



wwPDB EM Validation Summary Report ⓘ

Mar 22, 2026 – 11:07 AM UTC

PDB ID : 7AKD / pdb_00007akd
EMDB ID : EMD-11812
Title : Structure of the SARS-CoV-2 spike glycoprotein in complex with the 47D11 neutralizing antibody Fab fragment
Authors : Fedry, J.; Hurdiss, D.L.; Wang, C.; Li, W.; Obal, G.; Drulyte, I.; Howes, S.C.; van Kuppeveld, F.J.M.; Foerster, F.; Bosch, B.J.
Deposited on : 2020-09-30
Resolution : 4.00 Å(reported)

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

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

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:

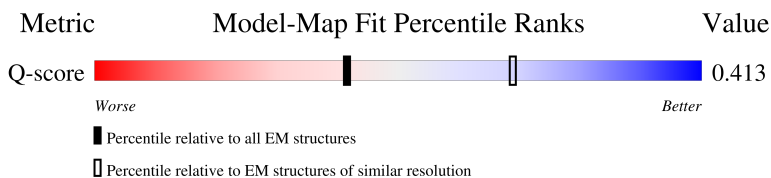
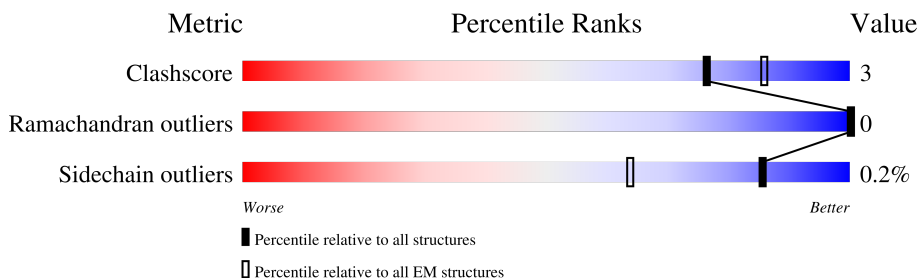
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13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

1 Overall quality at a glance

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

The reported resolution of this entry is 4.00 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	7587 (3.50 - 4.50)

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	1286	<p>13% (red), 71% (green), 5% (yellow), 25% (grey)</p>
1	B	1286	<p>6% (red), 72% (green), 5% (yellow), 23% (grey)</p>
1	C	1286	<p>71% (green), 6% (yellow), 23% (grey)</p>
2	D	121	<p>45% (red), 86% (green), 13% (yellow)</p>

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Mol	Chain	Length	Quality of chain
2	H	121	
3	E	106	
3	L	106	
4	F	2	
4	J	2	
4	K	2	
4	M	2	
4	P	2	
4	Q	2	
4	R	2	
4	V	2	
4	W	2	
4	X	2	
5	G	3	
5	I	3	
5	N	3	
6	O	5	
7	S	4	
8	T	6	
9	U	2	

2 Entry composition i

There are 12 unique types of molecules in this entry. The entry contains 27358 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
			Total	C	N	O	S		
1	A	970	Total 7517	C 4809	N 1252	O 1424	S 32	0	0
1	B	990	Total 7666	C 4898	N 1274	O 1460	S 34	0	0
1	C	992	Total 7685	C 4912	N 1279	O 1460	S 34	0	0

There are 249 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	682	GLY	ARG	conflict	UNP P0DTC2
A	683	SER	ARG	conflict	UNP P0DTC2
A	685	SER	ARG	conflict	UNP P0DTC2
A	986	PRO	LYS	conflict	UNP P0DTC2
A	987	PRO	VAL	conflict	UNP P0DTC2
A	1209	GLY	-	expression tag	UNP P0DTC2
A	1210	SER	-	expression tag	UNP P0DTC2
A	1211	GLY	-	expression tag	UNP P0DTC2
A	1212	TYR	-	expression tag	UNP P0DTC2
A	1213	ILE	-	expression tag	UNP P0DTC2
A	1214	PRO	-	expression tag	UNP P0DTC2
A	1215	GLU	-	expression tag	UNP P0DTC2
A	1216	ALA	-	expression tag	UNP P0DTC2
A	1217	PRO	-	expression tag	UNP P0DTC2
A	1218	ARG	-	expression tag	UNP P0DTC2
A	1219	ASP	-	expression tag	UNP P0DTC2
A	1220	GLY	-	expression tag	UNP P0DTC2
A	1221	GLN	-	expression tag	UNP P0DTC2
A	1222	ALA	-	expression tag	UNP P0DTC2
A	1223	TYR	-	expression tag	UNP P0DTC2
A	1224	VAL	-	expression tag	UNP P0DTC2
A	1225	ARG	-	expression tag	UNP P0DTC2
A	1226	LYS	-	expression tag	UNP P0DTC2
A	1227	ASP	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1228	GLY	-	expression tag	UNP P0DTC2
A	1229	GLU	-	expression tag	UNP P0DTC2
A	1230	TRP	-	expression tag	UNP P0DTC2
A	1231	VAL	-	expression tag	UNP P0DTC2
A	1232	LEU	-	expression tag	UNP P0DTC2
A	1233	LEU	-	expression tag	UNP P0DTC2
A	1234	SER	-	expression tag	UNP P0DTC2
A	1235	THR	-	expression tag	UNP P0DTC2
A	1236	PHE	-	expression tag	UNP P0DTC2
A	1237	LEU	-	expression tag	UNP P0DTC2
A	1238	GLY	-	expression tag	UNP P0DTC2
A	1239	ARG	-	expression tag	UNP P0DTC2
A	1240	SER	-	expression tag	UNP P0DTC2
A	1241	LEU	-	expression tag	UNP P0DTC2
A	1242	GLU	-	expression tag	UNP P0DTC2
A	1243	VAL	-	expression tag	UNP P0DTC2
A	1244	LEU	-	expression tag	UNP P0DTC2
A	1245	PHE	-	expression tag	UNP P0DTC2
A	1246	GLN	-	expression tag	UNP P0DTC2
A	1247	GLY	-	expression tag	UNP P0DTC2
A	1248	PRO	-	expression tag	UNP P0DTC2
A	1249	GLY	-	expression tag	UNP P0DTC2
A	1250	GLY	-	expression tag	UNP P0DTC2
A	1251	SER	-	expression tag	UNP P0DTC2
A	1252	ALA	-	expression tag	UNP P0DTC2
A	1253	GLY	-	expression tag	UNP P0DTC2
A	1254	GLY	-	expression tag	UNP P0DTC2
A	1255	SER	-	expression tag	UNP P0DTC2
A	1256	ALA	-	expression tag	UNP P0DTC2
A	1257	GLY	-	expression tag	UNP P0DTC2
A	1258	TRP	-	expression tag	UNP P0DTC2
A	1259	SER	-	expression tag	UNP P0DTC2
A	1260	HIS	-	expression tag	UNP P0DTC2
A	1261	PRO	-	expression tag	UNP P0DTC2
A	1262	GLN	-	expression tag	UNP P0DTC2
A	1263	PHE	-	expression tag	UNP P0DTC2
A	1264	GLU	-	expression tag	UNP P0DTC2
A	1265	LYS	-	expression tag	UNP P0DTC2
A	1266	GLY	-	expression tag	UNP P0DTC2
A	1267	GLY	-	expression tag	UNP P0DTC2
A	1268	GLY	-	expression tag	UNP P0DTC2
A	1269	SER	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1270	GLY	-	expression tag	UNP P0DTC2
A	1271	GLY	-	expression tag	UNP P0DTC2
A	1272	GLY	-	expression tag	UNP P0DTC2
A	1273	GLY	-	expression tag	UNP P0DTC2
A	1274	SER	-	expression tag	UNP P0DTC2
A	1275	GLY	-	expression tag	UNP P0DTC2
A	1276	GLY	-	expression tag	UNP P0DTC2
A	1277	SER	-	expression tag	UNP P0DTC2
A	1278	ALA	-	expression tag	UNP P0DTC2
A	1279	TRP	-	expression tag	UNP P0DTC2
A	1280	SER	-	expression tag	UNP P0DTC2
A	1281	HIS	-	expression tag	UNP P0DTC2
A	1282	PRO	-	expression tag	UNP P0DTC2
A	1283	GLN	-	expression tag	UNP P0DTC2
A	1284	PHE	-	expression tag	UNP P0DTC2
A	1285	GLU	-	expression tag	UNP P0DTC2
A	1286	LYS	-	expression tag	UNP P0DTC2
B	676F	GLY	ARG	conflict	UNP P0DTC2
B	676G	SER	ARG	conflict	UNP P0DTC2
B	676I	SER	ARG	conflict	UNP P0DTC2
B	986	PRO	LYS	conflict	UNP P0DTC2
B	987	PRO	VAL	conflict	UNP P0DTC2
B	1209	GLY	-	expression tag	UNP P0DTC2
B	1210	SER	-	expression tag	UNP P0DTC2
B	1211	GLY	-	expression tag	UNP P0DTC2
B	1212	TYR	-	expression tag	UNP P0DTC2
B	1213	ILE	-	expression tag	UNP P0DTC2
B	1214	PRO	-	expression tag	UNP P0DTC2
B	1215	GLU	-	expression tag	UNP P0DTC2
B	1216	ALA	-	expression tag	UNP P0DTC2
B	1217	PRO	-	expression tag	UNP P0DTC2
B	1218	ARG	-	expression tag	UNP P0DTC2
B	1219	ASP	-	expression tag	UNP P0DTC2
B	1220	GLY	-	expression tag	UNP P0DTC2
B	1221	GLN	-	expression tag	UNP P0DTC2
B	1222	ALA	-	expression tag	UNP P0DTC2
B	1223	TYR	-	expression tag	UNP P0DTC2
B	1224	VAL	-	expression tag	UNP P0DTC2
B	1225	ARG	-	expression tag	UNP P0DTC2
B	1226	LYS	-	expression tag	UNP P0DTC2
B	1227	ASP	-	expression tag	UNP P0DTC2
B	1228	GLY	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1229	GLU	-	expression tag	UNP P0DTC2
B	1230	TRP	-	expression tag	UNP P0DTC2
B	1231	VAL	-	expression tag	UNP P0DTC2
B	1232	LEU	-	expression tag	UNP P0DTC2
B	1233	LEU	-	expression tag	UNP P0DTC2
B	1234	SER	-	expression tag	UNP P0DTC2
B	1235	THR	-	expression tag	UNP P0DTC2
B	1236	PHE	-	expression tag	UNP P0DTC2
B	1237	LEU	-	expression tag	UNP P0DTC2
B	1238	GLY	-	expression tag	UNP P0DTC2
B	1239	ARG	-	expression tag	UNP P0DTC2
B	1240	SER	-	expression tag	UNP P0DTC2
B	1241	LEU	-	expression tag	UNP P0DTC2
B	1242	GLU	-	expression tag	UNP P0DTC2
B	1243	VAL	-	expression tag	UNP P0DTC2
B	1244	LEU	-	expression tag	UNP P0DTC2
B	1245	PHE	-	expression tag	UNP P0DTC2
B	1246	GLN	-	expression tag	UNP P0DTC2
B	1247	GLY	-	expression tag	UNP P0DTC2
B	1248	PRO	-	expression tag	UNP P0DTC2
B	1249	GLY	-	expression tag	UNP P0DTC2
B	1250	GLY	-	expression tag	UNP P0DTC2
B	1251	SER	-	expression tag	UNP P0DTC2
B	1252	ALA	-	expression tag	UNP P0DTC2
B	1253	GLY	-	expression tag	UNP P0DTC2
B	1254	GLY	-	expression tag	UNP P0DTC2
B	1255	SER	-	expression tag	UNP P0DTC2
B	1256	ALA	-	expression tag	UNP P0DTC2
B	1257	GLY	-	expression tag	UNP P0DTC2
B	1258	TRP	-	expression tag	UNP P0DTC2
B	1259	SER	-	expression tag	UNP P0DTC2
B	1260	HIS	-	expression tag	UNP P0DTC2
B	1261	PRO	-	expression tag	UNP P0DTC2
B	1262	GLN	-	expression tag	UNP P0DTC2
B	1263	PHE	-	expression tag	UNP P0DTC2
B	1264	GLU	-	expression tag	UNP P0DTC2
B	1265	LYS	-	expression tag	UNP P0DTC2
B	1266	GLY	-	expression tag	UNP P0DTC2
B	1267	GLY	-	expression tag	UNP P0DTC2
B	1268	GLY	-	expression tag	UNP P0DTC2
B	1269	SER	-	expression tag	UNP P0DTC2
B	1270	GLY	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1271	GLY	-	expression tag	UNP P0DTC2
B	1272	GLY	-	expression tag	UNP P0DTC2
B	1273	GLY	-	expression tag	UNP P0DTC2
B	1274	SER	-	expression tag	UNP P0DTC2
B	1275	GLY	-	expression tag	UNP P0DTC2
B	1276	GLY	-	expression tag	UNP P0DTC2
B	1277	SER	-	expression tag	UNP P0DTC2
B	1278	ALA	-	expression tag	UNP P0DTC2
B	1279	TRP	-	expression tag	UNP P0DTC2
B	1280	SER	-	expression tag	UNP P0DTC2
B	1281	HIS	-	expression tag	UNP P0DTC2
B	1282	PRO	-	expression tag	UNP P0DTC2
B	1283	GLN	-	expression tag	UNP P0DTC2
B	1284	PHE	-	expression tag	UNP P0DTC2
B	1285	GLU	-	expression tag	UNP P0DTC2
B	1286	LYS	-	expression tag	UNP P0DTC2
C	676F	GLY	ARG	conflict	UNP P0DTC2
C	676G	SER	ARG	conflict	UNP P0DTC2
C	676I	SER	ARG	conflict	UNP P0DTC2
C	986	PRO	LYS	conflict	UNP P0DTC2
C	987	PRO	VAL	conflict	UNP P0DTC2
C	1209	GLY	-	expression tag	UNP P0DTC2
C	1210	SER	-	expression tag	UNP P0DTC2
C	1211	GLY	-	expression tag	UNP P0DTC2
C	1212	TYR	-	expression tag	UNP P0DTC2
C	1213	ILE	-	expression tag	UNP P0DTC2
C	1214	PRO	-	expression tag	UNP P0DTC2
C	1215	GLU	-	expression tag	UNP P0DTC2
C	1216	ALA	-	expression tag	UNP P0DTC2
C	1217	PRO	-	expression tag	UNP P0DTC2
C	1218	ARG	-	expression tag	UNP P0DTC2
C	1219	ASP	-	expression tag	UNP P0DTC2
C	1220	GLY	-	expression tag	UNP P0DTC2
C	1221	GLN	-	expression tag	UNP P0DTC2
C	1222	ALA	-	expression tag	UNP P0DTC2
C	1223	TYR	-	expression tag	UNP P0DTC2
C	1224	VAL	-	expression tag	UNP P0DTC2
C	1225	ARG	-	expression tag	UNP P0DTC2
C	1226	LYS	-	expression tag	UNP P0DTC2
C	1227	ASP	-	expression tag	UNP P0DTC2
C	1228	GLY	-	expression tag	UNP P0DTC2
C	1229	GLU	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1230	TRP	-	expression tag	UNP P0DTC2
C	1231	VAL	-	expression tag	UNP P0DTC2
C	1232	LEU	-	expression tag	UNP P0DTC2
C	1233	LEU	-	expression tag	UNP P0DTC2
C	1234	SER	-	expression tag	UNP P0DTC2
C	1235	THR	-	expression tag	UNP P0DTC2
C	1236	PHE	-	expression tag	UNP P0DTC2
C	1237	LEU	-	expression tag	UNP P0DTC2
C	1238	GLY	-	expression tag	UNP P0DTC2
C	1239	ARG	-	expression tag	UNP P0DTC2
C	1240	SER	-	expression tag	UNP P0DTC2
C	1241	LEU	-	expression tag	UNP P0DTC2
C	1242	GLU	-	expression tag	UNP P0DTC2
C	1243	VAL	-	expression tag	UNP P0DTC2
C	1244	LEU	-	expression tag	UNP P0DTC2
C	1245	PHE	-	expression tag	UNP P0DTC2
C	1246	GLN	-	expression tag	UNP P0DTC2
C	1247	GLY	-	expression tag	UNP P0DTC2
C	1248	PRO	-	expression tag	UNP P0DTC2
C	1249	GLY	-	expression tag	UNP P0DTC2
C	1250	GLY	-	expression tag	UNP P0DTC2
C	1251	SER	-	expression tag	UNP P0DTC2
C	1252	ALA	-	expression tag	UNP P0DTC2
C	1253	GLY	-	expression tag	UNP P0DTC2
C	1254	GLY	-	expression tag	UNP P0DTC2
C	1255	SER	-	expression tag	UNP P0DTC2
C	1256	ALA	-	expression tag	UNP P0DTC2
C	1257	GLY	-	expression tag	UNP P0DTC2
C	1258	TRP	-	expression tag	UNP P0DTC2
C	1259	SER	-	expression tag	UNP P0DTC2
C	1260	HIS	-	expression tag	UNP P0DTC2
C	1261	PRO	-	expression tag	UNP P0DTC2
C	1262	GLN	-	expression tag	UNP P0DTC2
C	1263	PHE	-	expression tag	UNP P0DTC2
C	1264	GLU	-	expression tag	UNP P0DTC2
C	1265	LYS	-	expression tag	UNP P0DTC2
C	1266	GLY	-	expression tag	UNP P0DTC2
C	1267	GLY	-	expression tag	UNP P0DTC2
C	1268	GLY	-	expression tag	UNP P0DTC2
C	1269	SER	-	expression tag	UNP P0DTC2
C	1270	GLY	-	expression tag	UNP P0DTC2
C	1271	GLY	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1272	GLY	-	expression tag	UNP P0DTC2
C	1273	GLY	-	expression tag	UNP P0DTC2
C	1274	SER	-	expression tag	UNP P0DTC2
C	1275	GLY	-	expression tag	UNP P0DTC2
C	1276	GLY	-	expression tag	UNP P0DTC2
C	1277	SER	-	expression tag	UNP P0DTC2
C	1278	ALA	-	expression tag	UNP P0DTC2
C	1279	TRP	-	expression tag	UNP P0DTC2
C	1280	SER	-	expression tag	UNP P0DTC2
C	1281	HIS	-	expression tag	UNP P0DTC2
C	1282	PRO	-	expression tag	UNP P0DTC2
C	1283	GLN	-	expression tag	UNP P0DTC2
C	1284	PHE	-	expression tag	UNP P0DTC2
C	1285	GLU	-	expression tag	UNP P0DTC2
C	1286	LYS	-	expression tag	UNP P0DTC2

- Molecule 2 is a protein called 47D11 neutralizing antibody heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	D	120	925	593	152	177	3	0	0
2	H	120	925	593	152	177	3	0	0

- Molecule 3 is a protein called 47D11 neutralizing antibody light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	E	106	798	502	135	158	3	0	0
3	L	106	798	502	135	158	3	0	0

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



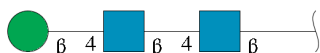
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	F	2	28	16	2	10	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	J	2	28	16	2	10	0	0
4	K	2	28	16	2	10	0	0
4	M	2	28	16	2	10	0	0
4	P	2	28	16	2	10	0	0
4	Q	2	28	16	2	10	0	0
4	R	2	28	16	2	10	0	0
4	V	2	28	16	2	10	0	0
4	W	2	28	16	2	10	0	0
4	X	2	28	16	2	10	0	0

- Molecule 5 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

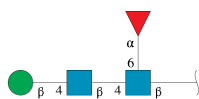


Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	G	3	39	22	2	15	0	0
5	I	3	39	22	2	15	0	0
5	N	3	39	22	2	15	0	0

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

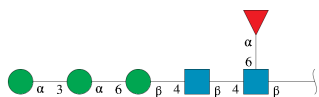
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	O	5	61	34	2	25	0	0

- Molecule 7 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms			AltConf	Trace	
			Total	C	N			O
7	S	4	49	28	2	19	0	0

- Molecule 8 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



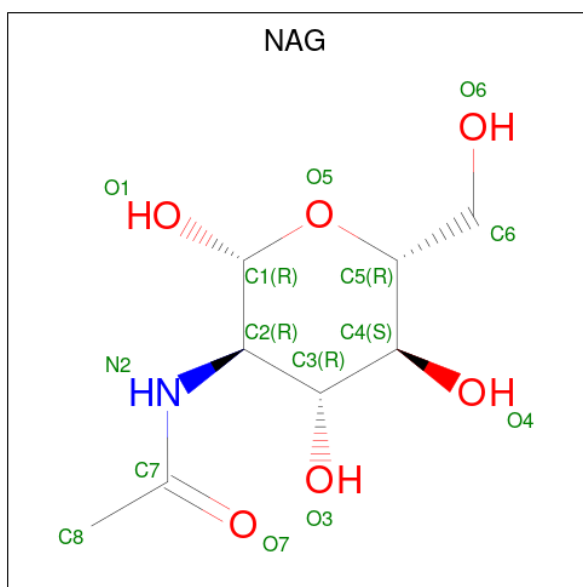
Mol	Chain	Residues	Atoms			AltConf	Trace	
			Total	C	N			O
8	T	6	71	40	2	29	0	0

- Molecule 9 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose.



Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	O		
9	U	2	22	10	0	0

- Molecule 10 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



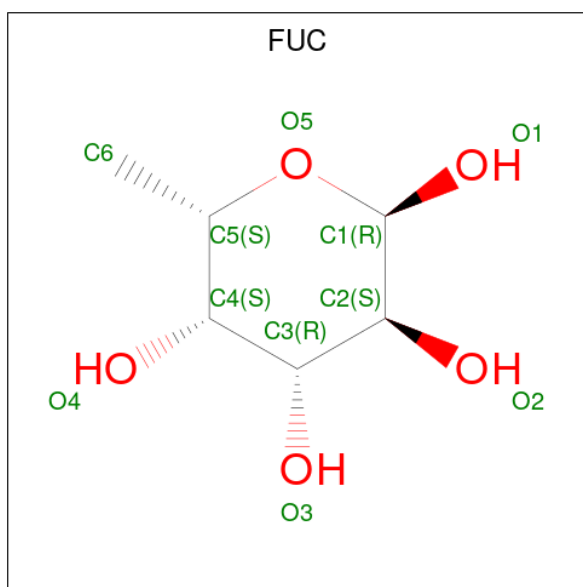
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
10	A	1	Total 14	8	1	5	0
10	A	1	Total 14	8	1	5	0
10	A	1	Total 14	8	1	5	0
10	A	1	Total 14	8	1	5	0
10	A	1	Total 14	8	1	5	0
10	A	1	Total 14	8	1	5	0
10	A	1	Total 14	8	1	5	0
10	A	1	Total 14	8	1	5	0
10	A	1	Total 14	8	1	5	0
10	B	1	Total 14	8	1	5	0
10	B	1	Total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

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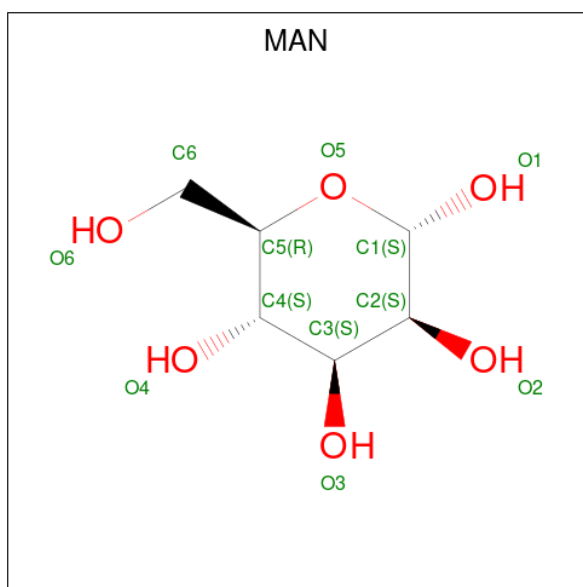
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
10	B	1	14	8	1	5	0
10	B	1	14	8	1	5	0
10	B	1	14	8	1	5	0
10	B	1	14	8	1	5	0
10	B	1	14	8	1	5	0
10	B	1	14	8	1	5	0
10	B	1	14	8	1	5	0
10	C	1	14	8	1	5	0
10	C	1	14	8	1	5	0
10	C	1	14	8	1	5	0
10	C	1	14	8	1	5	0
10	C	1	14	8	1	5	0
10	C	1	14	8	1	5	0
10	C	1	14	8	1	5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

- Molecule 11 is alpha-L-fucopyranose (CCD ID: FUC) (formula: C₆H₁₂O₅).



Mol	Chain	Residues	Atoms			AltConf
11	A	1	Total	C	O	0
			10	6	4	
11	B	1	Total	C	O	0
			10	6	4	
11	C	1	Total	C	O	0
			10	6	4	

- Molecule 12 is alpha-D-mannopyranose (CCD ID: MAN) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			AltConf
12	D	1	Total	C	O	0
			11	6	5	

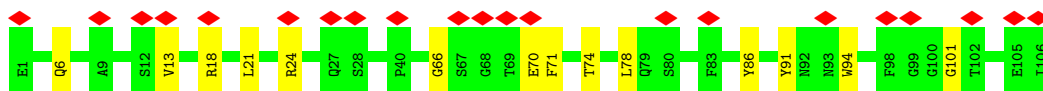
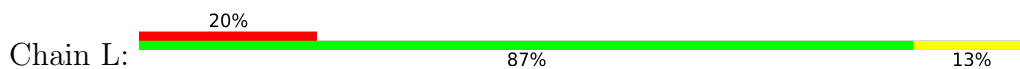
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Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
12	H	1	11	6	5	0



- Molecule 3: 47D11 neutralizing antibody light chain



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



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



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



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



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





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

Chain Q: 100%



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

Chain R: 100%



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

Chain V: 50%



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

Chain W: 50%



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

Chain X: 50%



- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G: 67%



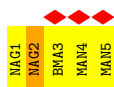
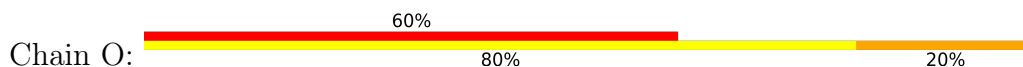
- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



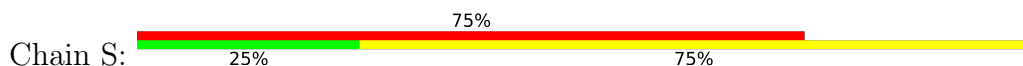
- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



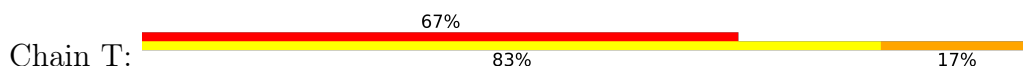
- Molecule 6: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(3-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 7: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 8: alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 9: alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	945232	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.148	Depositor
Minimum map value	-0.088	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.016	Depositor
Map size (Å)	432.00003, 432.00003, 432.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	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, MAN, BMA, FUC

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	0.13	0/7684	0.39	1/10461 (0.0%)
1	B	0.12	0/7838	0.38	0/10676
1	C	0.12	0/7857	0.39	0/10699
2	D	0.11	0/951	0.39	0/1297
2	H	0.11	0/951	0.42	0/1297
3	E	0.11	0/817	0.38	0/1112
3	L	0.11	0/817	0.38	0/1112
All	All	0.12	0/26915	0.39	1/36654 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	608	VAL	N-CA-CB	-6.65	104.67	112.32

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7517	0	7298	36	0
1	B	7666	0	7430	37	0
1	C	7685	0	7470	48	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	925	0	905	10	0
2	H	925	0	905	8	0
3	E	798	0	776	8	0
3	L	798	0	776	9	0
4	F	28	0	25	1	0
4	J	28	0	25	2	0
4	K	28	0	25	1	0
4	M	28	0	25	0	0
4	P	28	0	25	1	0
4	Q	28	0	25	0	0
4	R	28	0	25	0	0
4	V	28	0	25	1	0
4	W	28	0	25	2	0
4	X	28	0	25	0	0
5	G	39	0	34	1	0
5	I	39	0	34	1	0
5	N	39	0	34	1	0
6	O	61	0	50	2	0
7	S	49	0	43	1	0
8	T	71	0	61	2	0
9	U	22	0	19	1	0
10	A	126	0	117	4	0
10	B	168	0	156	5	0
10	C	98	0	91	1	0
11	A	10	0	10	0	0
11	B	10	0	10	0	0
11	C	10	0	10	0	0
12	D	11	0	10	1	0
12	H	11	0	10	0	0
All	All	27358	0	26499	159	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 159 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:B:61:ASN:HB3	10:B:1301:NAG:HN2	1.36	0.89
3:E:24:ARG:HB3	3:E:70:GLU:HG2	1.63	0.80
3:L:24:ARG:HB3	3:L:70:GLU:HG2	1.63	0.79
1:B:343:ASN:OD1	6:O:1:NAG:N2	2.22	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:61:ASN:HB3	10:B:1301:NAG:N2	2.05	0.72

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	950/1286 (74%)	923 (97%)	27 (3%)	0	100	100
1	B	974/1286 (76%)	947 (97%)	27 (3%)	0	100	100
1	C	974/1286 (76%)	952 (98%)	22 (2%)	0	100	100
2	D	118/121 (98%)	113 (96%)	5 (4%)	0	100	100
2	H	118/121 (98%)	113 (96%)	5 (4%)	0	100	100
3	E	104/106 (98%)	102 (98%)	2 (2%)	0	100	100
3	L	104/106 (98%)	102 (98%)	2 (2%)	0	100	100
All	All	3342/4312 (78%)	3252 (97%)	90 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	831/1106 (75%)	831 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	848/1106 (77%)	845 (100%)	3 (0%)	84	84
1	C	851/1106 (77%)	850 (100%)	1 (0%)	88	89
2	D	104/105 (99%)	103 (99%)	1 (1%)	68	76
2	H	104/105 (99%)	103 (99%)	1 (1%)	68	76
3	E	87/87 (100%)	87 (100%)	0	100	100
3	L	87/87 (100%)	87 (100%)	0	100	100
All	All	2912/3702 (79%)	2906 (100%)	6 (0%)	85	87

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	338	PHE
2	D	33	TYR
2	H	33	TYR
1	B	488	CYS
1	B	338	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	658	ASN
1	C	949	GLN
3	L	6	GLN
1	C	926	GLN
1	C	1010	GLN

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](#)

46 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	F	1	4,1	14,14,15	0.72	1 (7%)	17,19,21	0.64	0
4	NAG	F	2	4	14,14,15	0.50	0	17,19,21	1.33	2 (11%)
5	NAG	G	1	5,1	14,14,15	0.46	0	17,19,21	0.57	0
5	NAG	G	2	5	14,14,15	0.32	0	17,19,21	0.47	0
5	BMA	G	3	5	11,11,12	0.56	0	15,15,17	0.79	0
5	NAG	I	1	5,1	14,14,15	0.20	0	17,19,21	0.69	0
5	NAG	I	2	5	14,14,15	0.45	0	17,19,21	1.40	2 (11%)
5	BMA	I	3	5	11,11,12	0.70	0	15,15,17	0.84	1 (6%)
4	NAG	J	1	4,1	14,14,15	0.44	0	17,19,21	1.36	2 (11%)
4	NAG	J	2	4	14,14,15	0.55	0	17,19,21	1.35	2 (11%)
4	NAG	K	1	4	14,14,15	0.16	0	17,19,21	0.56	0
4	NAG	K	2	4	14,14,15	0.65	1 (7%)	17,19,21	1.33	1 (5%)
4	NAG	M	1	4,1	14,14,15	0.22	0	17,19,21	0.51	0
4	NAG	M	2	4	14,14,15	0.22	0	17,19,21	0.48	0
5	NAG	N	1	5,1	14,14,15	0.38	0	17,19,21	0.47	0
5	NAG	N	2	5	14,14,15	0.42	0	17,19,21	0.49	0
5	BMA	N	3	5	11,11,12	0.59	0	15,15,17	0.71	0
6	NAG	O	1	1,6	14,14,15	0.42	0	17,19,21	0.70	0
6	NAG	O	2	6	14,14,15	0.51	0	17,19,21	1.06	1 (5%)
6	BMA	O	3	6	11,11,12	0.86	1 (9%)	15,15,17	0.93	1 (6%)
6	MAN	O	4	6	11,11,12	0.56	0	15,15,17	0.89	1 (6%)
6	MAN	O	5	6	11,11,12	0.69	0	15,15,17	0.89	1 (6%)
4	NAG	P	1	4	14,14,15	0.19	0	17,19,21	0.57	0
4	NAG	P	2	4	14,14,15	0.39	0	17,19,21	0.67	1 (5%)
4	NAG	Q	1	4,1	14,14,15	0.21	0	17,19,21	0.58	0
4	NAG	Q	2	4	14,14,15	0.25	0	17,19,21	0.48	0
4	NAG	R	1	4	14,14,15	0.29	0	17,19,21	0.51	0
4	NAG	R	2	4	14,14,15	0.50	0	17,19,21	0.59	1 (5%)
7	NAG	S	1	7,1	14,14,15	0.41	0	17,19,21	0.83	0
7	NAG	S	2	7	14,14,15	0.37	0	17,19,21	0.72	1 (5%)
7	BMA	S	3	7	11,11,12	0.76	0	15,15,17	0.92	1 (6%)
7	FUC	S	4	7	10,10,11	0.73	0	14,14,16	0.63	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	NAG	T	1	8,1	14,14,15	0.26	0	17,19,21	0.50	0
8	NAG	T	2	8	14,14,15	0.23	0	17,19,21	0.82	1 (5%)
8	BMA	T	3	8	11,11,12	0.64	0	15,15,17	1.04	0
8	MAN	T	4	8	11,11,12	0.59	0	15,15,17	0.85	1 (6%)
8	MAN	T	5	8	11,11,12	0.79	1 (9%)	15,15,17	1.38	3 (20%)
8	FUC	T	6	8	10,10,11	1.84	2 (20%)	14,14,16	1.25	2 (14%)
9	MAN	U	1	9	11,11,12	0.90	1 (9%)	15,15,17	0.91	1 (6%)
9	MAN	U	2	9	11,11,12	0.88	1 (9%)	15,15,17	1.83	3 (20%)
4	NAG	V	1	4	14,14,15	0.19	0	17,19,21	0.58	0
4	NAG	V	2	4	14,14,15	0.46	0	17,19,21	1.44	3 (17%)
4	NAG	W	1	4,1	14,14,15	0.20	0	17,19,21	0.75	1 (5%)
4	NAG	W	2	4	14,14,15	0.47	0	17,19,21	0.58	0
4	NAG	X	1	4	14,14,15	0.23	0	17,19,21	0.61	1 (5%)
4	NAG	X	2	4	14,14,15	0.29	0	17,19,21	0.50	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	F	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	F	2	4	-	6/6/23/26	0/1/1/1
5	NAG	G	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	G	2	5	-	2/6/23/26	0/1/1/1
5	BMA	G	3	5	-	0/2/19/22	0/1/1/1
5	NAG	I	1	5,1	-	4/6/23/26	0/1/1/1
5	NAG	I	2	5	-	4/6/23/26	0/1/1/1
5	BMA	I	3	5	-	1/2/19/22	1/1/1/1
4	NAG	J	1	4,1	-	4/6/23/26	0/1/1/1
4	NAG	J	2	4	-	6/6/23/26	0/1/1/1
4	NAG	K	1	4	-	2/6/23/26	0/1/1/1
4	NAG	K	2	4	-	0/6/23/26	0/1/1/1
4	NAG	M	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	M	2	4	-	1/6/23/26	0/1/1/1
5	NAG	N	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	N	2	5	-	0/6/23/26	0/1/1/1
5	BMA	N	3	5	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	O	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	O	2	6	-	2/6/23/26	0/1/1/1
6	BMA	O	3	6	-	2/2/19/22	0/1/1/1
6	MAN	O	4	6	-	0/2/19/22	0/1/1/1
6	MAN	O	5	6	-	1/2/19/22	0/1/1/1
4	NAG	P	1	4	-	0/6/23/26	0/1/1/1
4	NAG	P	2	4	-	2/6/23/26	0/1/1/1
4	NAG	Q	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	Q	2	4	-	1/6/23/26	0/1/1/1
4	NAG	R	1	4	-	2/6/23/26	0/1/1/1
4	NAG	R	2	4	-	4/6/23/26	0/1/1/1
7	NAG	S	1	7,1	-	4/6/23/26	0/1/1/1
7	NAG	S	2	7	-	2/6/23/26	0/1/1/1
7	BMA	S	3	7	-	1/2/19/22	1/1/1/1
7	FUC	S	4	7	-	-	0/1/1/1
8	NAG	T	1	8,1	-	4/6/23/26	0/1/1/1
8	NAG	T	2	8	-	2/6/23/26	0/1/1/1
8	BMA	T	3	8	-	2/2/19/22	0/1/1/1
8	MAN	T	4	8	-	0/2/19/22	0/1/1/1
8	MAN	T	5	8	-	0/2/19/22	0/1/1/1
8	FUC	T	6	8	-	-	0/1/1/1
9	MAN	U	1	9	-	2/2/19/22	0/1/1/1
9	MAN	U	2	9	-	2/2/19/22	0/1/1/1
4	NAG	V	1	4	-	4/6/23/26	0/1/1/1
4	NAG	V	2	4	-	4/6/23/26	0/1/1/1
4	NAG	W	1	4,1	-	4/6/23/26	0/1/1/1
4	NAG	W	2	4	-	1/6/23/26	0/1/1/1
4	NAG	X	1	4	-	4/6/23/26	0/1/1/1
4	NAG	X	2	4	-	2/6/23/26	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	T	6	FUC	C1-C2	4.35	1.62	1.52
8	T	6	FUC	O5-C1	2.89	1.48	1.43
4	F	1	NAG	O5-C1	-2.60	1.39	1.43
9	U	2	MAN	C1-C2	2.45	1.58	1.52
9	U	1	MAN	O5-C1	-2.17	1.40	1.43

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	U	2	MAN	C1-O5-C5	5.47	119.52	112.19
4	K	2	NAG	C1-O5-C5	5.04	118.94	112.19
4	J	1	NAG	C2-N2-C7	4.63	129.11	122.90
4	V	2	NAG	C2-N2-C7	4.60	129.06	122.90
5	I	2	NAG	C2-N2-C7	4.56	129.01	122.90

There are no chirality outliers.

5 of 90 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	O	1	NAG	C4-C5-C6-O6
4	J	2	NAG	C4-C5-C6-O6
5	G	2	NAG	O5-C5-C6-O6
4	K	1	NAG	O5-C5-C6-O6
4	W	1	NAG	O5-C5-C6-O6

All (2) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	S	3	BMA	C1-C2-C3-C4-C5-O5
5	I	3	BMA	C1-C2-C3-C4-C5-O5

20 monomers are involved in 16 short contacts:

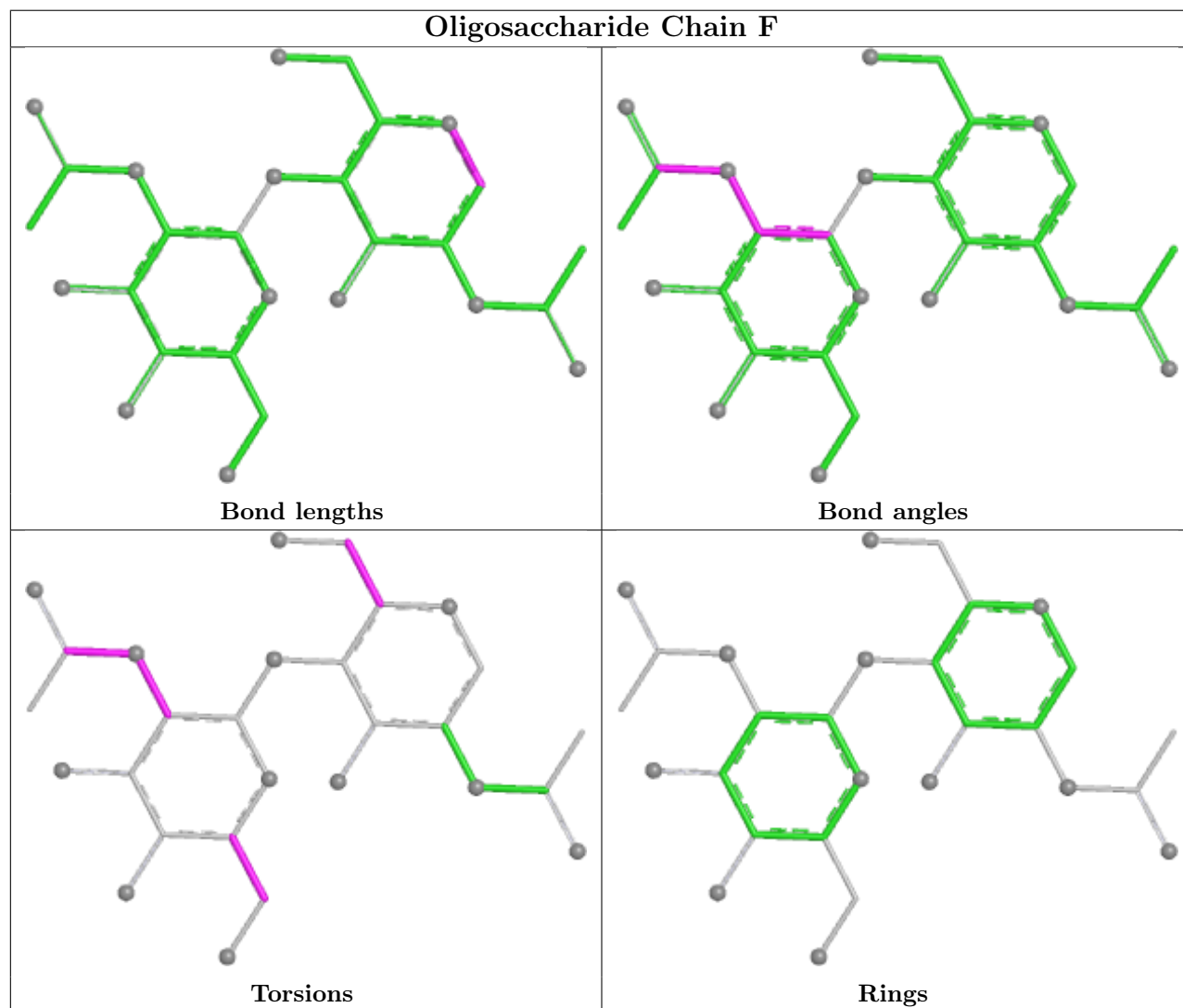
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	T	1	NAG	1	0
7	S	4	FUC	1	0
4	V	2	NAG	1	0
4	W	2	NAG	2	0
4	J	2	NAG	1	0
9	U	1	MAN	1	0
5	I	2	NAG	1	0
5	N	1	NAG	1	0
8	T	6	FUC	1	0
4	F	2	NAG	1	0
6	O	2	NAG	1	0
4	J	1	NAG	1	0
4	W	1	NAG	2	0
5	G	2	NAG	1	0
8	T	3	BMA	1	0
6	O	1	NAG	2	0

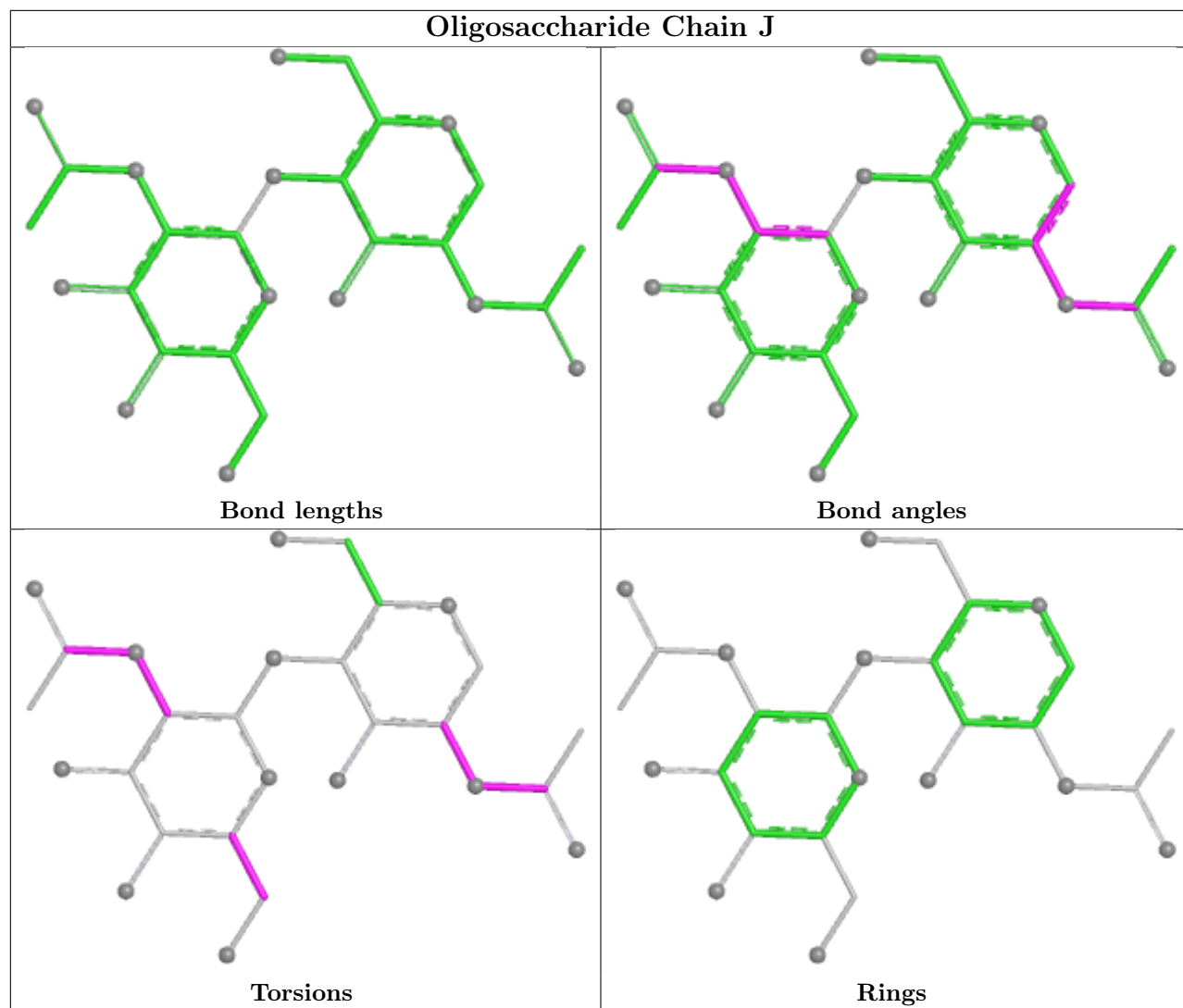
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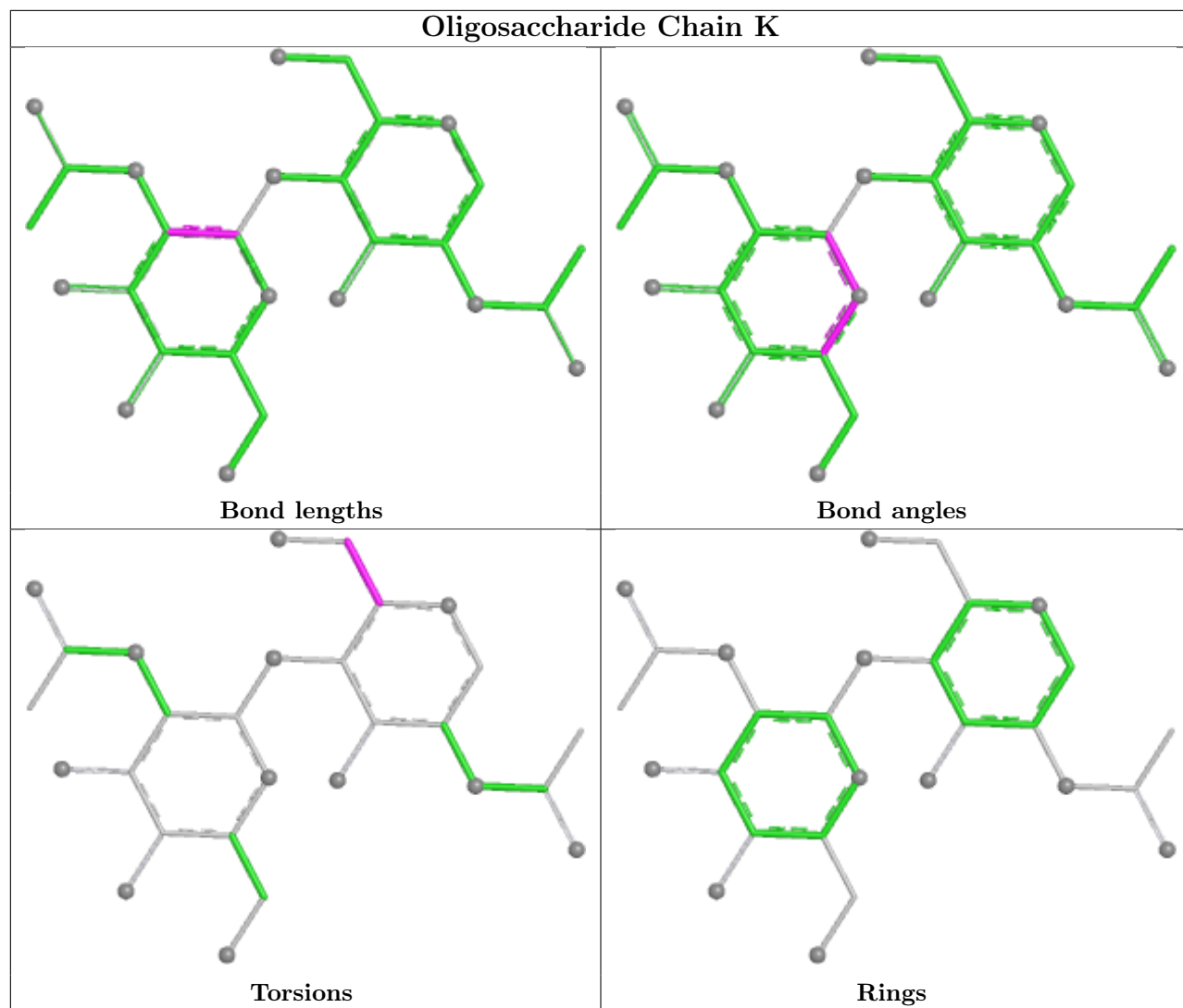
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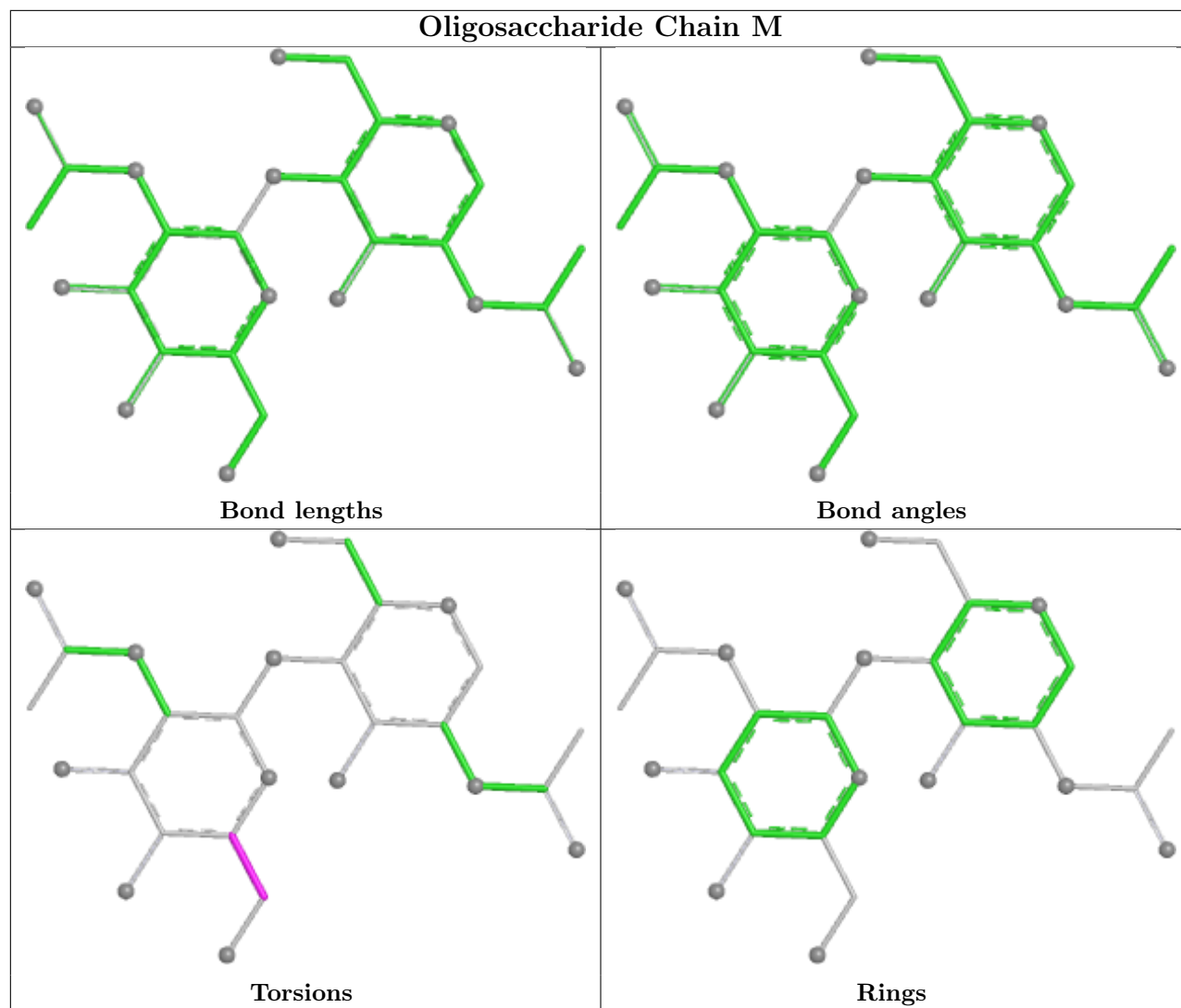
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	G	1	NAG	1	0
4	P	1	NAG	1	0
4	K	1	NAG	1	0
4	K	2	NAG	1	0

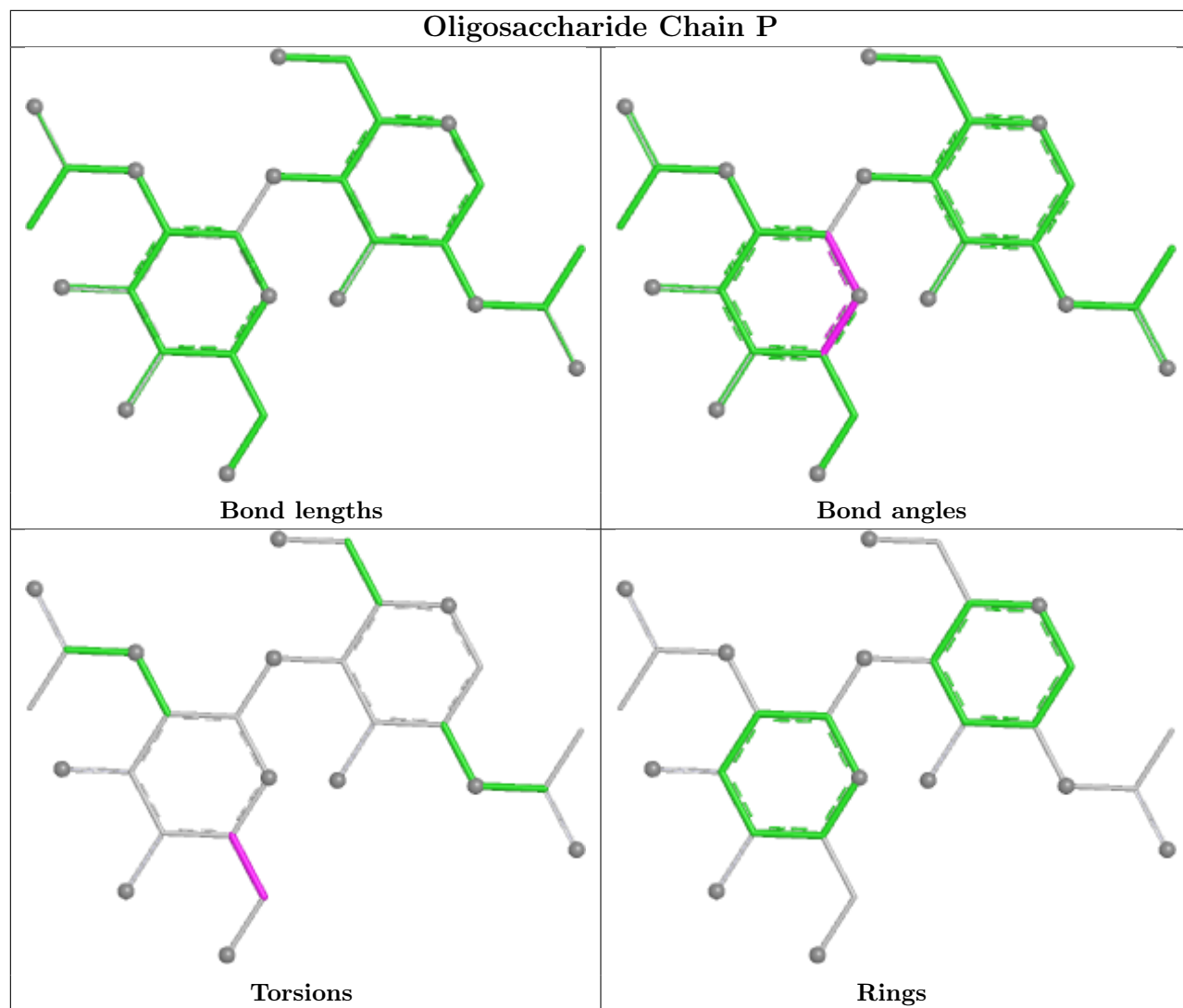
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

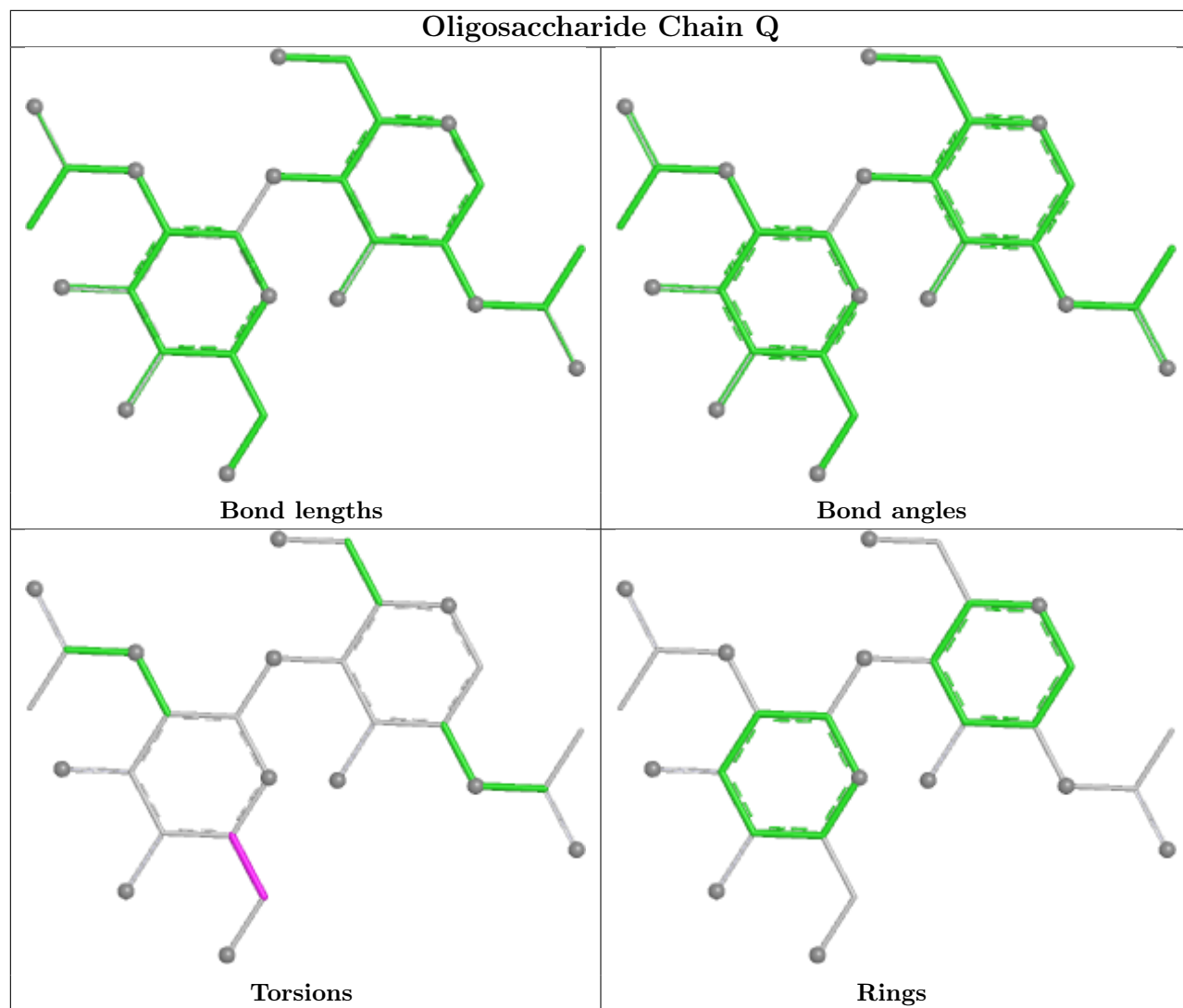


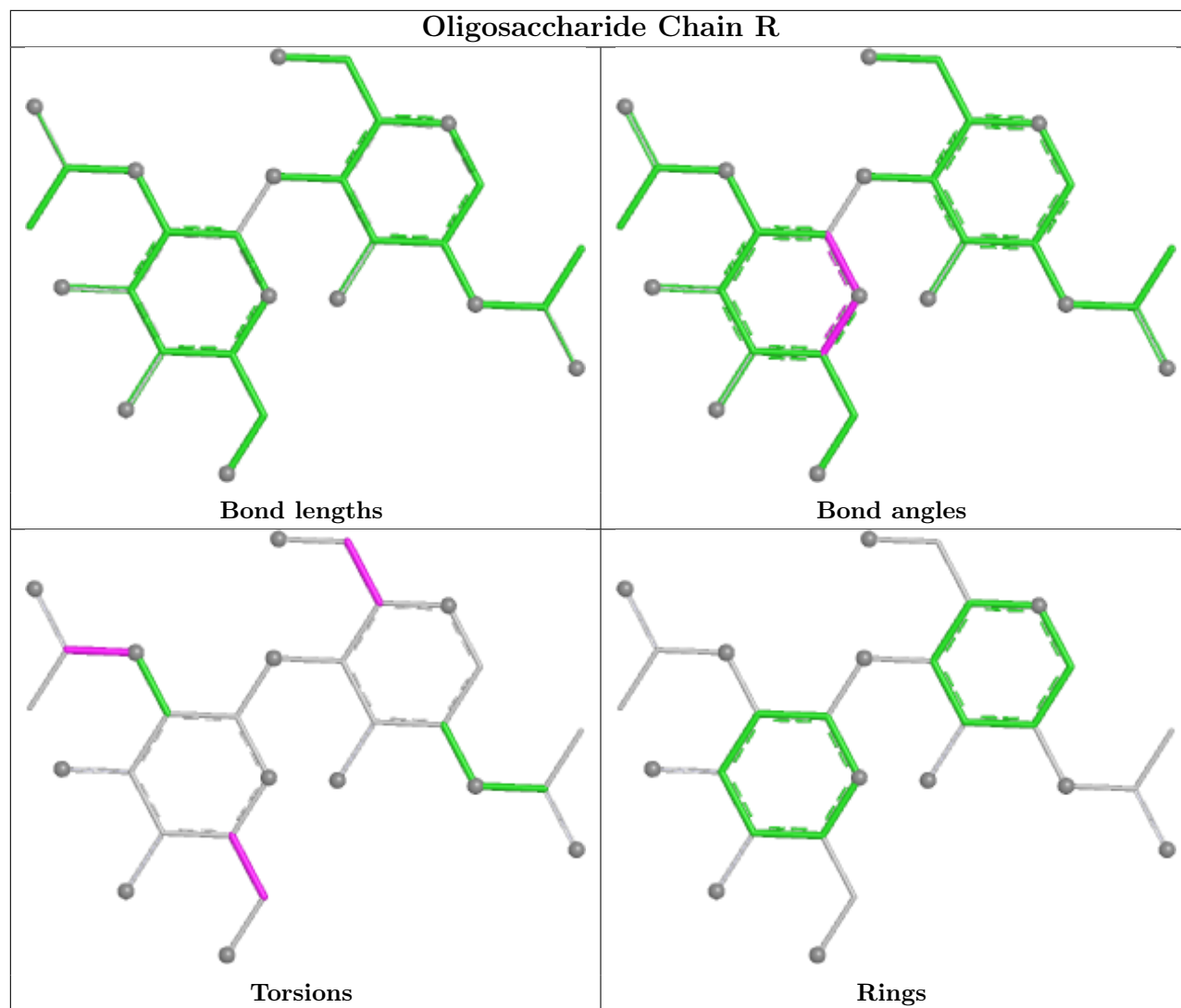


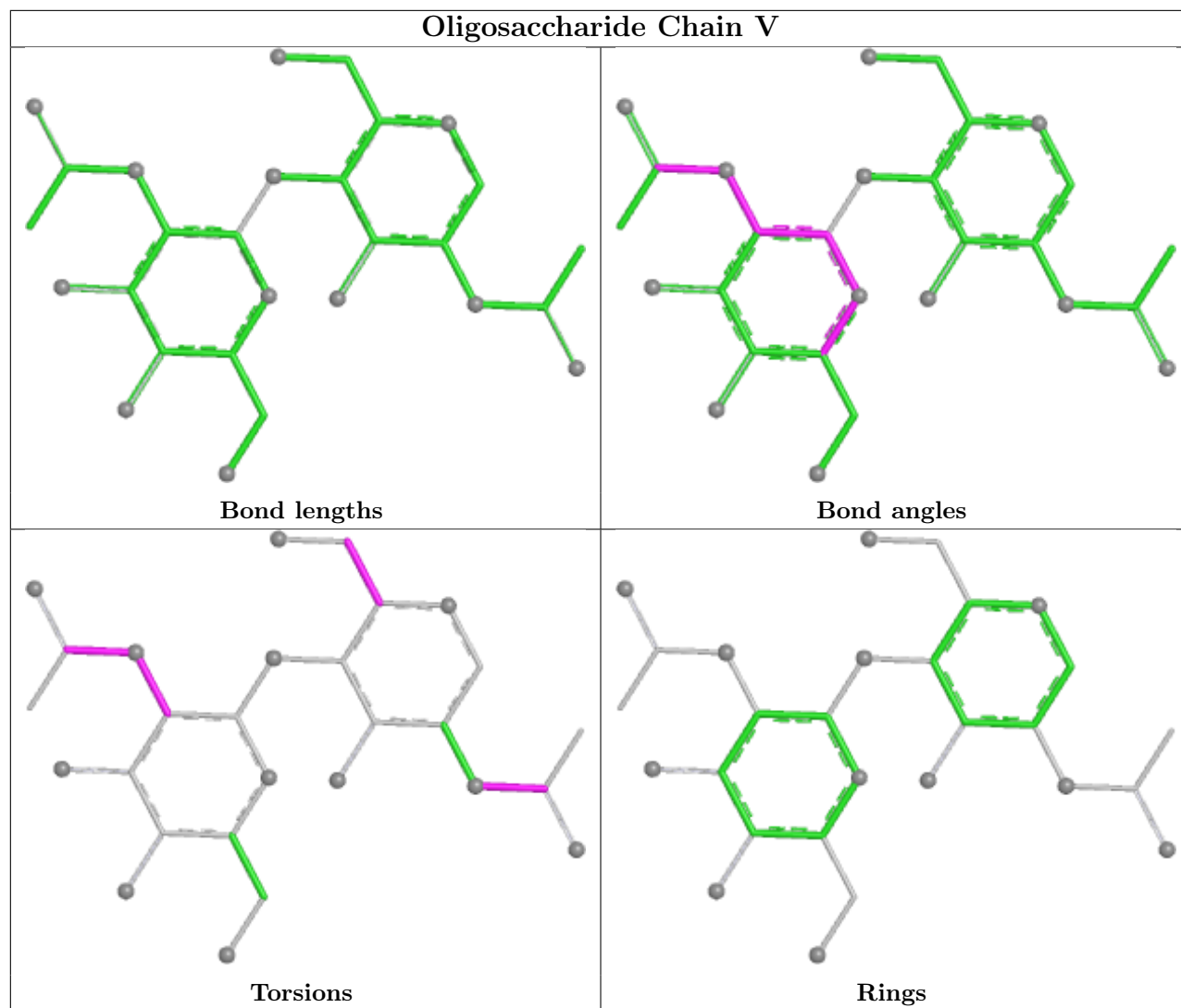


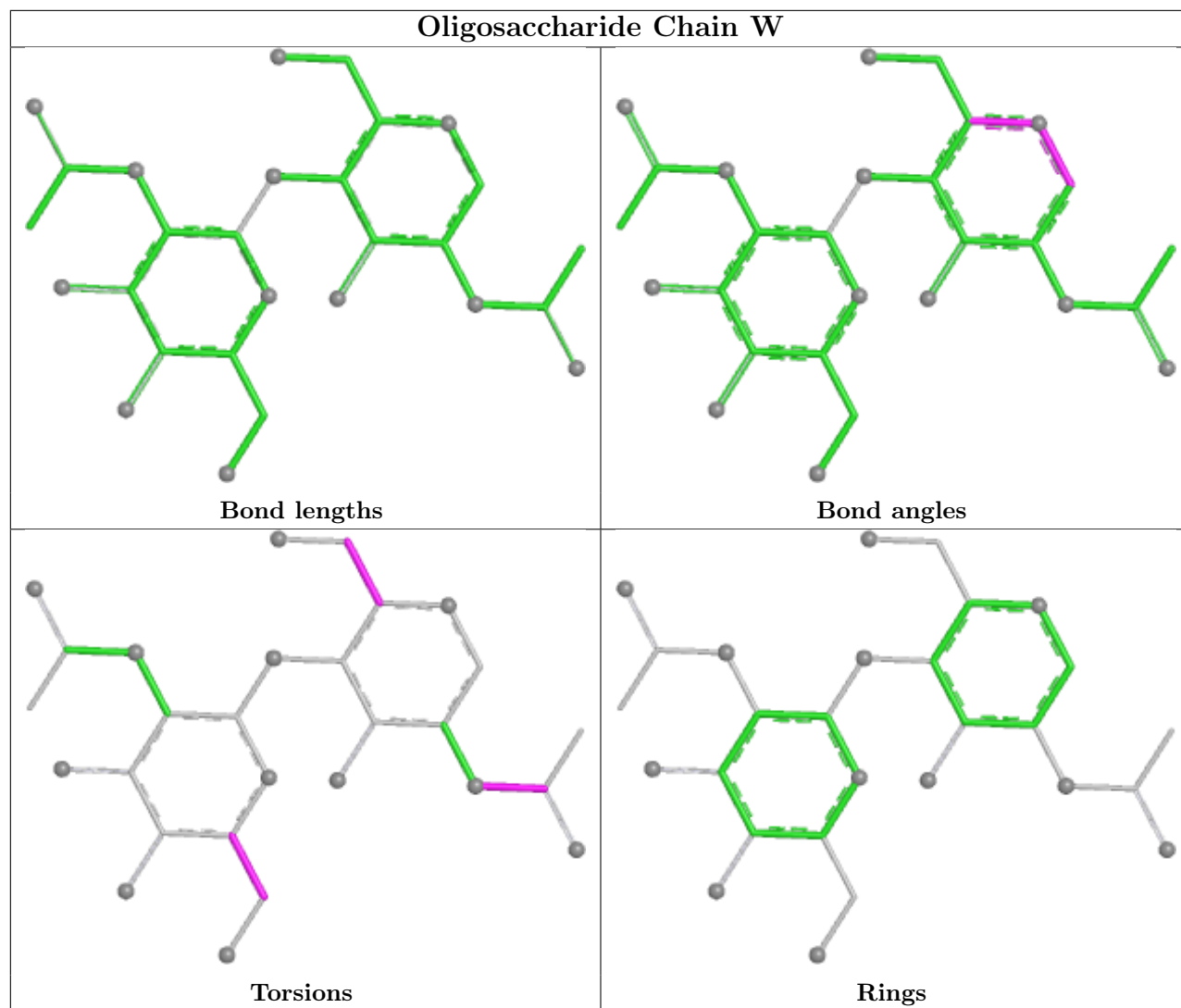


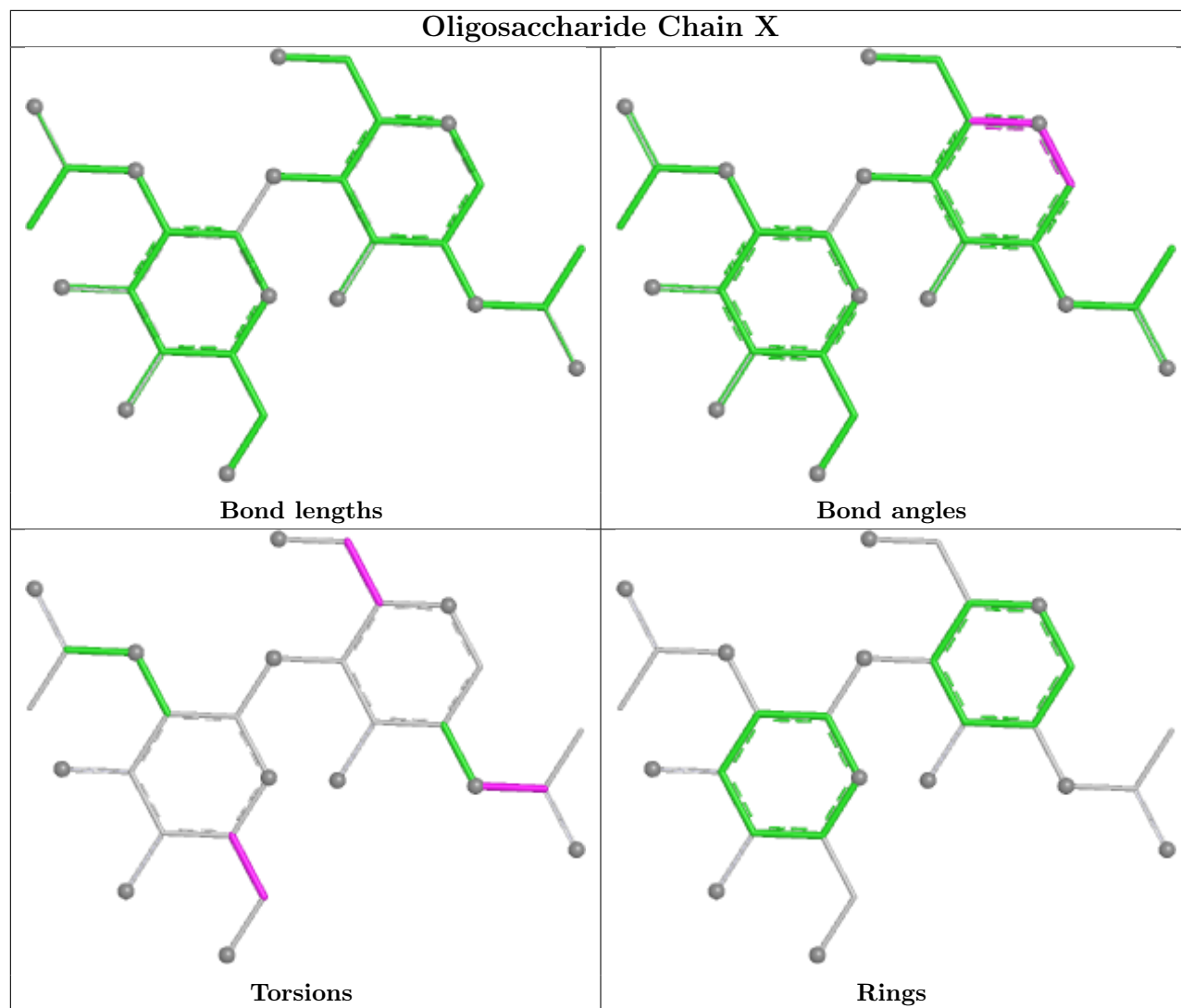


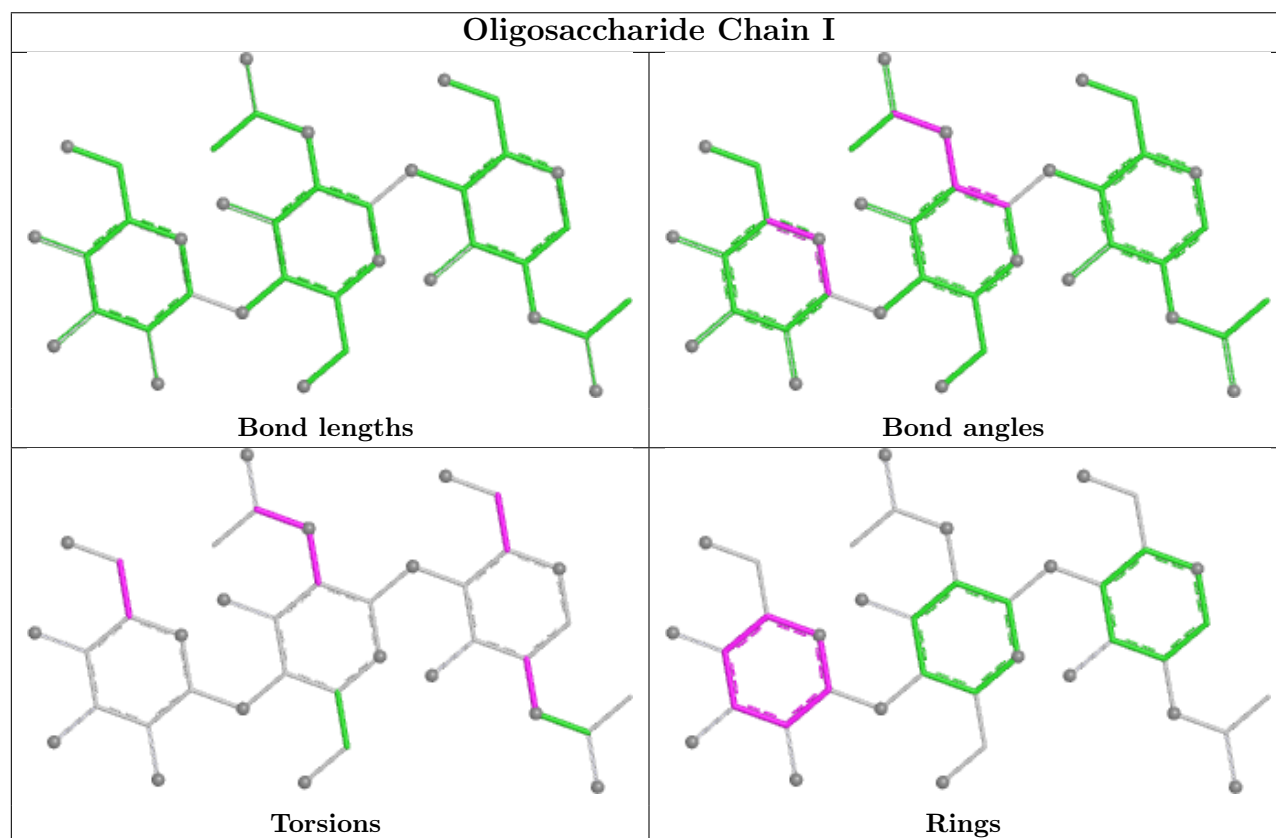
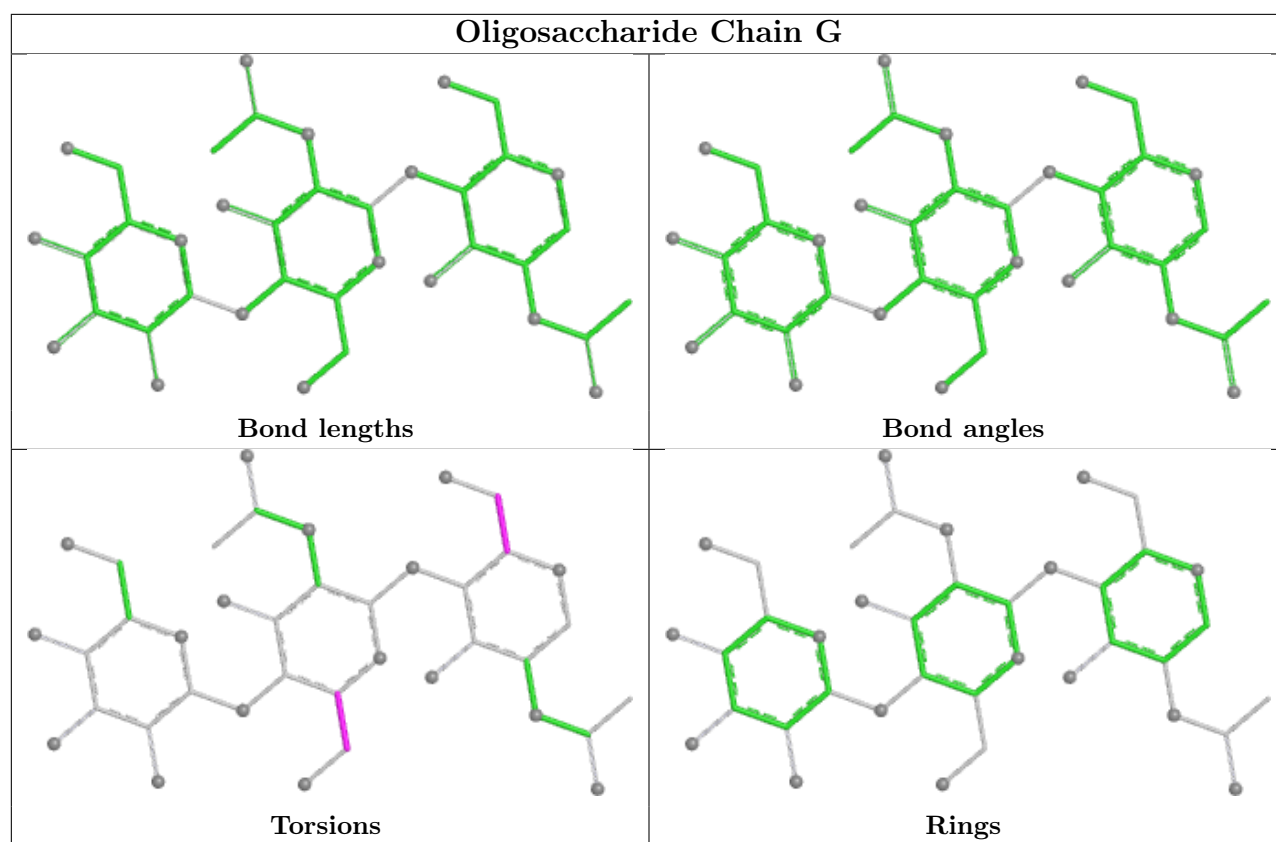


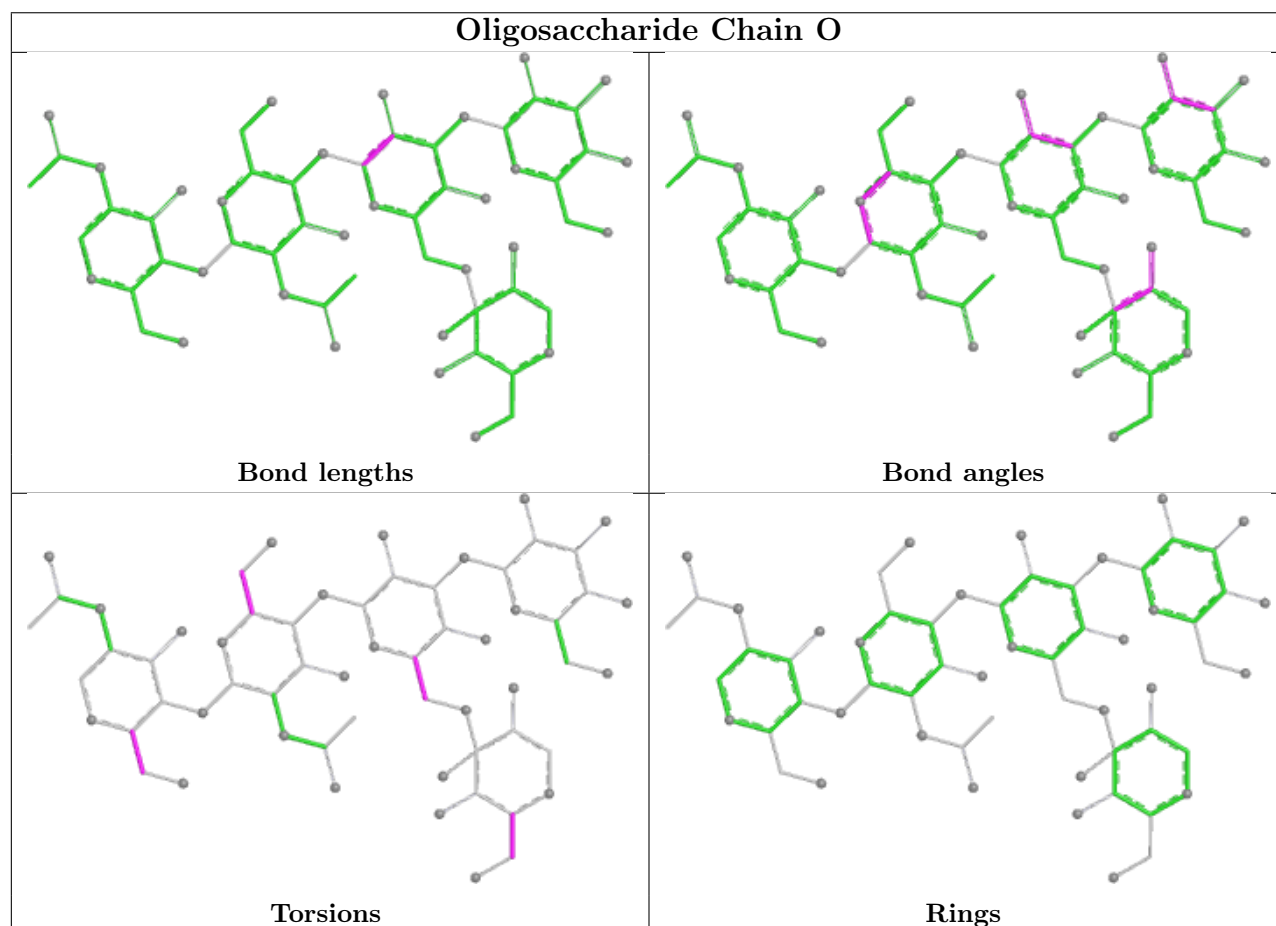
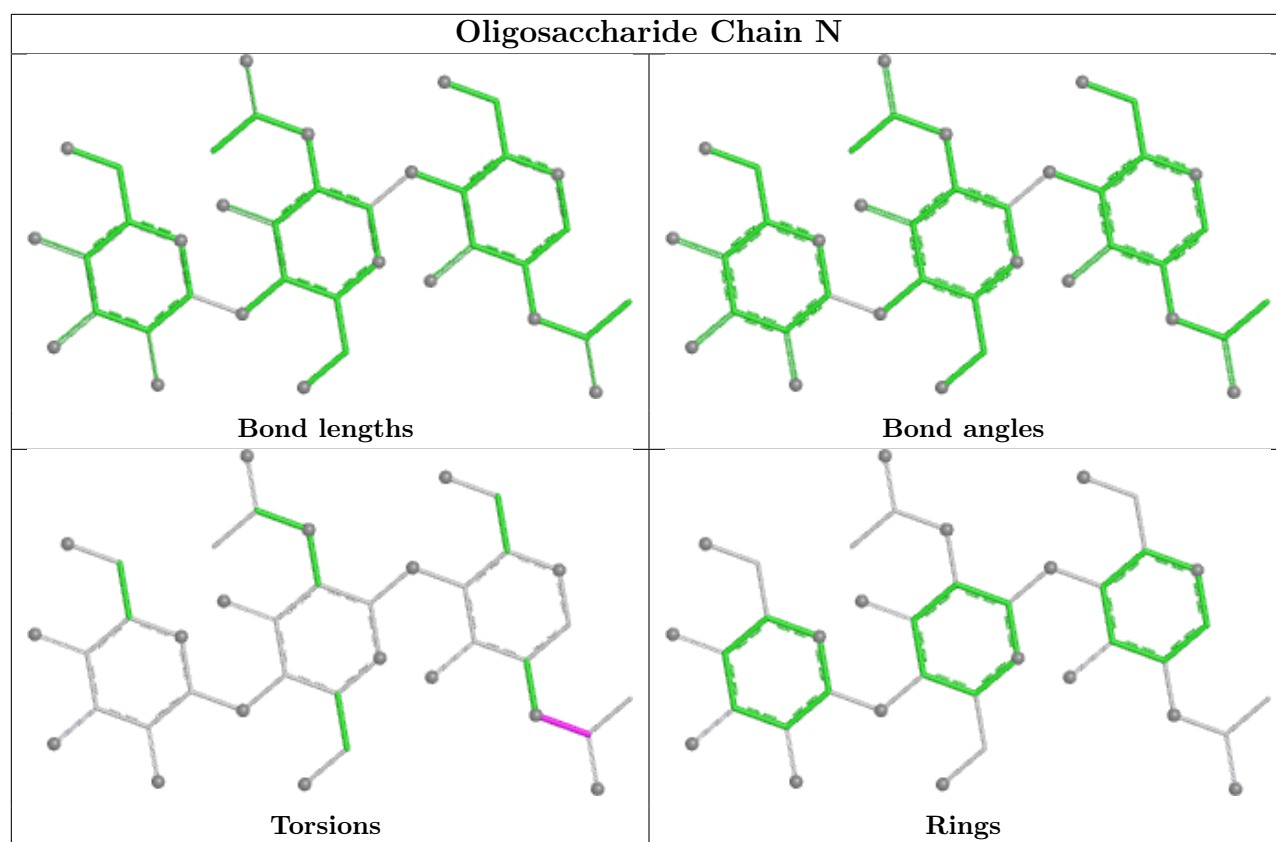


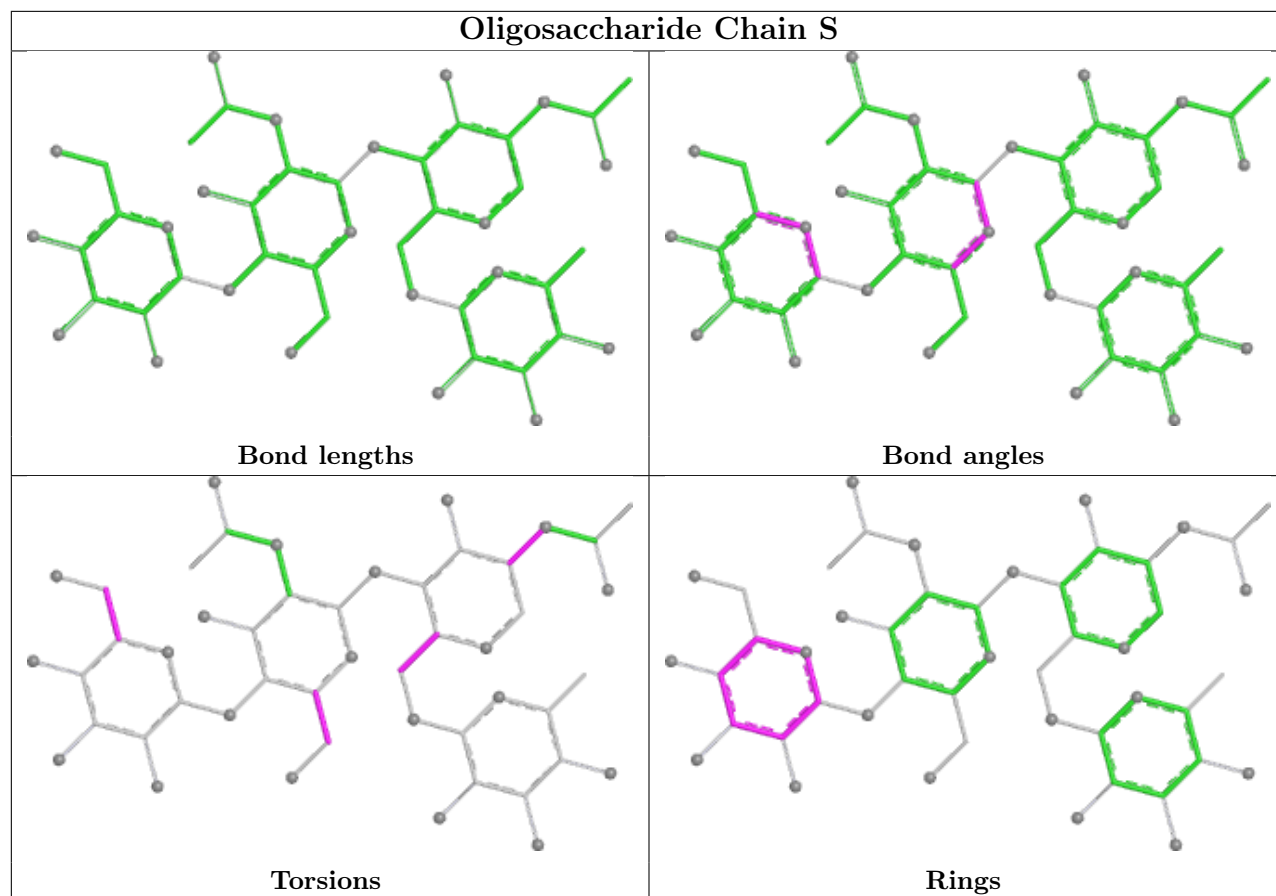


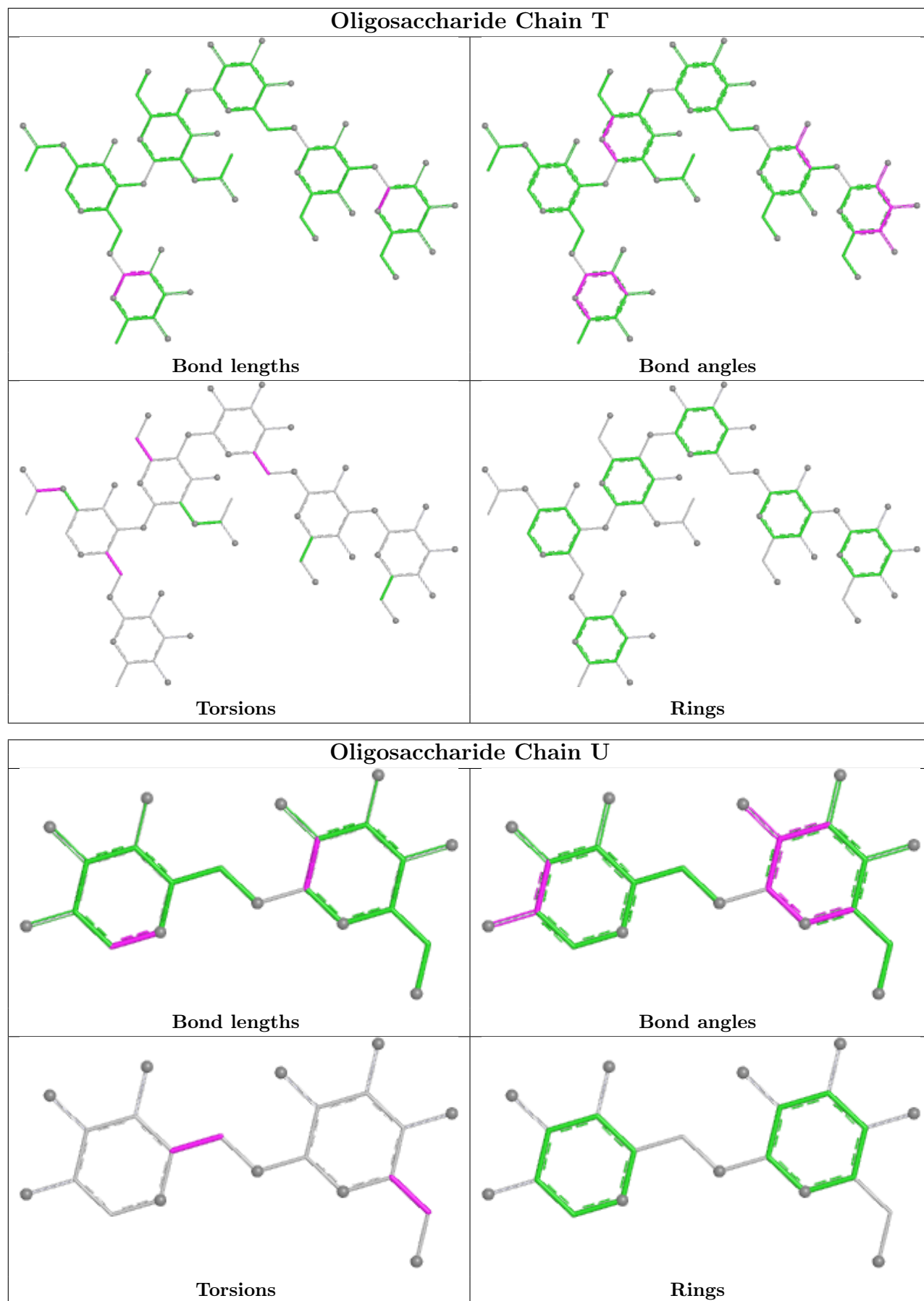












5.6 Ligand geometry

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
10	NAG	A	1303	1	14,14,15	0.30	0	17,19,21	0.44	0
10	NAG	B	1301	1	14,14,15	0.38	0	17,19,21	0.45	0
10	NAG	A	1301	1	14,14,15	0.28	0	17,19,21	0.46	0
10	NAG	A	1304	1	14,14,15	0.22	0	17,19,21	0.48	0
10	NAG	B	1312	-	14,14,15	0.19	0	17,19,21	0.51	0
10	NAG	A	1305	1	14,14,15	0.41	0	17,19,21	0.43	0
10	NAG	B	1307	1	14,14,15	0.45	0	17,19,21	0.40	0
10	NAG	B	1311	-	14,14,15	0.83	1 (7%)	17,19,21	0.71	0
10	NAG	B	1305	-	14,14,15	0.24	0	17,19,21	0.60	1 (5%)
10	NAG	A	1307	1	14,14,15	0.44	0	17,19,21	1.38	2 (11%)
11	FUC	A	1310	-	10,10,11	0.93	0	14,14,16	0.87	0
10	NAG	B	1302	-	14,14,15	0.24	0	17,19,21	0.56	0
10	NAG	B	1309	-	14,14,15	0.38	0	17,19,21	0.36	0
10	NAG	B	1310	1	14,14,15	0.34	0	17,19,21	0.80	1 (5%)
10	NAG	C	1301	-	14,14,15	0.30	0	17,19,21	0.52	0
10	NAG	C	1304	1	14,14,15	0.29	0	17,19,21	0.48	0
10	NAG	A	1302	1	14,14,15	0.64	1 (7%)	17,19,21	0.60	0
10	NAG	C	1305	-	14,14,15	0.38	0	17,19,21	0.36	0
12	MAN	H	201	-	11,11,12	0.69	0	15,15,17	0.88	1 (6%)
12	MAN	D	201	-	11,11,12	0.64	0	15,15,17	0.92	1 (6%)
10	NAG	B	1303	-	14,14,15	0.33	0	17,19,21	0.51	0
10	NAG	B	1304	1	14,14,15	0.35	0	17,19,21	0.47	0
10	NAG	A	1306	1	14,14,15	0.34	0	17,19,21	0.55	0
11	FUC	B	1306	-	10,10,11	0.69	0	14,14,16	0.60	0
10	NAG	C	1303	1	14,14,15	0.30	0	17,19,21	0.62	1 (5%)
10	NAG	A	1308	-	14,14,15	0.82	1 (7%)	17,19,21	0.71	0
10	NAG	B	1308	1	14,14,15	0.43	0	17,19,21	0.36	0
10	NAG	C	1307	1	14,14,15	0.30	0	17,19,21	0.63	0
10	NAG	C	1302	-	14,14,15	0.44	0	17,19,21	0.51	0
10	NAG	A	1309	1	14,14,15	0.31	0	17,19,21	0.69	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
11	FUC	C	1308	-	10,10,11	0.84	1 (10%)	14,14,16	0.60	0
10	NAG	C	1306	-	14,14,15	0.25	0	17,19,21	0.54	0
10	NAG	B	1313	-	14,14,15	0.24	0	17,19,21	0.59	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	NAG	A	1303	1	-	2/6/23/26	0/1/1/1
10	NAG	B	1301	1	-	0/6/23/26	0/1/1/1
10	NAG	A	1301	1	-	0/6/23/26	0/1/1/1
10	NAG	A	1304	1	-	2/6/23/26	0/1/1/1
10	NAG	B	1312	-	-	0/6/23/26	0/1/1/1
10	NAG	A	1305	1	-	3/6/23/26	0/1/1/1
10	NAG	B	1307	1	-	0/6/23/26	0/1/1/1
10	NAG	B	1311	-	-	2/6/23/26	0/1/1/1
10	NAG	B	1305	-	-	1/6/23/26	0/1/1/1
10	NAG	A	1307	1	-	6/6/23/26	0/1/1/1
11	FUC	A	1310	-	-	-	0/1/1/1
10	NAG	B	1302	-	-	4/6/23/26	0/1/1/1
10	NAG	B	1309	-	-	1/6/23/26	0/1/1/1
10	NAG	B	1310	1	-	4/6/23/26	0/1/1/1
10	NAG	C	1301	-	-	2/6/23/26	0/1/1/1
10	NAG	C	1304	1	-	4/6/23/26	0/1/1/1
10	NAG	A	1302	1	-	3/6/23/26	0/1/1/1
10	NAG	C	1305	-	-	2/6/23/26	0/1/1/1
12	MAN	H	201	-	-	2/2/19/22	0/1/1/1
12	MAN	D	201	-	-	2/2/19/22	1/1/1/1
10	NAG	B	1303	-	-	2/6/23/26	0/1/1/1
10	NAG	B	1304	1	-	2/6/23/26	0/1/1/1
10	NAG	A	1306	1	-	4/6/23/26	0/1/1/1
11	FUC	B	1306	-	-	-	0/1/1/1
10	NAG	C	1303	1	-	4/6/23/26	0/1/1/1
10	NAG	A	1308	-	-	2/6/23/26	0/1/1/1
10	NAG	B	1308	1	-	0/6/23/26	0/1/1/1
10	NAG	C	1307	1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	NAG	C	1302	-	-	4/6/23/26	0/1/1/1
10	NAG	A	1309	1	-	2/6/23/26	0/1/1/1
11	FUC	C	1308	-	-	-	0/1/1/1
10	NAG	C	1306	-	-	2/6/23/26	0/1/1/1
10	NAG	B	1313	-	-	0/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	B	1311	NAG	O5-C1	-2.98	1.38	1.43
10	A	1308	NAG	O5-C1	-2.96	1.38	1.43
10	A	1302	NAG	O5-C1	-2.26	1.39	1.43
11	C	1308	FUC	O5-C1	-2.04	1.40	1.43

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	1307	NAG	C2-N2-C7	4.67	129.16	122.90
10	B	1310	NAG	C1-O5-C5	2.67	115.77	112.19
10	C	1303	NAG	C1-O5-C5	2.21	115.14	112.19
10	A	1307	NAG	C1-C2-N2	2.19	113.88	110.43
12	H	201	MAN	O2-C2-C3	-2.16	105.69	110.15

There are no chirality outliers.

5 of 64 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	A	1308	NAG	C4-C5-C6-O6
10	B	1303	NAG	O5-C5-C6-O6
10	B	1310	NAG	C4-C5-C6-O6
12	D	201	MAN	O5-C5-C6-O6
10	A	1304	NAG	O5-C5-C6-O6

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	D	201	MAN	C1-C2-C3-C4-C5-O5

9 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	B	1301	NAG	2	0
10	A	1301	NAG	1	0
10	A	1305	NAG	1	0
10	B	1307	NAG	2	0
10	A	1307	NAG	1	0
10	A	1302	NAG	1	0
12	D	201	MAN	1	0
10	B	1304	NAG	1	0
10	C	1306	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.

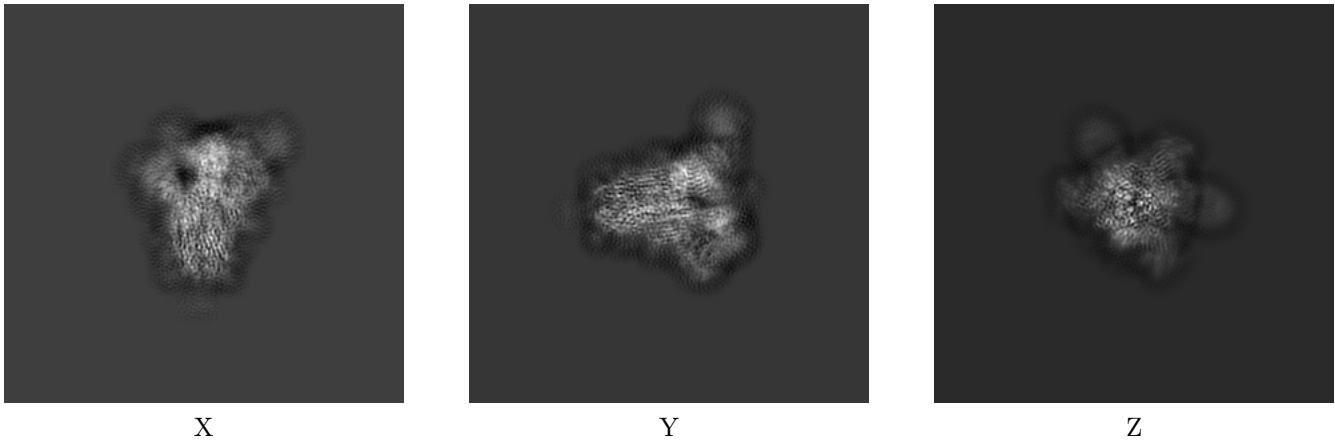
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11812. 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](#)

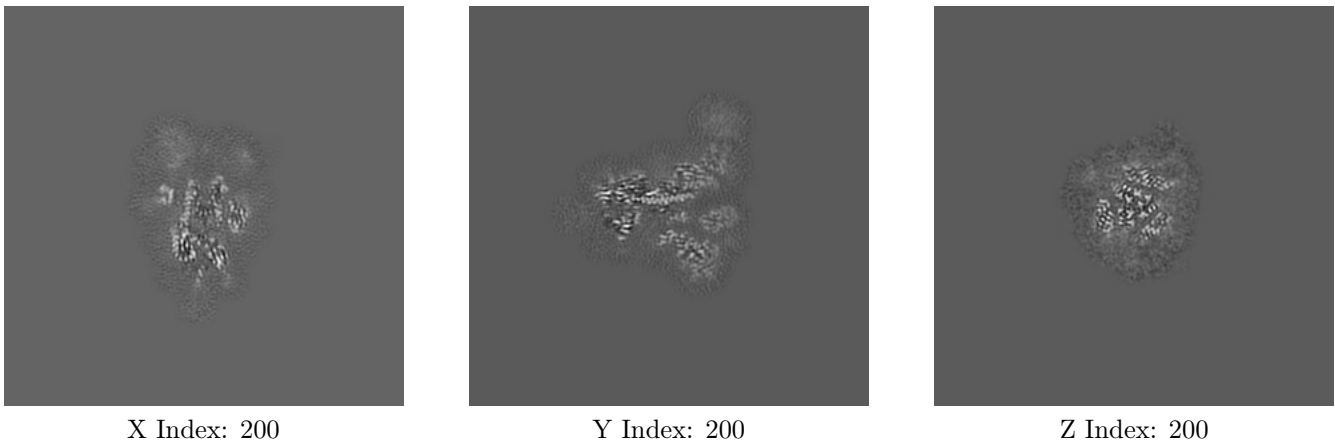
6.1.1 Primary map



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

6.2 Central slices [i](#)

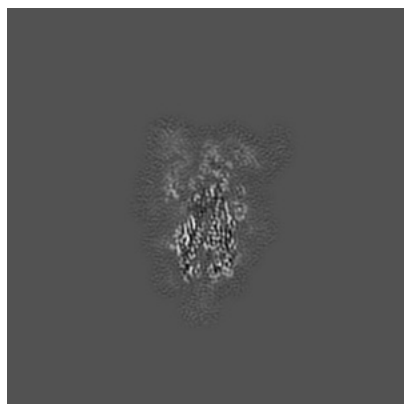
6.2.1 Primary map



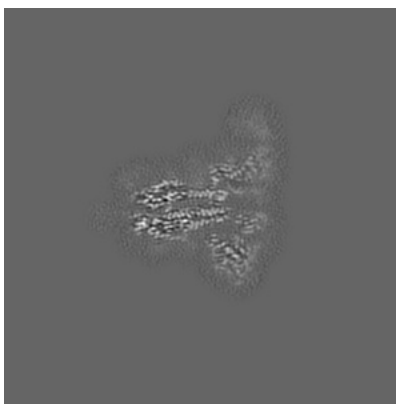
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

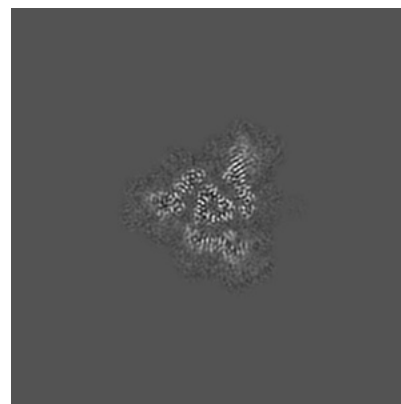
6.3.1 Primary map



X Index: 191



Y Index: 207

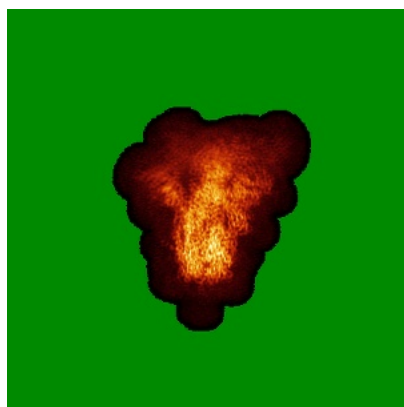


Z Index: 216

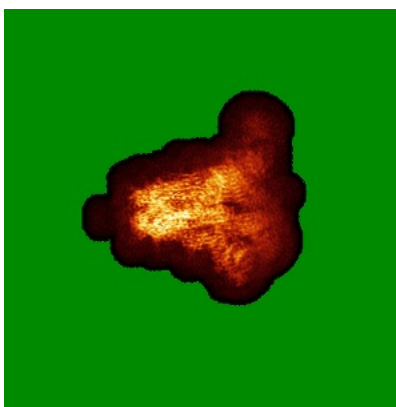
The images above show the largest variance slices of the map in three orthogonal directions.

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

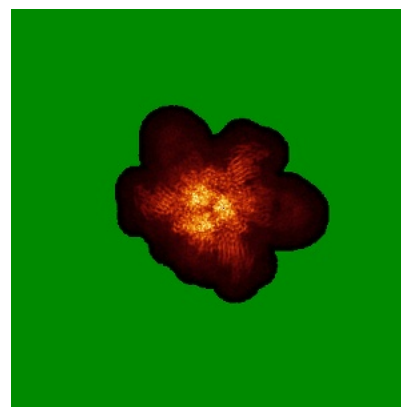
6.4.1 Primary map



X



Y



Z

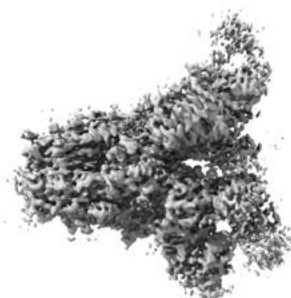
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

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 0.016. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

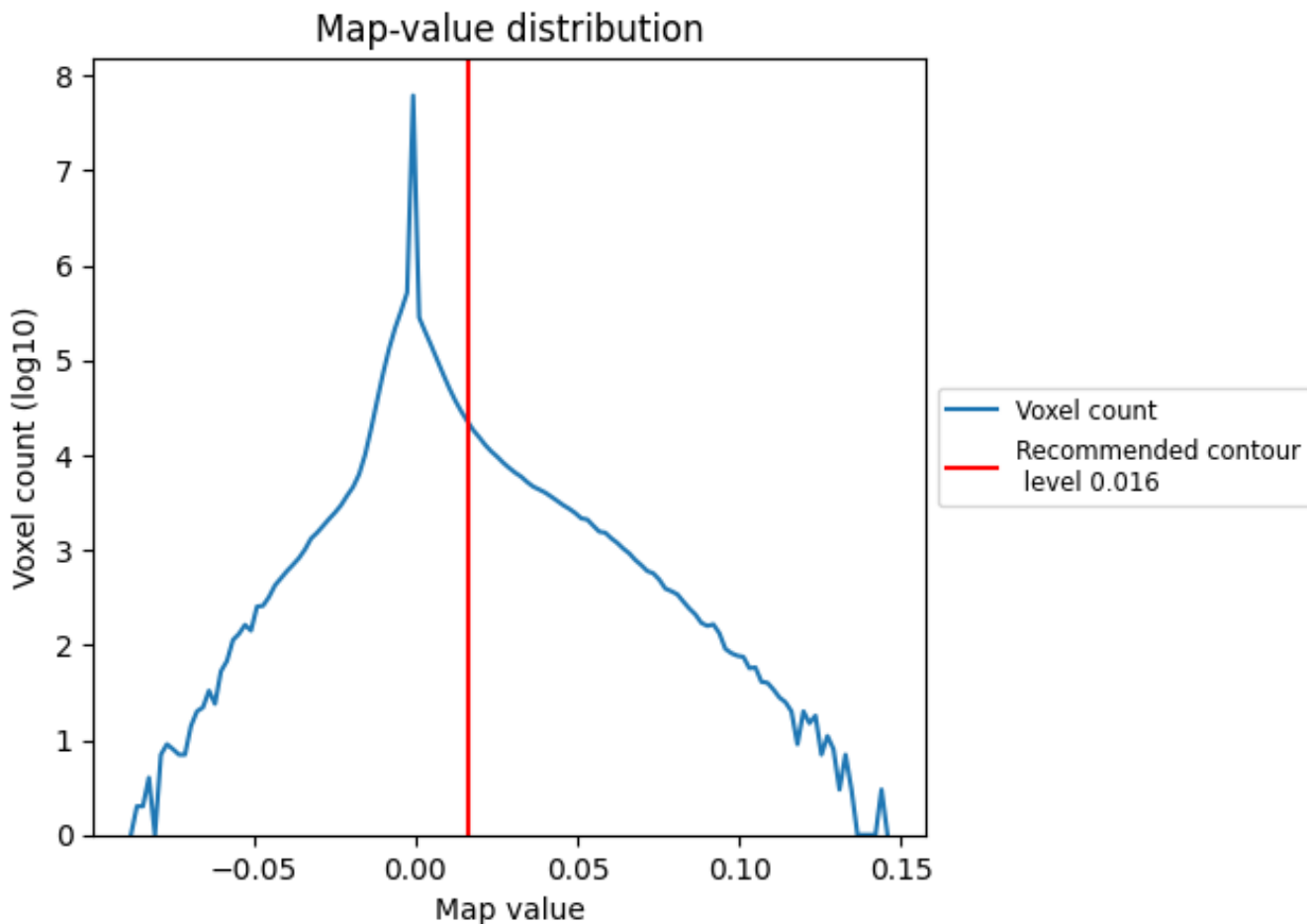
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

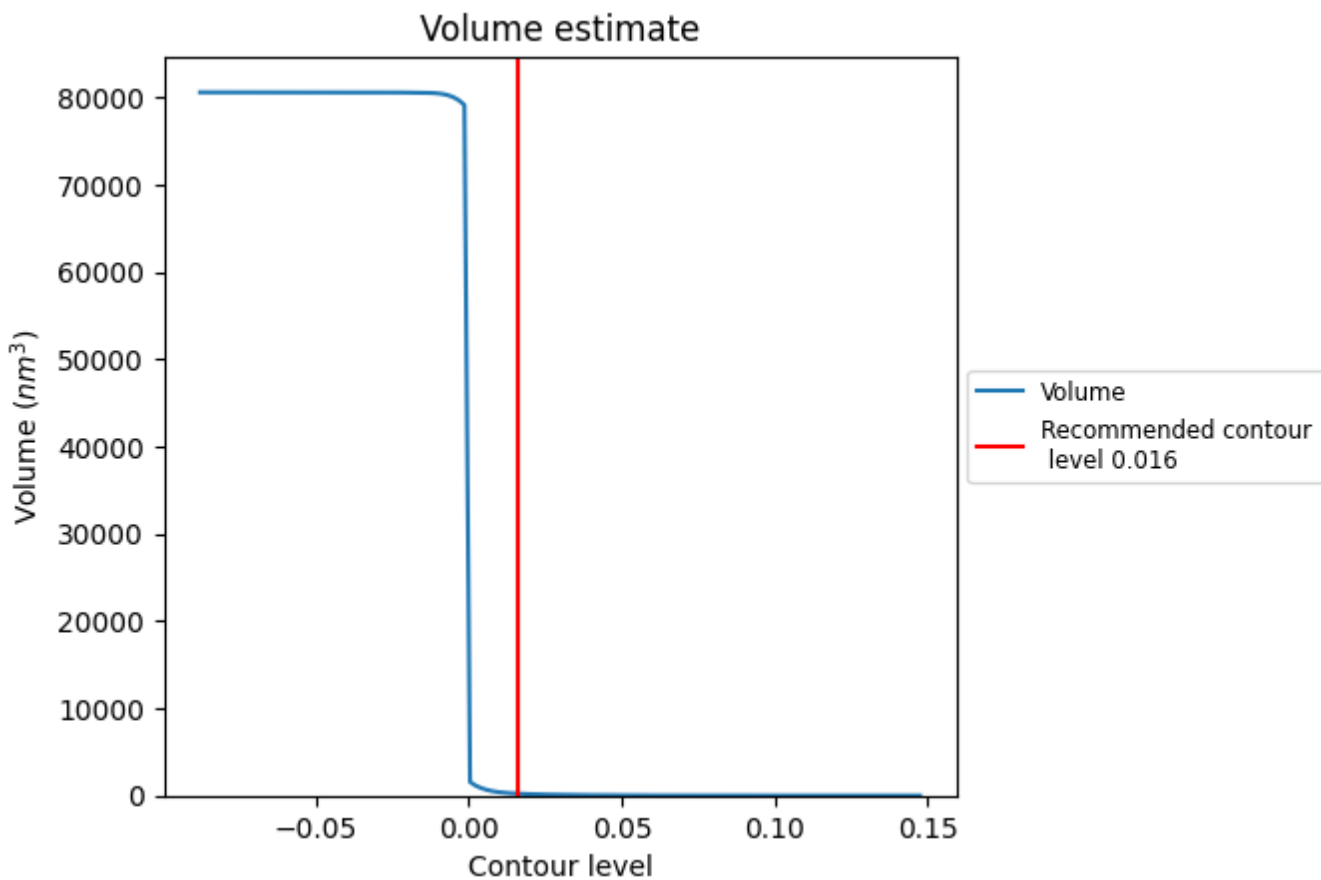
This section contains the results of statistical analysis of the map.

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.

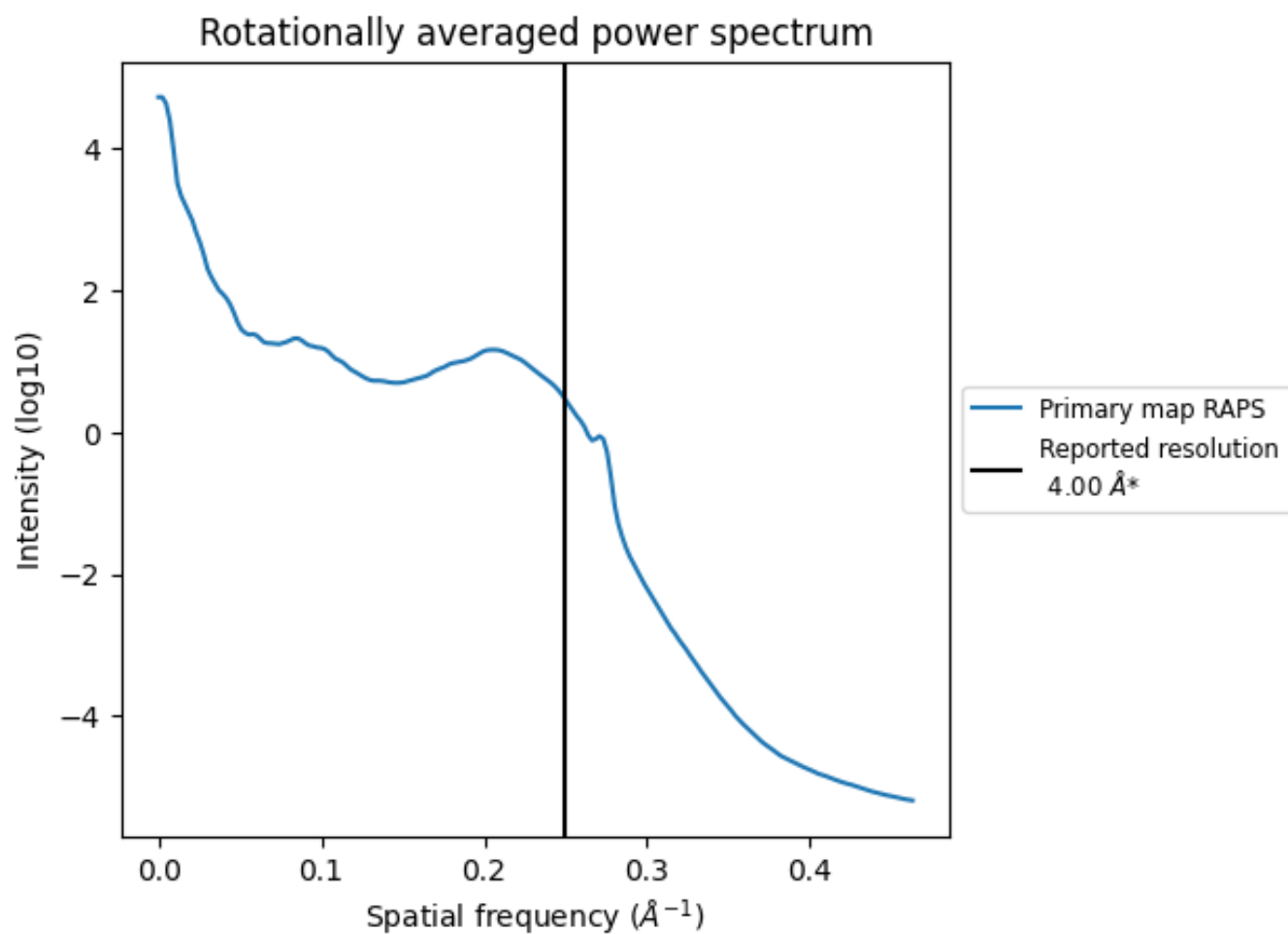
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 217 nm³; this corresponds to an approximate mass of 196 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 [i](#)

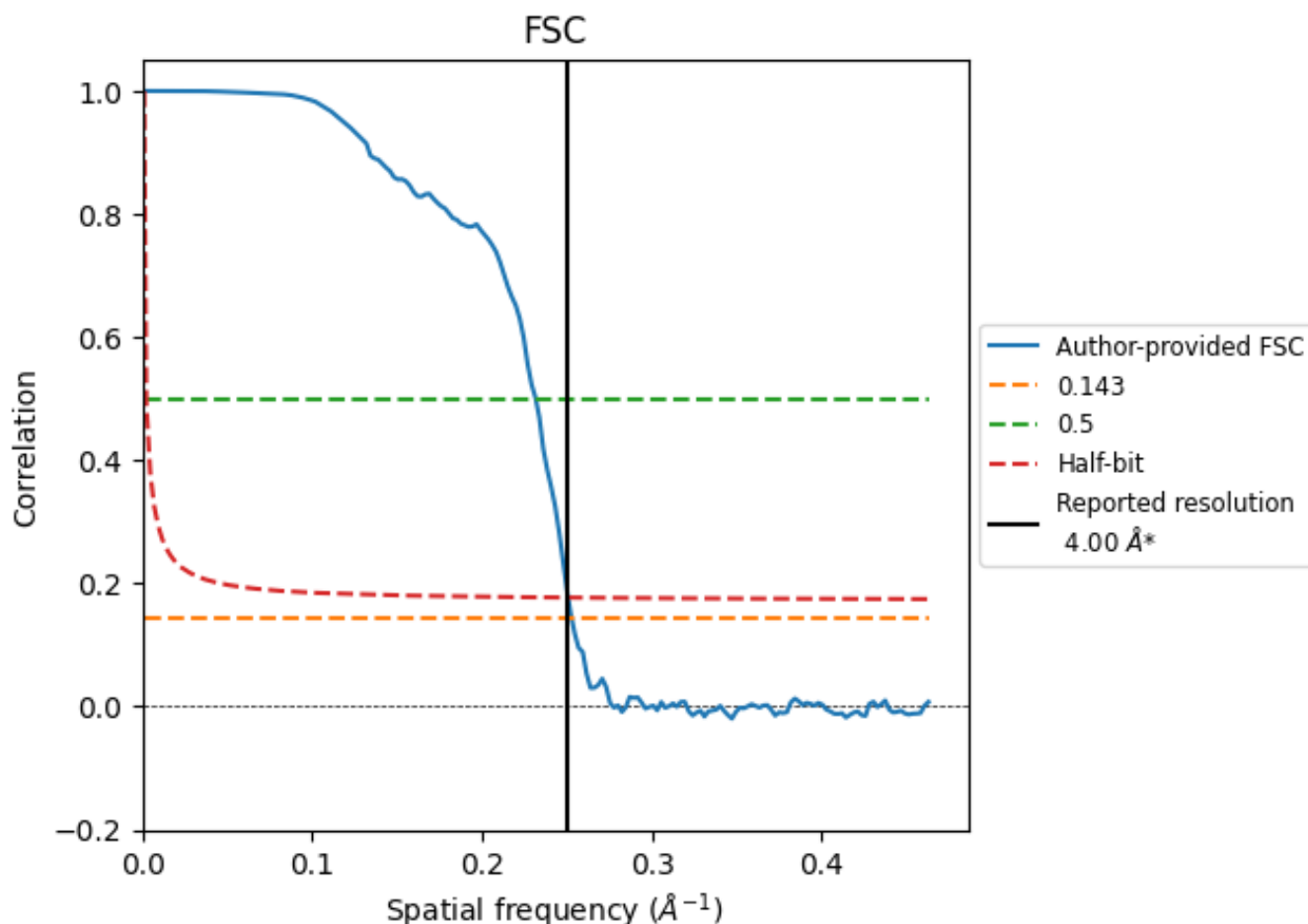


*Reported resolution corresponds to spatial frequency of 0.250 Å⁻¹

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 0.250 Å⁻¹

8.2 Resolution estimates [i](#)

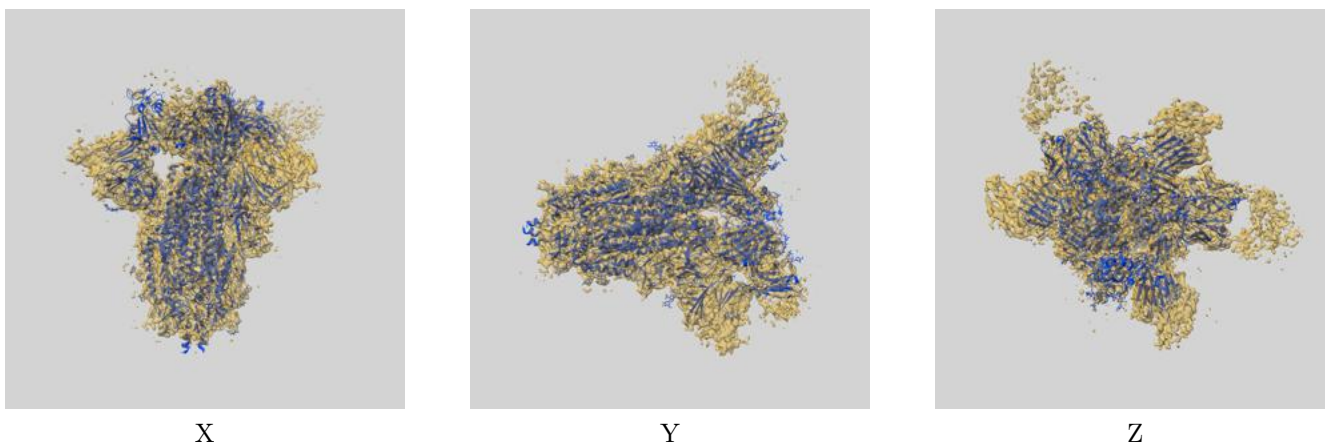
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	3.96	4.32	3.99
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

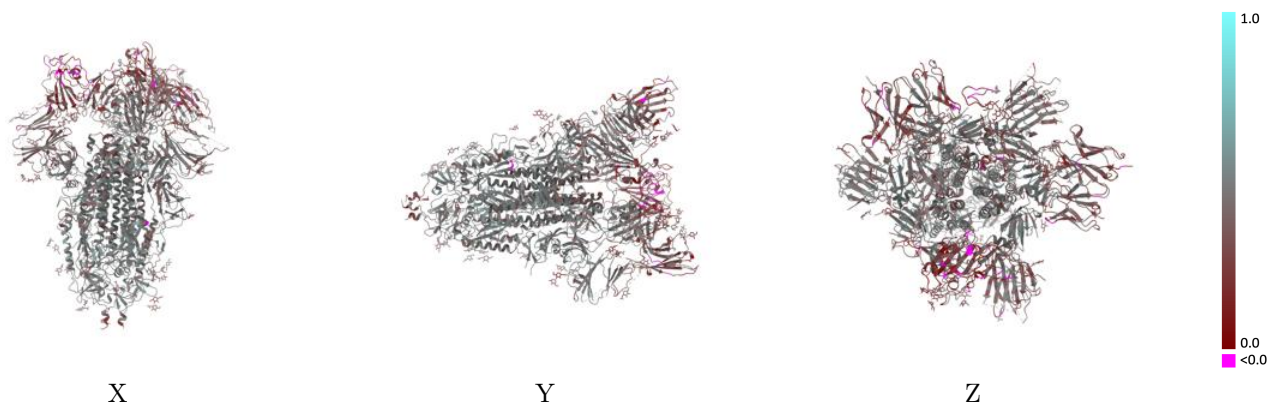
This section contains information regarding the fit between EMDB map EMD-11812 and PDB model 7AKD. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



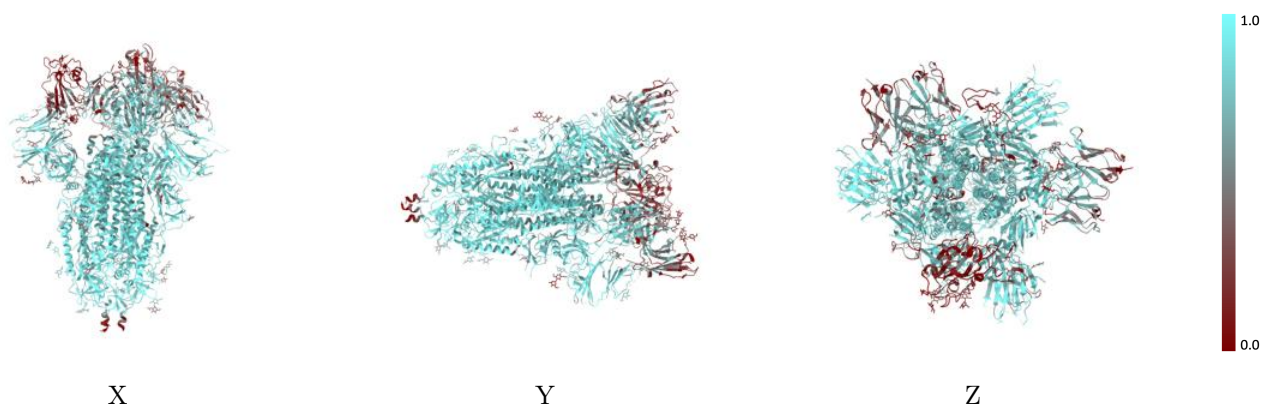
The images above show the 3D surface view of the map at the recommended contour level 0.016 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



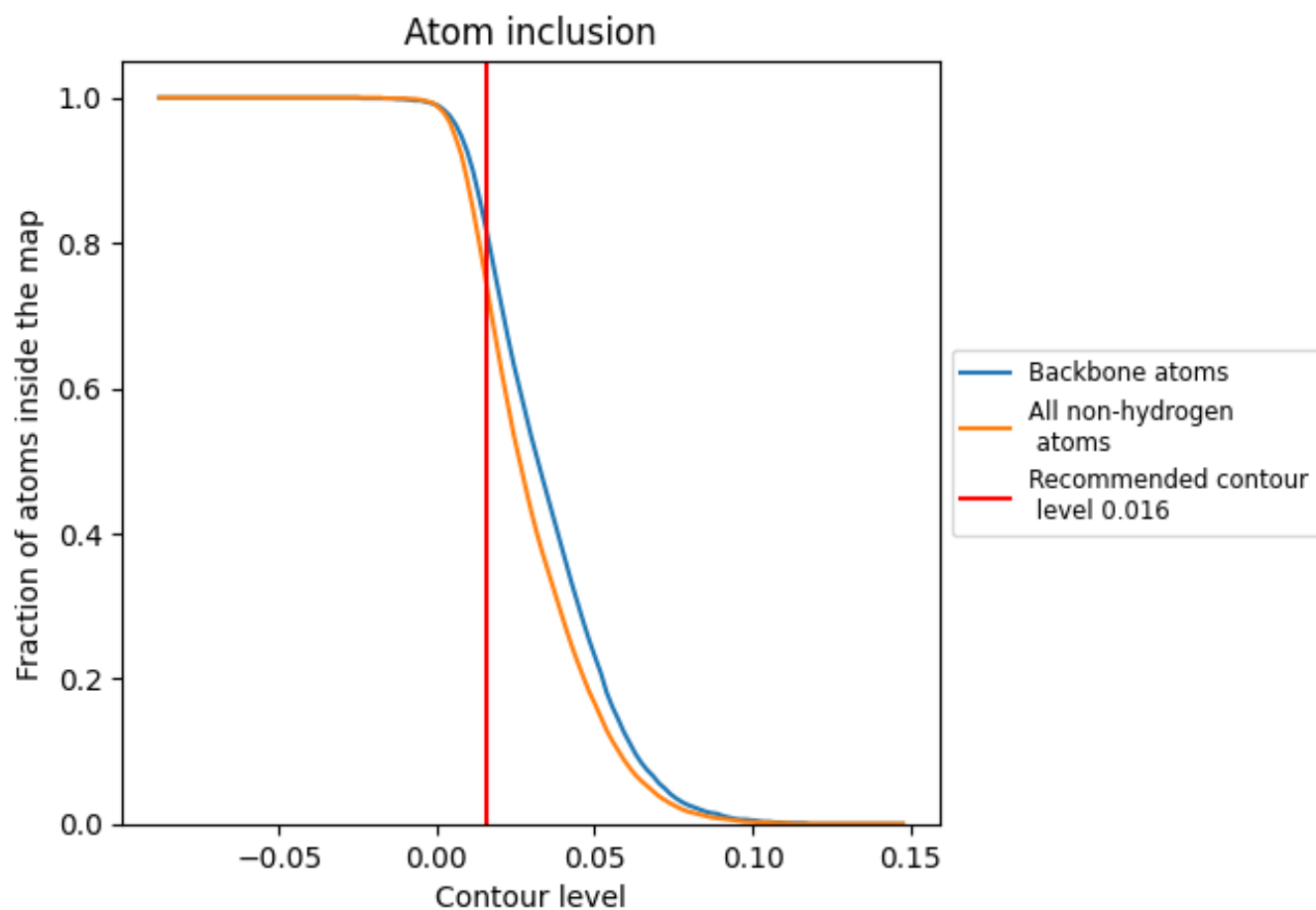
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.016).



















































9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 74% 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 (0.016) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7370	 0.4130
A	 0.7320	 0.4130
B	 0.7820	 0.4260
C	 0.8200	 0.4480
D	 0.4440	 0.3090
E	 0.5020	 0.3310
F	 0.3210	 0.2410
G	 0.2820	 0.2230
H	 0.5400	 0.3240
I	 0.3850	 0.2840
J	 0.2140	 0.2310
K	 0.6790	 0.3940
L	 0.5860	 0.3500
M	 0.5710	 0.3150
N	 0.2050	 0.2880
O	 0.4260	 0.3080
P	 0.6070	 0.3550
Q	 0.6790	 0.3870
R	 0.0710	 0.1520
S	 0.3060	 0.2830
T	 0.3240	 0.3190
U	 0.0910	 0.4840
V	 0.7860	 0.4100
W	 0.4640	 0.3240
X	 0.4640	 0.1970

