



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 08:54 AM UTC

PDB ID : 6VYB / pdb_00006vyb
EMDB ID : EMD-21457
Title : SARS-CoV-2 spike ectodomain structure (open state)
Authors : Walls, A.C.; Park, Y.J.; Tortorici, M.A.; Wall, A.; Seattle Structural Genomics Center for Infectious Disease (SSGCID); McGuire, A.T.; Veisler, D.
Deposited on : 2020-02-25
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

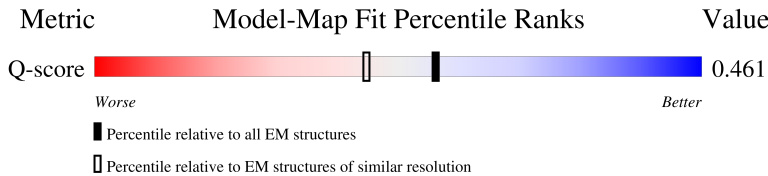
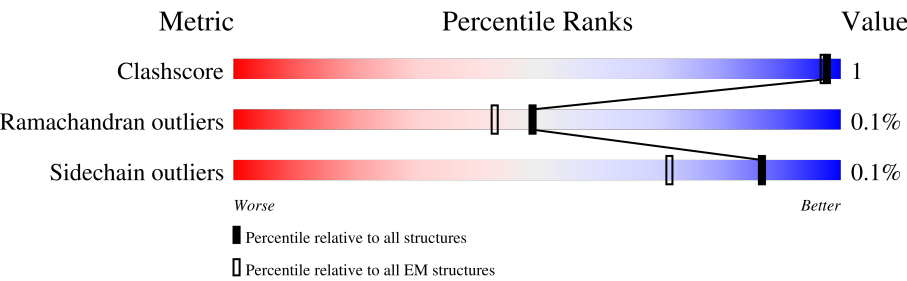
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMD archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	15020 (2.70 - 3.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1281	72% 25%
1	B	1281	70% 26%
1	C	1281	71% 25%
2	D	2	50% 100%

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Mol	Chain	Length	Quality of chain
2	E	2	 100%
2	F	2	 100%
2	G	2	 100%
2	H	2	 100%
2	I	2	 100%
2	J	2	 100%
2	K	2	 100%
2	L	2	 100%
2	M	2	 100%
2	N	2	 100%
2	O	2	 100%  50%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 22365 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	966	Total	C	N	O	S	0	0
			7393	4741	1235	1385	32		
1	B	949	Total	C	N	O	S	0	0
			6865	4365	1162	1306	32		
1	C	960	Total	C	N	O	S	0	0
			7281	4667	1221	1361	32		

There are 267 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	MET	-	expression tag	UNP P0DTC2
A	-17	GLY	-	expression tag	UNP P0DTC2
A	-16	ILE	-	expression tag	UNP P0DTC2
A	-15	LEU	-	expression tag	UNP P0DTC2
A	-14	PRO	-	expression tag	UNP P0DTC2
A	-13	SER	-	expression tag	UNP P0DTC2
A	-12	PRO	-	expression tag	UNP P0DTC2
A	-11	GLY	-	expression tag	UNP P0DTC2
A	-10	MET	-	expression tag	UNP P0DTC2
A	-9	PRO	-	expression tag	UNP P0DTC2
A	-8	ALA	-	expression tag	UNP P0DTC2
A	-7	LEU	-	expression tag	UNP P0DTC2
A	-6	LEU	-	expression tag	UNP P0DTC2
A	-5	SER	-	expression tag	UNP P0DTC2
A	-4	LEU	-	expression tag	UNP P0DTC2
A	-3	VAL	-	expression tag	UNP P0DTC2
A	-2	SER	-	expression tag	UNP P0DTC2
A	-1	LEU	-	expression tag	UNP P0DTC2
A	0	LEU	-	expression tag	UNP P0DTC2
A	1	SER	-	expression tag	UNP P0DTC2
A	2	VAL	-	expression tag	UNP P0DTC2
A	3	LEU	-	expression tag	UNP P0DTC2
A	4	LEU	-	expression tag	UNP P0DTC2
A	5	MET	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	6	GLY	-	expression tag	UNP P0DTC2
A	7	CYS	-	expression tag	UNP P0DTC2
A	8	VAL	-	expression tag	UNP P0DTC2
A	9	ALA	-	expression tag	UNP P0DTC2
A	10	GLU	-	expression tag	UNP P0DTC2
A	11	THR	-	expression tag	UNP P0DTC2
A	12	GLY	-	expression tag	UNP P0DTC2
A	13	THR	-	expression tag	UNP P0DTC2
A	607	GLU	GLN	conflict	UNP P0DTC2
A	682	SER	ARG	conflict	UNP P0DTC2
A	683	GLY	ARG	conflict	UNP P0DTC2
A	685	GLY	ARG	conflict	UNP P0DTC2
A	986	PRO	LYS	conflict	UNP P0DTC2
A	987	PRO	VAL	conflict	UNP P0DTC2
A	1212	GLY	-	expression tag	UNP P0DTC2
A	1213	SER	-	expression tag	UNP P0DTC2
A	1214	GLY	-	expression tag	UNP P0DTC2
A	1215	ARG	-	expression tag	UNP P0DTC2
A	1216	GLU	-	expression tag	UNP P0DTC2
A	1217	ASN	-	expression tag	UNP P0DTC2
A	1218	LEU	-	expression tag	UNP P0DTC2
A	1219	TYR	-	expression tag	UNP P0DTC2
A	1220	PHE	-	expression tag	UNP P0DTC2
A	1221	GLN	-	expression tag	UNP P0DTC2
A	1222	GLY	-	expression tag	UNP P0DTC2
A	1223	GLY	-	expression tag	UNP P0DTC2
A	1224	GLY	-	expression tag	UNP P0DTC2
A	1225	GLY	-	expression tag	UNP P0DTC2
A	1226	SER	-	expression tag	UNP P0DTC2
A	1227	GLY	-	expression tag	UNP P0DTC2
A	1228	TYR	-	expression tag	UNP P0DTC2
A	1229	ILE	-	expression tag	UNP P0DTC2
A	1230	PRO	-	expression tag	UNP P0DTC2
A	1231	GLU	-	expression tag	UNP P0DTC2
A	1232	ALA	-	expression tag	UNP P0DTC2
A	1233	PRO	-	expression tag	UNP P0DTC2
A	1234	ARG	-	expression tag	UNP P0DTC2
A	1235	ASP	-	expression tag	UNP P0DTC2
A	1236	GLY	-	expression tag	UNP P0DTC2
A	1237	GLN	-	expression tag	UNP P0DTC2
A	1238	ALA	-	expression tag	UNP P0DTC2
A	1239	TYR	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1240	VAL	-	expression tag	UNP P0DTC2
A	1241	ARG	-	expression tag	UNP P0DTC2
A	1242	LYS	-	expression tag	UNP P0DTC2
A	1243	ASP	-	expression tag	UNP P0DTC2
A	1244	GLY	-	expression tag	UNP P0DTC2
A	1245	GLU	-	expression tag	UNP P0DTC2
A	1246	TRP	-	expression tag	UNP P0DTC2
A	1247	VAL	-	expression tag	UNP P0DTC2
A	1248	LEU	-	expression tag	UNP P0DTC2
A	1249	LEU	-	expression tag	UNP P0DTC2
A	1250	SER	-	expression tag	UNP P0DTC2
A	1251	THR	-	expression tag	UNP P0DTC2
A	1252	PHE	-	expression tag	UNP P0DTC2
A	1253	LEU	-	expression tag	UNP P0DTC2
A	1254	GLY	-	expression tag	UNP P0DTC2
A	1255	HIS	-	expression tag	UNP P0DTC2
A	1256	HIS	-	expression tag	UNP P0DTC2
A	1257	HIS	-	expression tag	UNP P0DTC2
A	1258	HIS	-	expression tag	UNP P0DTC2
A	1259	HIS	-	expression tag	UNP P0DTC2
A	1260	HIS	-	expression tag	UNP P0DTC2
A	1261	HIS	-	expression tag	UNP P0DTC2
A	1262	HIS	-	expression tag	UNP P0DTC2
B	-18	MET	-	expression tag	UNP P0DTC2
B	-17	GLY	-	expression tag	UNP P0DTC2
B	-16	ILE	-	expression tag	UNP P0DTC2
B	-15	LEU	-	expression tag	UNP P0DTC2
B	-14	PRO	-	expression tag	UNP P0DTC2
B	-13	SER	-	expression tag	UNP P0DTC2
B	-12	PRO	-	expression tag	UNP P0DTC2
B	-11	GLY	-	expression tag	UNP P0DTC2
B	-10	MET	-	expression tag	UNP P0DTC2
B	-9	PRO	-	expression tag	UNP P0DTC2
B	-8	ALA	-	expression tag	UNP P0DTC2
B	-7	LEU	-	expression tag	UNP P0DTC2
B	-6	LEU	-	expression tag	UNP P0DTC2
B	-5	SER	-	expression tag	UNP P0DTC2
B	-4	LEU	-	expression tag	UNP P0DTC2
B	-3	VAL	-	expression tag	UNP P0DTC2
B	-2	SER	-	expression tag	UNP P0DTC2
B	-1	LEU	-	expression tag	UNP P0DTC2
B	0	LEU	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1	SER	-	expression tag	UNP P0DTC2
B	2	VAL	-	expression tag	UNP P0DTC2
B	3	LEU	-	expression tag	UNP P0DTC2
B	4	LEU	-	expression tag	UNP P0DTC2
B	5	MET	-	expression tag	UNP P0DTC2
B	6	GLY	-	expression tag	UNP P0DTC2
B	7	CYS	-	expression tag	UNP P0DTC2
B	8	VAL	-	expression tag	UNP P0DTC2
B	9	ALA	-	expression tag	UNP P0DTC2
B	10	GLU	-	expression tag	UNP P0DTC2
B	11	THR	-	expression tag	UNP P0DTC2
B	12	GLY	-	expression tag	UNP P0DTC2
B	13	THR	-	expression tag	UNP P0DTC2
B	607	GLU	GLN	conflict	UNP P0DTC2
B	682	SER	ARG	conflict	UNP P0DTC2
B	683	GLY	ARG	conflict	UNP P0DTC2
B	685	GLY	ARG	conflict	UNP P0DTC2
B	986	PRO	LYS	conflict	UNP P0DTC2
B	987	PRO	VAL	conflict	UNP P0DTC2
B	1212	GLY	-	expression tag	UNP P0DTC2
B	1213	SER	-	expression tag	UNP P0DTC2
B	1214	GLY	-	expression tag	UNP P0DTC2
B	1215	ARG	-	expression tag	UNP P0DTC2
B	1216	GLU	-	expression tag	UNP P0DTC2
B	1217	ASN	-	expression tag	UNP P0DTC2
B	1218	LEU	-	expression tag	UNP P0DTC2
B	1219	TYR	-	expression tag	UNP P0DTC2
B	1220	PHE	-	expression tag	UNP P0DTC2
B	1221	GLN	-	expression tag	UNP P0DTC2
B	1222	GLY	-	expression tag	UNP P0DTC2
B	1223	GLY	-	expression tag	UNP P0DTC2
B	1224	GLY	-	expression tag	UNP P0DTC2
B	1225	GLY	-	expression tag	UNP P0DTC2
B	1226	SER	-	expression tag	UNP P0DTC2
B	1227	GLY	-	expression tag	UNP P0DTC2
B	1228	TYR	-	expression tag	UNP P0DTC2
B	1229	ILE	-	expression tag	UNP P0DTC2
B	1230	PRO	-	expression tag	UNP P0DTC2
B	1231	GLU	-	expression tag	UNP P0DTC2
B	1232	ALA	-	expression tag	UNP P0DTC2
B	1233	PRO	-	expression tag	UNP P0DTC2
B	1234	ARG	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1235	ASP	-	expression tag	UNP P0DTC2
B	1236	GLY	-	expression tag	UNP P0DTC2
B	1237	GLN	-	expression tag	UNP P0DTC2
B	1238	ALA	-	expression tag	UNP P0DTC2
B	1239	TYR	-	expression tag	UNP P0DTC2
B	1240	VAL	-	expression tag	UNP P0DTC2
B	1241	ARG	-	expression tag	UNP P0DTC2
B	1242	LYS	-	expression tag	UNP P0DTC2
B	1243	ASP	-	expression tag	UNP P0DTC2
B	1244	GLY	-	expression tag	UNP P0DTC2
B	1245	GLU	-	expression tag	UNP P0DTC2
B	1246	TRP	-	expression tag	UNP P0DTC2
B	1247	VAL	-	expression tag	UNP P0DTC2
B	1248	LEU	-	expression tag	UNP P0DTC2
B	1249	LEU	-	expression tag	UNP P0DTC2
B	1250	SER	-	expression tag	UNP P0DTC2
B	1251	THR	-	expression tag	UNP P0DTC2
B	1252	PHE	-	expression tag	UNP P0DTC2
B	1253	LEU	-	expression tag	UNP P0DTC2
B	1254	GLY	-	expression tag	UNP P0DTC2
B	1255	HIS	-	expression tag	UNP P0DTC2
B	1256	HIS	-	expression tag	UNP P0DTC2
B	1257	HIS	-	expression tag	UNP P0DTC2
B	1258	HIS	-	expression tag	UNP P0DTC2
B	1259	HIS	-	expression tag	UNP P0DTC2
B	1260	HIS	-	expression tag	UNP P0DTC2
B	1261	HIS	-	expression tag	UNP P0DTC2
B	1262	HIS	-	expression tag	UNP P0DTC2
C	-18	MET	-	expression tag	UNP P0DTC2
C	-17	GLY	-	expression tag	UNP P0DTC2
C	-16	ILE	-	expression tag	UNP P0DTC2
C	-15	LEU	-	expression tag	UNP P0DTC2
C	-14	PRO	-	expression tag	UNP P0DTC2
C	-13	SER	-	expression tag	UNP P0DTC2
C	-12	PRO	-	expression tag	UNP P0DTC2
C	-11	GLY	-	expression tag	UNP P0DTC2
C	-10	MET	-	expression tag	UNP P0DTC2
C	-9	PRO	-	expression tag	UNP P0DTC2
C	-8	ALA	-	expression tag	UNP P0DTC2
C	-7	LEU	-	expression tag	UNP P0DTC2
C	-6	LEU	-	expression tag	UNP P0DTC2
C	-5	SER	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-4	LEU	-	expression tag	UNP P0DTC2
C	-3	VAL	-	expression tag	UNP P0DTC2
C	-2	SER	-	expression tag	UNP P0DTC2
C	-1	LEU	-	expression tag	UNP P0DTC2
C	0	LEU	-	expression tag	UNP P0DTC2
C	1	SER	-	expression tag	UNP P0DTC2
C	2	VAL	-	expression tag	UNP P0DTC2
C	3	LEU	-	expression tag	UNP P0DTC2
C	4	LEU	-	expression tag	UNP P0DTC2
C	5	MET	-	expression tag	UNP P0DTC2
C	6	GLY	-	expression tag	UNP P0DTC2
C	7	CYS	-	expression tag	UNP P0DTC2
C	8	VAL	-	expression tag	UNP P0DTC2
C	9	ALA	-	expression tag	UNP P0DTC2
C	10	GLU	-	expression tag	UNP P0DTC2
C	11	THR	-	expression tag	UNP P0DTC2
C	12	GLY	-	expression tag	UNP P0DTC2
C	13	THR	-	expression tag	UNP P0DTC2
C	607	GLU	GLN	conflict	UNP P0DTC2
C	682	SER	ARG	conflict	UNP P0DTC2
C	683	GLY	ARG	conflict	UNP P0DTC2
C	685	GLY	ARG	conflict	UNP P0DTC2
C	986	PRO	LYS	conflict	UNP P0DTC2
C	987	PRO	VAL	conflict	UNP P0DTC2
C	1212	GLY	-	expression tag	UNP P0DTC2
C	1213	SER	-	expression tag	UNP P0DTC2
C	1214	GLY	-	expression tag	UNP P0DTC2
C	1215	ARG	-	expression tag	UNP P0DTC2
C	1216	GLU	-	expression tag	UNP P0DTC2
C	1217	ASN	-	expression tag	UNP P0DTC2
C	1218	LEU	-	expression tag	UNP P0DTC2
C	1219	TYR	-	expression tag	UNP P0DTC2
C	1220	PHE	-	expression tag	UNP P0DTC2
C	1221	GLN	-	expression tag	UNP P0DTC2
C	1222	GLY	-	expression tag	UNP P0DTC2
C	1223	GLY	-	expression tag	UNP P0DTC2
C	1224	GLY	-	expression tag	UNP P0DTC2
C	1225	GLY	-	expression tag	UNP P0DTC2
C	1226	SER	-	expression tag	UNP P0DTC2
C	1227	GLY	-	expression tag	UNP P0DTC2
C	1228	TYR	-	expression tag	UNP P0DTC2
C	1229	ILE	-	expression tag	UNP P0DTC2

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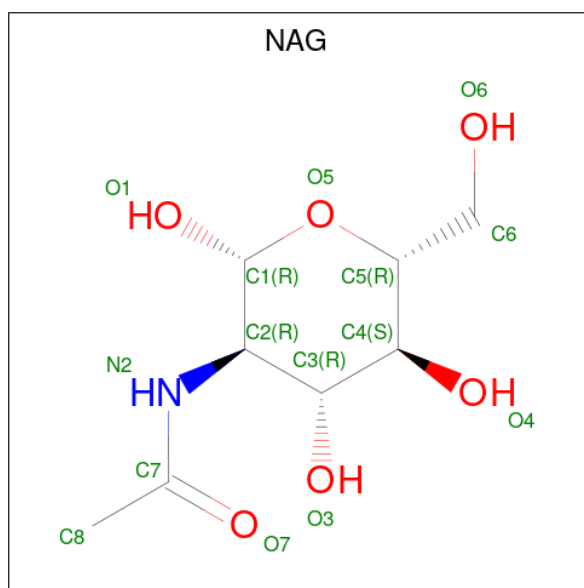
Chain	Residue	Modelled	Actual	Comment	Reference
C	1230	PRO	-	expression tag	UNP P0DTC2
C	1231	GLU	-	expression tag	UNP P0DTC2
C	1232	ALA	-	expression tag	UNP P0DTC2
C	1233	PRO	-	expression tag	UNP P0DTC2
C	1234	ARG	-	expression tag	UNP P0DTC2
C	1235	ASP	-	expression tag	UNP P0DTC2
C	1236	GLY	-	expression tag	UNP P0DTC2
C	1237	GLN	-	expression tag	UNP P0DTC2
C	1238	ALA	-	expression tag	UNP P0DTC2
C	1239	TYR	-	expression tag	UNP P0DTC2
C	1240	VAL	-	expression tag	UNP P0DTC2
C	1241	ARG	-	expression tag	UNP P0DTC2
C	1242	LYS	-	expression tag	UNP P0DTC2
C	1243	ASP	-	expression tag	UNP P0DTC2
C	1244	GLY	-	expression tag	UNP P0DTC2
C	1245	GLU	-	expression tag	UNP P0DTC2
C	1246	TRP	-	expression tag	UNP P0DTC2
C	1247	VAL	-	expression tag	UNP P0DTC2
C	1248	LEU	-	expression tag	UNP P0DTC2
C	1249	LEU	-	expression tag	UNP P0DTC2
C	1250	SER	-	expression tag	UNP P0DTC2
C	1251	THR	-	expression tag	UNP P0DTC2
C	1252	PHE	-	expression tag	UNP P0DTC2
C	1253	LEU	-	expression tag	UNP P0DTC2
C	1254	GLY	-	expression tag	UNP P0DTC2
C	1255	HIS	-	expression tag	UNP P0DTC2
C	1256	HIS	-	expression tag	UNP P0DTC2
C	1257	HIS	-	expression tag	UNP P0DTC2
C	1258	HIS	-	expression tag	UNP P0DTC2
C	1259	HIS	-	expression tag	UNP P0DTC2
C	1260	HIS	-	expression tag	UNP P0DTC2
C	1261	HIS	-	expression tag	UNP P0DTC2
C	1262	HIS	-	expression tag	UNP P0DTC2

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



Mol	Chain	Residues	Atoms				AltConf	Trace
2	D	2	Total	C	N	O	0	0
			28	16	2	10		
2	E	2	Total	C	N	O	0	0
			28	16	2	10		
2	F	2	Total	C	N	O	0	0
			28	16	2	10		
2	G	2	Total	C	N	O	0	0
			28	16	2	10		
2	H	2	Total	C	N	O	0	0
			28	16	2	10		
2	I	2	Total	C	N	O	0	0
			28	16	2	10		
2	J	2	Total	C	N	O	0	0
			28	16	2	10		
2	K	2	Total	C	N	O	0	0
			28	16	2	10		
2	L	2	Total	C	N	O	0	0
			28	16	2	10		
2	M	2	Total	C	N	O	0	0
			28	16	2	10		
2	N	2	Total	C	N	O	0	0
			28	16	2	10		
2	O	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

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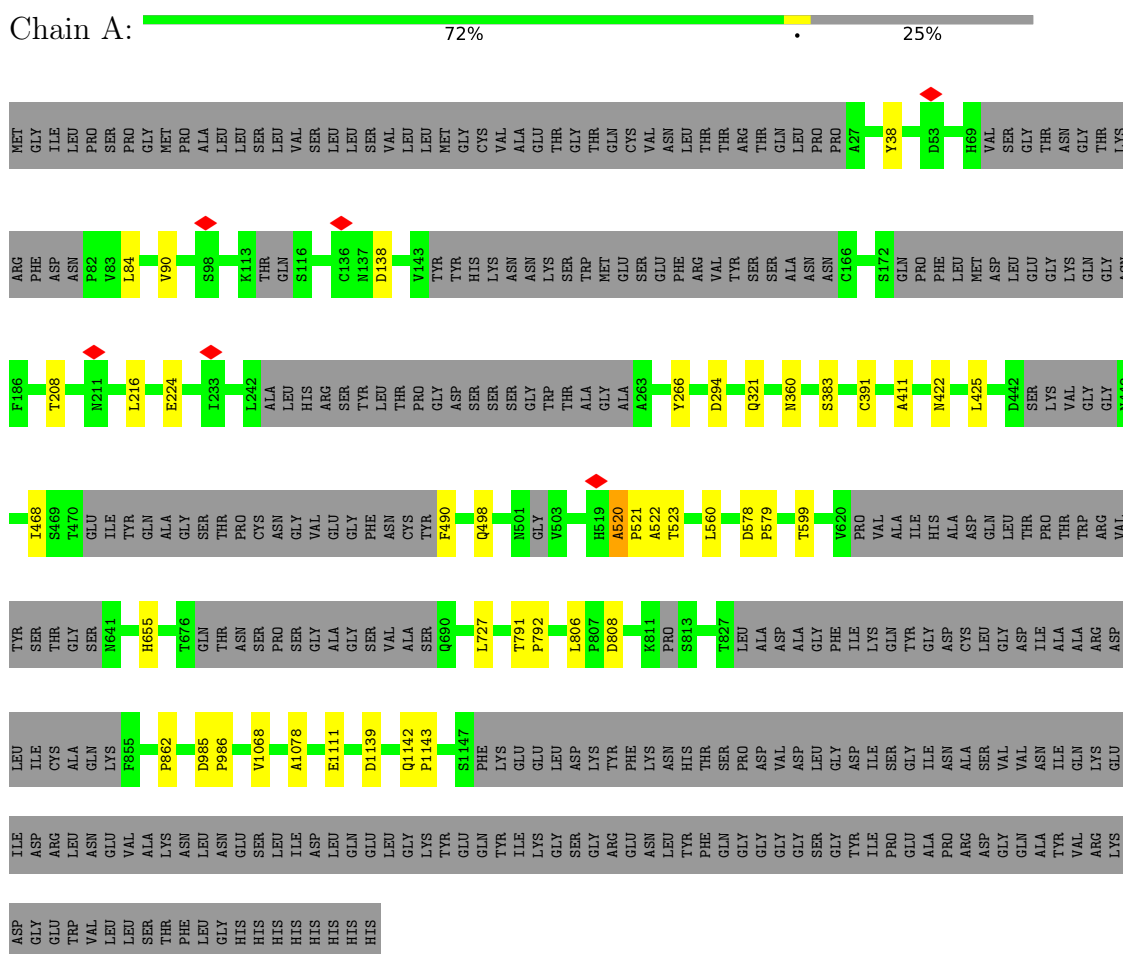
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Mol	Chain	Residues	Atoms				AltConf
3	B	1	Total	C	N	O	0
			14	8	1	5	
3	C	1	Total	C	N	O	0
			14	8	1	5	
3	C	1	Total	C	N	O	0
			14	8	1	5	
3	C	1	Total	C	N	O	0
			14	8	1	5	
3	C	1	Total	C	N	O	0
			14	8	1	5	
3	C	1	Total	C	N	O	0
			14	8	1	5	
3	C	1	Total	C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

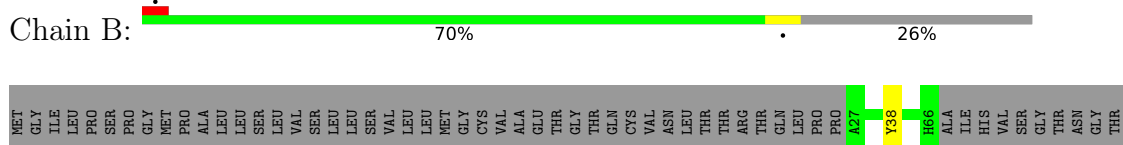
3 Residue-property plots

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 1: Spike glycoprotein





ASN ALA SER VAL ASN TLE GLN LYS GLU ASP ARG LEU ASN GLU VAL ALA LYS ASN LEU ASN GLU SER LEU TLE ASP LEU GLN TYR TYR TLE LYS GLY ARG GLU ASN LEU TYR PHE GLN GLY GLY GLY GLY TYR TLE PRO GLU ALA

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

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



MAG1
MAG2

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



MAG1
MAG2

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



MAG1
MAG2

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



MAG1
MAG2

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



MAG1
MAG2

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



MAG1
MAG2

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

Chain J:  100%MAG1
MAG2

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

Chain K:  100%MAG1
MAG2

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

Chain L:  100%MAG1
MAG2

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

Chain M:  100%MAG1
MAG2

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

Chain N:  100%MAG1
MAG2

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

Chain O:  50%
100%MAG1
MAG2

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	197005	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	70	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	3.233	Depositor
Minimum map value	-1.594	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.060	Depositor
Recommended contour level	0.4	Depositor
Map size (Å)	419.99997, 419.99997, 419.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.74	1/7554 (0.0%)	1.01	57/10291 (0.6%)
1	B	0.74	0/6998	1.07	64/9553 (0.7%)
1	C	0.74	1/7441 (0.0%)	1.04	67/10146 (0.7%)
All	All	0.74	2/21993 (0.0%)	1.04	188/29990 (0.6%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	422	ASN	CB-CG	-6.72	1.35	1.52
1	C	454	ARG	NE-CZ	5.01	1.38	1.33

All (188) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1070	ALA	N-CA-C	15.37	133.62	113.18
1	C	1070	ALA	N-CA-C	13.52	130.02	112.72
1	B	1071	GLN	N-CA-C	-10.86	91.69	109.40
1	C	1071	GLN	N-CA-C	-10.20	92.78	109.40
1	B	124	THR	N-CA-C	9.88	125.33	113.28
1	B	1070	ALA	CB-CA-C	-9.41	93.67	110.23
1	C	124	THR	N-CA-C	9.32	124.65	113.28
1	C	1070	ALA	CB-CA-C	-7.60	97.91	110.37
1	B	526	GLY	CA-C-N	7.46	127.39	119.85
1	B	526	GLY	C-N-CA	7.46	127.39	119.85
1	C	599	THR	CA-C-N	7.44	127.14	119.56
1	C	599	THR	C-N-CA	7.44	127.14	119.56
1	B	122	ASN	CA-CB-CG	7.37	119.97	112.60
1	C	792	PRO	CA-C-N	7.27	126.98	119.56
1	C	792	PRO	C-N-CA	7.27	126.98	119.56
1	A	792	PRO	CA-C-N	7.19	126.89	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	792	PRO	C-N-CA	7.19	126.89	119.56
1	C	1139	ASP	CA-C-N	7.10	126.80	119.56
1	C	1139	ASP	C-N-CA	7.10	126.80	119.56
1	B	498	GLN	CA-C-N	7.03	126.66	119.56
1	B	498	GLN	C-N-CA	7.03	126.66	119.56
1	C	498	GLN	CA-C-N	6.96	126.58	119.56
1	C	498	GLN	C-N-CA	6.96	126.58	119.56
1	B	862	PRO	CA-C-N	6.92	126.84	119.85
1	B	862	PRO	C-N-CA	6.92	126.84	119.85
1	A	1139	ASP	CA-C-N	6.92	126.62	119.56
1	A	1139	ASP	C-N-CA	6.92	126.62	119.56
1	B	138	ASP	CA-C-N	6.87	126.83	120.03
1	B	138	ASP	C-N-CA	6.87	126.83	120.03
1	C	383	SER	CA-C-N	6.87	126.57	119.56
1	C	383	SER	C-N-CA	6.87	126.57	119.56
1	A	862	PRO	CA-C-N	6.85	126.81	120.03
1	A	862	PRO	C-N-CA	6.85	126.81	120.03
1	B	1139	ASP	CA-C-N	6.84	126.53	119.56
1	B	1139	ASP	C-N-CA	6.84	126.53	119.56
1	B	383	SER	CA-C-N	6.81	126.44	119.56
1	B	383	SER	C-N-CA	6.81	126.44	119.56
1	A	138	ASP	CA-C-N	6.78	126.74	119.76
1	A	138	ASP	C-N-CA	6.78	126.74	119.76
1	B	792	PRO	CA-C-N	6.72	126.42	119.56
1	B	792	PRO	C-N-CA	6.72	126.42	119.56
1	C	862	PRO	CA-C-N	6.70	126.62	119.85
1	C	862	PRO	C-N-CA	6.70	126.62	119.85
1	A	383	SER	CA-C-N	6.63	126.32	119.56
1	A	383	SER	C-N-CA	6.63	126.32	119.56
1	A	578	ASP	CA-C-N	6.58	126.20	119.56
1	A	578	ASP	C-N-CA	6.58	126.20	119.56
1	C	138	ASP	CA-C-N	6.56	126.52	119.76
1	C	138	ASP	C-N-CA	6.56	126.52	119.76
1	C	294	ASP	CA-C-N	6.46	126.15	119.56
1	C	294	ASP	C-N-CA	6.46	126.15	119.56
1	C	1078	ALA	CA-C-N	6.32	125.95	119.56
1	C	1078	ALA	C-N-CA	6.32	125.95	119.56
1	A	985	ASP	CA-C-N	6.30	126.87	120.38
1	A	985	ASP	C-N-CA	6.30	126.87	120.38
1	B	808	ASP	CA-C-N	6.25	125.88	119.56
1	B	808	ASP	C-N-CA	6.25	125.88	119.56
1	A	498	GLN	CA-C-N	6.25	125.93	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	498	GLN	C-N-CA	6.25	125.93	119.56
1	A	38	TYR	CA-C-N	6.18	125.80	119.56
1	A	38	TYR	C-N-CA	6.18	125.80	119.56
1	C	791	THR	CA-C-N	6.17	126.74	120.38
1	C	791	THR	C-N-CA	6.17	126.74	120.38
1	C	985	ASP	CA-C-N	6.12	126.68	120.38
1	C	985	ASP	C-N-CA	6.12	126.68	120.38
1	B	1078	ALA	CA-C-N	6.11	125.73	119.56
1	B	1078	ALA	C-N-CA	6.11	125.73	119.56
1	C	425	LEU	CA-C-N	6.11	126.46	119.92
1	C	425	LEU	C-N-CA	6.11	126.46	119.92
1	C	578	ASP	CA-C-N	6.11	125.73	119.56
1	C	578	ASP	C-N-CA	6.11	125.73	119.56
1	A	1078	ALA	CA-C-N	6.04	125.66	119.56
1	A	1078	ALA	C-N-CA	6.04	125.66	119.56
1	C	38	TYR	CA-C-N	5.96	125.58	119.56
1	C	38	TYR	C-N-CA	5.96	125.58	119.56
1	B	578	ASP	CA-C-N	5.95	125.57	119.56
1	B	578	ASP	C-N-CA	5.95	125.57	119.56
1	B	294	ASP	CA-C-N	5.95	126.10	119.32
1	B	294	ASP	C-N-CA	5.95	126.10	119.32
1	B	791	THR	CA-C-N	5.92	126.48	120.38
1	B	791	THR	C-N-CA	5.92	126.48	120.38
1	B	84	LEU	CA-C-N	5.90	125.86	119.78
1	B	84	LEU	C-N-CA	5.90	125.86	119.78
1	B	38	TYR	CA-C-N	5.90	125.52	119.56
1	B	38	TYR	C-N-CA	5.90	125.52	119.56
1	B	425	LEU	CA-C-N	5.89	126.22	119.92
1	B	425	LEU	C-N-CA	5.89	126.22	119.92
1	A	90	VAL	N-CA-C	5.89	116.35	108.11
1	A	599	THR	CA-C-N	5.87	125.84	120.03
1	A	599	THR	C-N-CA	5.87	125.84	120.03
1	C	808	ASP	CA-C-N	5.86	125.96	119.87
1	C	808	ASP	C-N-CA	5.86	125.96	119.87
1	C	1068	VAL	CA-C-N	5.83	125.85	119.90
1	C	1068	VAL	C-N-CA	5.83	125.85	119.90
1	C	224	GLU	CA-C-N	5.83	125.59	119.76
1	C	224	GLU	C-N-CA	5.83	125.59	119.76
1	A	294	ASP	CA-C-N	5.81	125.48	119.56
1	A	294	ASP	C-N-CA	5.81	125.48	119.56
1	B	599	THR	CA-C-N	5.78	125.76	120.03
1	B	599	THR	C-N-CA	5.78	125.76	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	727	LEU	CA-C-N	5.77	125.71	119.76
1	C	727	LEU	C-N-CA	5.77	125.71	119.76
1	C	90	VAL	N-CA-C	5.75	116.15	108.11
1	A	84	LEU	CA-C-N	5.74	125.69	119.78
1	A	84	LEU	C-N-CA	5.74	125.69	119.78
1	B	985	ASP	CA-C-N	5.71	126.26	120.38
1	B	985	ASP	C-N-CA	5.71	126.26	120.38
1	A	321	GLN	CA-C-N	5.69	125.45	119.76
1	A	321	GLN	C-N-CA	5.69	125.45	119.76
1	A	490	PHE	CA-C-N	5.68	126.75	120.45
1	A	490	PHE	C-N-CA	5.68	126.75	120.45
1	B	806	LEU	CA-C-N	5.66	125.59	119.76
1	B	806	LEU	C-N-CA	5.66	125.59	119.76
1	A	425	LEU	CA-C-N	5.62	125.57	119.78
1	A	425	LEU	C-N-CA	5.62	125.57	119.78
1	C	321	GLN	CA-C-N	5.62	125.38	119.76
1	C	321	GLN	C-N-CA	5.62	125.38	119.76
1	C	411	ALA	CA-C-N	5.61	125.52	119.85
1	C	411	ALA	C-N-CA	5.61	125.52	119.85
1	B	329	PHE	CA-C-N	5.60	125.91	119.92
1	B	329	PHE	C-N-CA	5.60	125.91	119.92
1	C	336	CYS	CA-C-N	5.59	126.83	119.84
1	C	336	CYS	C-N-CA	5.59	126.83	119.84
1	A	808	ASP	CA-C-N	5.59	125.69	119.87
1	A	808	ASP	C-N-CA	5.59	125.69	119.87
1	B	1111	GLU	CA-C-N	5.55	125.72	119.90
1	B	1111	GLU	C-N-CA	5.55	125.72	119.90
1	C	208	THR	CA-C-N	5.55	125.31	119.76
1	C	208	THR	C-N-CA	5.55	125.31	119.76
1	C	123	ALA	N-CA-C	-5.51	99.07	110.80
1	C	806	LEU	CA-C-N	5.49	125.41	119.76
1	C	806	LEU	C-N-CA	5.49	125.41	119.76
1	C	84	LEU	CA-C-N	5.48	125.42	119.78
1	C	84	LEU	C-N-CA	5.48	125.42	119.78
1	C	124	THR	N-CA-CB	-5.46	101.88	110.46
1	B	120	VAL	N-CA-C	5.46	115.98	108.12
1	B	81	ASN	CA-C-N	5.43	125.41	120.03
1	B	81	ASN	C-N-CA	5.43	125.41	120.03
1	B	90	VAL	N-CA-C	5.42	115.70	108.11
1	C	560	LEU	CA-C-N	5.36	126.54	119.84
1	C	560	LEU	C-N-CA	5.36	126.54	119.84
1	A	411	ALA	CA-C-N	5.36	125.26	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	411	ALA	C-N-CA	5.36	125.26	119.85
1	B	560	LEU	CA-C-N	5.36	126.53	119.84
1	B	560	LEU	C-N-CA	5.36	126.53	119.84
1	A	1111	GLU	CA-C-N	5.35	125.11	119.76
1	A	1111	GLU	C-N-CA	5.35	125.11	119.76
1	C	271	GLN	CA-C-N	5.35	126.53	119.84
1	C	271	GLN	C-N-CA	5.35	126.53	119.84
1	A	727	LEU	CA-C-N	5.34	125.26	119.76
1	A	727	LEU	C-N-CA	5.34	125.26	119.76
1	B	411	ALA	CA-C-N	5.33	125.09	119.76
1	B	411	ALA	C-N-CA	5.33	125.09	119.76
1	A	560	LEU	CA-C-N	5.32	126.49	119.84
1	A	560	LEU	C-N-CA	5.32	126.49	119.84
1	B	321	GLN	CA-C-N	5.31	125.23	119.76
1	B	321	GLN	C-N-CA	5.31	125.23	119.76
1	A	224	GLU	CA-C-N	5.29	125.05	119.76
1	A	224	GLU	C-N-CA	5.29	125.05	119.76
1	A	986	PRO	N-CA-C	5.27	117.13	110.70
1	B	462	LYS	CA-C-N	5.27	125.56	119.93
1	B	462	LYS	C-N-CA	5.27	125.56	119.93
1	B	124	THR	N-CA-CB	-5.26	102.19	110.46
1	C	81	ASN	CA-C-N	5.26	125.72	120.14
1	C	81	ASN	C-N-CA	5.26	125.72	120.14
1	B	208	THR	CA-C-N	5.23	125.63	119.99
1	B	208	THR	C-N-CA	5.23	125.63	119.99
1	A	791	THR	CA-C-N	5.20	125.74	120.38
1	A	791	THR	C-N-CA	5.20	125.74	120.38
1	A	806	LEU	CA-C-N	5.20	125.11	119.76
1	A	806	LEU	C-N-CA	5.20	125.11	119.76
1	A	520	ALA	N-CA-C	-5.20	98.33	109.81
1	C	462	LYS	CA-C-N	5.15	125.40	119.83
1	C	462	LYS	C-N-CA	5.15	125.40	119.83
1	C	1111	GLU	CA-C-N	5.14	124.90	119.76
1	C	1111	GLU	C-N-CA	5.14	124.90	119.76
1	C	519	HIS	N-CA-C	-5.11	106.98	114.39
1	A	208	THR	CA-C-N	5.09	124.85	119.76
1	A	208	THR	C-N-CA	5.09	124.85	119.76
1	A	1068	VAL	CA-C-N	5.04	125.32	119.93
1	A	1068	VAL	C-N-CA	5.04	125.32	119.93
1	A	216	LEU	CA-C-N	5.03	124.96	119.78
1	A	216	LEU	C-N-CA	5.03	124.96	119.78
1	B	224	GLU	CA-C-N	5.03	125.18	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	224	GLU	C-N-CA	5.03	125.18	119.90
1	C	986	PRO	N-CA-C	5.01	116.81	110.70
1	B	727	LEU	CA-C-N	5.01	124.91	119.85
1	B	727	LEU	C-N-CA	5.01	124.91	119.85

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	7393	0	7130	8	0
1	B	6865	0	6288	7	0
1	C	7281	0	6950	8	0
2	D	28	0	25	0	0
2	E	28	0	25	0	0
2	F	28	0	25	0	0
2	G	28	0	25	0	0
2	H	28	0	25	0	0
2	I	28	0	25	0	0
2	J	28	0	25	0	0
2	K	28	0	25	0	0
2	L	28	0	25	0	0
2	M	28	0	25	0	0
2	N	28	0	25	0	0
2	O	28	0	25	0	0
3	A	140	0	130	2	0
3	B	182	0	169	3	0
3	C	168	0	156	0	0
All	All	22365	0	21123	23	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

All (23) 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:655:HIS:O	3:A:1310:NAG:H81	2.10	0.51
1:A:520:ALA:HB1	1:A:521:PRO:HD2	1.92	0.50
1:A:360:ASN:H	1:A:523:THR:HG22	1.76	0.50
1:C:360:ASN:H	1:C:523:THR:HG22	1.79	0.48
1:B:574:ASP:OD1	1:B:575:ALA:N	2.48	0.47
1:C:353:TRP:CD1	1:C:353:TRP:H	2.33	0.46
1:B:655:HIS:O	3:B:1309:NAG:H81	2.16	0.46
1:B:1028:LYS:NZ	1:B:1042:PHE:O	2.50	0.45
1:C:202:LYS:NZ	1:C:228:ASP:OD2	2.50	0.45
1:B:343:ASN:OD1	3:B:1306:NAG:C7	2.65	0.44
1:C:1142:GLN:N	1:C:1143:PRO:CD	2.81	0.44
1:B:811:LYS:NZ	1:B:820:ASP:OD2	2.41	0.44
1:C:796:ASP:OD1	1:C:796:ASP:N	2.51	0.44
1:B:123:ALA:HB3	3:B:1302:NAG:H82	1.99	0.43
1:B:290:ASP:OD1	1:B:290:ASP:C	2.60	0.43
1:A:579:PRO:O	3:A:1306:NAG:H82	2.19	0.43
1:A:360:ASN:H	1:A:523:THR:CG2	2.30	0.43
1:A:1142:GLN:N	1:A:1143:PRO:CD	2.82	0.42
1:C:520:ALA:HB1	1:C:521:PRO:HD2	2.02	0.42
1:C:599:THR:HG22	1:C:601:GLY:H	1.85	0.41
1:A:266:TYR:CD1	1:A:266:TYR:N	2.89	0.41
1:C:391:CYS:SG	1:C:522:ALA:HB1	2.60	0.41
1:A:391:CYS:SG	1:A:522:ALA:HB1	2.61	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	940/1281 (73%)	916 (97%)	23 (2%)	1 (0%)	48	79
1	B	921/1281 (72%)	898 (98%)	22 (2%)	1 (0%)	48	79
1	C	936/1281 (73%)	913 (98%)	23 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	2797/3843 (73%)	2727 (98%)	68 (2%)	2 (0%)	49 79

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	332	ILE
1	A	468	ILE

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	801/1107 (72%)	801 (100%)	0	100 100
1	B	682/1107 (62%)	680 (100%)	2 (0%)	86 88
1	C	775/1107 (70%)	774 (100%)	1 (0%)	88 91
All	All	2258/3321 (68%)	2255 (100%)	3 (0%)	87 91

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	122	ASN
1	B	603	ASN
1	C	331	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	69	HIS
1	A	439	ASN
1	A	703	ASN
1	A	856	ASN
1	A	1010	GLN
1	A	1088	HIS

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Mol	Chain	Res	Type
1	B	196	ASN
1	B	787	GLN
1	B	856	ASN
1	B	1071	GLN
1	C	314	GLN
1	C	450	ASN
1	C	519	HIS
1	C	613	GLN
1	C	655	HIS
1	C	675	GLN
1	C	913	GLN
1	C	1088	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

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	$\# Z > 2$
2	NAG	D	1	2,1	14,14,15	1.71	2 (14%)	17,19,21	0.68	0
2	NAG	D	2	2	14,14,15	1.36	2 (14%)	17,19,21	0.66	0
2	NAG	E	1	2,1	14,14,15	1.50	2 (14%)	17,19,21	0.67	0
2	NAG	E	2	2	14,14,15	1.47	2 (14%)	17,19,21	0.66	0
2	NAG	F	1	2,1	14,14,15	1.57	2 (14%)	17,19,21	0.65	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	F	2	2	14,14,15	1.42	2 (14%)	17,19,21	0.63	0
2	NAG	G	1	2,1	14,14,15	1.59	2 (14%)	17,19,21	0.78	0
2	NAG	G	2	2	14,14,15	1.47	2 (14%)	17,19,21	0.63	0
2	NAG	H	1	2,1	14,14,15	1.63	2 (14%)	17,19,21	0.74	0
2	NAG	H	2	2	14,14,15	1.48	2 (14%)	17,19,21	0.62	0
2	NAG	I	1	2,1	14,14,15	1.56	2 (14%)	17,19,21	0.62	0
2	NAG	I	2	2	14,14,15	1.46	2 (14%)	17,19,21	0.63	0
2	NAG	J	1	2,1	14,14,15	1.53	2 (14%)	17,19,21	0.79	0
2	NAG	J	2	2	14,14,15	1.43	2 (14%)	17,19,21	0.65	0
2	NAG	K	1	2,1	14,14,15	1.51	2 (14%)	17,19,21	0.70	0
2	NAG	K	2	2	14,14,15	1.44	2 (14%)	17,19,21	0.63	0
2	NAG	L	1	2,1	14,14,15	1.50	2 (14%)	17,19,21	0.77	0
2	NAG	L	2	2	14,14,15	1.46	2 (14%)	17,19,21	0.67	0
2	NAG	M	1	2,1	14,14,15	1.58	2 (14%)	17,19,21	0.71	0
2	NAG	M	2	2	14,14,15	1.47	2 (14%)	17,19,21	0.60	0
2	NAG	N	1	2,1	14,14,15	1.54	2 (14%)	17,19,21	0.85	0
2	NAG	N	2	2	14,14,15	1.37	2 (14%)	17,19,21	0.63	0
2	NAG	O	1	2,1	14,14,15	1.54	2 (14%)	17,19,21	0.70	0
2	NAG	O	2	2	14,14,15	1.49	2 (14%)	17,19,21	0.63	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
2	NAG	D	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	D	2	2	-	1/6/23/26	0/1/1/1
2	NAG	E	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	E	2	2	-	0/6/23/26	0/1/1/1
2	NAG	F	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	F	2	2	-	0/6/23/26	0/1/1/1
2	NAG	G	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	G	2	2	-	0/6/23/26	0/1/1/1
2	NAG	H	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	H	2	2	-	0/6/23/26	0/1/1/1
2	NAG	I	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	I	2	2	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	J	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	J	2	2	-	0/6/23/26	0/1/1/1
2	NAG	K	1	2,1	-	1/6/23/26	0/1/1/1
2	NAG	K	2	2	-	0/6/23/26	0/1/1/1
2	NAG	L	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	L	2	2	-	0/6/23/26	0/1/1/1
2	NAG	M	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	M	2	2	-	0/6/23/26	0/1/1/1
2	NAG	N	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	N	2	2	-	0/6/23/26	0/1/1/1
2	NAG	O	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	O	2	2	-	0/6/23/26	0/1/1/1

All (48) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1	NAG	C1-C2	4.96	1.59	1.52
2	M	1	NAG	C1-C2	4.56	1.58	1.52
2	H	1	NAG	C1-C2	4.48	1.58	1.52
2	N	1	NAG	C1-C2	4.34	1.58	1.52
2	F	1	NAG	C1-C2	4.30	1.58	1.52
2	I	1	NAG	C1-C2	4.25	1.58	1.52
2	L	1	NAG	C1-C2	4.17	1.58	1.52
2	O	1	NAG	C1-C2	4.13	1.58	1.52
2	G	1	NAG	C1-C2	4.10	1.57	1.52
2	J	1	NAG	C1-C2	4.09	1.57	1.52
2	E	1	NAG	C1-C2	4.07	1.57	1.52
2	K	1	NAG	C1-C2	4.03	1.57	1.52
2	O	2	NAG	C1-C2	3.88	1.57	1.52
2	H	2	NAG	C1-C2	3.85	1.57	1.52
2	M	2	NAG	C1-C2	3.83	1.57	1.52
2	I	2	NAG	C1-C2	3.76	1.57	1.52
2	G	2	NAG	C1-C2	3.69	1.57	1.52
2	E	2	NAG	C1-C2	3.67	1.57	1.52
2	F	2	NAG	C1-C2	3.65	1.57	1.52
2	K	2	NAG	C1-C2	3.65	1.57	1.52
2	L	2	NAG	C1-C2	3.61	1.57	1.52
2	J	2	NAG	C1-C2	3.60	1.57	1.52
2	D	2	NAG	C1-C2	3.23	1.56	1.52
2	N	2	NAG	C1-C2	3.12	1.56	1.52
2	G	1	NAG	O5-C5	2.66	1.48	1.43
2	G	2	NAG	O5-C5	2.60	1.48	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	2	NAG	O5-C5	2.59	1.48	1.43
2	I	2	NAG	O5-C5	2.57	1.48	1.43
2	N	2	NAG	O5-C5	2.55	1.48	1.43
2	J	2	NAG	O5-C5	2.50	1.48	1.43
2	J	1	NAG	O5-C5	2.49	1.48	1.43
2	H	2	NAG	O5-C5	2.47	1.48	1.43
2	M	2	NAG	O5-C5	2.45	1.48	1.43
2	E	2	NAG	O5-C5	2.45	1.48	1.43
2	K	2	NAG	O5-C5	2.44	1.48	1.43
2	O	2	NAG	O5-C5	2.43	1.48	1.43
2	H	1	NAG	O5-C5	2.42	1.48	1.43
2	D	2	NAG	O5-C5	2.39	1.48	1.43
2	F	2	NAG	O5-C5	2.36	1.48	1.43
2	F	1	NAG	O5-C5	2.35	1.48	1.43
2	N	1	NAG	O5-C5	2.35	1.48	1.43
2	D	1	NAG	O5-C5	2.33	1.48	1.43
2	K	1	NAG	O5-C5	2.28	1.47	1.43
2	L	1	NAG	O5-C5	2.28	1.47	1.43
2	M	1	NAG	O5-C5	2.25	1.47	1.43
2	O	1	NAG	O5-C5	2.24	1.47	1.43
2	E	1	NAG	O5-C5	2.23	1.47	1.43
2	I	1	NAG	O5-C5	2.18	1.47	1.43

There are no bond angle outliers.

There are no chirality outliers.

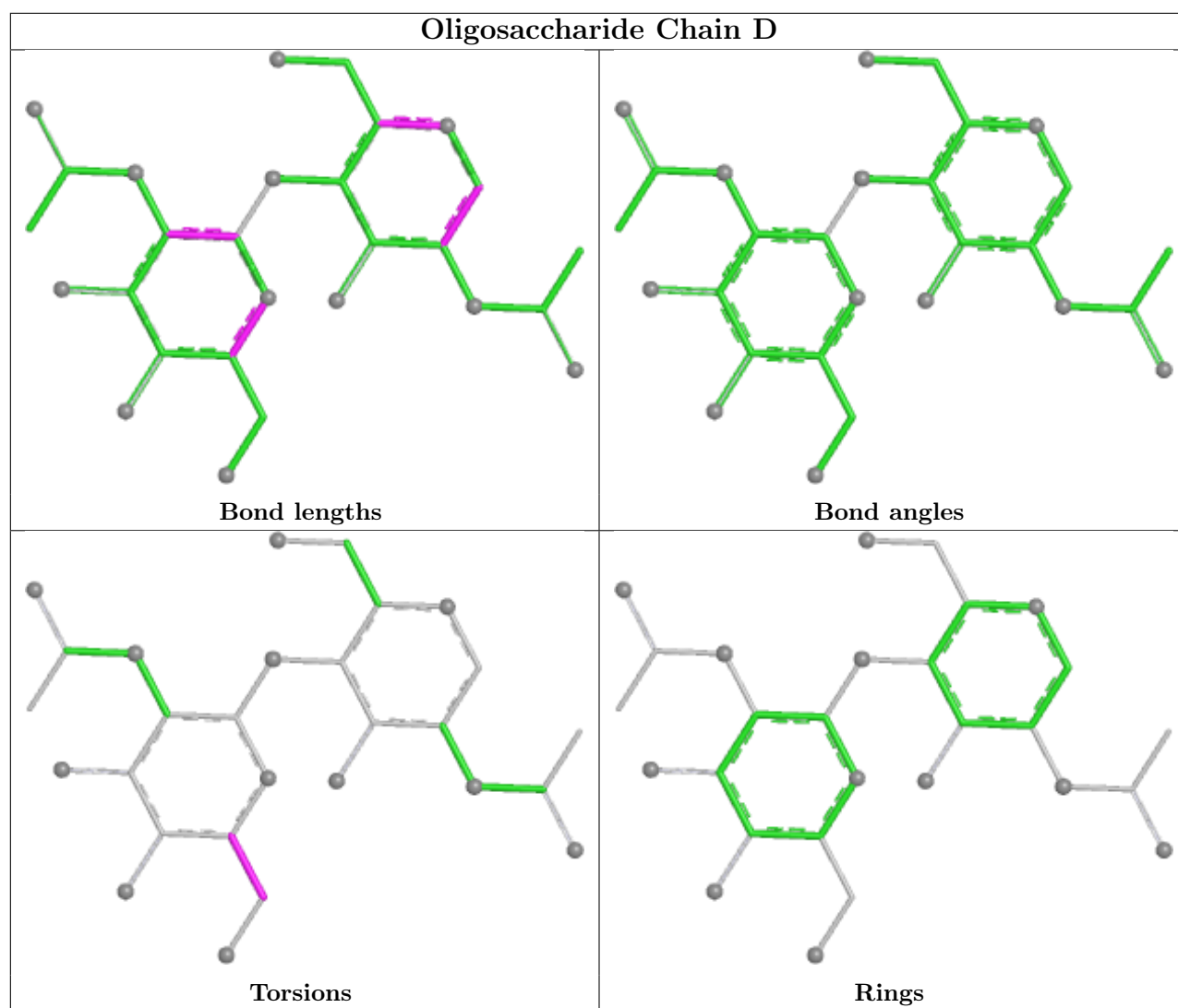
All (2) torsion outliers are listed below:

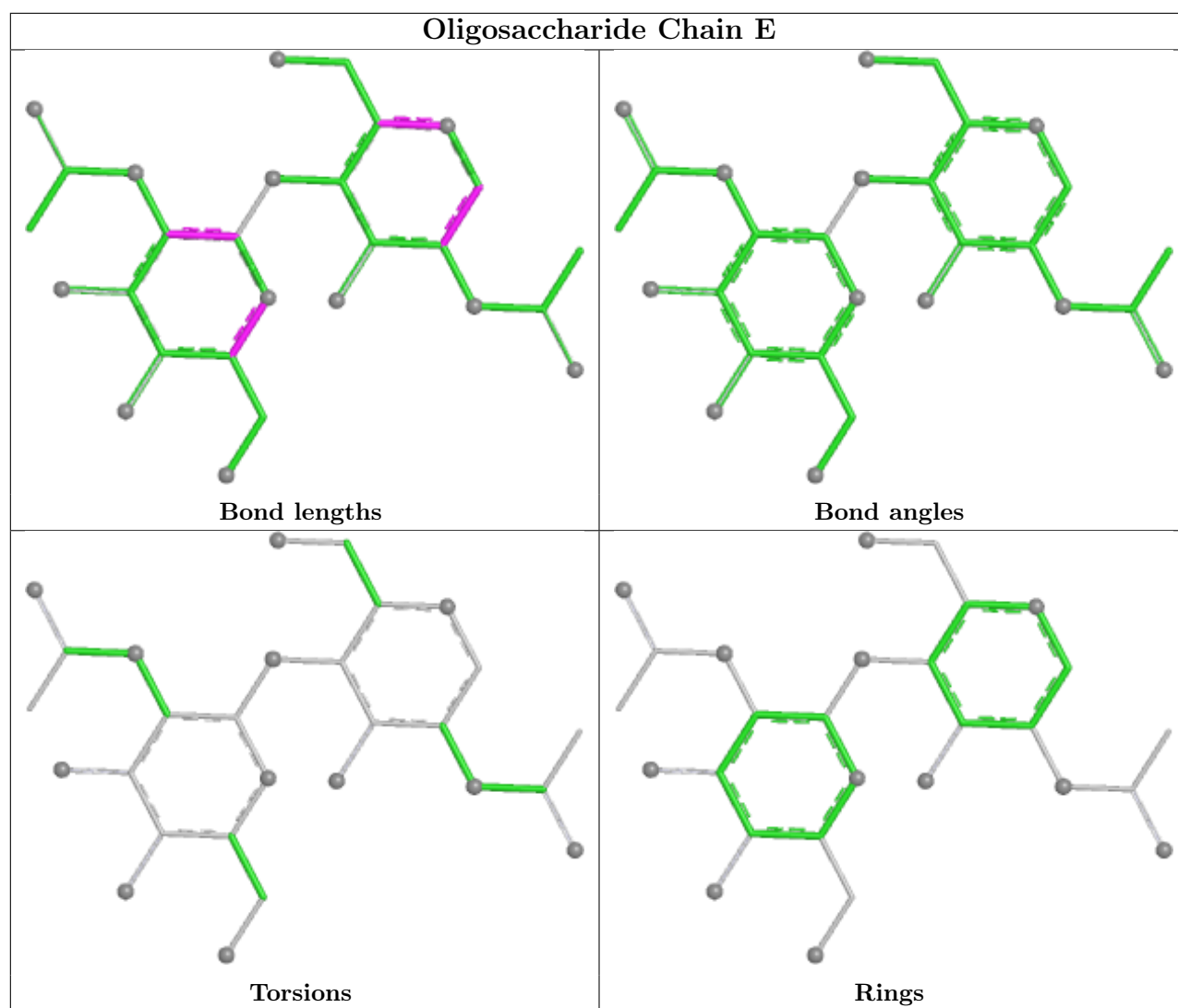
Mol	Chain	Res	Type	Atoms
2	D	2	NAG	O5-C5-C6-O6
2	K	1	NAG	C1-C2-N2-C7

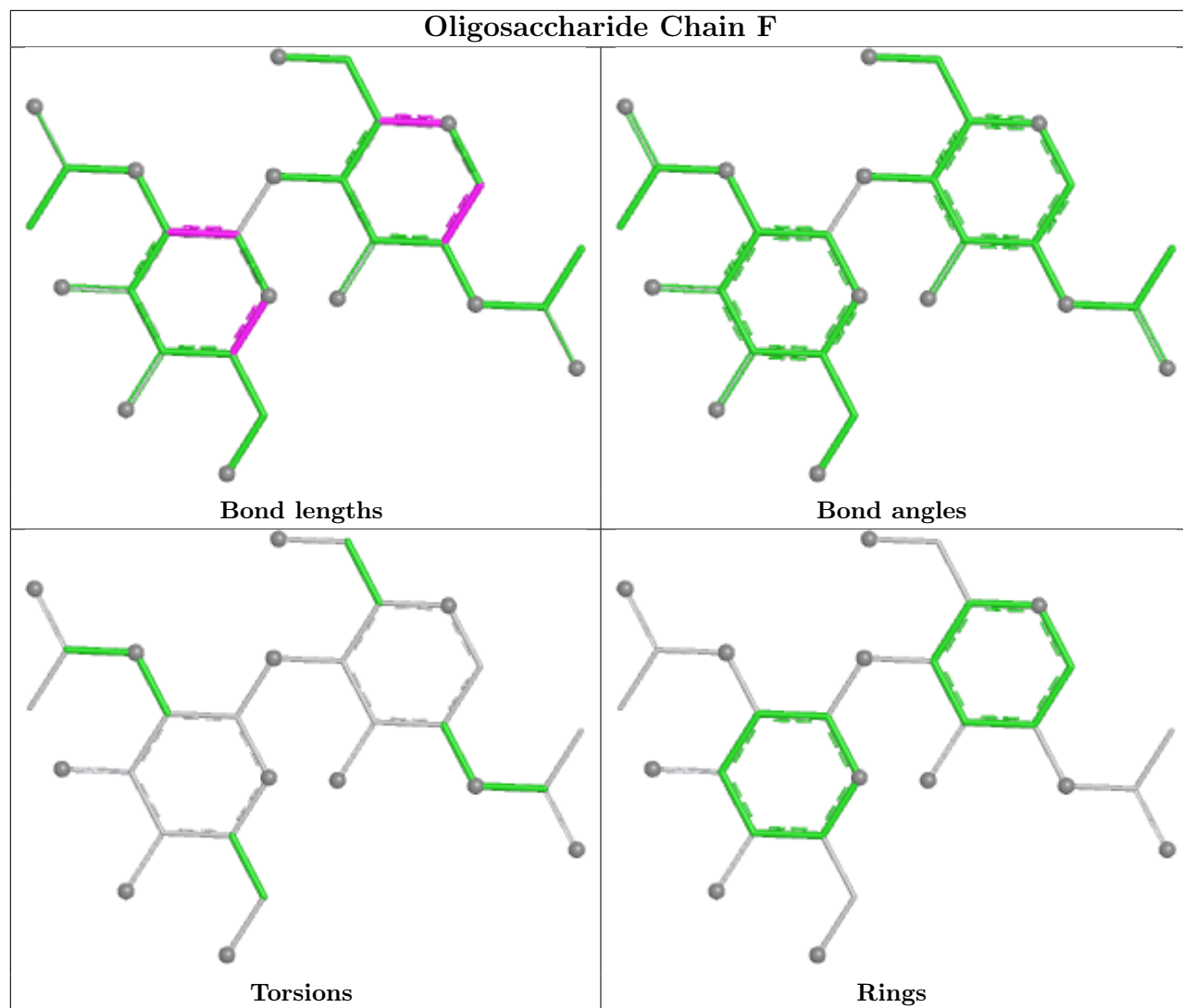
There are no ring outliers.

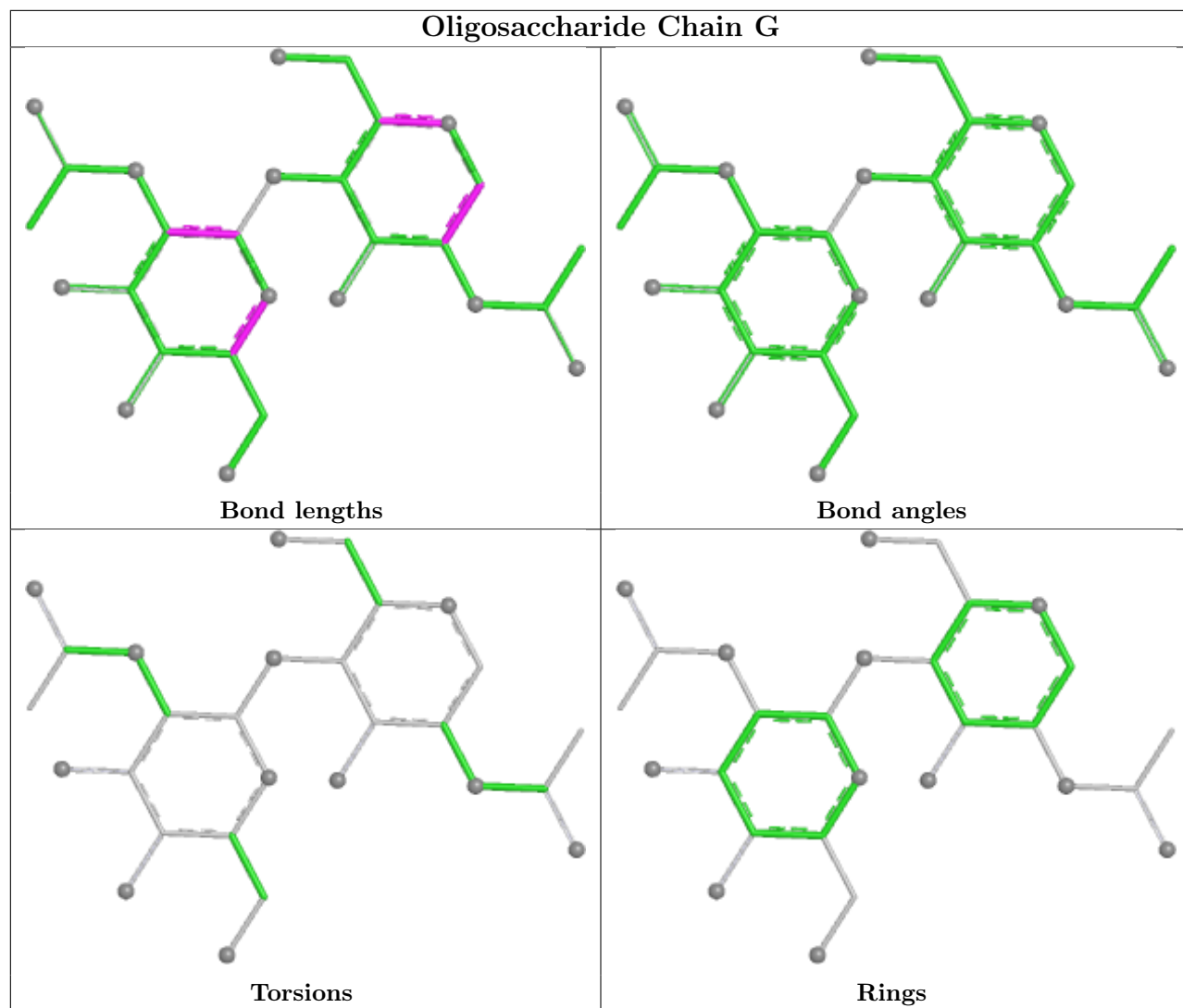
No monomer is involved in short contacts.

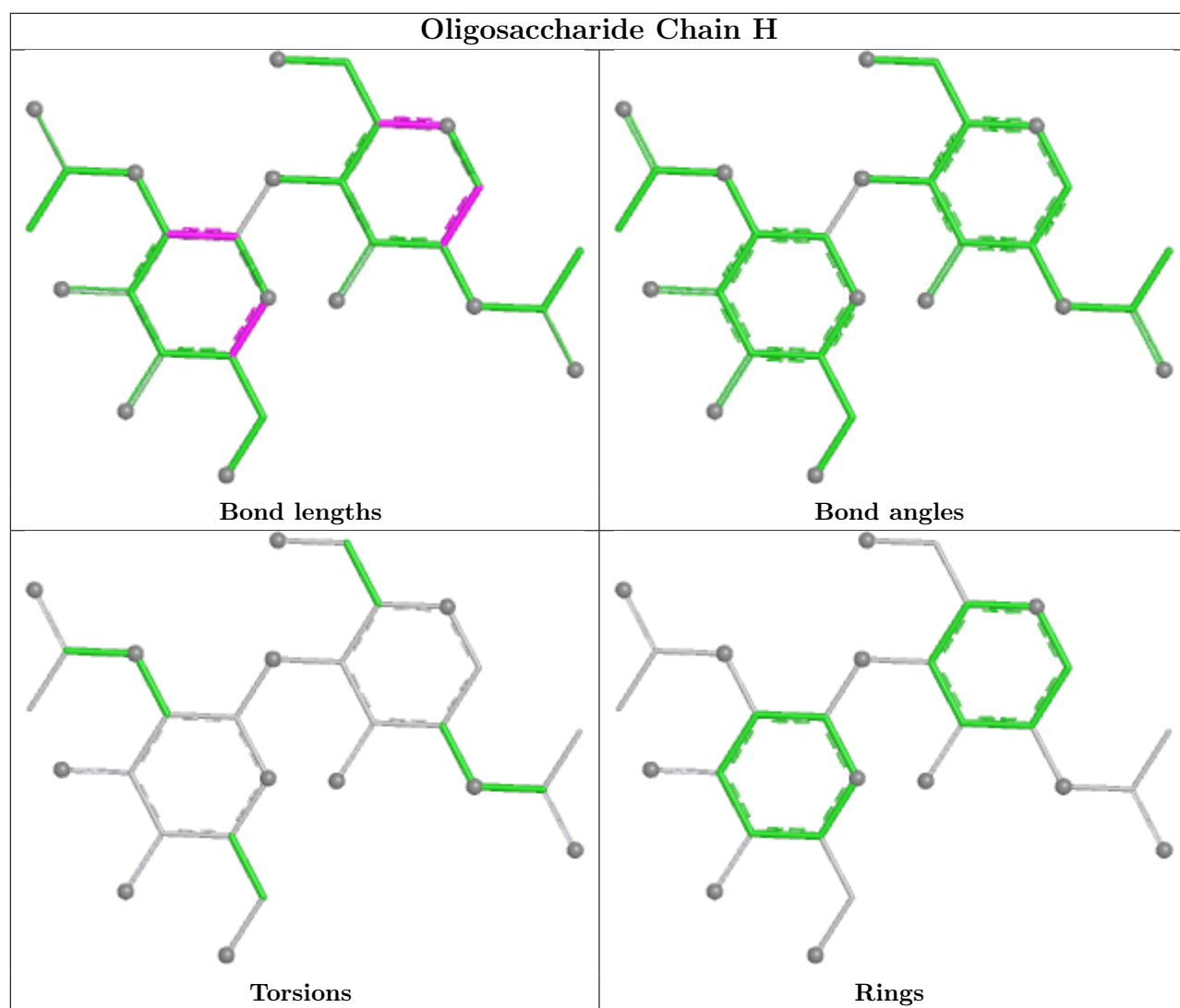
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

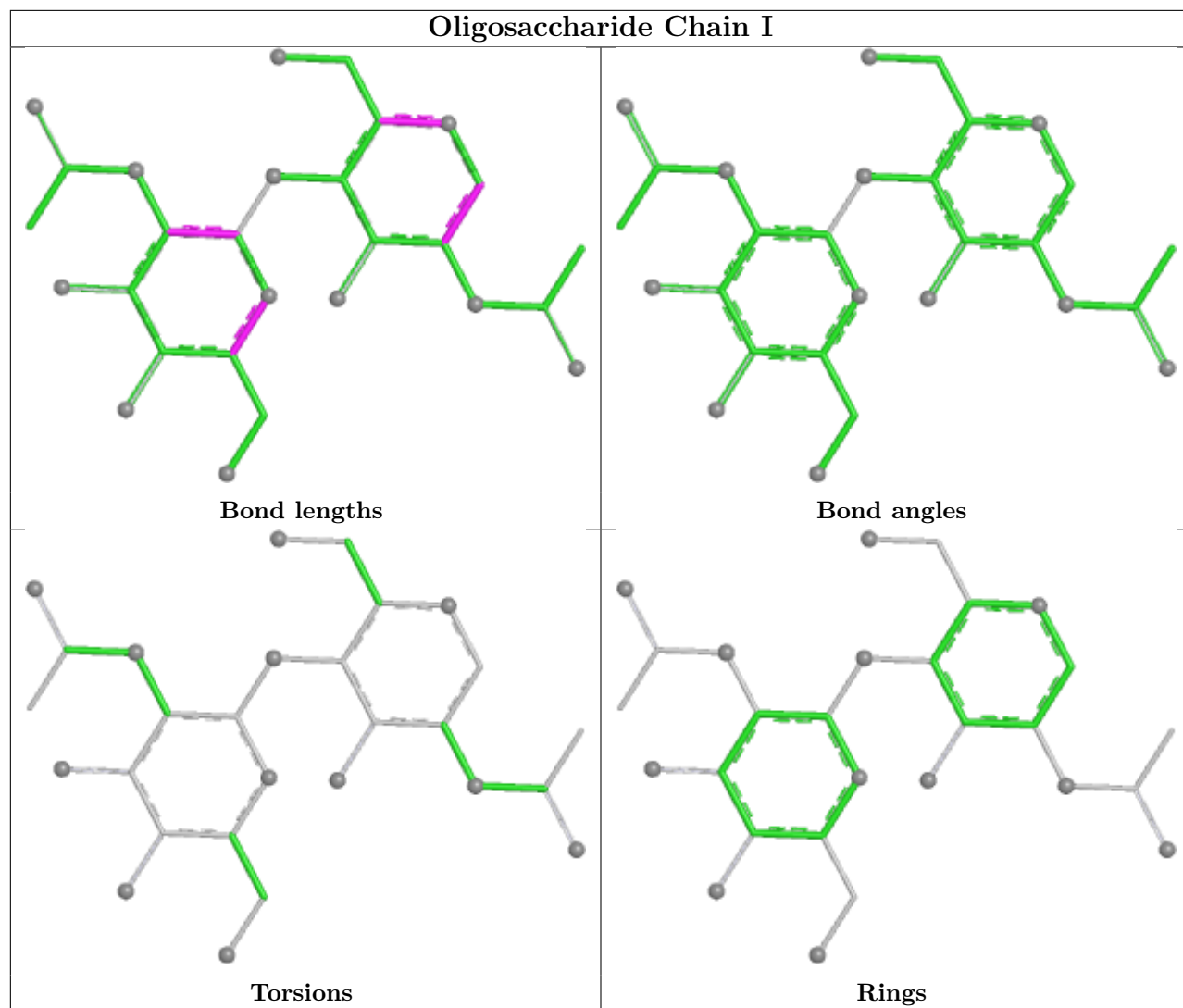


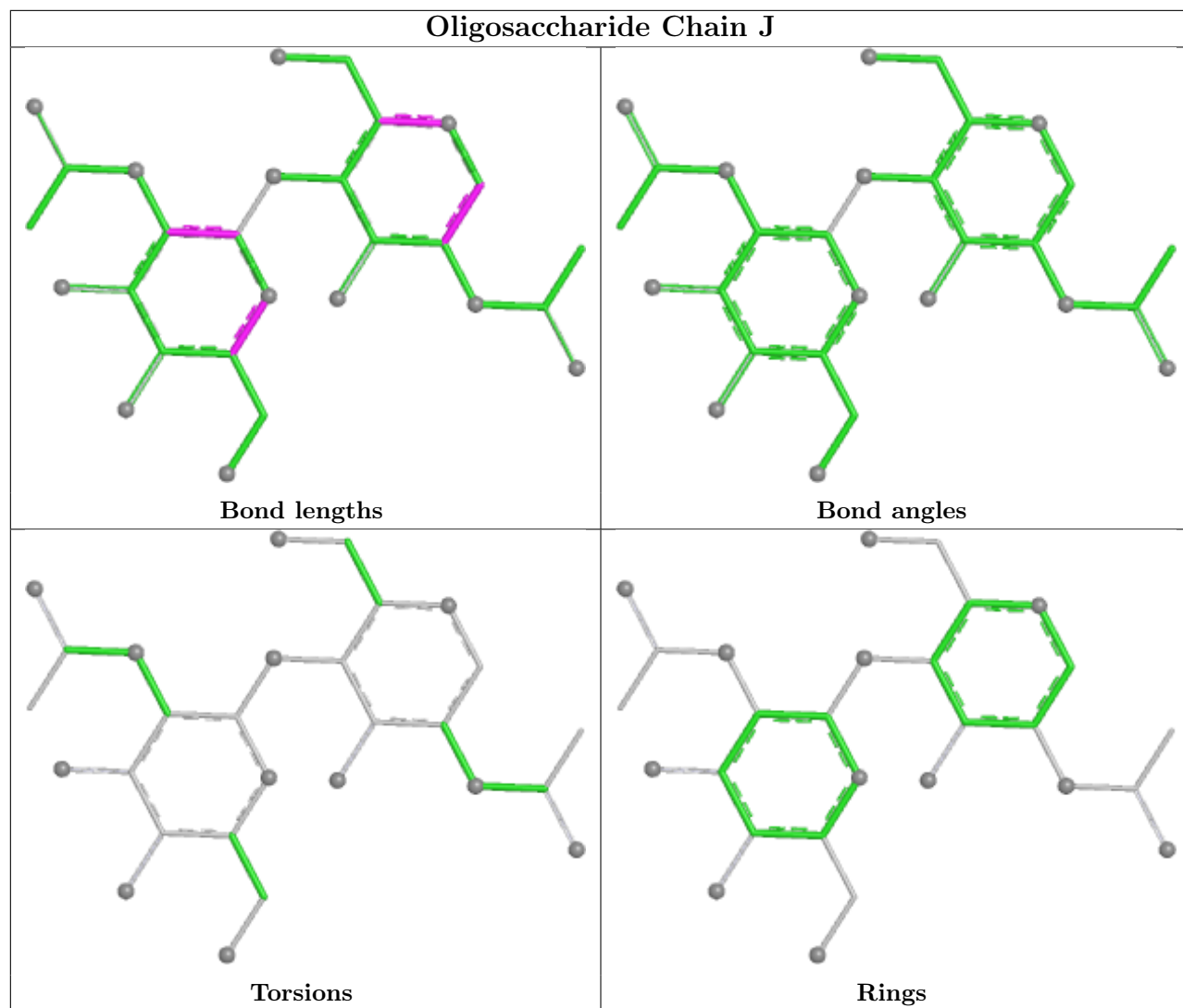


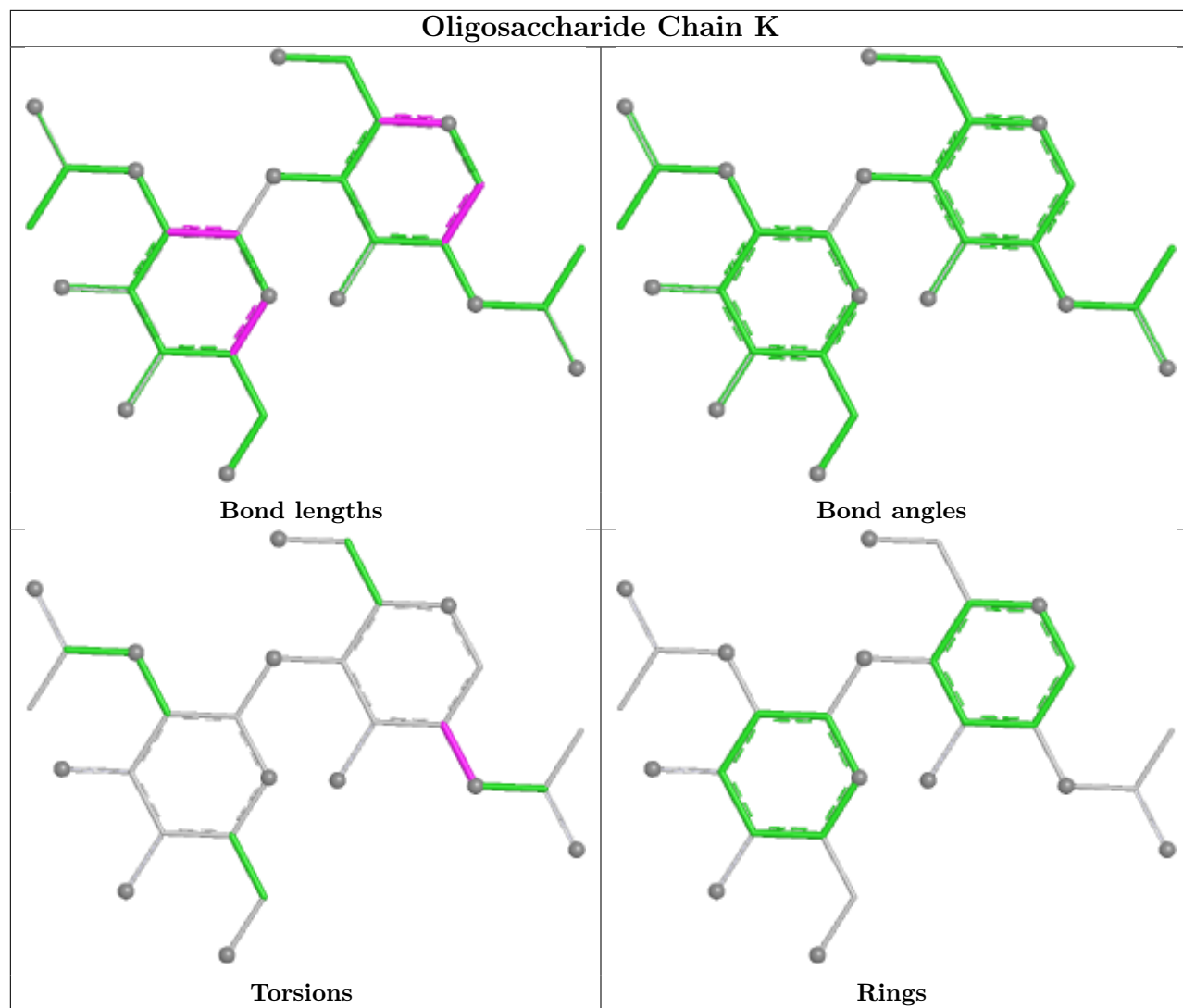


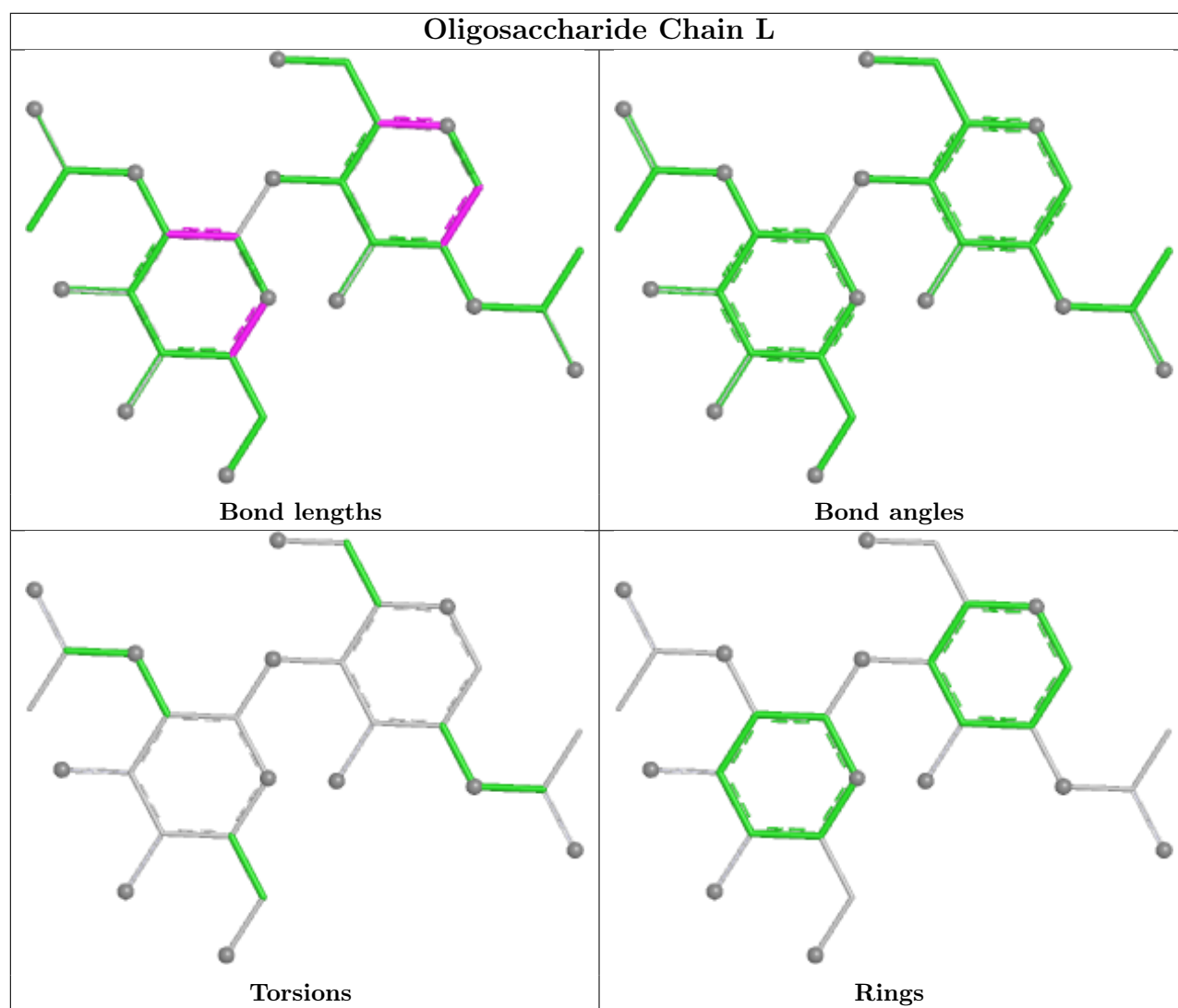


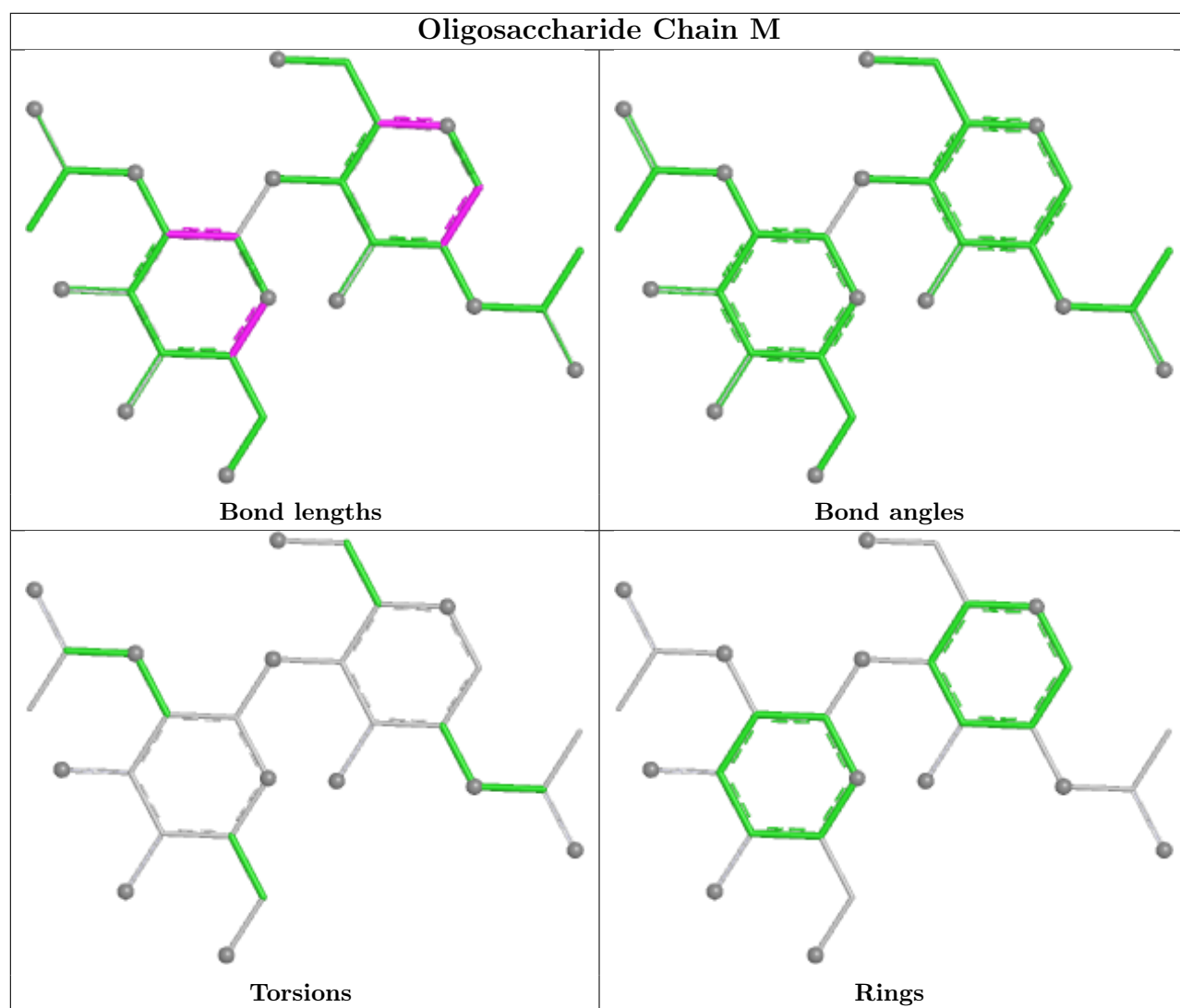


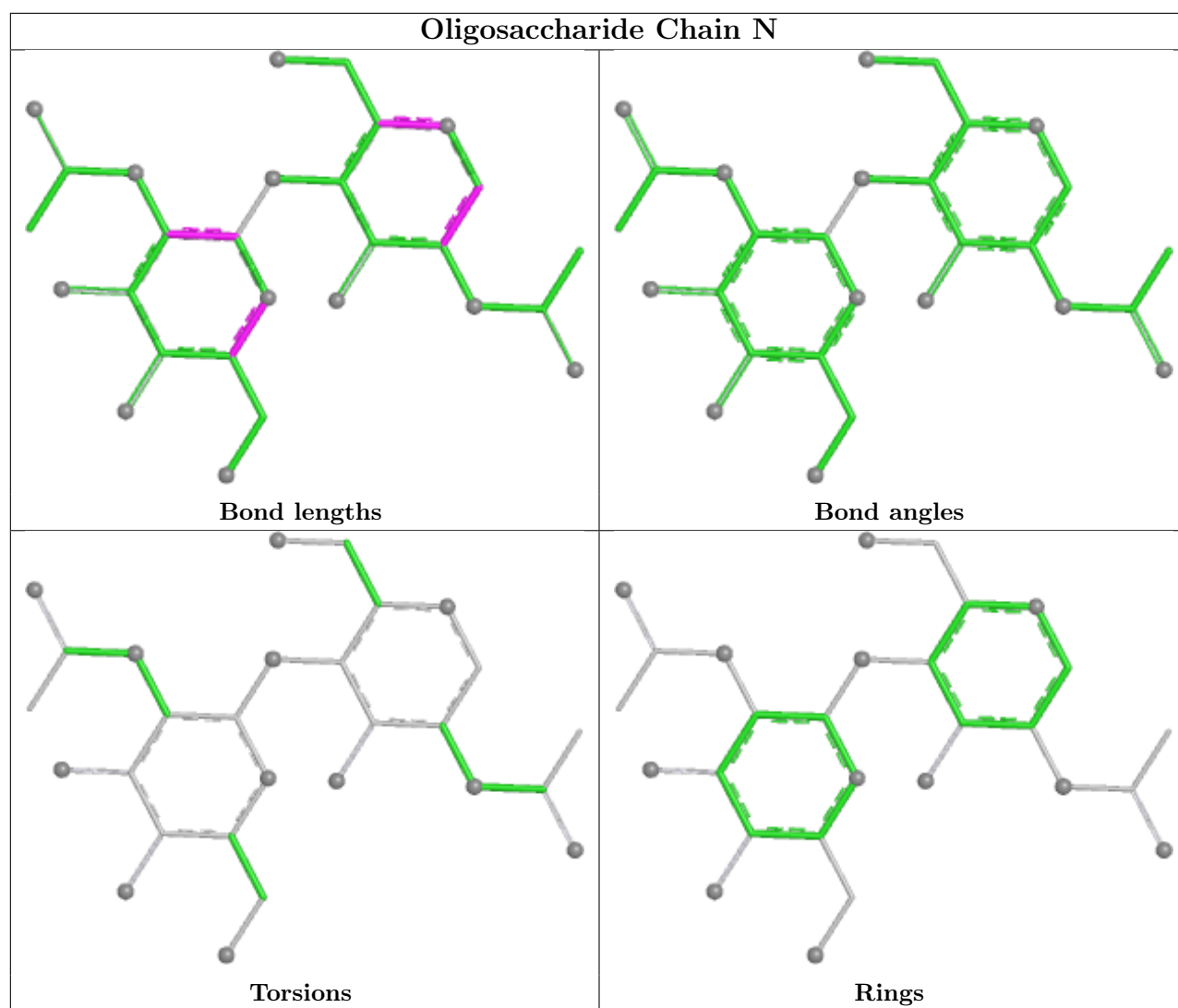


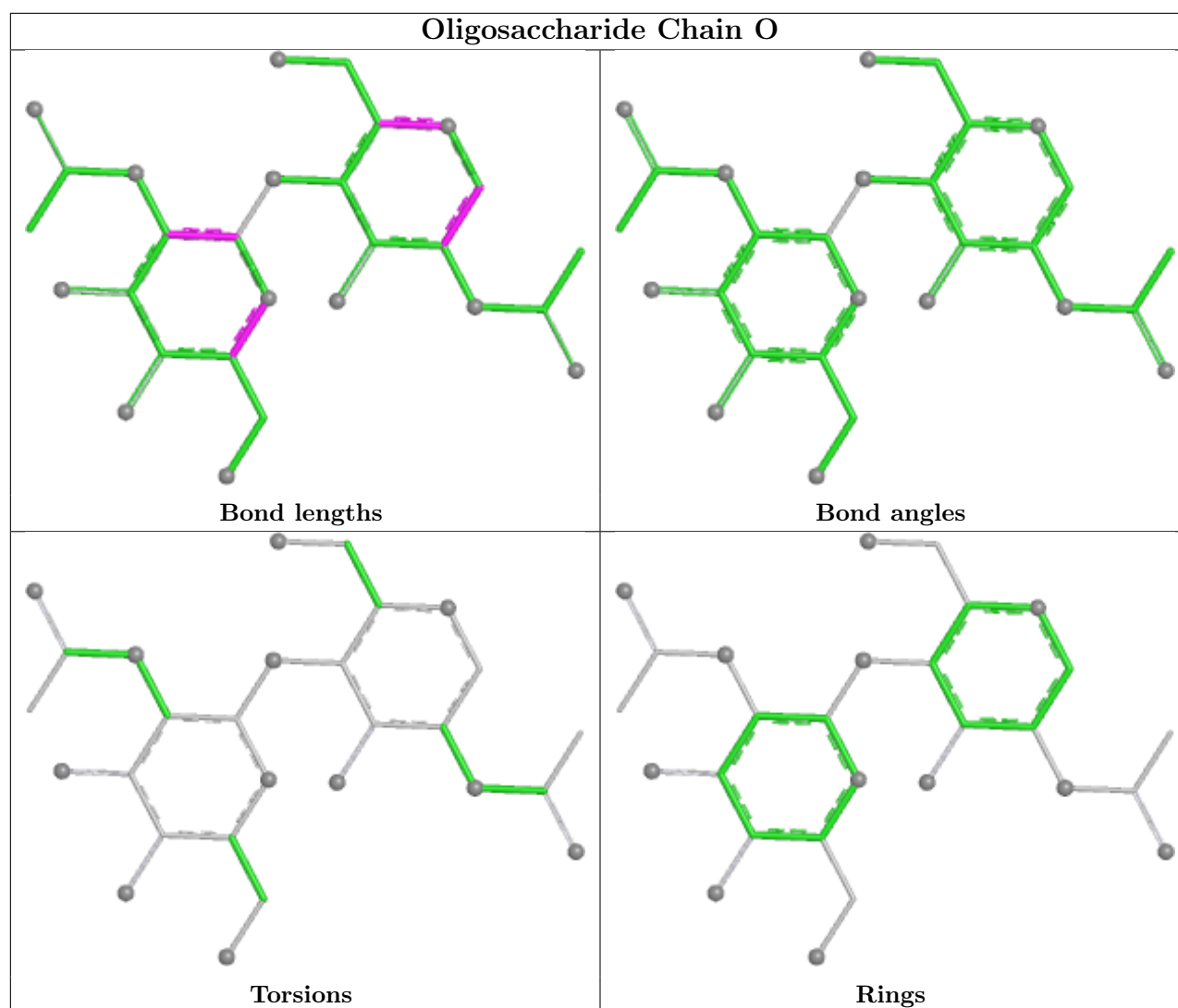












5.6 Ligand geometry [i](#)

35 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	NAG	B	1302	1	14,14,15	1.94	3 (21%)	17,19,21	0.91	1 (5%)
3	NAG	B	1304	1	14,14,15	1.60	2 (14%)	17,19,21	0.70	0
3	NAG	B	1310	1	14,14,15	1.53	3 (21%)	17,19,21	0.65	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	C	1310	1	14,14,15	1.56	2 (14%)	17,19,21	0.70	0
3	NAG	B	1301	1	14,14,15	1.63	2 (14%)	17,19,21	0.66	0
3	NAG	C	1305	1	14,14,15	1.65	2 (14%)	17,19,21	0.65	0
3	NAG	C	1320	1	14,14,15	1.57	2 (14%)	17,19,21	0.71	0
3	NAG	B	1303	1	14,14,15	1.68	2 (14%)	17,19,21	0.68	0
3	NAG	C	1303	1	14,14,15	1.64	2 (14%)	17,19,21	0.70	0
3	NAG	A	1311	1	14,14,15	1.53	2 (14%)	17,19,21	0.70	0
3	NAG	C	1309	1	14,14,15	1.70	2 (14%)	17,19,21	0.66	0
3	NAG	B	1305	1	14,14,15	1.65	2 (14%)	17,19,21	0.71	0
3	NAG	C	1315	1	14,14,15	1.60	2 (14%)	17,19,21	0.68	0
3	NAG	A	1307	1	14,14,15	1.63	2 (14%)	17,19,21	0.65	0
3	NAG	A	1305	1	14,14,15	1.58	2 (14%)	17,19,21	0.72	0
3	NAG	B	1319	1	14,14,15	1.67	3 (21%)	17,19,21	0.73	0
3	NAG	C	1302	1	14,14,15	1.58	2 (14%)	17,19,21	0.72	0
3	NAG	A	1310	1	14,14,15	1.67	2 (14%)	17,19,21	0.71	0
3	NAG	B	1311	1	14,14,15	1.57	2 (14%)	17,19,21	0.79	0
3	NAG	A	1301	1	14,14,15	1.65	2 (14%)	17,19,21	0.65	0
3	NAG	C	1306	1	14,14,15	1.60	2 (14%)	17,19,21	0.70	0
3	NAG	A	1309	1	14,14,15	1.63	2 (14%)	17,19,21	0.69	0
3	NAG	B	1307	1	14,14,15	1.61	2 (14%)	17,19,21	0.66	0
3	NAG	A	1306	1	14,14,15	1.71	2 (14%)	17,19,21	0.69	0
3	NAG	C	1307	1	14,14,15	1.61	2 (14%)	17,19,21	0.72	0
3	NAG	B	1306	1	14,14,15	1.71	2 (14%)	17,19,21	0.91	1 (5%)
3	NAG	A	1316	1	14,14,15	1.58	2 (14%)	17,19,21	0.73	0
3	NAG	A	1302	1	14,14,15	1.65	2 (14%)	17,19,21	0.73	0
3	NAG	B	1309	1	14,14,15	1.70	2 (14%)	17,19,21	0.71	0
3	NAG	C	1308	1	14,14,15	1.57	2 (14%)	17,19,21	0.70	0
3	NAG	B	1314	1	14,14,15	1.58	2 (14%)	17,19,21	0.70	0
3	NAG	C	1304	1	14,14,15	1.63	2 (14%)	17,19,21	0.72	0
3	NAG	B	1308	1	14,14,15	1.62	2 (14%)	17,19,21	0.63	0
3	NAG	A	1308	1	14,14,15	1.61	2 (14%)	17,19,21	0.65	0
3	NAG	C	1301	1	14,14,15	1.61	2 (14%)	17,19,21	0.64	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	B	1302	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1304	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1310	1	-	0/6/23/26	0/1/1/1
3	NAG	C	1310	1	-	1/6/23/26	0/1/1/1
3	NAG	B	1301	1	-	0/6/23/26	0/1/1/1
3	NAG	C	1305	1	-	0/6/23/26	0/1/1/1
3	NAG	C	1320	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1303	1	-	0/6/23/26	0/1/1/1
3	NAG	C	1303	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1311	1	-	1/6/23/26	0/1/1/1
3	NAG	C	1309	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1305	1	-	0/6/23/26	0/1/1/1
3	NAG	C	1315	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1307	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1305	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1319	1	-	0/6/23/26	0/1/1/1
3	NAG	C	1302	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1310	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1311	1	-	1/6/23/26	0/1/1/1
3	NAG	A	1301	1	-	0/6/23/26	0/1/1/1
3	NAG	C	1306	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1309	1	-	1/6/23/26	0/1/1/1
3	NAG	B	1307	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1306	1	-	0/6/23/26	0/1/1/1
3	NAG	C	1307	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1306	1	-	2/6/23/26	0/1/1/1
3	NAG	A	1316	1	-	1/6/23/26	0/1/1/1
3	NAG	A	1302	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1309	1	-	0/6/23/26	0/1/1/1
3	NAG	C	1308	1	-	1/6/23/26	0/1/1/1
3	NAG	B	1314	1	-	0/6/23/26	0/1/1/1
3	NAG	C	1304	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1308	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1308	1	-	0/6/23/26	0/1/1/1
3	NAG	C	1301	1	-	0/6/23/26	0/1/1/1

All (73) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1302	NAG	C1-C2	5.62	1.60	1.52
3	A	1306	NAG	C1-C2	5.08	1.59	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1309	NAG	C1-C2	4.93	1.59	1.52
3	C	1309	NAG	C1-C2	4.80	1.58	1.52
3	B	1305	NAG	C1-C2	4.73	1.58	1.52
3	A	1310	NAG	C1-C2	4.72	1.58	1.52
3	A	1301	NAG	C1-C2	4.71	1.58	1.52
3	B	1303	NAG	C1-C2	4.70	1.58	1.52
3	A	1302	NAG	C1-C2	4.65	1.58	1.52
3	B	1308	NAG	C1-C2	4.61	1.58	1.52
3	B	1319	NAG	C1-C2	4.60	1.58	1.52
3	C	1304	NAG	C1-C2	4.56	1.58	1.52
3	B	1301	NAG	C1-C2	4.54	1.58	1.52
3	C	1315	NAG	C1-C2	4.54	1.58	1.52
3	B	1306	NAG	C1-C2	4.53	1.58	1.52
3	A	1309	NAG	C1-C2	4.52	1.58	1.52
3	C	1301	NAG	C1-C2	4.50	1.58	1.52
3	B	1314	NAG	C1-C2	4.50	1.58	1.52
3	B	1307	NAG	C1-C2	4.49	1.58	1.52
3	C	1305	NAG	C1-C2	4.47	1.58	1.52
3	C	1306	NAG	C1-C2	4.46	1.58	1.52
3	C	1303	NAG	C1-C2	4.46	1.58	1.52
3	C	1302	NAG	C1-C2	4.45	1.58	1.52
3	A	1307	NAG	C1-C2	4.45	1.58	1.52
3	B	1311	NAG	C1-C2	4.45	1.58	1.52
3	B	1304	NAG	C1-C2	4.41	1.58	1.52
3	A	1305	NAG	C1-C2	4.41	1.58	1.52
3	A	1316	NAG	C1-C2	4.39	1.58	1.52
3	A	1308	NAG	C1-C2	4.39	1.58	1.52
3	C	1307	NAG	C1-C2	4.36	1.58	1.52
3	C	1310	NAG	C1-C2	4.31	1.58	1.52
3	C	1308	NAG	C1-C2	4.28	1.58	1.52
3	C	1320	NAG	C1-C2	4.16	1.58	1.52
3	A	1311	NAG	C1-C2	4.12	1.58	1.52
3	B	1310	NAG	C1-C2	3.55	1.57	1.52
3	B	1302	NAG	O5-C5	2.93	1.49	1.43
3	C	1305	NAG	O5-C5	2.71	1.48	1.43
3	B	1306	NAG	O5-C5	2.70	1.48	1.43
3	C	1303	NAG	O5-C5	2.68	1.48	1.43
3	A	1310	NAG	O5-C5	2.62	1.48	1.43
3	A	1308	NAG	O5-C5	2.61	1.48	1.43
3	B	1303	NAG	O5-C5	2.57	1.48	1.43
3	C	1309	NAG	O5-C5	2.56	1.48	1.43
3	C	1320	NAG	O5-C5	2.56	1.48	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1311	NAG	O5-C5	2.55	1.48	1.43
3	B	1304	NAG	O5-C5	2.53	1.48	1.43
3	A	1301	NAG	O5-C5	2.49	1.48	1.43
3	B	1305	NAG	O5-C5	2.49	1.48	1.43
3	C	1301	NAG	O5-C5	2.49	1.48	1.43
3	B	1311	NAG	O5-C5	2.47	1.48	1.43
3	B	1319	NAG	O5-C5	2.47	1.48	1.43
3	C	1310	NAG	O5-C5	2.47	1.48	1.43
3	A	1307	NAG	O5-C5	2.47	1.48	1.43
3	C	1304	NAG	O5-C5	2.46	1.48	1.43
3	C	1308	NAG	O5-C5	2.46	1.48	1.43
3	C	1307	NAG	O5-C5	2.45	1.48	1.43
3	B	1301	NAG	O5-C5	2.45	1.48	1.43
3	B	1309	NAG	O5-C5	2.44	1.48	1.43
3	B	1307	NAG	O5-C5	2.44	1.48	1.43
3	A	1305	NAG	O5-C5	2.44	1.48	1.43
3	B	1310	NAG	O5-C5	2.43	1.48	1.43
3	C	1302	NAG	O5-C5	2.43	1.48	1.43
3	B	1308	NAG	O5-C5	2.43	1.48	1.43
3	A	1309	NAG	O5-C5	2.41	1.48	1.43
3	C	1306	NAG	O5-C5	2.39	1.48	1.43
3	A	1302	NAG	O5-C5	2.38	1.48	1.43
3	B	1314	NAG	O5-C5	2.38	1.48	1.43
3	B	1310	NAG	O5-C1	2.34	1.47	1.43
3	A	1316	NAG	O5-C5	2.34	1.48	1.43
3	A	1306	NAG	O5-C5	2.28	1.47	1.43
3	C	1315	NAG	O5-C5	2.24	1.47	1.43
3	B	1302	NAG	O5-C1	2.17	1.47	1.43
3	B	1319	NAG	C3-C2	2.05	1.56	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1306	NAG	O5-C1-C2	-2.38	107.61	111.29
3	B	1302	NAG	C2-N2-C7	2.04	125.63	122.90

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	1306	NAG	O5-C5-C6-O6
3	B	1306	NAG	C4-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
3	A	1309	NAG	O5-C5-C6-O6
3	A	1316	NAG	O5-C5-C6-O6
3	C	1308	NAG	C4-C5-C6-O6
3	A	1311	NAG	C1-C2-N2-C7
3	C	1310	NAG	C1-C2-N2-C7
3	B	1311	NAG	C4-C5-C6-O6

There are no ring outliers.

5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1302	NAG	1	0
3	A	1310	NAG	1	0
3	A	1306	NAG	1	0
3	B	1306	NAG	1	0
3	B	1309	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.

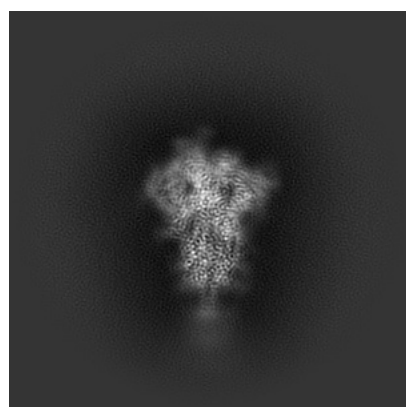
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21457. These allow visual inspection of the internal detail of the map and identification of artifacts.

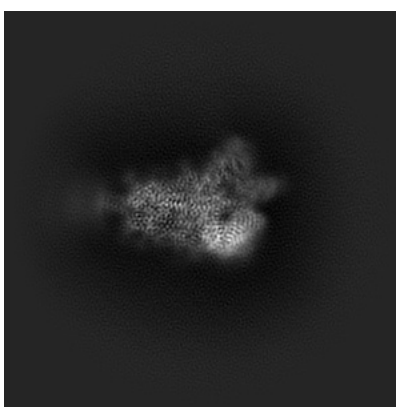
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

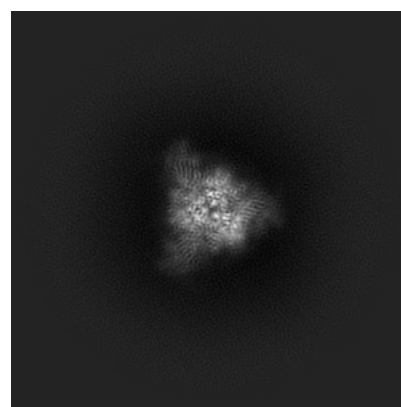
6.1.1 Primary map



X



Y



Z

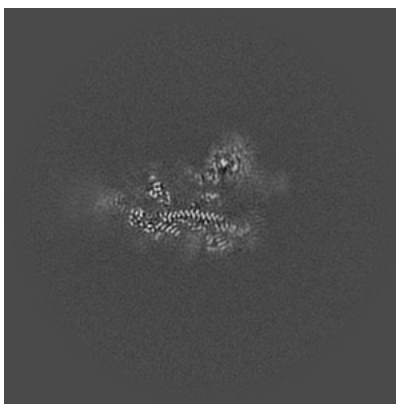
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

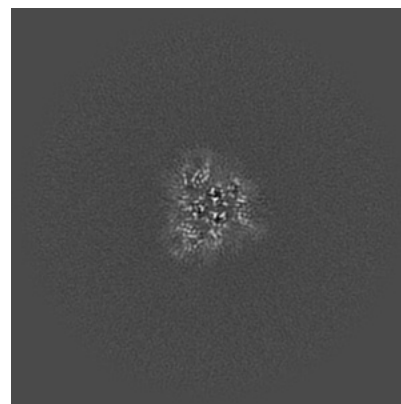
6.2.1 Primary map



X Index: 200



Y Index: 200

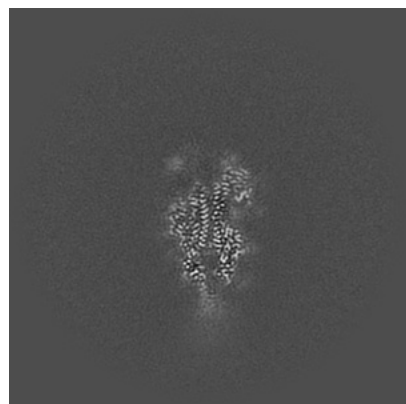


Z Index: 200

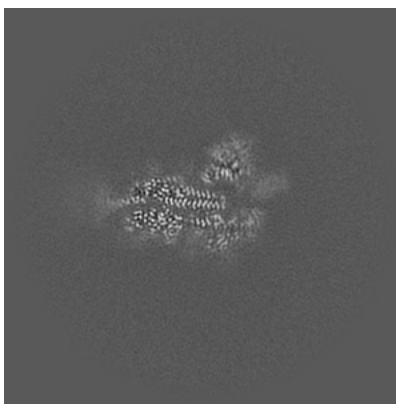
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

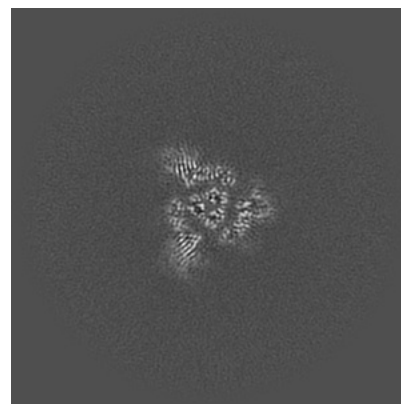
6.3.1 Primary map



X Index: 205



Y Index: 194



Z Index: 213

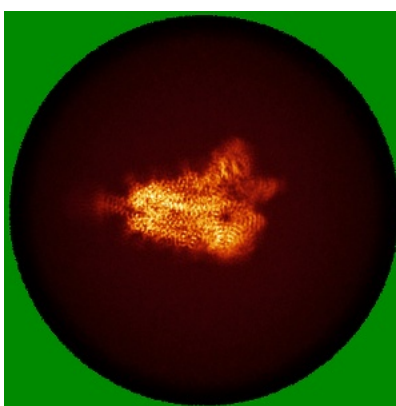
The images above show the largest variance slices of the map in three orthogonal directions.

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

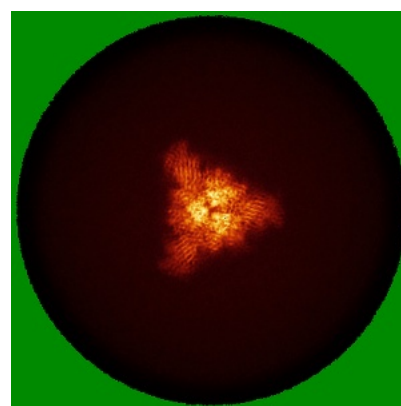
6.4.1 Primary map



X



Y



Z

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](#)

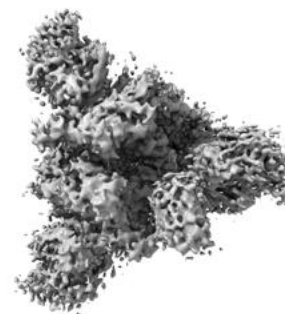
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.4. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

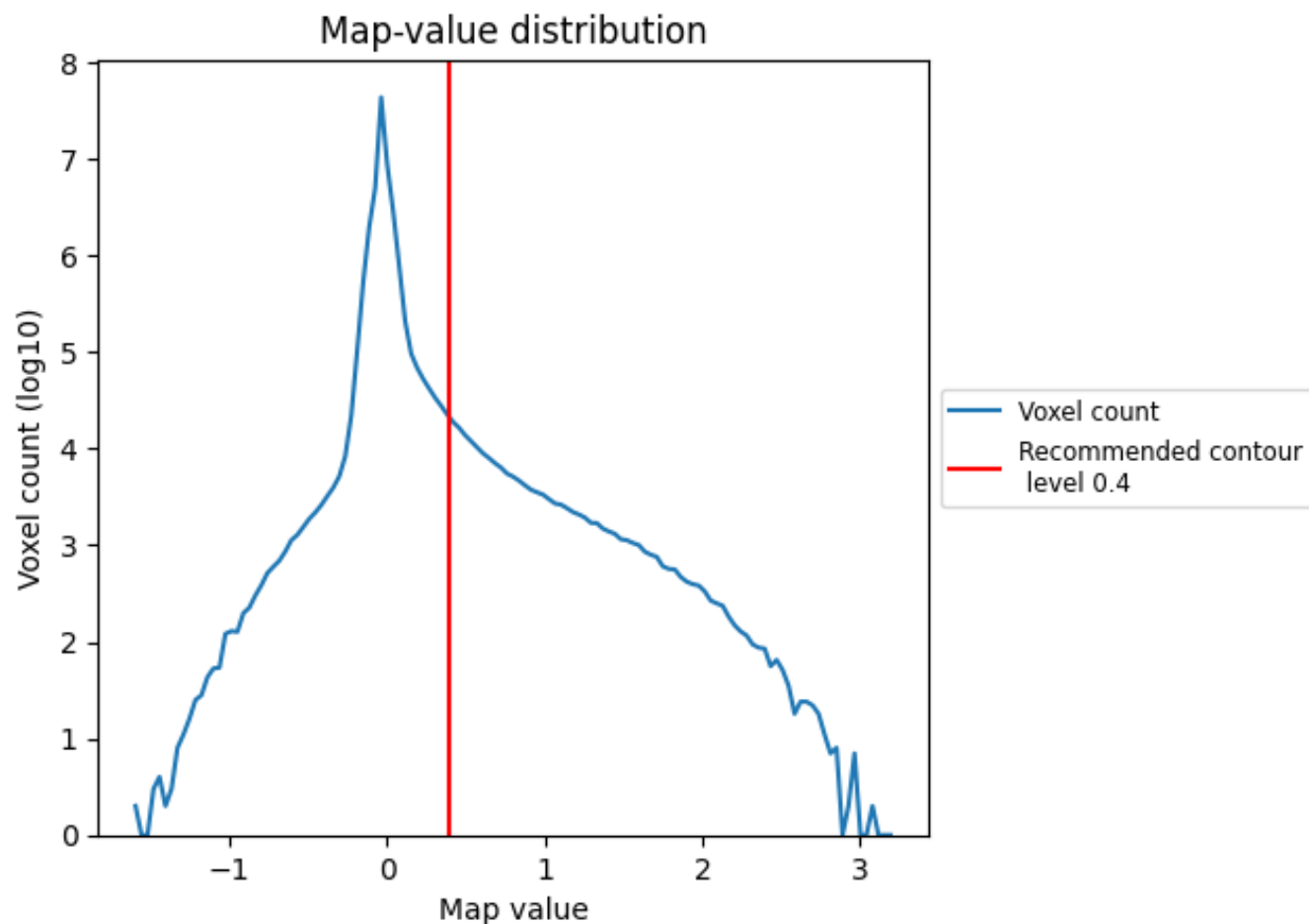
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

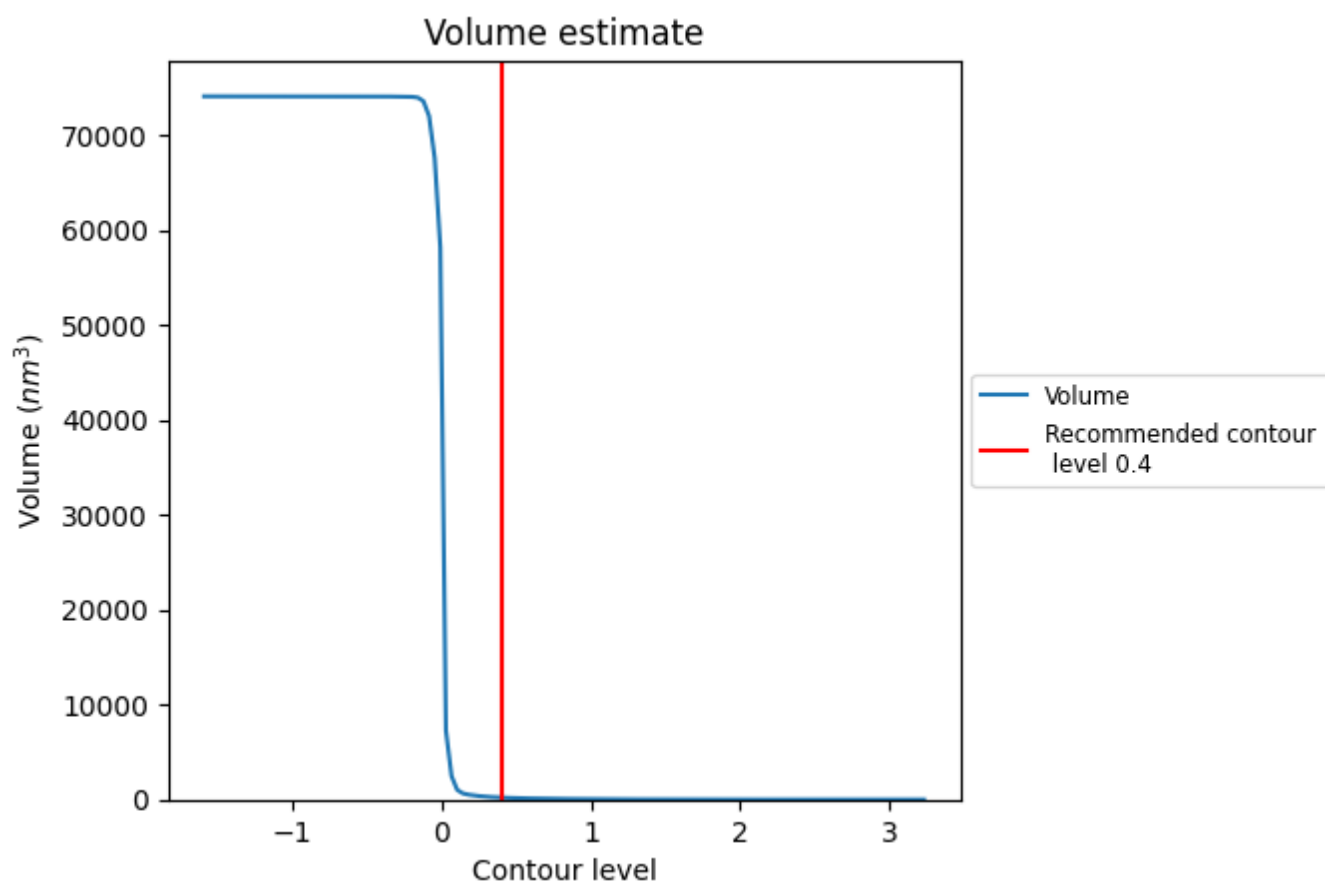
This section contains the results of statistical analysis of the map.

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.

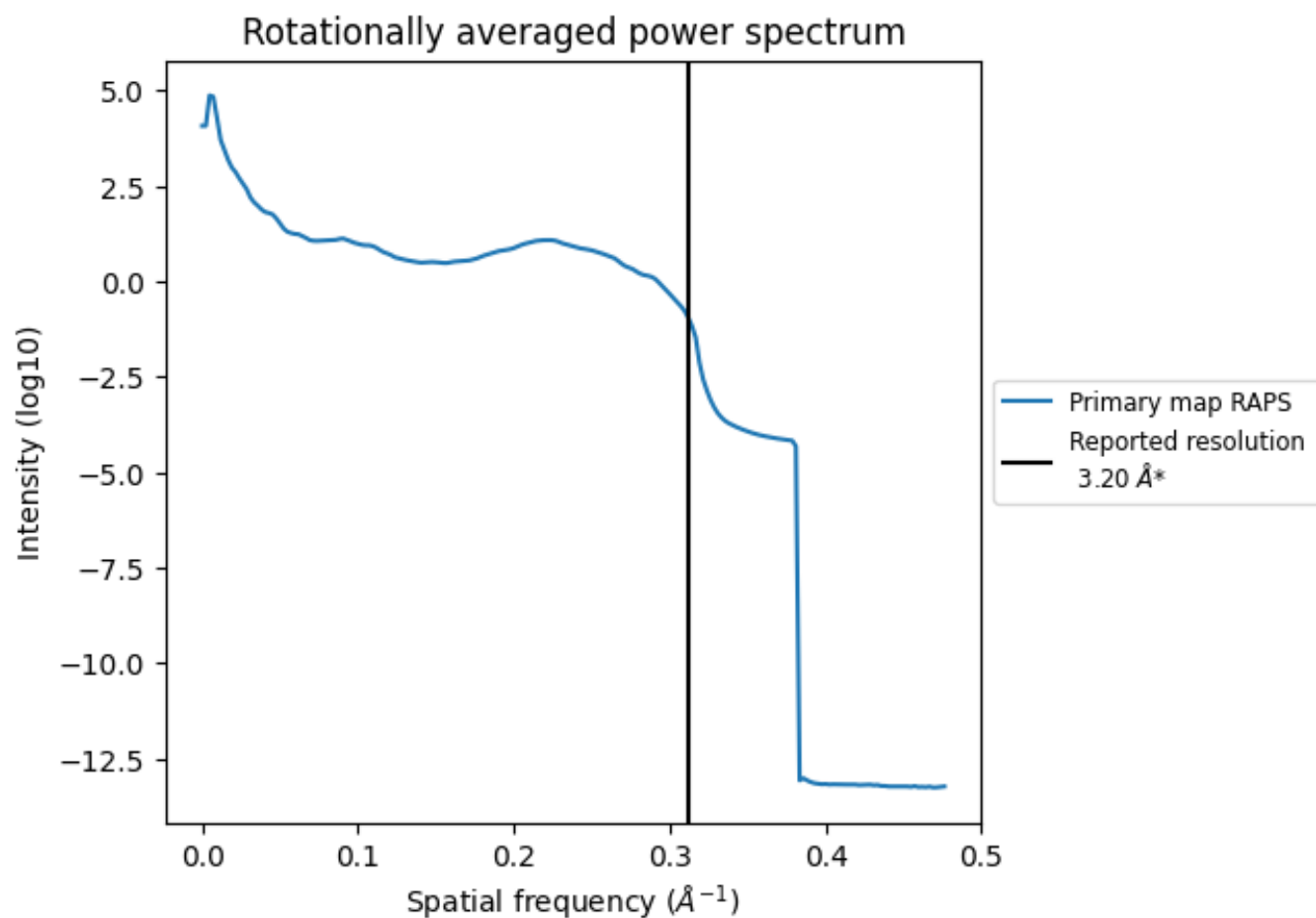
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 209 nm^3 ; this corresponds to an approximate mass of 189 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



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

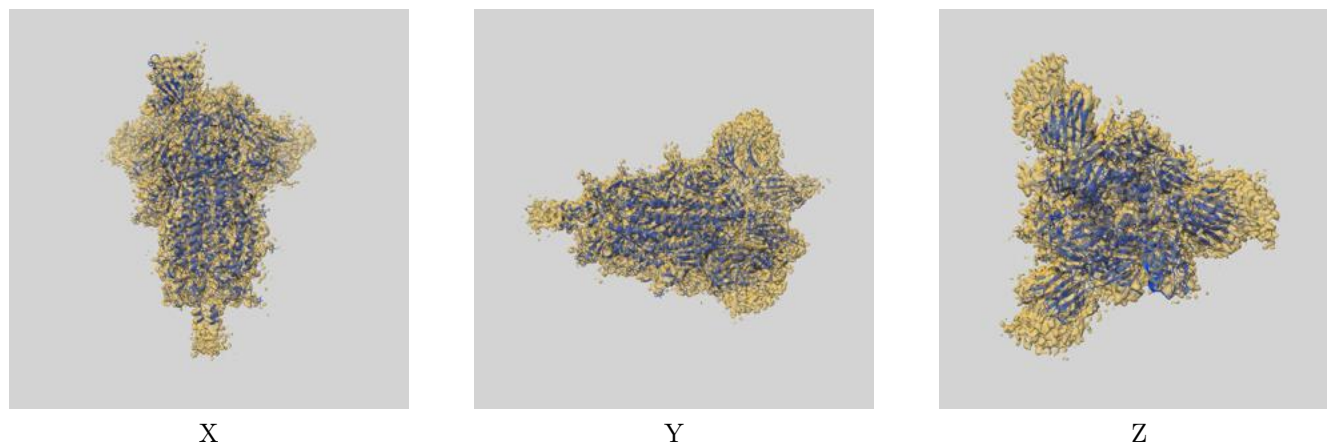
8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

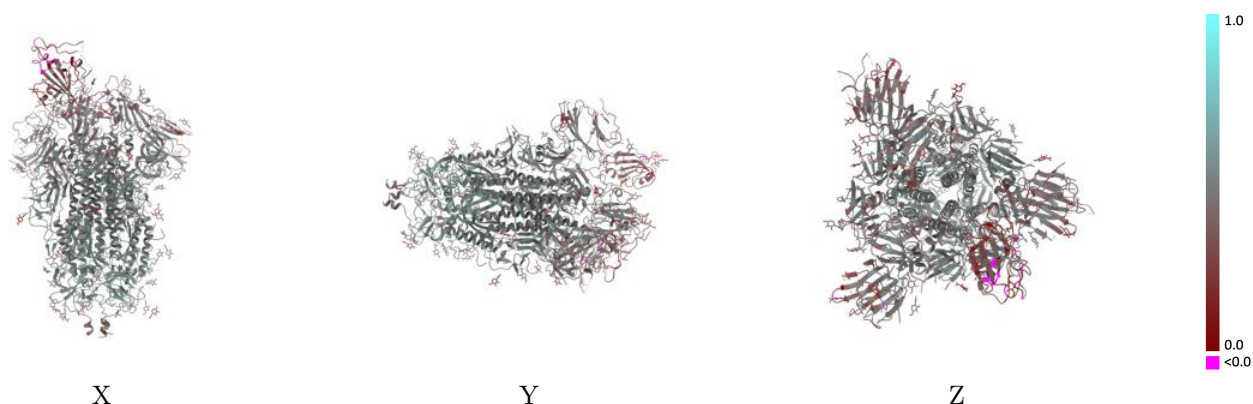
This section contains information regarding the fit between EMDB map EMD-21457 and PDB model 6VYB. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



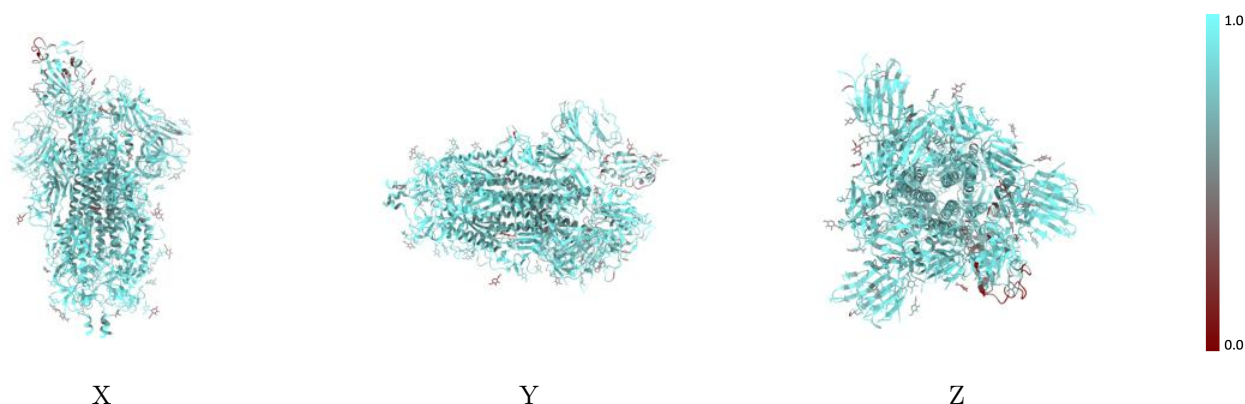
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



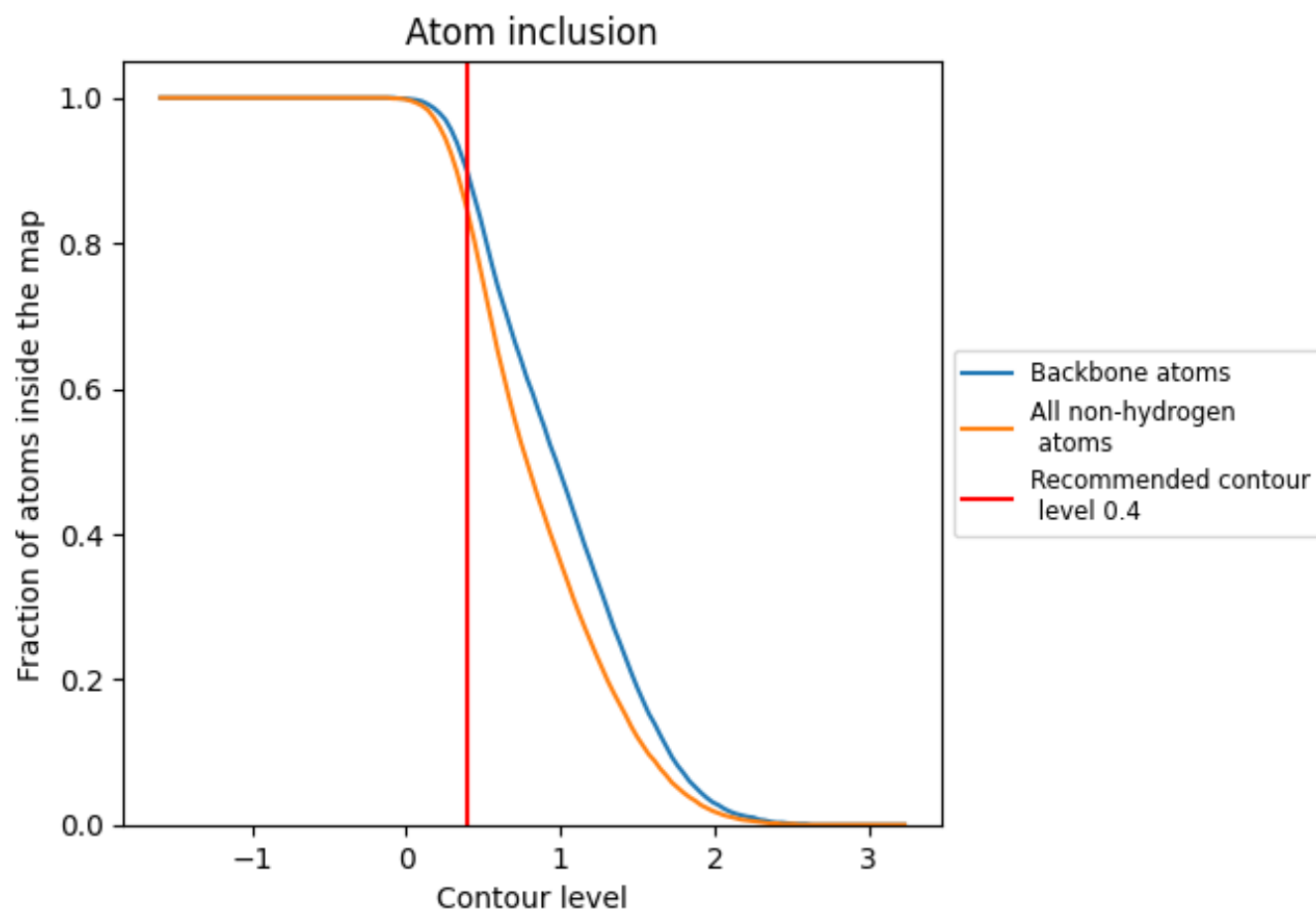
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 84% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8420	0.4610
A	0.8510	0.4670
B	0.8280	0.4540
C	0.8540	0.4680
D	0.4640	0.2980
E	0.7140	0.4260
F	0.6790	0.4010
G	0.7500	0.4180
H	0.6430	0.2520
I	0.7140	0.3810
J	0.6790	0.3530
K	0.6790	0.3840
L	0.7140	0.3920
M	0.6790	0.3090
N	0.6430	0.3820
O	0.5710	0.3370

1.0

0.0

<0.0