



wwPDB EM Validation Summary Report ⓘ

Aug 19, 2024 – 11:12 AM EDT

PDB ID : 8UG9
EMDB ID : EMD-42218
Title : XBB.1.5 spike/Nb5 complex
Authors : Ye, G.; Bu, F.; Liu, B.; Li, F.
Deposited on : 2023-10-05
Resolution : 3.49 Å(reported)
Based on initial model : 8IOS

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev92
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 : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

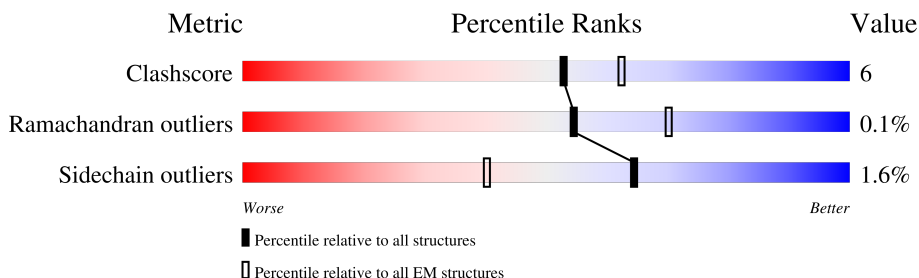
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.49 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 ≥ 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	M	135	
1	N	135	
1	O	135	
2	A	1230	
2	B	1230	
2	C	1230	
3	D	2	
3	E	2	

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Mol	Chain	Length	Quality of chain
3	F	2	<div><div></div><div>50%</div><div></div><div>50%</div></div>
3	G	2	<div><div></div><div>100%</div><div></div></div>
3	H	2	<div><div></div><div>100%</div><div></div></div>
3	I	2	<div><div></div><div>50%</div><div></div><div>50%</div></div>
3	J	2	<div><div></div><div>100%</div><div></div></div>
3	K	2	<div><div></div><div>100%</div><div></div></div>
3	L	2	<div><div></div><div>50%</div><div></div><div>50%</div></div>
3	P	2	<div><div></div><div>100%</div><div></div></div>
3	Q	2	<div><div></div><div>100%</div><div></div></div>
3	R	2	<div><div></div><div>50%</div><div></div><div>50%</div></div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 28383 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 Nanosota-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	M	114	Total	C	N	O	S	0	0
			881	541	159	175	6		
1	N	114	Total	C	N	O	S	0	0
			881	541	159	175	6		
1	O	114	Total	C	N	O	S	0	0
			881	541	159	175	6		

- Molecule 2 is a protein called Spike glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	1063	Total	C	N	O	S	0	0
			8314	5315	1387	1574	38		
2	B	1063	Total	C	N	O	S	0	0
			8314	5315	1387	1574	38		
2	C	1063	Total	C	N	O	S	0	0
			8314	5315	1387	1574	38		

There are 255 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	19	ILE	THR	conflict	UNP P0DTC2
A	?	-	LEU	deletion	UNP P0DTC2
A	?	-	PRO	deletion	UNP P0DTC2
A	?	-	PRO	deletion	UNP P0DTC2
A	24	SER	ALA	conflict	UNP P0DTC2
A	80	ALA	VAL	conflict	UNP P0DTC2
A	139	ASP	GLY	conflict	UNP P0DTC2
A	?	-	TYR	deletion	UNP P0DTC2
A	142	GLN	HIS	conflict	UNP P0DTC2
A	179	GLU	GLN	conflict	UNP P0DTC2
A	209	GLU	VAL	conflict	UNP P0DTC2
A	335	HIS	GLY	conflict	UNP P0DTC2
A	342	THR	ARG	conflict	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	364	ILE	LEU	conflict	UNP P0DTC2
A	367	PHE	SER	conflict	UNP P0DTC2
A	369	PRO	SER	conflict	UNP P0DTC2
A	371	PHE	SER	conflict	UNP P0DTC2
A	372	ALA	THR	conflict	UNP P0DTC2
A	401	ASN	ASP	conflict	UNP P0DTC2
A	404	SER	ARG	conflict	UNP P0DTC2
A	413	ASN	LYS	conflict	UNP P0DTC2
A	436	LYS	ASN	conflict	UNP P0DTC2
A	441	PRO	VAL	conflict	UNP P0DTC2
A	442	SER	GLY	conflict	UNP P0DTC2
A	456	LYS	ASN	conflict	UNP P0DTC2
A	473	ASN	SER	conflict	UNP P0DTC2
A	474	LYS	THR	conflict	UNP P0DTC2
A	480	ALA	GLU	conflict	UNP P0DTC2
A	482	PRO	PHE	conflict	UNP P0DTC2
A	486	SER	PHE	conflict	UNP P0DTC2
A	494	ARG	GLN	conflict	UNP P0DTC2
A	497	TYR	ASN	conflict	UNP P0DTC2
A	501	HIS	TYR	conflict	UNP P0DTC2
A	610	GLY	ASP	conflict	UNP P0DTC2
A	651	TYR	HIS	conflict	UNP P0DTC2
A	675	LYS	ASN	conflict	UNP P0DTC2
A	677	HIS	PRO	conflict	UNP P0DTC2
A	678	ALA	ARG	conflict	UNP P0DTC2
A	679	GLY	ARG	conflict	UNP P0DTC2
A	760	LYS	ASN	conflict	UNP P0DTC2
A	792	TYR	ASP	conflict	UNP P0DTC2
A	813	PRO	PHE	conflict	UNP P0DTC2
A	888	PRO	ALA	conflict	UNP P0DTC2
A	895	PRO	ALA	conflict	UNP P0DTC2
A	938	PRO	ALA	conflict	UNP P0DTC2
A	950	HIS	GLN	conflict	UNP P0DTC2
A	965	LYS	ASN	conflict	UNP P0DTC2
A	982	PRO	LYS	conflict	UNP P0DTC2
A	983	PRO	VAL	conflict	UNP P0DTC2
A	1208	GLY	-	expression tag	UNP P0DTC2
A	1209	SER	-	expression tag	UNP P0DTC2
A	1210	GLY	-	expression tag	UNP P0DTC2
A	1211	TYR	-	expression tag	UNP P0DTC2
A	1212	ILE	-	expression tag	UNP P0DTC2
A	1213	PRO	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1214	GLU	-	expression tag	UNP P0DTC2
A	1215	ALA	-	expression tag	UNP P0DTC2
A	1216	PRO	-	expression tag	UNP P0DTC2
A	1217	ARG	-	expression tag	UNP P0DTC2
A	1218	ASP	-	expression tag	UNP P0DTC2
A	1219	GLY	-	expression tag	UNP P0DTC2
A	1220	GLN	-	expression tag	UNP P0DTC2
A	1221	ALA	-	expression tag	UNP P0DTC2
A	1222	TYR	-	expression tag	UNP P0DTC2
A	1223	VAL	-	expression tag	UNP P0DTC2
A	1224	ARG	-	expression tag	UNP P0DTC2
A	1225	LYS	-	expression tag	UNP P0DTC2
A	1226	ASP	-	expression tag	UNP P0DTC2
A	1227	GLY	-	expression tag	UNP P0DTC2
A	1228	GLU	-	expression tag	UNP P0DTC2
A	1229	TRP	-	expression tag	UNP P0DTC2
A	1230	VAL	-	expression tag	UNP P0DTC2
A	1231	LEU	-	expression tag	UNP P0DTC2
A	1232	LEU	-	expression tag	UNP P0DTC2
A	1233	SER	-	expression tag	UNP P0DTC2
A	1234	THR	-	expression tag	UNP P0DTC2
A	1235	PHE	-	expression tag	UNP P0DTC2
A	1236	LEU	-	expression tag	UNP P0DTC2
A	1237	GLY	-	expression tag	UNP P0DTC2
A	1238	HIS	-	expression tag	UNP P0DTC2
A	1239	HIS	-	expression tag	UNP P0DTC2
A	1240	HIS	-	expression tag	UNP P0DTC2
A	1241	HIS	-	expression tag	UNP P0DTC2
A	1242	HIS	-	expression tag	UNP P0DTC2
A	1243	HIS	-	expression tag	UNP P0DTC2
B	19	ILE	THR	conflict	UNP P0DTC2
B	?	-	LEU	deletion	UNP P0DTC2
B	?	-	PRO	deletion	UNP P0DTC2
B	?	-	PRO	deletion	UNP P0DTC2
B	24	SER	ALA	conflict	UNP P0DTC2
B	80	ALA	VAL	conflict	UNP P0DTC2
B	139	ASP	GLY	conflict	UNP P0DTC2
B	?	-	TYR	deletion	UNP P0DTC2
B	142	GLN	HIS	conflict	UNP P0DTC2
B	179	GLU	GLN	conflict	UNP P0DTC2
B	209	GLU	VAL	conflict	UNP P0DTC2
B	335	HIS	GLY	conflict	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	342	THR	ARG	conflict	UNP P0DTC2
B	364	ILE	LEU	conflict	UNP P0DTC2
B	367	PHE	SER	conflict	UNP P0DTC2
B	369	PRO	SER	conflict	UNP P0DTC2
B	371	PHE	SER	conflict	UNP P0DTC2
B	372	ALA	THR	conflict	UNP P0DTC2
B	401	ASN	ASP	conflict	UNP P0DTC2
B	404	SER	ARG	conflict	UNP P0DTC2
B	413	ASN	LYS	conflict	UNP P0DTC2
B	436	LYS	ASN	conflict	UNP P0DTC2
B	441	PRO	VAL	conflict	UNP P0DTC2
B	442	SER	GLY	conflict	UNP P0DTC2
B	456	LYS	ASN	conflict	UNP P0DTC2
B	473	ASN	SER	conflict	UNP P0DTC2
B	474	LYS	THR	conflict	UNP P0DTC2
B	480	ALA	GLU	conflict	UNP P0DTC2
B	482	PRO	PHE	conflict	UNP P0DTC2
B	486	SER	PHE	conflict	UNP P0DTC2
B	494	ARG	GLN	conflict	UNP P0DTC2
B	497	TYR	ASN	conflict	UNP P0DTC2
B	501	HIS	TYR	conflict	UNP P0DTC2
B	610	GLY	ASP	conflict	UNP P0DTC2
B	651	TYR	HIS	conflict	UNP P0DTC2
B	675	LYS	ASN	conflict	UNP P0DTC2
B	677	HIS	PRO	conflict	UNP P0DTC2
B	678	ALA	ARG	conflict	UNP P0DTC2
B	679	GLY	ARG	conflict	UNP P0DTC2
B	760	LYS	ASN	conflict	UNP P0DTC2
B	792	TYR	ASP	conflict	UNP P0DTC2
B	813	PRO	PHE	conflict	UNP P0DTC2
B	888	PRO	ALA	conflict	UNP P0DTC2
B	895	PRO	ALA	conflict	UNP P0DTC2
B	938	PRO	ALA	conflict	UNP P0DTC2
B	950	HIS	GLN	conflict	UNP P0DTC2
B	965	LYS	ASN	conflict	UNP P0DTC2
B	982	PRO	LYS	conflict	UNP P0DTC2
B	983	PRO	VAL	conflict	UNP P0DTC2
B	1208	GLY	-	expression tag	UNP P0DTC2
B	1209	SER	-	expression tag	UNP P0DTC2
B	1210	GLY	-	expression tag	UNP P0DTC2
B	1211	TYR	-	expression tag	UNP P0DTC2
B	1212	ILE	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1213	PRO	-	expression tag	UNP P0DTC2
B	1214	GLU	-	expression tag	UNP P0DTC2
B	1215	ALA	-	expression tag	UNP P0DTC2
B	1216	PRO	-	expression tag	UNP P0DTC2
B	1217	ARG	-	expression tag	UNP P0DTC2
B	1218	ASP	-	expression tag	UNP P0DTC2
B	1219	GLY	-	expression tag	UNP P0DTC2
B	1220	GLN	-	expression tag	UNP P0DTC2
B	1221	ALA	-	expression tag	UNP P0DTC2
B	1222	TYR	-	expression tag	UNP P0DTC2
B	1223	VAL	-	expression tag	UNP P0DTC2
B	1224	ARG	-	expression tag	UNP P0DTC2
B	1225	LYS	-	expression tag	UNP P0DTC2
B	1226	ASP	-	expression tag	UNP P0DTC2
B	1227	GLY	-	expression tag	UNP P0DTC2
B	1228	GLU	-	expression tag	UNP P0DTC2
B	1229	TRP	-	expression tag	UNP P0DTC2
B	1230	VAL	-	expression tag	UNP P0DTC2
B	1231	LEU	-	expression tag	UNP P0DTC2
B	1232	LEU	-	expression tag	UNP P0DTC2
B	1233	SER	-	expression tag	UNP P0DTC2
B	1234	THR	-	expression tag	UNP P0DTC2
B	1235	PHE	-	expression tag	UNP P0DTC2
B	1236	LEU	-	expression tag	UNP P0DTC2
B	1237	GLY	-	expression tag	UNP P0DTC2
B	1238	HIS	-	expression tag	UNP P0DTC2
B	1239	HIS	-	expression tag	UNP P0DTC2
B	1240	HIS	-	expression tag	UNP P0DTC2
B	1241	HIS	-	expression tag	UNP P0DTC2
B	1242	HIS	-	expression tag	UNP P0DTC2
B	1243	HIS	-	expression tag	UNP P0DTC2
C	19	ILE	THR	conflict	UNP P0DTC2
C	?	-	LEU	deletion	UNP P0DTC2
C	?	-	PRO	deletion	UNP P0DTC2
C	?	-	PRO	deletion	UNP P0DTC2
C	24	SER	ALA	conflict	UNP P0DTC2
C	80	ALA	VAL	conflict	UNP P0DTC2
C	139	ASP	GLY	conflict	UNP P0DTC2
C	?	-	TYR	deletion	UNP P0DTC2
C	142	GLN	HIS	conflict	UNP P0DTC2
C	179	GLU	GLN	conflict	UNP P0DTC2
C	209	GLU	VAL	conflict	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	335	HIS	GLY	conflict	UNP P0DTC2
C	342	THR	ARG	conflict	UNP P0DTC2
C	364	ILE	LEU	conflict	UNP P0DTC2
C	367	PHE	SER	conflict	UNP P0DTC2
C	369	PRO	SER	conflict	UNP P0DTC2
C	371	PHE	SER	conflict	UNP P0DTC2
C	372	ALA	THR	conflict	UNP P0DTC2
C	401	ASN	ASP	conflict	UNP P0DTC2
C	404	SER	ARG	conflict	UNP P0DTC2
C	413	ASN	LYS	conflict	UNP P0DTC2
C	436	LYS	ASN	conflict	UNP P0DTC2
C	441	PRO	VAL	conflict	UNP P0DTC2
C	442	SER	GLY	conflict	UNP P0DTC2
C	456	LYS	ASN	conflict	UNP P0DTC2
C	473	ASN	SER	conflict	UNP P0DTC2
C	474	LYS	THR	conflict	UNP P0DTC2
C	480	ALA	GLU	conflict	UNP P0DTC2
C	482	PRO	PHE	conflict	UNP P0DTC2
C	486	SER	PHE	conflict	UNP P0DTC2
C	494	ARG	GLN	conflict	UNP P0DTC2
C	497	TYR	ASN	conflict	UNP P0DTC2
C	501	HIS	TYR	conflict	UNP P0DTC2
C	610	GLY	ASP	conflict	UNP P0DTC2
C	651	TYR	HIS	conflict	UNP P0DTC2
C	675	LYS	ASN	conflict	UNP P0DTC2
C	677	HIS	PRO	conflict	UNP P0DTC2
C	678	ALA	ARG	conflict	UNP P0DTC2
C	679	GLY	ARG	conflict	UNP P0DTC2
C	760	LYS	ASN	conflict	UNP P0DTC2
C	792	TYR	ASP	conflict	UNP P0DTC2
C	813	PRO	PHE	conflict	UNP P0DTC2
C	888	PRO	ALA	conflict	UNP P0DTC2
C	895	PRO	ALA	conflict	UNP P0DTC2
C	938	PRO	ALA	conflict	UNP P0DTC2
C	950	HIS	GLN	conflict	UNP P0DTC2
C	965	LYS	ASN	conflict	UNP P0DTC2
C	982	PRO	LYS	conflict	UNP P0DTC2
C	983	PRO	VAL	conflict	UNP P0DTC2
C	1208	GLY	-	expression tag	UNP P0DTC2
C	1209	SER	-	expression tag	UNP P0DTC2
C	1210	GLY	-	expression tag	UNP P0DTC2
C	1211	TYR	-	expression tag	UNP P0DTC2

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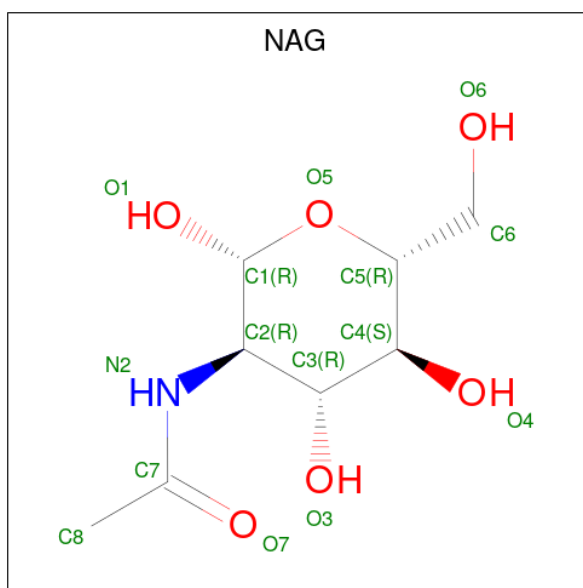
Chain	Residue	Modelled	Actual	Comment	Reference
C	1212	ILE	-	expression tag	UNP P0DTC2
C	1213	PRO	-	expression tag	UNP P0DTC2
C	1214	GLU	-	expression tag	UNP P0DTC2
C	1215	ALA	-	expression tag	UNP P0DTC2
C	1216	PRO	-	expression tag	UNP P0DTC2
C	1217	ARG	-	expression tag	UNP P0DTC2
C	1218	ASP	-	expression tag	UNP P0DTC2
C	1219	GLY	-	expression tag	UNP P0DTC2
C	1220	GLN	-	expression tag	UNP P0DTC2
C	1221	ALA	-	expression tag	UNP P0DTC2
C	1222	TYR	-	expression tag	UNP P0DTC2
C	1223	VAL	-	expression tag	UNP P0DTC2
C	1224	ARG	-	expression tag	UNP P0DTC2
C	1225	LYS	-	expression tag	UNP P0DTC2
C	1226	ASP	-	expression tag	UNP P0DTC2
C	1227	GLY	-	expression tag	UNP P0DTC2
C	1228	GLU	-	expression tag	UNP P0DTC2
C	1229	TRP	-	expression tag	UNP P0DTC2
C	1230	VAL	-	expression tag	UNP P0DTC2
C	1231	LEU	-	expression tag	UNP P0DTC2
C	1232	LEU	-	expression tag	UNP P0DTC2
C	1233	SER	-	expression tag	UNP P0DTC2
C	1234	THR	-	expression tag	UNP P0DTC2
C	1235	PHE	-	expression tag	UNP P0DTC2
C	1236	LEU	-	expression tag	UNP P0DTC2
C	1237	GLY	-	expression tag	UNP P0DTC2
C	1238	HIS	-	expression tag	UNP P0DTC2
C	1239	HIS	-	expression tag	UNP P0DTC2
C	1240	HIS	-	expression tag	UNP P0DTC2
C	1241	HIS	-	expression tag	UNP P0DTC2
C	1242	HIS	-	expression tag	UNP P0DTC2
C	1243	HIS	-	expression tag	UNP P0DTC2

- Molecule 3 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
3	D	2	Total	C	N	O	0	0
			28	16	2	10		
3	E	2	Total	C	N	O	0	0
			28	16	2	10		
3	F	2	Total	C	N	O	0	0
			28	16	2	10		
3	G	2	Total	C	N	O	0	0
			28	16	2	10		
3	H	2	Total	C	N	O	0	0
			28	16	2	10		
3	I	2	Total	C	N	O	0	0
			28	16	2	10		
3	J	2	Total	C	N	O	0	0
			28	16	2	10		
3	K	2	Total	C	N	O	0	0
			28	16	2	10		
3	L	2	Total	C	N	O	0	0
			28	16	2	10		
3	P	2	Total	C	N	O	0	0
			28	16	2	10		
3	Q	2	Total	C	N	O	0	0
			28	16	2	10		
3	R	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

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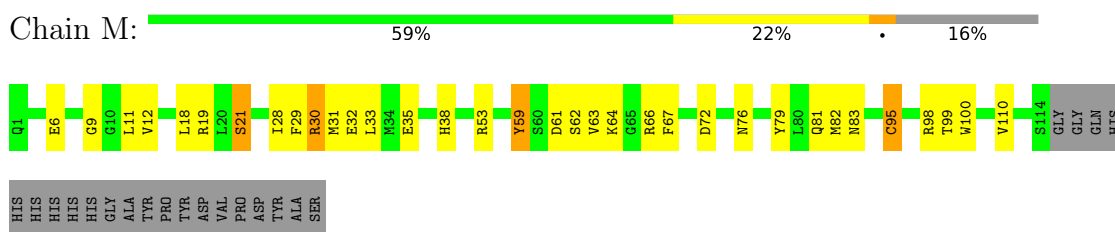
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Mol	Chain	Residues	Atoms				AltConf
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C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

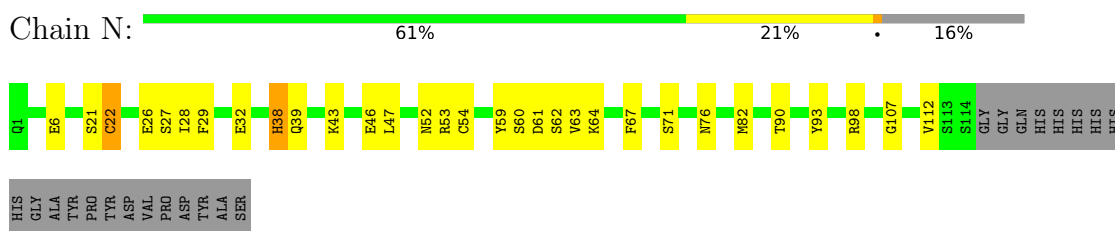
3 Residue-property plots [i](#)

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

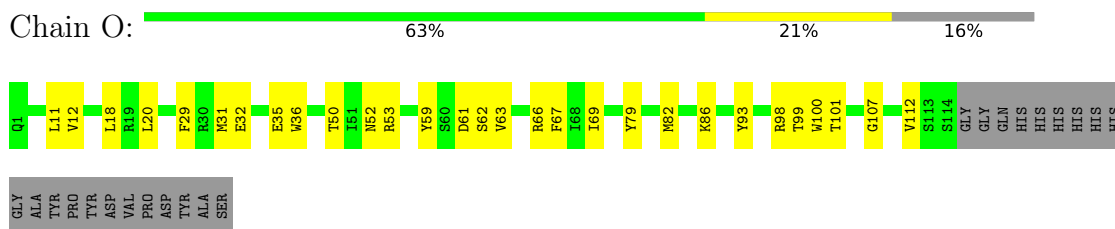
• Molecule 1: Nanosota-5



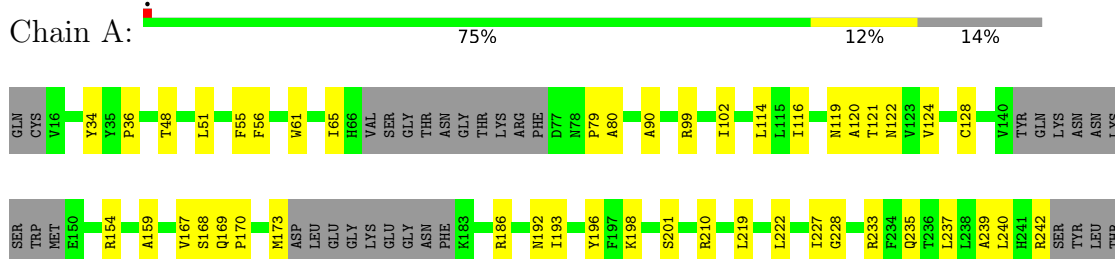
• Molecule 1: Nanosota-5

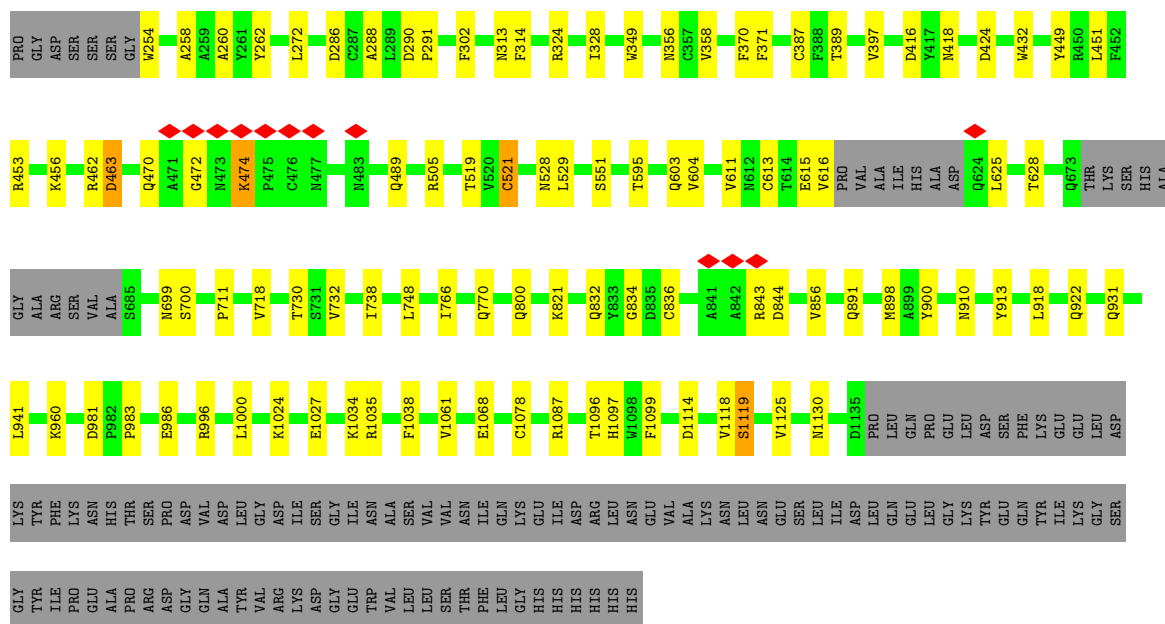


• Molecule 1: Nanosota-5



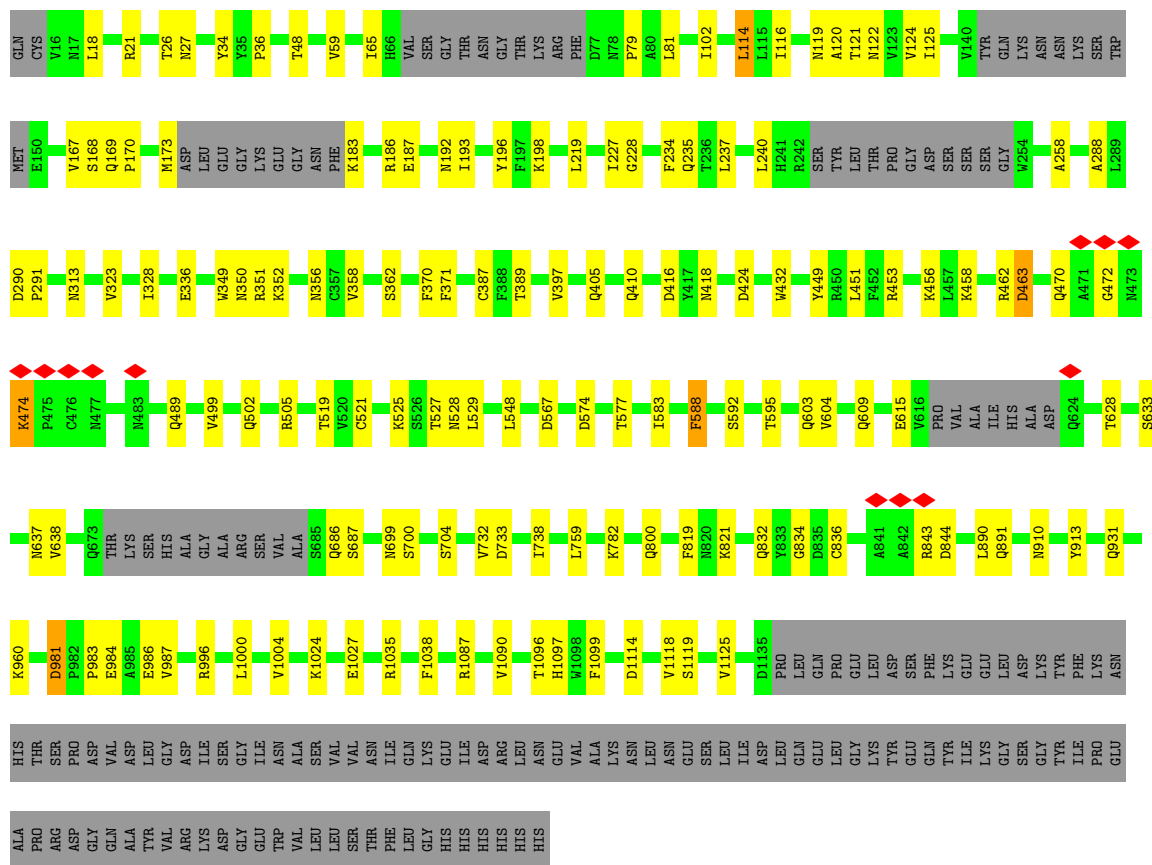
• Molecule 2: Spike glycoprotein



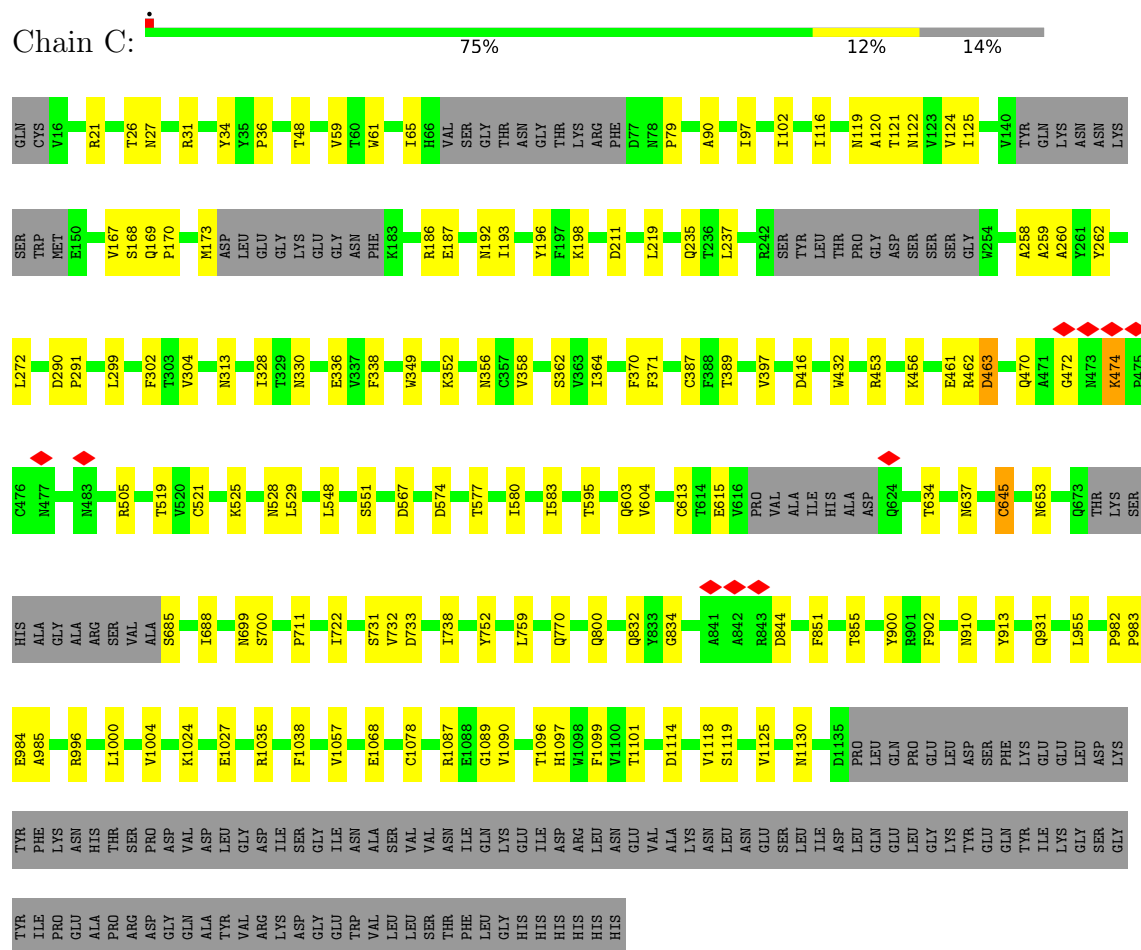


• Molecule 2: Spike glycoprotein

Chain B:



• Molecule 2: Spike glycoprotein



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D: 

MAG1
MAG2

- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E: 

MAG1
MAG2

- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F: 

MAG1
MAG2

- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:  100%



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H:  100%



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:  50% 50%



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:  100%



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:  100%



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L:  50% 50%



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P:  100%



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Q:  100%



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain R:  50% 50%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	81718	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.817	Depositor
Minimum map value	-0.343	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.103	Depositor
Map size (\AA)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.1, 1.1, 1.1	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	M	0.25	0/896	0.58	1/1209 (0.1%)
1	N	0.24	0/896	0.52	0/1209
1	O	0.25	0/896	0.52	0/1209
2	A	0.26	0/8510	0.49	0/11584
2	B	0.26	0/8510	0.48	0/11584
2	C	0.26	0/8510	0.48	0/11584
All	All	0.26	0/28218	0.49	1/38379 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	72	ASP	CB-CG-OD1	5.38	123.14	118.30

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	M	881	0	848	21	0
1	N	881	0	848	19	0
1	O	881	0	848	19	0
2	A	8314	0	8118	95	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	8314	0	8118	93	0
2	C	8314	0	8118	88	0
3	D	28	0	25	1	0
3	E	28	0	25	3	0
3	F	28	0	25	0	0
3	G	28	0	25	0	0
3	H	28	0	25	1	0
3	I	28	0	25	1	0
3	J	28	0	25	0	0
3	K	28	0	25	0	0
3	L	28	0	25	2	0
3	P	28	0	25	0	0
3	Q	28	0	25	0	0
3	R	28	0	25	1	0
4	A	154	0	143	3	0
4	B	154	0	143	2	0
4	C	154	0	143	3	0
All	All	28383	0	27627	311	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 6.

The worst 5 of 311 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)
2:C:387:CYS:HA	2:C:521:CYS:HB3	1.53	0.91
1:N:98:ARG:HD3	2:B:603:GLN:HE22	1.35	0.90
2:B:387:CYS:HA	2:B:521:CYS:HB3	1.57	0.86
2:A:242:ARG:HB3	2:A:254:TRP:CD1	2.17	0.78
2:A:102:ILE:HB	2:A:235:GLN:HB3	1.67	0.77

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	M	112/135 (83%)	104 (93%)	8 (7%)	0	100	100
1	N	112/135 (83%)	105 (94%)	7 (6%)	0	100	100
1	O	112/135 (83%)	104 (93%)	8 (7%)	0	100	100
2	A	1049/1230 (85%)	1011 (96%)	38 (4%)	0	100	100
2	B	1049/1230 (85%)	1011 (96%)	37 (4%)	1 (0%)	51	84
2	C	1049/1230 (85%)	1013 (97%)	35 (3%)	1 (0%)	51	84
All	All	3483/4095 (85%)	3348 (96%)	133 (4%)	2 (0%)	54	84

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	687	SER
2	C	688	ILE

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	M	96/112 (86%)	90 (94%)	6 (6%)	18	51
1	N	96/112 (86%)	91 (95%)	5 (5%)	23	56
1	O	96/112 (86%)	93 (97%)	3 (3%)	40	70
2	A	927/1070 (87%)	917 (99%)	10 (1%)	73	88
2	B	927/1070 (87%)	915 (99%)	12 (1%)	69	86
2	C	927/1070 (87%)	915 (99%)	12 (1%)	69	86
All	All	3069/3546 (86%)	3021 (98%)	48 (2%)	64	83

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	463	ASP

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Mol	Chain	Res	Type
2	B	981	ASP
2	B	474	LYS
2	B	819	PHE
2	C	313	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	603	GLN
2	B	1102	GLN
2	C	603	GLN
2	C	235	GLN
2	B	235	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

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	$\# Z > 2$
3	NAG	D	1	2,3	14,14,15	0.99	1 (7%)	17,19,21	0.98	1 (5%)
3	NAG	D	2	3	14,14,15	0.62	1 (7%)	17,19,21	0.36	0
3	NAG	E	1	2,3	14,14,15	0.55	0	17,19,21	0.53	0
3	NAG	E	2	3	14,14,15	0.18	0	17,19,21	0.38	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	F	1	2,3	14,14,15	1.13	2 (14%)	17,19,21	0.80	0
3	NAG	F	2	3	14,14,15	0.28	0	17,19,21	0.54	0
3	NAG	G	1	2,3	14,14,15	0.45	0	17,19,21	0.42	0
3	NAG	G	2	3	14,14,15	0.19	0	17,19,21	0.33	0
3	NAG	H	1	2,3	14,14,15	0.27	0	17,19,21	0.43	0
3	NAG	H	2	3	14,14,15	0.25	0	17,19,21	0.39	0
3	NAG	I	1	2,3	14,14,15	0.21	0	17,19,21	0.44	0
3	NAG	I	2	3	14,14,15	0.23	0	17,19,21	0.40	0
3	NAG	J	1	2,3	14,14,15	0.28	0	17,19,21	0.37	0
3	NAG	J	2	3	14,14,15	0.24	0	17,19,21	0.36	0
3	NAG	K	1	2,3	14,14,15	0.27	0	17,19,21	0.45	0
3	NAG	K	2	3	14,14,15	0.24	0	17,19,21	0.41	0
3	NAG	L	1	2,3	14,14,15	0.20	0	17,19,21	0.46	0
3	NAG	L	2	3	14,14,15	0.24	0	17,19,21	0.40	0
3	NAG	P	1	2,3	14,14,15	0.27	0	17,19,21	0.43	0
3	NAG	P	2	3	14,14,15	0.22	0	17,19,21	0.39	0
3	NAG	Q	1	2,3	14,14,15	0.25	0	17,19,21	0.43	0
3	NAG	Q	2	3	14,14,15	0.24	0	17,19,21	0.41	0
3	NAG	R	1	2,3	14,14,15	0.23	0	17,19,21	0.45	0
3	NAG	R	2	3	14,14,15	0.22	0	17,19,21	0.39	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	D	1	2,3	-	3/6/23/26	0/1/1/1
3	NAG	D	2	3	-	3/6/23/26	0/1/1/1
3	NAG	E	1	2,3	-	4/6/23/26	0/1/1/1
3	NAG	E	2	3	-	2/6/23/26	0/1/1/1
3	NAG	F	1	2,3	-	4/6/23/26	0/1/1/1
3	NAG	F	2	3	-	3/6/23/26	0/1/1/1
3	NAG	G	1	2,3	-	1/6/23/26	0/1/1/1
3	NAG	G	2	3	-	0/6/23/26	0/1/1/1
3	NAG	H	1	2,3	-	2/6/23/26	0/1/1/1
3	NAG	H	2	3	-	2/6/23/26	0/1/1/1
3	NAG	I	1	2,3	-	0/6/23/26	0/1/1/1
3	NAG	I	2	3	-	0/6/23/26	0/1/1/1
3	NAG	J	1	2,3	-	0/6/23/26	0/1/1/1
3	NAG	J	2	3	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	K	1	2,3	-	0/6/23/26	0/1/1/1
3	NAG	K	2	3	-	2/6/23/26	0/1/1/1
3	NAG	L	1	2,3	-	0/6/23/26	0/1/1/1
3	NAG	L	2	3	-	2/6/23/26	0/1/1/1
3	NAG	P	1	2,3	-	2/6/23/26	0/1/1/1
3	NAG	P	2	3	-	0/6/23/26	0/1/1/1
3	NAG	Q	1	2,3	-	2/6/23/26	0/1/1/1
3	NAG	Q	2	3	-	2/6/23/26	0/1/1/1
3	NAG	R	1	2,3	-	0/6/23/26	0/1/1/1
3	NAG	R	2	3	-	2/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	1	NAG	O5-C1	-3.56	1.38	1.43
3	F	1	NAG	C1-C2	3.45	1.57	1.52
3	D	2	NAG	O5-C1	-2.20	1.40	1.43
3	F	1	NAG	O5-C1	2.02	1.46	1.43

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	1	NAG	C3-C4-C5	2.61	114.90	110.24

There are no chirality outliers.

5 of 36 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	H	2	NAG	O5-C5-C6-O6
3	F	1	NAG	O5-C5-C6-O6
3	E	1	NAG	O5-C5-C6-O6
3	E	1	NAG	C4-C5-C6-O6
3	Q	2	NAG	O5-C5-C6-O6

There are no ring outliers.

7 monomers are involved in 9 short contacts:

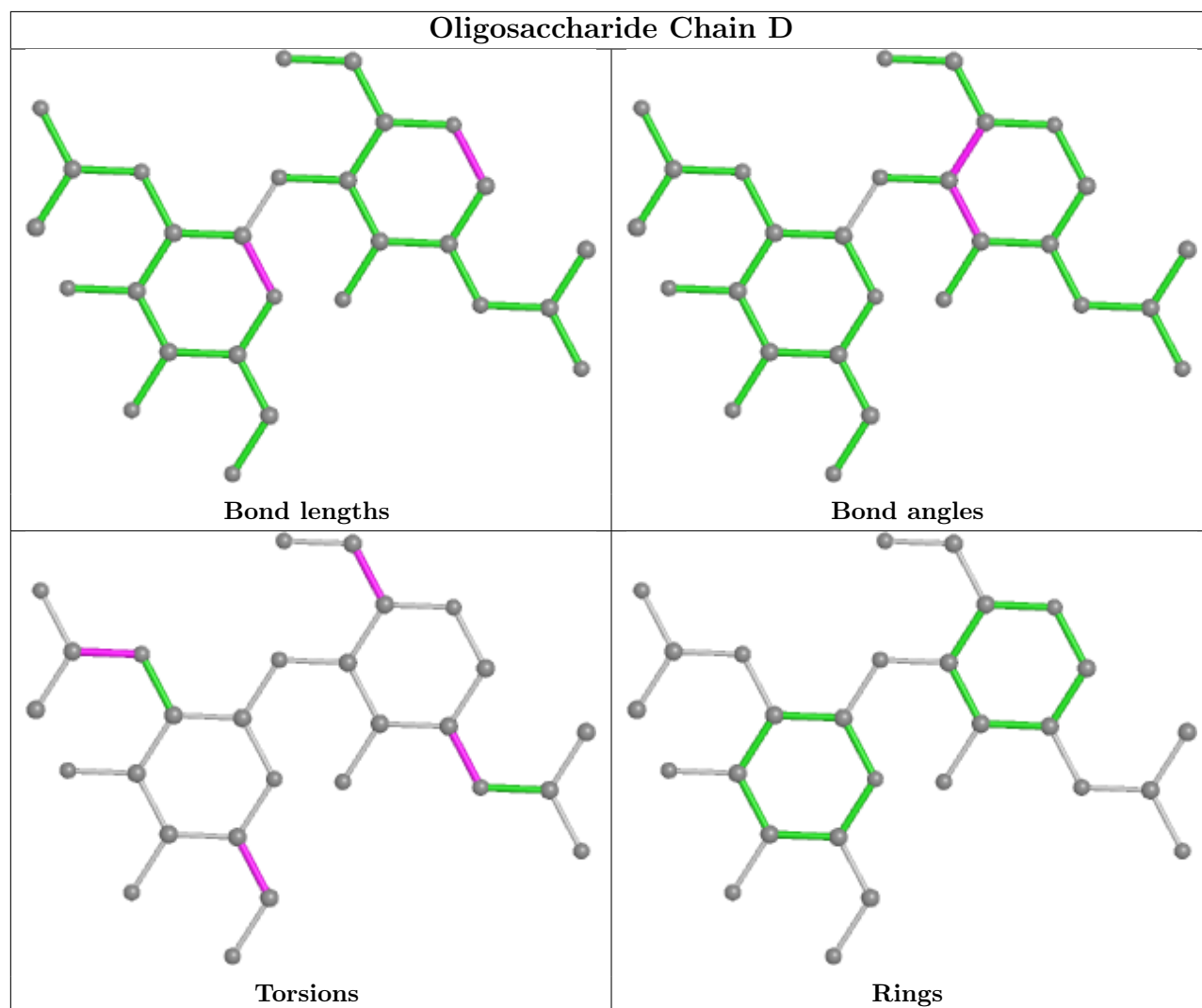
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	1	NAG	3	0

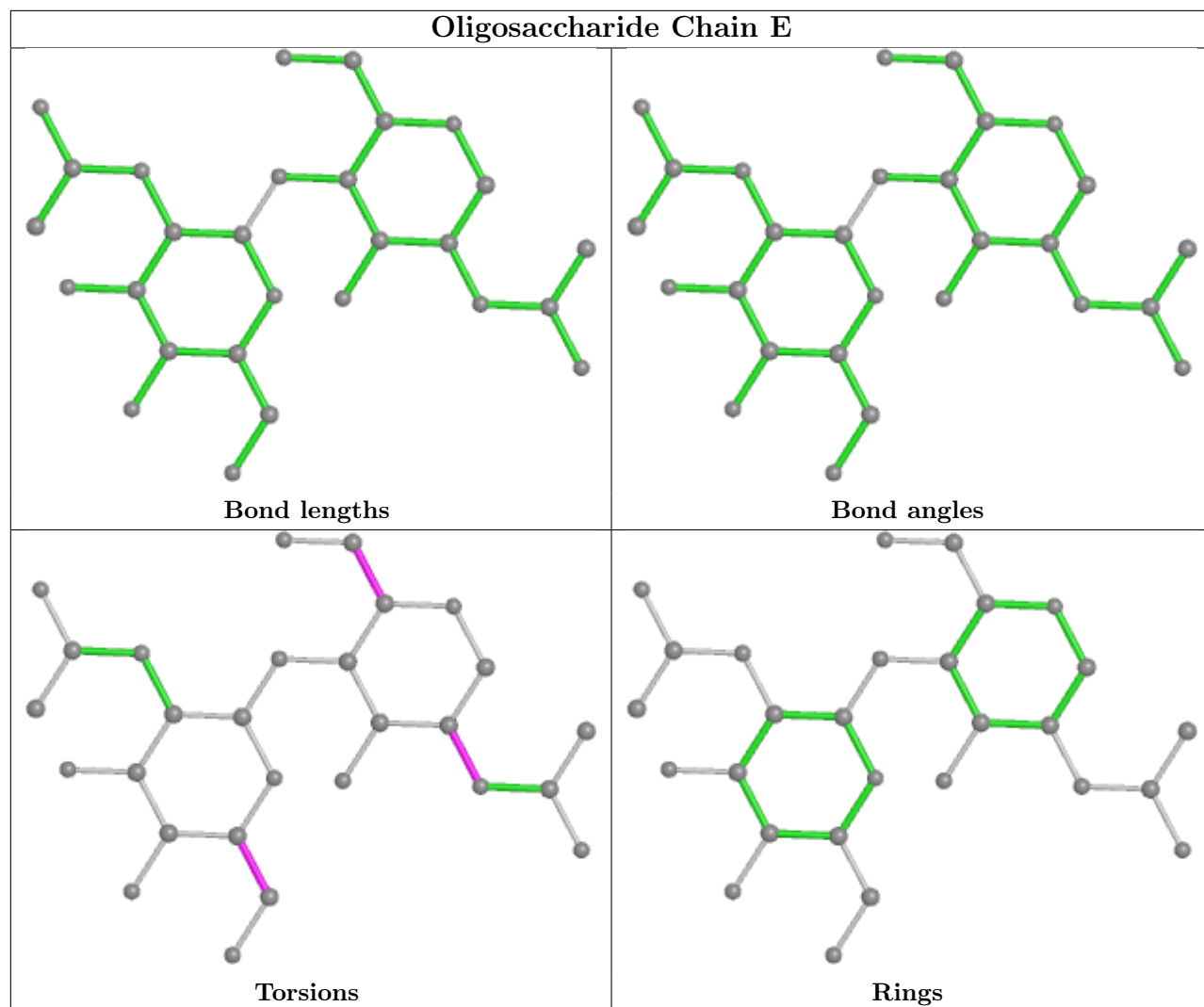
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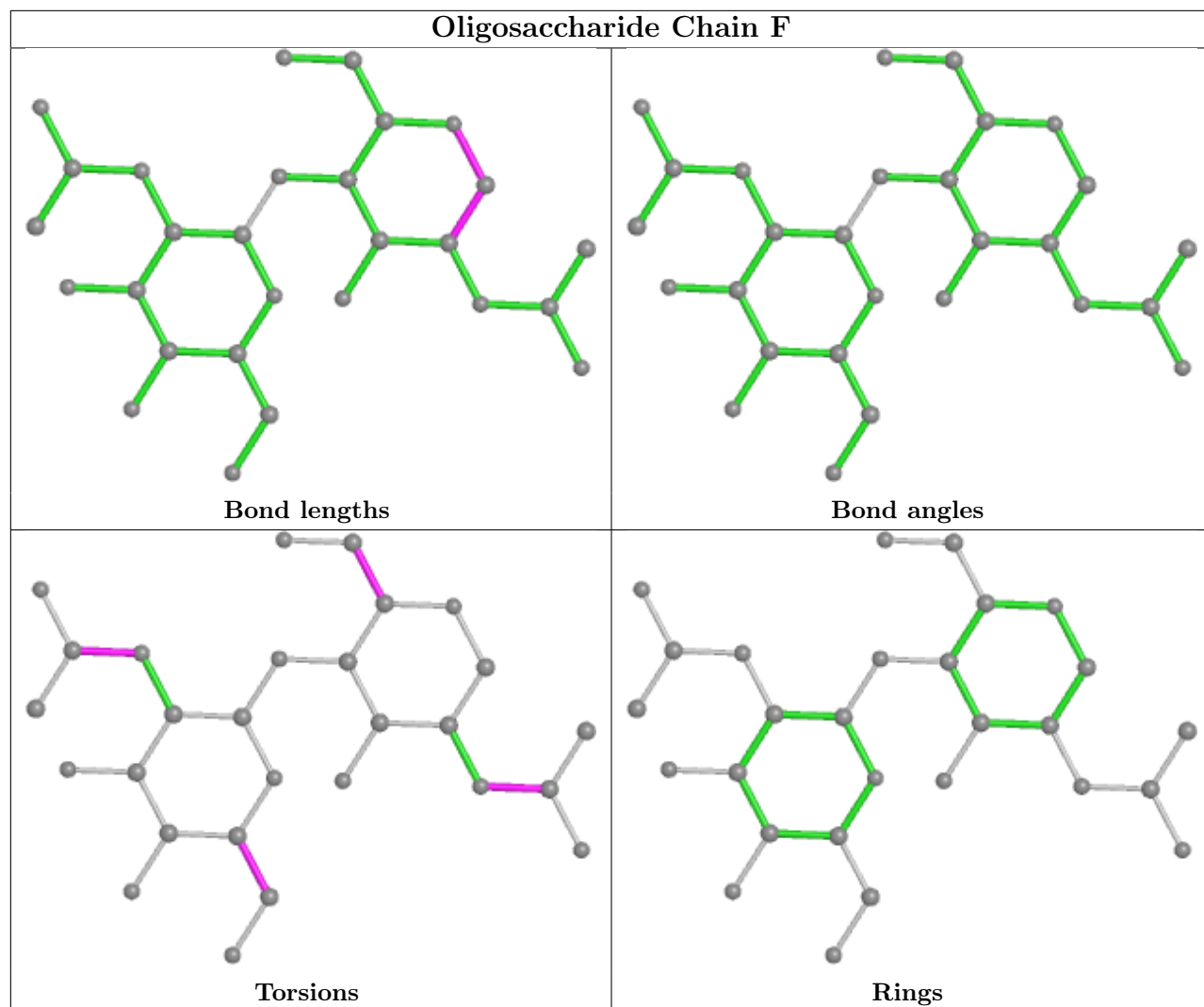
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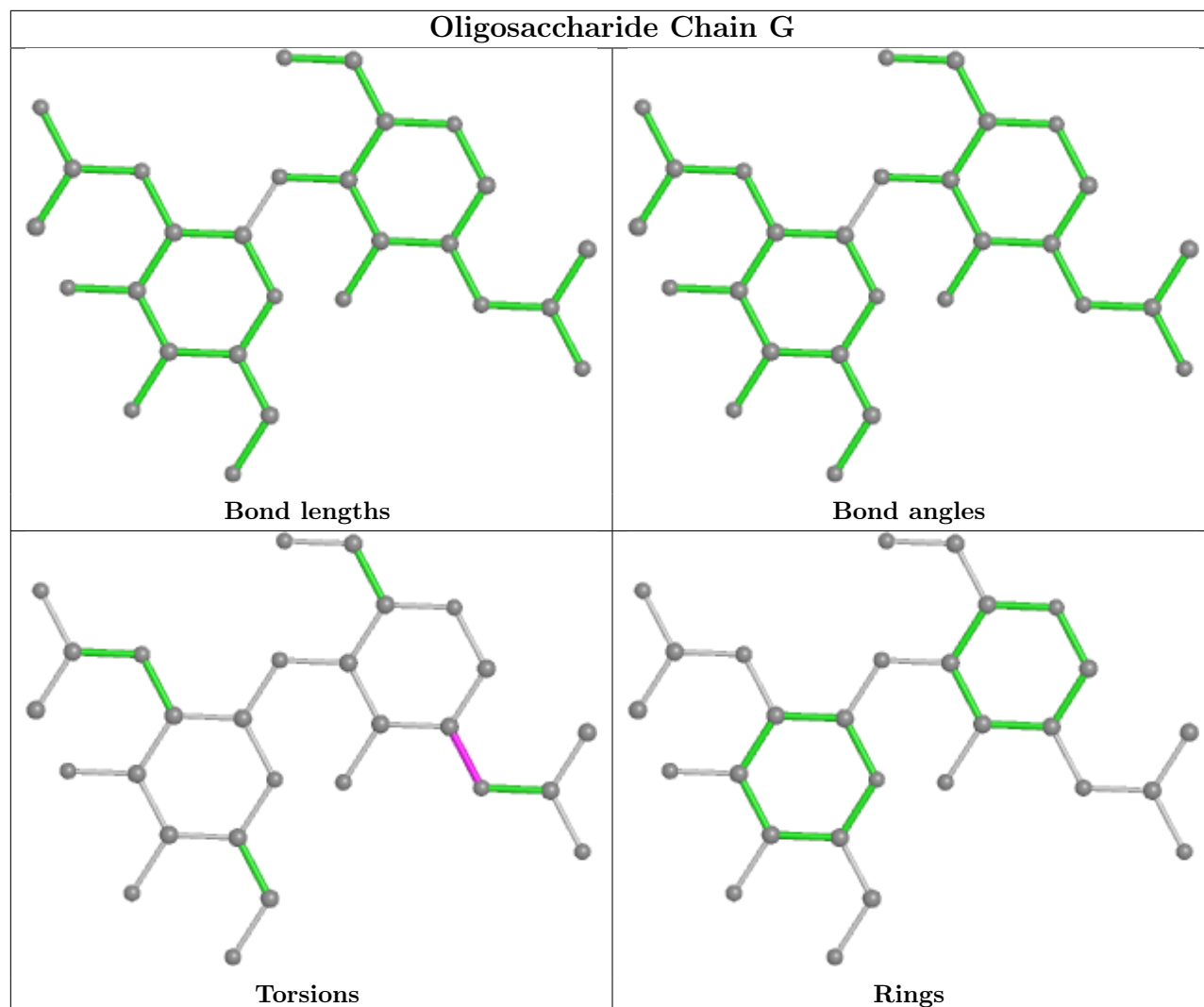
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	2	NAG	1	0
3	H	1	NAG	1	0
3	D	1	NAG	1	0
3	I	1	NAG	1	0
3	R	1	NAG	1	0
3	L	1	NAG	2	0

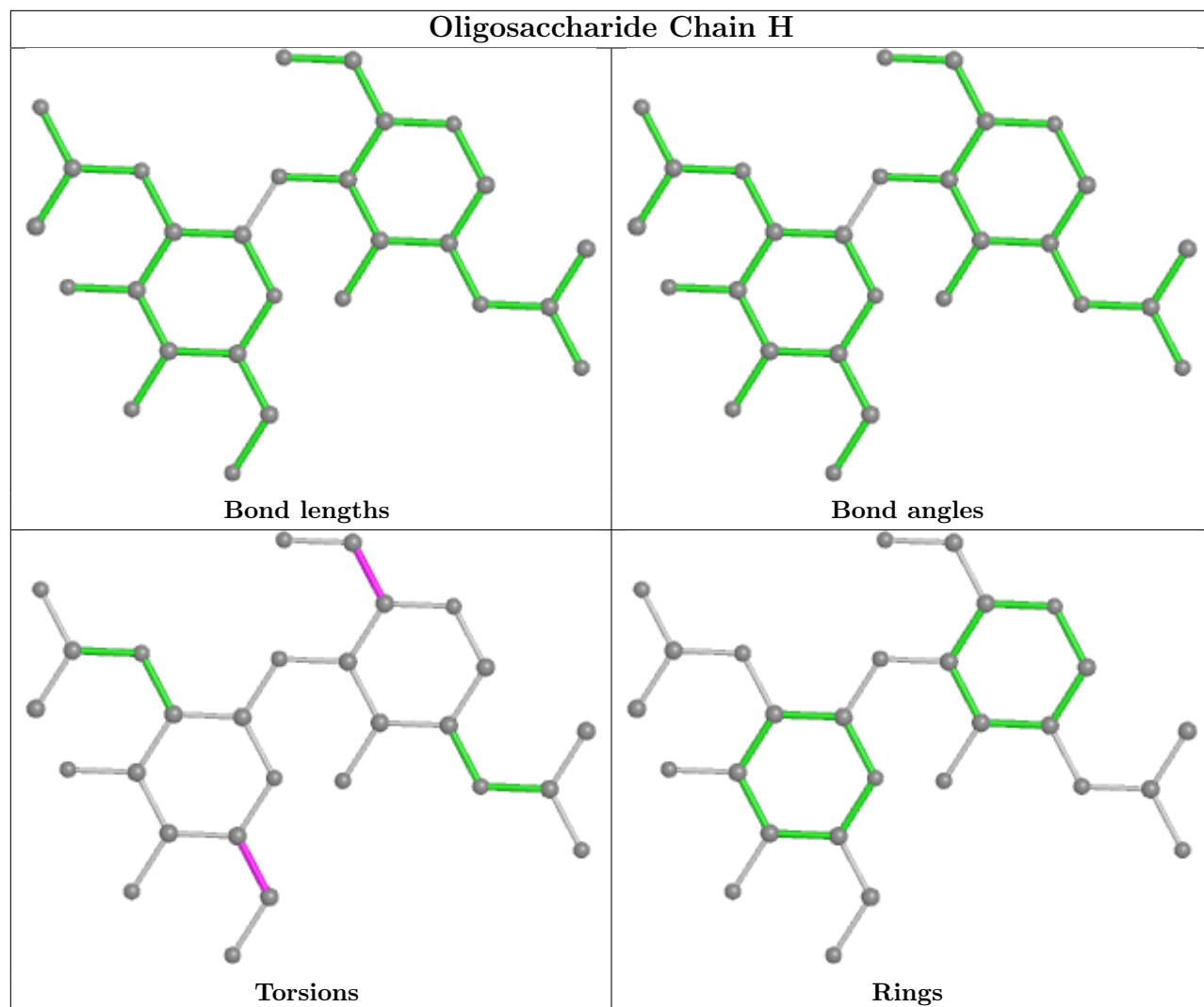
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

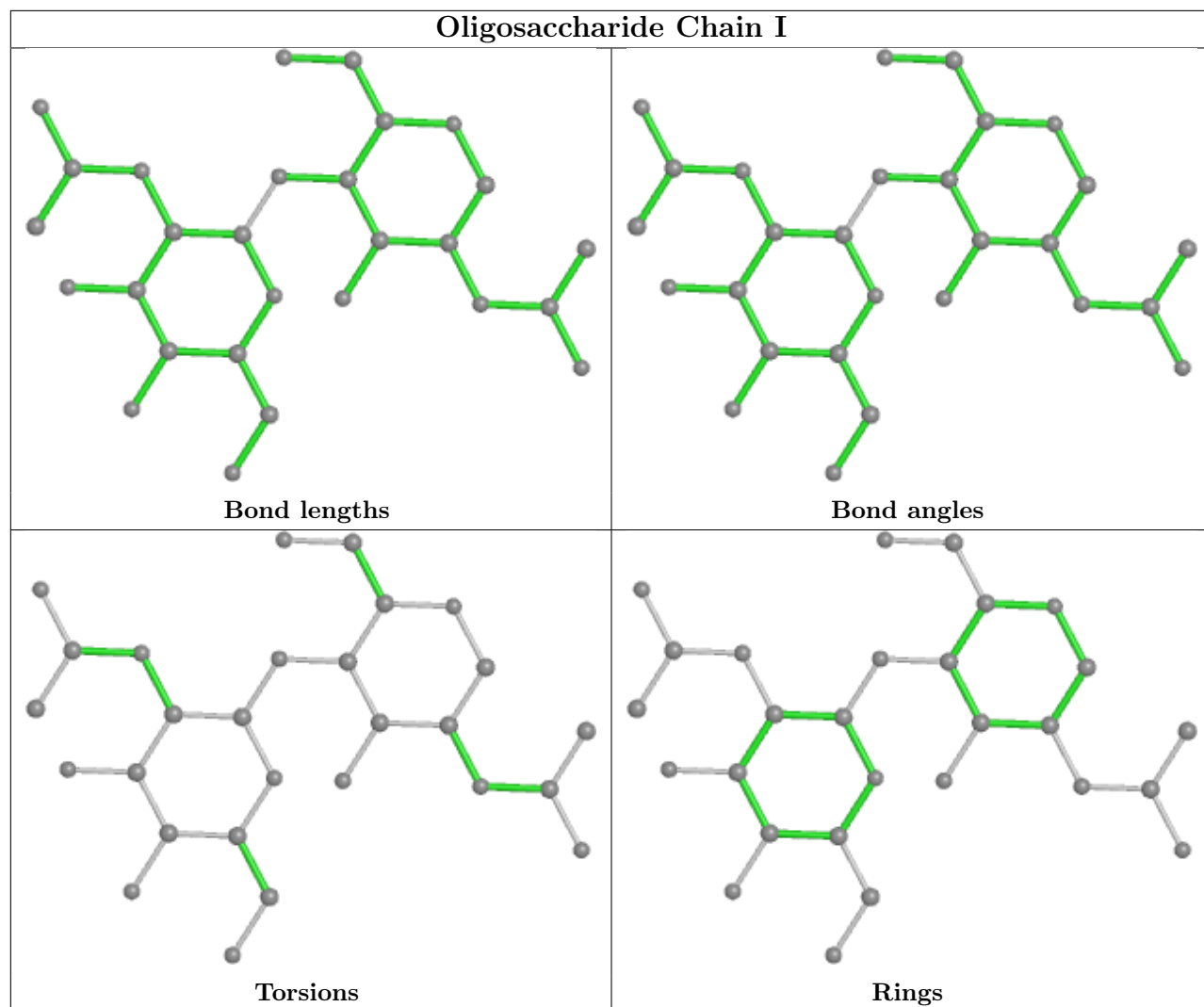


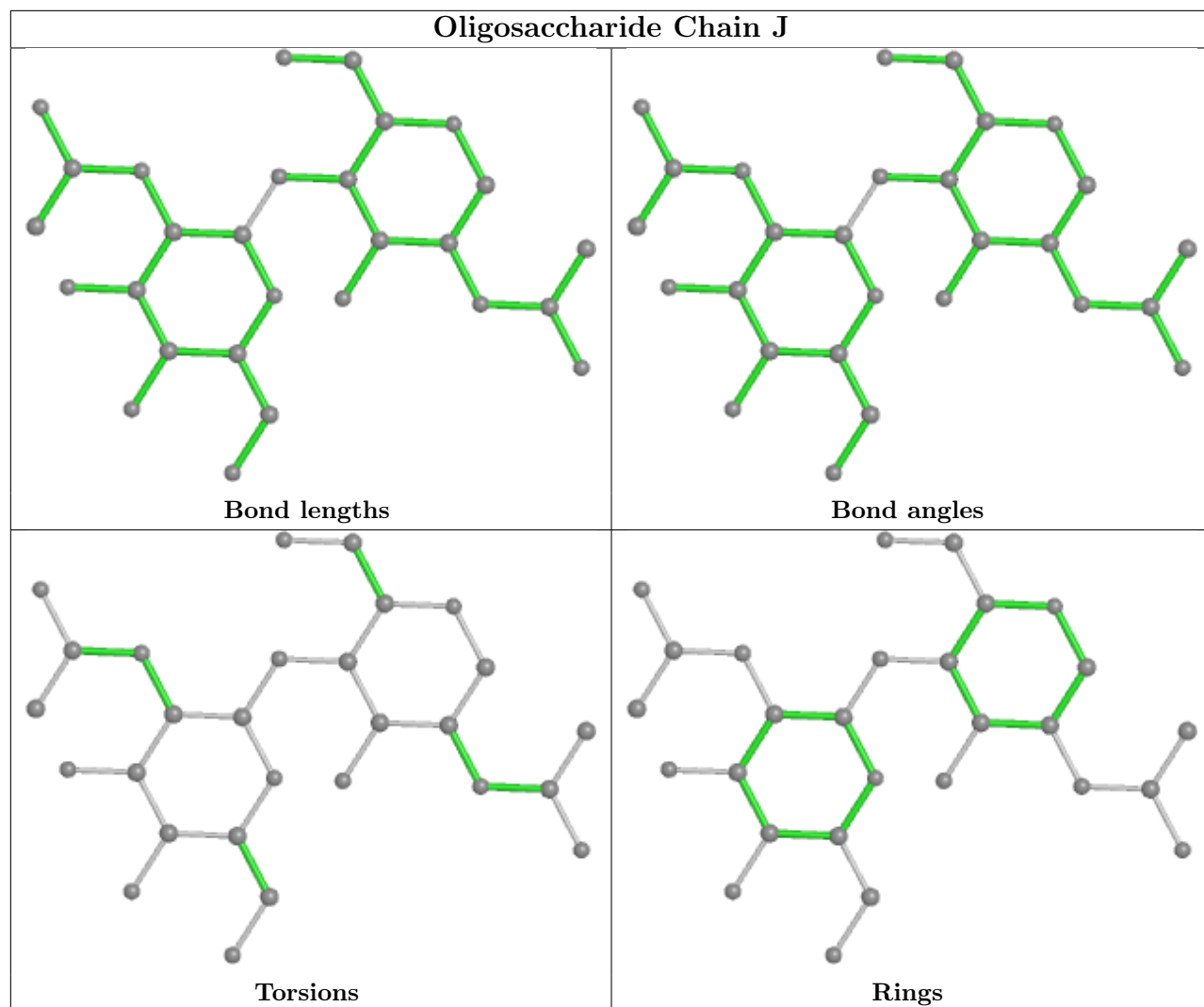


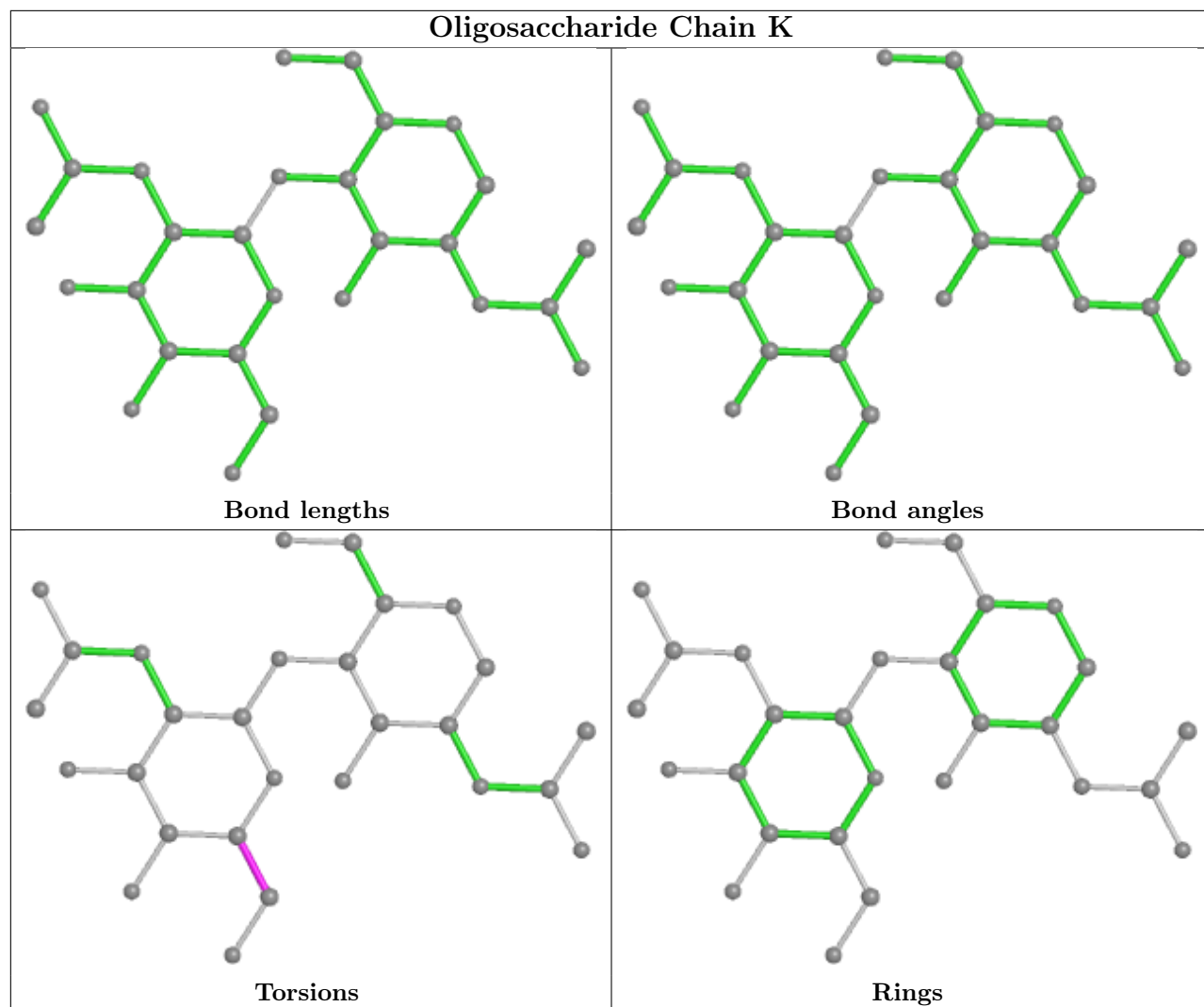


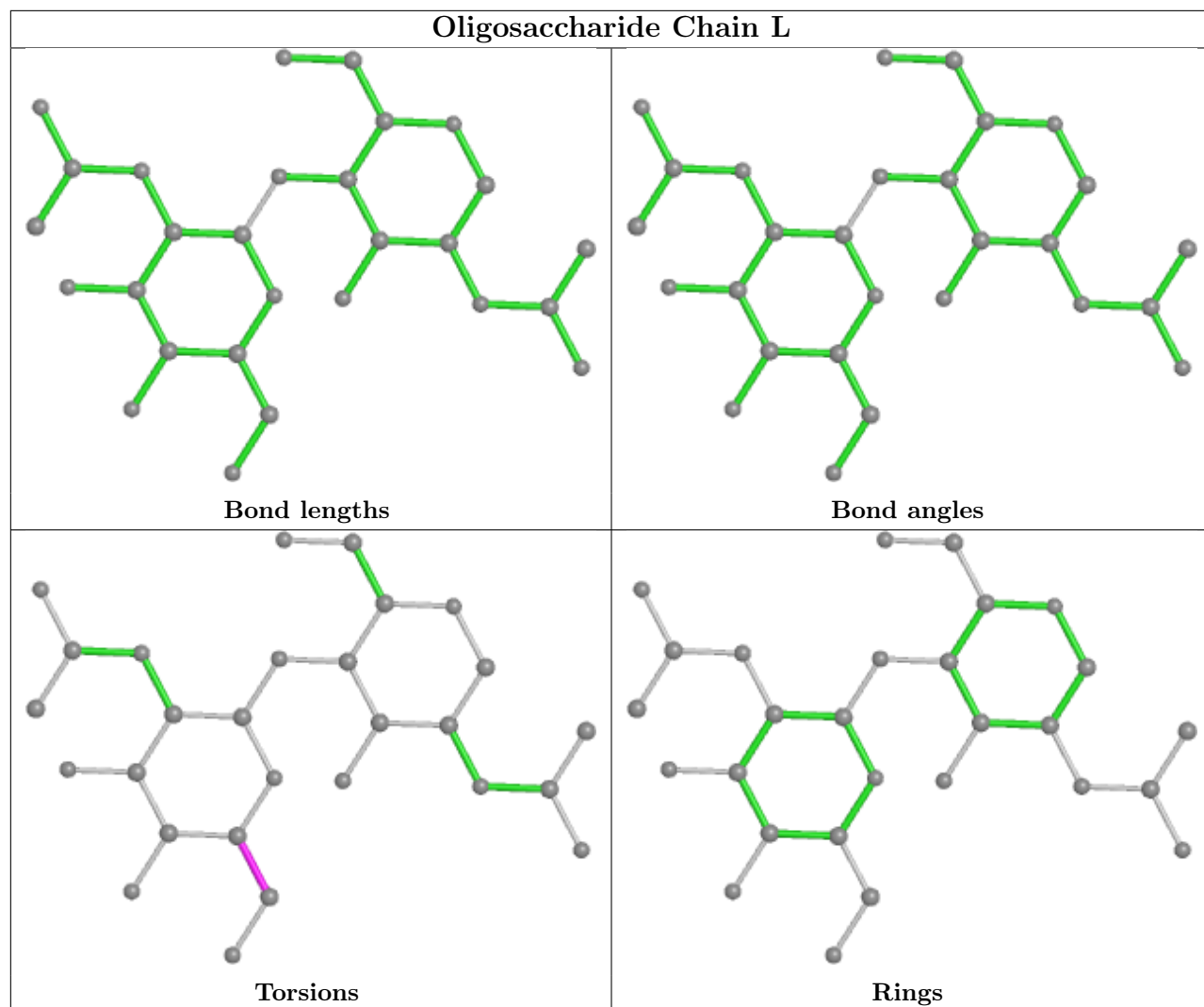


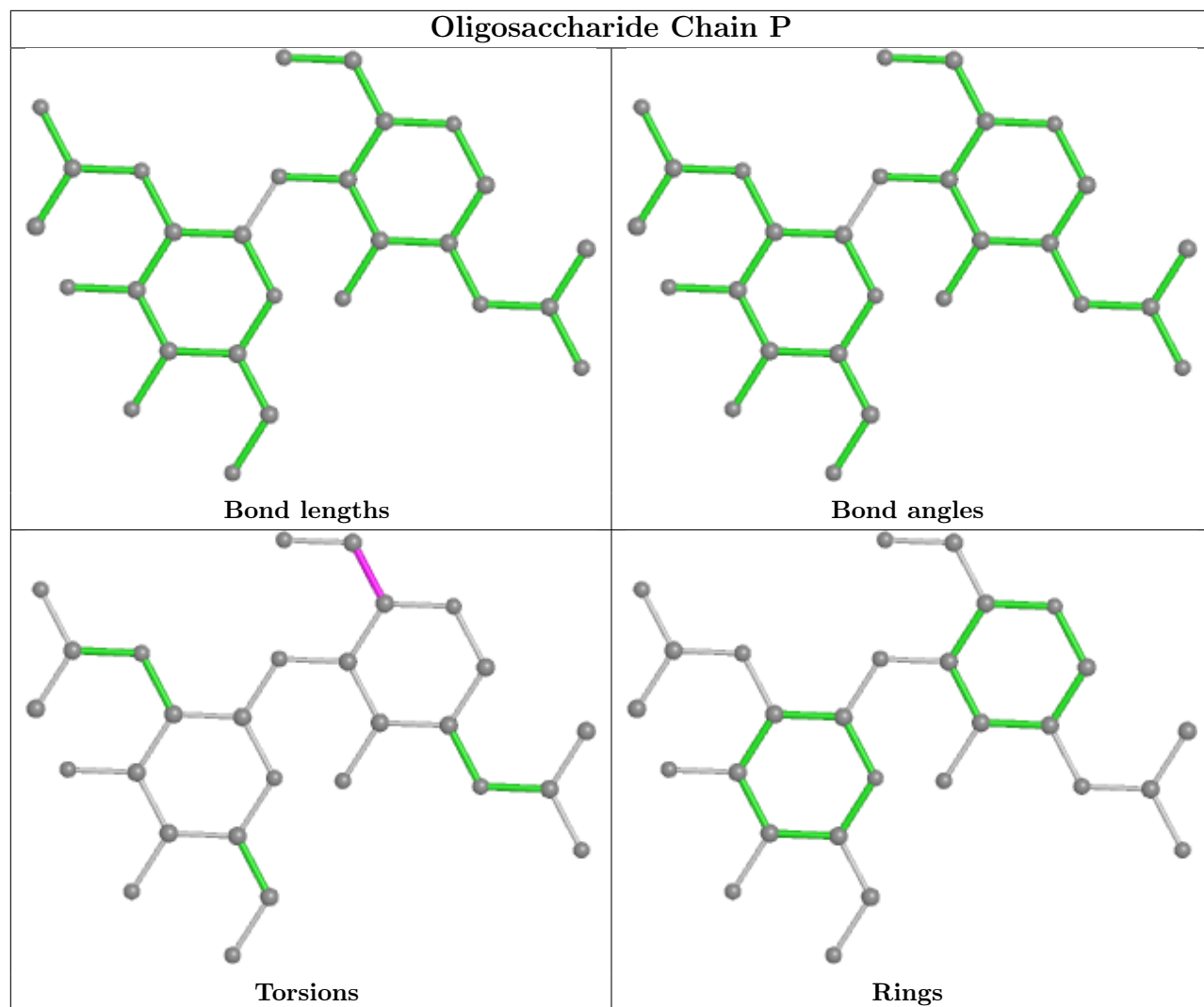


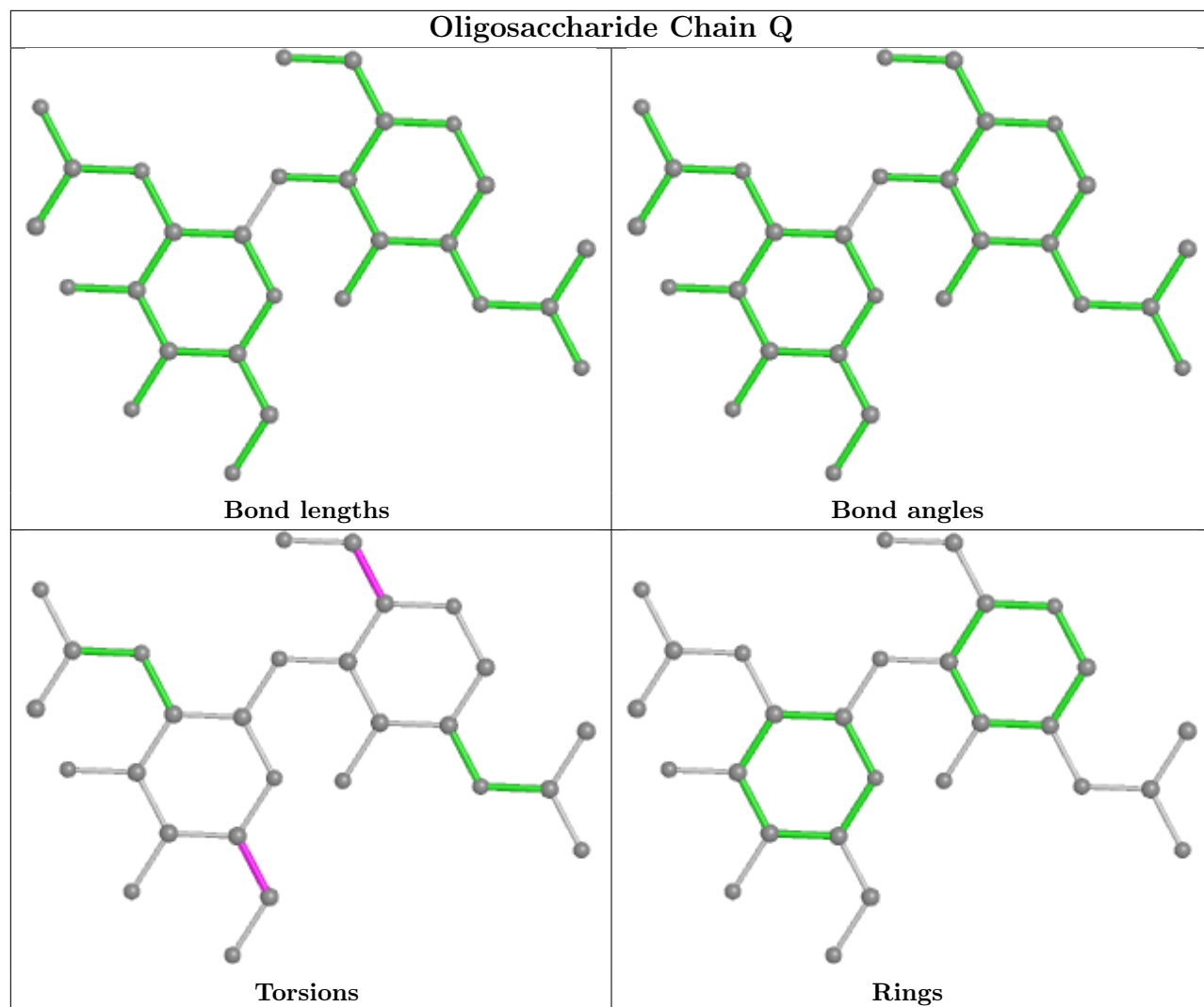


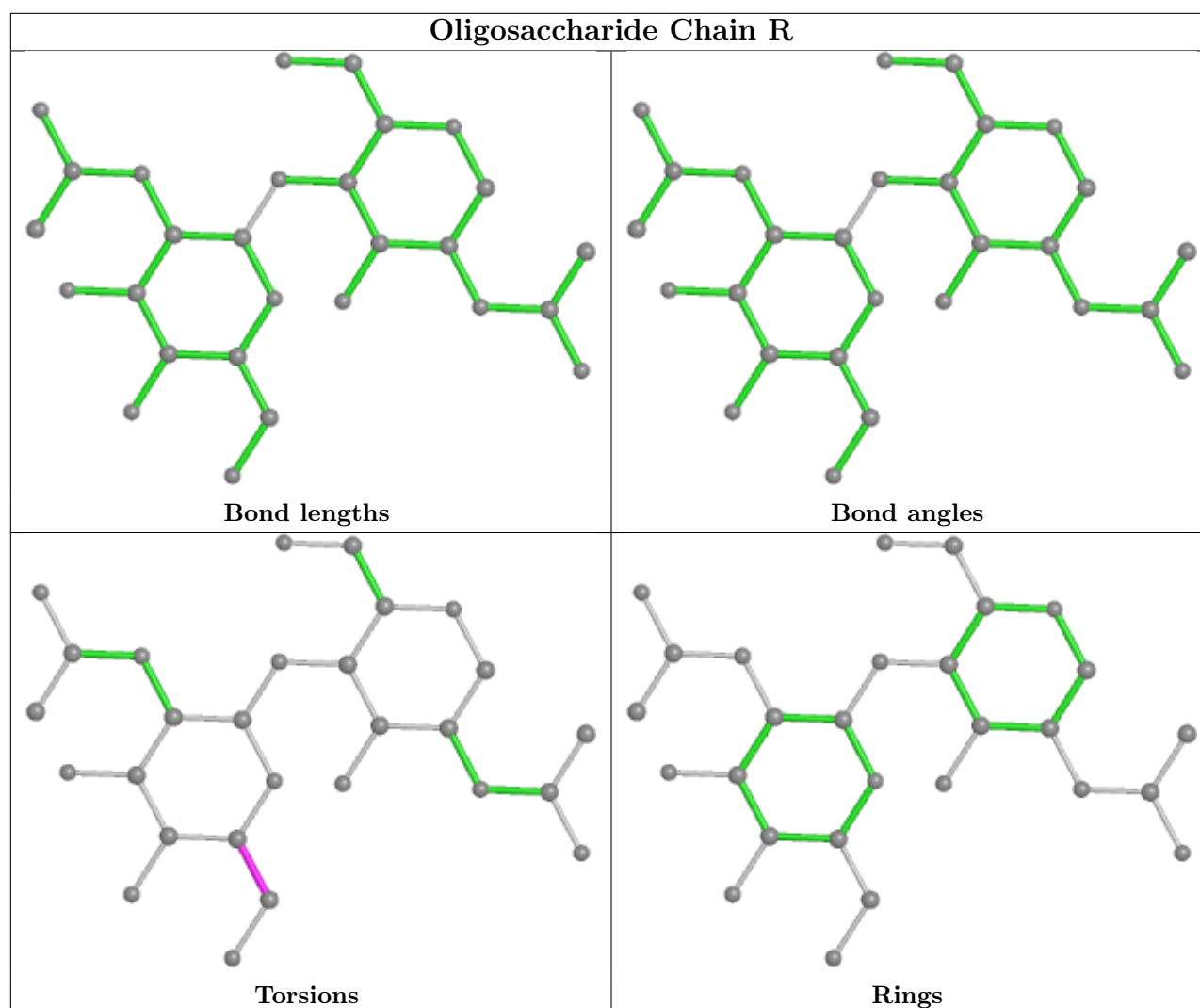












5.6 Ligand geometry [i](#)

33 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	$\# Z > 2$
4	NAG	A	1309	2	14,14,15	0.49	0	17,19,21	0.47	0
4	NAG	A	1307	2	14,14,15	0.38	0	17,19,21	0.62	0
4	NAG	A	1308	2	14,14,15	0.26	0	17,19,21	0.58	0
4	NAG	A	1311	2	14,14,15	0.58	0	17,19,21	0.51	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	B	1304	2	14,14,15	0.34	0	17,19,21	0.40	0
4	NAG	B	1301	2	14,14,15	0.31	0	17,19,21	0.45	0
4	NAG	C	1304	2	14,14,15	0.29	0	17,19,21	0.43	0
4	NAG	C	1301	2	14,14,15	0.35	0	17,19,21	0.47	0
4	NAG	A	1305	2	14,14,15	0.19	0	17,19,21	0.44	0
4	NAG	C	1305	2	14,14,15	0.18	0	17,19,21	0.44	0
4	NAG	A	1303	2	14,14,15	0.99	2 (14%)	17,19,21	1.39	1 (5%)
4	NAG	A	1310	2	14,14,15	0.32	0	17,19,21	0.50	0
4	NAG	B	1303	2	14,14,15	0.21	0	17,19,21	0.53	0
4	NAG	B	1306	2	14,14,15	0.24	0	17,19,21	0.37	0
4	NAG	B	1310	2	14,14,15	0.31	0	17,19,21	0.50	0
4	NAG	A	1306	2	14,14,15	0.37	0	17,19,21	0.43	0
4	NAG	C	1306	2	14,14,15	0.87	1 (7%)	17,19,21	0.85	1 (5%)
4	NAG	C	1310	2	14,14,15	0.25	0	17,19,21	0.47	0
4	NAG	A	1304	2	14,14,15	0.24	0	17,19,21	0.40	0
4	NAG	A	1301	2	14,14,15	0.32	0	17,19,21	0.46	0
4	NAG	B	1311	2	14,14,15	0.48	0	17,19,21	0.44	0
4	NAG	C	1311	2	14,14,15	0.48	0	17,19,21	0.53	0
4	NAG	B	1308	2	14,14,15	0.31	0	17,19,21	0.59	0
4	NAG	B	1309	2	14,14,15	0.33	0	17,19,21	0.36	0
4	NAG	B	1302	2	14,14,15	0.32	0	17,19,21	0.55	0
4	NAG	C	1309	2	14,14,15	0.26	0	17,19,21	0.36	0
4	NAG	A	1302	2	14,14,15	0.33	0	17,19,21	0.55	0
4	NAG	C	1302	2	14,14,15	0.31	0	17,19,21	0.54	0
4	NAG	C	1308	2	14,14,15	0.86	1 (7%)	17,19,21	0.99	1 (5%)
4	NAG	C	1303	2	14,14,15	0.25	0	17,19,21	0.59	0
4	NAG	B	1305	2	14,14,15	0.23	0	17,19,21	0.46	0
4	NAG	C	1307	2	14,14,15	0.37	0	17,19,21	0.42	0
4	NAG	B	1307	2	14,14,15	0.23	0	17,19,21	0.46	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	A	1309	2	-	2/6/23/26	0/1/1/1
4	NAG	A	1307	2	-	2/6/23/26	0/1/1/1
4	NAG	A	1308	2	-	2/6/23/26	0/1/1/1
4	NAG	A	1311	2	-	4/6/23/26	0/1/1/1
4	NAG	B	1304	2	-	2/6/23/26	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	B	1301	2	-	2/6/23/26	0/1/1/1
4	NAG	C	1304	2	-	0/6/23/26	0/1/1/1
4	NAG	C	1301	2	-	2/6/23/26	0/1/1/1
4	NAG	A	1305	2	-	0/6/23/26	0/1/1/1
4	NAG	C	1305	2	-	0/6/23/26	0/1/1/1
4	NAG	A	1303	2	-	3/6/23/26	0/1/1/1
4	NAG	A	1310	2	-	2/6/23/26	0/1/1/1
4	NAG	B	1303	2	-	1/6/23/26	0/1/1/1
4	NAG	B	1306	2	-	2/6/23/26	0/1/1/1
4	NAG	B	1310	2	-	0/6/23/26	0/1/1/1
4	NAG	A	1306	2	-	3/6/23/26	0/1/1/1
4	NAG	C	1306	2	-	3/6/23/26	0/1/1/1
4	NAG	C	1310	2	-	2/6/23/26	0/1/1/1
4	NAG	A	1304	2	-	2/6/23/26	0/1/1/1
4	NAG	A	1301	2	-	2/6/23/26	0/1/1/1
4	NAG	B	1311	2	-	0/6/23/26	0/1/1/1
4	NAG	C	1311	2	-	0/6/23/26	0/1/1/1
4	NAG	B	1308	2	-	3/6/23/26	0/1/1/1
4	NAG	B	1309	2	-	2/6/23/26	0/1/1/1
4	NAG	B	1302	2	-	3/6/23/26	0/1/1/1
4	NAG	C	1309	2	-	2/6/23/26	0/1/1/1
4	NAG	A	1302	2	-	3/6/23/26	0/1/1/1
4	NAG	C	1302	2	-	3/6/23/26	0/1/1/1
4	NAG	C	1308	2	-	0/6/23/26	0/1/1/1
4	NAG	C	1303	2	-	3/6/23/26	0/1/1/1
4	NAG	B	1305	2	-	1/6/23/26	0/1/1/1
4	NAG	C	1307	2	-	2/6/23/26	0/1/1/1
4	NAG	B	1307	2	-	2/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	1308	NAG	O5-C1	3.05	1.48	1.43
4	A	1303	NAG	O5-C1	2.90	1.48	1.43
4	C	1306	NAG	O5-C1	2.56	1.47	1.43
4	A	1303	NAG	C1-C2	2.03	1.55	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1303	NAG	C1-O5-C5	5.33	119.41	112.19
4	C	1308	NAG	C1-O5-C5	3.56	117.02	112.19
4	C	1306	NAG	C1-O5-C5	3.29	116.65	112.19

There are no chirality outliers.

5 of 60 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1301	NAG	C4-C5-C6-O6
4	C	1301	NAG	C4-C5-C6-O6
4	C	1310	NAG	O5-C5-C6-O6
4	C	1309	NAG	O5-C5-C6-O6
4	A	1307	NAG	C4-C5-C6-O6

There are no ring outliers.

8 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1311	NAG	1	0
4	B	1301	NAG	1	0
4	C	1301	NAG	1	0
4	A	1303	NAG	1	0
4	A	1301	NAG	1	0
4	B	1309	NAG	1	0
4	C	1308	NAG	1	0
4	C	1303	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.

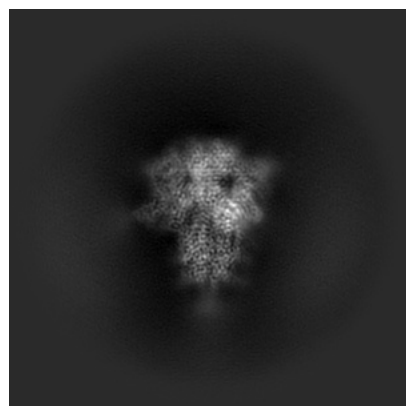
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42218. These allow visual inspection of the internal detail of the map and identification of artifacts.

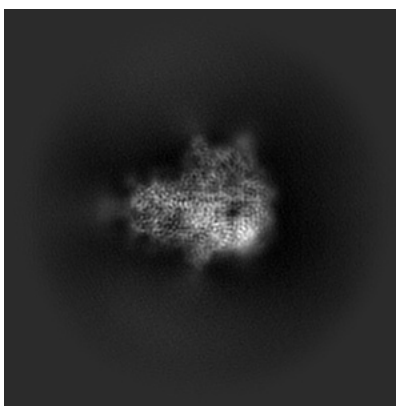
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

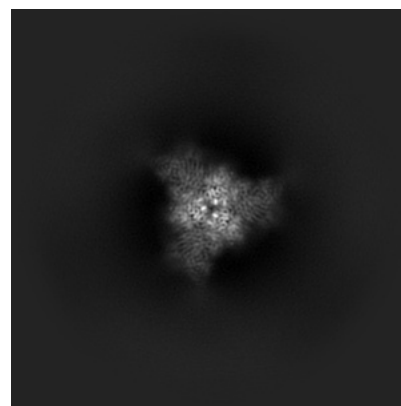
6.1.1 Primary map



X

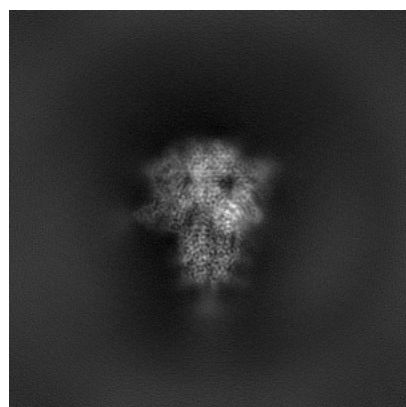


Y

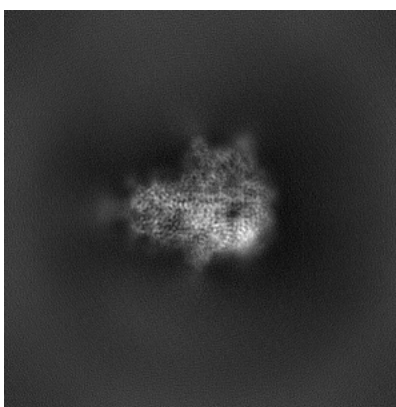


Z

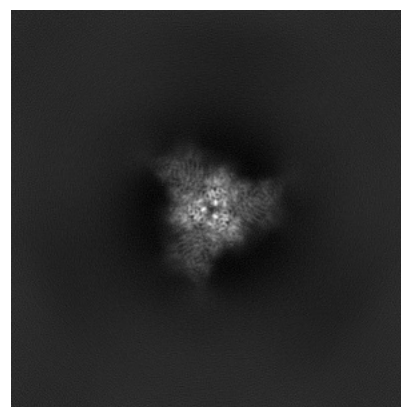
6.1.2 Raw map



X



Y

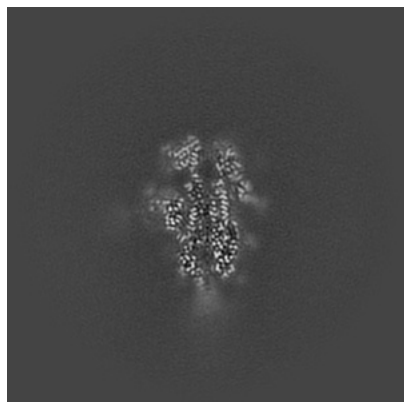


Z

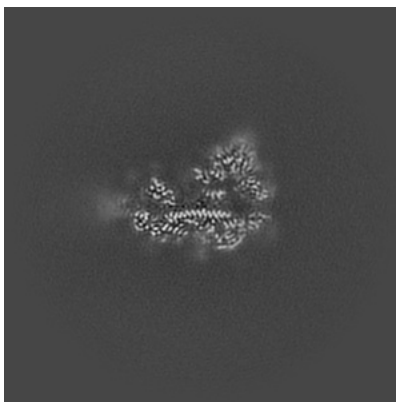
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

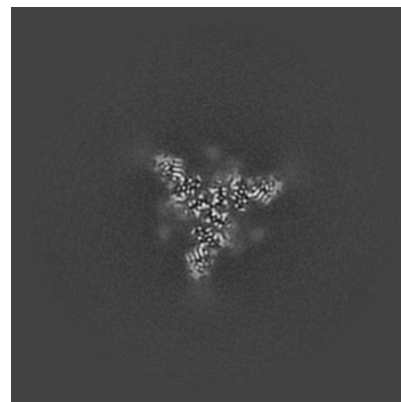
6.2.1 Primary map



X Index: 192

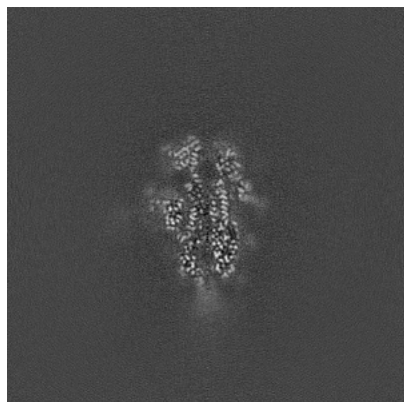


Y Index: 192

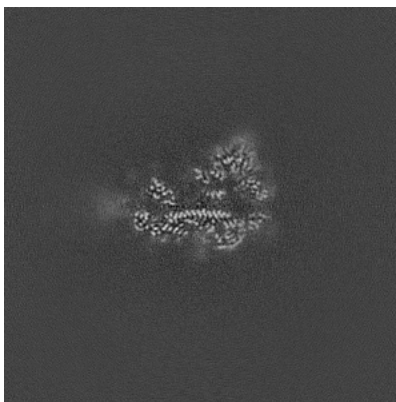


Z Index: 192

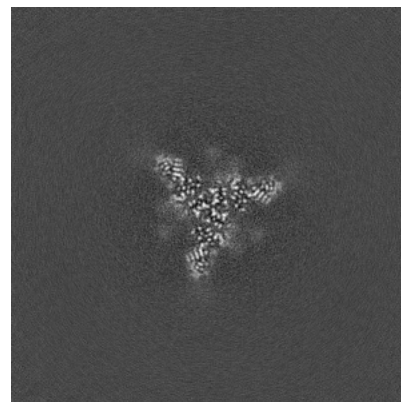
6.2.2 Raw map



X Index: 192



Y Index: 192

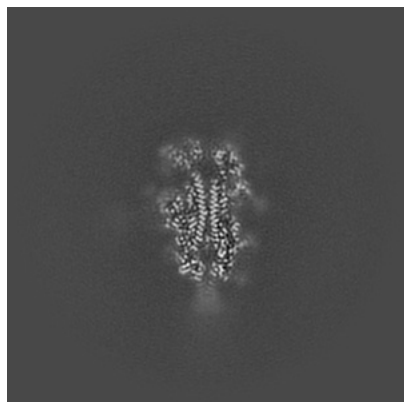


Z Index: 192

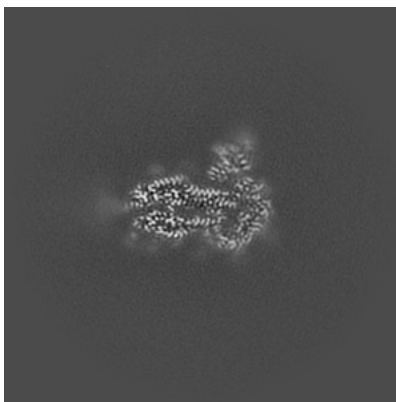
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

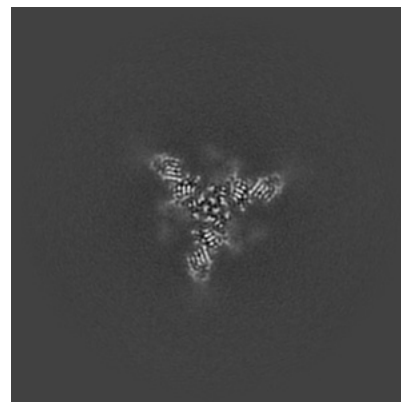
6.3.1 Primary map



X Index: 195

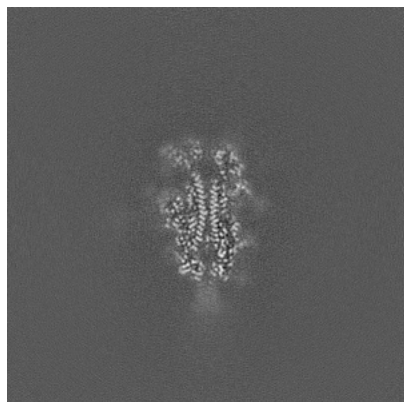


Y Index: 183

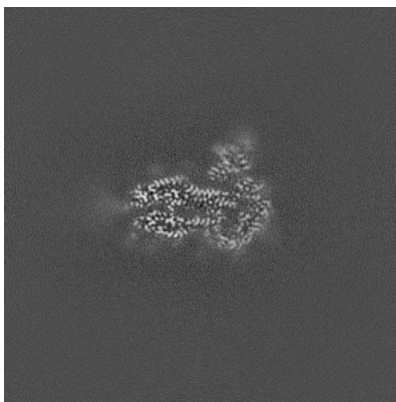


Z Index: 190

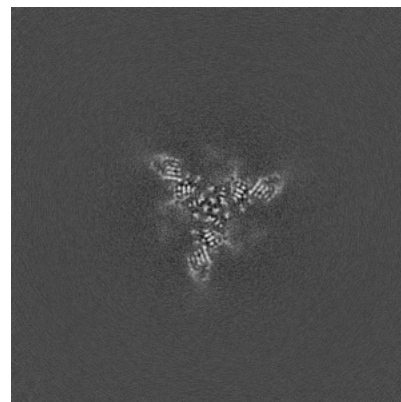
6.3.2 Raw map



X Index: 195



Y Index: 183

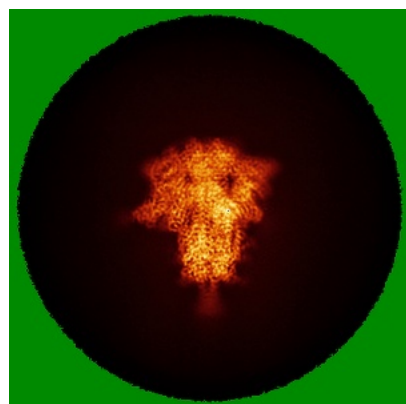


Z Index: 190

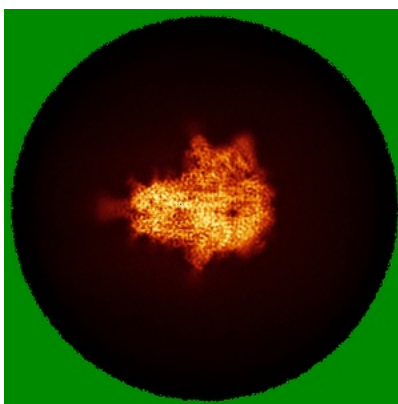
The images above show the largest variance slices of the map in three orthogonal directions.

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

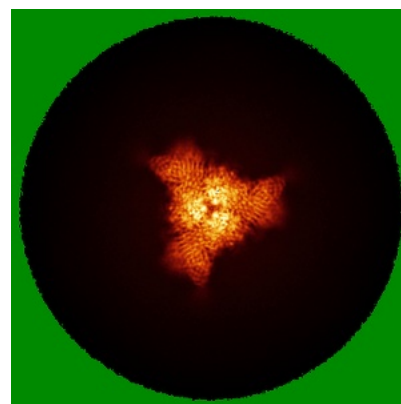
6.4.1 Primary map



X

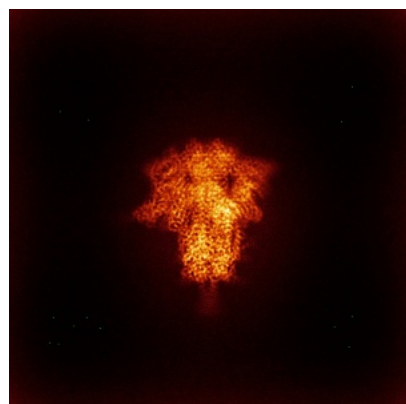


Y

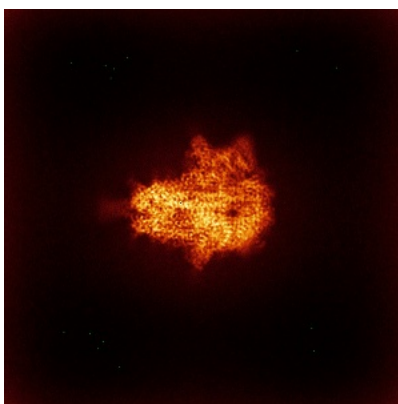


Z

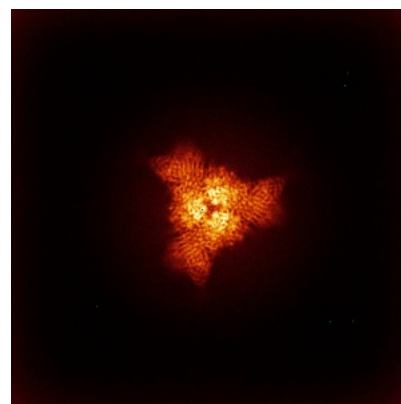
6.4.2 Raw map



X



Y

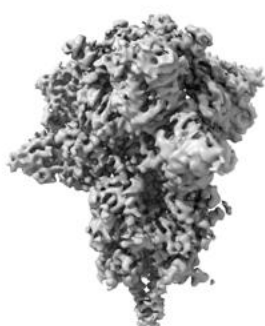


Z

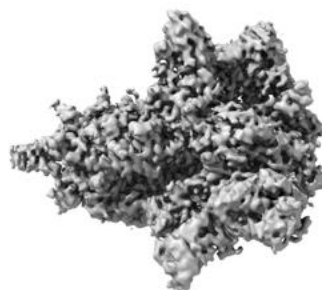
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

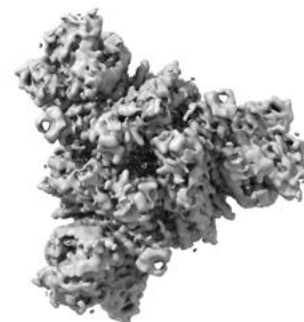
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.103. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

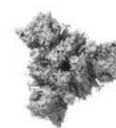
6.5.2 Raw map



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.

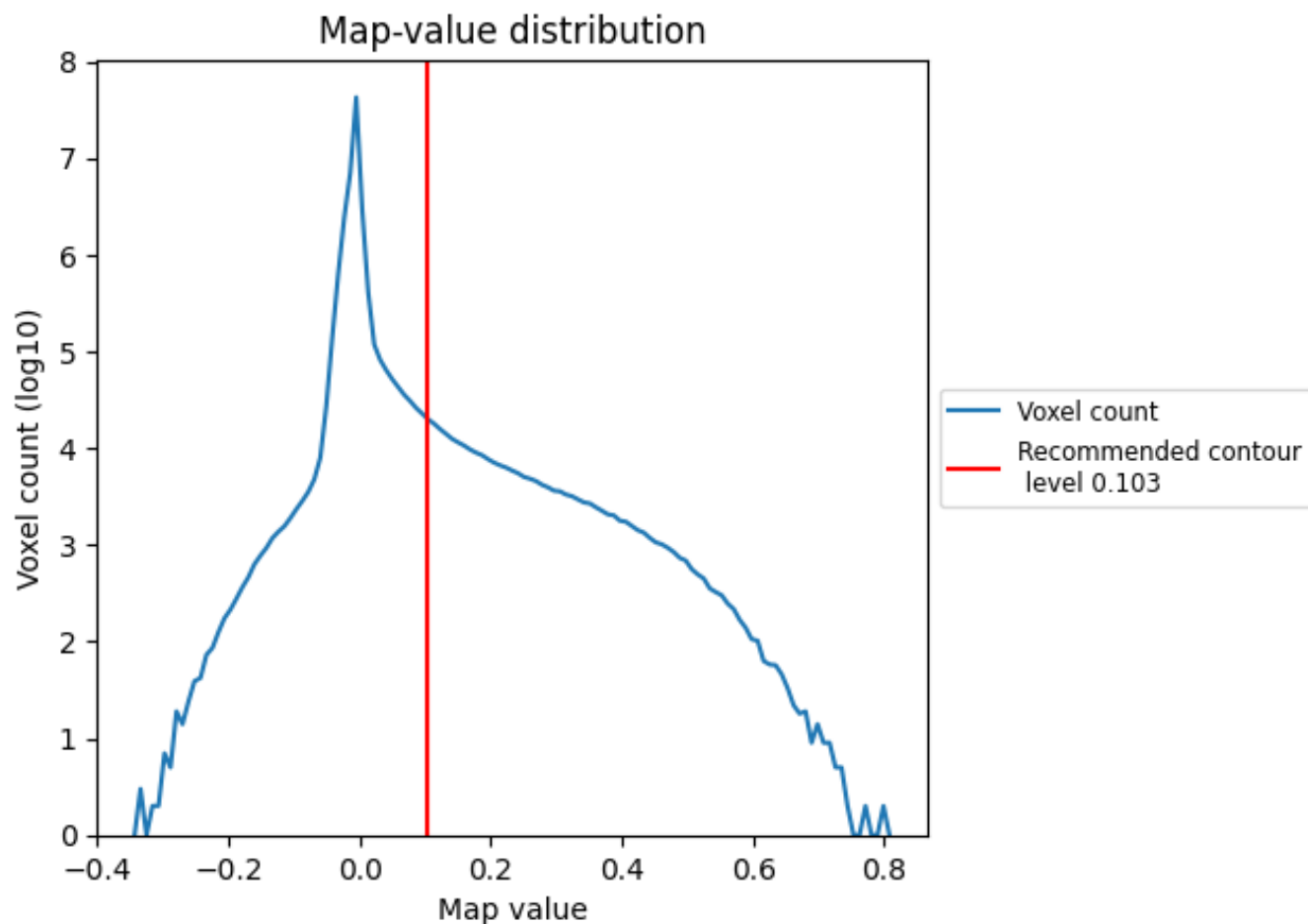
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

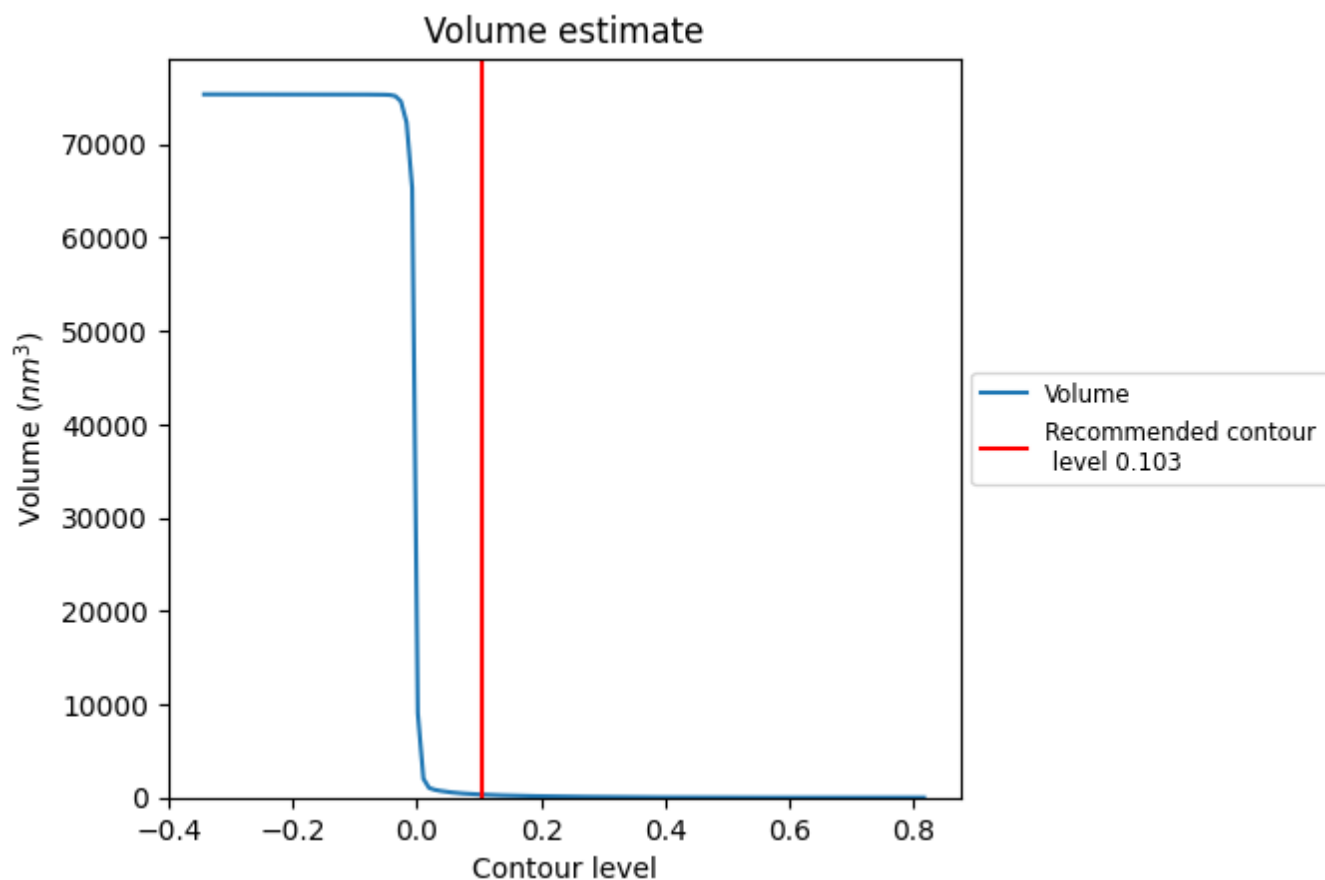
This section contains the results of statistical analysis of the map.

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.

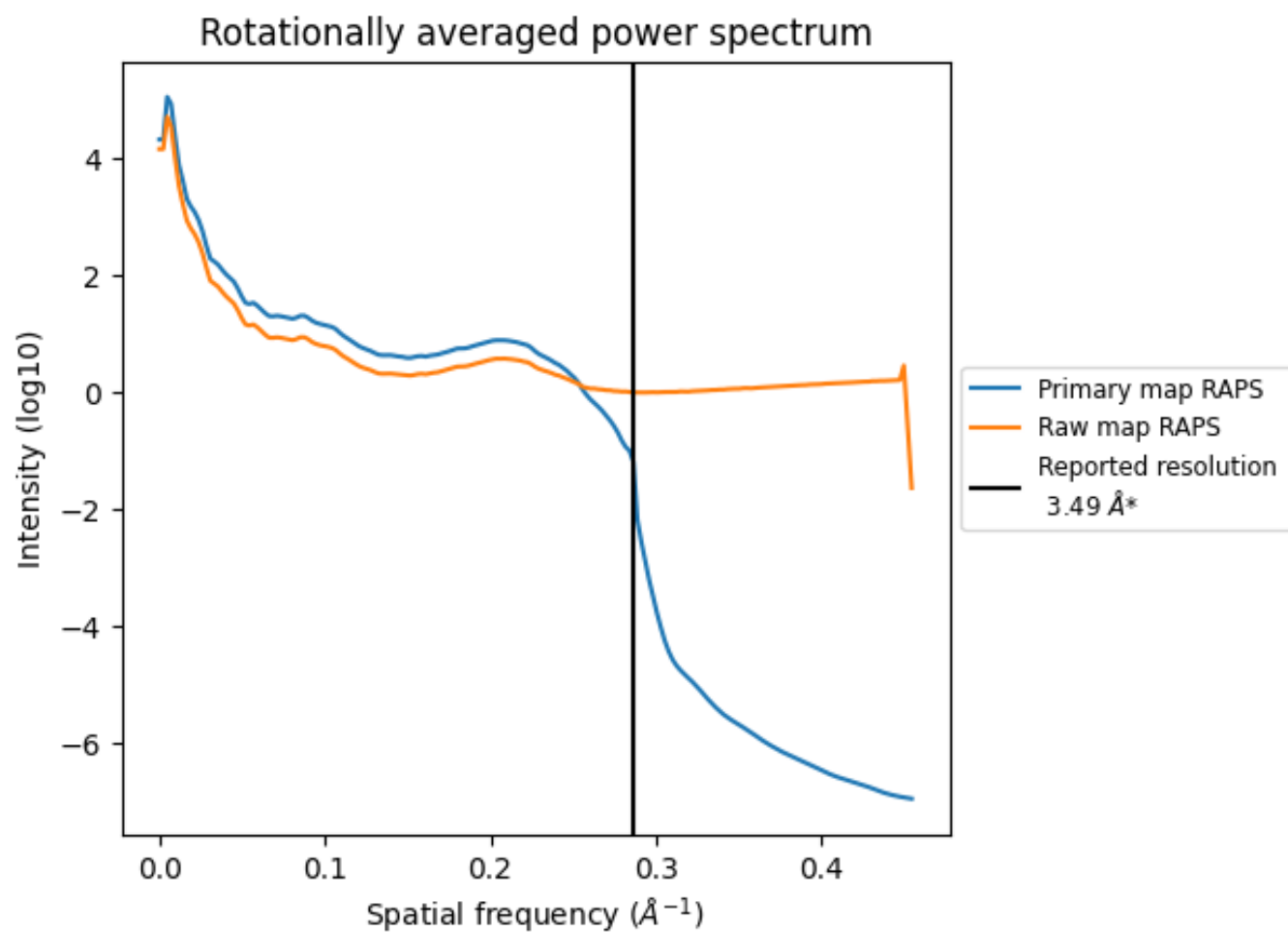
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 324 nm³; this corresponds to an approximate mass of 293 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 ⓘ

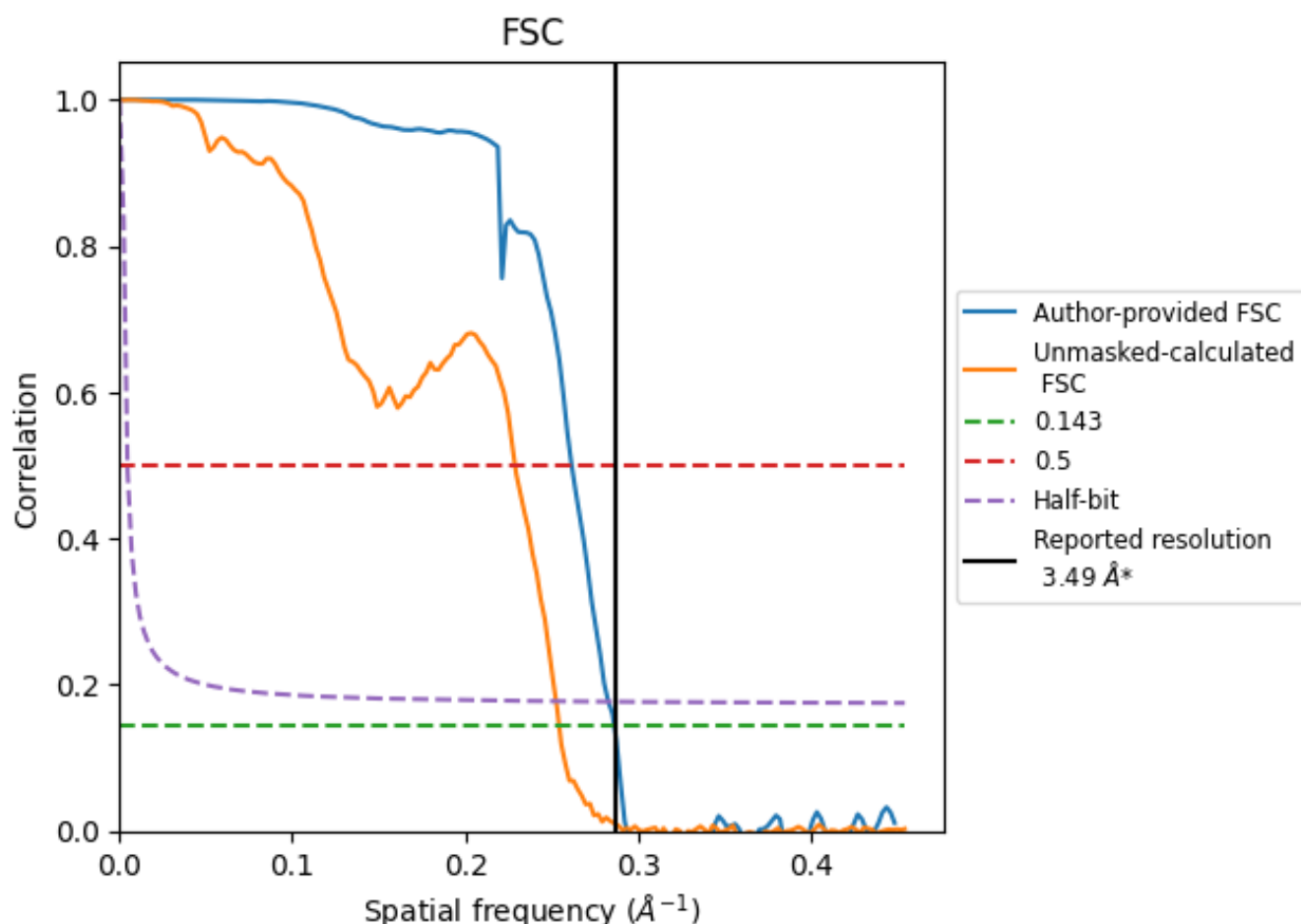


*Reported resolution corresponds to spatial frequency of 0.287 Å⁻¹

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 0.287 Å⁻¹

8.2 Resolution estimates [i](#)

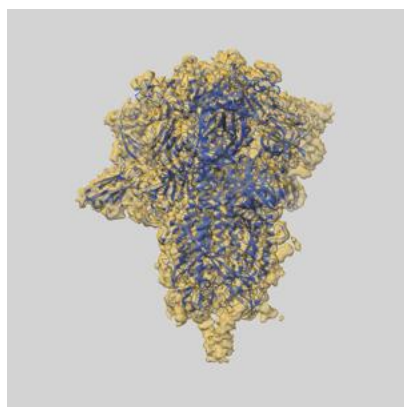
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.49	-	-
Author-provided FSC curve	3.49	3.82	3.53
Unmasked-calculated*	3.93	4.37	3.96

*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 3.93 differs from the reported value 3.49 by more than 10 %

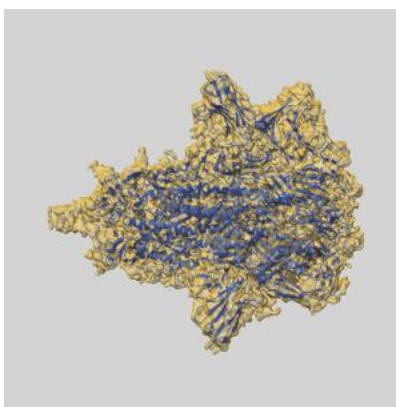
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-42218 and PDB model 8UG9. Per-residue inclusion information can be found in section 3 on page 14.

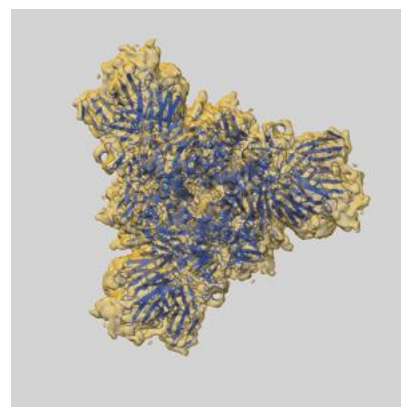
9.1 Map-model overlay [i](#)



X



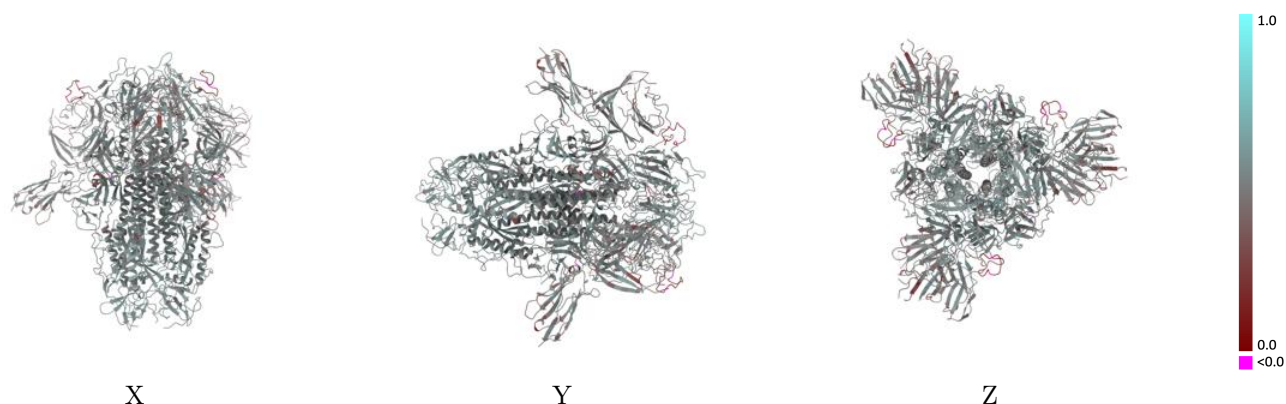
Y



Z

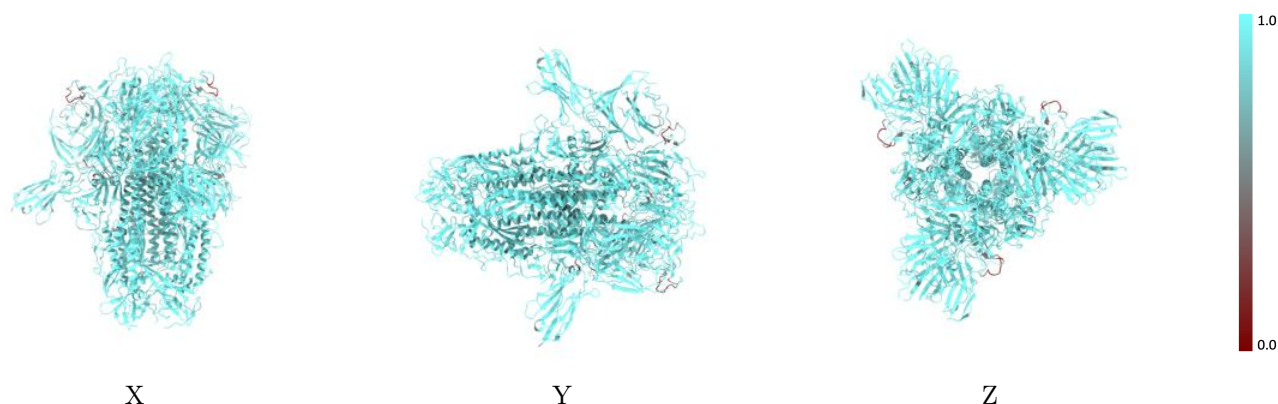
The images above show the 3D surface view of the map at the recommended contour level 0.103 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



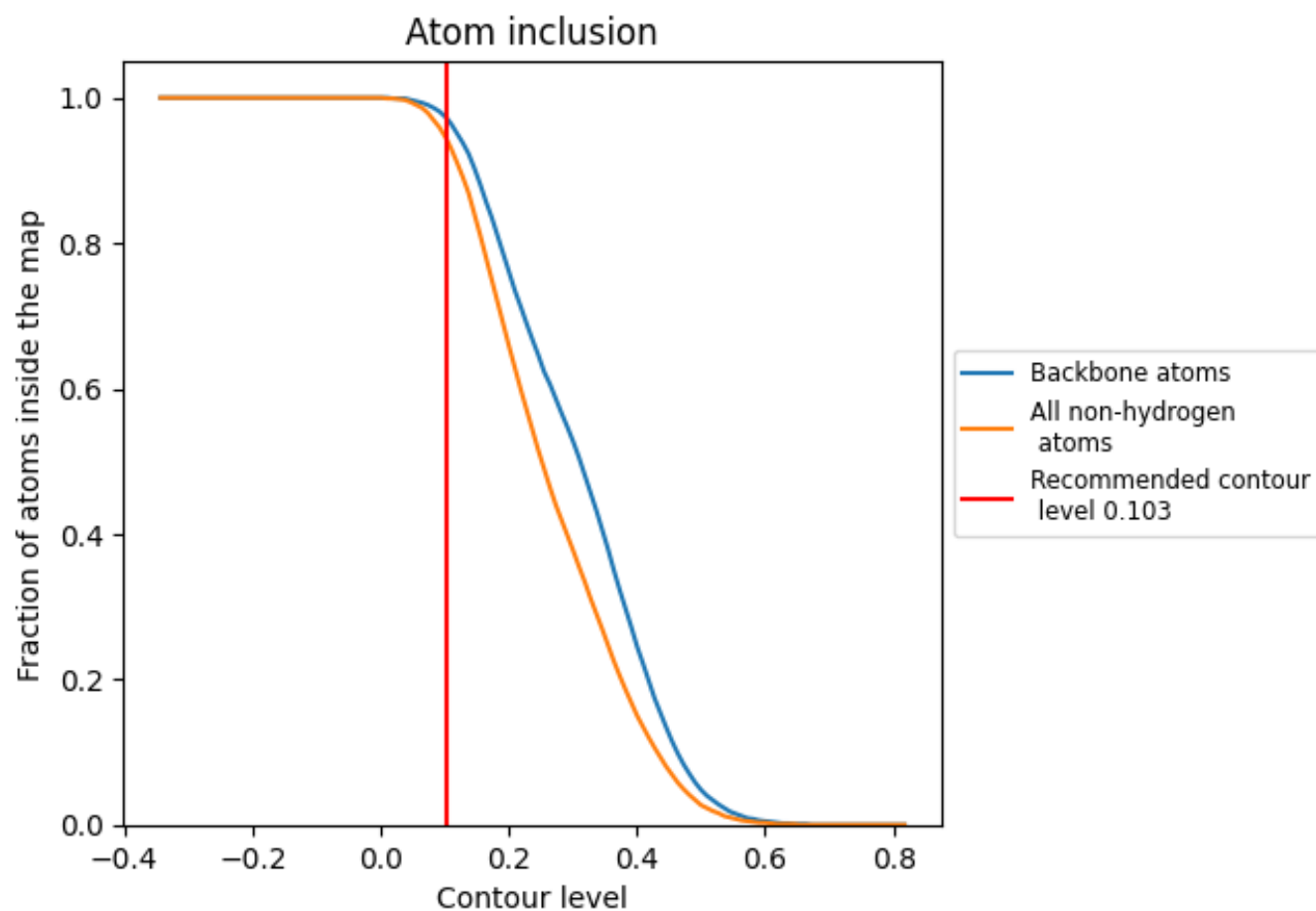
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.103).







































9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 94% 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 (0.103) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9430	 0.4920
A	 0.9410	 0.4950
B	 0.9410	 0.4950
C	 0.9420	 0.4960
D	 0.9290	 0.4280
E	 0.8930	 0.4200
F	 0.7860	 0.3720
G	 1.0000	 0.4780
H	 0.8930	 0.4230
I	 0.8570	 0.4650
J	 1.0000	 0.4800
K	 0.8930	 0.4350
L	 0.9290	 0.4520
M	 0.9630	 0.4690
N	 0.9580	 0.4670
O	 0.9640	 0.4790
P	 1.0000	 0.4860
Q	 0.8570	 0.4080
R	 0.9290	 0.4590

