	-	expression tag	UNP Q696P8
B	-4	LEU	-	expression tag	UNP Q696P8
B	-3	GLN	-	expression tag	UNP Q696P8
B	-2	PRO	-	expression tag	UNP Q696P8
B	-1	LEU	-	expression tag	UNP Q696P8
B	0	ALA	-	expression tag	UNP Q696P8
B	1	THR	-	expression tag	UNP Q696P8
B	2	LEU	-	expression tag	UNP Q696P8
B	3	TYR	-	expression tag	UNP Q696P8
B	4	LEU	-	expression tag	UNP Q696P8
B	5	LEU	-	expression tag	UNP Q696P8
B	6	GLY	-	expression tag	UNP Q696P8
B	7	MET	-	expression tag	UNP Q696P8
B	8	LEU	-	expression tag	UNP Q696P8
B	9	VAL	-	expression tag	UNP Q696P8
B	10	ALA	-	expression tag	UNP Q696P8
B	11	SER	-	expression tag	UNP Q696P8
B	12	VAL	-	expression tag	UNP Q696P8
B	13	LEU	-	expression tag	UNP Q696P8
B	1266	LEU	-	expression tag	UNP Q696P8
B	1267	ILE	-	expression tag	UNP Q696P8
B	1268	LYS	-	expression tag	UNP Q696P8
B	1269	ARG	-	expression tag	UNP Q696P8
B	1270	MET	-	expression tag	UNP Q696P8
B	1271	LYS	-	expression tag	UNP Q696P8
B	1272	GLN	-	expression tag	UNP Q696P8
B	1273	ILE	-	expression tag	UNP Q696P8
B	1274	GLU	-	expression tag	UNP Q696P8
B	1275	ASP	-	expression tag	UNP Q696P8
B	1276	LYS	-	expression tag	UNP Q696P8
B	1277	ILE	-	expression tag	UNP Q696P8
B	1278	GLU	-	expression tag	UNP Q696P8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1279	GLU	-	expression tag	UNP Q696P8
B	1280	ILE	-	expression tag	UNP Q696P8
B	1281	GLU	-	expression tag	UNP Q696P8
B	1282	SER	-	expression tag	UNP Q696P8
B	1283	LYS	-	expression tag	UNP Q696P8
B	1284	GLN	-	expression tag	UNP Q696P8
B	1285	LYS	-	expression tag	UNP Q696P8
B	1286	LYS	-	expression tag	UNP Q696P8
B	1287	ILE	-	expression tag	UNP Q696P8
B	1288	GLU	-	expression tag	UNP Q696P8
B	1289	ASN	-	expression tag	UNP Q696P8
B	1290	GLU	-	expression tag	UNP Q696P8
B	1291	ILE	-	expression tag	UNP Q696P8
B	1292	ALA	-	expression tag	UNP Q696P8
B	1293	ARG	-	expression tag	UNP Q696P8
B	1294	ILE	-	expression tag	UNP Q696P8
B	1295	LYS	-	expression tag	UNP Q696P8
B	1296	LYS	-	expression tag	UNP Q696P8
B	1297	ILE	-	expression tag	UNP Q696P8
B	1298	LYS	-	expression tag	UNP Q696P8
B	1299	LEU	-	expression tag	UNP Q696P8
B	1300	VAL	-	expression tag	UNP Q696P8
B	1301	PRO	-	expression tag	UNP Q696P8
B	1302	ARG	-	expression tag	UNP Q696P8
B	1303	GLY	-	expression tag	UNP Q696P8
B	1304	SER	-	expression tag	UNP Q696P8
B	1305	LEU	-	expression tag	UNP Q696P8
B	1306	GLU	-	expression tag	UNP Q696P8
B	1307	TRP	-	expression tag	UNP Q696P8
B	1308	SER	-	expression tag	UNP Q696P8
B	1309	HIS	-	expression tag	UNP Q696P8
B	1310	PRO	-	expression tag	UNP Q696P8
B	1311	GLN	-	expression tag	UNP Q696P8
B	1312	PHE	-	expression tag	UNP Q696P8
B	1313	GLU	-	expression tag	UNP Q696P8
B	1314	LYS	-	expression tag	UNP Q696P8
C	-9	MET	-	initiating methionine	UNP Q696P8
C	-8	PRO	-	expression tag	UNP Q696P8
C	-7	MET	-	expression tag	UNP Q696P8
C	-6	GLY	-	expression tag	UNP Q696P8
C	-5	SER	-	expression tag	UNP Q696P8
C	-4	LEU	-	expression tag	UNP Q696P8

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-3	GLN	-	expression tag	UNP Q696P8
C	-2	PRO	-	expression tag	UNP Q696P8
C	-1	LEU	-	expression tag	UNP Q696P8
C	0	ALA	-	expression tag	UNP Q696P8
C	1	THR	-	expression tag	UNP Q696P8
C	2	LEU	-	expression tag	UNP Q696P8
C	3	TYR	-	expression tag	UNP Q696P8
C	4	LEU	-	expression tag	UNP Q696P8
C	5	LEU	-	expression tag	UNP Q696P8
C	6	GLY	-	expression tag	UNP Q696P8
C	7	MET	-	expression tag	UNP Q696P8
C	8	LEU	-	expression tag	UNP Q696P8
C	9	VAL	-	expression tag	UNP Q696P8
C	10	ALA	-	expression tag	UNP Q696P8
C	11	SER	-	expression tag	UNP Q696P8
C	12	VAL	-	expression tag	UNP Q696P8
C	13	LEU	-	expression tag	UNP Q696P8
C	1266	LEU	-	expression tag	UNP Q696P8
C	1267	ILE	-	expression tag	UNP Q696P8
C	1268	LYS	-	expression tag	UNP Q696P8
C	1269	ARG	-	expression tag	UNP Q696P8
C	1270	MET	-	expression tag	UNP Q696P8
C	1271	LYS	-	expression tag	UNP Q696P8
C	1272	GLN	-	expression tag	UNP Q696P8
C	1273	ILE	-	expression tag	UNP Q696P8
C	1274	GLU	-	expression tag	UNP Q696P8
C	1275	ASP	-	expression tag	UNP Q696P8
C	1276	LYS	-	expression tag	UNP Q696P8
C	1277	ILE	-	expression tag	UNP Q696P8
C	1278	GLU	-	expression tag	UNP Q696P8
C	1279	GLU	-	expression tag	UNP Q696P8
C	1280	ILE	-	expression tag	UNP Q696P8
C	1281	GLU	-	expression tag	UNP Q696P8
C	1282	SER	-	expression tag	UNP Q696P8
C	1283	LYS	-	expression tag	UNP Q696P8
C	1284	GLN	-	expression tag	UNP Q696P8
C	1285	LYS	-	expression tag	UNP Q696P8
C	1286	LYS	-	expression tag	UNP Q696P8
C	1287	ILE	-	expression tag	UNP Q696P8
C	1288	GLU	-	expression tag	UNP Q696P8
C	1289	ASN	-	expression tag	UNP Q696P8
C	1290	GLU	-	expression tag	UNP Q696P8

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1291	ILE	-	expression tag	UNP Q696P8
C	1292	ALA	-	expression tag	UNP Q696P8
C	1293	ARG	-	expression tag	UNP Q696P8
C	1294	ILE	-	expression tag	UNP Q696P8
C	1295	LYS	-	expression tag	UNP Q696P8
C	1296	LYS	-	expression tag	UNP Q696P8
C	1297	ILE	-	expression tag	UNP Q696P8
C	1298	LYS	-	expression tag	UNP Q696P8
C	1299	LEU	-	expression tag	UNP Q696P8
C	1300	VAL	-	expression tag	UNP Q696P8
C	1301	PRO	-	expression tag	UNP Q696P8
C	1302	ARG	-	expression tag	UNP Q696P8
C	1303	GLY	-	expression tag	UNP Q696P8
C	1304	SER	-	expression tag	UNP Q696P8
C	1305	LEU	-	expression tag	UNP Q696P8
C	1306	GLU	-	expression tag	UNP Q696P8
C	1307	TRP	-	expression tag	UNP Q696P8
C	1308	SER	-	expression tag	UNP Q696P8
C	1309	HIS	-	expression tag	UNP Q696P8
C	1310	PRO	-	expression tag	UNP Q696P8
C	1311	GLN	-	expression tag	UNP Q696P8
C	1312	PHE	-	expression tag	UNP Q696P8
C	1313	GLU	-	expression tag	UNP Q696P8
C	1314	LYS	-	expression tag	UNP Q696P8

- Molecule 2 is a protein called 46C12 antibody light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L	112	Total	C	N	O	S	0	0
			847	534	141	168	4		
2	D	112	Total	C	N	O	S	0	0
			847	534	141	168	4		
2	E	112	Total	C	N	O	S	0	0
			847	534	141	168	4		

- Molecule 3 is a protein called 46C12 antibody heavy chain.

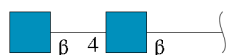
Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	121	Total	C	N	O	S	0	0
			959	607	166	182	4		
3	G	121	Total	C	N	O	S	0	0
			959	607	166	182	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	I	121	Total	C	N	O	S	0	0
			959	607	166	182	4		

- Molecule 4 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
4	F	2	Total	C	N	O	0	0
			28	16	2	10		
4	J	2	Total	C	N	O	0	0
			28	16	2	10		
4	K	2	Total	C	N	O	0	0
			28	16	2	10		
4	M	2	Total	C	N	O	0	0
			28	16	2	10		
4	N	2	Total	C	N	O	0	0
			28	16	2	10		
4	O	2	Total	C	N	O	0	0
			28	16	2	10		
4	P	2	Total	C	N	O	0	0
			28	16	2	10		
4	Q	2	Total	C	N	O	0	0
			28	16	2	10		
4	R	2	Total	C	N	O	0	0
			28	16	2	10		
4	S	2	Total	C	N	O	0	0
			28	16	2	10		
4	T	2	Total	C	N	O	0	0
			28	16	2	10		
4	U	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 5 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
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	

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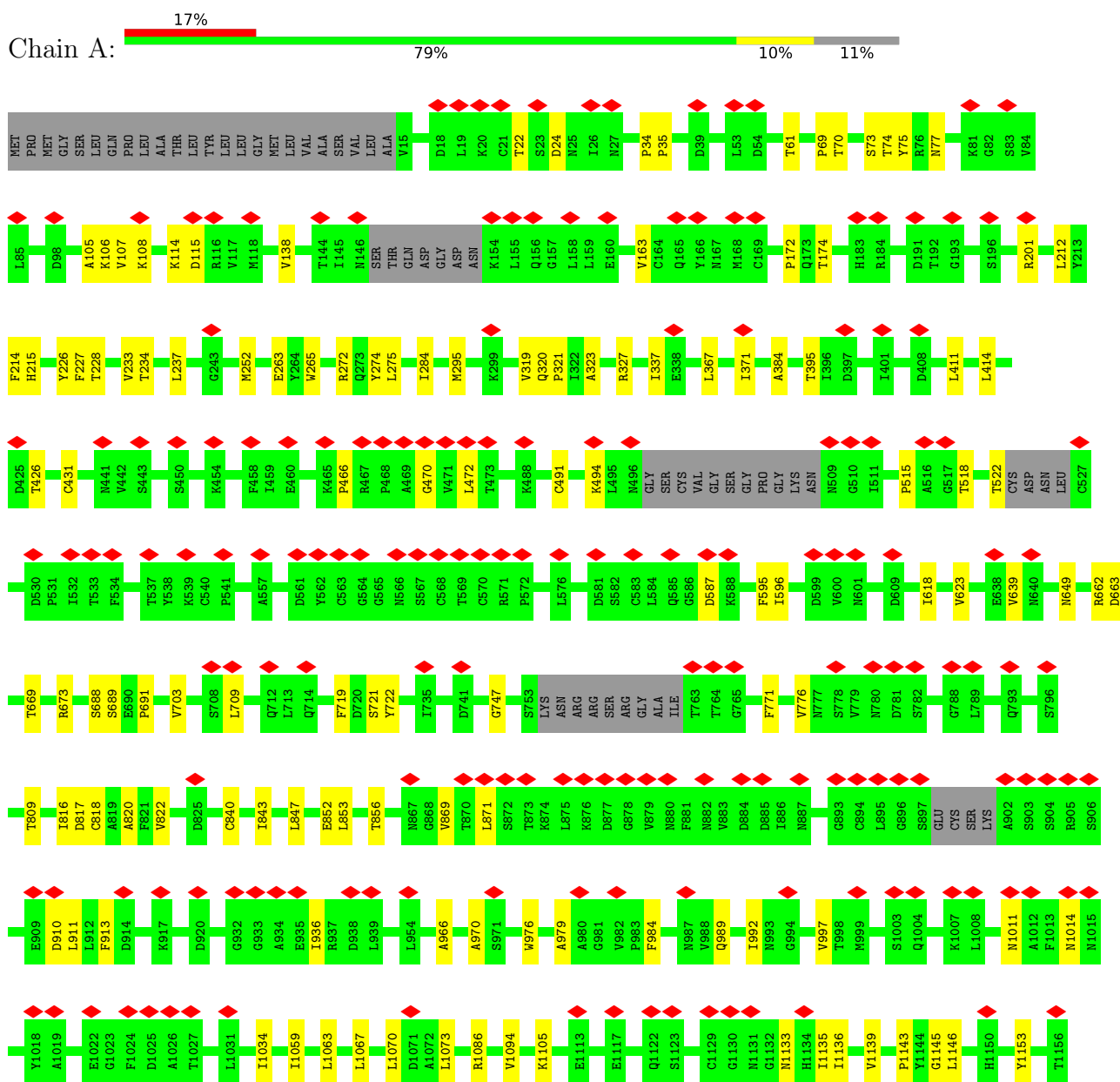
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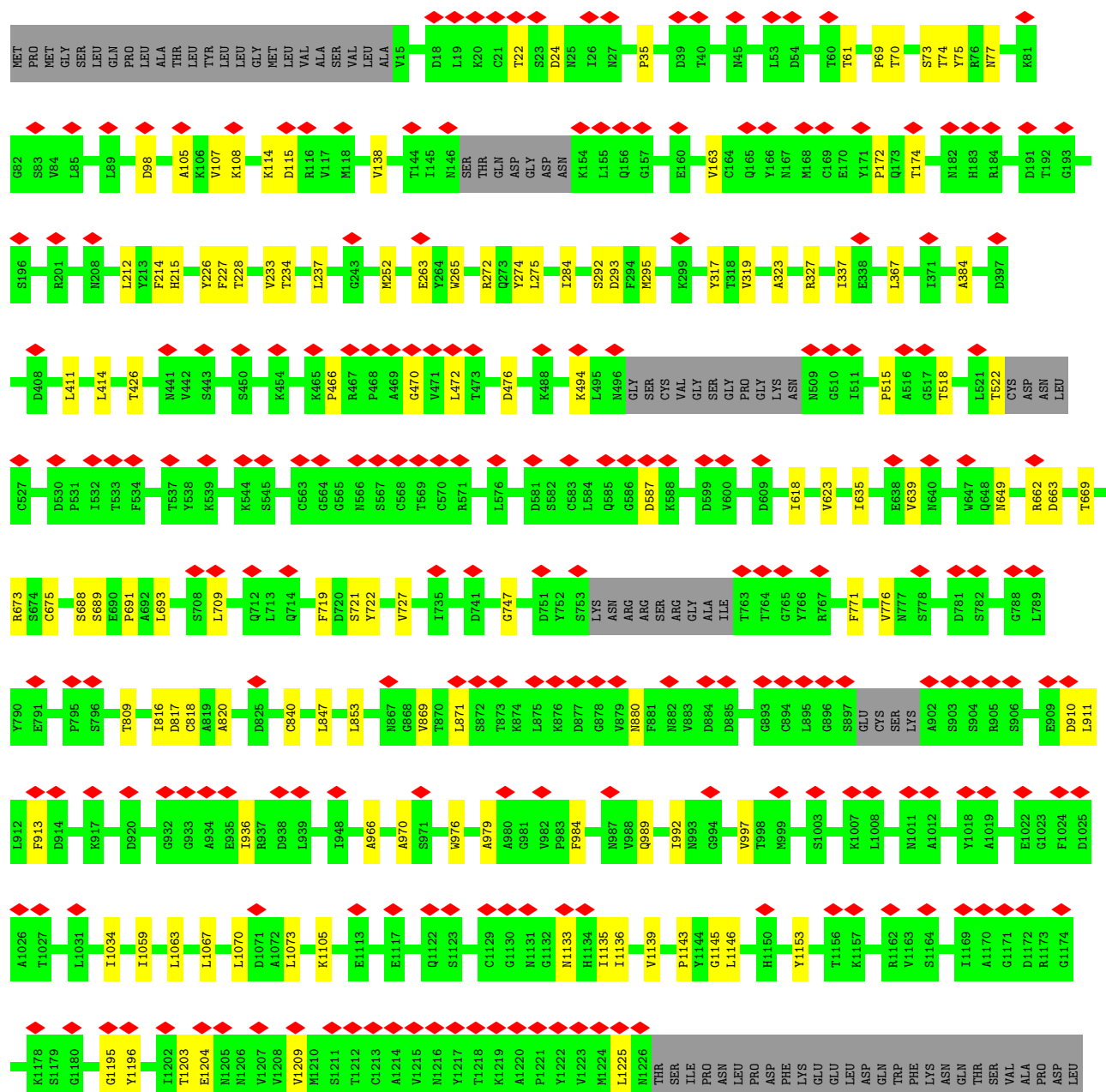
Mol	Chain	Residues	Atoms				AltConf
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	C	1	Total	C	N	O	0
			14	8	1	5	
5	C	1	Total	C	N	O	0
			14	8	1	5	
5	C	1	Total	C	N	O	0
			14	8	1	5	
5	C	1	Total	C	N	O	0
			14	8	1	5	
5	C	1	Total	C	N	O	0
			14	8	1	5	
5	C	1	Total	C	N	O	0
			14	8	1	5	

### 3 Residue-property plots

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

#### • Molecule 1: Spike glycoprotein

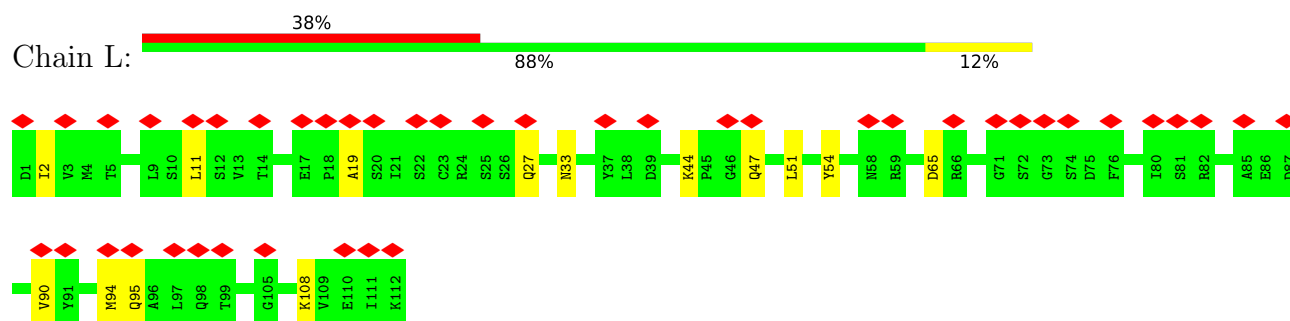




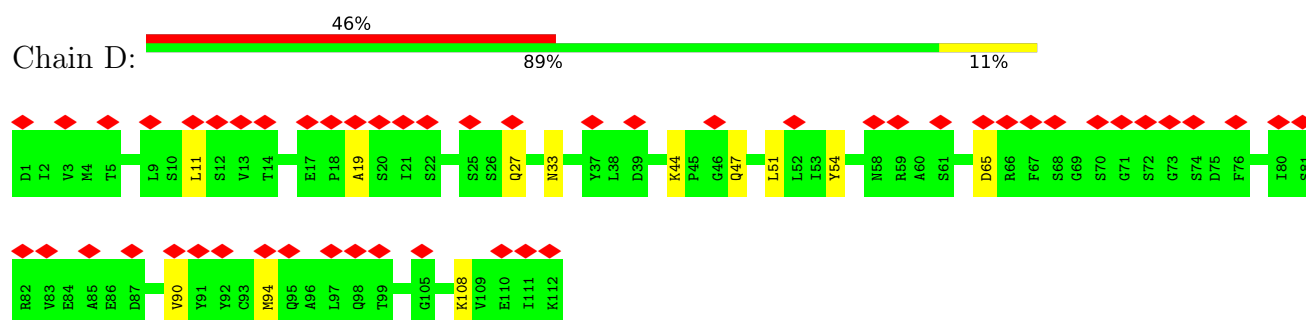




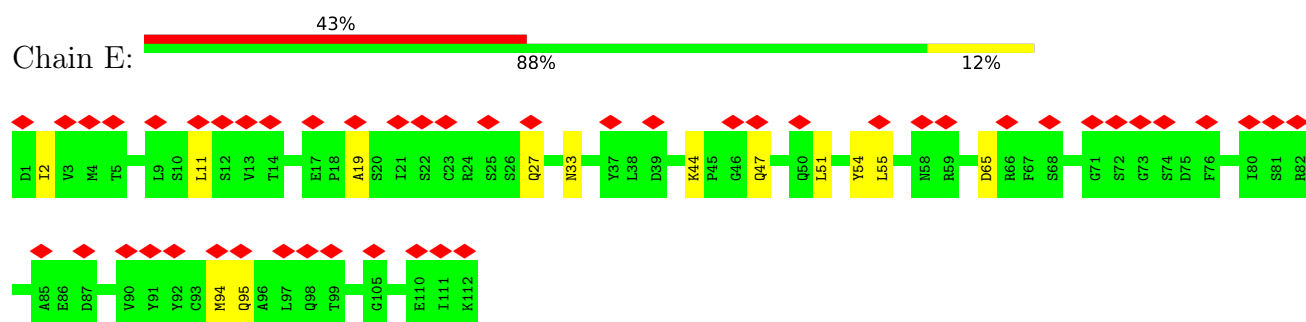
- Molecule 2: 46C12 antibody light chain



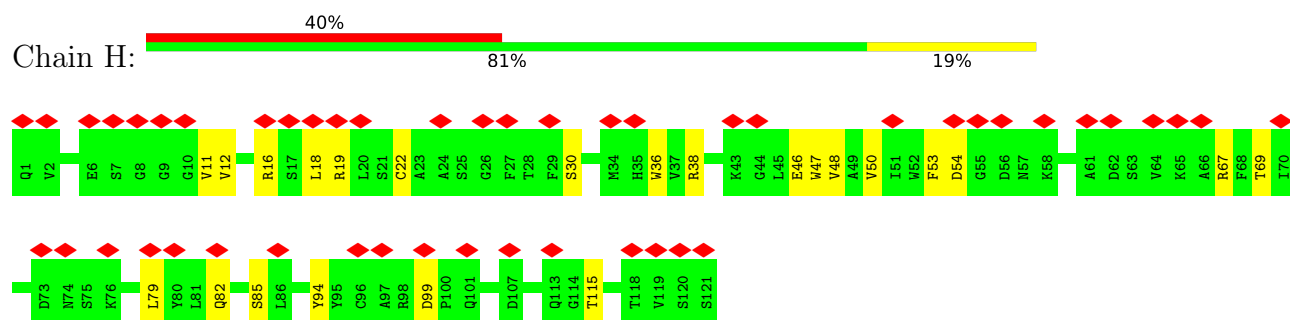
- Molecule 2: 46C12 antibody light chain



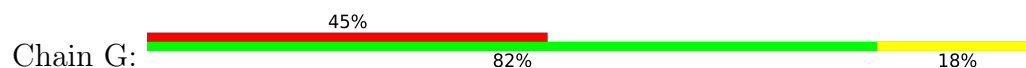
- Molecule 2: 46C12 antibody light chain

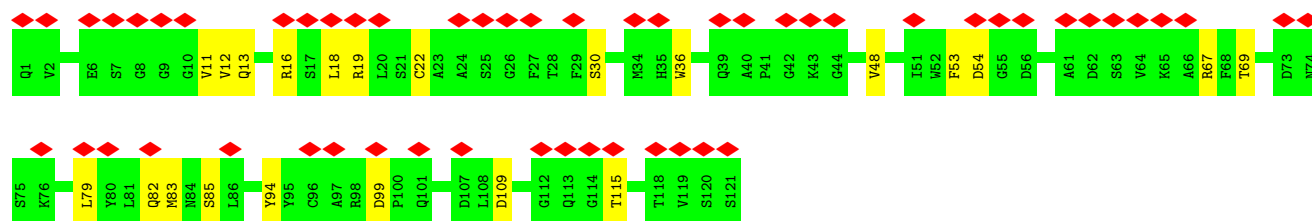


- Molecule 3: 46C12 antibody heavy chain

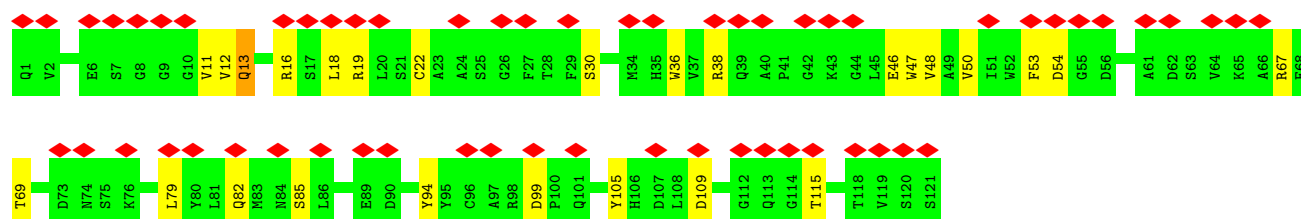
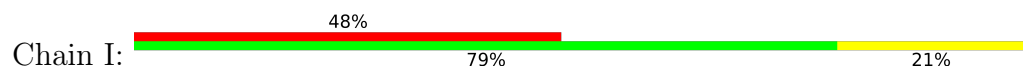


- Molecule 3: 46C12 antibody heavy chain





- Molecule 3: 46C12 antibody heavy chain



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



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



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



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





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



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



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



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



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



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

Chain S:  100%

NAG1  
NAG2

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

Chain T:  50%  
 100%

NAG1  
NAG2

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

Chain U:  100%  
 100%

NAG1  
NAG2

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	76638	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	52	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	1.980	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.035	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	340.80002, 340.80002, 340.80002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.065, 1.065, 1.065	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	0.27	0/9359	0.54	1/12744 (0.0%)
1	B	0.27	0/9359	0.54	1/12744 (0.0%)
1	C	0.27	0/9359	0.54	1/12744 (0.0%)
2	D	0.26	0/865	0.54	0/1172
2	E	0.26	0/865	0.54	0/1172
2	L	0.26	0/865	0.54	0/1172
3	G	0.25	0/984	0.55	0/1339
3	H	0.25	0/984	0.55	0/1339
3	I	0.25	0/984	0.54	0/1339
All	All	0.27	0/33624	0.54	3/45765 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	911	LEU	CA-CB-CG	5.88	128.82	115.30
1	B	911	LEU	CA-CB-CG	5.81	128.66	115.30
1	C	911	LEU	CA-CB-CG	5.81	128.66	115.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	9150	0	8851	81	0
1	B	9150	0	8851	75	0
1	C	9150	0	8851	78	0
2	D	847	0	837	7	0
2	E	847	0	837	8	0
2	L	847	0	837	8	0
3	G	959	0	911	15	0
3	H	959	0	911	15	0
3	I	959	0	911	18	0
4	F	28	0	25	0	0
4	J	28	0	25	1	0
4	K	28	0	25	0	0
4	M	28	0	25	0	0
4	N	28	0	25	0	0
4	O	28	0	25	0	0
4	P	28	0	25	0	0
4	Q	28	0	25	0	0
4	R	28	0	25	0	0
4	S	28	0	25	0	0
4	T	28	0	25	0	0
4	U	28	0	25	0	0
5	A	112	0	104	1	0
5	B	112	0	104	1	0
5	C	112	0	104	1	0
All	All	33540	0	32409	285	0

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

The worst 5 of 285 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:215:HIS:HB2	1:A:226:TYR:HB2	1.80	0.63
1:B:1133:ASN:HB3	1:B:1153:TYR:HB3	1.81	0.62
1:C:1133:ASN:HB3	1:C:1153:TYR:HB3	1.81	0.62
1:A:1133:ASN:HB3	1:A:1153:TYR:HB3	1.81	0.61
1:B:215:HIS:HB2	1:B:226:TYR:HB2	1.82	0.61

There are no symmetry-related clashes.



## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	1163/1322 (88%)	1119 (96%)	44 (4%)	0	100	100
1	B	1163/1322 (88%)	1124 (97%)	39 (3%)	0	100	100
1	C	1163/1322 (88%)	1124 (97%)	39 (3%)	0	100	100
2	D	110/112 (98%)	102 (93%)	8 (7%)	0	100	100
2	E	110/112 (98%)	103 (94%)	7 (6%)	0	100	100
2	L	110/112 (98%)	102 (93%)	8 (7%)	0	100	100
3	G	119/121 (98%)	111 (93%)	8 (7%)	0	100	100
3	H	119/121 (98%)	112 (94%)	7 (6%)	0	100	100
3	I	119/121 (98%)	112 (94%)	7 (6%)	0	100	100
All	All	4176/4665 (90%)	4009 (96%)	167 (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	1022/1154 (89%)	1022 (100%)	0	100	100
1	B	1022/1154 (89%)	1022 (100%)	0	100	100
1	C	1022/1154 (89%)	1020 (100%)	2 (0%)	92	96
2	D	96/96 (100%)	95 (99%)	1 (1%)	73	82
2	E	96/96 (100%)	95 (99%)	1 (1%)	73	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	L	96/96 (100%)	95 (99%)	1 (1%)	73	82
3	G	102/102 (100%)	101 (99%)	1 (1%)	73	82
3	H	102/102 (100%)	102 (100%)	0	100	100
3	I	102/102 (100%)	101 (99%)	1 (1%)	73	82
All	All	3660/4056 (90%)	3653 (100%)	7 (0%)	91	96

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	453	ASN
1	C	1051	GLN
3	I	13	GLN
2	E	27	GLN
3	G	83	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	453	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 ⓘ

24 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	$\# Z  > 2$
4	NAG	F	1	4,1	14,14,15	0.25	0	17,19,21	0.43	0
4	NAG	F	2	4	14,14,15	0.34	0	17,19,21	0.48	0
4	NAG	J	1	4,1	14,14,15	0.25	0	17,19,21	0.47	0
4	NAG	J	2	4	14,14,15	0.35	0	17,19,21	0.45	0
4	NAG	K	1	4,1	14,14,15	0.25	0	17,19,21	0.46	0
4	NAG	K	2	4	14,14,15	0.32	0	17,19,21	0.47	0
4	NAG	M	1	4,1	14,14,15	0.32	0	17,19,21	0.50	0
4	NAG	M	2	4	14,14,15	0.39	0	17,19,21	0.51	0
4	NAG	N	1	4,1	14,14,15	0.24	0	17,19,21	0.43	0
4	NAG	N	2	4	14,14,15	0.34	0	17,19,21	0.48	0
4	NAG	O	1	4,1	14,14,15	0.26	0	17,19,21	0.46	0
4	NAG	O	2	4	14,14,15	0.35	0	17,19,21	0.46	0
4	NAG	P	1	4,1	14,14,15	0.27	0	17,19,21	0.47	0
4	NAG	P	2	4	14,14,15	0.33	0	17,19,21	0.48	0
4	NAG	Q	1	4,1	14,14,15	0.31	0	17,19,21	0.50	0
4	NAG	Q	2	4	14,14,15	0.41	0	17,19,21	0.51	0
4	NAG	R	1	4,1	14,14,15	0.26	0	17,19,21	0.43	0
4	NAG	R	2	4	14,14,15	0.33	0	17,19,21	0.48	0
4	NAG	S	1	4,1	14,14,15	0.25	0	17,19,21	0.47	0
4	NAG	S	2	4	14,14,15	0.38	0	17,19,21	0.46	0
4	NAG	T	1	4,1	14,14,15	0.25	0	17,19,21	0.45	0
4	NAG	T	2	4	14,14,15	0.31	0	17,19,21	0.48	0
4	NAG	U	1	4,1	14,14,15	0.30	0	17,19,21	0.51	0
4	NAG	U	2	4	14,14,15	0.42	0	17,19,21	0.50	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
4	NAG	F	1	4,1	-	1/6/23/26	0/1/1/1
4	NAG	F	2	4	-	2/6/23/26	0/1/1/1
4	NAG	J	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	J	2	4	-	2/6/23/26	0/1/1/1
4	NAG	K	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	K	2	4	-	2/6/23/26	0/1/1/1
4	NAG	M	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	M	2	4	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	N	1	4,1	-	1/6/23/26	0/1/1/1
4	NAG	N	2	4	-	2/6/23/26	0/1/1/1
4	NAG	O	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	O	2	4	-	2/6/23/26	0/1/1/1
4	NAG	P	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	P	2	4	-	2/6/23/26	0/1/1/1
4	NAG	Q	1	4,1	-	1/6/23/26	0/1/1/1
4	NAG	Q	2	4	-	1/6/23/26	0/1/1/1
4	NAG	R	1	4,1	-	1/6/23/26	0/1/1/1
4	NAG	R	2	4	-	2/6/23/26	0/1/1/1
4	NAG	S	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	S	2	4	-	2/6/23/26	0/1/1/1
4	NAG	T	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	T	2	4	-	2/6/23/26	0/1/1/1
4	NAG	U	1	4,1	-	1/6/23/26	0/1/1/1
4	NAG	U	2	4	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 33 torsion outliers are listed below:

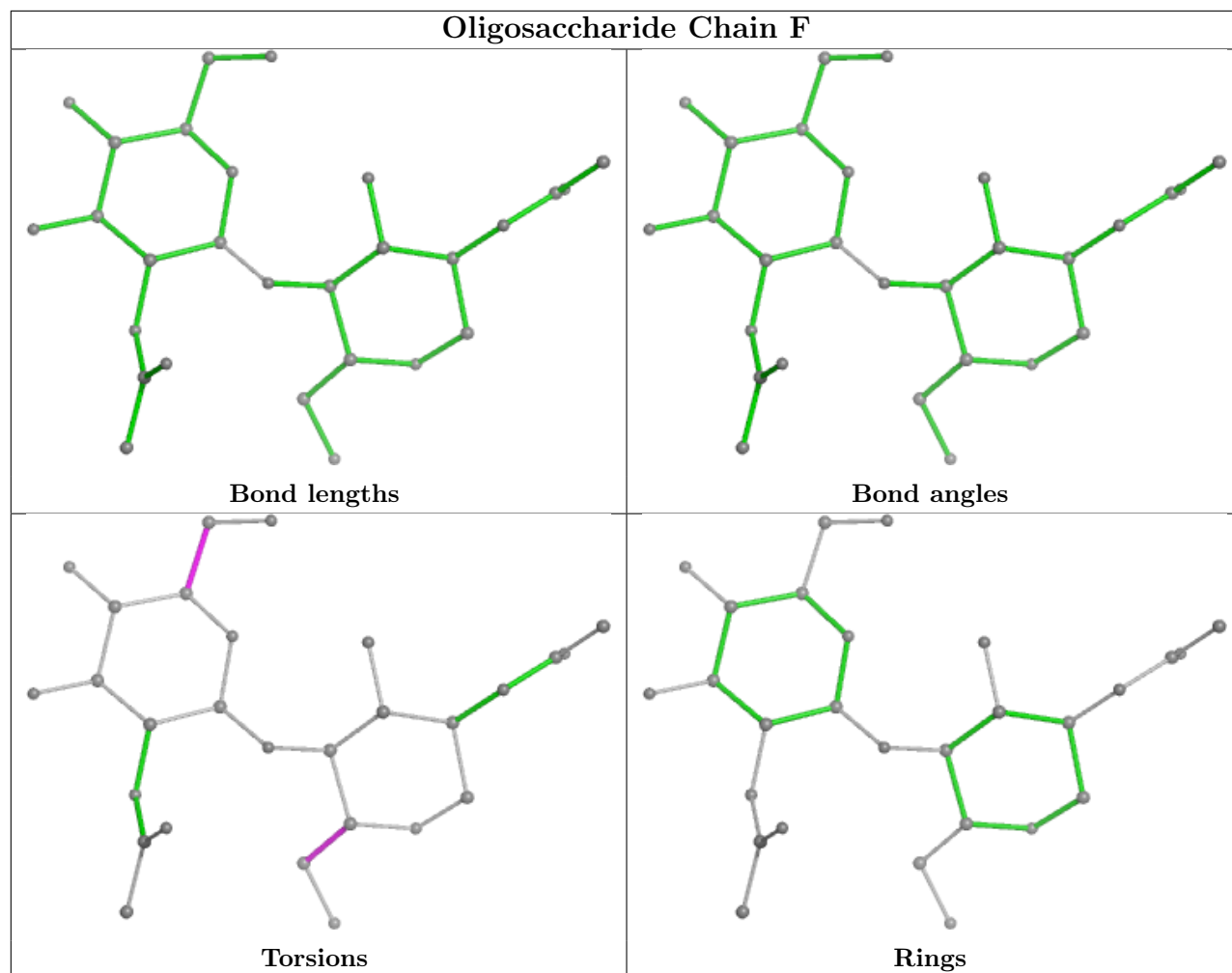
Mol	Chain	Res	Type	Atoms
4	T	1	NAG	O5-C5-C6-O6
4	F	2	NAG	O5-C5-C6-O6
4	R	2	NAG	O5-C5-C6-O6
4	N	2	NAG	O5-C5-C6-O6
4	K	1	NAG	O5-C5-C6-O6

There are no ring outliers.

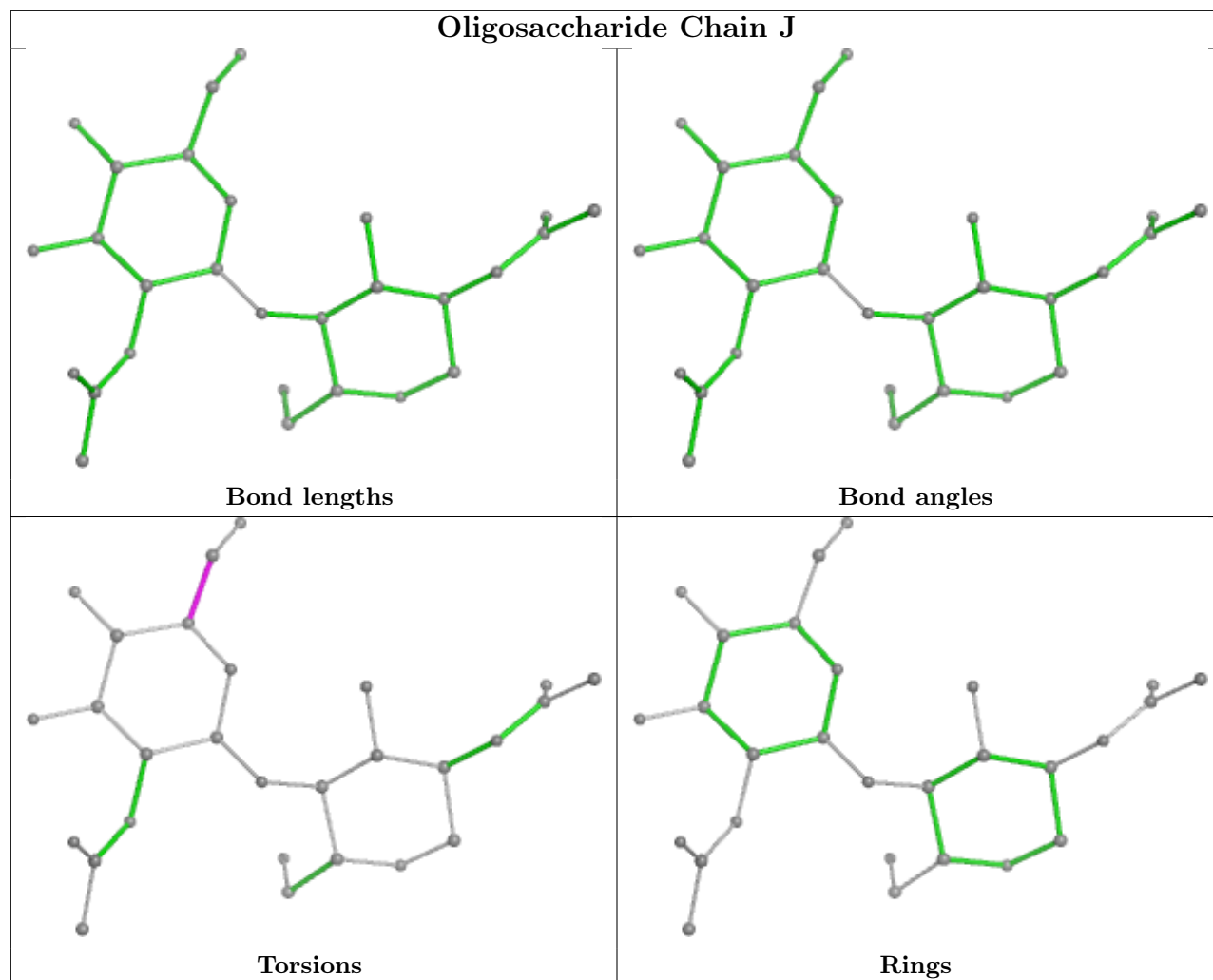
1 monomer is involved in 1 short contact:

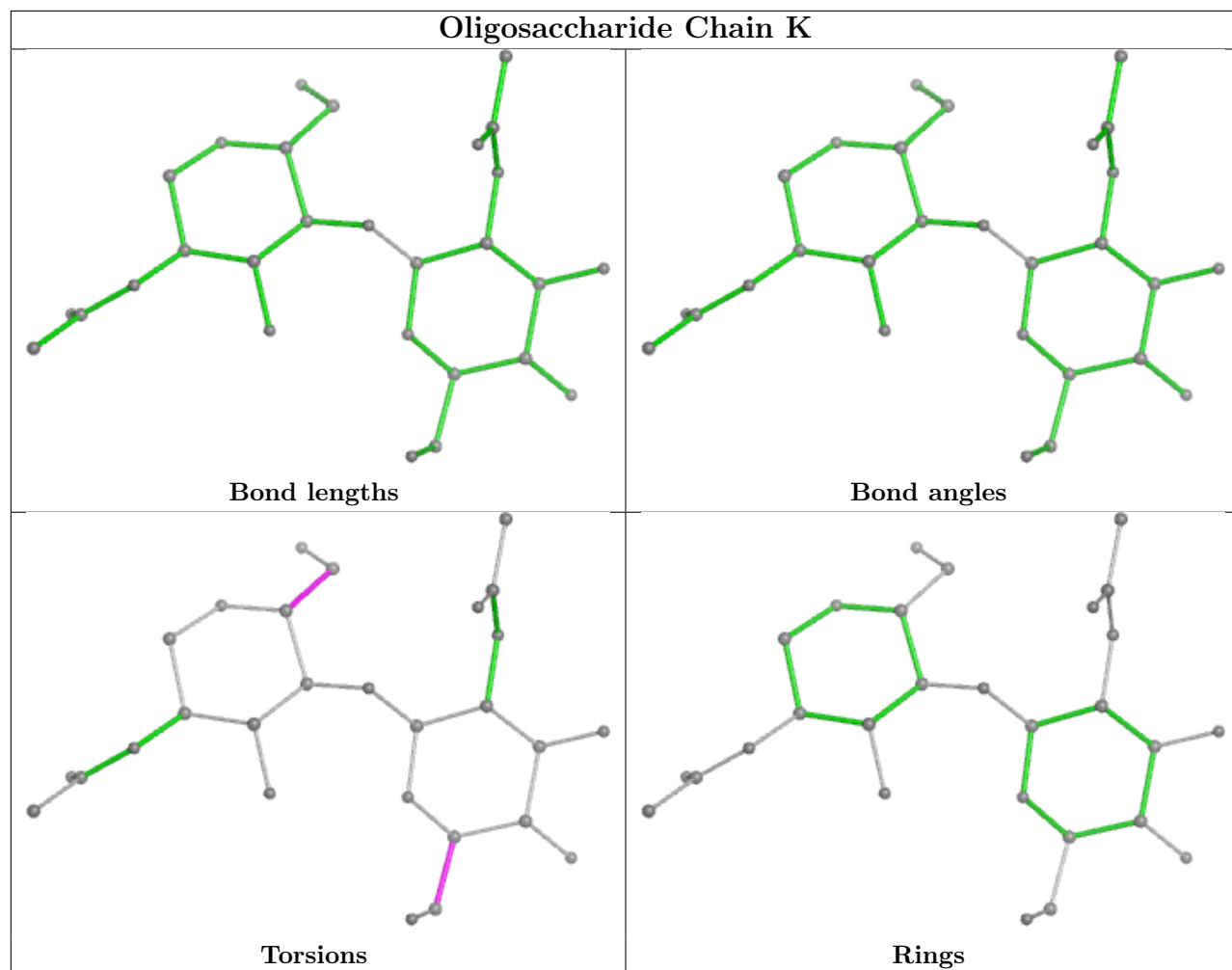
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	J	1	NAG	1	0

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

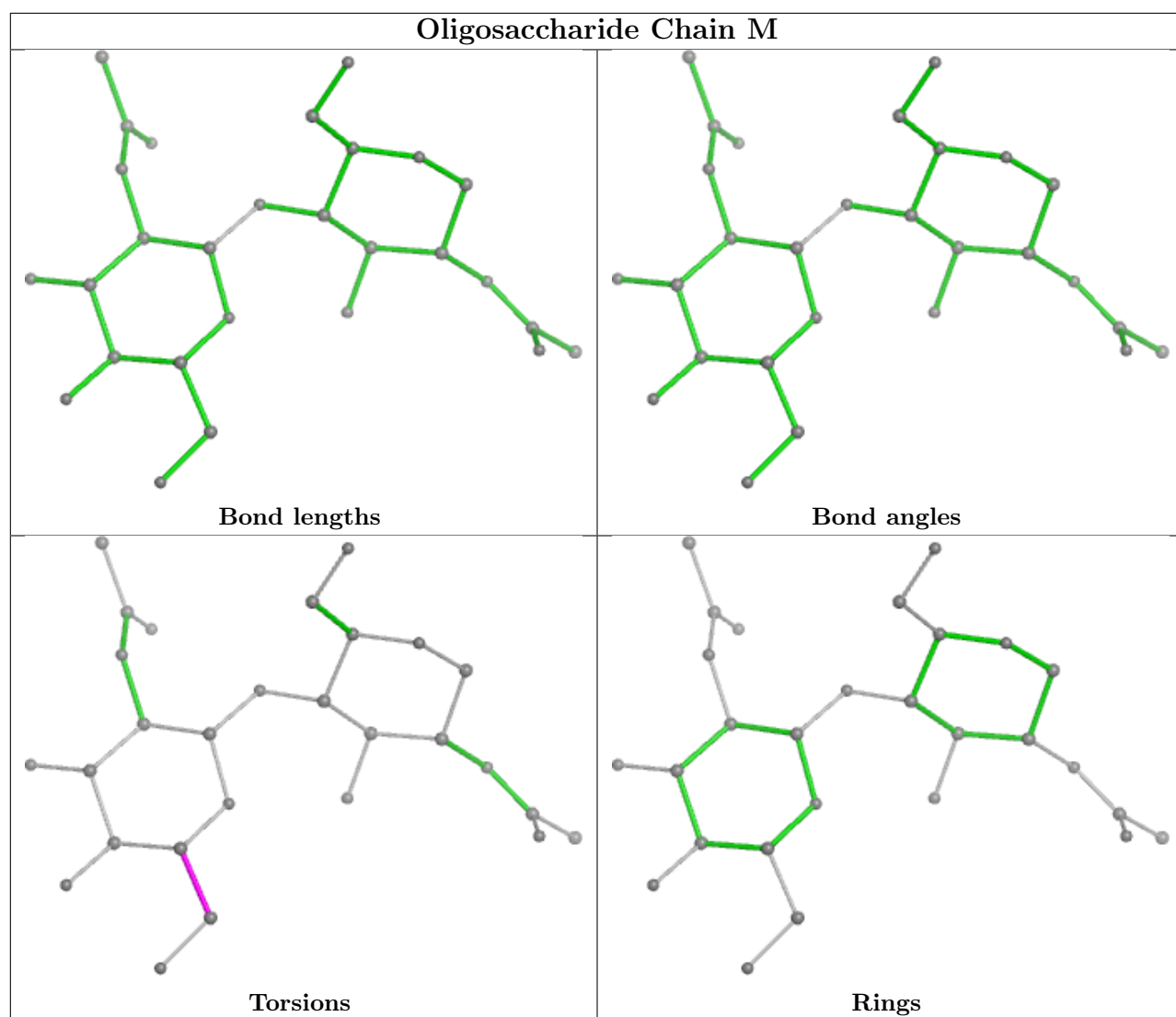


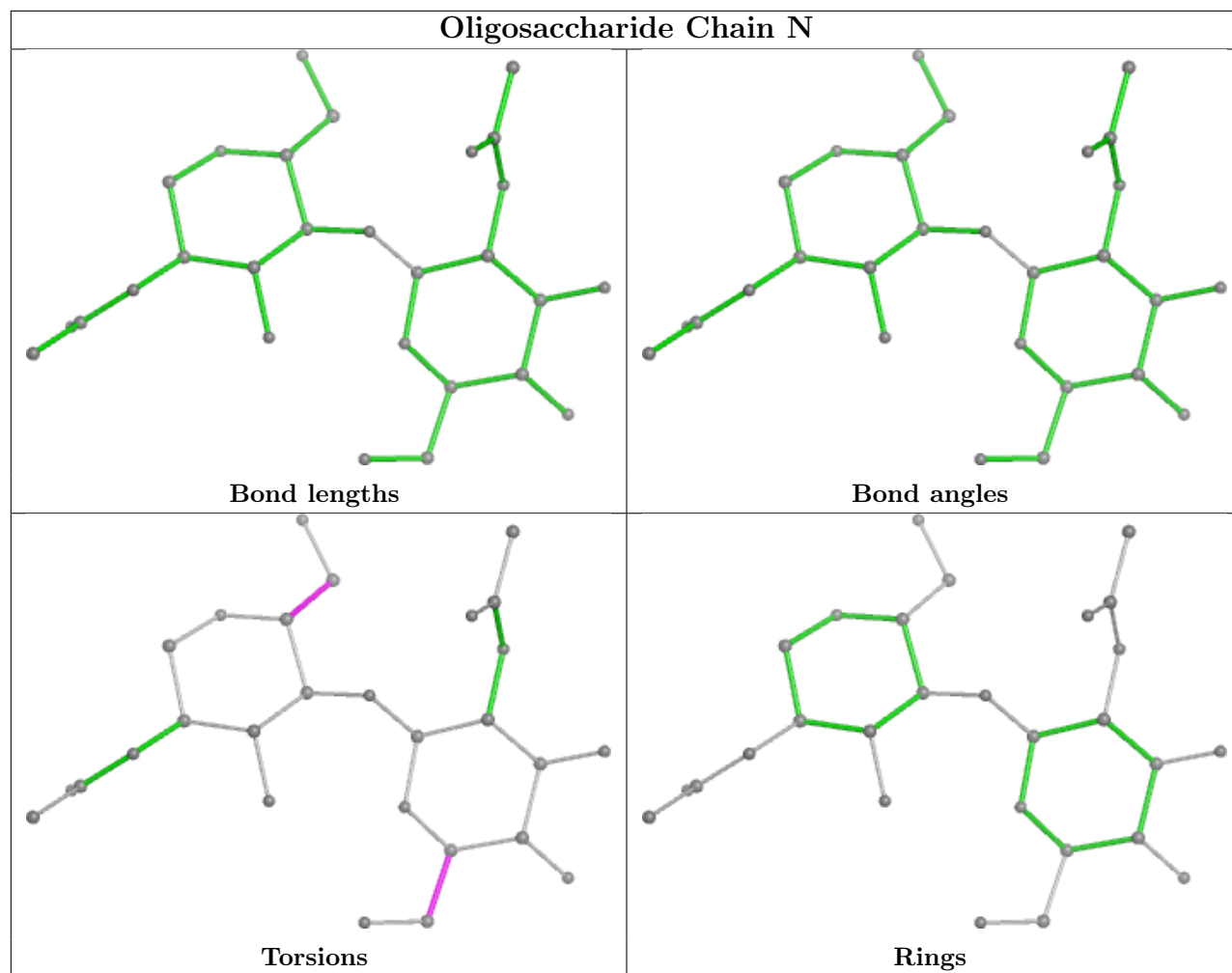
## Oligosaccharide Chain J

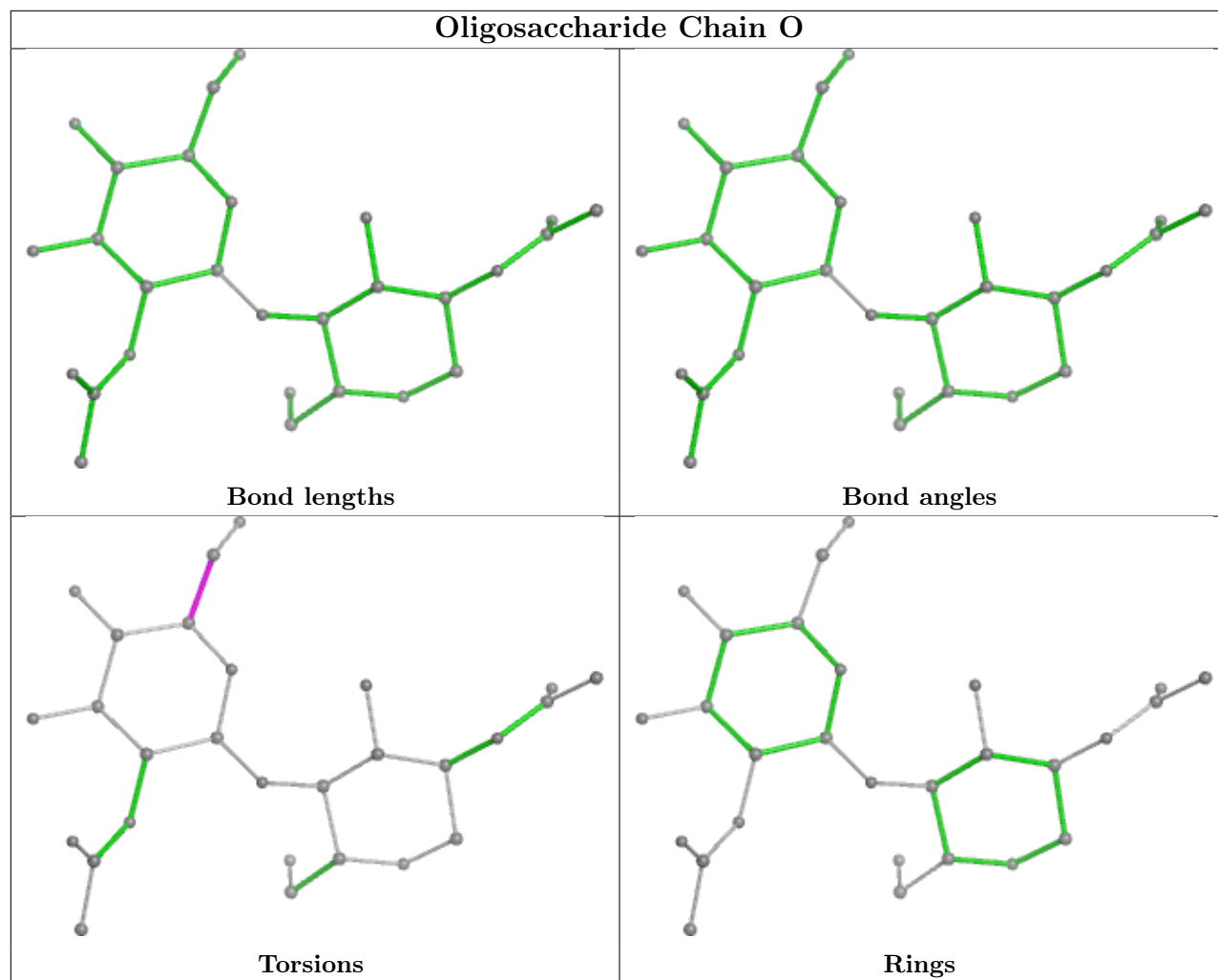


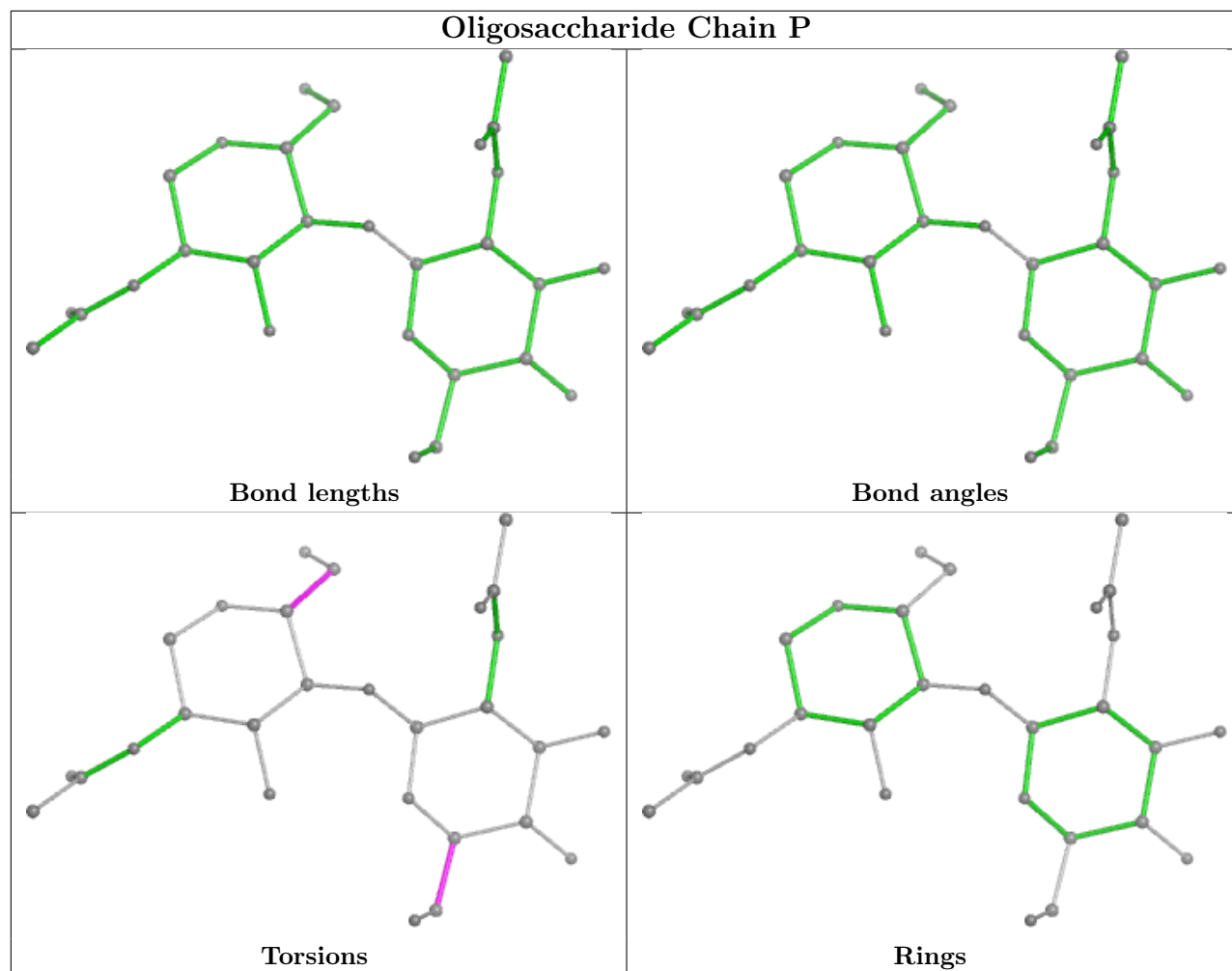


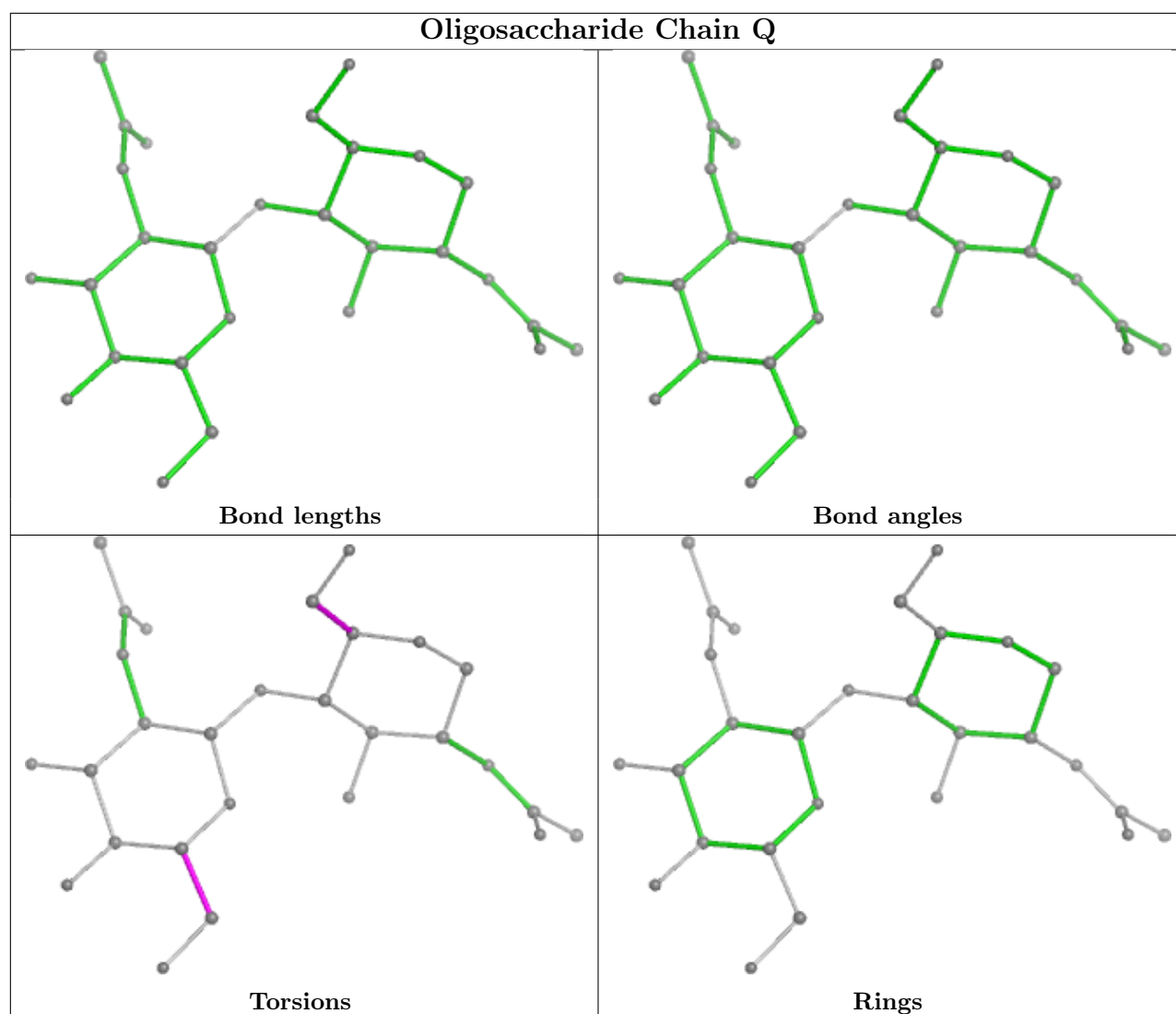


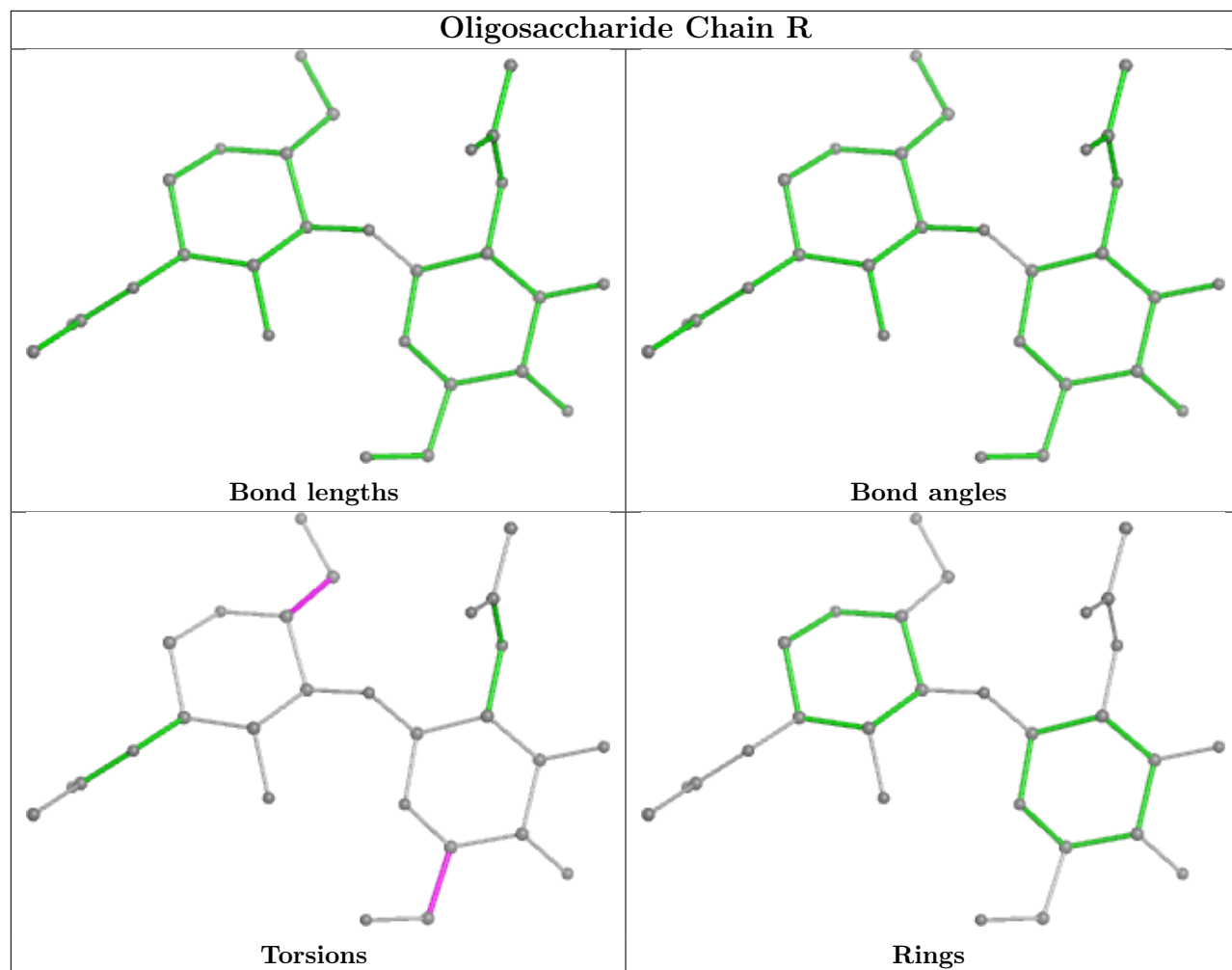


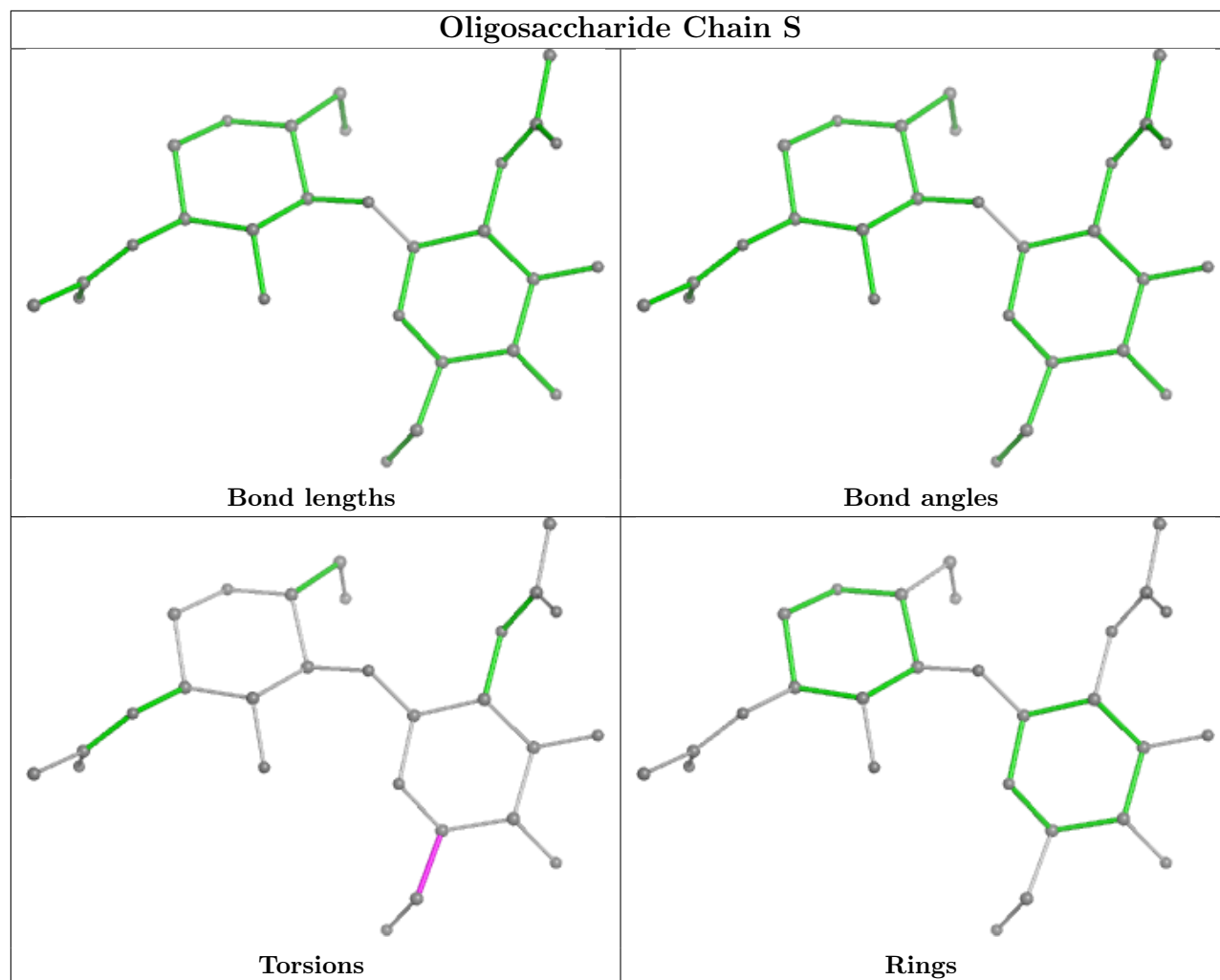


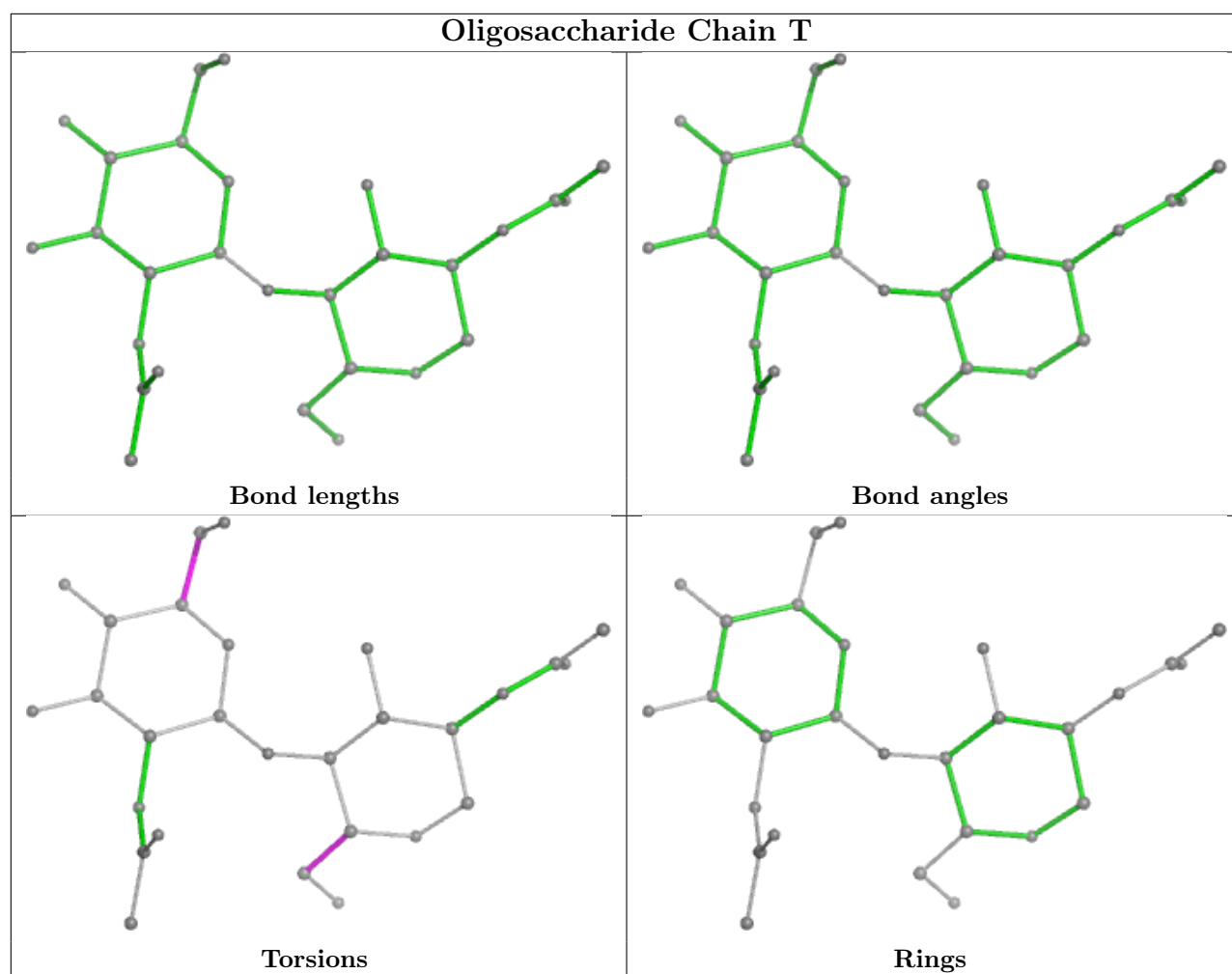




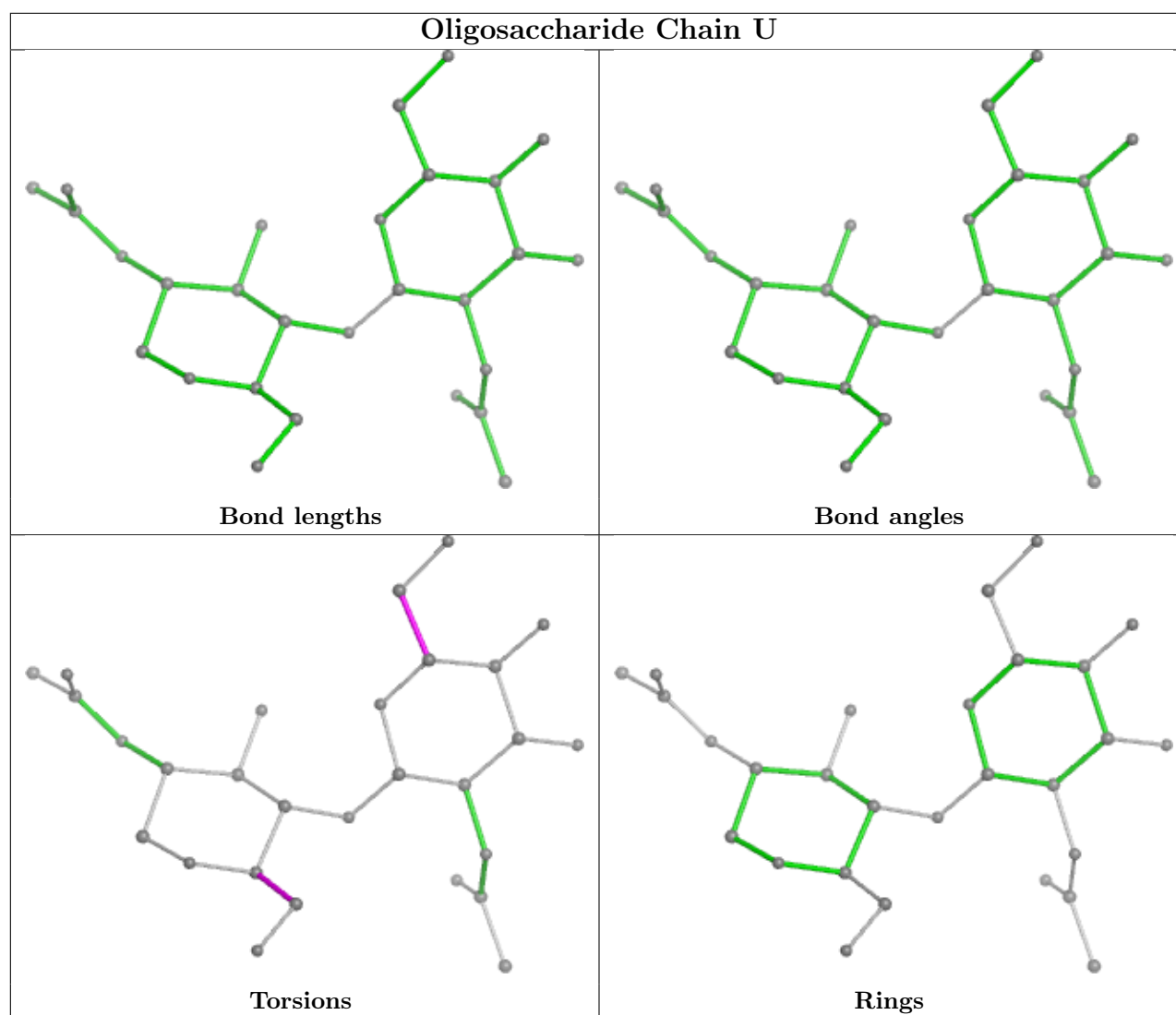












## 5.6 Ligand geometry [i](#)

24 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	C	1401	1	14,14,15	0.36	0	17,19,21	0.49	0
5	NAG	B	1402	1	14,14,15	0.40	0	17,19,21	0.48	0
5	NAG	C	1406	1	14,14,15	0.36	0	17,19,21	0.50	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	NAG	A	1401	1	14,14,15	0.34	0	17,19,21	0.48	0
5	NAG	B	1403	1	14,14,15	0.35	0	17,19,21	0.53	0
5	NAG	C	1408	1	14,14,15	0.38	0	17,19,21	0.54	0
5	NAG	C	1403	1	14,14,15	0.34	0	17,19,21	0.54	0
5	NAG	C	1404	1	14,14,15	1.26	1 (7%)	17,19,21	1.32	1 (5%)
5	NAG	A	1404	1	14,14,15	1.27	1 (7%)	17,19,21	1.33	1 (5%)
5	NAG	B	1405	1	14,14,15	0.62	0	17,19,21	0.46	0
5	NAG	C	1405	1	14,14,15	0.63	0	17,19,21	0.46	0
5	NAG	B	1407	1	14,14,15	0.34	0	17,19,21	0.41	0
5	NAG	B	1401	1	14,14,15	0.37	0	17,19,21	0.50	0
5	NAG	A	1406	1	14,14,15	0.35	0	17,19,21	0.50	0
5	NAG	A	1408	1	14,14,15	0.38	0	17,19,21	0.55	0
5	NAG	A	1402	1	14,14,15	0.39	0	17,19,21	0.47	0
5	NAG	A	1403	1	14,14,15	0.34	0	17,19,21	0.53	0
5	NAG	B	1408	1	14,14,15	0.39	0	17,19,21	0.54	0
5	NAG	B	1406	1	14,14,15	0.35	0	17,19,21	0.50	0
5	NAG	B	1404	1	14,14,15	1.25	1 (7%)	17,19,21	1.32	1 (5%)
5	NAG	C	1402	1	14,14,15	0.38	0	17,19,21	0.47	0
5	NAG	A	1405	1	14,14,15	0.63	0	17,19,21	0.47	0
5	NAG	C	1407	1	14,14,15	0.33	0	17,19,21	0.41	0
5	NAG	A	1407	1	14,14,15	0.33	0	17,19,21	0.41	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	C	1401	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1402	1	-	0/6/23/26	0/1/1/1
5	NAG	C	1406	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1401	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1403	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1408	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1403	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1404	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1404	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1405	1	-	1/6/23/26	0/1/1/1
5	NAG	C	1405	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1407	1	-	2/6/23/26	0/1/1/1

Continued on next page...

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	B	1401	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1406	1	-	1/6/23/26	0/1/1/1
5	NAG	A	1408	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1402	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1403	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1408	1	-	1/6/23/26	0/1/1/1
5	NAG	B	1406	1	-	1/6/23/26	0/1/1/1
5	NAG	B	1404	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1402	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1405	1	-	1/6/23/26	0/1/1/1
5	NAG	C	1407	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1407	1	-	2/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	1404	NAG	O5-C1	4.29	1.50	1.43
5	A	1404	NAG	O5-C1	4.28	1.50	1.43
5	B	1404	NAG	O5-C1	4.26	1.50	1.43

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1404	NAG	C1-O5-C5	5.28	119.34	112.19
5	C	1404	NAG	C1-O5-C5	5.25	119.31	112.19
5	B	1404	NAG	C1-O5-C5	5.24	119.29	112.19

There are no chirality outliers.

5 of 35 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1403	NAG	O5-C5-C6-O6
5	B	1403	NAG	O5-C5-C6-O6
5	C	1401	NAG	O5-C5-C6-O6
5	A	1401	NAG	O5-C5-C6-O6
5	C	1403	NAG	O5-C5-C6-O6

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	1403	NAG	1	0
5	C	1403	NAG	1	0
5	A	1403	NAG	1	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.

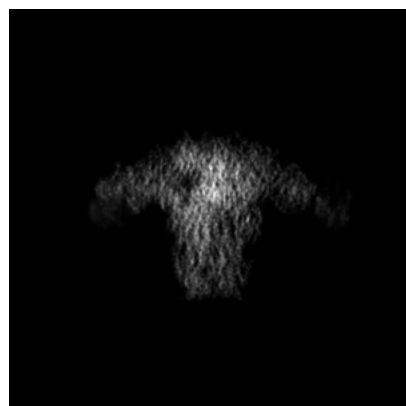
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13549. These allow visual inspection of the internal detail of the map and identification of artifacts.

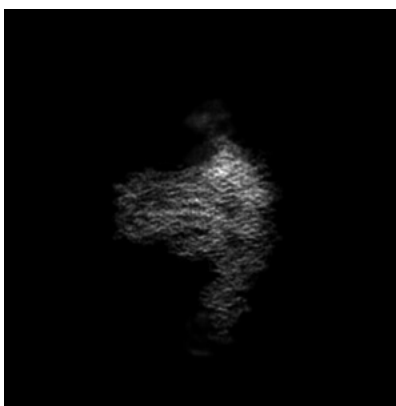
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

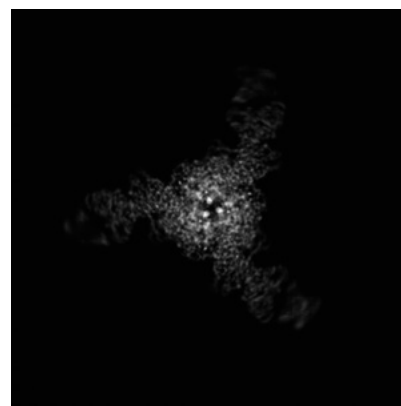
#### 6.1.1 Primary map



X

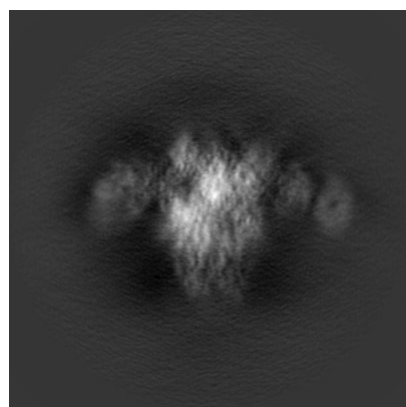


Y

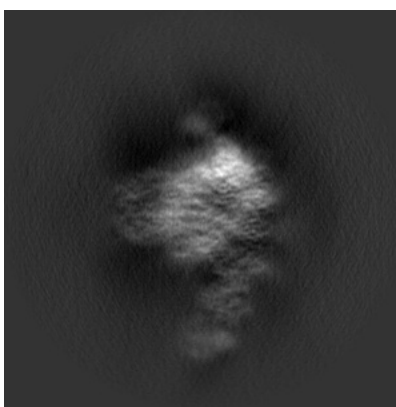


Z

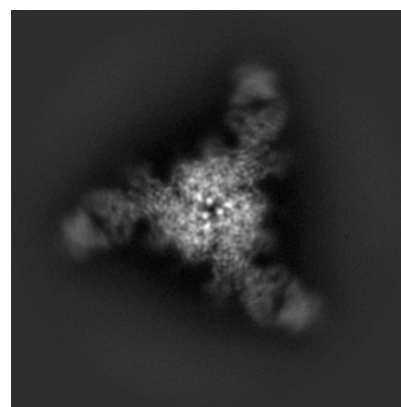
#### 6.1.2 Raw map



X



Y



Z

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

## 6.2 Central slices [i](#)

### 6.2.1 Primary map



X Index: 160

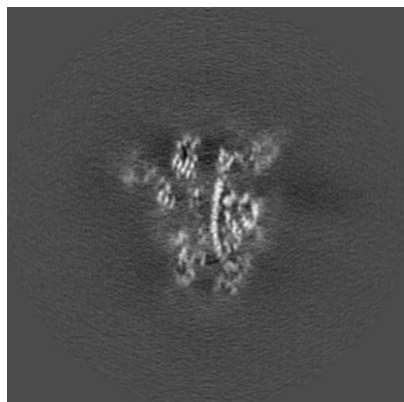


Y Index: 160

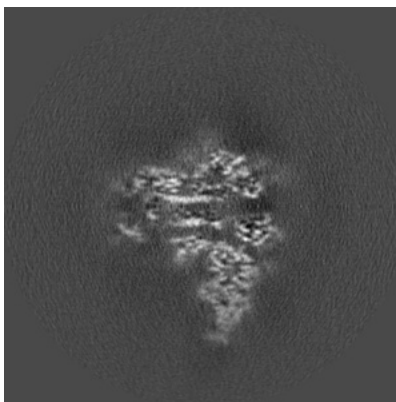


Z Index: 160

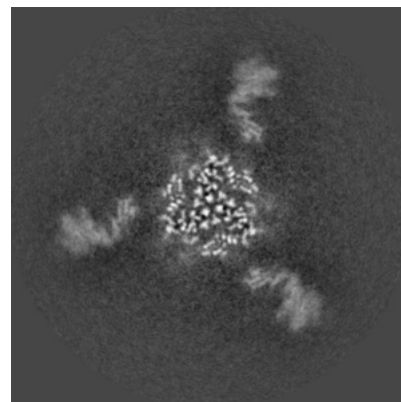
### 6.2.2 Raw map



X Index: 160



Y Index: 160



Z Index: 160

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

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

### 6.3.1 Primary map



X Index: 156

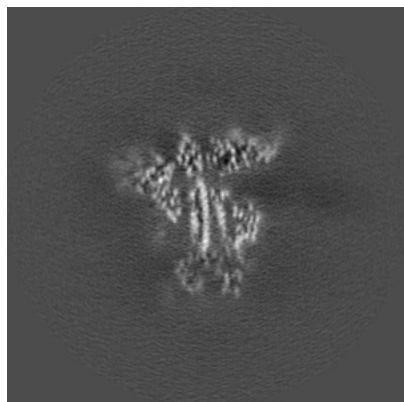


Y Index: 155

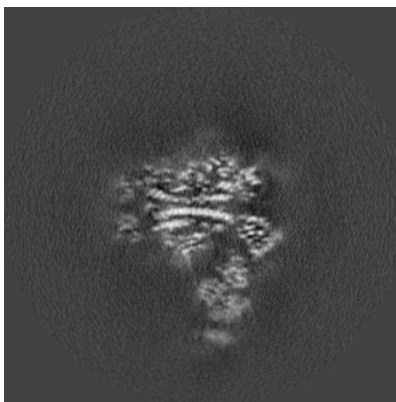


Z Index: 171

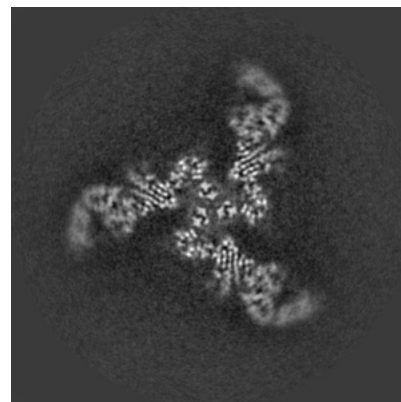
### 6.3.2 Raw map



X Index: 167



Y Index: 156

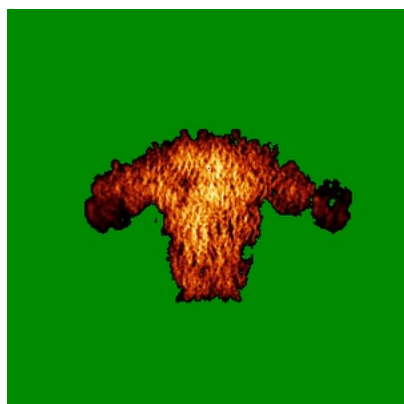


Z Index: 176

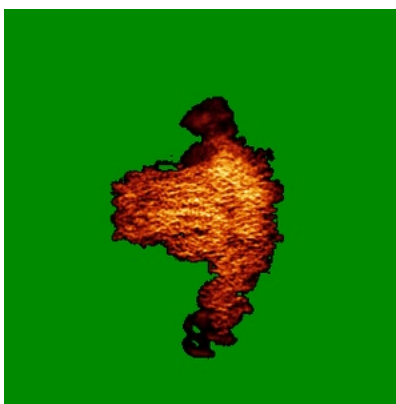
The images above show the largest variance slices of the map in three orthogonal directions.

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

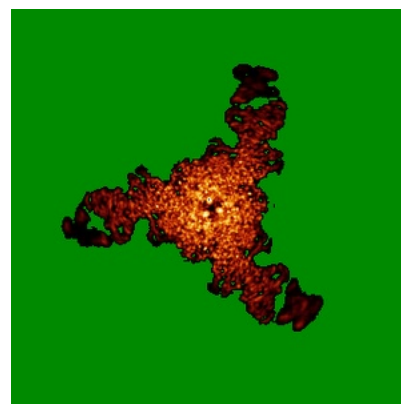
### 6.4.1 Primary map



X

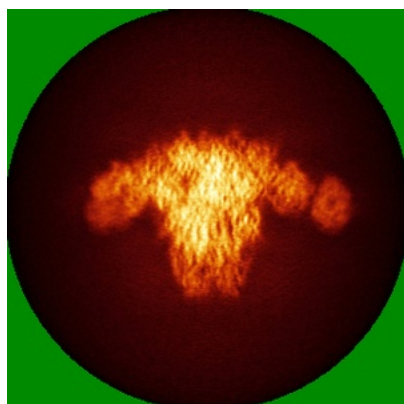


Y

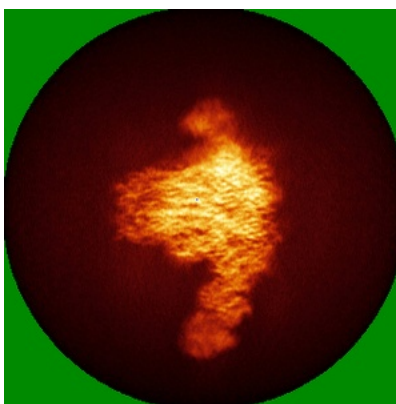


Z

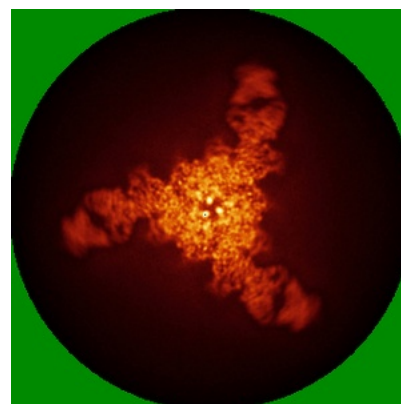
### 6.4.2 Raw map



X



Y



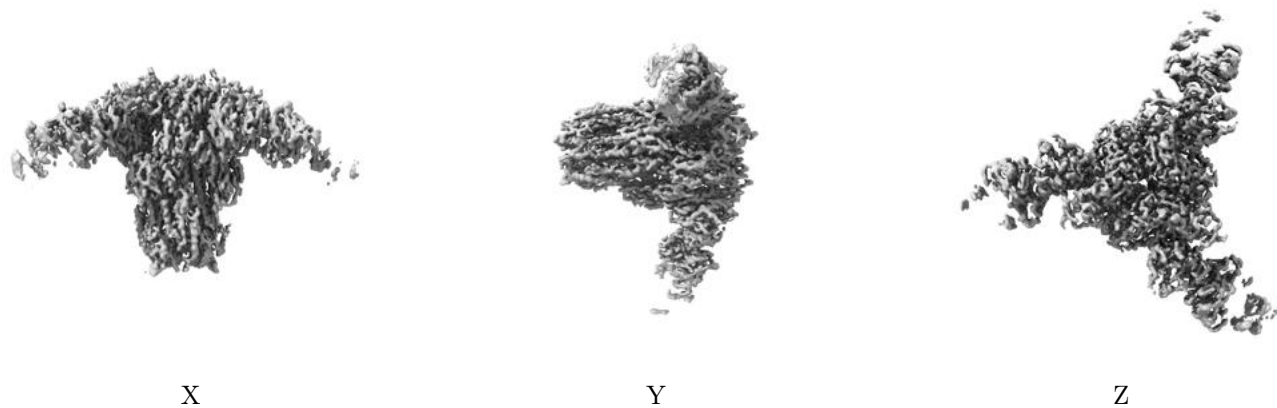
Z

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.



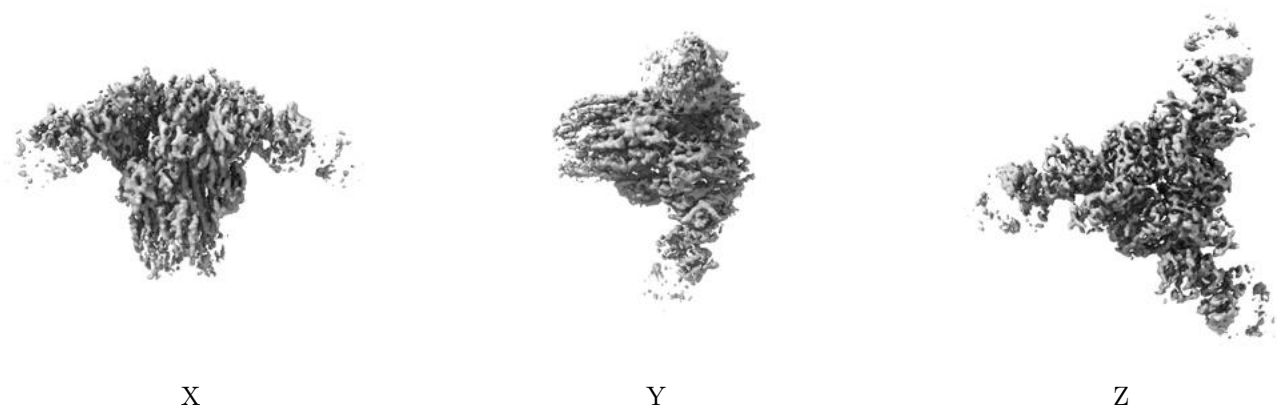
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



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



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.

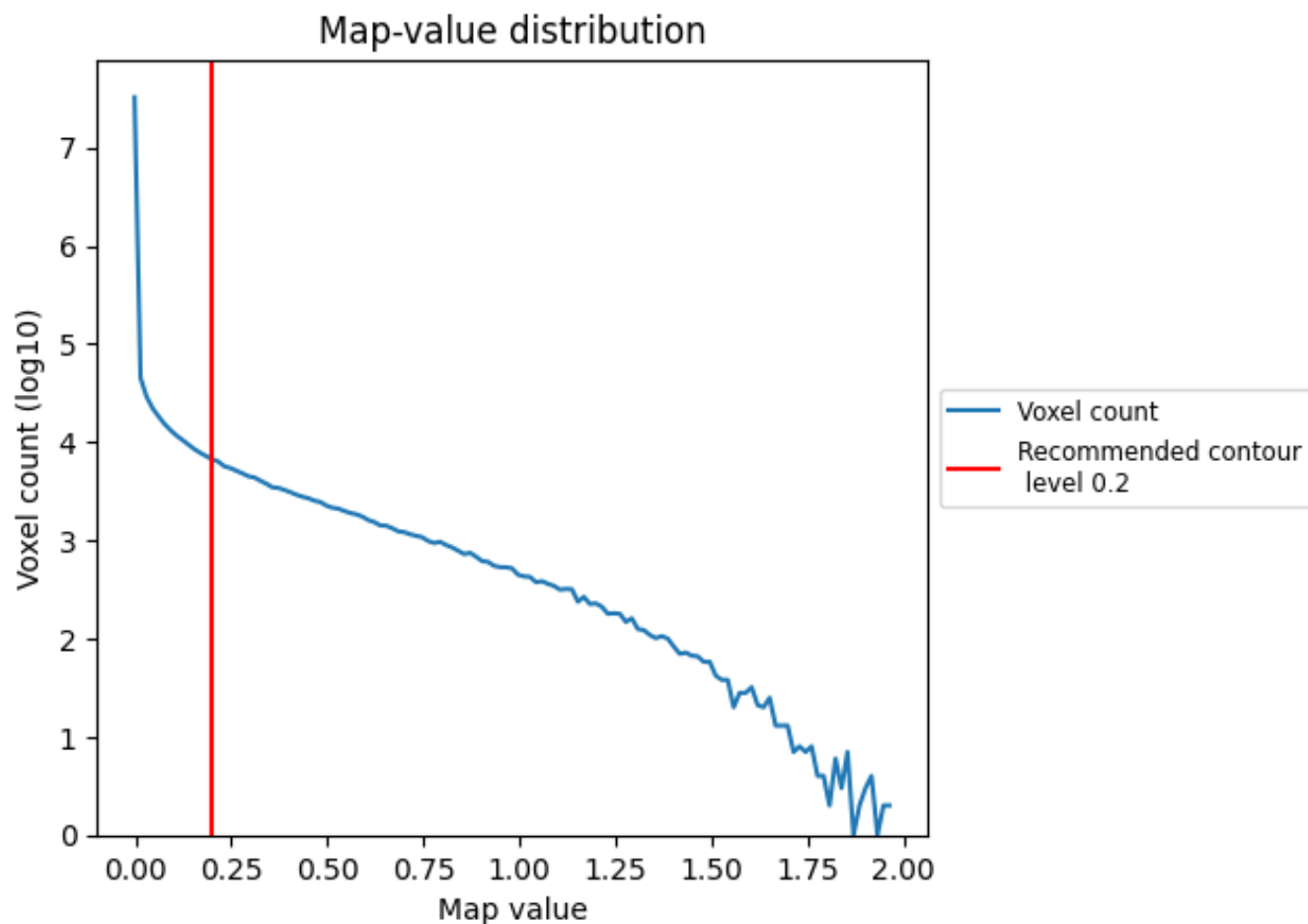
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

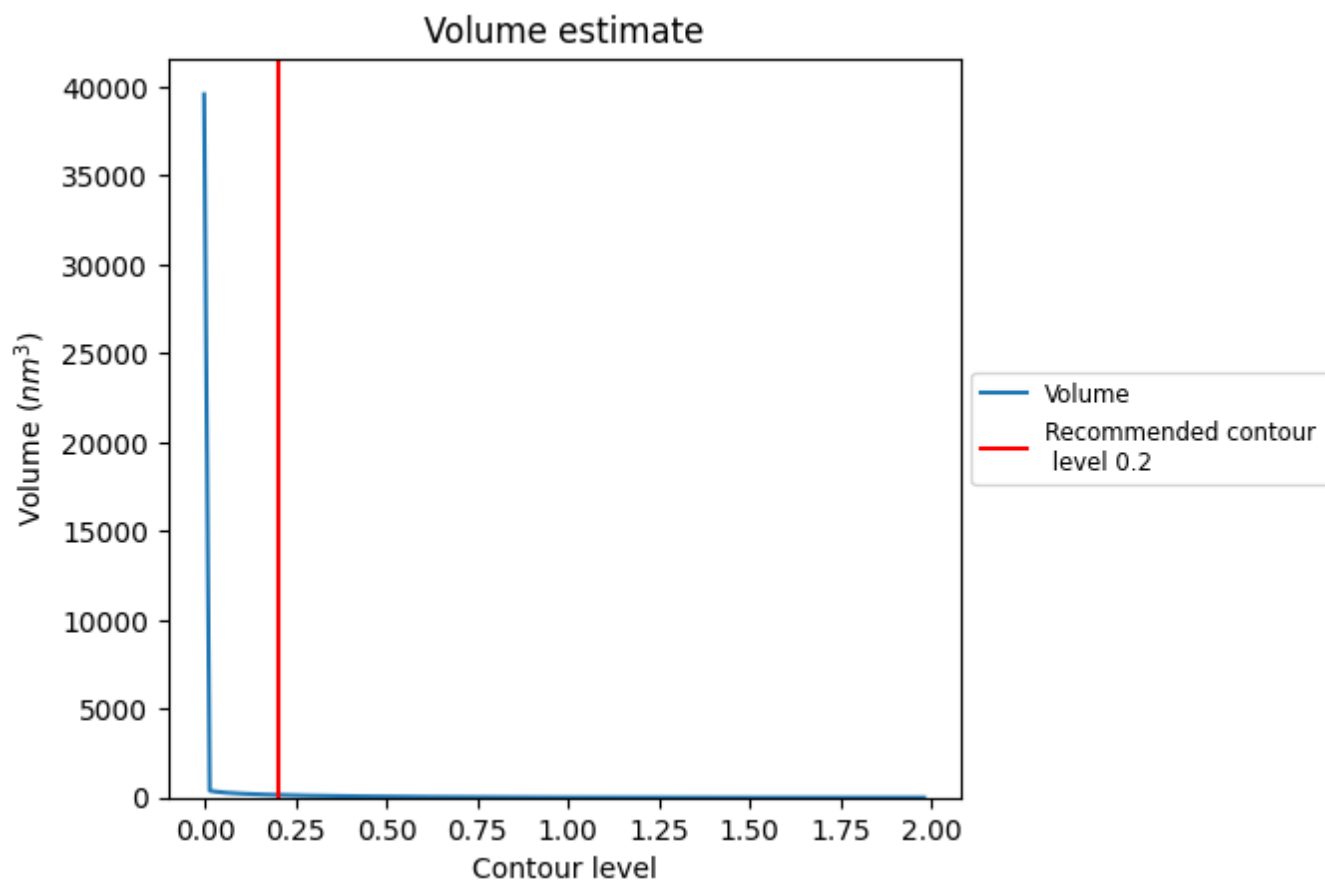
This section contains the results of statistical analysis of the map.

### 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.

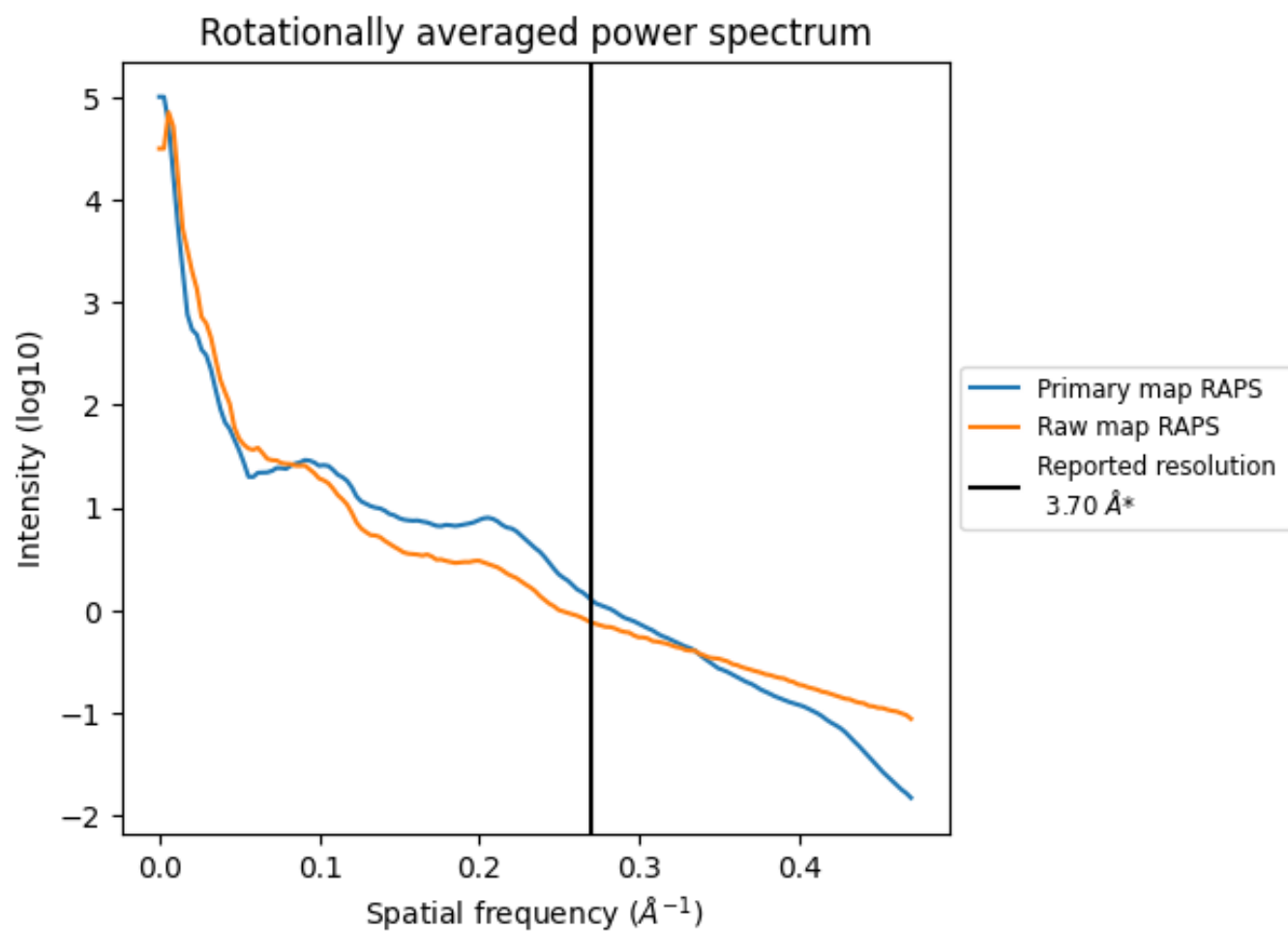
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 149  $\text{nm}^3$ ; this corresponds to an approximate mass of 134 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 ⓘ

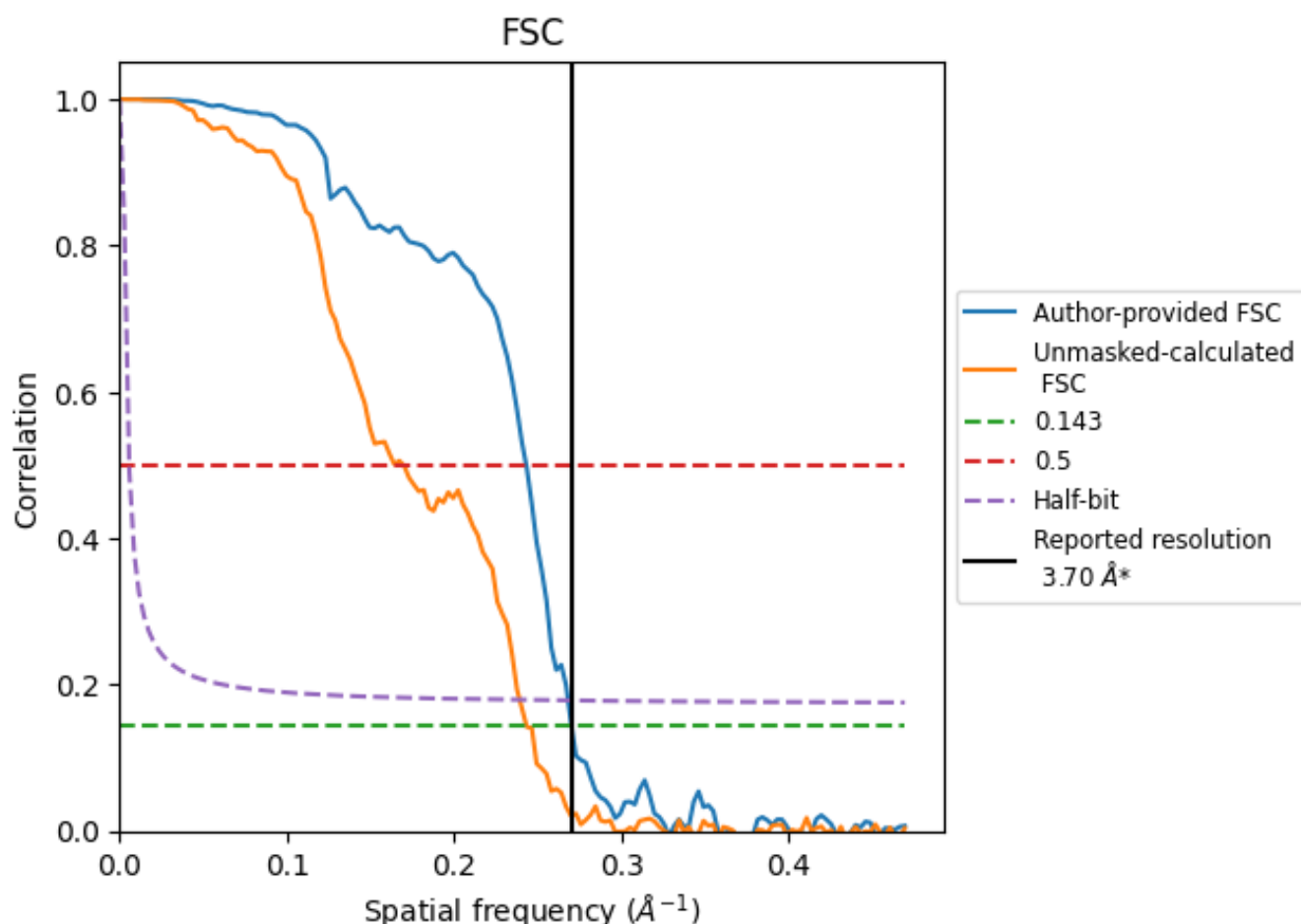


\*Reported resolution corresponds to spatial frequency of 0.270 Å<sup>-1</sup>

## 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 0.270 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

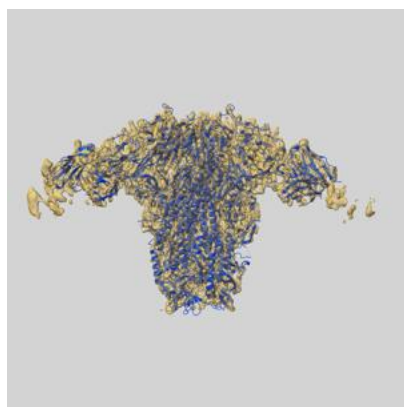
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.70	4.11	3.73
Unmasked-calculated*	4.11	5.89	4.18

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.11 differs from the reported value 3.7 by more than 10 %

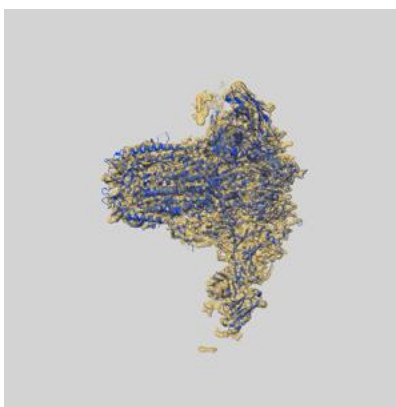
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13549 and PDB model 7PNM. Per-residue inclusion information can be found in section [3](#) on page [13](#).

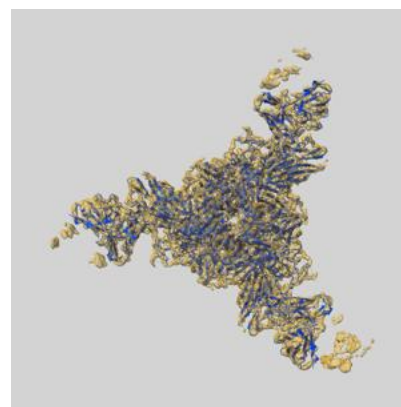
### 9.1 Map-model overlay [i](#)



X



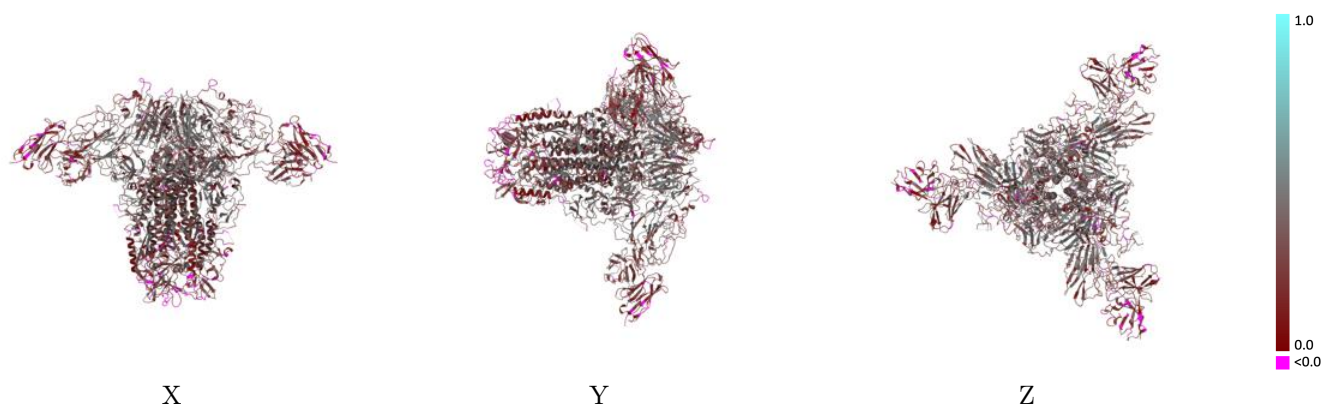
Y



Z

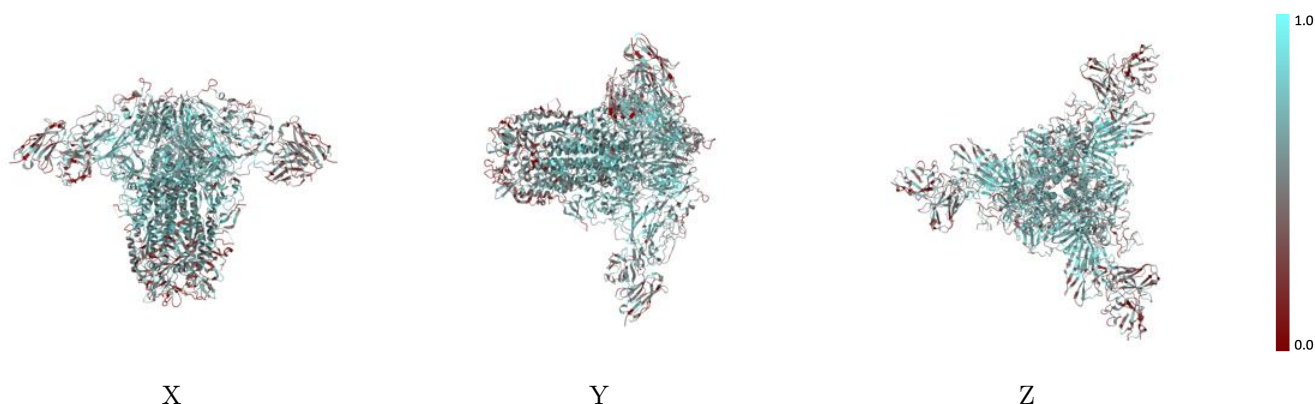
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 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.

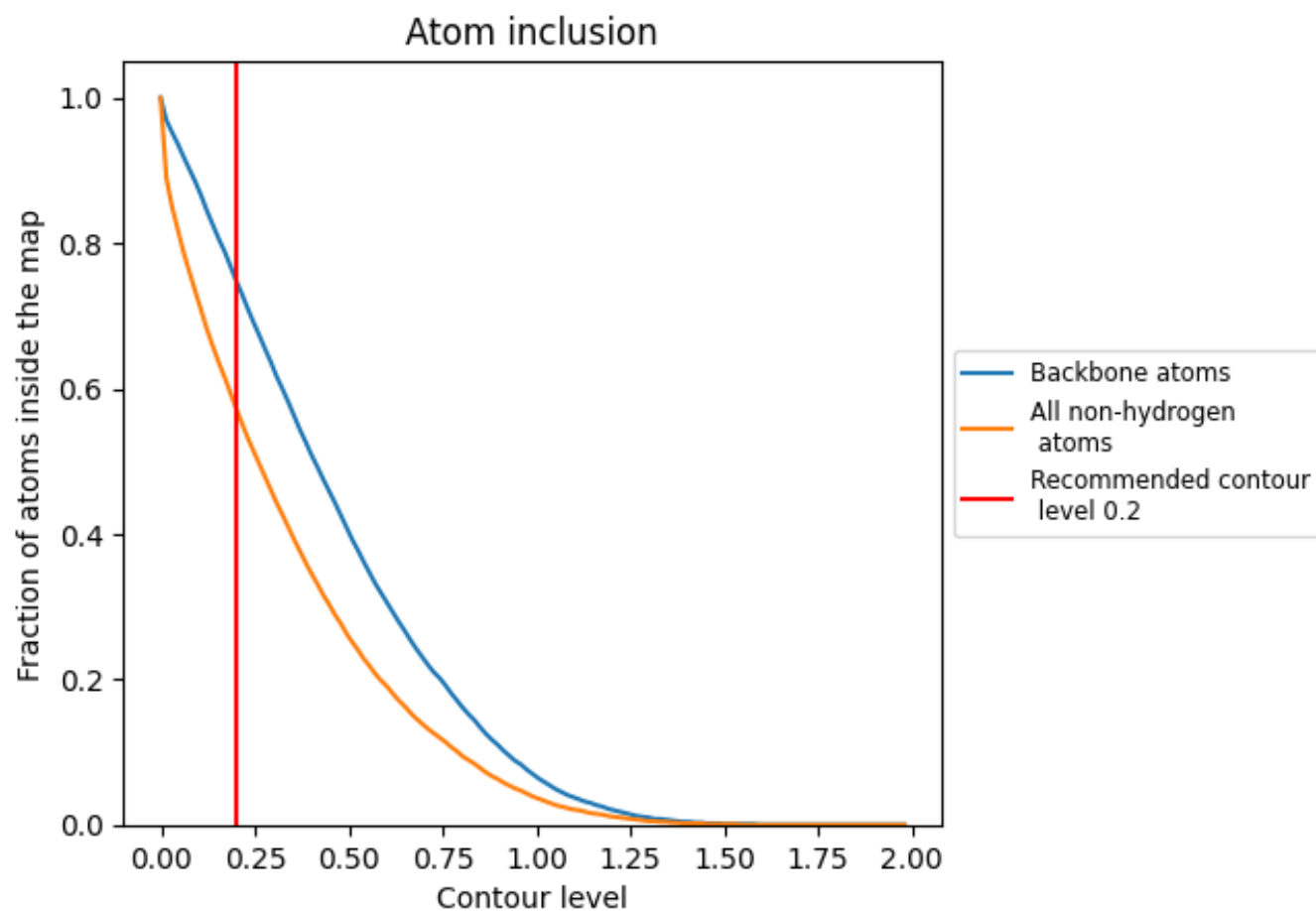
## 9.3 Atom inclusion mapped to coordinate model [i](#)



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 [i](#)



At the recommended contour level, 75% of all backbone atoms, 57% 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	 0.5720	 0.3150
A	 0.6010	 0.3330
B	 0.6010	 0.3310
C	 0.5970	 0.3310
D	 0.4440	 0.2620
E	 0.4270	 0.2650
F	 0.4290	 0.2910
G	 0.4290	 0.2100
H	 0.4640	 0.2130
I	 0.4080	 0.2040
J	 0.5360	 0.3490
K	 0.4640	 0.2820
L	 0.4800	 0.2640
M	 0.0710	 0.1510
N	 0.5000	 0.2880
O	 0.4290	 0.3400
P	 0.4640	 0.3180
Q	 0.0710	 0.0660
R	 0.4640	 0.2830
S	 0.5360	 0.3340
T	 0.4290	 0.2830
U	 0.0710	 0.2650

