



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 09:39 AM UTC

PDB ID : 8DLW / pdb_00008dlw
EMDB ID : EMD-27518
Title : Cryo-EM structure of SARS-CoV-2 Epsilon (B.1.429) spike protein in complex with Fab S2M11
Authors : Zhu, X.; Mannar, D.; Saville, J.W.; Srivastava, S.S.; Berezuk, A.M.; Zhou, S.; Tuttle, K.S.; Subramaniam, S.
Deposited on : 2022-07-08
Resolution : 2.16 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:

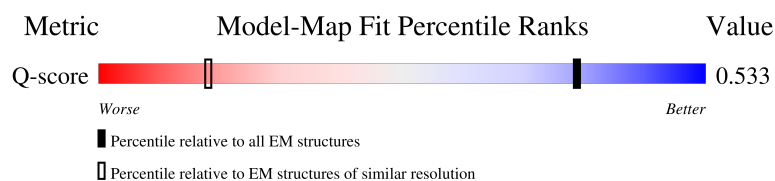
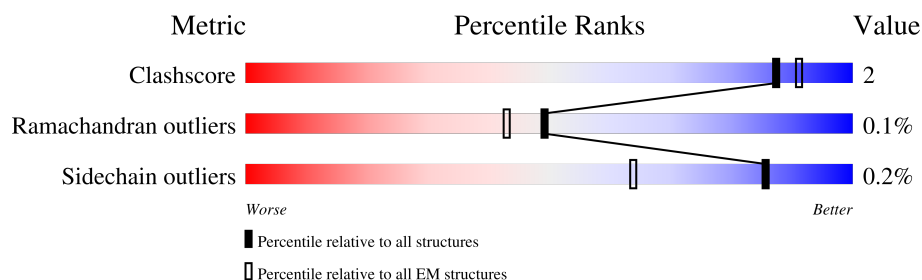
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 2.16 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.



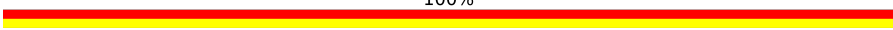
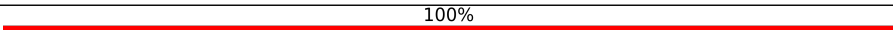
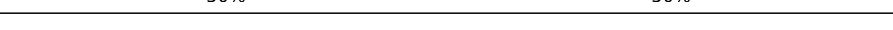
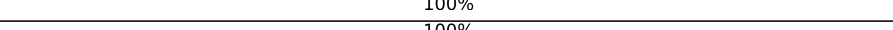
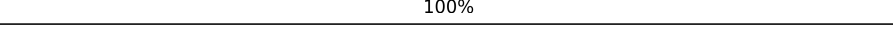
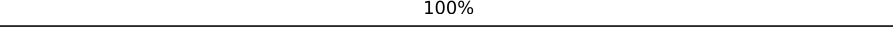
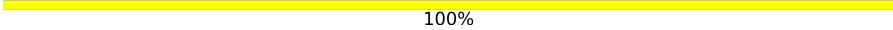
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2609 (1.67 - 2.66)

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	1288	
1	B	1288	
1	E	1288	
2	C	255	

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Mol	Chain	Length	Quality of chain
2	F	255	 45% 52%
2	H	255	 44% 52%
3	D	234	 42% 55%
3	G	234	 41% 55%
3	L	234	 41% 55%
4	I	2	 100%
4	J	2	 100%
4	M	2	 50% 50%
4	N	2	 50% 50%
4	O	2	 50% 50%
4	P	2	 100%
4	Q	2	 100%
4	R	2	 100%
4	T	2	 50% 50%
4	U	2	 50% 50%
4	V	2	 50% 50%
4	W	2	 100%
4	X	2	 100%
4	Y	2	 100%
4	a	2	 50% 50%
4	b	2	 50% 50%
4	c	2	 50% 50%
4	d	2	 100%
5	K	4	 50% 50%
5	S	4	 50% 50%

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Mol	Chain	Length	Quality of chain
5	Z	4	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 30267 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	1029	Total	C	N	O	S	0	0
			7978	5099	1334	1506	39		
1	B	1029	Total	C	N	O	S	0	0
			7978	5099	1334	1506	39		
1	E	1029	Total	C	N	O	S	0	0
			7978	5099	1334	1506	39		

There are 279 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	13	ILE	SER	conflict	UNP P0DTC2
A	152	CYS	TRP	conflict	UNP P0DTC2
A	452	ARG	LEU	conflict	UNP P0DTC2
A	614	GLY	ASP	conflict	UNP P0DTC2
A	682	GLY	ARG	conflict	UNP P0DTC2
A	683	SER	ARG	conflict	UNP P0DTC2
A	685	SER	ARG	conflict	UNP P0DTC2
A	817	PRO	PHE	conflict	UNP P0DTC2
A	892	PRO	ALA	conflict	UNP P0DTC2
A	899	PRO	ALA	conflict	UNP P0DTC2
A	942	PRO	ALA	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

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Chain	Residue	Modelled	Actual	Comment	Reference
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
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	HIS	-	expression tag	UNP P0DTC2
A	1251	HIS	-	expression tag	UNP P0DTC2
A	1252	HIS	-	expression tag	UNP P0DTC2
A	1253	HIS	-	expression tag	UNP P0DTC2
A	1254	HIS	-	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	SER	-	expression tag	UNP P0DTC2
A	1259	ALA	-	expression tag	UNP P0DTC2
A	1260	TRP	-	expression tag	UNP P0DTC2
A	1261	SER	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1262	HIS	-	expression tag	UNP P0DTC2
A	1263	PRO	-	expression tag	UNP P0DTC2
A	1264	GLN	-	expression tag	UNP P0DTC2
A	1265	PHE	-	expression tag	UNP P0DTC2
A	1266	GLU	-	expression tag	UNP P0DTC2
A	1267	LYS	-	expression tag	UNP P0DTC2
A	1268	GLY	-	expression tag	UNP P0DTC2
A	1269	GLY	-	expression tag	UNP P0DTC2
A	1270	GLY	-	expression tag	UNP P0DTC2
A	1271	SER	-	expression tag	UNP P0DTC2
A	1272	GLY	-	expression tag	UNP P0DTC2
A	1273	GLY	-	expression tag	UNP P0DTC2
A	1274	GLY	-	expression tag	UNP P0DTC2
A	1275	GLY	-	expression tag	UNP P0DTC2
A	1276	SER	-	expression tag	UNP P0DTC2
A	1277	GLY	-	expression tag	UNP P0DTC2
A	1278	GLY	-	expression tag	UNP P0DTC2
A	1279	SER	-	expression tag	UNP P0DTC2
A	1280	ALA	-	expression tag	UNP P0DTC2
A	1281	TRP	-	expression tag	UNP P0DTC2
A	1282	SER	-	expression tag	UNP P0DTC2
A	1283	HIS	-	expression tag	UNP P0DTC2
A	1284	PRO	-	expression tag	UNP P0DTC2
A	1285	GLN	-	expression tag	UNP P0DTC2
A	1286	PHE	-	expression tag	UNP P0DTC2
A	1287	GLU	-	expression tag	UNP P0DTC2
A	1288	LYS	-	expression tag	UNP P0DTC2
B	13	ILE	SER	conflict	UNP P0DTC2
B	152	CYS	TRP	conflict	UNP P0DTC2
B	452	ARG	LEU	conflict	UNP P0DTC2
B	614	GLY	ASP	conflict	UNP P0DTC2
B	682	GLY	ARG	conflict	UNP P0DTC2
B	683	SER	ARG	conflict	UNP P0DTC2
B	685	SER	ARG	conflict	UNP P0DTC2
B	817	PRO	PHE	conflict	UNP P0DTC2
B	892	PRO	ALA	conflict	UNP P0DTC2
B	899	PRO	ALA	conflict	UNP P0DTC2
B	942	PRO	ALA	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

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Chain	Residue	Modelled	Actual	Comment	Reference
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
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	HIS	-	expression tag	UNP P0DTC2
B	1251	HIS	-	expression tag	UNP P0DTC2
B	1252	HIS	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1253	HIS	-	expression tag	UNP P0DTC2
B	1254	HIS	-	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	SER	-	expression tag	UNP P0DTC2
B	1259	ALA	-	expression tag	UNP P0DTC2
B	1260	TRP	-	expression tag	UNP P0DTC2
B	1261	SER	-	expression tag	UNP P0DTC2
B	1262	HIS	-	expression tag	UNP P0DTC2
B	1263	PRO	-	expression tag	UNP P0DTC2
B	1264	GLN	-	expression tag	UNP P0DTC2
B	1265	PHE	-	expression tag	UNP P0DTC2
B	1266	GLU	-	expression tag	UNP P0DTC2
B	1267	LYS	-	expression tag	UNP P0DTC2
B	1268	GLY	-	expression tag	UNP P0DTC2
B	1269	GLY	-	expression tag	UNP P0DTC2
B	1270	GLY	-	expression tag	UNP P0DTC2
B	1271	SER	-	expression tag	UNP P0DTC2
B	1272	GLY	-	expression tag	UNP P0DTC2
B	1273	GLY	-	expression tag	UNP P0DTC2
B	1274	GLY	-	expression tag	UNP P0DTC2
B	1275	GLY	-	expression tag	UNP P0DTC2
B	1276	SER	-	expression tag	UNP P0DTC2
B	1277	GLY	-	expression tag	UNP P0DTC2
B	1278	GLY	-	expression tag	UNP P0DTC2
B	1279	SER	-	expression tag	UNP P0DTC2
B	1280	ALA	-	expression tag	UNP P0DTC2
B	1281	TRP	-	expression tag	UNP P0DTC2
B	1282	SER	-	expression tag	UNP P0DTC2
B	1283	HIS	-	expression tag	UNP P0DTC2
B	1284	PRO	-	expression tag	UNP P0DTC2
B	1285	GLN	-	expression tag	UNP P0DTC2
B	1286	PHE	-	expression tag	UNP P0DTC2
B	1287	GLU	-	expression tag	UNP P0DTC2
B	1288	LYS	-	expression tag	UNP P0DTC2
E	13	ILE	SER	conflict	UNP P0DTC2
E	152	CYS	TRP	conflict	UNP P0DTC2
E	452	ARG	LEU	conflict	UNP P0DTC2
E	614	GLY	ASP	conflict	UNP P0DTC2
E	682	GLY	ARG	conflict	UNP P0DTC2
E	683	SER	ARG	conflict	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
E	685	SER	ARG	conflict	UNP P0DTC2
E	817	PRO	PHE	conflict	UNP P0DTC2
E	892	PRO	ALA	conflict	UNP P0DTC2
E	899	PRO	ALA	conflict	UNP P0DTC2
E	942	PRO	ALA	conflict	UNP P0DTC2
E	986	PRO	LYS	conflict	UNP P0DTC2
E	987	PRO	VAL	conflict	UNP P0DTC2
E	1209	GLY	-	expression tag	UNP P0DTC2
E	1210	SER	-	expression tag	UNP P0DTC2
E	1211	GLY	-	expression tag	UNP P0DTC2
E	1212	TYR	-	expression tag	UNP P0DTC2
E	1213	ILE	-	expression tag	UNP P0DTC2
E	1214	PRO	-	expression tag	UNP P0DTC2
E	1215	GLU	-	expression tag	UNP P0DTC2
E	1216	ALA	-	expression tag	UNP P0DTC2
E	1217	PRO	-	expression tag	UNP P0DTC2
E	1218	ARG	-	expression tag	UNP P0DTC2
E	1219	ASP	-	expression tag	UNP P0DTC2
E	1220	GLY	-	expression tag	UNP P0DTC2
E	1221	GLN	-	expression tag	UNP P0DTC2
E	1222	ALA	-	expression tag	UNP P0DTC2
E	1223	TYR	-	expression tag	UNP P0DTC2
E	1224	VAL	-	expression tag	UNP P0DTC2
E	1225	ARG	-	expression tag	UNP P0DTC2
E	1226	LYS	-	expression tag	UNP P0DTC2
E	1227	ASP	-	expression tag	UNP P0DTC2
E	1228	GLY	-	expression tag	UNP P0DTC2
E	1229	GLU	-	expression tag	UNP P0DTC2
E	1230	TRP	-	expression tag	UNP P0DTC2
E	1231	VAL	-	expression tag	UNP P0DTC2
E	1232	LEU	-	expression tag	UNP P0DTC2
E	1233	LEU	-	expression tag	UNP P0DTC2
E	1234	SER	-	expression tag	UNP P0DTC2
E	1235	THR	-	expression tag	UNP P0DTC2
E	1236	PHE	-	expression tag	UNP P0DTC2
E	1237	LEU	-	expression tag	UNP P0DTC2
E	1238	GLY	-	expression tag	UNP P0DTC2
E	1239	ARG	-	expression tag	UNP P0DTC2
E	1240	SER	-	expression tag	UNP P0DTC2
E	1241	LEU	-	expression tag	UNP P0DTC2
E	1242	GLU	-	expression tag	UNP P0DTC2
E	1243	VAL	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
E	1244	LEU	-	expression tag	UNP P0DTC2
E	1245	PHE	-	expression tag	UNP P0DTC2
E	1246	GLN	-	expression tag	UNP P0DTC2
E	1247	GLY	-	expression tag	UNP P0DTC2
E	1248	PRO	-	expression tag	UNP P0DTC2
E	1249	GLY	-	expression tag	UNP P0DTC2
E	1250	HIS	-	expression tag	UNP P0DTC2
E	1251	HIS	-	expression tag	UNP P0DTC2
E	1252	HIS	-	expression tag	UNP P0DTC2
E	1253	HIS	-	expression tag	UNP P0DTC2
E	1254	HIS	-	expression tag	UNP P0DTC2
E	1255	HIS	-	expression tag	UNP P0DTC2
E	1256	HIS	-	expression tag	UNP P0DTC2
E	1257	HIS	-	expression tag	UNP P0DTC2
E	1258	SER	-	expression tag	UNP P0DTC2
E	1259	ALA	-	expression tag	UNP P0DTC2
E	1260	TRP	-	expression tag	UNP P0DTC2
E	1261	SER	-	expression tag	UNP P0DTC2
E	1262	HIS	-	expression tag	UNP P0DTC2
E	1263	PRO	-	expression tag	UNP P0DTC2
E	1264	GLN	-	expression tag	UNP P0DTC2
E	1265	PHE	-	expression tag	UNP P0DTC2
E	1266	GLU	-	expression tag	UNP P0DTC2
E	1267	LYS	-	expression tag	UNP P0DTC2
E	1268	GLY	-	expression tag	UNP P0DTC2
E	1269	GLY	-	expression tag	UNP P0DTC2
E	1270	GLY	-	expression tag	UNP P0DTC2
E	1271	SER	-	expression tag	UNP P0DTC2
E	1272	GLY	-	expression tag	UNP P0DTC2
E	1273	GLY	-	expression tag	UNP P0DTC2
E	1274	GLY	-	expression tag	UNP P0DTC2
E	1275	GLY	-	expression tag	UNP P0DTC2
E	1276	SER	-	expression tag	UNP P0DTC2
E	1277	GLY	-	expression tag	UNP P0DTC2
E	1278	GLY	-	expression tag	UNP P0DTC2
E	1279	SER	-	expression tag	UNP P0DTC2
E	1280	ALA	-	expression tag	UNP P0DTC2
E	1281	TRP	-	expression tag	UNP P0DTC2
E	1282	SER	-	expression tag	UNP P0DTC2
E	1283	HIS	-	expression tag	UNP P0DTC2
E	1284	PRO	-	expression tag	UNP P0DTC2
E	1285	GLN	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
E	1286	PHE	-	expression tag	UNP P0DTC2
E	1287	GLU	-	expression tag	UNP P0DTC2
E	1288	LYS	-	expression tag	UNP P0DTC2

- Molecule 2 is a protein called Fab S2M11 heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	122	Total	C	N	O	S	0	0
			962	618	156	182	6		
2	F	122	Total	C	N	O	S	0	0
			962	618	156	182	6		
2	H	122	Total	C	N	O	S	0	0
			962	618	156	182	6		

- Molecule 3 is a protein called Fab S2M11 light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	105	Total	C	N	O	S	0	0
			792	497	135	156	4		
3	G	105	Total	C	N	O	S	0	0
			792	497	135	156	4		
3	L	105	Total	C	N	O	S	0	0
			792	497	135	156	4		

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



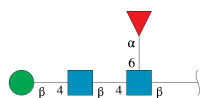
Mol	Chain	Residues	Atoms					AltConf	Trace
4	I	2	Total	C	N	O		0	0
			28	16	2	10			
4	J	2	Total	C	N	O		0	0
			28	16	2	10			
4	M	2	Total	C	N	O		0	0
			28	16	2	10			
4	N	2	Total	C	N	O		0	0
			28	16	2	10			
4	O	2	Total	C	N	O		0	0
			28	16	2	10			

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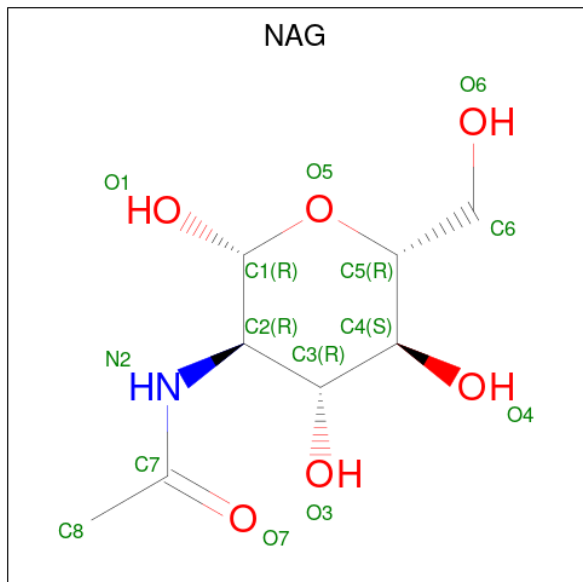
Mol	Chain	Residues	Atoms				AltConf	Trace
4	P	2	Total	C	N	O	0	0
			28	16	2	10		
4	Q	2	Total	C	N	O	0	0
			28	16	2	10		
4	R	2	Total	C	N	O	0	0
			28	16	2	10		
4	T	2	Total	C	N	O	0	0
			28	16	2	10		
4	U	2	Total	C	N	O	0	0
			28	16	2	10		
4	V	2	Total	C	N	O	0	0
			28	16	2	10		
4	W	2	Total	C	N	O	0	0
			28	16	2	10		
4	X	2	Total	C	N	O	0	0
			28	16	2	10		
4	Y	2	Total	C	N	O	0	0
			28	16	2	10		
4	a	2	Total	C	N	O	0	0
			28	16	2	10		
4	b	2	Total	C	N	O	0	0
			28	16	2	10		
4	c	2	Total	C	N	O	0	0
			28	16	2	10		
4	d	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 5 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
5	K	4	Total	C	N	O	0	0
			49	28	2	19		
5	S	4	Total	C	N	O	0	0
			49	28	2	19		
5	Z	4	Total	C	N	O	0	0
			49	28	2	19		

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

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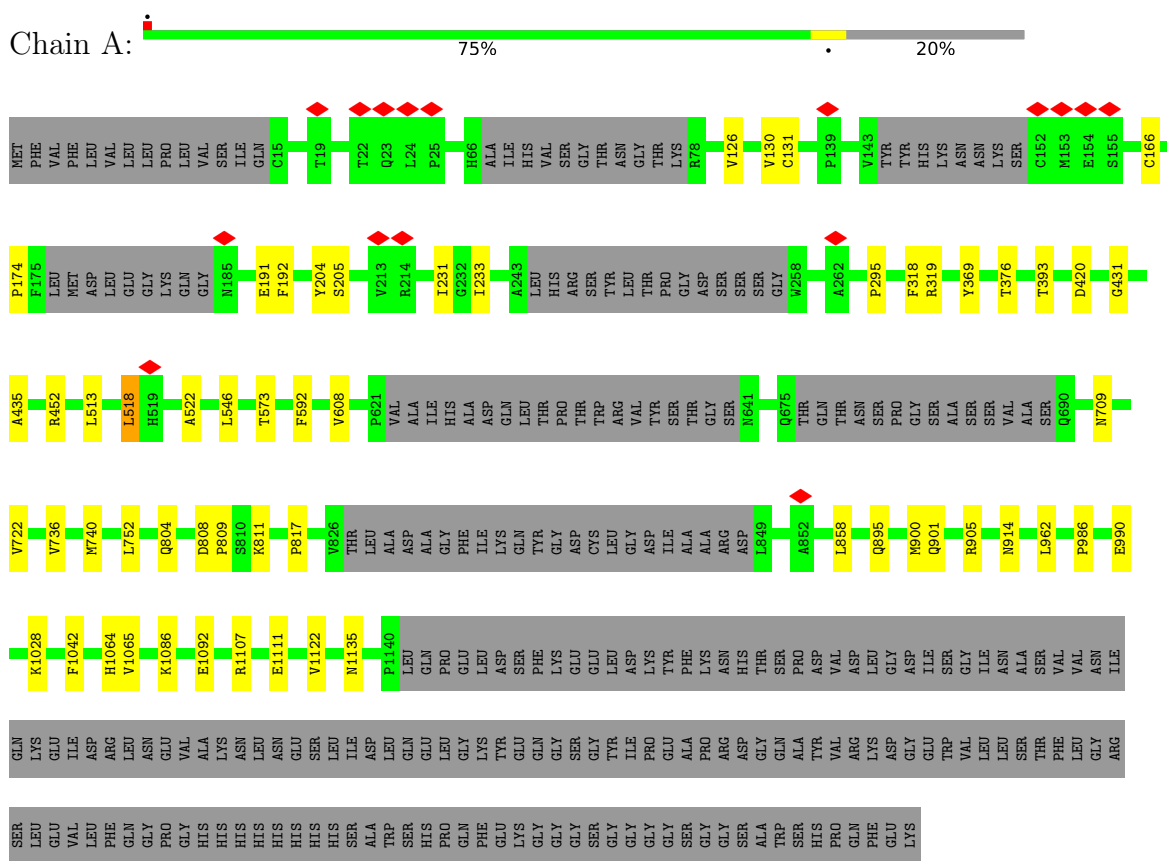
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Mol	Chain	Residues	Atoms				AltConf
6	B	1	Total	C	N	O	0
			14	8	1	5	
6	B	1	Total	C	N	O	0
			14	8	1	5	
6	B	1	Total	C	N	O	0
			14	8	1	5	
6	B	1	Total	C	N	O	0
			14	8	1	5	
6	B	1	Total	C	N	O	0
			14	8	1	5	
6	B	1	Total	C	N	O	0
			14	8	1	5	
6	B	1	Total	C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

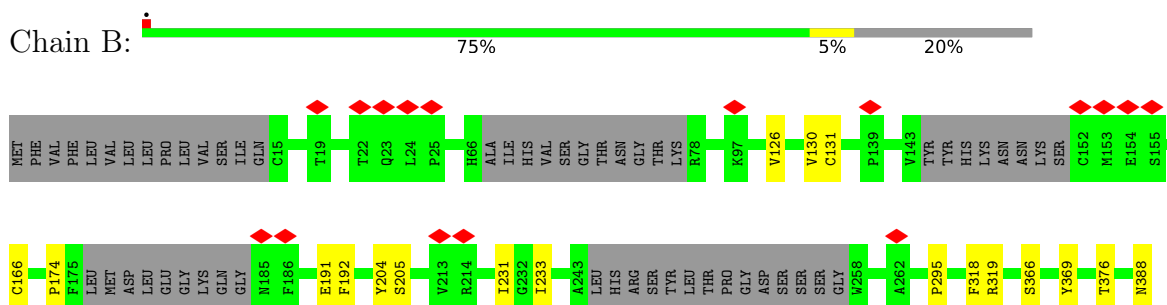
3 Residue-property plots

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



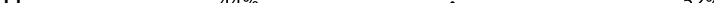
THR	THR	GLY
ILE	ALA	ALA
CYS	ASN	ALA
GLY	VAL	LEU
ASN	ASN	GLY
HIS	HIS	CYS
LYS	LYS	LEU
PRO	PRO	VAL
SER	SER	LYS
ASN	ASN	ASP
THR	THR	PHE
LYS	LYS	PRO
VAL	VAL	GLU
GLU	VAL	VAL
PRO	PRO	THR
THR	THR	VAL
CYS	CYS	SER
GLY	GLY	GLY
SER	SER	ALA
HIS	HIS	LEU
HIS	HIS	THR
HIS	HIS	SER
HIS	HIS	GLY
HIS	HIS	VAL
		THR
		THR
		PHE
		PRO
		ALA
		VAL
		LEU
		GLN
		SER
		SER
		GLY
		GLY
		LEU
		THR
		SER
		LEU
		SER
		VAL
		THR
		VAL
		PRO
		SER
		SER
		GLY
		THR
		THR
		GLN

- Molecule 2: Fab S2M11 heavy chain

Chain F: 45% . 52%

CYS	ASN	VAL	ASN	HIS	PRO	SER	ASN	THR	LYS	VAL	ASP	LYS	LYS	VAL	GLU	PRO	VAL	THR	GLY	SER	LYS	PRO	LYS	GLY	SER	HIS	HIS	HIS	HIS	HIS
ALA	ALA	LEU	GLY	CYS	LEU	VAL	LYS	ASP	PHE	PRO	GLU	PRO	VAL	THR	VAL	THR	ASN	TRP	SER	GLY	GLY	ALA	THR	SER	GLY	VAL	HIS	THR	GLN	SER
MET	ASP	TRP	TRP	TRP	ARG	VAL	PHE	CYS	LEU	ALA	VAL	ALA	PRO	GLY	ALA	HIS	GLU	V2	K19	M34	T51	M81	T91	Y103	T122	V123	SER	SER	ALA	SER

- Molecule 2: Fab S2M11 heavy chain

Chain H:  44% . 52%

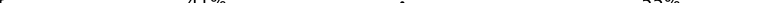
[illegible]

- Molecule 3: Fab S2M11 light chain

Chain D:  42% . 55%

[illegible]

- Molecule 3: Fab S2M11 light chain

Chain G:  41% 0 55%

[illegible]

LYS
SER
HIS
ARG
SER
TYR
SER
CYS
GLN
VAL
THR
THR
HIS
GLU
GLY
SER
THR
VAL
GLU
LYS
THR
VAL
ALA
ALA
PRO
THR
GLU
CYS
SER

- Molecule 3: Fab S2M11 light chain

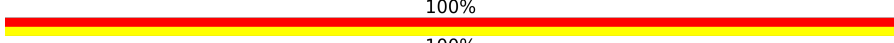
Chain L:  41% 55%

MET
VAL
LEU
GLN
THR
THR
GLN
VAL
PHE
ILE
SER
LEU
LEU
LEU
TRP
ILE
SER
THR
GLY
ALA
VAL
TYR
GLY
E1
I2
S26
Q38
L48
I49
Y50
A56
R62
D63
V105
GLU
ILE
LYS
GLN
GLN
PRO
LYS
LYS
ASN
ALA
PRO
THR
VAL
THR
LEU
PHE
PRO
PRO
SER
SER
GLU
GLU
LEU

GLN
ALA
ASN
LYS
SER
THR
LEU
VAL
CYS
GLN
ILE
THR
SER
ASP
PHE
THR
PRO
SER
GLY
ALA
VAL
THR
VAL
VAL
TRP
LYS
ALA
ASP
GLY
SER
PRO
VAL
LYS
ALA
GLY
VAL
GLU
THR
THR
LYS
PRO
SER
LYS
GLN
SER
ASN
ASN
LYS
TYR
ALA
ALA
SER
SER
TYR
LEU
SER
LEU
THR
PRO
GLU
TRP

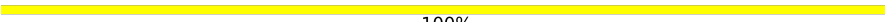
LYS
SER
HIS
ARG
SER
TYR
SER
CYS
GLN
VAL
THR
THR
HIS
GLU
GLY
SER
THR
VAL
GLU
LYS
THR
VAL
VAL
ALA
PRO
THR
GLU
CYS
SER

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

Chain I:  100% 100%

MAG1
MAG2

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

Chain J:  100%

MAG1
MAG2

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

Chain M:  50% 50%

MAG1
MAG2

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

Chain N:  50% 50%

MAG1
MAG2

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

Chain O:  50% 50%

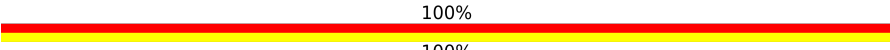


- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P:  100%



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

Chain Q:  100% 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 T:  50% 50%



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

Chain U:  50% 50%



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

Chain V:  50% 50%



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

Chain W:  100%



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

Chain X:  100%
100%



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

Chain Y:  100%



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

Chain a:  50% 50%



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

Chain b:  50% 50%

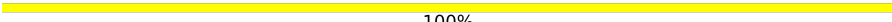


- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain c:  50% 50%



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

Chain d:  100%

NAG1
NAG2

- Molecule 5: 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

Chain K:  50% 50%

NAG1
NAG2
BMA3
FUC4

- Molecule 5: 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

Chain S:  50% 50%

NAG1
NAG2
BMA3
FUC4

- Molecule 5: 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

Chain Z:  50% 50%

NAG1
NAG2
BMA3
FUC4

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	124473	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.977	Depositor
Minimum map value	-0.576	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.047	Depositor
Recommended contour level	0.236	Depositor
Map size (Å)	400.0, 400.0, 400.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0, 1.0, 1.0	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FUC, NAG, BMA

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	0.28	0/8163	0.65	1/11116 (0.0%)
1	B	0.28	0/8163	0.65	1/11116 (0.0%)
1	E	0.28	0/8163	0.65	1/11116 (0.0%)
2	C	0.22	0/992	0.62	0/1351
2	F	0.23	0/992	0.63	0/1351
2	H	0.24	0/992	0.64	1/1351 (0.1%)
3	D	0.22	0/811	0.60	0/1100
3	G	0.23	0/811	0.63	0/1100
3	L	0.23	0/811	0.60	0/1100
All	All	0.27	0/29898	0.64	4/40701 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	986	PRO	N-CA-C	5.57	117.50	110.70
1	E	986	PRO	N-CA-C	5.55	117.47	110.70
1	B	986	PRO	N-CA-C	5.44	117.33	110.70
2	H	103	TYR	CA-CB-CG	5.03	122.95	113.90

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	7978	0	7726	33	0
1	B	7978	0	7726	35	0
1	E	7978	0	7726	35	0
2	C	962	0	902	5	0
2	F	962	0	902	4	0
2	H	962	0	902	5	0
3	D	792	0	762	4	0
3	G	792	0	762	4	0
3	L	792	0	762	4	0
4	I	28	0	25	0	0
4	J	28	0	25	0	0
4	M	28	0	25	0	0
4	N	28	0	25	0	0
4	O	28	0	25	0	0
4	P	28	0	25	0	0
4	Q	28	0	25	0	0
4	R	28	0	25	0	0
4	T	28	0	25	0	0
4	U	28	0	25	0	0
4	V	28	0	25	0	0
4	W	28	0	25	0	0
4	X	28	0	25	0	0
4	Y	28	0	25	0	0
4	a	28	0	25	0	0
4	b	28	0	25	0	0
4	c	28	0	25	0	0
4	d	28	0	25	0	0
5	K	49	0	43	0	0
5	S	49	0	43	0	0
5	Z	49	0	43	0	0
6	A	140	0	130	0	0
6	B	140	0	130	0	0
6	E	140	0	130	0	0
All	All	30267	0	29139	117	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 2.

The worst 5 of 117 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:19:LYS:HA	2:H:81:MET:O	1.84	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:19:LYS:HA	2:C:81:MET:O	1.87	0.74
2:F:19:LYS:HA	2:F:81:MET:O	1.89	0.72
1:B:901:GLN:HE21	1:B:905:ARG:HE	1.43	0.67
1:A:901:GLN:HE21	1:A:905:ARG:HE	1.42	0.67

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1013/1288 (79%)	987 (97%)	25 (2%)	1 (0%)	48	50
1	B	1013/1288 (79%)	987 (97%)	26 (3%)	0	100	100
1	E	1013/1288 (79%)	987 (97%)	25 (2%)	1 (0%)	48	50
2	C	120/255 (47%)	120 (100%)	0	0	100	100
2	F	120/255 (47%)	118 (98%)	2 (2%)	0	100	100
2	H	120/255 (47%)	120 (100%)	0	0	100	100
3	D	103/234 (44%)	101 (98%)	2 (2%)	0	100	100
3	G	103/234 (44%)	100 (97%)	3 (3%)	0	100	100
3	L	103/234 (44%)	101 (98%)	2 (2%)	0	100	100
All	All	3708/5331 (70%)	3621 (98%)	85 (2%)	2 (0%)	49	50

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	809	PRO
1	E	809	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	881/1115 (79%)	879 (100%)	2 (0%)	87	92
1	B	881/1115 (79%)	879 (100%)	2 (0%)	87	92
1	E	881/1115 (79%)	879 (100%)	2 (0%)	87	92
2	C	100/214 (47%)	100 (100%)	0	100	100
2	F	100/214 (47%)	100 (100%)	0	100	100
2	H	100/214 (47%)	100 (100%)	0	100	100
3	D	85/197 (43%)	85 (100%)	0	100	100
3	G	85/197 (43%)	85 (100%)	0	100	100
3	L	85/197 (43%)	85 (100%)	0	100	100
All	All	3198/4578 (70%)	3192 (100%)	6 (0%)	85	92

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

Mol	Chain	Res	Type
1	B	1135	ASN
1	E	518	LEU
1	E	1135	ASN
1	A	1135	ASN
1	A	518	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	949	GLN
1	E	655	HIS
1	E	185	ASN
1	E	690	GLN
1	B	134	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

48 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	I	1	4,1	14,14,15	0.43	0	17,19,21	0.72	1 (5%)
4	NAG	I	2	4	14,14,15	0.54	0	17,19,21	0.67	1 (5%)
4	NAG	J	1	4,1	14,14,15	0.39	0	17,19,21	0.72	1 (5%)
4	NAG	J	2	4	14,14,15	0.53	0	17,19,21	0.65	1 (5%)
5	NAG	K	1	5,1	14,14,15	0.42	0	17,19,21	0.84	1 (5%)
5	NAG	K	2	5	14,14,15	0.66	0	17,19,21	0.44	0
5	BMA	K	3	5	11,11,12	0.83	0	15,15,17	0.83	0
5	FUC	K	4	5	10,10,11	1.10	1 (10%)	14,14,16	0.77	0
4	NAG	M	1	4,1	14,14,15	0.31	0	17,19,21	0.64	1 (5%)
4	NAG	M	2	4	14,14,15	0.56	0	17,19,21	0.56	0
4	NAG	N	1	4,1	14,14,15	0.31	0	17,19,21	0.72	1 (5%)
4	NAG	N	2	4	14,14,15	0.55	0	17,19,21	0.53	0
4	NAG	O	1	4,1	14,14,15	0.39	0	17,19,21	0.60	1 (5%)
4	NAG	O	2	4	14,14,15	0.53	0	17,19,21	0.51	0
4	NAG	P	1	4,1	14,14,15	0.35	0	17,19,21	0.79	1 (5%)
4	NAG	P	2	4	14,14,15	0.46	0	17,19,21	0.70	1 (5%)
4	NAG	Q	1	4,1	14,14,15	0.42	0	17,19,21	0.70	1 (5%)
4	NAG	Q	2	4	14,14,15	0.54	0	17,19,21	0.69	1 (5%)
4	NAG	R	1	4,1	14,14,15	0.39	0	17,19,21	0.72	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	R	2	4	14,14,15	0.53	0	17,19,21	0.64	1 (5%)
5	NAG	S	1	5,1	14,14,15	0.40	0	17,19,21	0.84	1 (5%)
5	NAG	S	2	5	14,14,15	0.65	0	17,19,21	0.42	0
5	BMA	S	3	5	11,11,12	0.81	0	15,15,17	0.81	0
5	FUC	S	4	5	10,10,11	1.04	1 (10%)	14,14,16	0.76	0
4	NAG	T	1	4,1	14,14,15	0.32	0	17,19,21	0.64	1 (5%)
4	NAG	T	2	4	14,14,15	0.53	0	17,19,21	0.55	0
4	NAG	U	1	4,1	14,14,15	0.32	0	17,19,21	0.73	1 (5%)
4	NAG	U	2	4	14,14,15	0.55	0	17,19,21	0.53	0
4	NAG	V	1	4,1	14,14,15	0.38	0	17,19,21	0.60	1 (5%)
4	NAG	V	2	4	14,14,15	0.53	0	17,19,21	0.52	0
4	NAG	W	1	4,1	14,14,15	0.35	0	17,19,21	0.79	1 (5%)
4	NAG	W	2	4	14,14,15	0.46	0	17,19,21	0.71	1 (5%)
4	NAG	X	1	4,1	14,14,15	0.42	0	17,19,21	0.70	1 (5%)
4	NAG	X	2	4	14,14,15	0.54	0	17,19,21	0.69	1 (5%)
4	NAG	Y	1	4,1	14,14,15	0.39	0	17,19,21	0.72	1 (5%)
4	NAG	Y	2	4	14,14,15	0.55	0	17,19,21	0.65	1 (5%)
5	NAG	Z	1	5,1	14,14,15	0.40	0	17,19,21	0.84	1 (5%)
5	NAG	Z	2	5	14,14,15	0.65	0	17,19,21	0.42	0
5	BMA	Z	3	5	11,11,12	0.80	0	15,15,17	0.82	0
5	FUC	Z	4	5	10,10,11	1.03	1 (10%)	14,14,16	0.74	0
4	NAG	a	1	4,1	14,14,15	0.32	0	17,19,21	0.65	1 (5%)
4	NAG	a	2	4	14,14,15	0.58	0	17,19,21	0.55	0
4	NAG	b	1	4,1	14,14,15	0.31	0	17,19,21	0.73	1 (5%)
4	NAG	b	2	4	14,14,15	0.54	0	17,19,21	0.54	0
4	NAG	c	1	4,1	14,14,15	0.38	0	17,19,21	0.60	1 (5%)
4	NAG	c	2	4	14,14,15	0.54	0	17,19,21	0.51	0
4	NAG	d	1	4,1	14,14,15	0.34	0	17,19,21	0.78	1 (5%)
4	NAG	d	2	4	14,14,15	0.45	0	17,19,21	0.71	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	I	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	I	2	4	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	J	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	J	2	4	-	2/6/23/26	0/1/1/1
5	NAG	K	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	K	2	5	-	0/6/23/26	0/1/1/1
5	BMA	K	3	5	-	1/2/19/22	0/1/1/1
5	FUC	K	4	5	-	-	0/1/1/1
4	NAG	M	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	M	2	4	-	3/6/23/26	0/1/1/1
4	NAG	N	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	N	2	4	-	3/6/23/26	0/1/1/1
4	NAG	O	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	O	2	4	-	2/6/23/26	0/1/1/1
4	NAG	P	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	P	2	4	-	0/6/23/26	0/1/1/1
4	NAG	Q	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	Q	2	4	-	2/6/23/26	0/1/1/1
4	NAG	R	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	R	2	4	-	1/6/23/26	0/1/1/1
5	NAG	S	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	S	2	5	-	0/6/23/26	0/1/1/1
5	BMA	S	3	5	-	1/2/19/22	0/1/1/1
5	FUC	S	4	5	-	-	0/1/1/1
4	NAG	T	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	T	2	4	-	2/6/23/26	0/1/1/1
4	NAG	U	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	U	2	4	-	3/6/23/26	0/1/1/1
4	NAG	V	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	V	2	4	-	2/6/23/26	0/1/1/1
4	NAG	W	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	W	2	4	-	0/6/23/26	0/1/1/1
4	NAG	X	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	X	2	4	-	2/6/23/26	0/1/1/1
4	NAG	Y	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	Y	2	4	-	2/6/23/26	0/1/1/1
5	NAG	Z	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	Z	2	5	-	2/6/23/26	0/1/1/1
5	BMA	Z	3	5	-	1/2/19/22	0/1/1/1
5	FUC	Z	4	5	-	-	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	a	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	a	2	4	-	2/6/23/26	0/1/1/1
4	NAG	b	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	b	2	4	-	2/6/23/26	0/1/1/1
4	NAG	c	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	c	2	4	-	2/6/23/26	0/1/1/1
4	NAG	d	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	d	2	4	-	0/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	K	4	FUC	C2-C3	2.29	1.56	1.52
5	S	4	FUC	C2-C3	2.15	1.55	1.52
5	Z	4	FUC	C2-C3	2.03	1.55	1.52

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	P	1	NAG	C1-O5-C5	2.95	116.14	112.19
4	W	1	NAG	C1-O5-C5	2.94	116.13	112.19
4	d	1	NAG	C1-O5-C5	2.88	116.05	112.19
5	K	1	NAG	C1-O5-C5	2.81	115.95	112.19
5	S	1	NAG	C1-O5-C5	2.80	115.94	112.19

There are no chirality outliers.

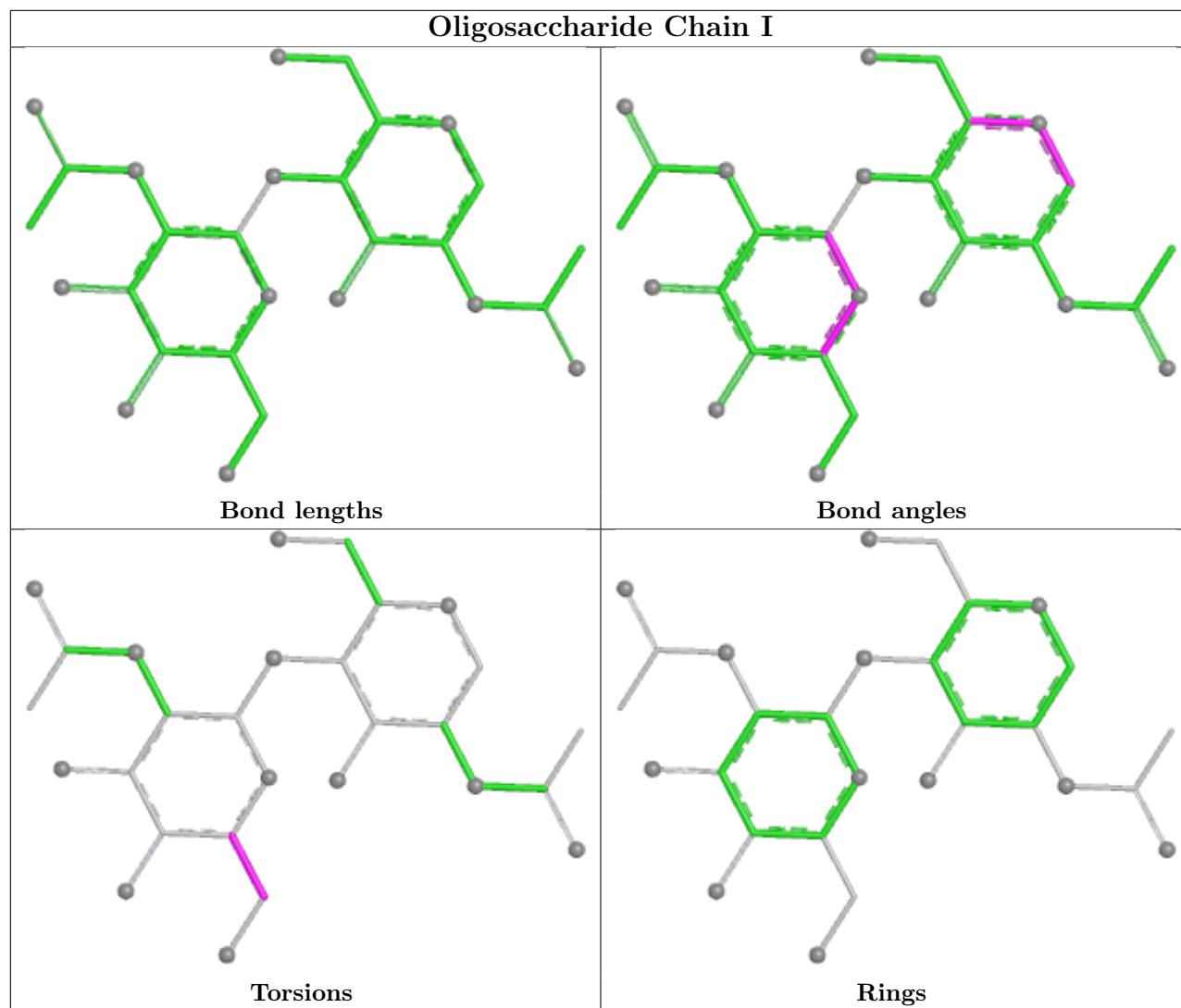
5 of 49 torsion outliers are listed below:

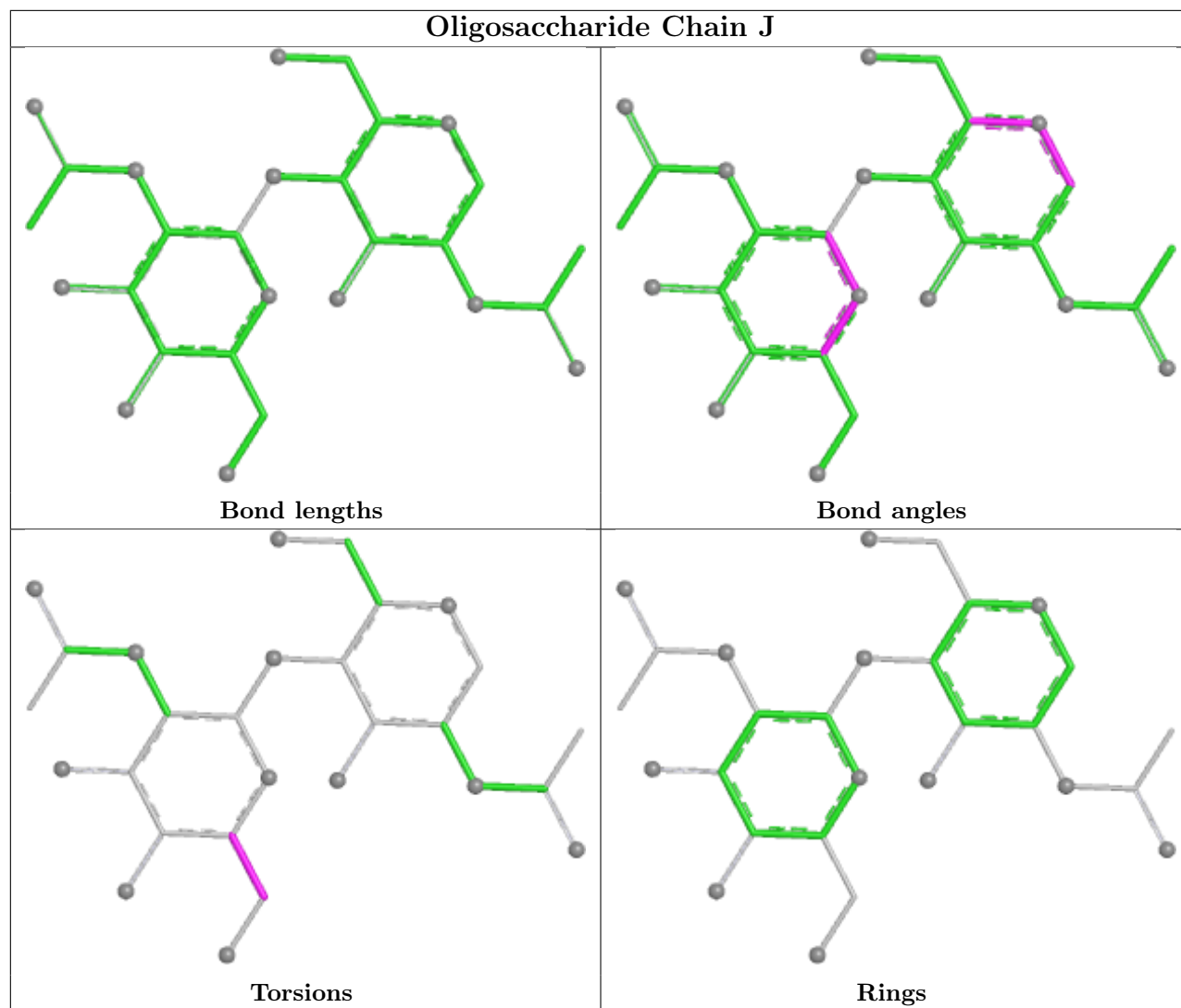
Mol	Chain	Res	Type	Atoms
4	b	1	NAG	O5-C5-C6-O6
4	U	1	NAG	O5-C5-C6-O6
4	O	2	NAG	O5-C5-C6-O6
4	V	2	NAG	O5-C5-C6-O6
4	M	2	NAG	O5-C5-C6-O6

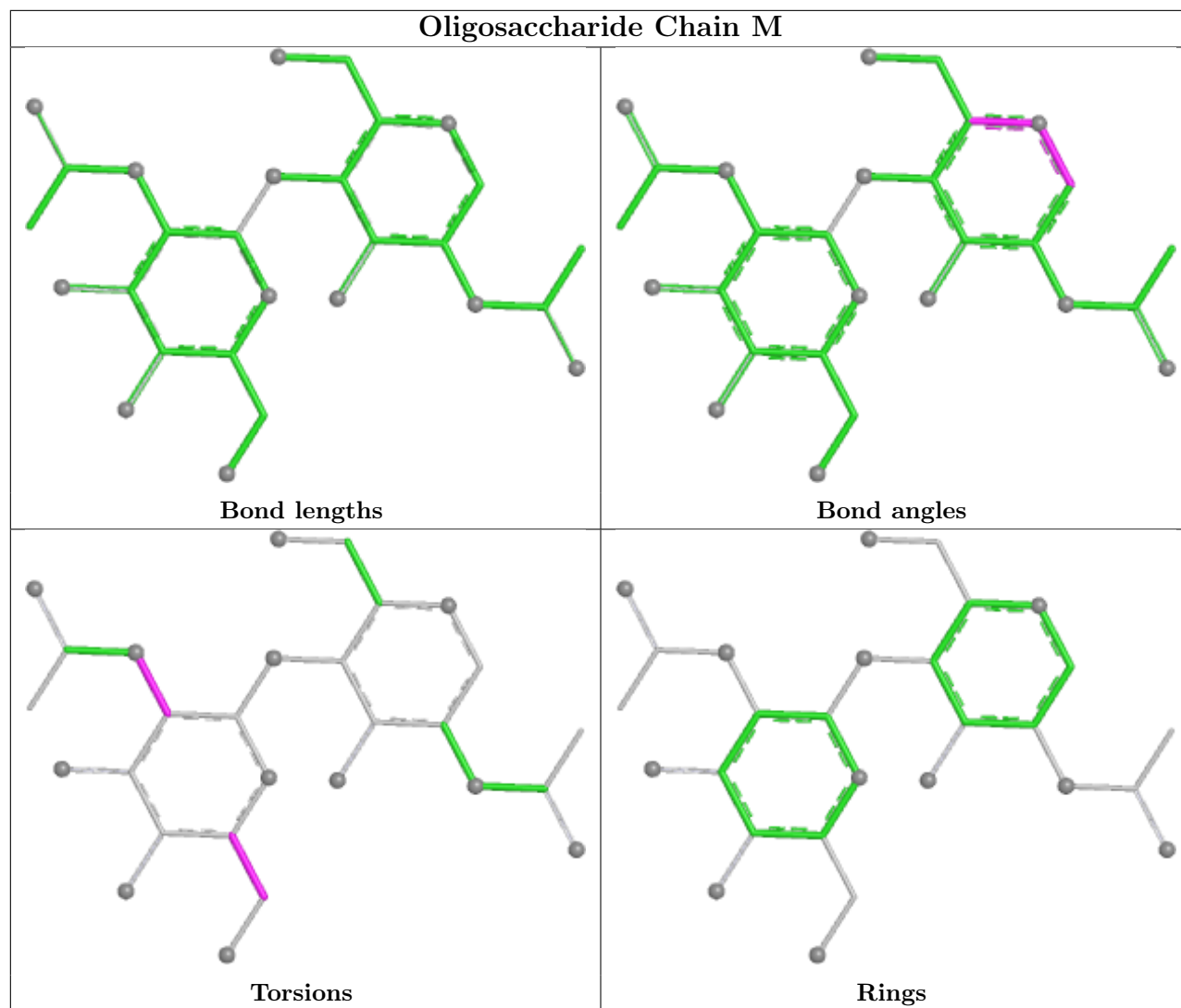
There are no ring outliers.

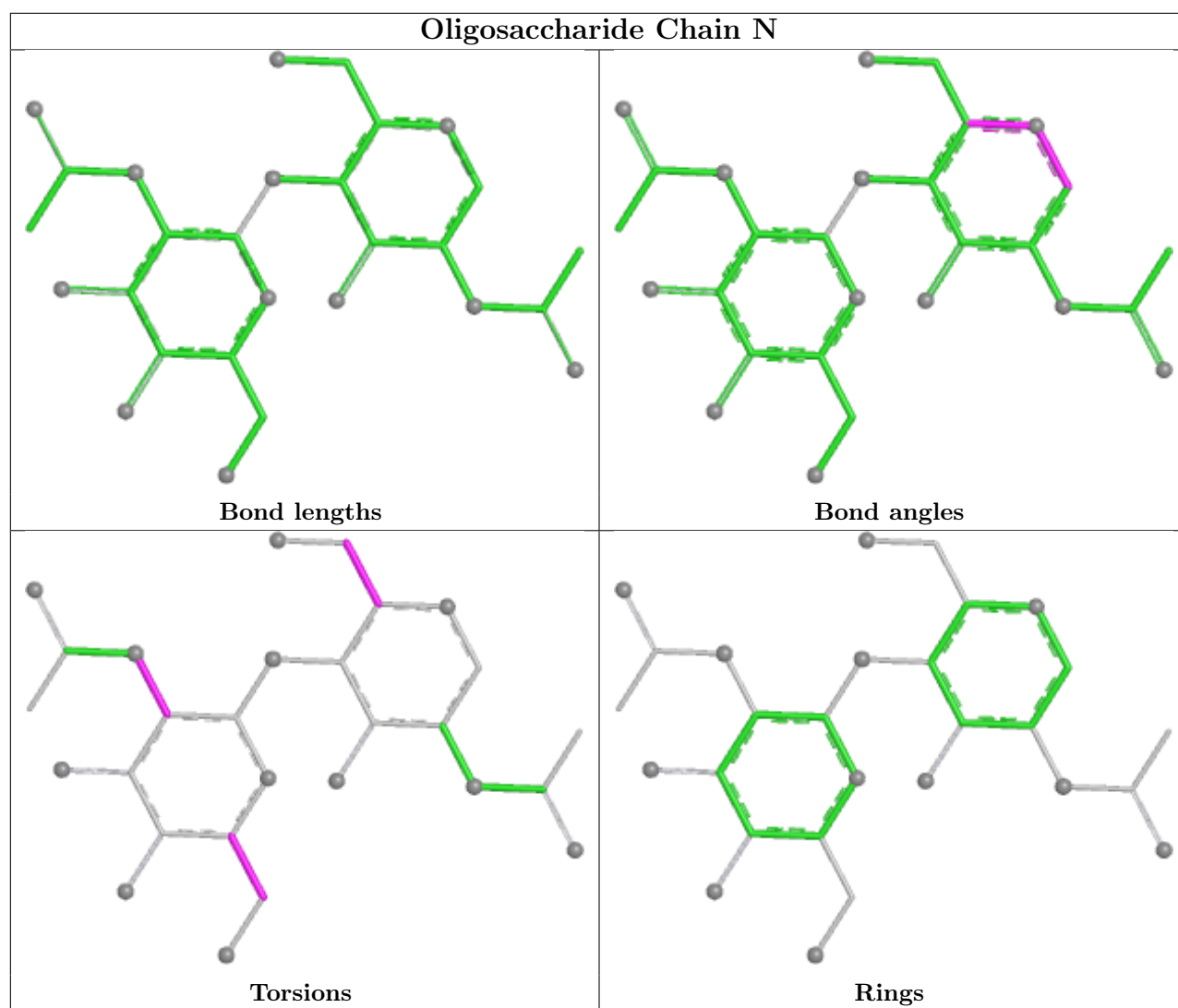
No monomer is involved in short contacts.

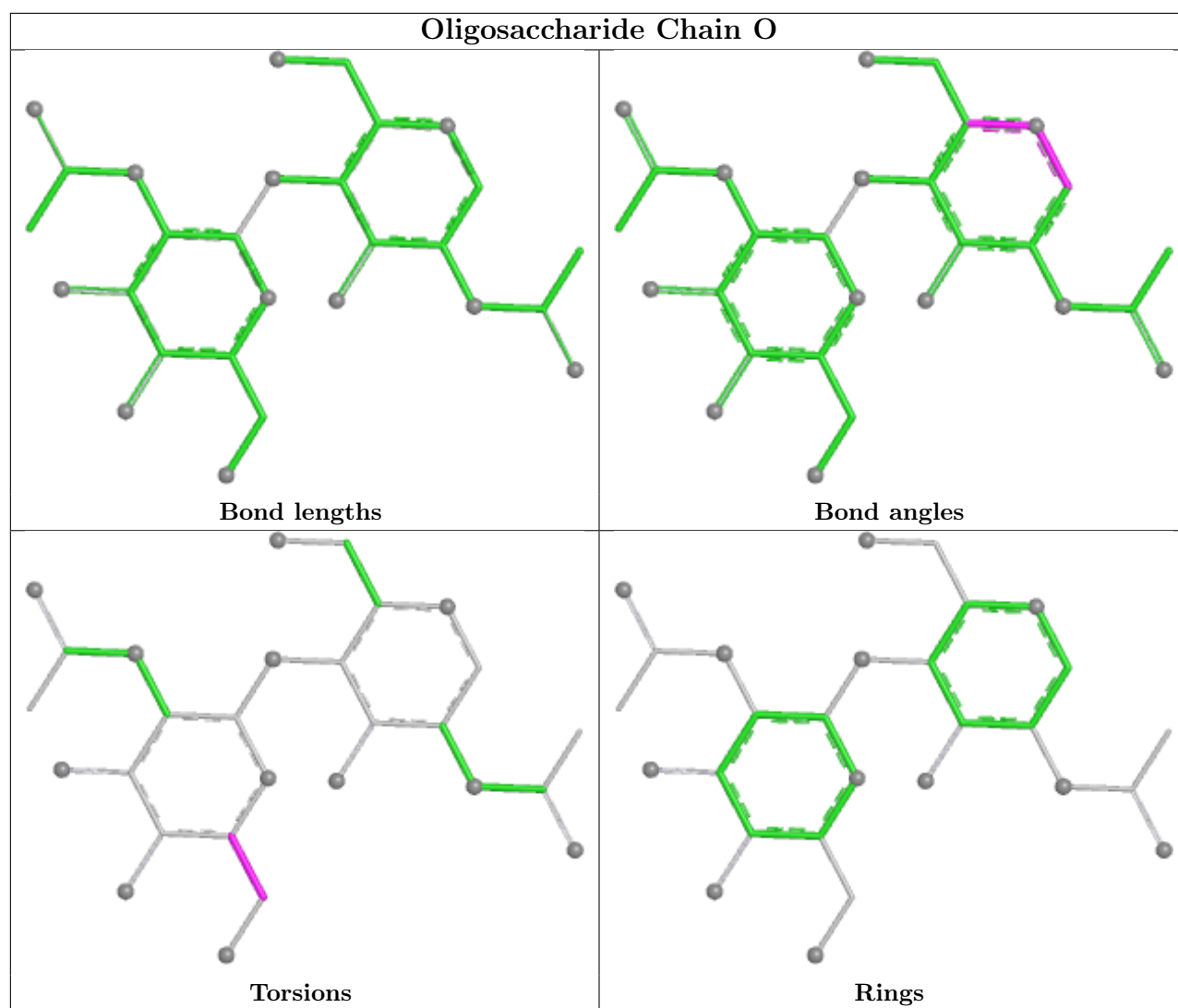
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

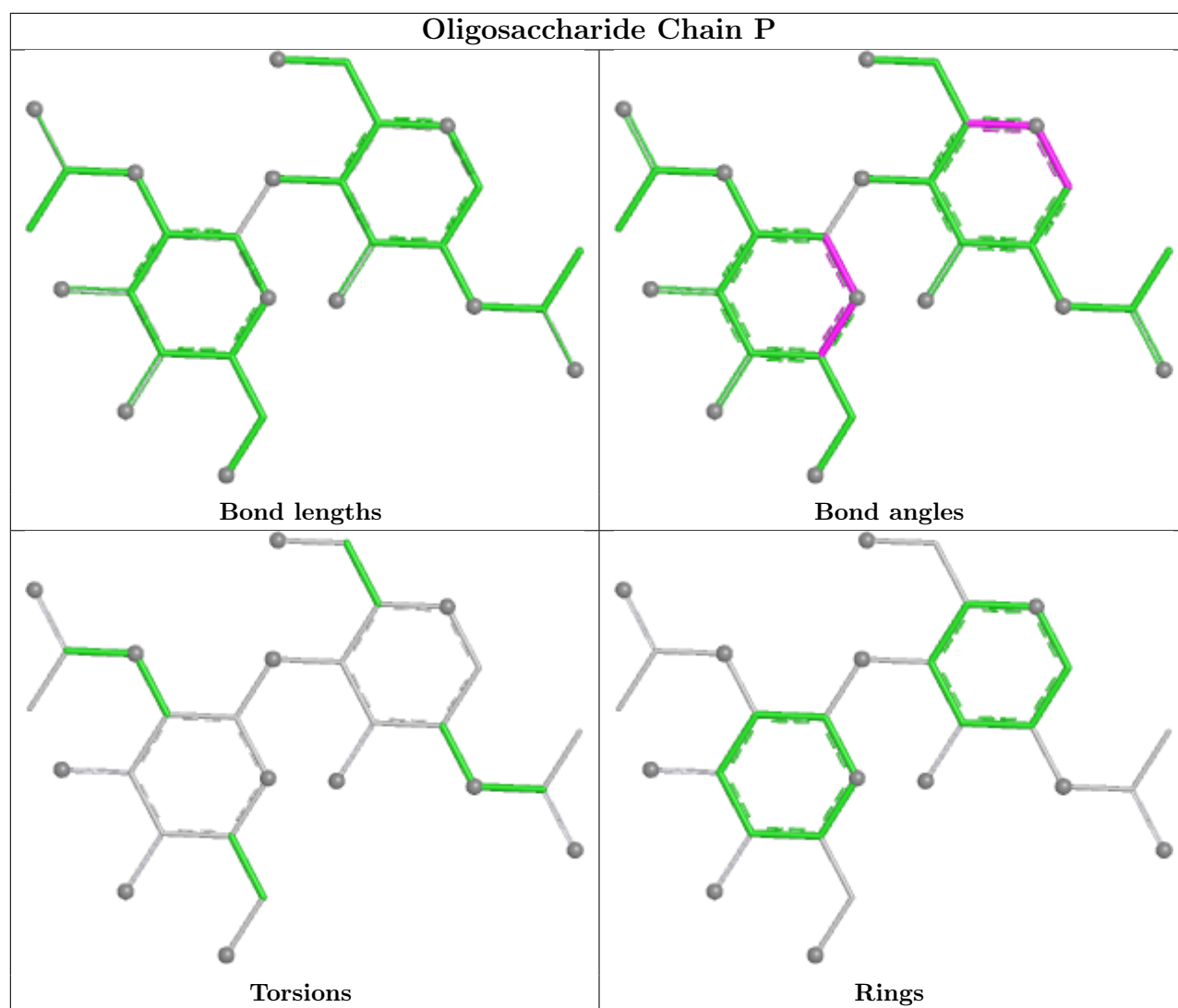


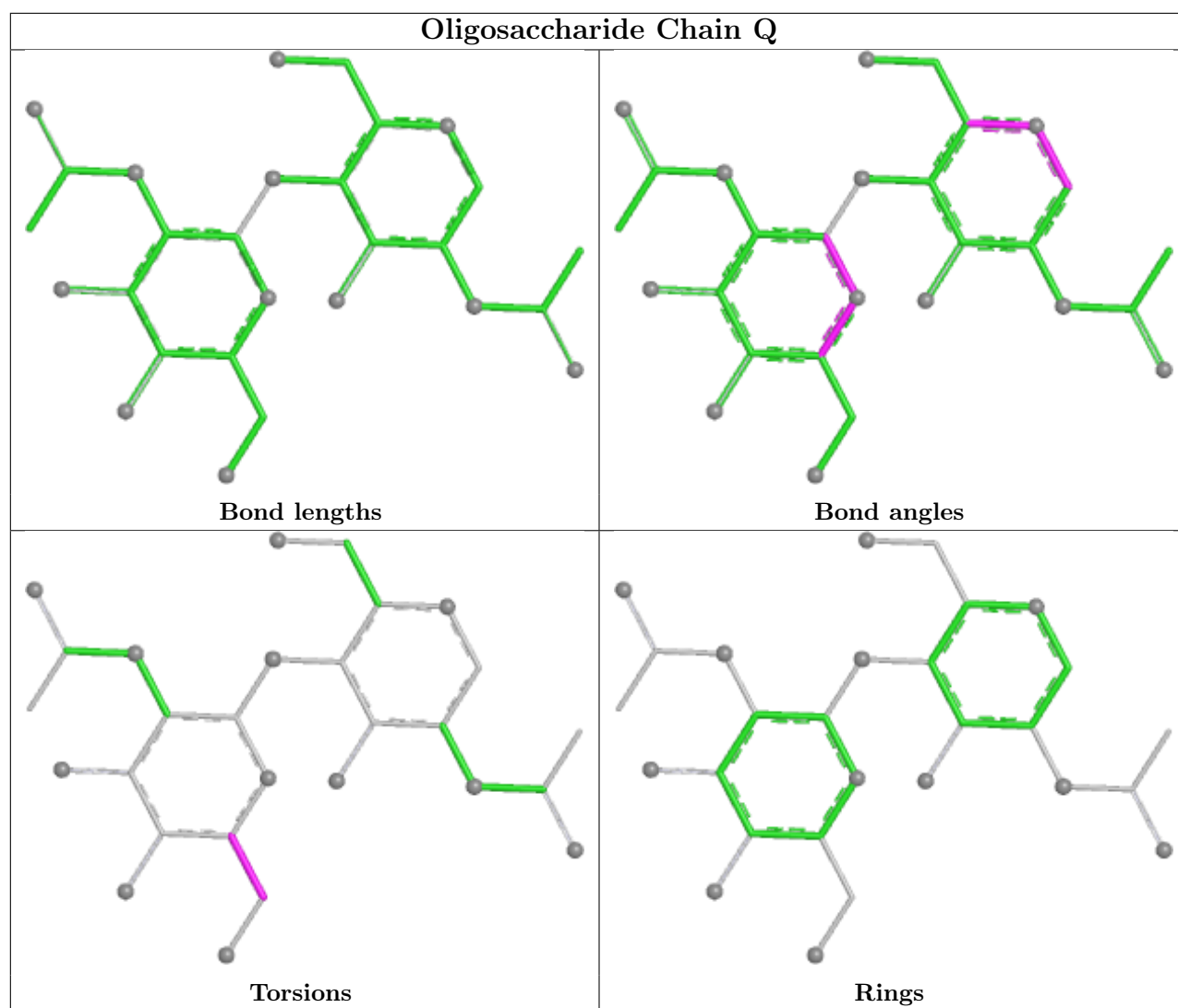


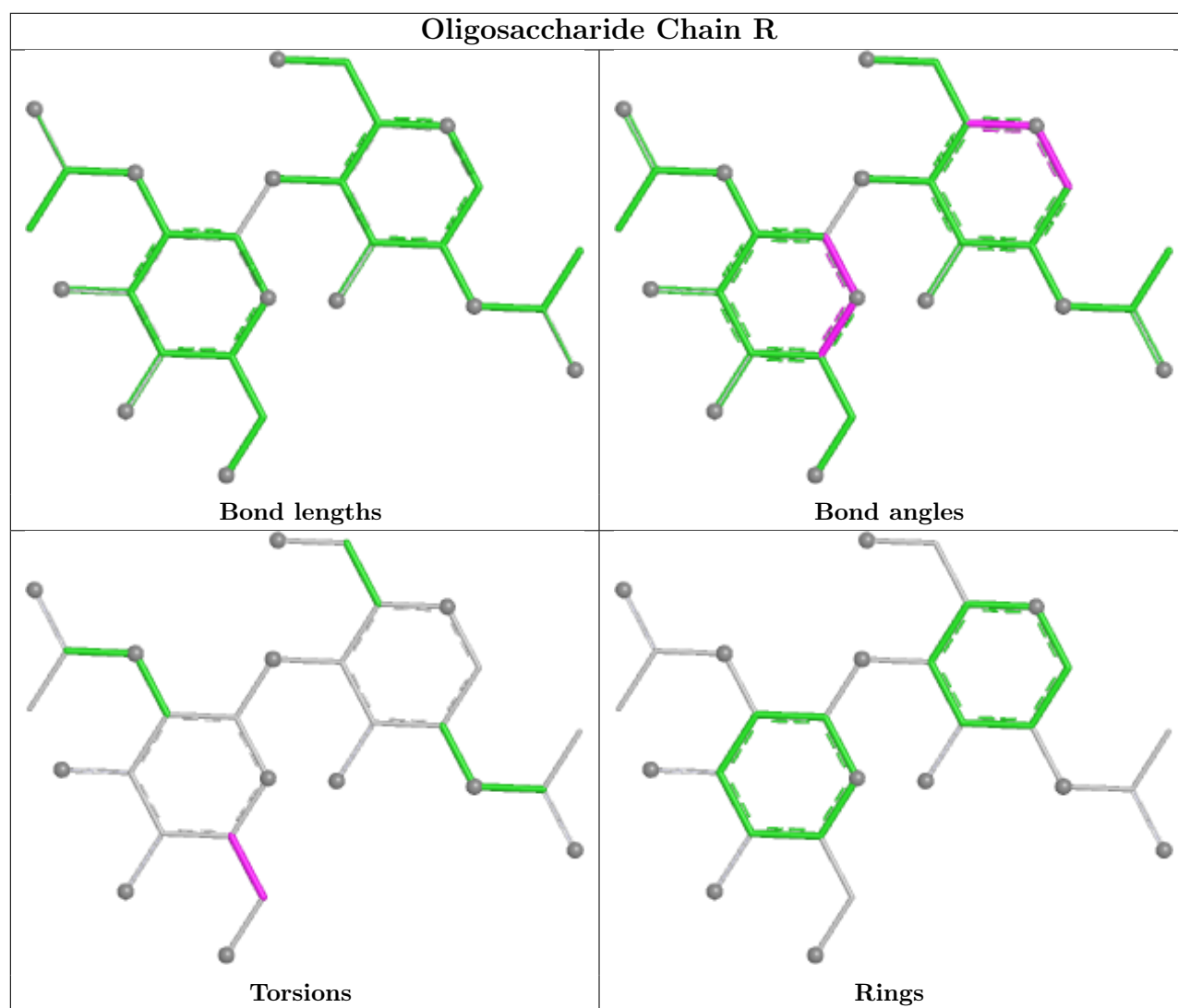


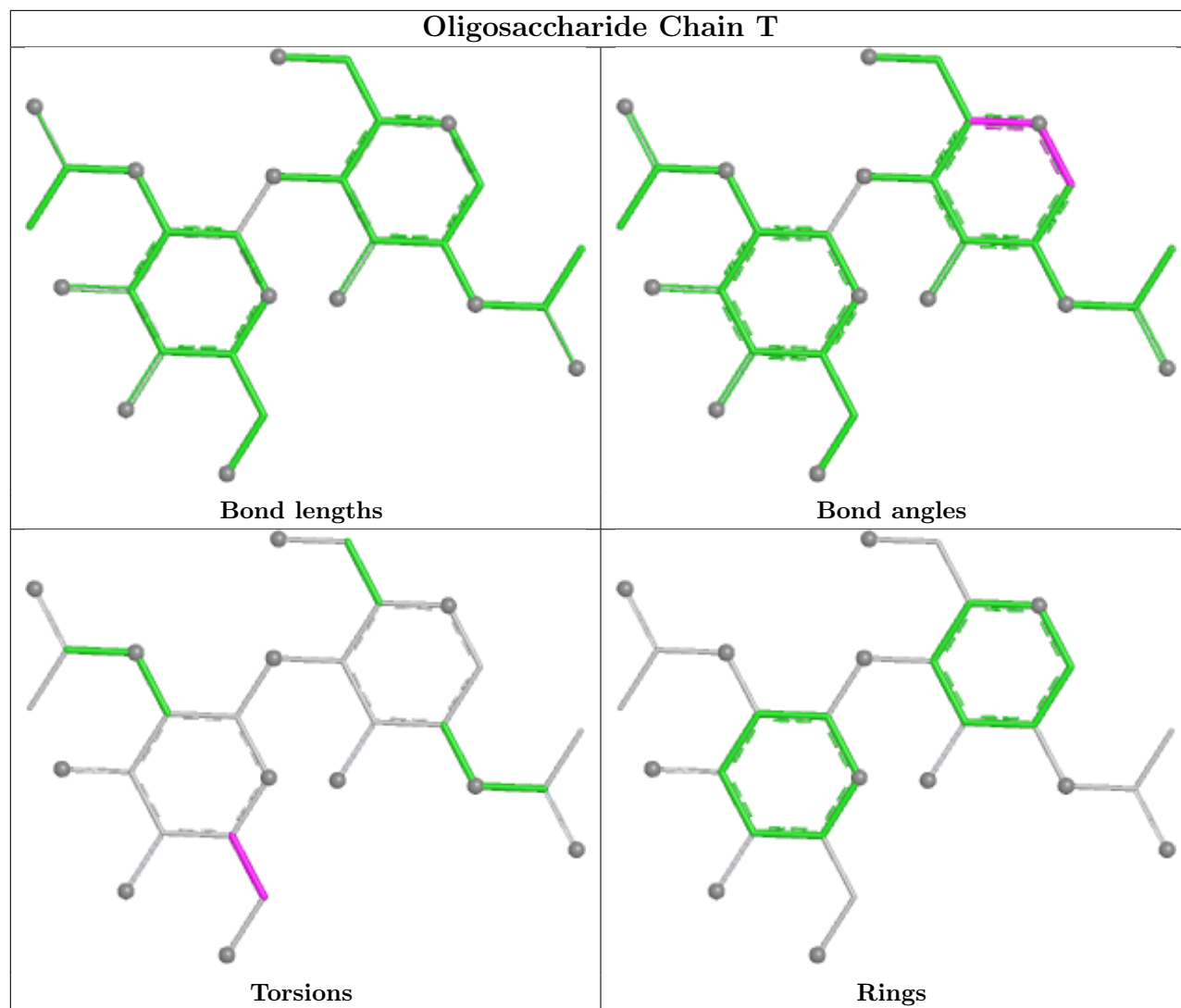


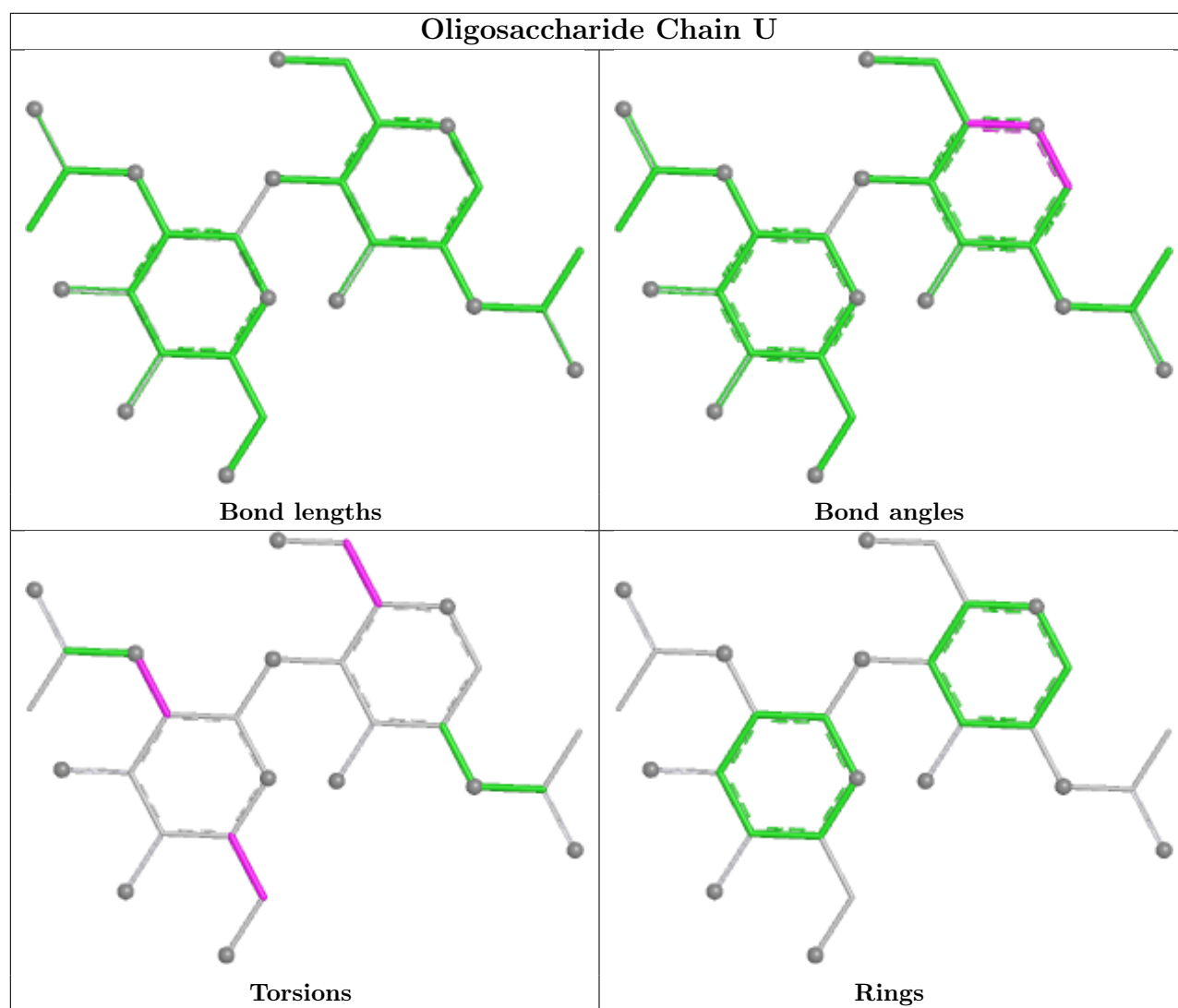


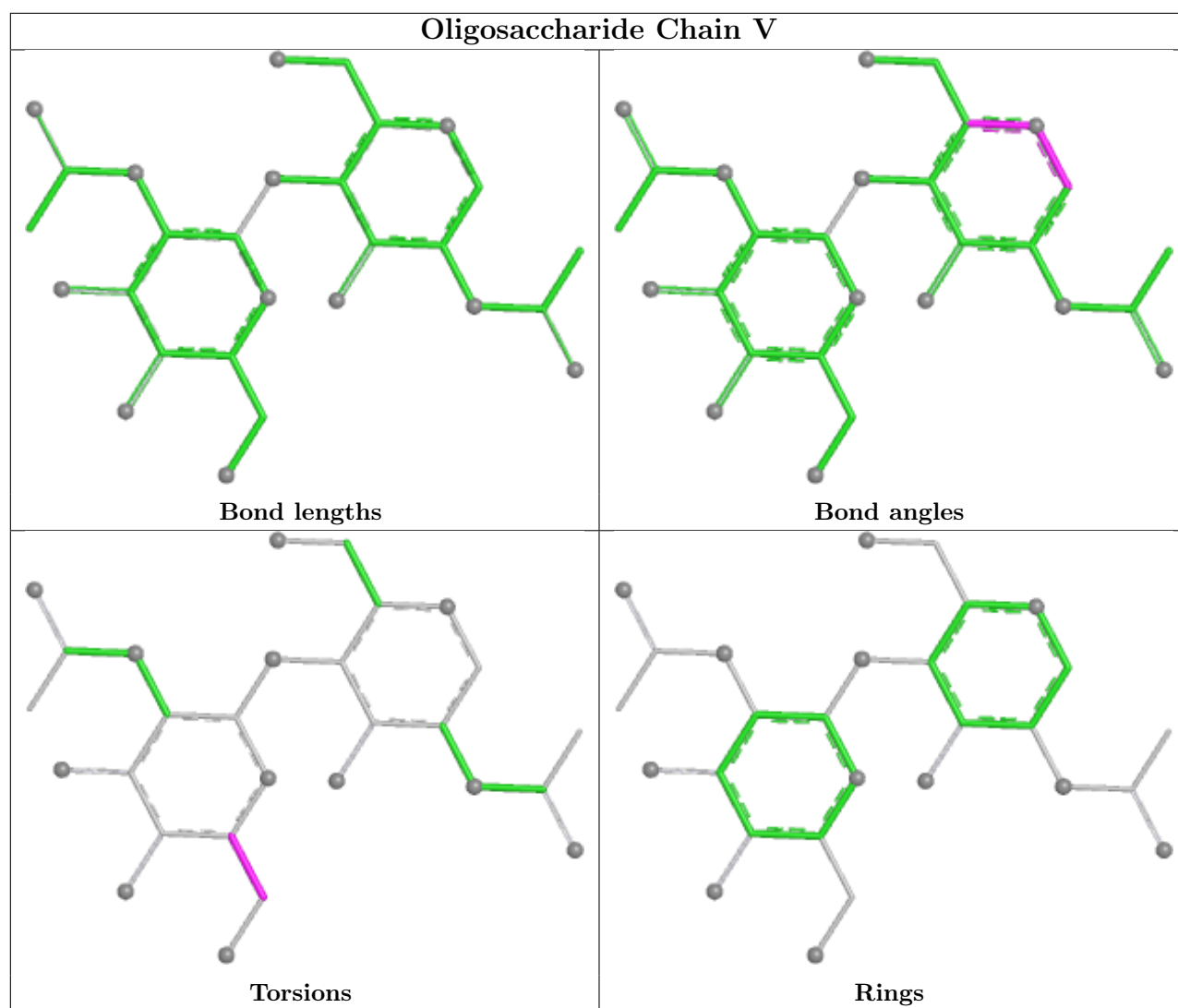


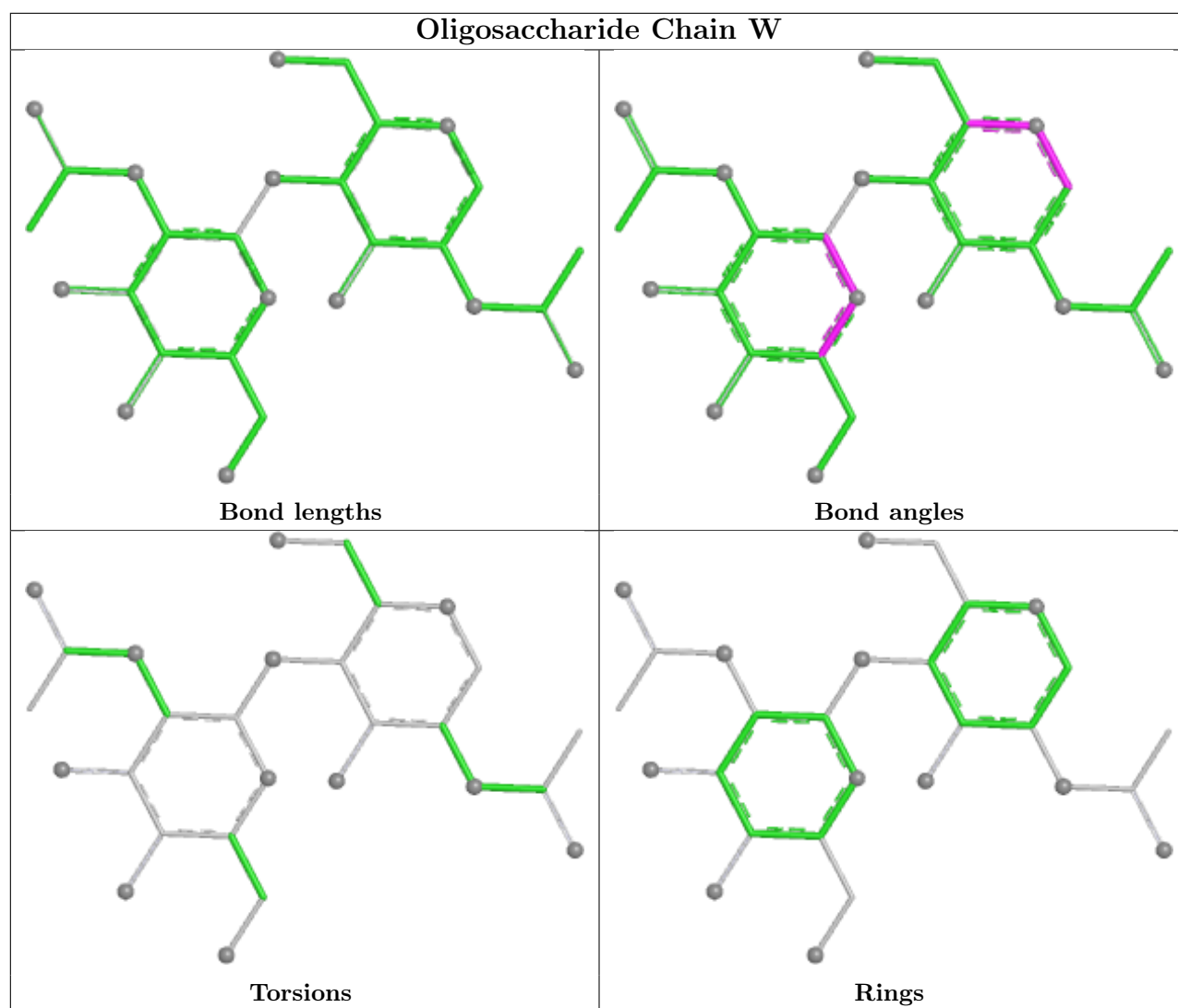


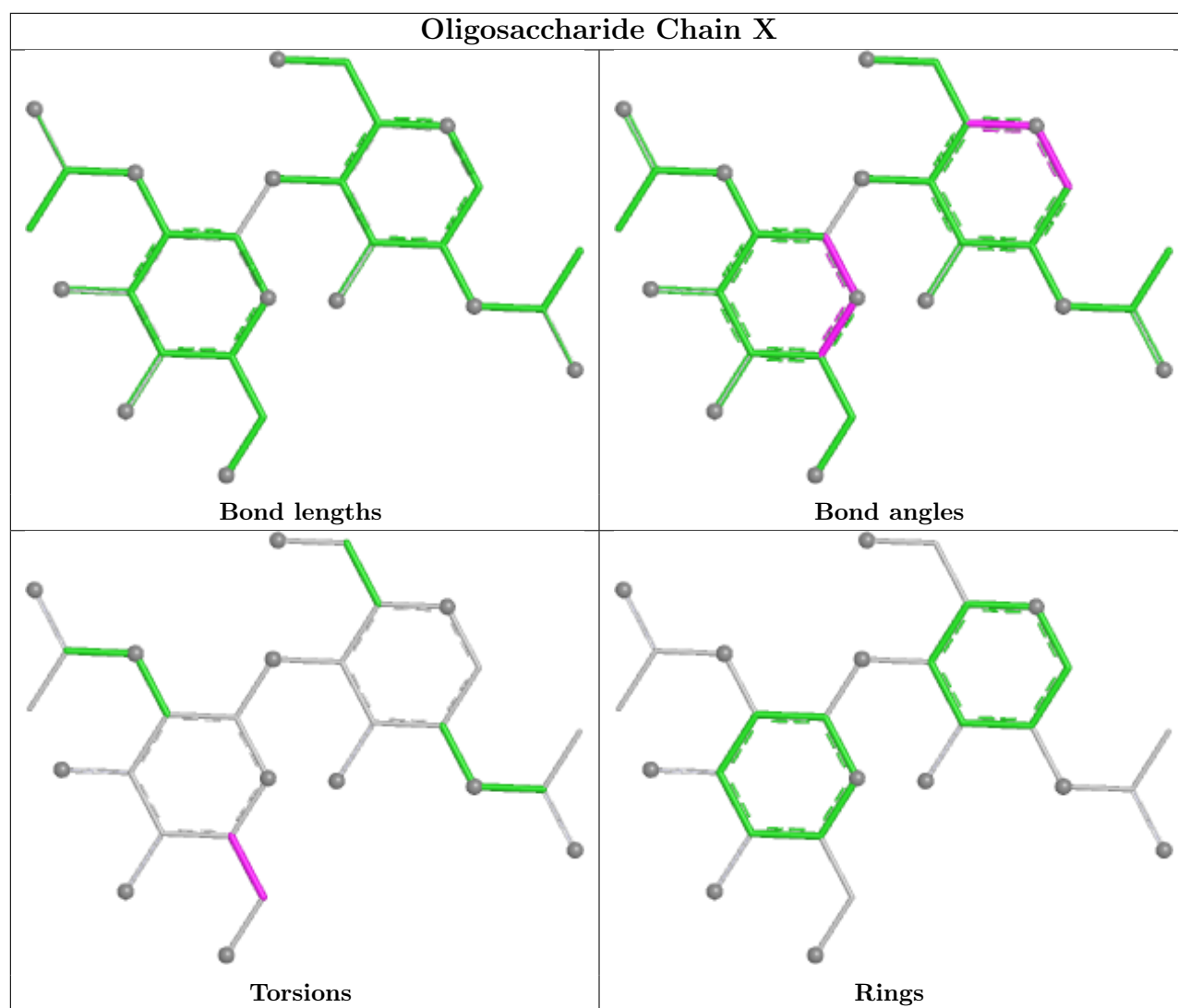


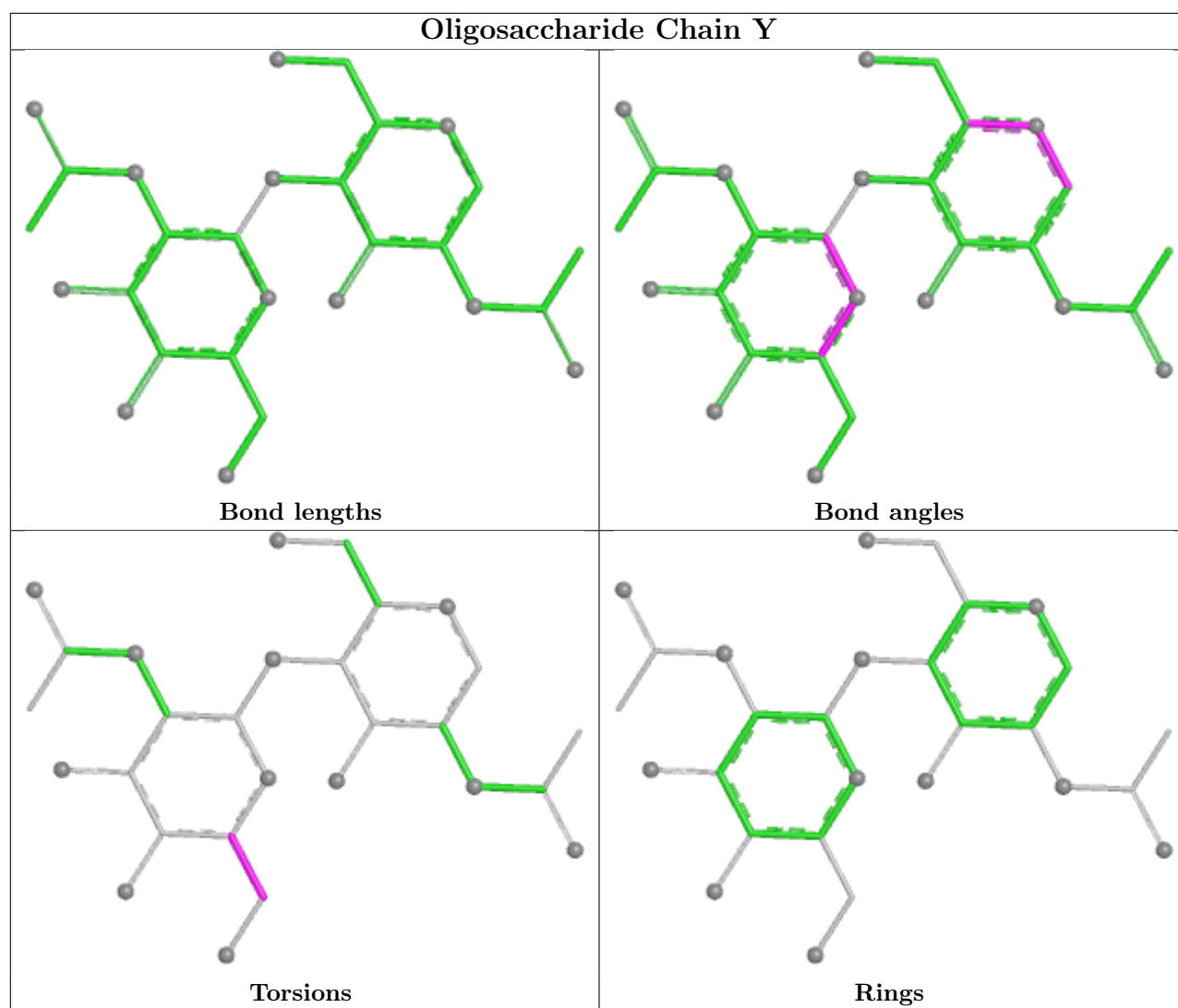


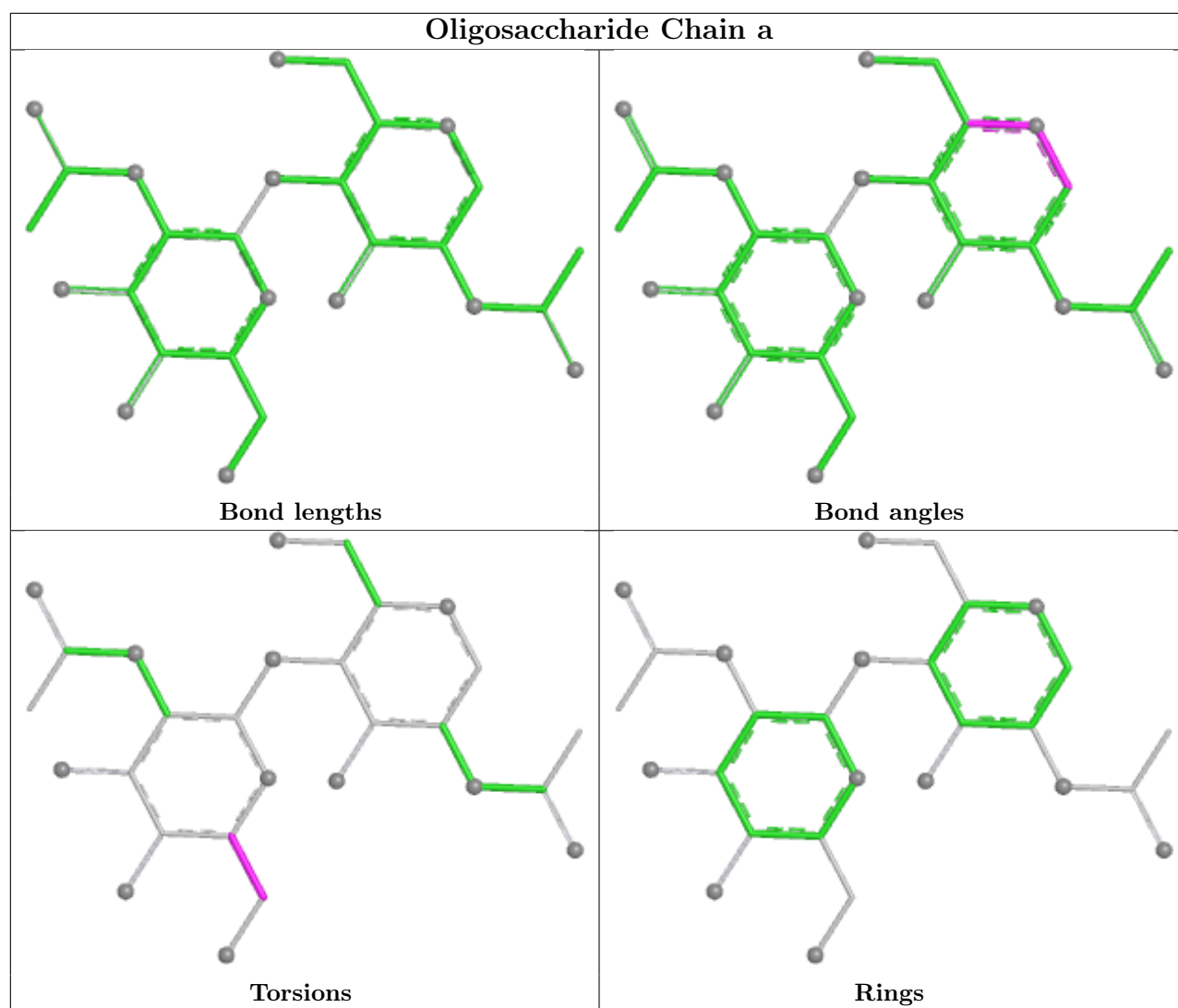


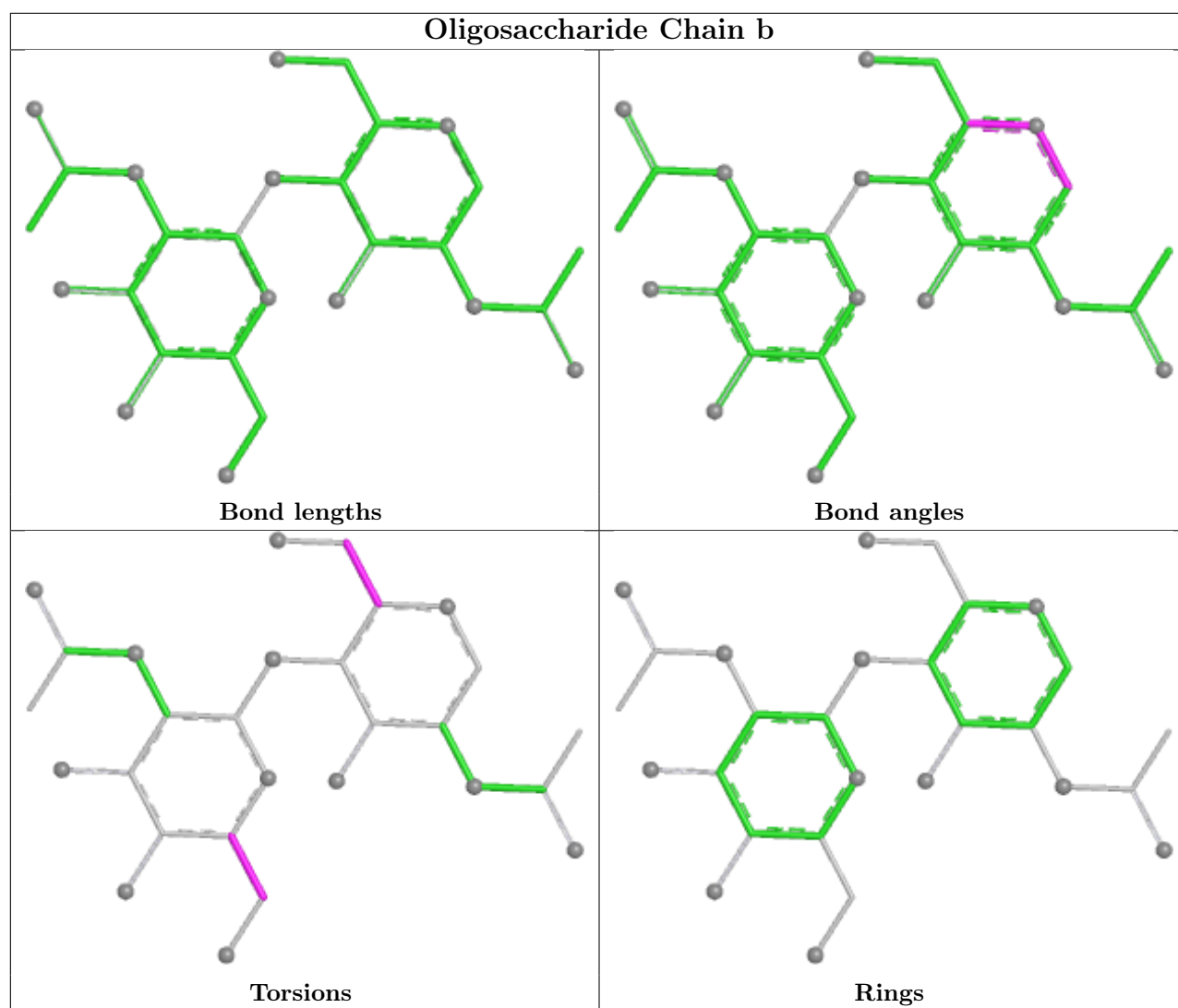


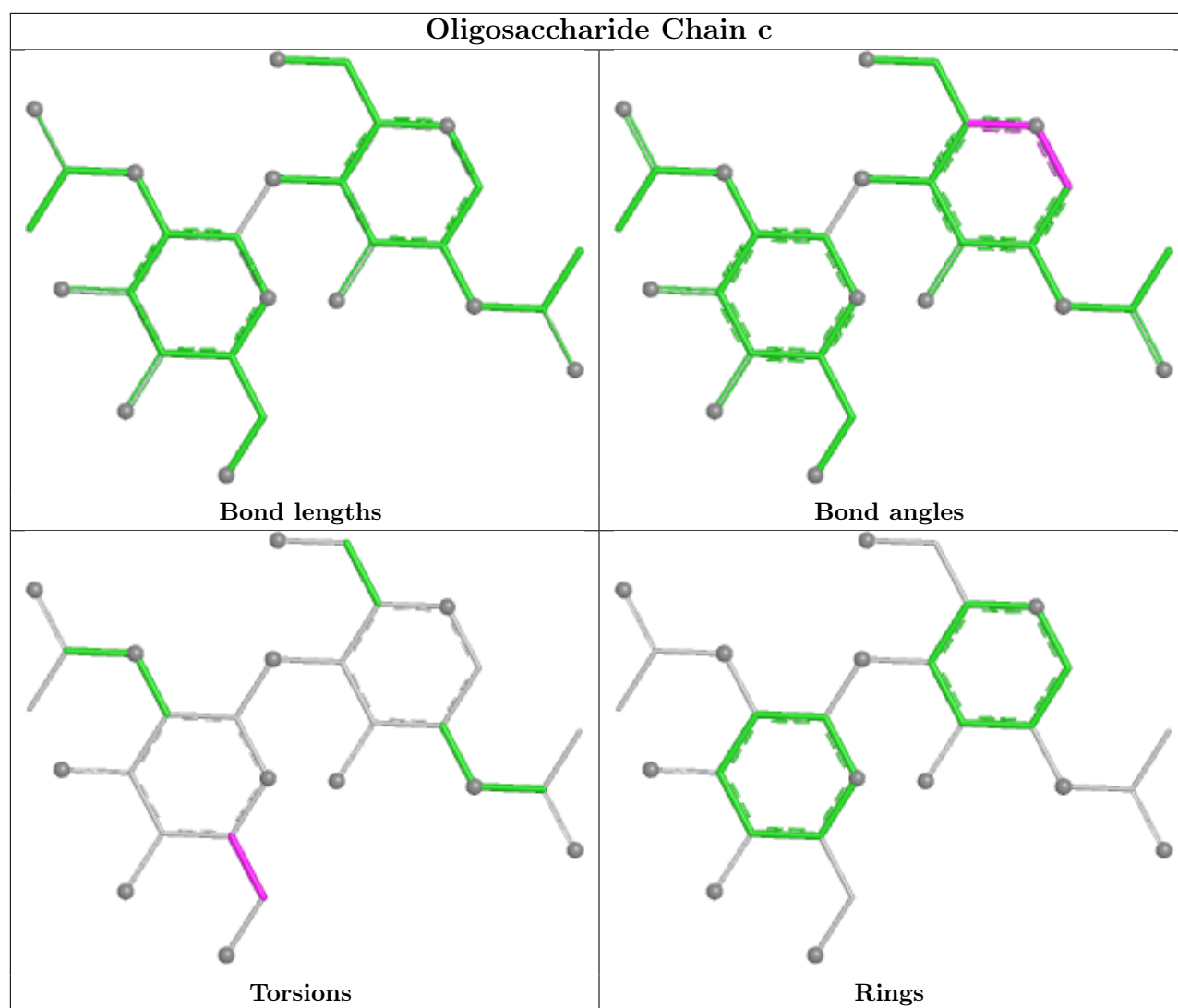


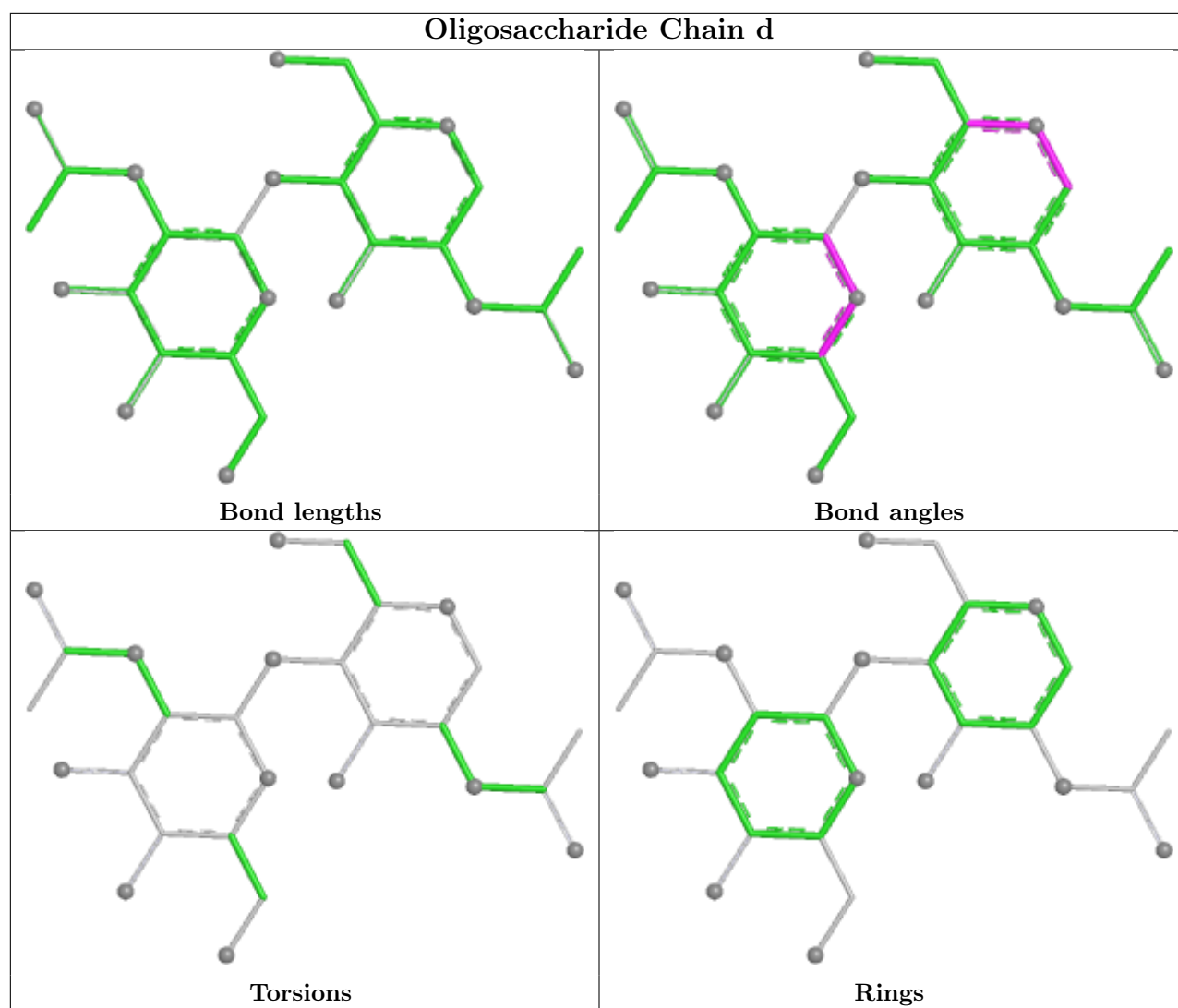


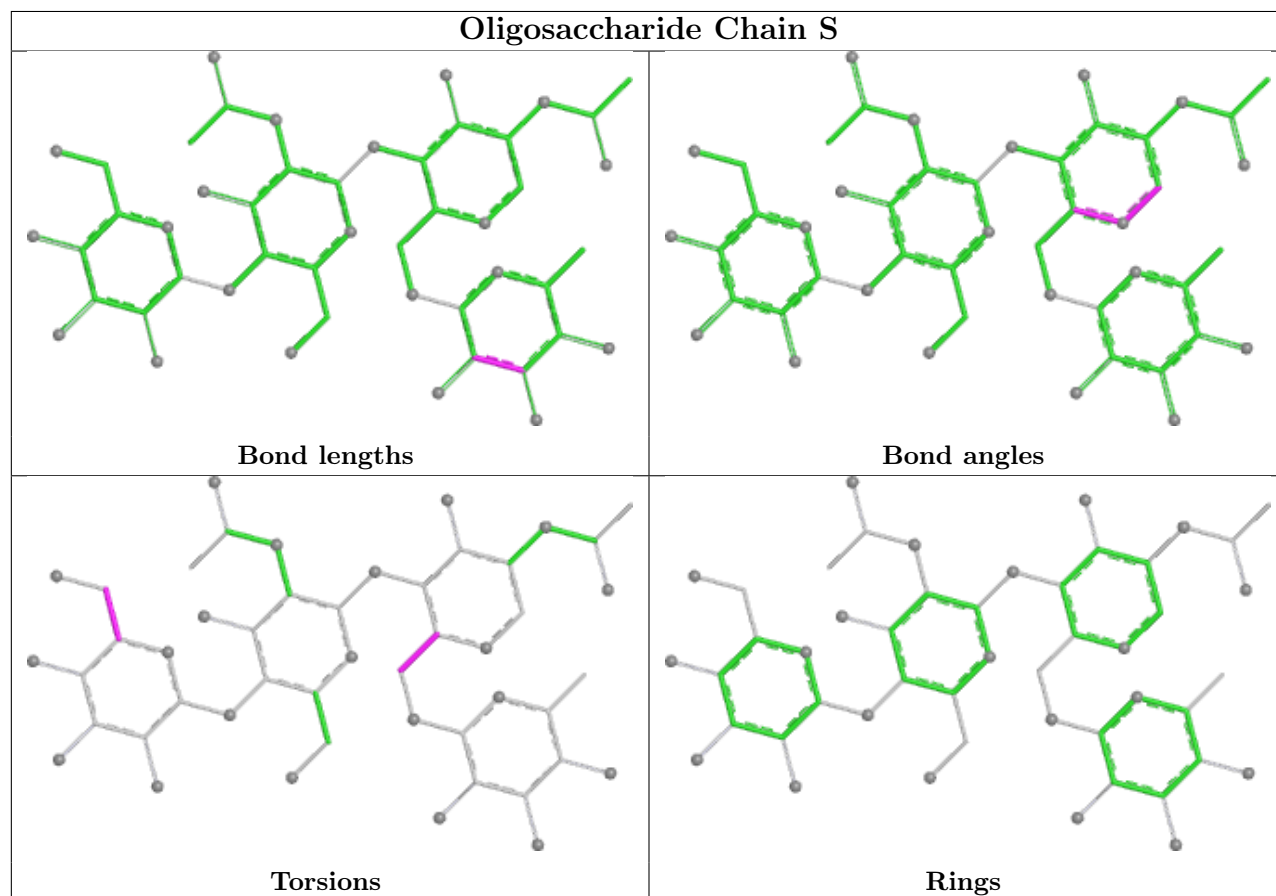
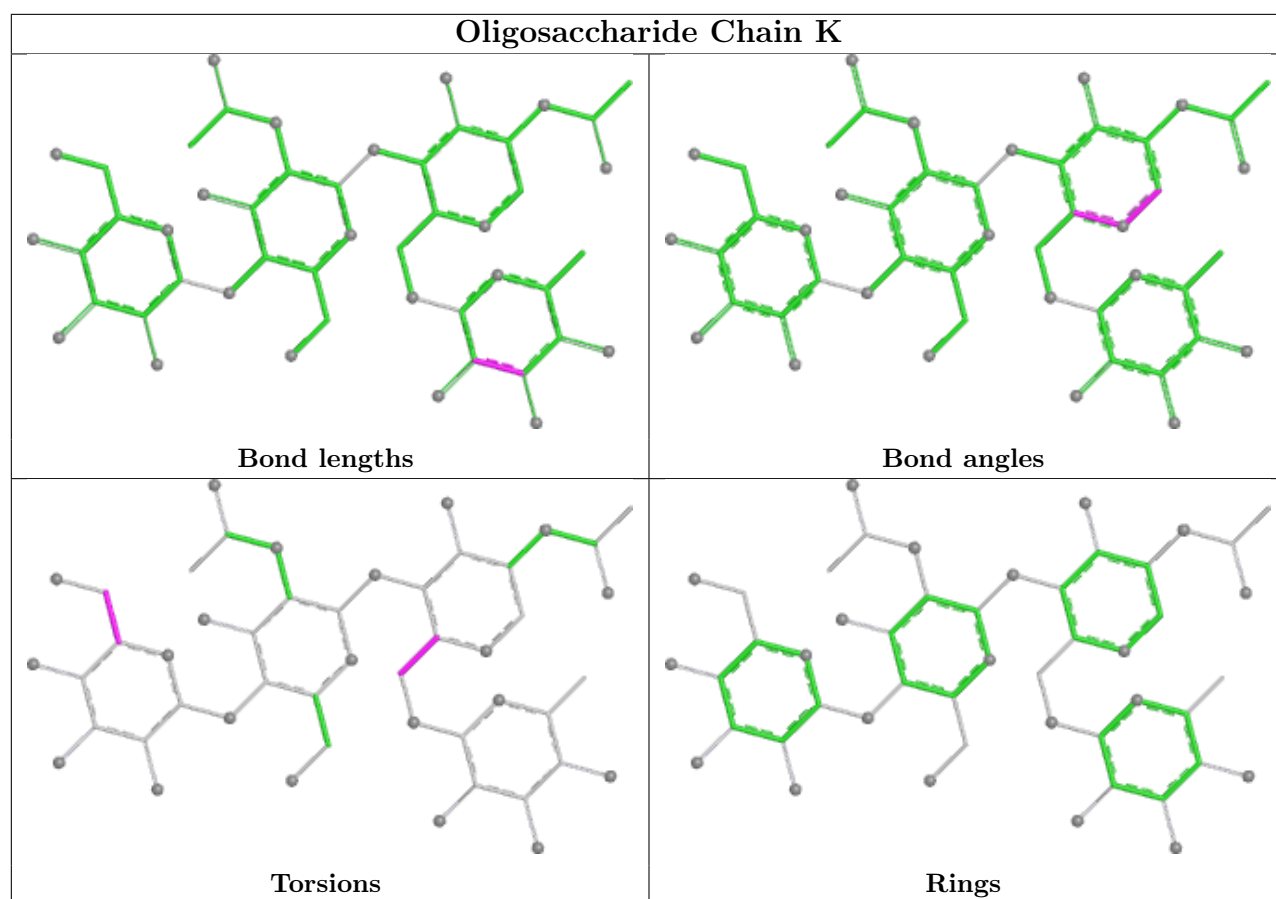


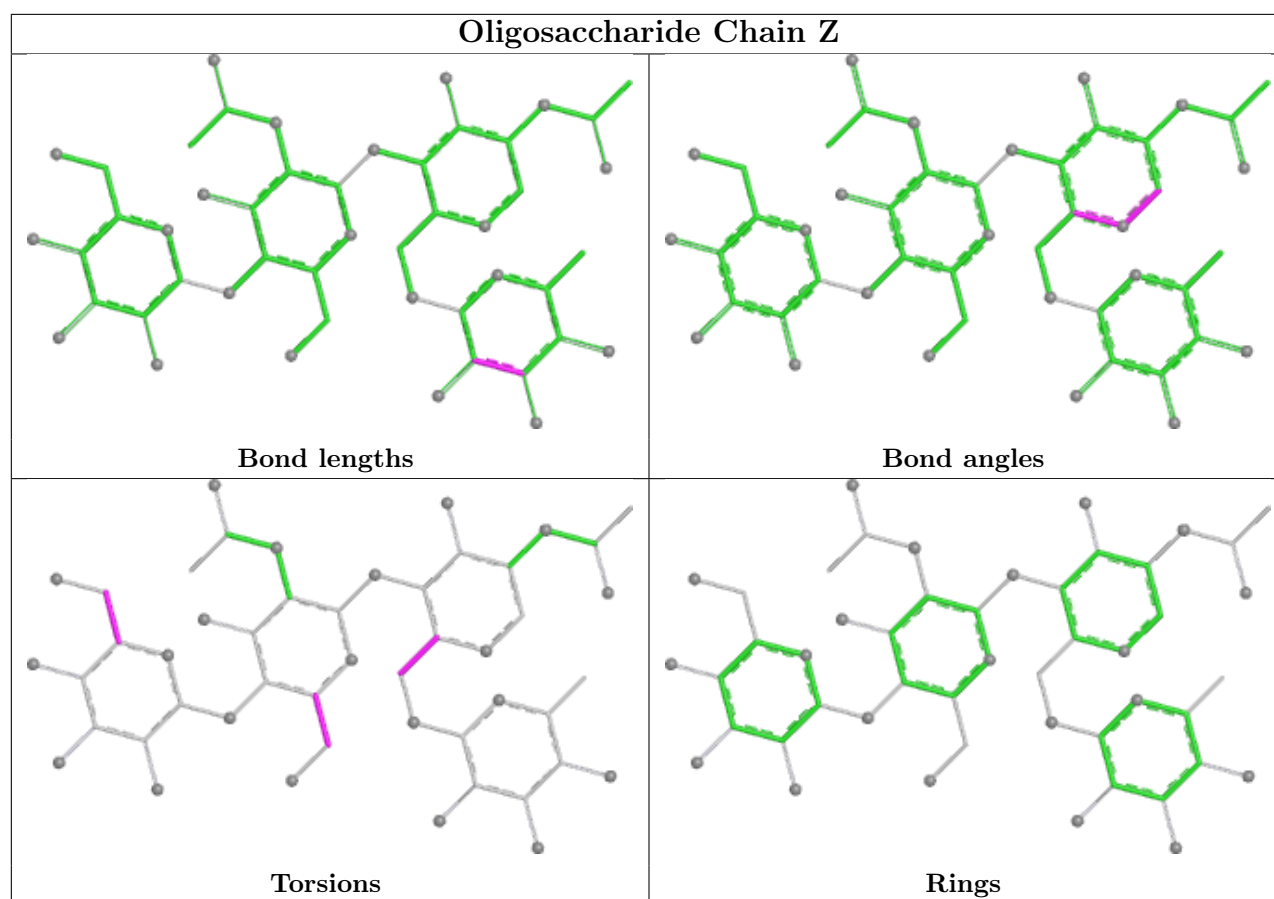












5.6 Ligand geometry [i](#)

30 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	$\# Z > 2$
6	NAG	A	1310	1	14,14,15	0.44	0	17,19,21	0.73	1 (5%)
6	NAG	B	1301	1	14,14,15	0.41	0	17,19,21	0.61	1 (5%)
6	NAG	E	1301	1	14,14,15	0.41	0	17,19,21	0.62	1 (5%)
6	NAG	E	1307	1	14,14,15	0.52	0	17,19,21	0.79	1 (5%)
6	NAG	A	1309	1	14,14,15	0.48	0	17,19,21	0.77	1 (5%)
6	NAG	B	1310	1	14,14,15	0.44	0	17,19,21	0.73	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NAG	A	1307	1	14,14,15	0.50	0	17,19,21	0.80	1 (5%)
6	NAG	B	1303	1	14,14,15	0.56	0	17,19,21	0.92	1 (5%)
6	NAG	A	1308	1	14,14,15	0.51	0	17,19,21	0.85	1 (5%)
6	NAG	A	1303	1	14,14,15	0.56	0	17,19,21	0.92	1 (5%)
6	NAG	A	1302	1	14,14,15	0.48	0	17,19,21	0.80	1 (5%)
6	NAG	E	1304	1	14,14,15	0.48	0	17,19,21	0.83	1 (5%)
6	NAG	E	1305	1	14,14,15	0.52	0	17,19,21	0.58	0
6	NAG	A	1306	1	14,14,15	0.52	0	17,19,21	0.75	1 (5%)
6	NAG	A	1305	1	14,14,15	0.51	0	17,19,21	0.59	0
6	NAG	A	1301	1	14,14,15	0.41	0	17,19,21	0.62	1 (5%)
6	NAG	B	1305	1	14,14,15	0.49	0	17,19,21	0.59	0
6	NAG	B	1304	1	14,14,15	0.47	0	17,19,21	0.84	1 (5%)
6	NAG	A	1304	1	14,14,15	0.48	0	17,19,21	0.83	1 (5%)
6	NAG	E	1309	1	14,14,15	0.51	0	17,19,21	0.77	1 (5%)
6	NAG	B	1309	1	14,14,15	0.47	0	17,19,21	0.77	1 (5%)
6	NAG	E	1306	1	14,14,15	0.53	0	17,19,21	0.74	1 (5%)
6	NAG	E	1310	1	14,14,15	0.41	0	17,19,21	0.75	1 (5%)
6	NAG	B	1307	1	14,14,15	0.50	0	17,19,21	0.79	1 (5%)
6	NAG	B	1306	1	14,14,15	0.52	0	17,19,21	0.75	1 (5%)
6	NAG	B	1308	1	14,14,15	0.51	0	17,19,21	0.85	1 (5%)
6	NAG	E	1303	1	14,14,15	0.57	0	17,19,21	0.91	1 (5%)
6	NAG	E	1302	1	14,14,15	0.49	0	17,19,21	0.79	1 (5%)
6	NAG	E	1308	1	14,14,15	0.50	0	17,19,21	0.86	1 (5%)
6	NAG	B	1302	1	14,14,15	0.48	0	17,19,21	0.80	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
6	NAG	A	1310	1	-	2/6/23/26	0/1/1/1
6	NAG	B	1301	1	-	0/6/23/26	0/1/1/1
6	NAG	E	1301	1	-	0/6/23/26	0/1/1/1
6	NAG	E	1307	1	-	2/6/23/26	0/1/1/1
6	NAG	A	1309	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1310	1	-	2/6/23/26	0/1/1/1

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

There are no bond length outliers.

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	1303	NAG	C1-O5-C5	3.55	116.94	112.19
6	A	1303	NAG	C1-O5-C5	3.55	116.94	112.19
6	E	1303	NAG	C1-O5-C5	3.52	116.91	112.19
6	E	1308	NAG	C1-O5-C5	3.33	116.65	112.19
6	B	1308	NAG	C1-O5-C5	3.29	116.60	112.19

There are no chirality outliers.

5 of 27 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	E	1303	NAG	C4-C5-C6-O6
6	A	1303	NAG	C4-C5-C6-O6
6	B	1303	NAG	C4-C5-C6-O6
6	E	1310	NAG	C4-C5-C6-O6
6	E	1303	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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.

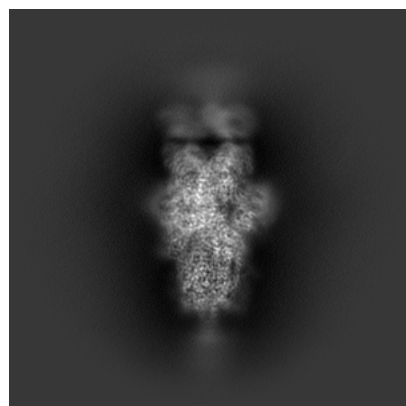
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27518. These allow visual inspection of the internal detail of the map and identification of artifacts.

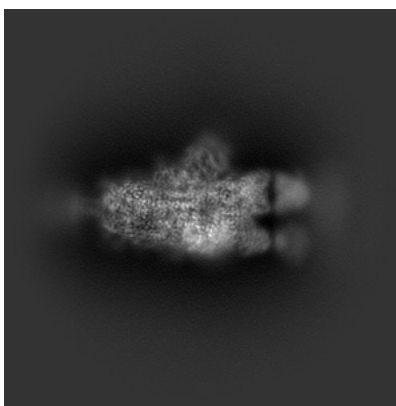
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

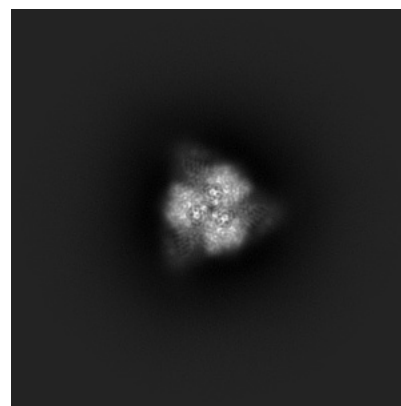
6.1.1 Primary map



X

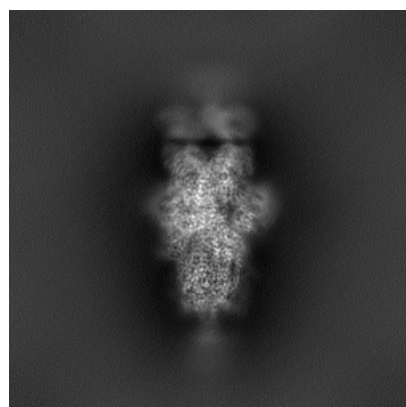


Y

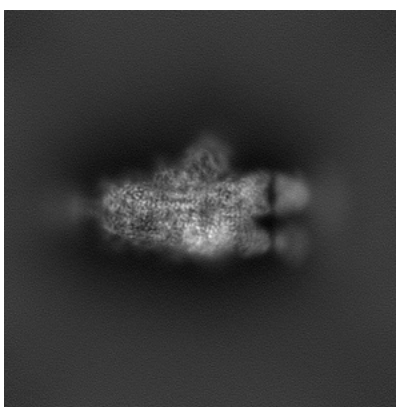


Z

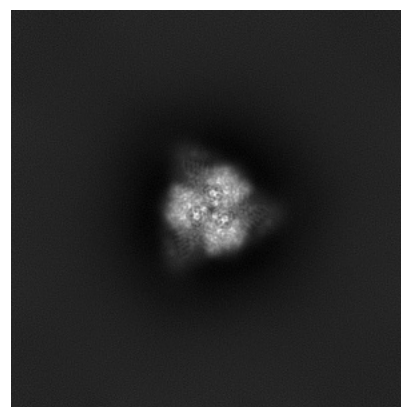
6.1.2 Raw map



X



Y

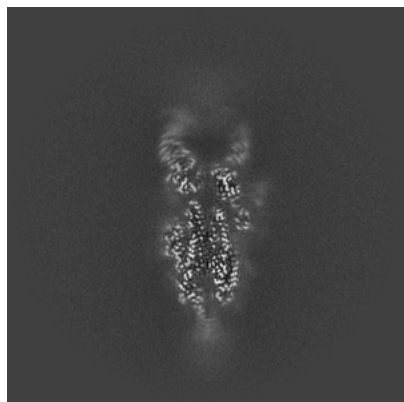


Z

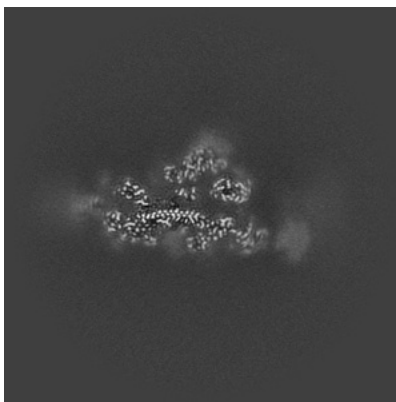
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

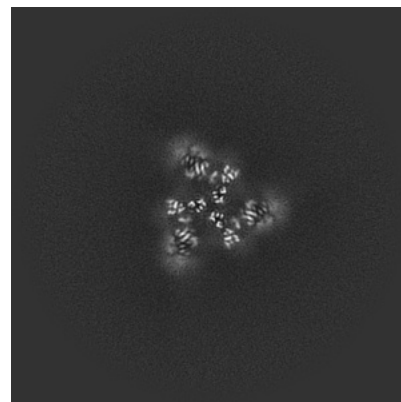
6.2.1 Primary map



X Index: 200

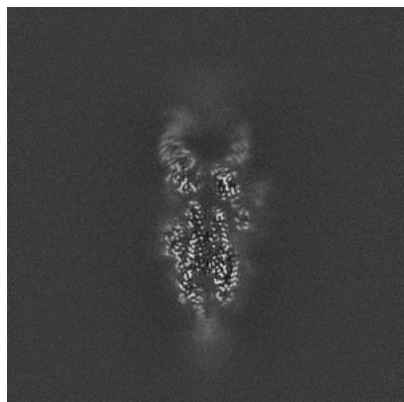


Y Index: 200

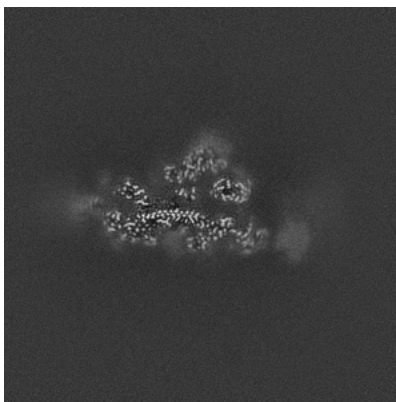


Z Index: 200

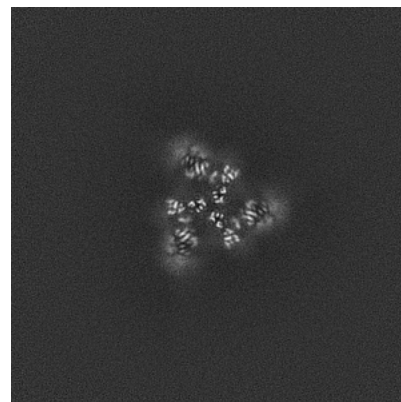
6.2.2 Raw map



X Index: 200



Y Index: 200

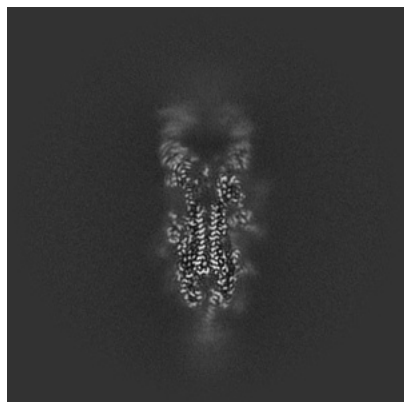


Z Index: 200

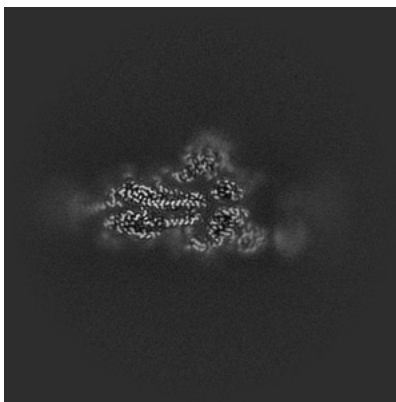
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

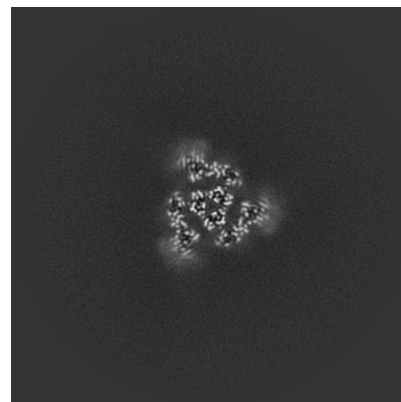
6.3.1 Primary map



X Index: 205

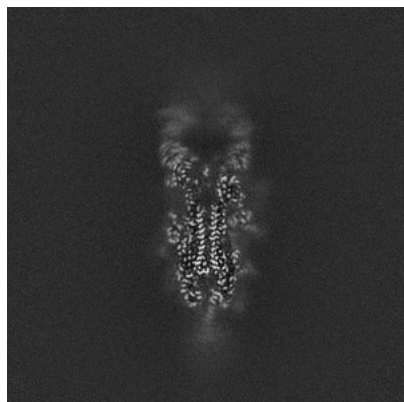


Y Index: 193

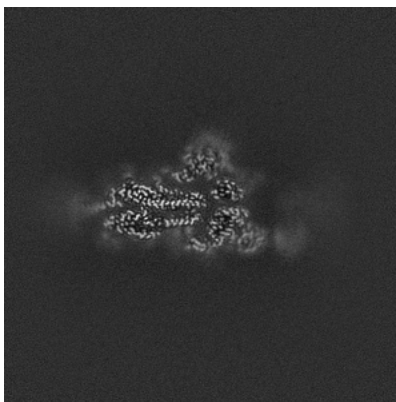


Z Index: 193

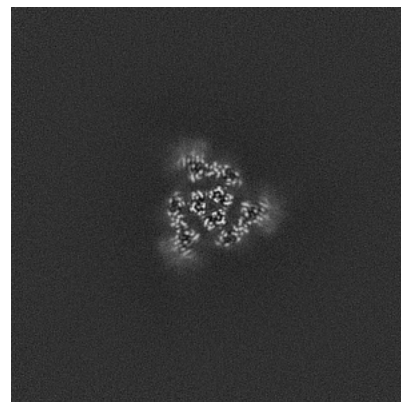
6.3.2 Raw map



X Index: 205



Y Index: 193

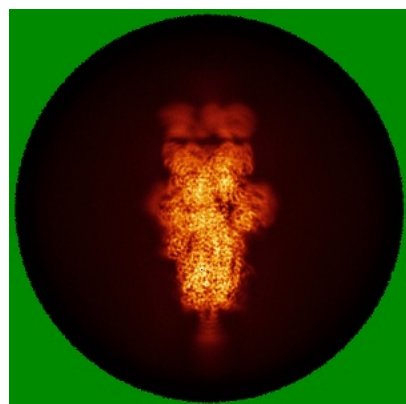


Z Index: 193

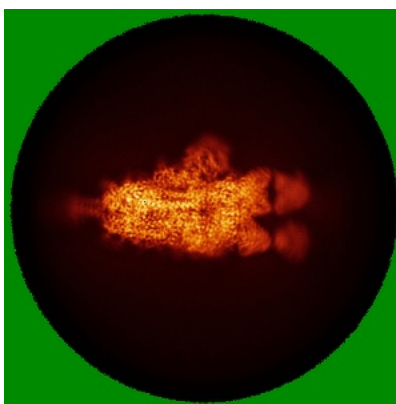
The images above show the largest variance slices of the map in three orthogonal directions.

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

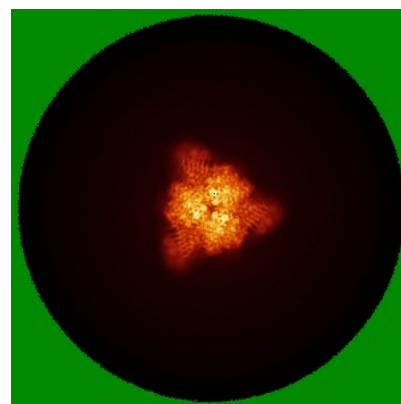
6.4.1 Primary map



X

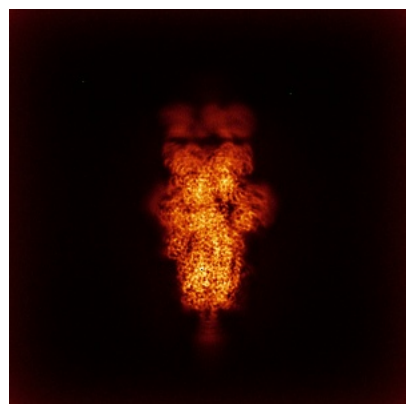


Y

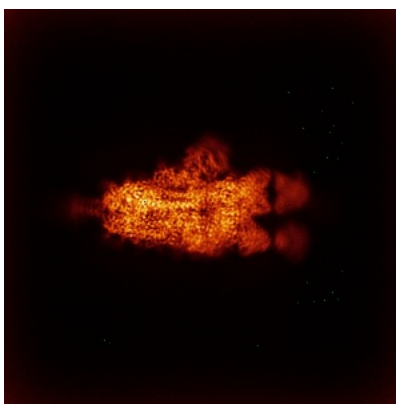


Z

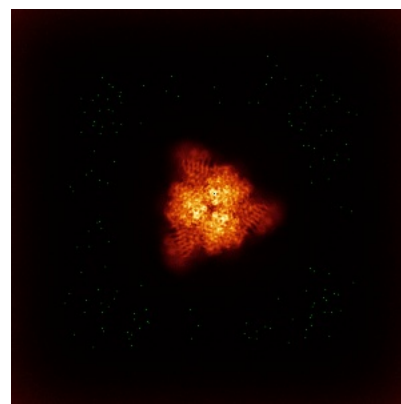
6.4.2 Raw map



X



Y

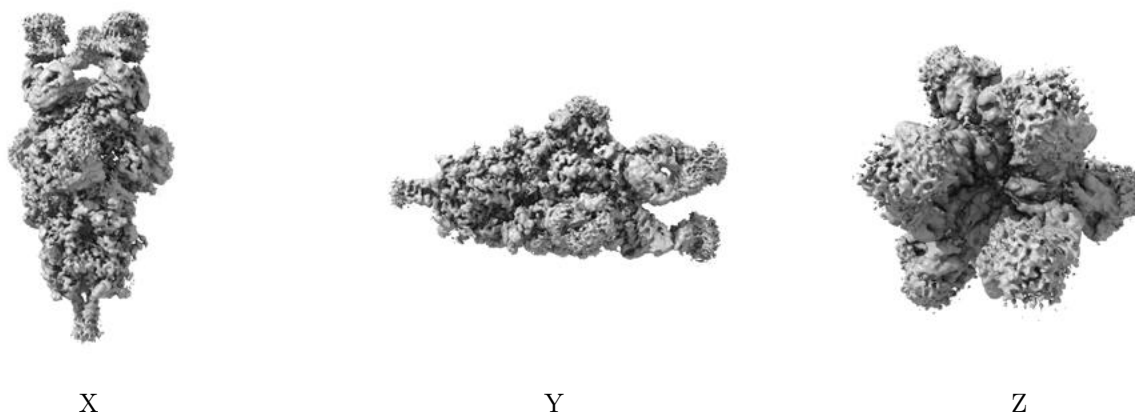


Z

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

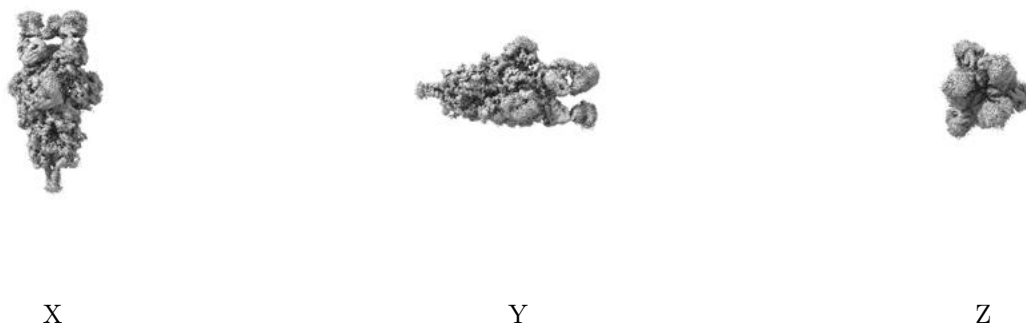
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.236. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

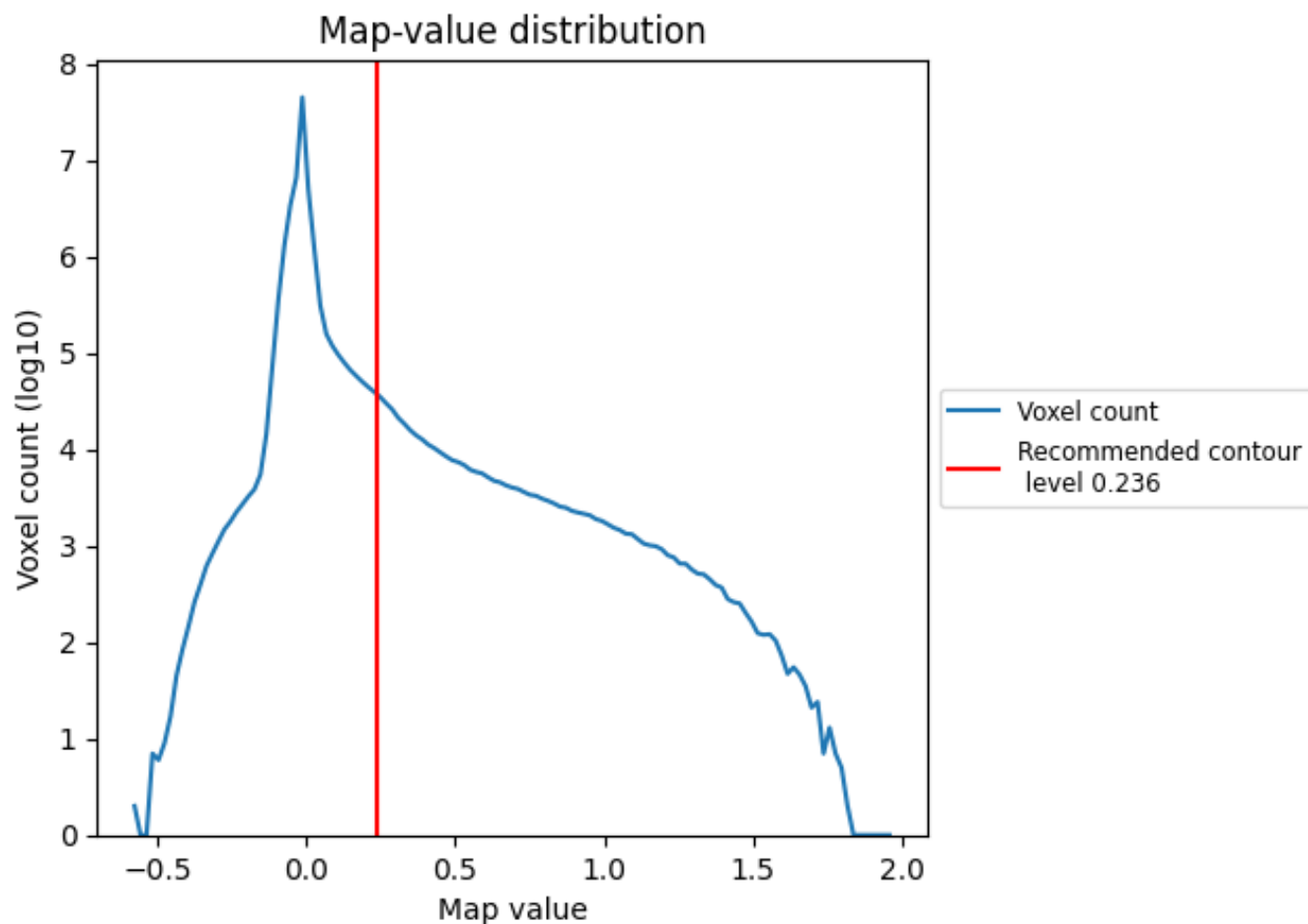
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

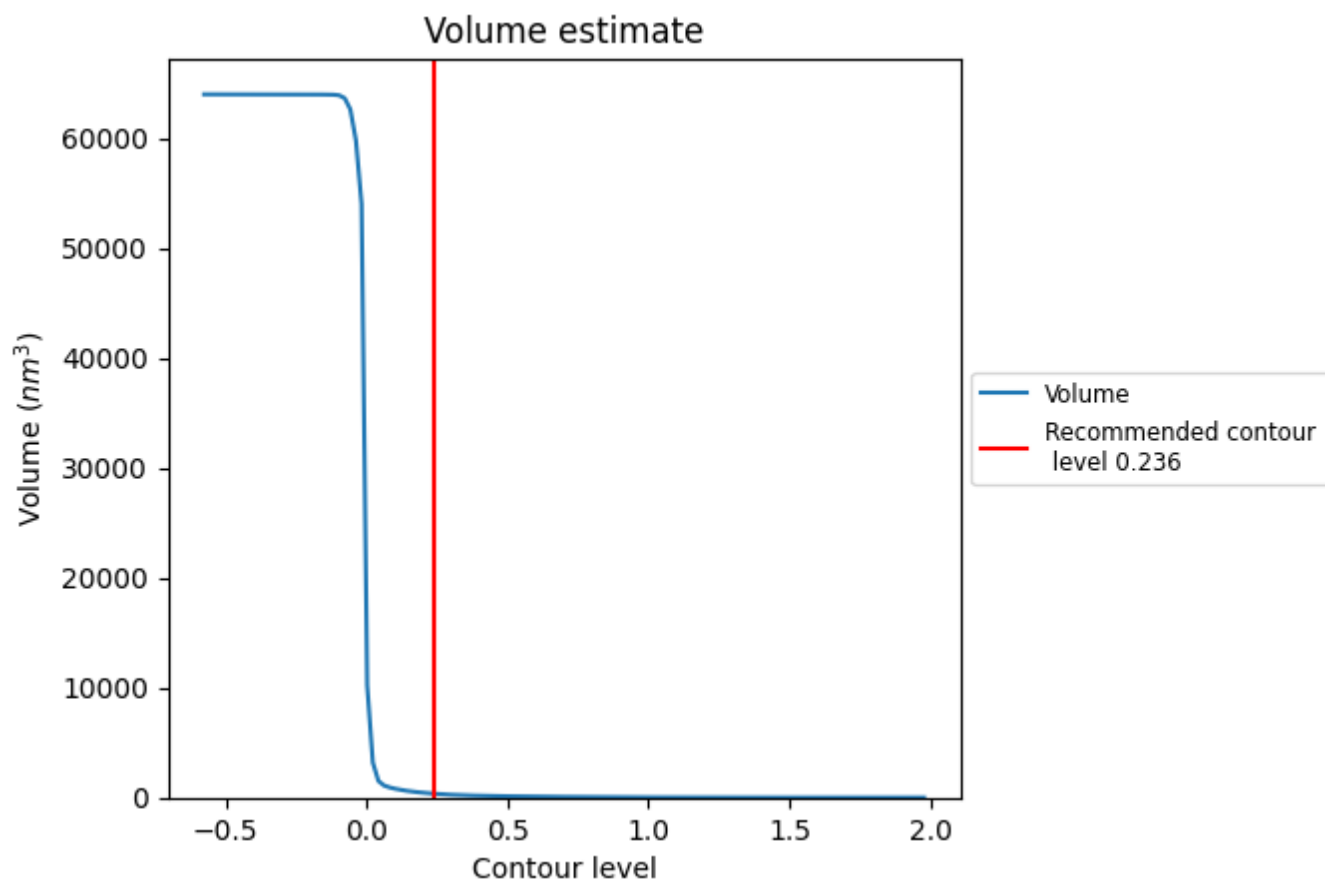
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

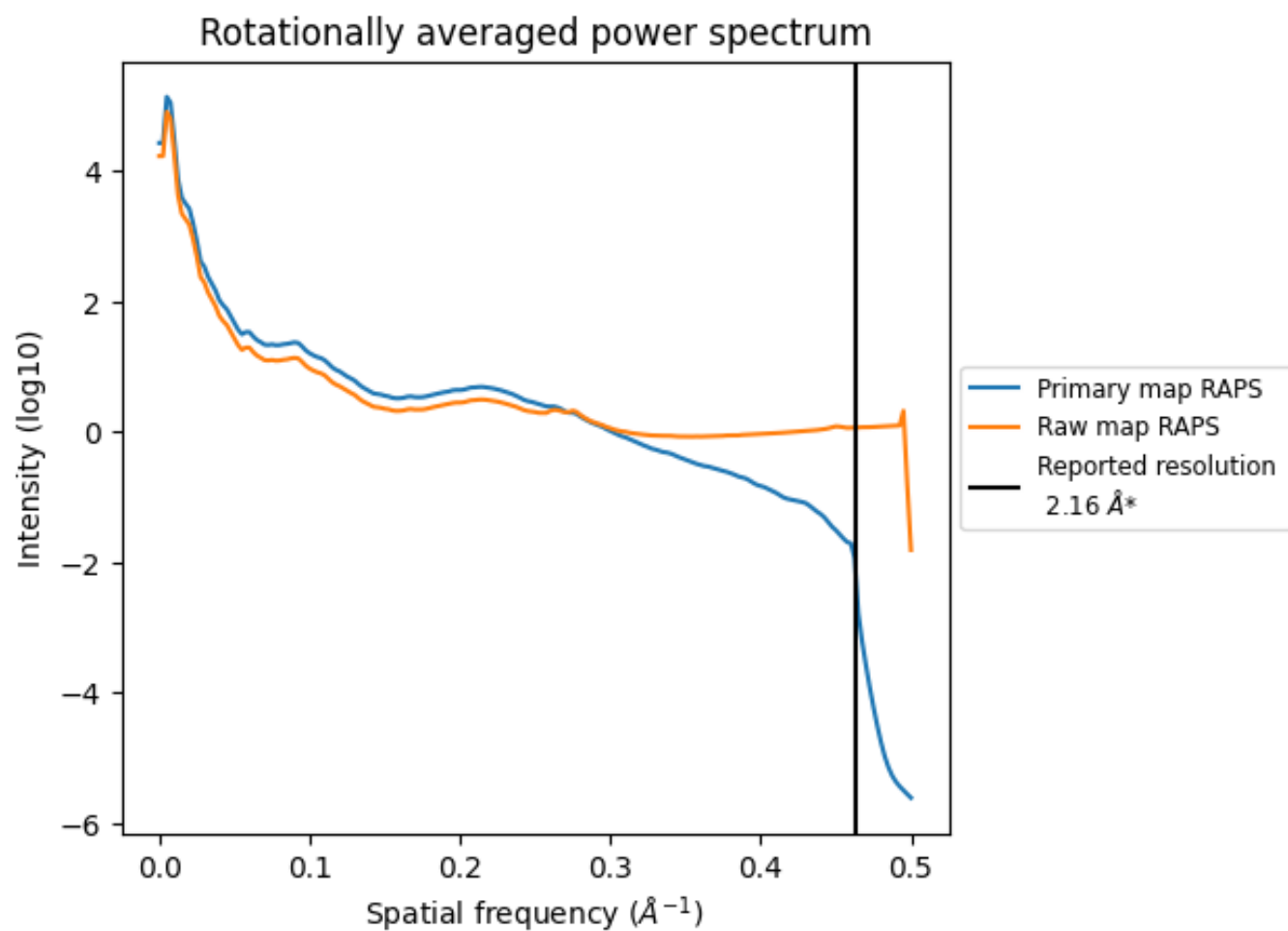
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 358 nm^3 ; this corresponds to an approximate mass of 323 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 ⓘ

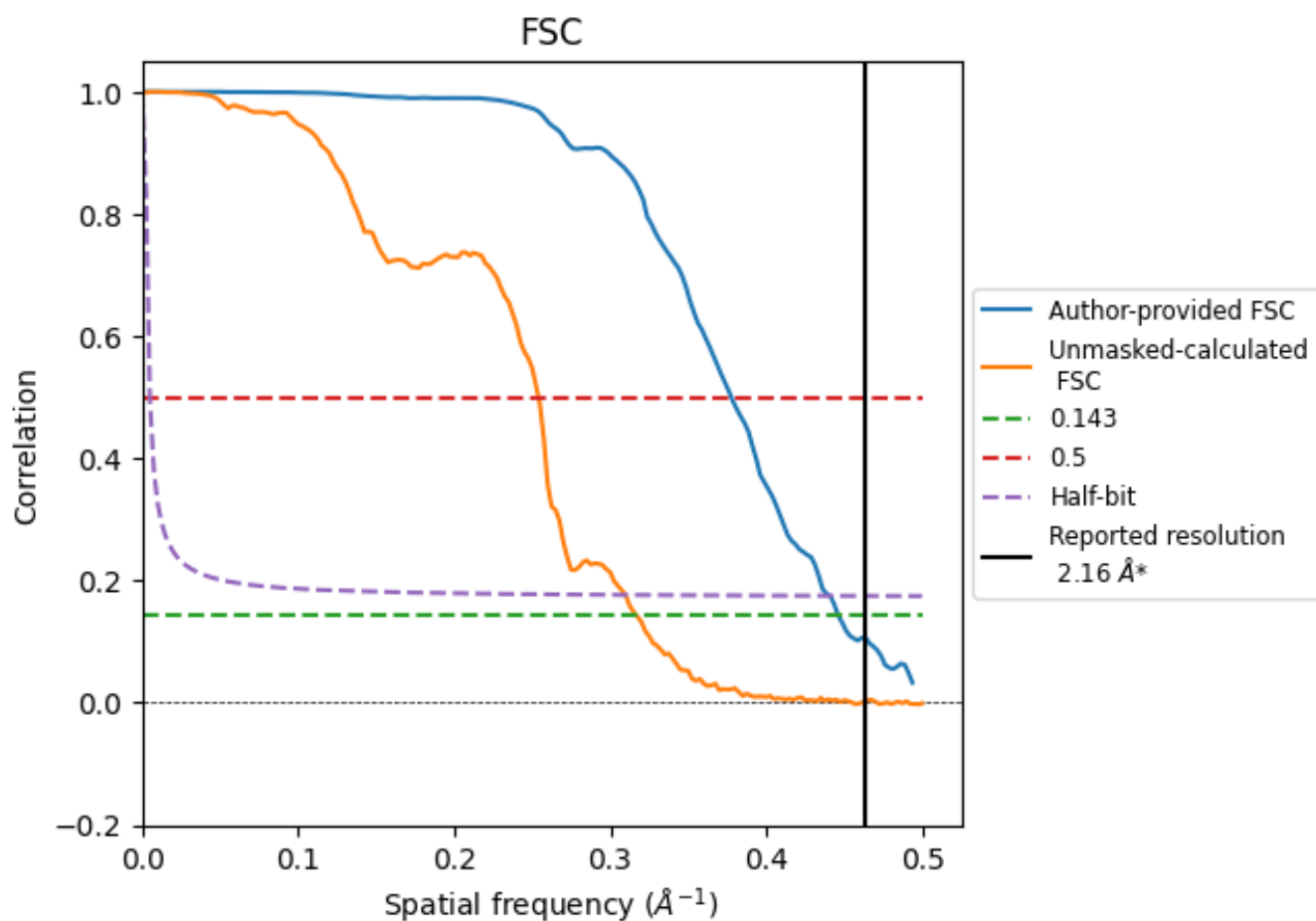


*Reported resolution corresponds to spatial frequency of 0.463 Å⁻¹

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 0.463 Å⁻¹

8.2 Resolution estimates [i](#)

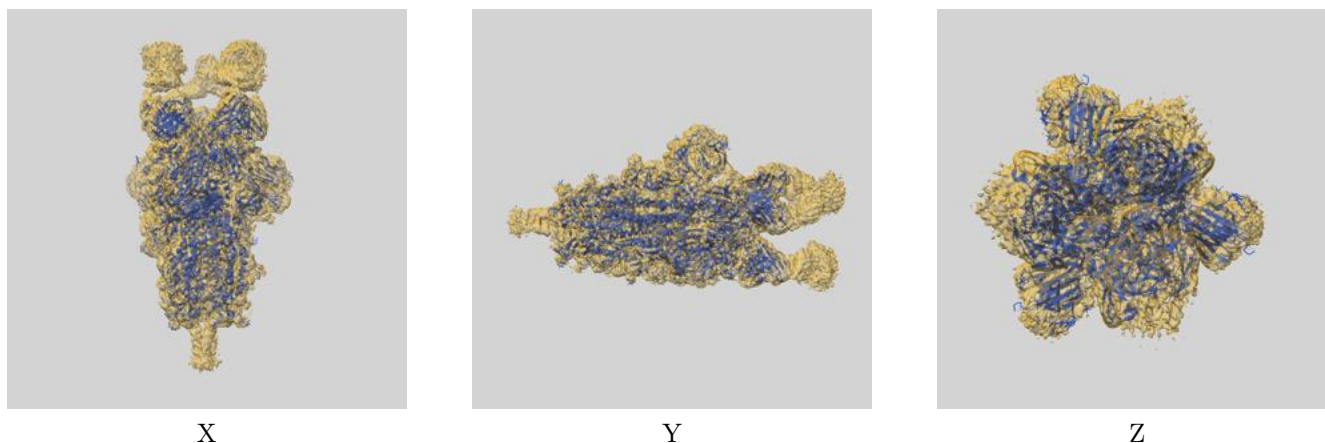
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.16	-	-
Author-provided FSC curve	2.24	2.65	2.27
Unmasked-calculated*	3.16	3.94	3.23

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.16 differs from the reported value 2.16 by more than 10 %

9 Map-model fit [i](#)

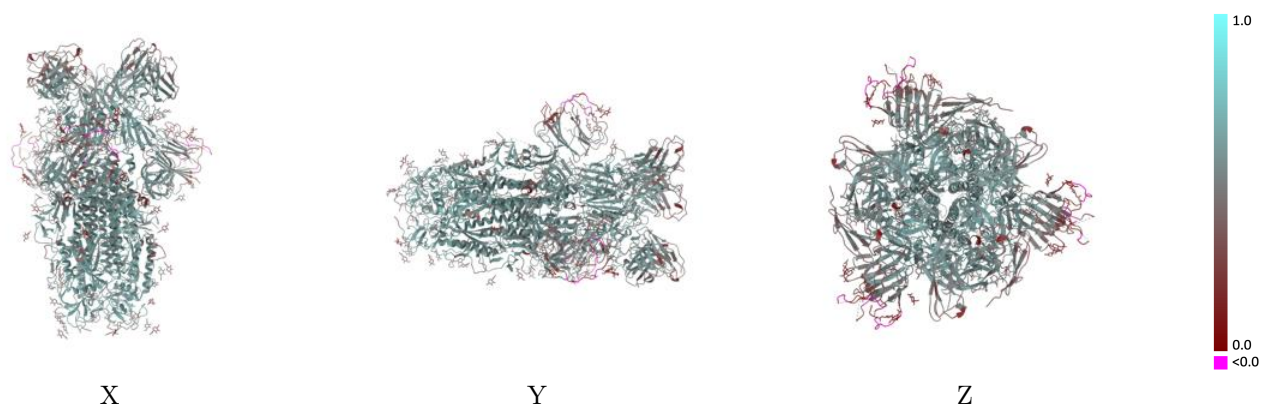
This section contains information regarding the fit between EMDB map EMD-27518 and PDB model 8DLW. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

9.1 Map-model overlay [i](#)



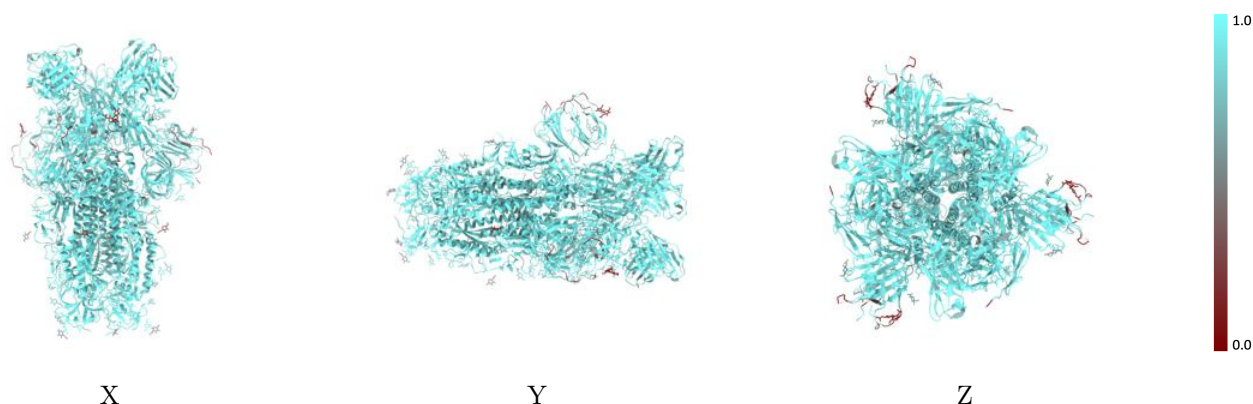
The images above show the 3D surface view of the map at the recommended contour level 0.236 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



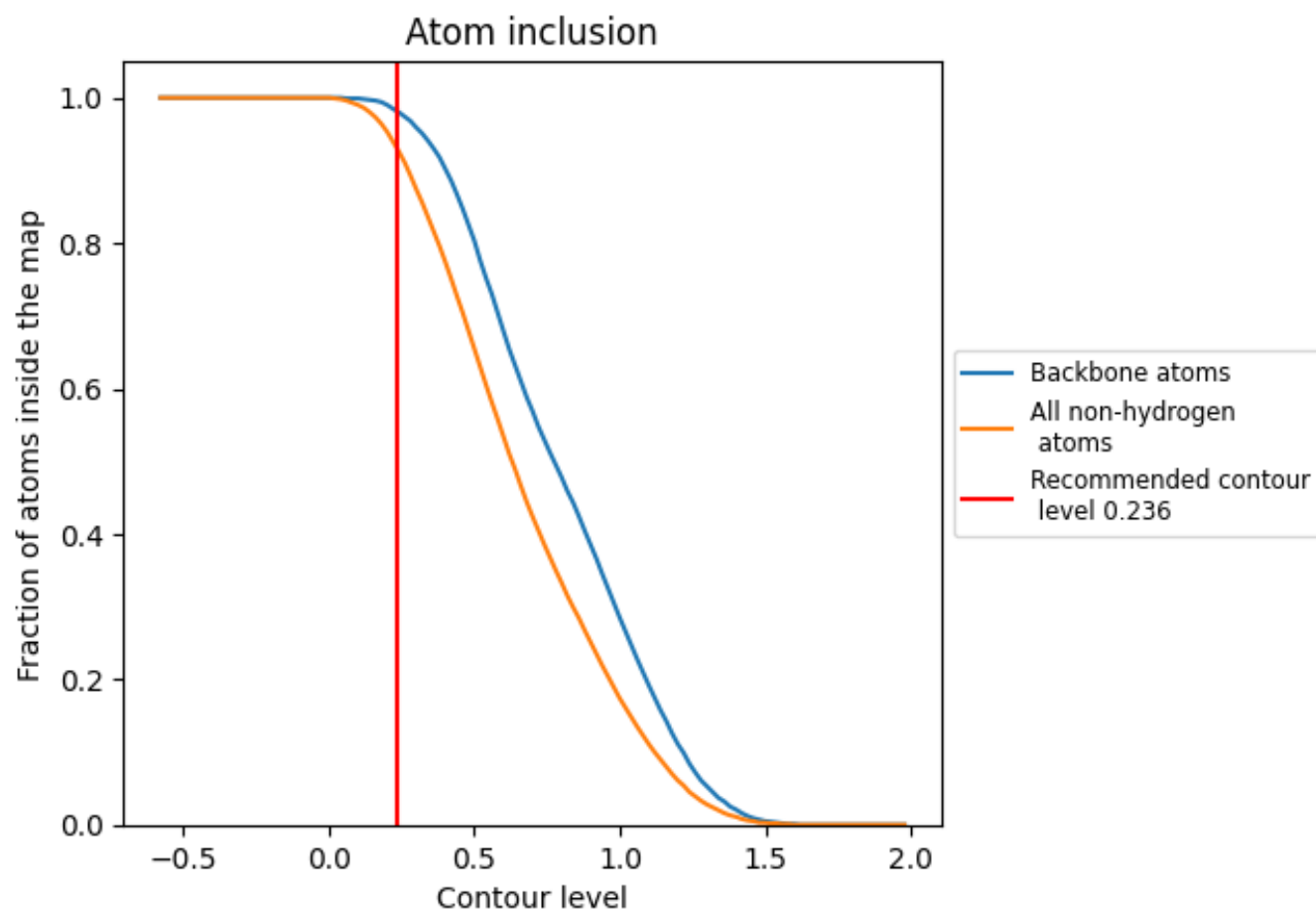
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.236).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 93% 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 (0.236) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9300	 0.5330
A	 0.9380	 0.5470
B	 0.9380	 0.5480
C	 0.9430	 0.5240
D	 0.9080	 0.4690
E	 0.9380	 0.5450
F	 0.9380	 0.5130
G	 0.9080	 0.4640
H	 0.9410	 0.5160
I	 0.0360	 0.1230
J	 0.6790	 0.2230
K	 0.8780	 0.4940
L	 0.8990	 0.4550
M	 0.8210	 0.4650
N	 0.8570	 0.3950
O	 0.7140	 0.3640
P	 0.7140	 0.4190
Q	 0.0360	 0.1230
R	 0.7140	 0.2260
S	 0.8570	 0.5020
T	 0.8210	 0.4440
U	 0.8570	 0.3840
V	 0.7140	 0.3700
W	 0.7140	 0.4080
X	 0.0360	 0.1340
Y	 0.7140	 0.1870
Z	 0.8370	 0.4770
a	 0.8210	 0.4300
b	 0.8570	 0.3820
c	 0.6790	 0.3530
d	 0.7140	 0.3750

