



Full wwPDB EM Validation Report ⓘ

Oct 26, 2024 – 07:46 PM EDT

PDB ID : 6OHW
EMDB ID : EMD-20070
Title : Structural basis for human coronavirus attachment to sialic acid receptors.
Apo-HCoV-OC43 S
Authors : Tortorici, M.A.; Walls, A.C.; Lang, Y.; Wang, C.; Li, Z.; Koerhuis, D.; Boons, G.J.; Bosch, B.J.; Rey, F.A.; de Groot, R.; Veerler, D.
Deposited on : 2019-04-07
Resolution : 2.90 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

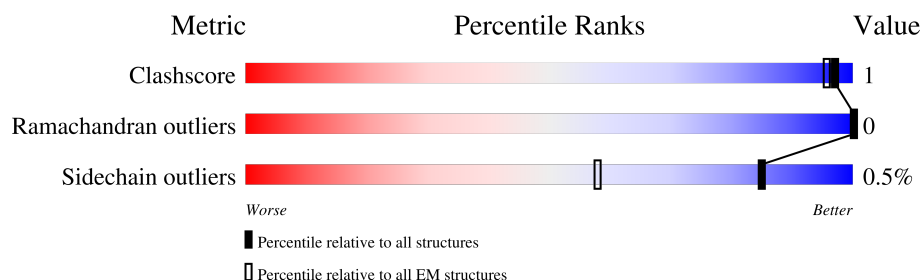
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	1322	<div> <div>15%</div> <div>82%</div> <div>7%</div> <div>11%</div> </div>
1	B	1322	<div> <div>15%</div> <div>82%</div> <div>7%</div> <div>11%</div> </div>
1	C	1322	<div> <div>15%</div> <div>82%</div> <div>6%</div> <div>11%</div> </div>
2	D	3	<div> <div>100%</div> <div>67%</div> <div>33%</div> </div>
2	E	3	<div> <div>100%</div> <div>67%</div> <div>33%</div> </div>
2	F	3	<div> <div>100%</div> <div>100%</div> </div>
2	G	3	<div> <div>67%</div> <div>33%</div> <div>67%</div> </div>
2	M	3	<div> <div>100%</div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain
2	N	3	100%
2	O	3	67%
2	P	3	100%
2	Q	3	67%
2	W	3	100%
2	X	3	100%
2	Y	3	100%
2	Z	3	100%
2	a	3	67%
2	g	3	100%
3	H	2	100%
3	I	2	100%
3	K	2	100%
3	L	2	100%
3	R	2	100%
3	S	2	100%
3	U	2	100%
3	V	2	100%
3	b	2	100%
3	c	2	100%
3	e	2	100%
3	f	2	100%
4	J	4	75%
4	T	4	75%
4	d	4	75%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 28917 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 surface glycoprotein.

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

There are 225 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-9	MET	-	initiating methionine	UNP Q696P8
A	-8	PRO	-	expression tag	UNP Q696P8
A	-7	MET	-	expression tag	UNP Q696P8
A	-6	GLY	-	expression tag	UNP Q696P8
A	-5	SER	-	expression tag	UNP Q696P8
A	-4	LEU	-	expression tag	UNP Q696P8
A	-3	GLN	-	expression tag	UNP Q696P8
A	-2	PRO	-	expression tag	UNP Q696P8
A	-1	LEU	-	expression tag	UNP Q696P8
A	0	ALA	-	expression tag	UNP Q696P8
A	1	THR	-	expression tag	UNP Q696P8
A	2	LEU	-	expression tag	UNP Q696P8
A	3	TYR	-	expression tag	UNP Q696P8
A	4	LEU	-	expression tag	UNP Q696P8
A	5	LEU	-	expression tag	UNP Q696P8
A	6	GLY	-	expression tag	UNP Q696P8
A	7	MET	-	expression tag	UNP Q696P8
A	8	LEU	-	expression tag	UNP Q696P8
A	9	VAL	-	expression tag	UNP Q696P8
A	10	ALA	-	expression tag	UNP Q696P8
A	11	SER	-	expression tag	UNP Q696P8
A	12	VAL	-	expression tag	UNP Q696P8
A	13	LEU	-	expression tag	UNP Q696P8
A	764	GLY	ARG	engineered mutation	UNP Q696P8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	765	GLY	ARG	engineered mutation	UNP Q696P8
A	767	GLY	ARG	engineered mutation	UNP Q696P8
A	1274	LEU	-	expression tag	UNP Q696P8
A	1275	ILE	-	expression tag	UNP Q696P8
A	1276	LYS	-	expression tag	UNP Q696P8
A	1277	ARG	-	expression tag	UNP Q696P8
A	1278	MET	-	expression tag	UNP Q696P8
A	1279	LYS	-	expression tag	UNP Q696P8
A	1280	GLN	-	expression tag	UNP Q696P8
A	1281	ILE	-	expression tag	UNP Q696P8
A	1282	GLU	-	expression tag	UNP Q696P8
A	1283	ASP	-	expression tag	UNP Q696P8
A	1284	LYS	-	expression tag	UNP Q696P8
A	1285	ILE	-	expression tag	UNP Q696P8
A	1286	GLU	-	expression tag	UNP Q696P8
A	1287	GLU	-	expression tag	UNP Q696P8
A	1288	ILE	-	expression tag	UNP Q696P8
A	1289	GLU	-	expression tag	UNP Q696P8
A	1290	SER	-	expression tag	UNP Q696P8
A	1291	LYS	-	expression tag	UNP Q696P8
A	1292	GLN	-	expression tag	UNP Q696P8
A	1293	LYS	-	expression tag	UNP Q696P8
A	1294	LYS	-	expression tag	UNP Q696P8
A	1295	ILE	-	expression tag	UNP Q696P8
A	1296	GLU	-	expression tag	UNP Q696P8
A	1297	ASN	-	expression tag	UNP Q696P8
A	1298	GLU	-	expression tag	UNP Q696P8
A	1299	ILE	-	expression tag	UNP Q696P8
A	1300	ALA	-	expression tag	UNP Q696P8
A	1301	ARG	-	expression tag	UNP Q696P8
A	1302	ILE	-	expression tag	UNP Q696P8
A	1303	LYS	-	expression tag	UNP Q696P8
A	1304	LYS	-	expression tag	UNP Q696P8
A	1305	ILE	-	expression tag	UNP Q696P8
A	1306	LYS	-	expression tag	UNP Q696P8
A	1307	LEU	-	expression tag	UNP Q696P8
A	1308	VAL	-	expression tag	UNP Q696P8
A	1309	PRO	-	expression tag	UNP Q696P8
A	1310	ARG	-	expression tag	UNP Q696P8
A	1311	GLY	-	expression tag	UNP Q696P8
A	1312	SER	-	expression tag	UNP Q696P8
A	1313	LEU	-	expression tag	UNP Q696P8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1314	GLU	-	expression tag	UNP Q696P8
A	1315	TRP	-	expression tag	UNP Q696P8
A	1316	SER	-	expression tag	UNP Q696P8
A	1317	HIS	-	expression tag	UNP Q696P8
A	1318	PRO	-	expression tag	UNP Q696P8
A	1319	GLN	-	expression tag	UNP Q696P8
A	1320	PHE	-	expression tag	UNP Q696P8
A	1321	GLU	-	expression tag	UNP Q696P8
A	1322	LYS	-	expression tag	UNP Q696P8
B	-9	MET	-	initiating methionine	UNP Q696P8
B	-8	PRO	-	expression tag	UNP Q696P8
B	-7	MET	-	expression tag	UNP Q696P8
B	-6	GLY	-	expression tag	UNP Q696P8
B	-5	SER	-	expression tag	UNP Q696P8
B	-4	LEU	-	expression tag	UNP Q696P8
B	-3	GLN	-	expression tag	UNP Q696P8
B	-2	PRO	-	expression tag	UNP Q696P8
B	-1	LEU	-	expression tag	UNP Q696P8
B	0	ALA	-	expression tag	UNP Q696P8
B	1	THR	-	expression tag	UNP Q696P8
B	2	LEU	-	expression tag	UNP Q696P8
B	3	TYR	-	expression tag	UNP Q696P8
B	4	LEU	-	expression tag	UNP Q696P8
B	5	LEU	-	expression tag	UNP Q696P8
B	6	GLY	-	expression tag	UNP Q696P8
B	7	MET	-	expression tag	UNP Q696P8
B	8	LEU	-	expression tag	UNP Q696P8
B	9	VAL	-	expression tag	UNP Q696P8
B	10	ALA	-	expression tag	UNP Q696P8
B	11	SER	-	expression tag	UNP Q696P8
B	12	VAL	-	expression tag	UNP Q696P8
B	13	LEU	-	expression tag	UNP Q696P8
B	764	GLY	ARG	engineered mutation	UNP Q696P8
B	765	GLY	ARG	engineered mutation	UNP Q696P8
B	767	GLY	ARG	engineered mutation	UNP Q696P8
B	1274	LEU	-	expression tag	UNP Q696P8
B	1275	ILE	-	expression tag	UNP Q696P8
B	1276	LYS	-	expression tag	UNP Q696P8
B	1277	ARG	-	expression tag	UNP Q696P8
B	1278	MET	-	expression tag	UNP Q696P8
B	1279	LYS	-	expression tag	UNP Q696P8
B	1280	GLN	-	expression tag	UNP Q696P8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1281	ILE	-	expression tag	UNP Q696P8
B	1282	GLU	-	expression tag	UNP Q696P8
B	1283	ASP	-	expression tag	UNP Q696P8
B	1284	LYS	-	expression tag	UNP Q696P8
B	1285	ILE	-	expression tag	UNP Q696P8
B	1286	GLU	-	expression tag	UNP Q696P8
B	1287	GLU	-	expression tag	UNP Q696P8
B	1288	ILE	-	expression tag	UNP Q696P8
B	1289	GLU	-	expression tag	UNP Q696P8
B	1290	SER	-	expression tag	UNP Q696P8
B	1291	LYS	-	expression tag	UNP Q696P8
B	1292	GLN	-	expression tag	UNP Q696P8
B	1293	LYS	-	expression tag	UNP Q696P8
B	1294	LYS	-	expression tag	UNP Q696P8
B	1295	ILE	-	expression tag	UNP Q696P8
B	1296	GLU	-	expression tag	UNP Q696P8
B	1297	ASN	-	expression tag	UNP Q696P8
B	1298	GLU	-	expression tag	UNP Q696P8
B	1299	ILE	-	expression tag	UNP Q696P8
B	1300	ALA	-	expression tag	UNP Q696P8
B	1301	ARG	-	expression tag	UNP Q696P8
B	1302	ILE	-	expression tag	UNP Q696P8
B	1303	LYS	-	expression tag	UNP Q696P8
B	1304	LYS	-	expression tag	UNP Q696P8
B	1305	ILE	-	expression tag	UNP Q696P8
B	1306	LYS	-	expression tag	UNP Q696P8
B	1307	LEU	-	expression tag	UNP Q696P8
B	1308	VAL	-	expression tag	UNP Q696P8
B	1309	PRO	-	expression tag	UNP Q696P8
B	1310	ARG	-	expression tag	UNP Q696P8
B	1311	GLY	-	expression tag	UNP Q696P8
B	1312	SER	-	expression tag	UNP Q696P8
B	1313	LEU	-	expression tag	UNP Q696P8
B	1314	GLU	-	expression tag	UNP Q696P8
B	1315	TRP	-	expression tag	UNP Q696P8
B	1316	SER	-	expression tag	UNP Q696P8
B	1317	HIS	-	expression tag	UNP Q696P8
B	1318	PRO	-	expression tag	UNP Q696P8
B	1319	GLN	-	expression tag	UNP Q696P8
B	1320	PHE	-	expression tag	UNP Q696P8
B	1321	GLU	-	expression tag	UNP Q696P8
B	1322	LYS	-	expression tag	UNP Q696P8

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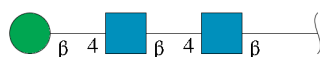
Chain	Residue	Modelled	Actual	Comment	Reference
C	-9	MET	-	initiating methionine	UNP Q696P8
C	-8	PRO	-	expression tag	UNP Q696P8
C	-7	MET	-	expression tag	UNP Q696P8
C	-6	GLY	-	expression tag	UNP Q696P8
C	-5	SER	-	expression tag	UNP Q696P8
C	-4	LEU	-	expression tag	UNP Q696P8
C	-3	GLN	-	expression tag	UNP Q696P8
C	-2	PRO	-	expression tag	UNP Q696P8
C	-1	LEU	-	expression tag	UNP Q696P8
C	0	ALA	-	expression tag	UNP Q696P8
C	1	THR	-	expression tag	UNP Q696P8
C	2	LEU	-	expression tag	UNP Q696P8
C	3	TYR	-	expression tag	UNP Q696P8
C	4	LEU	-	expression tag	UNP Q696P8
C	5	LEU	-	expression tag	UNP Q696P8
C	6	GLY	-	expression tag	UNP Q696P8
C	7	MET	-	expression tag	UNP Q696P8
C	8	LEU	-	expression tag	UNP Q696P8
C	9	VAL	-	expression tag	UNP Q696P8
C	10	ALA	-	expression tag	UNP Q696P8
C	11	SER	-	expression tag	UNP Q696P8
C	12	VAL	-	expression tag	UNP Q696P8
C	13	LEU	-	expression tag	UNP Q696P8
C	764	GLY	ARG	engineered mutation	UNP Q696P8
C	765	GLY	ARG	engineered mutation	UNP Q696P8
C	767	GLY	ARG	engineered mutation	UNP Q696P8
C	1274	LEU	-	expression tag	UNP Q696P8
C	1275	ILE	-	expression tag	UNP Q696P8
C	1276	LYS	-	expression tag	UNP Q696P8
C	1277	ARG	-	expression tag	UNP Q696P8
C	1278	MET	-	expression tag	UNP Q696P8
C	1279	LYS	-	expression tag	UNP Q696P8
C	1280	GLN	-	expression tag	UNP Q696P8
C	1281	ILE	-	expression tag	UNP Q696P8
C	1282	GLU	-	expression tag	UNP Q696P8
C	1283	ASP	-	expression tag	UNP Q696P8
C	1284	LYS	-	expression tag	UNP Q696P8
C	1285	ILE	-	expression tag	UNP Q696P8
C	1286	GLU	-	expression tag	UNP Q696P8
C	1287	GLU	-	expression tag	UNP Q696P8
C	1288	ILE	-	expression tag	UNP Q696P8
C	1289	GLU	-	expression tag	UNP Q696P8

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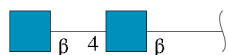
Chain	Residue	Modelled	Actual	Comment	Reference
C	1290	SER	-	expression tag	UNP Q696P8
C	1291	LYS	-	expression tag	UNP Q696P8
C	1292	GLN	-	expression tag	UNP Q696P8
C	1293	LYS	-	expression tag	UNP Q696P8
C	1294	LYS	-	expression tag	UNP Q696P8
C	1295	ILE	-	expression tag	UNP Q696P8
C	1296	GLU	-	expression tag	UNP Q696P8
C	1297	ASN	-	expression tag	UNP Q696P8
C	1298	GLU	-	expression tag	UNP Q696P8
C	1299	ILE	-	expression tag	UNP Q696P8
C	1300	ALA	-	expression tag	UNP Q696P8
C	1301	ARG	-	expression tag	UNP Q696P8
C	1302	ILE	-	expression tag	UNP Q696P8
C	1303	LYS	-	expression tag	UNP Q696P8
C	1304	LYS	-	expression tag	UNP Q696P8
C	1305	ILE	-	expression tag	UNP Q696P8
C	1306	LYS	-	expression tag	UNP Q696P8
C	1307	LEU	-	expression tag	UNP Q696P8
C	1308	VAL	-	expression tag	UNP Q696P8
C	1309	PRO	-	expression tag	UNP Q696P8
C	1310	ARG	-	expression tag	UNP Q696P8
C	1311	GLY	-	expression tag	UNP Q696P8
C	1312	SER	-	expression tag	UNP Q696P8
C	1313	LEU	-	expression tag	UNP Q696P8
C	1314	GLU	-	expression tag	UNP Q696P8
C	1315	TRP	-	expression tag	UNP Q696P8
C	1316	SER	-	expression tag	UNP Q696P8
C	1317	HIS	-	expression tag	UNP Q696P8
C	1318	PRO	-	expression tag	UNP Q696P8
C	1319	GLN	-	expression tag	UNP Q696P8
C	1320	PHE	-	expression tag	UNP Q696P8
C	1321	GLU	-	expression tag	UNP Q696P8
C	1322	LYS	-	expression tag	UNP Q696P8

- Molecule 2 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
2	D	3	Total	C	N	O	0	0
			39	22	2	15		
2	E	3	Total	C	N	O	0	0
			39	22	2	15		
2	F	3	Total	C	N	O	0	0
			39	22	2	15		
2	G	3	Total	C	N	O	0	0
			39	22	2	15		
2	M	3	Total	C	N	O	0	0
			39	22	2	15		
2	N	3	Total	C	N	O	0	0
			39	22	2	15		
2	O	3	Total	C	N	O	0	0
			39	22	2	15		
2	P	3	Total	C	N	O	0	0
			39	22	2	15		
2	Q	3	Total	C	N	O	0	0
			39	22	2	15		
2	W	3	Total	C	N	O	0	0
			39	22	2	15		
2	X	3	Total	C	N	O	0	0
			39	22	2	15		
2	Y	3	Total	C	N	O	0	0
			39	22	2	15		
2	Z	3	Total	C	N	O	0	0
			39	22	2	15		
2	a	3	Total	C	N	O	0	0
			39	22	2	15		
2	g	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



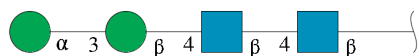
Mol	Chain	Residues	Atoms				AltConf	Trace
3	H	2	Total	C	N	O	0	0
			28	16	2	10		
3	I	2	Total	C	N	O	0	0
			28	16	2	10		

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Mol	Chain	Residues	Atoms				AltConf	Trace
3	K	2	Total	C	N	O	0	0
			28	16	2	10		
3	L	2	Total	C	N	O	0	0
			28	16	2	10		
3	R	2	Total	C	N	O	0	0
			28	16	2	10		
3	S	2	Total	C	N	O	0	0
			28	16	2	10		
3	U	2	Total	C	N	O	0	0
			28	16	2	10		
3	V	2	Total	C	N	O	0	0
			28	16	2	10		
3	b	2	Total	C	N	O	0	0
			28	16	2	10		
3	c	2	Total	C	N	O	0	0
			28	16	2	10		
3	e	2	Total	C	N	O	0	0
			28	16	2	10		
3	f	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-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
4	J	4	Total	C	N	O	0	0
			50	28	2	20		
4	T	4	Total	C	N	O	0	0
			50	28	2	20		
4	d	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



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

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

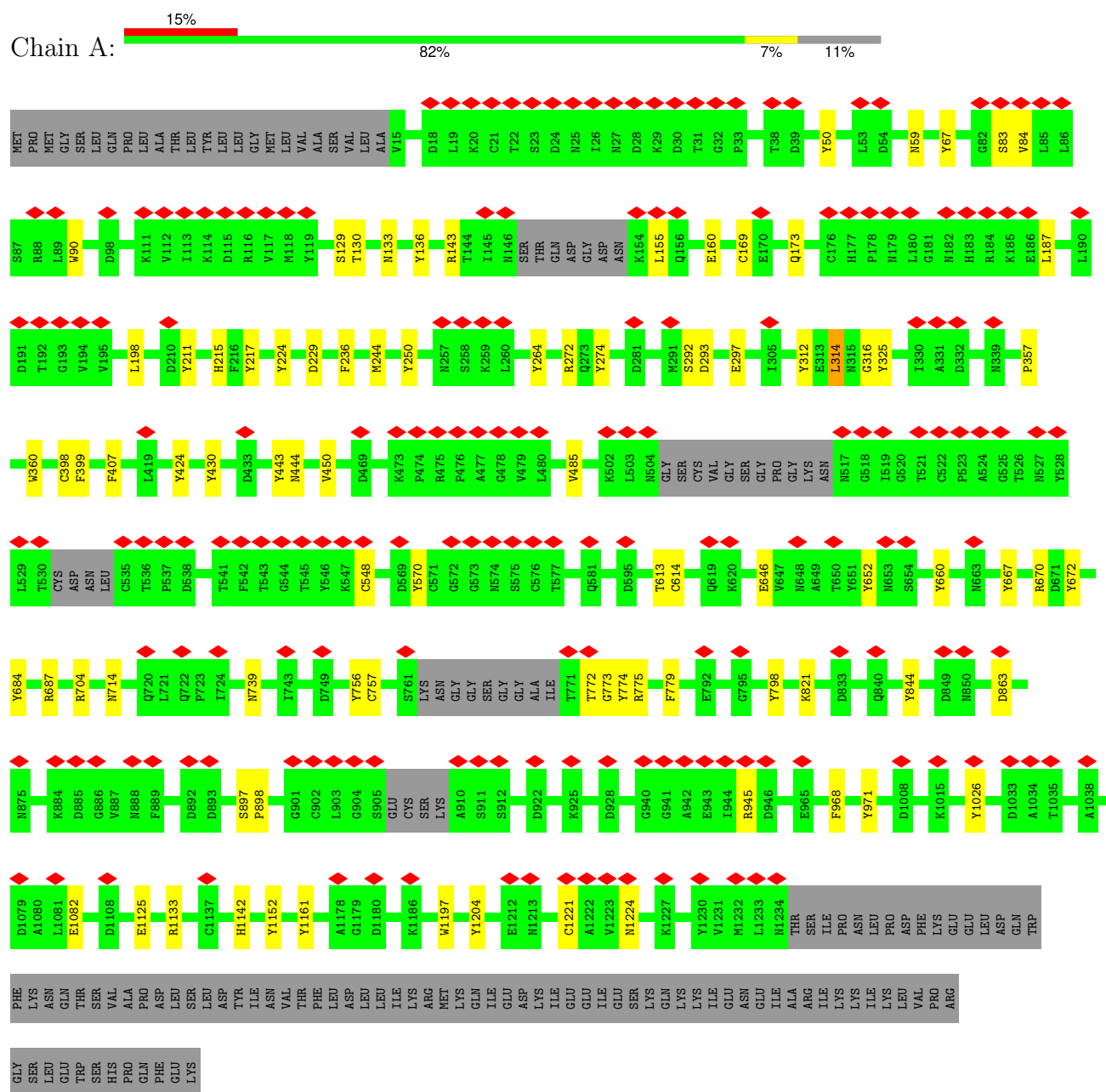
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		AltConf
6	A	62	Total	O	0
			62	62	
6	B	62	Total	O	0
			62	62	
6	C	62	Total	O	0
			62	62	

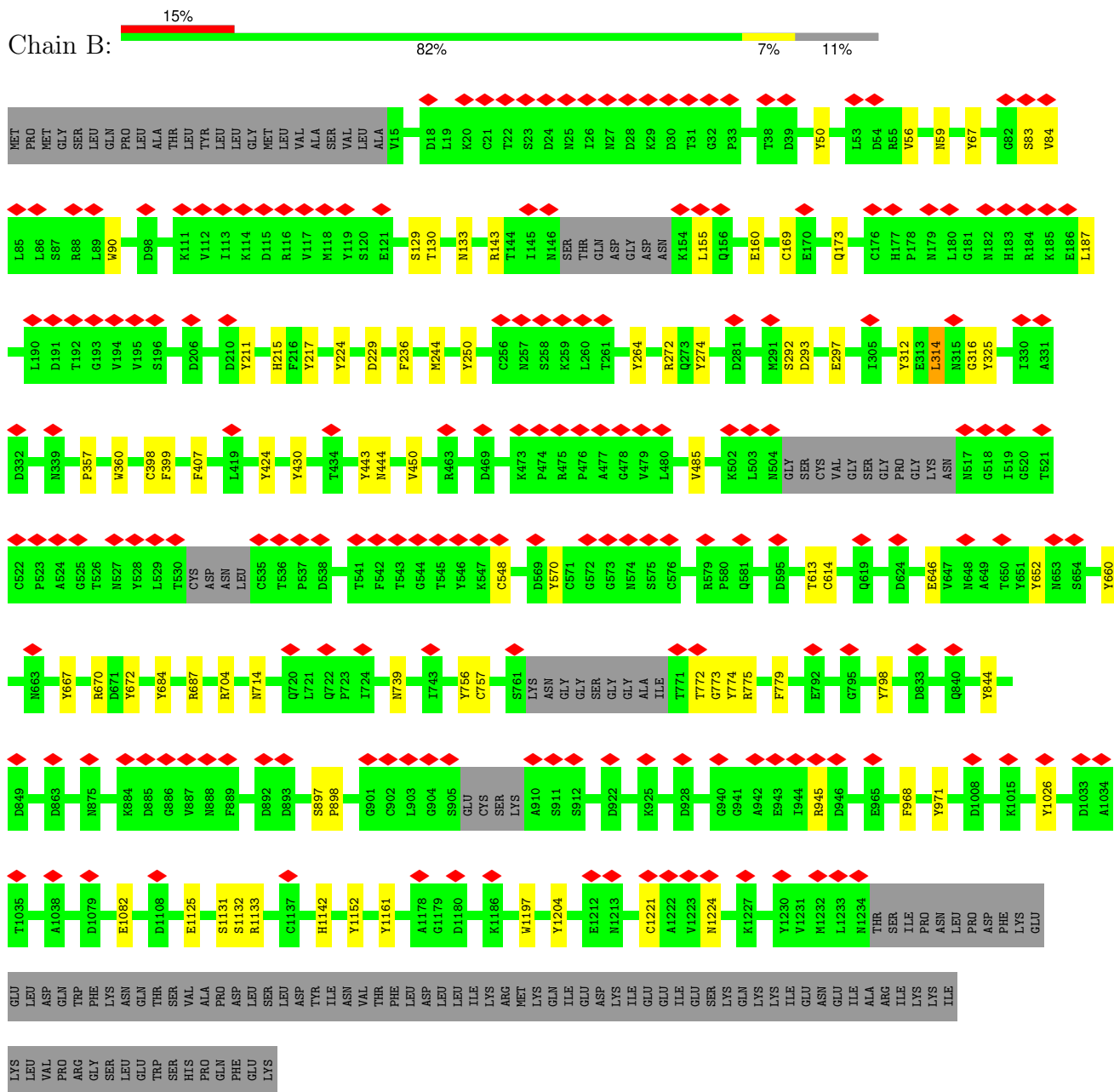
3 Residue-property plots

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.

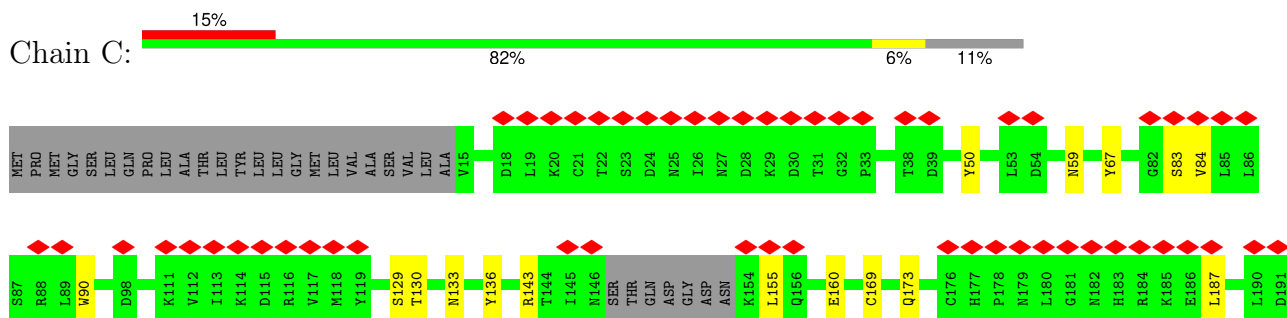
• Molecule 1: Spike surface glycoprotein



Chain B:



Chain C:





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



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



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



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



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



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



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



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



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



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



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



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

Chain g:  100%
100%



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

Chain H:  100%
100%



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

Chain I:  100%
100%



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

Chain K:  100%
100%



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

Chain L:  100%
100%



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

Chain R:  100%
100%



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



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



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



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



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



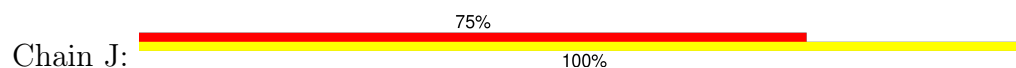
- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



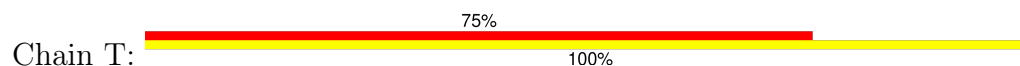
- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



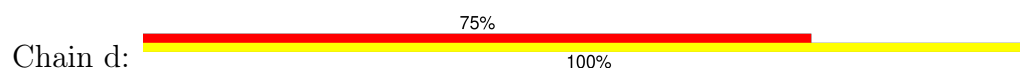
- Molecule 4: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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



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



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	105919	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	70	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	5.098	Depositor
Minimum map value	-3.037	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.080	Depositor
Recommended contour level	1	Depositor
Map size (Å)	419.99997, 419.99997, 419.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor

5 Model quality

5.1 Standard geometry

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

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	1.41	57/9359 (0.6%)	0.95	27/12744 (0.2%)
1	B	1.41	58/9359 (0.6%)	0.95	27/12744 (0.2%)
1	C	1.41	60/9359 (0.6%)	0.95	26/12744 (0.2%)
All	All	1.41	175/28077 (0.6%)	0.95	80/38232 (0.2%)

All (175) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	169	CYS	CB-SG	-10.16	1.65	1.82
1	C	169	CYS	CB-SG	-10.16	1.65	1.82
1	A	169	CYS	CB-SG	-10.16	1.65	1.82
1	C	757	CYS	CB-SG	-9.84	1.65	1.82
1	A	757	CYS	CB-SG	-9.81	1.65	1.82
1	B	757	CYS	CB-SG	-9.80	1.65	1.82
1	B	485	VAL	CB-CG1	-8.17	1.35	1.52
1	A	485	VAL	CB-CG1	-8.17	1.35	1.52
1	C	485	VAL	CB-CG1	-8.16	1.35	1.52
1	C	357	PRO	N-CD	-6.45	1.38	1.47
1	C	844	TYR	CB-CG	-6.44	1.42	1.51
1	A	844	TYR	CB-CG	-6.44	1.42	1.51
1	B	844	TYR	CB-CG	-6.43	1.42	1.51
1	B	357	PRO	N-CD	-6.42	1.38	1.47
1	A	357	PRO	N-CD	-6.41	1.38	1.47
1	B	224	TYR	CB-CG	-6.41	1.42	1.51
1	C	224	TYR	CB-CG	-6.39	1.42	1.51
1	A	224	TYR	CB-CG	-6.38	1.42	1.51
1	C	50	TYR	CB-CG	-6.32	1.42	1.51
1	A	50	TYR	CB-CG	-6.30	1.42	1.51
1	B	50	TYR	CB-CG	-6.25	1.42	1.51
1	A	443	TYR	CD2-CE2	-6.17	1.30	1.39
1	B	1161	TYR	CB-CG	-6.16	1.42	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	430	TYR	CG-CD1	-6.14	1.31	1.39
1	B	443	TYR	CD2-CE2	-6.14	1.30	1.39
1	A	1161	TYR	CB-CG	-6.14	1.42	1.51
1	C	443	TYR	CD2-CE2	-6.13	1.30	1.39
1	B	430	TYR	CG-CD1	-6.12	1.31	1.39
1	C	1161	TYR	CB-CG	-6.12	1.42	1.51
1	A	430	TYR	CG-CD1	-6.10	1.31	1.39
1	C	968	PHE	CB-CG	-6.04	1.41	1.51
1	B	614	CYS	CB-SG	6.04	1.92	1.82
1	B	968	PHE	CB-CG	-6.03	1.41	1.51
1	A	968	PHE	CB-CG	-6.03	1.41	1.51
1	A	215	HIS	CB-CG	-6.01	1.39	1.50
1	C	215	HIS	CB-CG	-6.01	1.39	1.50
1	B	215	HIS	CB-CG	-6.01	1.39	1.50
1	A	614	CYS	CB-SG	6.00	1.92	1.82
1	A	1161	TYR	CG-CD1	-5.98	1.31	1.39
1	C	450	VAL	CB-CG2	-5.97	1.40	1.52
1	C	614	CYS	CB-SG	5.97	1.92	1.82
1	C	1161	TYR	CG-CD1	-5.96	1.31	1.39
1	A	450	VAL	CB-CG2	-5.96	1.40	1.52
1	B	1161	TYR	CG-CD1	-5.95	1.31	1.39
1	B	450	VAL	CB-CG2	-5.93	1.40	1.52
1	B	160	GLU	CD-OE1	-5.86	1.19	1.25
1	C	160	GLU	CD-OE1	-5.85	1.19	1.25
1	A	160	GLU	CD-OE1	-5.83	1.19	1.25
1	A	672	TYR	CG-CD1	-5.79	1.31	1.39
1	C	672	TYR	CG-CD1	-5.78	1.31	1.39
1	B	672	TYR	CG-CD1	-5.77	1.31	1.39
1	C	215	HIS	C-N	-5.76	1.20	1.34
1	B	215	HIS	C-N	-5.75	1.20	1.34
1	A	215	HIS	C-N	-5.74	1.20	1.34
1	B	1125	GLU	CG-CD	-5.74	1.43	1.51
1	C	1125	GLU	CG-CD	-5.73	1.43	1.51
1	B	798	TYR	CB-CG	-5.72	1.43	1.51
1	A	1125	GLU	CG-CD	-5.71	1.43	1.51
1	A	444	ASN	CB-CG	-5.71	1.38	1.51
1	B	444	ASN	CB-CG	-5.70	1.38	1.51
1	C	444	ASN	CB-CG	-5.70	1.38	1.51
1	A	1026	TYR	CB-CG	-5.69	1.43	1.51
1	B	756	TYR	CB-CG	-5.69	1.43	1.51
1	C	1026	TYR	CB-CG	-5.68	1.43	1.51
1	C	756	TYR	CB-CG	-5.67	1.43	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	798	TYR	CB-CG	-5.67	1.43	1.51
1	B	297	GLU	CG-CD	-5.67	1.43	1.51
1	B	1026	TYR	CB-CG	-5.67	1.43	1.51
1	A	756	TYR	CB-CG	-5.66	1.43	1.51
1	B	485	VAL	CB-CG2	-5.66	1.41	1.52
1	C	297	GLU	CG-CD	-5.66	1.43	1.51
1	A	297	GLU	CG-CD	-5.65	1.43	1.51
1	A	570	TYR	CB-CG	-5.64	1.43	1.51
1	C	485	VAL	CB-CG2	-5.64	1.41	1.52
1	A	485	VAL	CB-CG2	-5.64	1.41	1.52
1	C	570	TYR	CB-CG	-5.64	1.43	1.51
1	C	798	TYR	CB-CG	-5.64	1.43	1.51
1	B	570	TYR	CB-CG	-5.60	1.43	1.51
1	C	325	TYR	CE2-CZ	-5.59	1.31	1.38
1	C	443	TYR	CE2-CZ	-5.56	1.31	1.38
1	B	325	TYR	CE2-CZ	-5.56	1.31	1.38
1	A	325	TYR	CE2-CZ	-5.53	1.31	1.38
1	A	443	TYR	CE2-CZ	-5.53	1.31	1.38
1	B	264	TYR	CG-CD2	-5.53	1.31	1.39
1	A	264	TYR	CG-CD2	-5.52	1.31	1.39
1	B	443	TYR	CE2-CZ	-5.50	1.31	1.38
1	C	264	TYR	CG-CD2	-5.49	1.32	1.39
1	B	430	TYR	CE1-CZ	-5.42	1.31	1.38
1	C	217	TYR	CB-CG	-5.42	1.43	1.51
1	A	430	TYR	CE1-CZ	-5.42	1.31	1.38
1	C	430	TYR	CE1-CZ	-5.41	1.31	1.38
1	A	217	TYR	CB-CG	-5.40	1.43	1.51
1	C	430	TYR	CE2-CZ	-5.39	1.31	1.38
1	B	774	TYR	CG-CD2	-5.39	1.32	1.39
1	C	774	TYR	CG-CD2	-5.38	1.32	1.39
1	A	774	TYR	CG-CD2	-5.37	1.32	1.39
1	B	660	TYR	CG-CD2	-5.37	1.32	1.39
1	C	90	TRP	CB-CG	-5.37	1.40	1.50
1	A	660	TYR	CG-CD2	-5.36	1.32	1.39
1	C	660	TYR	CG-CD2	-5.36	1.32	1.39
1	A	90	TRP	CB-CG	-5.35	1.40	1.50
1	B	217	TYR	CB-CG	-5.34	1.43	1.51
1	B	1142	HIS	CB-CG	-5.34	1.40	1.50
1	C	297	GLU	CD-OE2	-5.34	1.19	1.25
1	B	90	TRP	CB-CG	-5.33	1.40	1.50
1	B	297	GLU	CD-OE2	-5.33	1.19	1.25
1	B	1197	TRP	CD2-CE2	-5.32	1.34	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	430	TYR	CE2-CZ	-5.32	1.31	1.38
1	A	430	TYR	CE2-CZ	-5.32	1.31	1.38
1	A	297	GLU	CD-OE2	-5.31	1.19	1.25
1	A	67	TYR	CB-CG	-5.30	1.43	1.51
1	C	67	TYR	CB-CG	-5.30	1.43	1.51
1	C	297	GLU	CD-OE1	-5.29	1.19	1.25
1	C	1197	TRP	CD2-CE2	-5.29	1.35	1.41
1	C	1142	HIS	CB-CG	-5.29	1.40	1.50
1	A	1142	HIS	CB-CG	-5.28	1.40	1.50
1	B	67	TYR	CB-CG	-5.28	1.43	1.51
1	A	297	GLU	CD-OE1	-5.28	1.19	1.25
1	C	1204	TYR	CE2-CZ	-5.28	1.31	1.38
1	A	1197	TRP	CD2-CE2	-5.27	1.35	1.41
1	B	297	GLU	CD-OE1	-5.26	1.19	1.25
1	A	1204	TYR	CE2-CZ	-5.25	1.31	1.38
1	B	1204	TYR	CE2-CZ	-5.22	1.31	1.38
1	C	407	PHE	CG-CD2	-5.20	1.30	1.38
1	A	407	PHE	CG-CD2	-5.19	1.30	1.38
1	B	407	PHE	CG-CD2	-5.18	1.30	1.38
1	B	236	PHE	CB-CG	-5.18	1.42	1.51
1	C	1082	GLU	CD-OE1	-5.17	1.20	1.25
1	A	1125	GLU	CD-OE2	-5.17	1.20	1.25
1	A	236	PHE	CB-CG	-5.17	1.42	1.51
1	C	236	PHE	CB-CG	-5.17	1.42	1.51
1	A	1082	GLU	CD-OE1	-5.17	1.20	1.25
1	B	1082	GLU	CD-OE1	-5.16	1.20	1.25
1	B	1125	GLU	CD-OE2	-5.14	1.20	1.25
1	C	173	GLN	CG-CD	-5.14	1.39	1.51
1	B	50	TYR	CD2-CE2	-5.13	1.31	1.39
1	C	1125	GLU	CD-OE2	-5.13	1.20	1.25
1	B	548	CYS	CB-SG	-5.13	1.73	1.81
1	C	50	TYR	CD2-CE2	-5.12	1.31	1.39
1	A	50	TYR	CD2-CE2	-5.12	1.31	1.39
1	A	548	CYS	CB-SG	-5.12	1.73	1.81
1	A	173	GLN	CG-CD	-5.12	1.39	1.51
1	B	173	GLN	CG-CD	-5.12	1.39	1.51
1	A	360	TRP	CZ3-CH2	-5.11	1.31	1.40
1	B	360	TRP	CZ3-CH2	-5.11	1.31	1.40
1	C	312	TYR	CG-CD2	-5.11	1.32	1.39
1	C	360	TRP	CZ3-CH2	-5.11	1.31	1.40
1	C	652	TYR	CG-CD1	-5.11	1.32	1.39
1	A	667	TYR	CG-CD2	-5.10	1.32	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	312	TYR	CG-CD2	-5.10	1.32	1.39
1	A	646	GLU	CD-OE1	-5.10	1.20	1.25
1	C	50	TYR	CE2-CZ	-5.09	1.31	1.38
1	A	1204	TYR	CG-CD2	-5.08	1.32	1.39
1	A	50	TYR	CE2-CZ	-5.08	1.31	1.38
1	B	1204	TYR	CG-CD2	-5.08	1.32	1.39
1	B	1221	CYS	CB-SG	-5.08	1.73	1.81
1	C	1204	TYR	CG-CD2	-5.07	1.32	1.39
1	A	652	TYR	CG-CD1	-5.07	1.32	1.39
1	B	667	TYR	CG-CD2	-5.07	1.32	1.39
1	C	548	CYS	CB-SG	-5.07	1.73	1.81
1	B	652	TYR	CG-CD1	-5.07	1.32	1.39
1	C	646	GLU	CD-OE1	-5.06	1.20	1.25
1	C	667	TYR	CG-CD2	-5.05	1.32	1.39
1	C	779	PHE	CB-CG	-5.05	1.42	1.51
1	B	779	PHE	CB-CG	-5.05	1.42	1.51
1	B	50	TYR	CE2-CZ	-5.05	1.31	1.38
1	B	646	GLU	CD-OE1	-5.04	1.20	1.25
1	A	779	PHE	CB-CG	-5.04	1.42	1.51
1	C	265	TRP	CD2-CE2	-5.04	1.35	1.41
1	A	1221	CYS	CB-SG	-5.03	1.73	1.81
1	B	312	TYR	CG-CD2	-5.03	1.32	1.39
1	C	1221	CYS	CB-SG	-5.03	1.73	1.81
1	C	667	TYR	CB-CG	-5.02	1.44	1.51
1	B	56	VAL	CB-CG2	-5.02	1.42	1.52
1	C	250	TYR	CB-CG	-5.01	1.44	1.51

All (80) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	399	PHE	N-CA-CB	-12.15	88.72	110.60
1	B	399	PHE	N-CA-CB	-12.15	88.73	110.60
1	C	399	PHE	N-CA-CB	-12.14	88.74	110.60
1	A	398	CYS	CB-CA-C	-8.03	94.34	110.40
1	B	398	CYS	CB-CA-C	-8.03	94.35	110.40
1	C	398	CYS	CB-CA-C	-8.00	94.40	110.40
1	B	272	ARG	NE-CZ-NH2	-7.98	116.31	120.30
1	A	272	ARG	NE-CZ-NH2	-7.97	116.32	120.30
1	C	272	ARG	NE-CZ-NH2	-7.92	116.34	120.30
1	C	274	TYR	CB-CG-CD2	-7.86	116.29	121.00
1	B	274	TYR	CB-CG-CD2	-7.85	116.29	121.00
1	A	274	TYR	CB-CG-CD2	-7.84	116.30	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	704	ARG	NE-CZ-NH2	-7.74	116.43	120.30
1	C	704	ARG	NE-CZ-NH2	-7.72	116.44	120.30
1	A	704	ARG	NE-CZ-NH2	-7.71	116.44	120.30
1	A	660	TYR	CB-CG-CD2	-6.95	116.83	121.00
1	C	660	TYR	CB-CG-CD2	-6.95	116.83	121.00
1	B	50	TYR	CB-CG-CD2	-6.94	116.84	121.00
1	C	50	TYR	CB-CG-CD2	-6.92	116.85	121.00
1	A	50	TYR	CB-CG-CD2	-6.90	116.86	121.00
1	B	660	TYR	CB-CG-CD2	-6.87	116.88	121.00
1	C	314	LEU	CB-CA-C	6.84	123.19	110.20
1	C	613	THR	N-CA-C	-6.84	92.54	111.00
1	B	314	LEU	CB-CA-C	6.83	123.19	110.20
1	A	613	THR	N-CA-C	-6.83	92.56	111.00
1	B	613	THR	N-CA-C	-6.82	92.58	111.00
1	A	314	LEU	CB-CA-C	6.82	123.16	110.20
1	A	775	ARG	NE-CZ-NH2	-6.64	116.98	120.30
1	C	775	ARG	NE-CZ-NH2	-6.63	116.98	120.30
1	B	775	ARG	NE-CZ-NH2	-6.63	116.98	120.30
1	C	684	TYR	CB-CG-CD1	-6.52	117.09	121.00
1	A	684	TYR	CB-CG-CD1	-6.50	117.10	121.00
1	C	211	TYR	CB-CG-CD2	-6.45	117.13	121.00
1	A	211	TYR	CB-CG-CD2	-6.42	117.15	121.00
1	B	211	TYR	CB-CG-CD2	-6.41	117.15	121.00
1	B	684	TYR	CB-CG-CD1	-6.41	117.16	121.00
1	B	1133	ARG	NE-CZ-NH2	-6.15	117.22	120.30
1	A	1133	ARG	NE-CZ-NH2	-6.09	117.26	120.30
1	C	1133	ARG	NE-CZ-NH2	-6.05	117.28	120.30
1	A	670	ARG	NE-CZ-NH2	-5.84	117.38	120.30
1	B	670	ARG	NE-CZ-NH2	-5.80	117.40	120.30
1	C	670	ARG	NE-CZ-NH2	-5.78	117.41	120.30
1	A	971	TYR	CB-CG-CD1	-5.74	117.56	121.00
1	C	971	TYR	CB-CG-CD1	-5.71	117.58	121.00
1	B	971	TYR	CB-CG-CD1	-5.70	117.58	121.00
1	C	143	ARG	NE-CZ-NH2	-5.59	117.50	120.30
1	A	143	ARG	NE-CZ-NH2	-5.59	117.50	120.30
1	B	143	ARG	NE-CZ-NH2	-5.58	117.51	120.30
1	C	316	GLY	N-CA-C	5.53	126.94	113.10
1	A	316	GLY	N-CA-C	5.51	126.89	113.10
1	B	316	GLY	N-CA-C	5.50	126.85	113.10
1	C	1152	TYR	CB-CG-CD2	-5.40	117.76	121.00
1	A	1152	TYR	CB-CG-CD2	-5.35	117.79	121.00
1	B	1152	TYR	CB-CG-CD2	-5.32	117.81	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	844	TYR	CB-CG-CD2	-5.31	117.81	121.00
1	C	250	TYR	CB-CG-CD1	-5.30	117.82	121.00
1	B	424	TYR	CB-CG-CD1	-5.30	117.82	121.00
1	B	844	TYR	CB-CG-CD2	-5.29	117.82	121.00
1	C	67	TYR	CB-CG-CD2	-5.29	117.82	121.00
1	A	424	TYR	CB-CG-CD1	-5.29	117.83	121.00
1	C	424	TYR	CB-CG-CD1	-5.29	117.83	121.00
1	C	844	TYR	CB-CG-CD2	-5.29	117.83	121.00
1	B	67	TYR	CB-CG-CD2	-5.28	117.83	121.00
1	A	67	TYR	CB-CG-CD2	-5.27	117.84	121.00
1	A	250	TYR	CB-CG-CD1	-5.24	117.86	121.00
1	C	704	ARG	NE-CZ-NH1	5.23	122.92	120.30
1	A	614	CYS	CB-CA-C	-5.21	99.97	110.40
1	B	614	CYS	CB-CA-C	-5.21	99.98	110.40
1	A	704	ARG	NE-CZ-NH1	5.21	122.90	120.30
1	C	614	CYS	CB-CA-C	-5.21	99.99	110.40
1	B	704	ARG	NE-CZ-NH1	5.20	122.90	120.30
1	B	250	TYR	CB-CG-CD1	-5.17	117.90	121.00
1	A	667	TYR	CB-CG-CD1	-5.06	117.96	121.00
1	C	614	CYS	N-CA-C	5.06	124.65	111.00
1	A	945	ARG	NE-CZ-NH1	5.05	122.83	120.30
1	A	614	CYS	N-CA-C	5.05	124.64	111.00
1	C	667	TYR	CB-CG-CD1	-5.05	117.97	121.00
1	B	614	CYS	N-CA-C	5.05	124.63	111.00
1	B	667	TYR	CB-CG-CD1	-5.04	117.98	121.00
1	B	945	ARG	NE-CZ-NH1	5.00	122.80	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	9150	0	8848	12	0
1	B	9150	0	8848	11	0
1	C	9150	0	8848	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	39	0	34	0	0
2	E	39	0	34	0	0
2	F	39	0	34	0	0
2	G	39	0	34	0	0
2	M	39	0	34	0	0
2	N	39	0	34	0	0
2	O	39	0	34	0	0
2	P	39	0	34	0	0
2	Q	39	0	34	0	0
2	W	39	0	34	0	0
2	X	39	0	34	0	0
2	Y	39	0	34	0	0
2	Z	39	0	34	0	0
2	a	39	0	34	0	0
2	g	39	0	34	0	0
3	H	28	0	25	0	0
3	I	28	0	25	0	0
3	K	28	0	25	0	0
3	L	28	0	25	0	0
3	R	28	0	25	0	0
3	S	28	0	25	0	0
3	U	28	0	25	0	0
3	V	28	0	25	0	0
3	b	28	0	25	0	0
3	c	28	0	25	0	0
3	e	28	0	25	0	0
3	f	28	0	25	0	0
4	J	50	0	43	0	0
4	T	50	0	43	0	0
4	d	50	0	43	0	0
5	A	70	0	65	1	0
5	B	70	0	65	1	0
5	C	70	0	65	1	0
6	A	62	0	0	0	0
6	B	62	0	0	0	0
6	C	62	0	0	0	0
All	All	28917	0	27678	34	0

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

All (34) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:314:LEU:O	1:A:687:ARG:HB3	2.10	0.52
1:C:314:LEU:O	1:C:687:ARG:HB3	2.10	0.52
1:B:314:LEU:O	1:B:687:ARG:HB3	2.10	0.51
1:C:229:ASP:OD1	1:C:229:ASP:N	2.41	0.49
1:C:292:SER:OG	1:C:293:ASP:N	2.46	0.49
1:B:129:SER:OG	1:B:130:THR:N	2.47	0.48
1:A:129:SER:OG	1:A:130:THR:N	2.47	0.48
1:C:129:SER:OG	1:C:130:THR:N	2.47	0.48
1:B:83:SER:OG	1:B:84:VAL:N	2.48	0.47
1:A:292:SER:OG	1:A:293:ASP:N	2.46	0.46
1:B:229:ASP:OD1	1:B:229:ASP:N	2.41	0.46
1:C:897:SER:N	1:C:898:PRO:CD	2.79	0.46
1:B:772:THR:OG1	1:B:773:GLY:N	2.49	0.46
1:B:897:SER:N	1:B:898:PRO:CD	2.79	0.45
1:A:897:SER:N	1:A:898:PRO:CD	2.79	0.45
1:C:133:ASN:N	1:C:133:ASN:OD1	2.48	0.45
1:A:155:LEU:HD21	5:A:1429:NAG:H82	1.98	0.45
1:C:155:LEU:HD21	5:C:1429:NAG:H82	1.98	0.45
1:A:821:LYS:NZ	1:A:863:ASP:OD2	2.41	0.45
1:A:772:THR:OG1	1:A:773:GLY:N	2.49	0.44
1:A:229:ASP:OD1	1:A:229:ASP:N	2.41	0.44
1:C:772:THR:OG1	1:C:773:GLY:N	2.49	0.44
1:B:155:LEU:HD21	5:B:1429:NAG:H82	1.98	0.44
1:A:133:ASN:N	1:A:133:ASN:OD1	2.48	0.44
1:B:133:ASN:OD1	1:B:133:ASN:N	2.48	0.44
1:C:83:SER:OG	1:C:84:VAL:N	2.48	0.44
1:B:1131:SER:OG	1:B:1132:SER:N	2.50	0.44
1:B:292:SER:OG	1:B:293:ASP:N	2.46	0.43
1:A:83:SER:OG	1:A:84:VAL:N	2.48	0.41
1:A:739:ASN:OD1	1:A:739:ASN:C	2.58	0.41
1:B:739:ASN:C	1:B:739:ASN:OD1	2.58	0.41
1:A:136:TYR:CE2	1:A:198:LEU:HG	2.56	0.41
1:C:136:TYR:CE2	1:C:198:LEU:HG	2.56	0.40
1:C:739:ASN:C	1:C:739:ASN:OD1	2.58	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1163/1322 (88%)	1141 (98%)	22 (2%)	0	100	100
1	B	1163/1322 (88%)	1141 (98%)	22 (2%)	0	100	100
1	C	1163/1322 (88%)	1141 (98%)	22 (2%)	0	100	100
All	All	3489/3966 (88%)	3423 (98%)	66 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1022/1151 (89%)	1017 (100%)	5 (0%)	86	96
1	B	1022/1151 (89%)	1017 (100%)	5 (0%)	86	96
1	C	1022/1151 (89%)	1017 (100%)	5 (0%)	86	96
All	All	3066/3453 (89%)	3051 (100%)	15 (0%)	85	96

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	59	ASN
1	A	187	LEU
1	A	244	MET
1	A	714	ASN
1	A	1224	ASN

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Mol	Chain	Res	Type
1	B	59	ASN
1	B	187	LEU
1	B	244	MET
1	B	714	ASN
1	B	1224	ASN
1	C	59	ASN
1	C	187	LEU
1	C	244	MET
1	C	714	ASN
1	C	1224	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	183	HIS
1	B	183	HIS
1	C	183	HIS

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 ⓘ

81 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	NAG	D	1	1,2	14,14,15	0.71	0	17,19,21	0.81	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	D	2	2	14,14,15	0.78	1 (7%)	17,19,21	0.75	0
2	BMA	D	3	2	11,11,12	0.60	0	15,15,17	0.74	0
2	NAG	E	1	1,2	14,14,15	0.74	1 (7%)	17,19,21	1.13	2 (11%)
2	NAG	E	2	2	14,14,15	0.76	0	17,19,21	1.16	1 (5%)
2	BMA	E	3	2	11,11,12	0.72	0	15,15,17	0.71	0
2	NAG	F	1	1,2	14,14,15	0.92	1 (7%)	17,19,21	1.21	2 (11%)
2	NAG	F	2	2	14,14,15	0.87	1 (7%)	17,19,21	1.65	4 (23%)
2	BMA	F	3	2	11,11,12	0.64	0	15,15,17	0.75	1 (6%)
2	NAG	G	1	1,2	14,14,15	0.63	0	17,19,21	1.12	1 (5%)
2	NAG	G	2	2	14,14,15	0.78	0	17,19,21	0.96	1 (5%)
2	BMA	G	3	2	11,11,12	0.54	0	15,15,17	0.64	0
3	NAG	H	1	1,3	14,14,15	0.65	0	17,19,21	0.98	1 (5%)
3	NAG	H	2	3	14,14,15	0.67	1 (7%)	17,19,21	0.90	1 (5%)
3	NAG	I	1	1,3	14,14,15	0.80	1 (7%)	17,19,21	1.34	3 (17%)
3	NAG	I	2	3	14,14,15	0.88	1 (7%)	17,19,21	0.82	1 (5%)
4	NAG	J	1	1,4	14,14,15	0.64	0	17,19,21	0.85	1 (5%)
4	NAG	J	2	4	14,14,15	0.76	0	17,19,21	1.28	2 (11%)
4	BMA	J	3	4	11,11,12	0.78	0	15,15,17	1.03	1 (6%)
4	MAN	J	4	4	11,11,12	0.66	0	15,15,17	0.75	1 (6%)
3	NAG	K	1	1,3	14,14,15	0.72	0	17,19,21	0.79	1 (5%)
3	NAG	K	2	3	14,14,15	0.86	1 (7%)	17,19,21	0.76	1 (5%)
3	NAG	L	1	1,3	14,14,15	0.66	0	17,19,21	0.83	1 (5%)
3	NAG	L	2	3	14,14,15	0.84	1 (7%)	17,19,21	0.77	1 (5%)
2	NAG	M	1	1,2	14,14,15	0.76	1 (7%)	17,19,21	1.36	3 (17%)
2	NAG	M	2	2	14,14,15	0.82	0	17,19,21	1.38	3 (17%)
2	BMA	M	3	2	11,11,12	0.82	1 (9%)	15,15,17	0.73	0
2	NAG	N	1	1,2	14,14,15	0.71	0	17,19,21	0.81	0
2	NAG	N	2	2	14,14,15	0.78	1 (7%)	17,19,21	0.75	0
2	BMA	N	3	2	11,11,12	0.61	0	15,15,17	0.74	0
2	NAG	O	1	1,2	14,14,15	0.73	1 (7%)	17,19,21	1.13	2 (11%)
2	NAG	O	2	2	14,14,15	0.77	0	17,19,21	1.17	1 (5%)
2	BMA	O	3	2	11,11,12	0.72	0	15,15,17	0.71	0
2	NAG	P	1	1,2	14,14,15	0.92	1 (7%)	17,19,21	1.21	2 (11%)
2	NAG	P	2	2	14,14,15	0.88	1 (7%)	17,19,21	1.65	4 (23%)
2	BMA	P	3	2	11,11,12	0.63	0	15,15,17	0.76	1 (6%)
2	NAG	Q	1	1,2	14,14,15	0.63	0	17,19,21	1.13	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	Q	2	2	14,14,15	0.78	1 (7%)	17,19,21	0.96	1 (5%)
2	BMA	Q	3	2	11,11,12	0.53	0	15,15,17	0.64	0
3	NAG	R	1	1,3	14,14,15	0.66	0	17,19,21	0.98	1 (5%)
3	NAG	R	2	3	14,14,15	0.67	1 (7%)	17,19,21	0.90	1 (5%)
3	NAG	S	1	1,3	14,14,15	0.80	1 (7%)	17,19,21	1.34	3 (17%)
3	NAG	S	2	3	14,14,15	0.88	1 (7%)	17,19,21	0.81	1 (5%)
4	NAG	T	1	1,4	14,14,15	0.63	0	17,19,21	0.86	1 (5%)
4	NAG	T	2	4	14,14,15	0.76	0	17,19,21	1.28	2 (11%)
4	BMA	T	3	4	11,11,12	0.78	0	15,15,17	1.03	1 (6%)
4	MAN	T	4	4	11,11,12	0.65	0	15,15,17	0.75	1 (6%)
3	NAG	U	1	1,3	14,14,15	0.72	0	17,19,21	0.79	1 (5%)
3	NAG	U	2	3	14,14,15	0.85	1 (7%)	17,19,21	0.75	1 (5%)
3	NAG	V	1	1,3	14,14,15	0.66	0	17,19,21	0.84	1 (5%)
3	NAG	V	2	3	14,14,15	0.82	1 (7%)	17,19,21	0.77	1 (5%)
2	NAG	W	1	1,2	14,14,15	0.76	1 (7%)	17,19,21	1.36	3 (17%)
2	NAG	W	2	2	14,14,15	0.82	0	17,19,21	1.39	3 (17%)
2	BMA	W	3	2	11,11,12	0.82	1 (9%)	15,15,17	0.73	0
2	NAG	X	1	1,2	14,14,15	0.70	0	17,19,21	0.81	0
2	NAG	X	2	2	14,14,15	0.79	1 (7%)	17,19,21	0.75	0
2	BMA	X	3	2	11,11,12	0.60	0	15,15,17	0.74	0
2	NAG	Y	1	1,2	14,14,15	0.73	1 (7%)	17,19,21	1.13	2 (11%)
2	NAG	Y	2	2	14,14,15	0.76	0	17,19,21	1.15	1 (5%)
2	BMA	Y	3	2	11,11,12	0.72	0	15,15,17	0.72	0
2	NAG	Z	1	1,2	14,14,15	0.92	1 (7%)	17,19,21	1.22	2 (11%)
2	NAG	Z	2	2	14,14,15	0.87	1 (7%)	17,19,21	1.64	4 (23%)
2	BMA	Z	3	2	11,11,12	0.63	0	15,15,17	0.76	1 (6%)
2	NAG	a	1	1,2	14,14,15	0.61	0	17,19,21	1.12	1 (5%)
2	NAG	a	2	2	14,14,15	0.78	1 (7%)	17,19,21	0.96	1 (5%)
2	BMA	a	3	2	11,11,12	0.53	0	15,15,17	0.64	0
3	NAG	b	1	1,3	14,14,15	0.65	0	17,19,21	0.98	1 (5%)
3	NAG	b	2	3	14,14,15	0.65	0	17,19,21	0.90	1 (5%)
3	NAG	c	1	1,3	14,14,15	0.80	1 (7%)	17,19,21	1.34	2 (11%)
3	NAG	c	2	3	14,14,15	0.88	1 (7%)	17,19,21	0.82	1 (5%)
4	NAG	d	1	1,4	14,14,15	0.63	0	17,19,21	0.85	1 (5%)
4	NAG	d	2	4	14,14,15	0.76	0	17,19,21	1.27	2 (11%)
4	BMA	d	3	4	11,11,12	0.79	0	15,15,17	1.03	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	MAN	d	4	4	11,11,12	0.67	0	15,15,17	0.75	1 (6%)
3	NAG	e	1	1,3	14,14,15	0.73	0	17,19,21	0.80	1 (5%)
3	NAG	e	2	3	14,14,15	0.86	1 (7%)	17,19,21	0.75	1 (5%)
3	NAG	f	1	1,3	14,14,15	0.66	0	17,19,21	0.83	1 (5%)
3	NAG	f	2	3	14,14,15	0.83	1 (7%)	17,19,21	0.77	1 (5%)
2	NAG	g	1	1,2	14,14,15	0.75	1 (7%)	17,19,21	1.36	3 (17%)
2	NAG	g	2	2	14,14,15	0.82	0	17,19,21	1.38	3 (17%)
2	BMA	g	3	2	11,11,12	0.82	1 (9%)	15,15,17	0.73	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	D	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1
2	BMA	D	3	2	-	1/2/19/22	0/1/1/1
2	NAG	E	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	E	2	2	-	2/6/23/26	0/1/1/1
2	BMA	E	3	2	-	1/2/19/22	0/1/1/1
2	NAG	F	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	F	2	2	-	2/6/23/26	0/1/1/1
2	BMA	F	3	2	-	1/2/19/22	0/1/1/1
2	NAG	G	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	G	2	2	-	2/6/23/26	0/1/1/1
2	BMA	G	3	2	-	2/2/19/22	0/1/1/1
3	NAG	H	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	H	2	3	-	0/6/23/26	0/1/1/1
3	NAG	I	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	I	2	3	-	2/6/23/26	0/1/1/1
4	NAG	J	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	J	2	4	-	2/6/23/26	0/1/1/1
4	BMA	J	3	4	-	1/2/19/22	0/1/1/1
4	MAN	J	4	4	-	1/2/19/22	0/1/1/1
3	NAG	K	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	K	2	3	-	1/6/23/26	0/1/1/1
3	NAG	L	1	1,3	-	0/6/23/26	0/1/1/1

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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BMA	Z	3	2	-	1/2/19/22	0/1/1/1
2	NAG	a	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	a	2	2	-	2/6/23/26	0/1/1/1
2	BMA	a	3	2	-	2/2/19/22	0/1/1/1
3	NAG	b	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	b	2	3	-	0/6/23/26	0/1/1/1
3	NAG	c	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	c	2	3	-	2/6/23/26	0/1/1/1
4	NAG	d	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	d	2	4	-	2/6/23/26	0/1/1/1
4	BMA	d	3	4	-	1/2/19/22	0/1/1/1
4	MAN	d	4	4	-	1/2/19/22	0/1/1/1
3	NAG	e	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	e	2	3	-	1/6/23/26	0/1/1/1
3	NAG	f	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	f	2	3	-	1/6/23/26	0/1/1/1
2	NAG	g	1	1,2	-	1/6/23/26	0/1/1/1
2	NAG	g	2	2	-	2/6/23/26	0/1/1/1
2	BMA	g	3	2	-	1/2/19/22	0/1/1/1

All (34) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	2	NAG	C1-C2	2.88	1.56	1.52
3	S	2	NAG	C1-C2	2.87	1.56	1.52
3	c	2	NAG	C1-C2	2.85	1.56	1.52
3	e	2	NAG	C1-C2	2.82	1.56	1.52
3	K	2	NAG	C1-C2	2.82	1.56	1.52
3	U	2	NAG	C1-C2	2.78	1.56	1.52
2	Z	1	NAG	C1-C2	2.76	1.56	1.52
2	F	1	NAG	C1-C2	2.72	1.56	1.52
2	P	1	NAG	C1-C2	2.72	1.56	1.52
3	L	2	NAG	C1-C2	2.65	1.56	1.52
3	f	2	NAG	C1-C2	2.60	1.55	1.52
3	V	2	NAG	C1-C2	2.56	1.55	1.52
2	P	2	NAG	C1-C2	2.51	1.55	1.52
2	F	2	NAG	C1-C2	2.49	1.55	1.52
2	Z	2	NAG	C1-C2	2.47	1.55	1.52
3	S	1	NAG	C1-C2	2.46	1.55	1.52
3	c	1	NAG	C1-C2	2.45	1.55	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	1	NAG	C1-C2	2.44	1.55	1.52
2	X	2	NAG	C1-C2	2.32	1.55	1.52
2	D	2	NAG	C1-C2	2.29	1.55	1.52
2	N	2	NAG	C1-C2	2.26	1.55	1.52
2	g	3	BMA	C1-C2	2.26	1.57	1.52
2	M	3	BMA	C1-C2	2.25	1.57	1.52
2	W	3	BMA	C1-C2	2.24	1.57	1.52
2	M	1	NAG	C1-C2	2.18	1.55	1.52
2	W	1	NAG	C1-C2	2.18	1.55	1.52
2	g	1	NAG	C1-C2	2.16	1.55	1.52
2	E	1	NAG	C1-C2	2.13	1.55	1.52
2	Y	1	NAG	C1-C2	2.11	1.55	1.52
2	O	1	NAG	C1-C2	2.10	1.55	1.52
3	R	2	NAG	C1-C2	2.01	1.55	1.52
3	H	2	NAG	C1-C2	2.01	1.55	1.52
2	a	2	NAG	C1-C2	2.00	1.55	1.52
2	Q	2	NAG	C1-C2	2.00	1.55	1.52

All (98) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	2	NAG	C4-C3-C2	-4.39	104.59	111.02
2	P	2	NAG	C4-C3-C2	-4.39	104.59	111.02
2	Z	2	NAG	C4-C3-C2	-4.36	104.63	111.02
3	c	1	NAG	C1-O5-C5	-3.58	107.38	112.19
3	I	1	NAG	C1-O5-C5	-3.57	107.40	112.19
3	S	1	NAG	C1-O5-C5	-3.55	107.43	112.19
2	g	1	NAG	C3-C4-C5	-3.16	104.51	110.23
2	M	1	NAG	C3-C4-C5	-3.14	104.53	110.23
2	W	1	NAG	C3-C4-C5	-3.14	104.55	110.23
2	M	1	NAG	O4-C4-C3	-3.13	103.01	110.38
2	g	1	NAG	O4-C4-C3	-3.12	103.01	110.38
2	W	1	NAG	O4-C4-C3	-3.12	103.03	110.38
2	Y	1	NAG	C3-C4-C5	-3.02	104.75	110.23
2	O	1	NAG	C3-C4-C5	-3.01	104.78	110.23
2	E	1	NAG	C3-C4-C5	-3.00	104.79	110.23
3	b	2	NAG	C4-C3-C2	-2.83	106.86	111.02
3	H	2	NAG	C4-C3-C2	-2.82	106.89	111.02
3	R	2	NAG	C4-C3-C2	-2.81	106.90	111.02
2	Q	1	NAG	C3-C4-C5	-2.81	105.14	110.23
2	G	1	NAG	C3-C4-C5	-2.78	105.19	110.23
2	a	1	NAG	C3-C4-C5	-2.77	105.22	110.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	W	2	NAG	C3-C4-C5	-2.67	105.40	110.23
2	M	2	NAG	C3-C4-C5	-2.64	105.44	110.23
2	g	2	NAG	C3-C4-C5	-2.63	105.46	110.23
2	g	2	NAG	O4-C4-C3	2.56	116.41	110.38
4	d	2	NAG	C3-C4-C5	-2.56	105.59	110.23
2	W	2	NAG	O4-C4-C3	2.56	116.41	110.38
4	J	2	NAG	C3-C4-C5	-2.55	105.60	110.23
2	M	2	NAG	O4-C4-C3	2.55	116.39	110.38
4	T	2	NAG	C3-C4-C5	-2.55	105.61	110.23
3	U	1	NAG	C3-C4-C5	-2.44	105.81	110.23
2	P	2	NAG	O5-C1-C2	-2.44	107.52	111.29
3	e	1	NAG	C3-C4-C5	-2.43	105.82	110.23
3	K	1	NAG	C3-C4-C5	-2.43	105.82	110.23
2	O	2	NAG	C3-C4-C5	-2.43	105.83	110.23
2	E	2	NAG	C3-C4-C5	-2.42	105.84	110.23
2	F	2	NAG	O5-C1-C2	-2.42	107.55	111.29
2	Y	2	NAG	C3-C4-C5	-2.40	105.88	110.23
2	F	1	NAG	C1-O5-C5	-2.40	108.97	112.19
2	P	1	NAG	C1-O5-C5	-2.39	108.98	112.19
2	Z	2	NAG	O5-C1-C2	-2.38	107.60	111.29
3	I	1	NAG	O4-C4-C5	-2.37	103.49	109.32
2	Z	1	NAG	C1-O5-C5	-2.37	109.01	112.19
3	S	1	NAG	O4-C4-C5	-2.36	103.50	109.32
4	J	2	NAG	O4-C4-C3	2.36	115.94	110.38
4	T	2	NAG	O4-C4-C3	2.36	115.94	110.38
3	c	1	NAG	O4-C4-C5	-2.36	103.52	109.32
4	d	2	NAG	O4-C4-C3	2.36	115.93	110.38
2	Z	2	NAG	O4-C4-C5	2.35	115.12	109.32
2	F	2	NAG	O4-C4-C5	2.35	115.10	109.32
2	P	2	NAG	O4-C4-C5	2.34	115.09	109.32
3	c	2	NAG	C4-C3-C2	-2.33	107.61	111.02
3	f	1	NAG	C3-C4-C5	-2.32	106.02	110.23
3	V	1	NAG	C3-C4-C5	-2.32	106.03	110.23
3	L	1	NAG	C3-C4-C5	-2.32	106.03	110.23
3	I	2	NAG	C4-C3-C2	-2.30	107.64	111.02
3	S	2	NAG	C4-C3-C2	-2.28	107.68	111.02
2	Y	1	NAG	O4-C4-C3	-2.27	105.02	110.38
2	O	1	NAG	O4-C4-C3	-2.27	105.03	110.38
3	e	2	NAG	C4-C3-C2	-2.26	107.70	111.02
2	E	1	NAG	O4-C4-C3	-2.26	105.05	110.38
3	K	2	NAG	C4-C3-C2	-2.25	107.72	111.02
3	U	2	NAG	C4-C3-C2	-2.24	107.73	111.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	P	2	NAG	C1-O5-C5	2.24	115.19	112.19
2	a	2	NAG	C3-C4-C5	-2.22	106.21	110.23
2	G	2	NAG	C3-C4-C5	-2.22	106.21	110.23
2	W	2	NAG	O3-C3-C2	-2.21	104.81	109.40
2	Q	2	NAG	C3-C4-C5	-2.21	106.23	110.23
2	M	2	NAG	O3-C3-C2	-2.20	104.83	109.40
2	F	2	NAG	C1-O5-C5	2.20	115.14	112.19
2	g	2	NAG	O3-C3-C2	-2.19	104.86	109.40
2	F	1	NAG	C3-C4-C5	-2.18	106.28	110.23
2	Z	1	NAG	C3-C4-C5	-2.18	106.28	110.23
2	Z	2	NAG	C1-O5-C5	2.17	115.10	112.19
2	P	1	NAG	C3-C4-C5	-2.17	106.30	110.23
2	Z	3	BMA	C2-C3-C4	-2.17	107.05	110.86
2	F	3	BMA	C2-C3-C4	-2.16	107.06	110.86
2	P	3	BMA	C2-C3-C4	-2.15	107.08	110.86
2	W	1	NAG	C4-C3-C2	2.12	114.12	111.02
2	M	1	NAG	C4-C3-C2	2.11	114.11	111.02
2	g	1	NAG	C4-C3-C2	2.10	114.10	111.02
4	T	3	BMA	C2-C3-C4	-2.09	107.19	110.86
4	T	4	MAN	C2-C3-C4	-2.09	107.19	110.86
4	J	4	MAN	C2-C3-C4	-2.09	107.19	110.86
3	V	2	NAG	C4-C3-C2	-2.09	107.96	111.02
4	d	4	MAN	C2-C3-C4	-2.08	107.20	110.86
4	J	3	BMA	C2-C3-C4	-2.08	107.21	110.86
3	H	1	NAG	C4-C3-C2	-2.06	108.00	111.02
3	L	2	NAG	C4-C3-C2	-2.05	108.01	111.02
3	f	2	NAG	C4-C3-C2	-2.05	108.02	111.02
4	d	3	BMA	C2-C3-C4	-2.05	107.26	110.86
3	R	1	NAG	C4-C3-C2	-2.04	108.03	111.02
3	b	1	NAG	C4-C3-C2	-2.04	108.03	111.02
3	S	1	NAG	C3-C4-C5	-2.04	106.54	110.23
3	I	1	NAG	C3-C4-C5	-2.02	106.56	110.23
4	T	1	NAG	C3-C4-C5	-2.02	106.57	110.23
4	J	1	NAG	C3-C4-C5	-2.01	106.59	110.23
4	d	1	NAG	C3-C4-C5	-2.01	106.59	110.23

There are no chirality outliers.

All (93) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	2	NAG	O5-C5-C6-O6
2	O	2	NAG	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
2	Y	2	NAG	O5-C5-C6-O6
3	H	1	NAG	O5-C5-C6-O6
3	R	1	NAG	O5-C5-C6-O6
3	b	1	NAG	O5-C5-C6-O6
2	D	2	NAG	O5-C5-C6-O6
2	N	2	NAG	O5-C5-C6-O6
2	X	2	NAG	O5-C5-C6-O6
3	I	2	NAG	O5-C5-C6-O6
3	S	2	NAG	O5-C5-C6-O6
3	c	2	NAG	O5-C5-C6-O6
2	D	2	NAG	C4-C5-C6-O6
2	F	2	NAG	C4-C5-C6-O6
2	N	2	NAG	C4-C5-C6-O6
2	P	2	NAG	C4-C5-C6-O6
2	X	2	NAG	C4-C5-C6-O6
2	G	2	NAG	O5-C5-C6-O6
2	Q	2	NAG	O5-C5-C6-O6
2	a	2	NAG	O5-C5-C6-O6
2	Z	2	NAG	C4-C5-C6-O6
3	H	1	NAG	C4-C5-C6-O6
3	R	1	NAG	C4-C5-C6-O6
3	b	1	NAG	C4-C5-C6-O6
2	G	3	BMA	O5-C5-C6-O6
2	Q	3	BMA	O5-C5-C6-O6
2	a	3	BMA	O5-C5-C6-O6
4	T	2	NAG	O5-C5-C6-O6
2	E	2	NAG	C4-C5-C6-O6
2	O	2	NAG	C4-C5-C6-O6
2	Y	2	NAG	C4-C5-C6-O6
4	J	1	NAG	O5-C5-C6-O6
4	J	2	NAG	O5-C5-C6-O6
4	d	1	NAG	O5-C5-C6-O6
4	d	2	NAG	O5-C5-C6-O6
2	M	2	NAG	O5-C5-C6-O6
2	W	2	NAG	O5-C5-C6-O6
2	g	2	NAG	O5-C5-C6-O6
4	T	1	NAG	O5-C5-C6-O6
2	M	2	NAG	C4-C5-C6-O6
2	W	2	NAG	C4-C5-C6-O6
2	g	2	NAG	C4-C5-C6-O6
2	G	1	NAG	O5-C5-C6-O6
2	Q	1	NAG	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
2	a	1	NAG	O5-C5-C6-O6
4	J	2	NAG	C4-C5-C6-O6
4	T	2	NAG	C4-C5-C6-O6
4	d	2	NAG	C4-C5-C6-O6
2	G	2	NAG	C4-C5-C6-O6
2	Q	2	NAG	C4-C5-C6-O6
2	a	2	NAG	C4-C5-C6-O6
4	J	4	MAN	O5-C5-C6-O6
4	T	4	MAN	O5-C5-C6-O6
4	d	4	MAN	O5-C5-C6-O6
2	F	2	NAG	O5-C5-C6-O6
2	P	2	NAG	O5-C5-C6-O6
2	Z	2	NAG	O5-C5-C6-O6
4	J	1	NAG	C4-C5-C6-O6
4	T	1	NAG	C4-C5-C6-O6
4	d	1	NAG	C4-C5-C6-O6
3	I	2	NAG	C4-C5-C6-O6
3	S	2	NAG	C4-C5-C6-O6
3	c	2	NAG	C4-C5-C6-O6
2	G	1	NAG	C4-C5-C6-O6
2	Q	1	NAG	C4-C5-C6-O6
2	a	1	NAG	C4-C5-C6-O6
2	D	3	BMA	O5-C5-C6-O6
2	N	3	BMA	O5-C5-C6-O6
2	X	3	BMA	O5-C5-C6-O6
2	E	3	BMA	O5-C5-C6-O6
2	O	3	BMA	O5-C5-C6-O6
2	Y	3	BMA	O5-C5-C6-O6
2	M	3	BMA	O5-C5-C6-O6
2	W	3	BMA	O5-C5-C6-O6
2	g	3	BMA	O5-C5-C6-O6
2	F	3	BMA	O5-C5-C6-O6
2	P	3	BMA	O5-C5-C6-O6
2	Z	3	BMA	O5-C5-C6-O6
3	L	2	NAG	O5-C5-C6-O6
3	V	2	NAG	O5-C5-C6-O6
3	f	2	NAG	O5-C5-C6-O6
4	J	3	BMA	O5-C5-C6-O6
4	T	3	BMA	O5-C5-C6-O6
4	d	3	BMA	O5-C5-C6-O6
3	K	2	NAG	O5-C5-C6-O6
3	U	2	NAG	O5-C5-C6-O6

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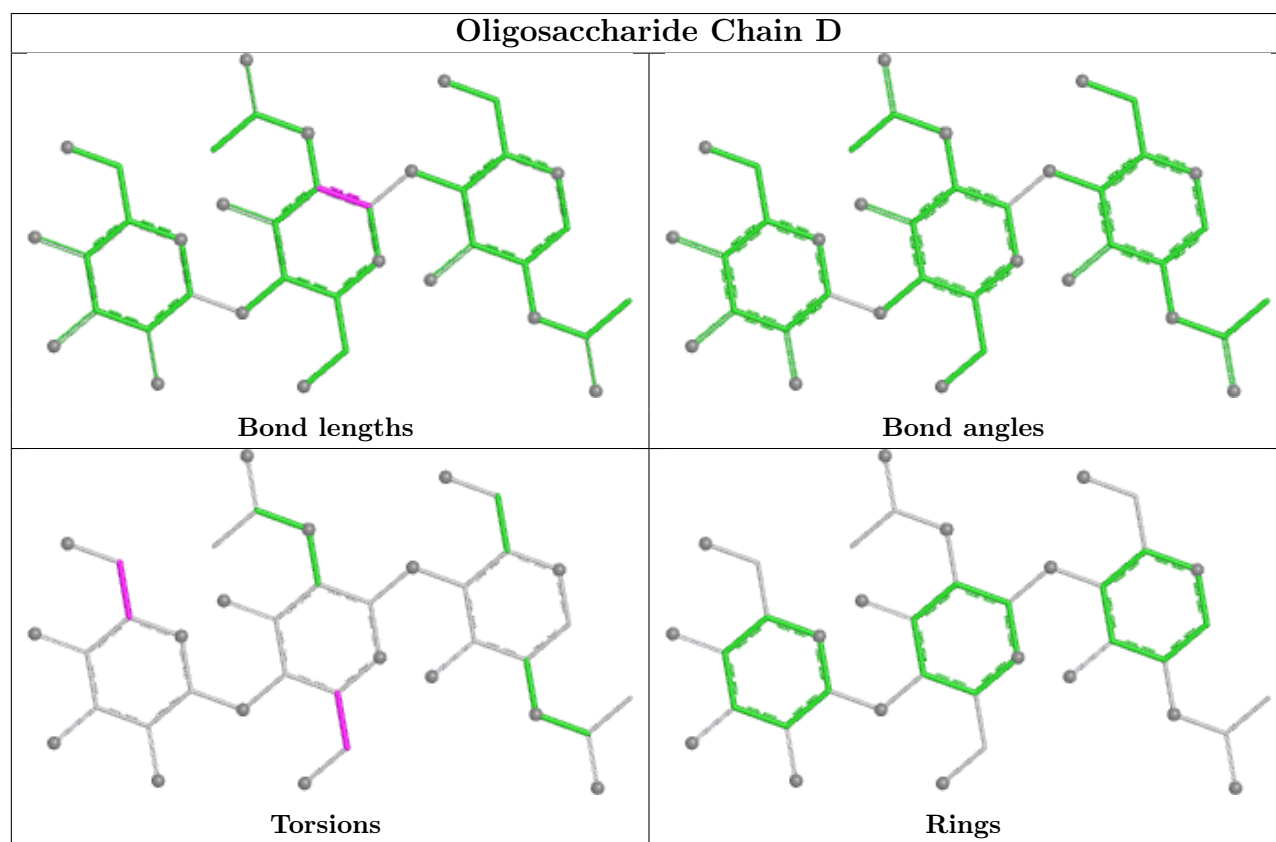
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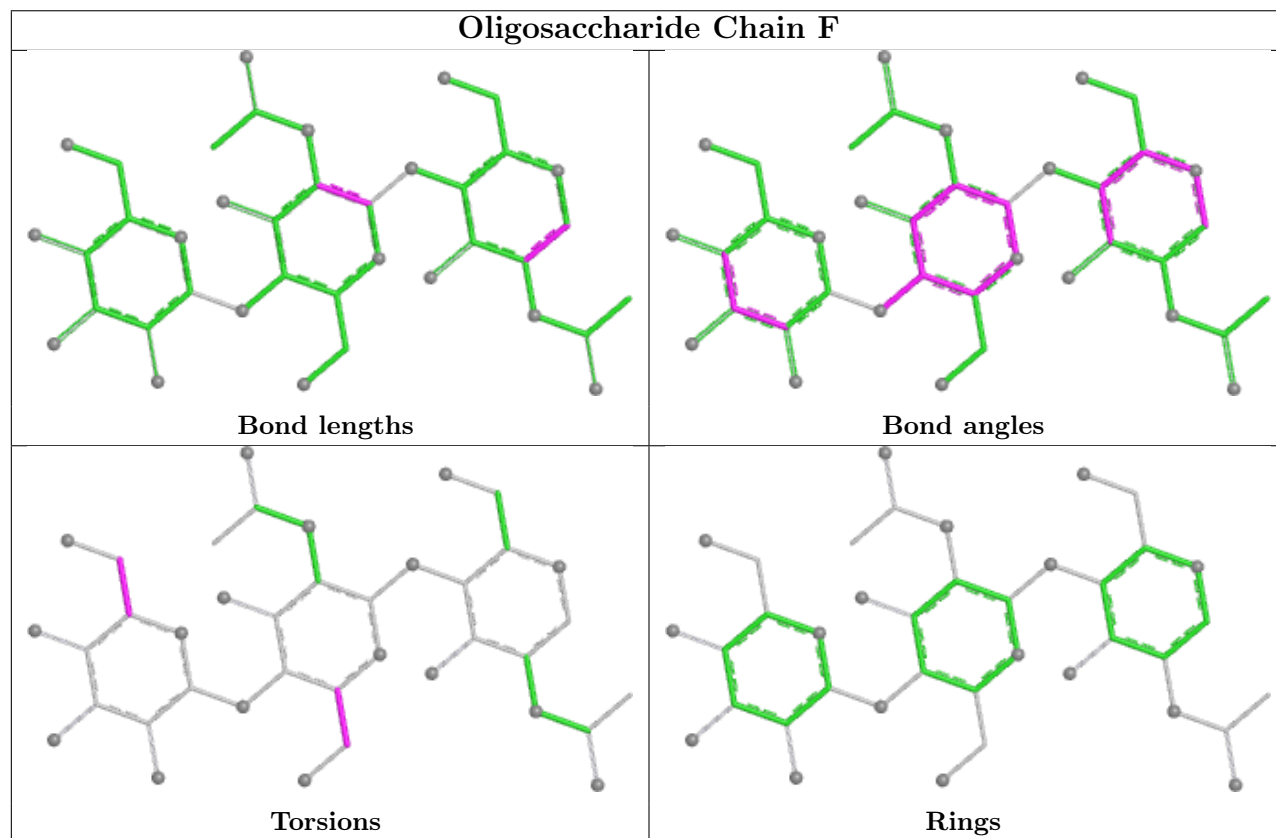
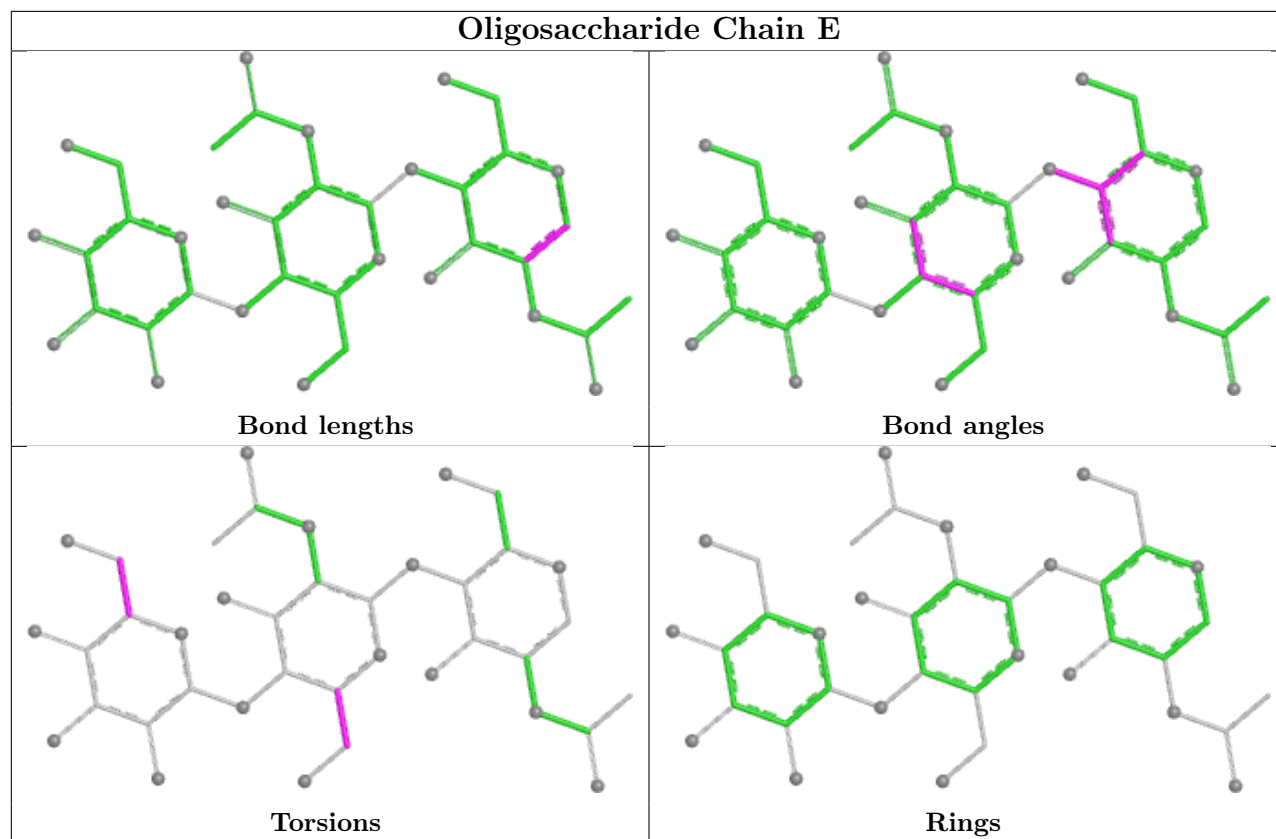
Mol	Chain	Res	Type	Atoms
3	e	2	NAG	O5-C5-C6-O6
2	M	1	NAG	O5-C5-C6-O6
2	W	1	NAG	O5-C5-C6-O6
2	g	1	NAG	O5-C5-C6-O6
2	Q	3	BMA	C4-C5-C6-O6
2	a	3	BMA	C4-C5-C6-O6
2	G	3	BMA	C4-C5-C6-O6

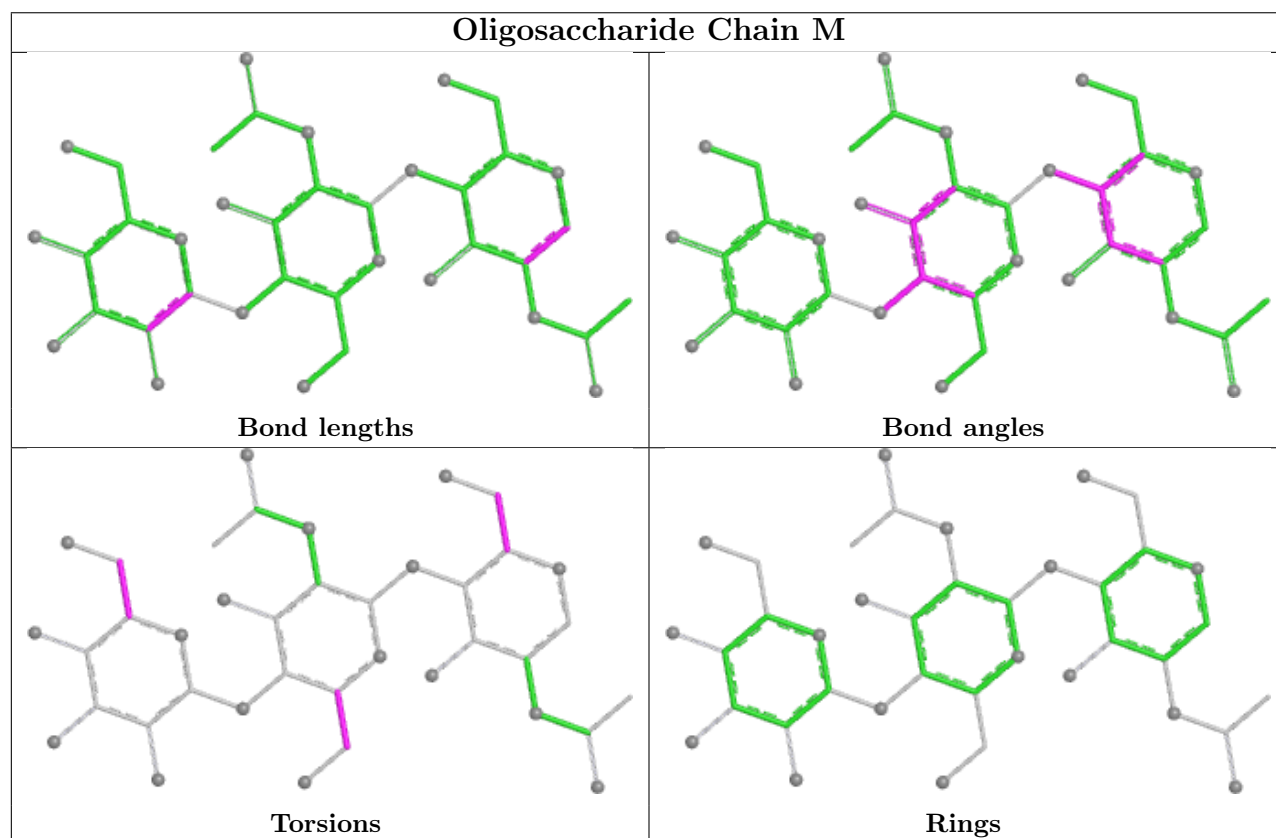
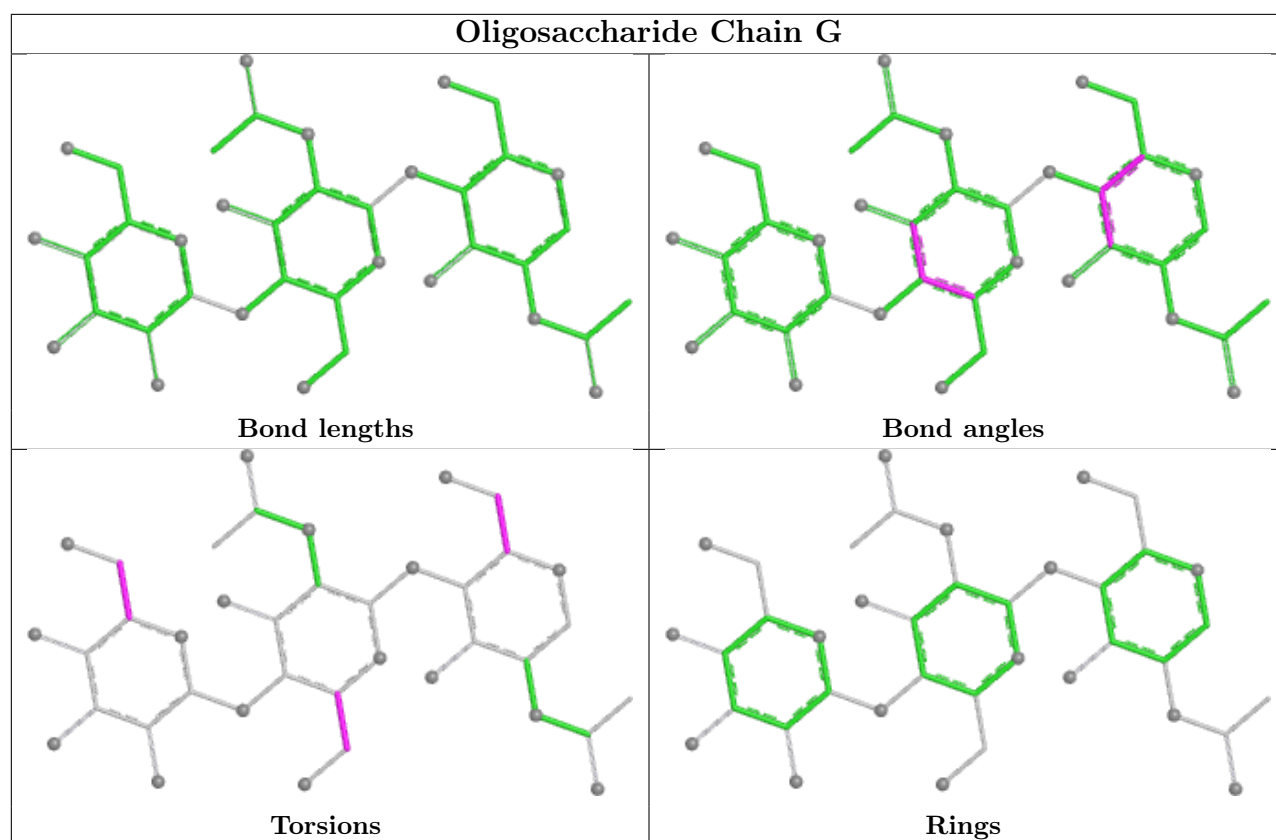
There are no ring outliers.

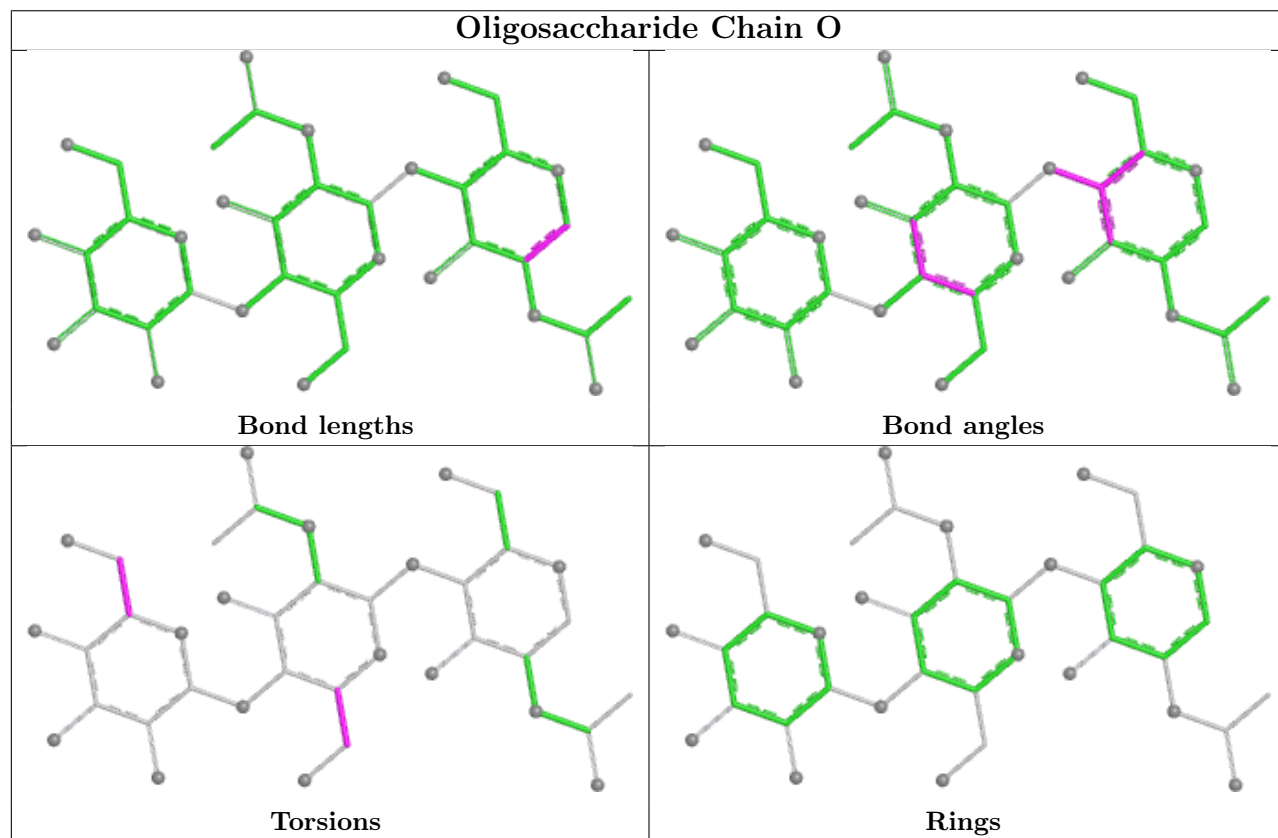
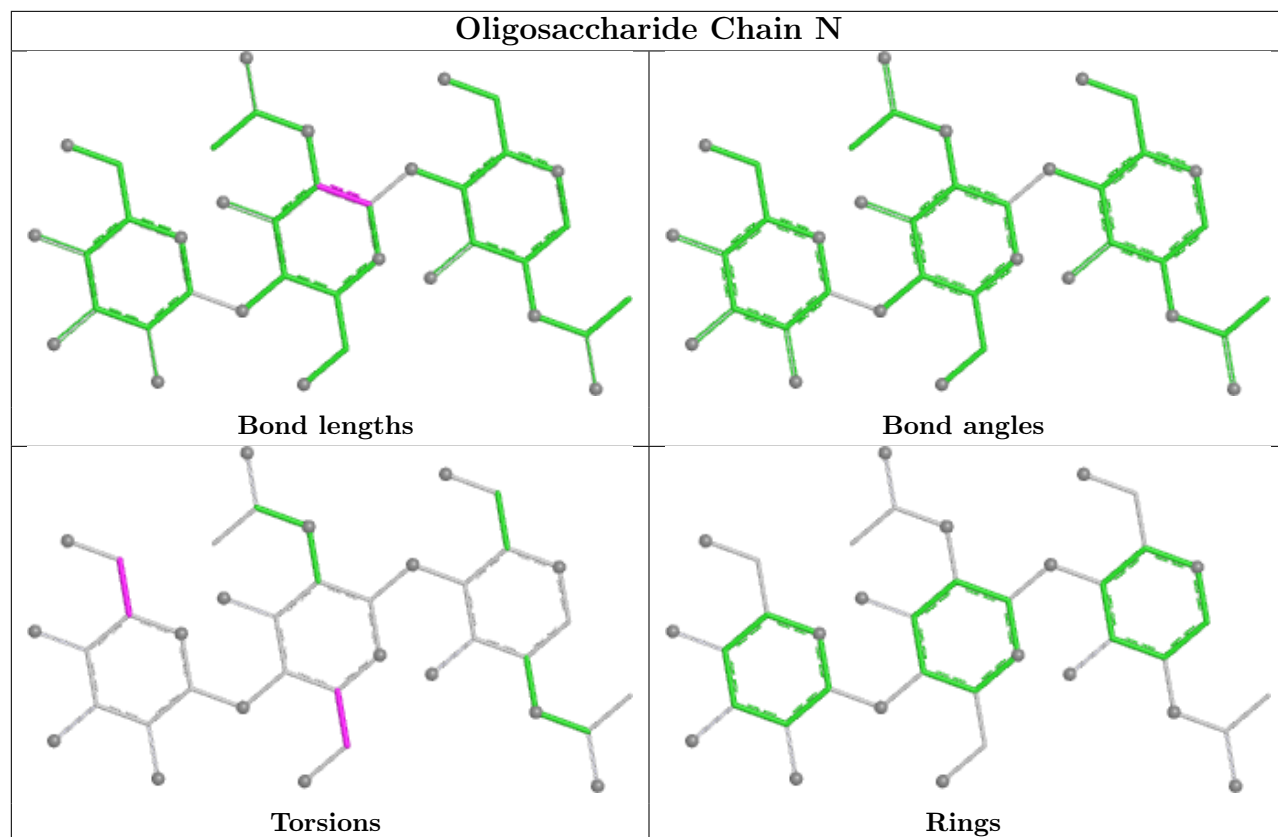
No monomer is involved in short contacts.

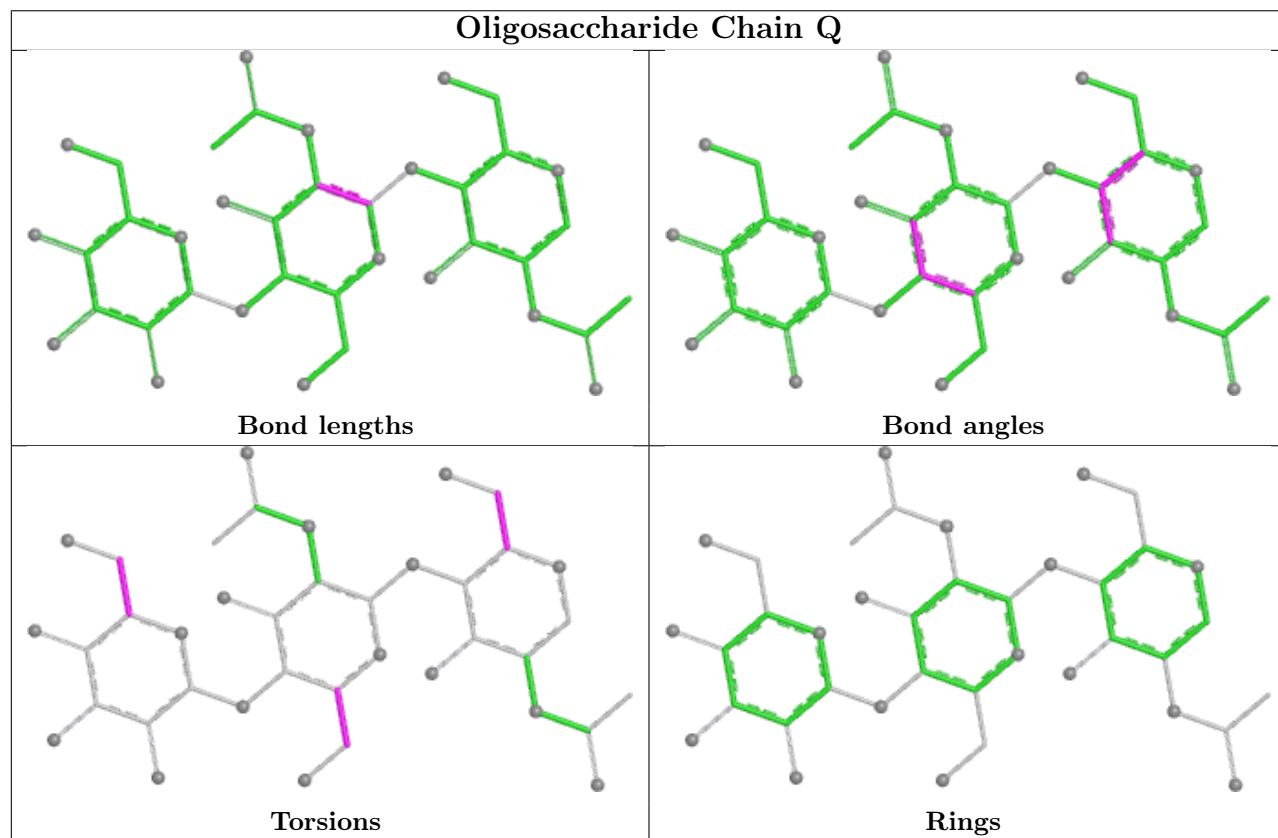
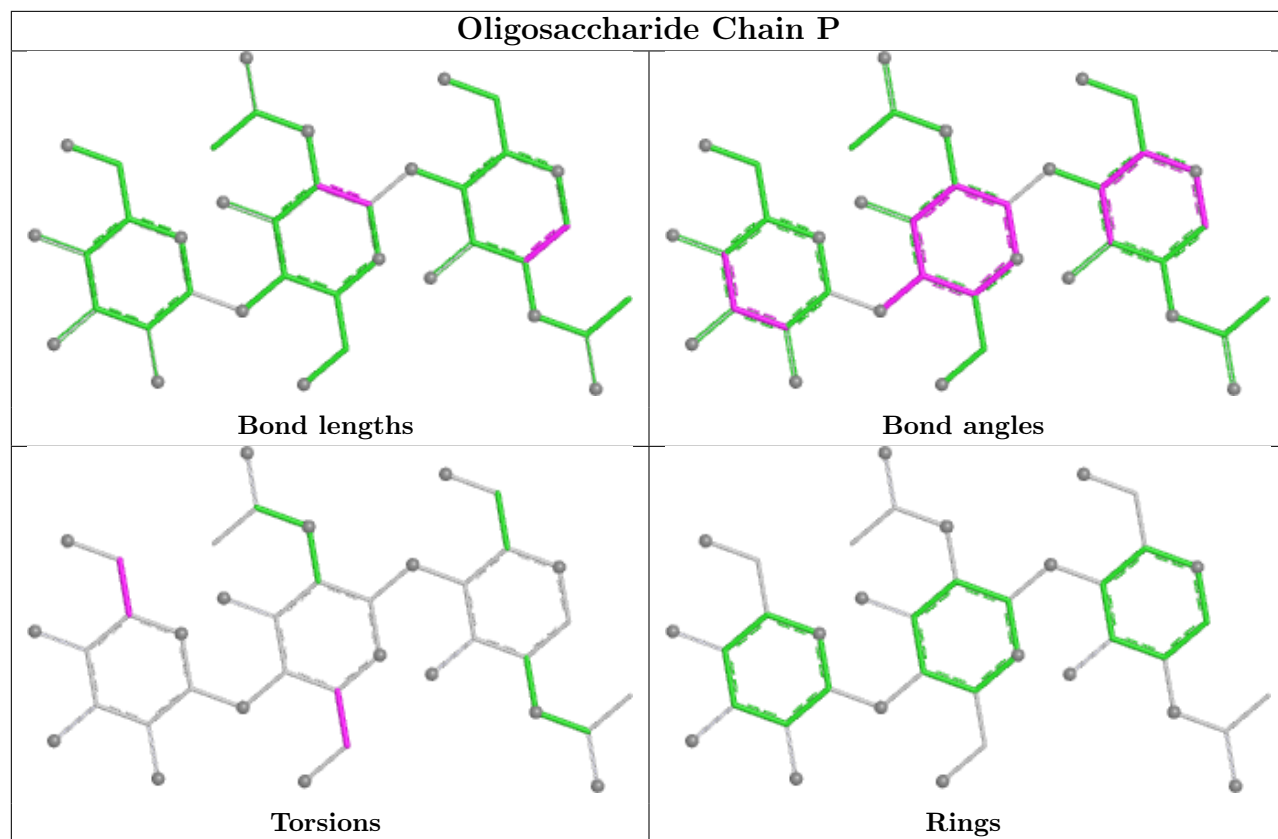
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

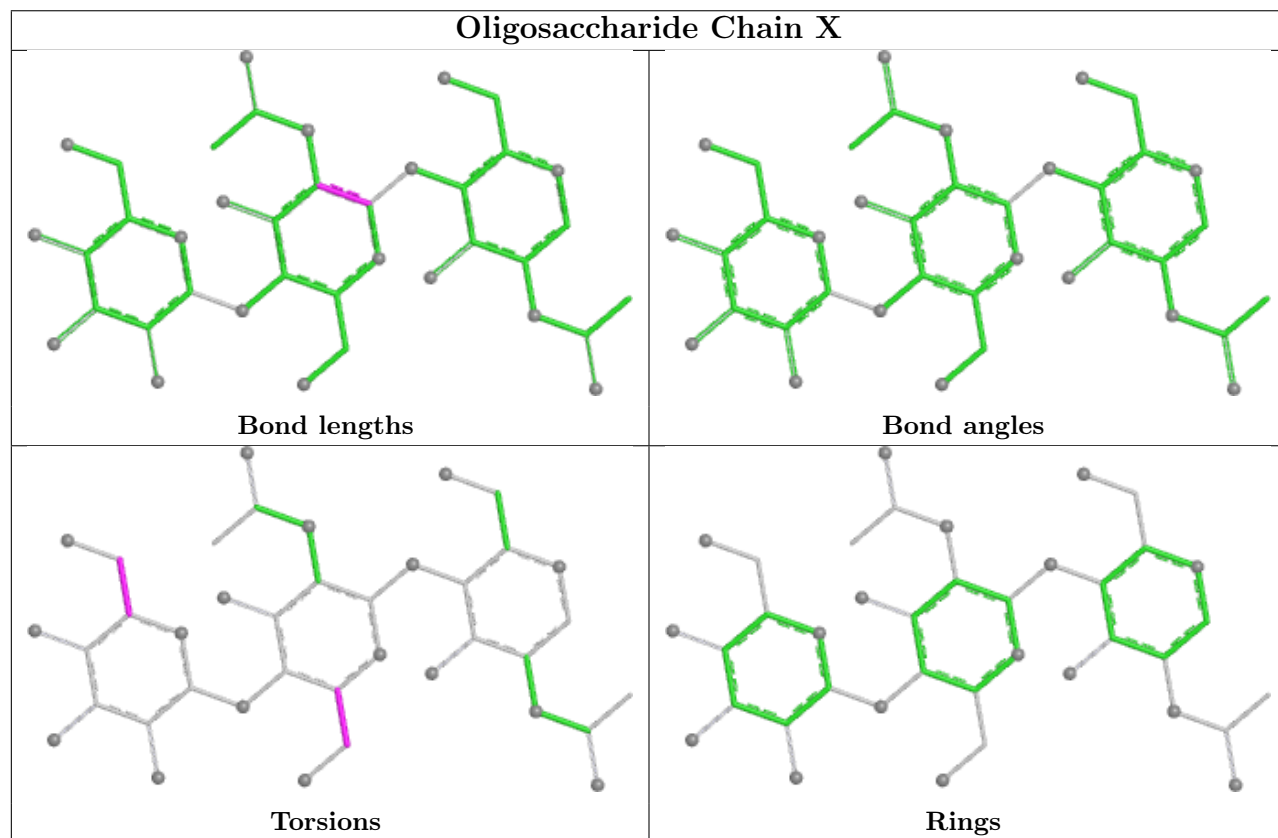
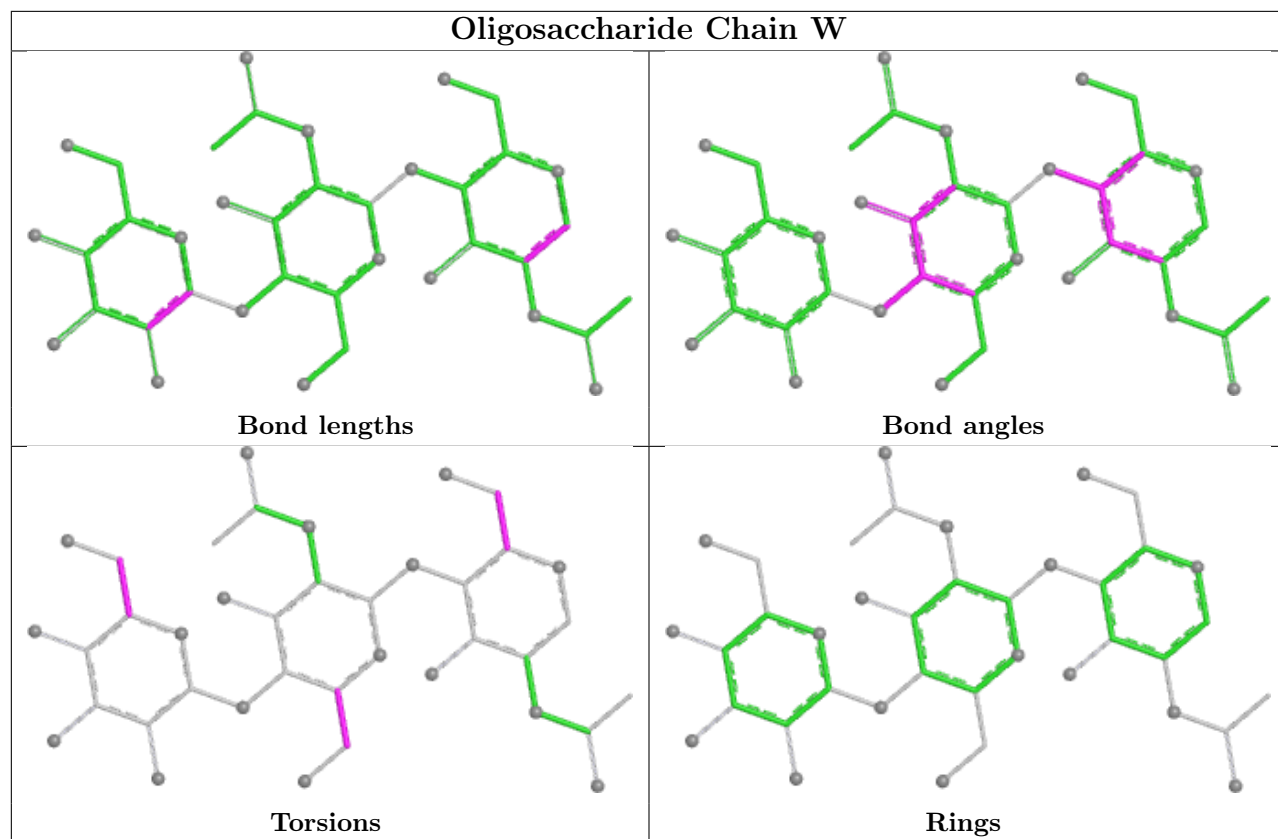


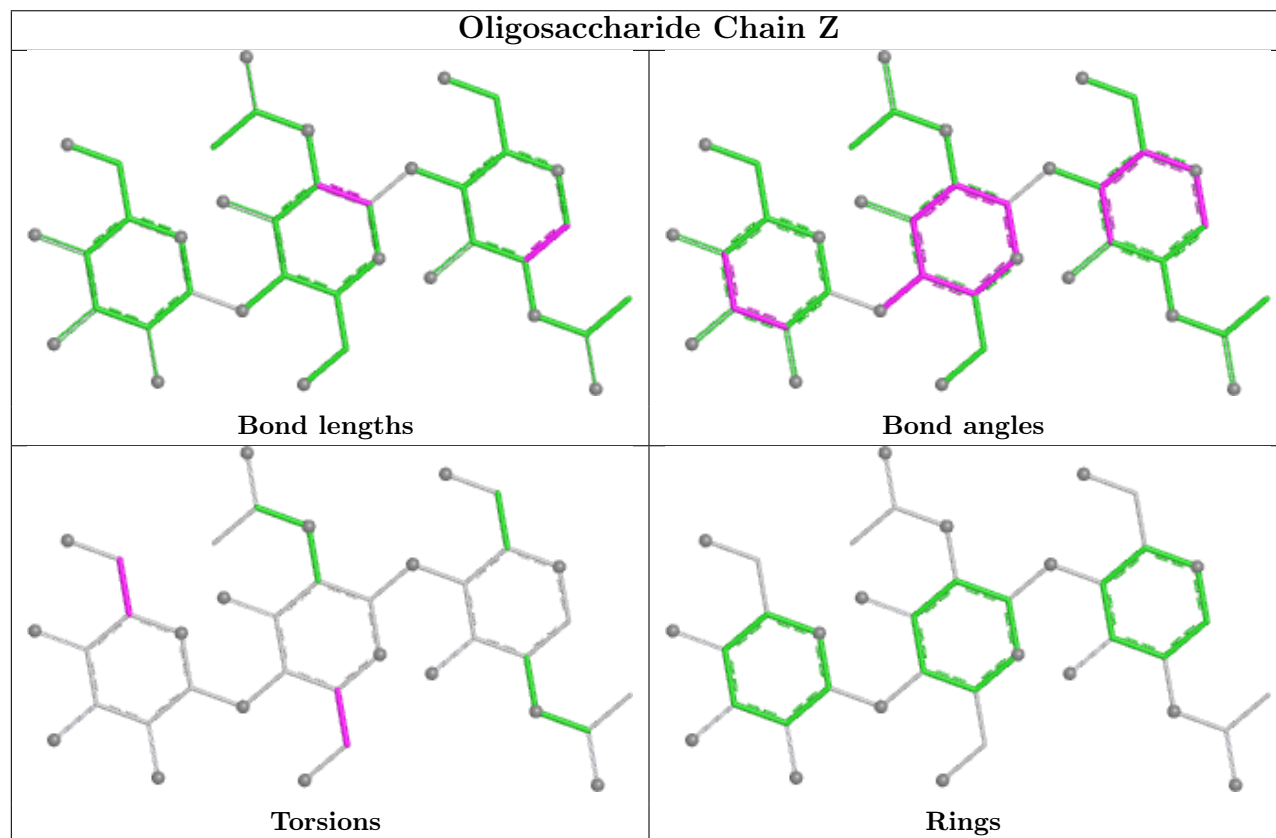
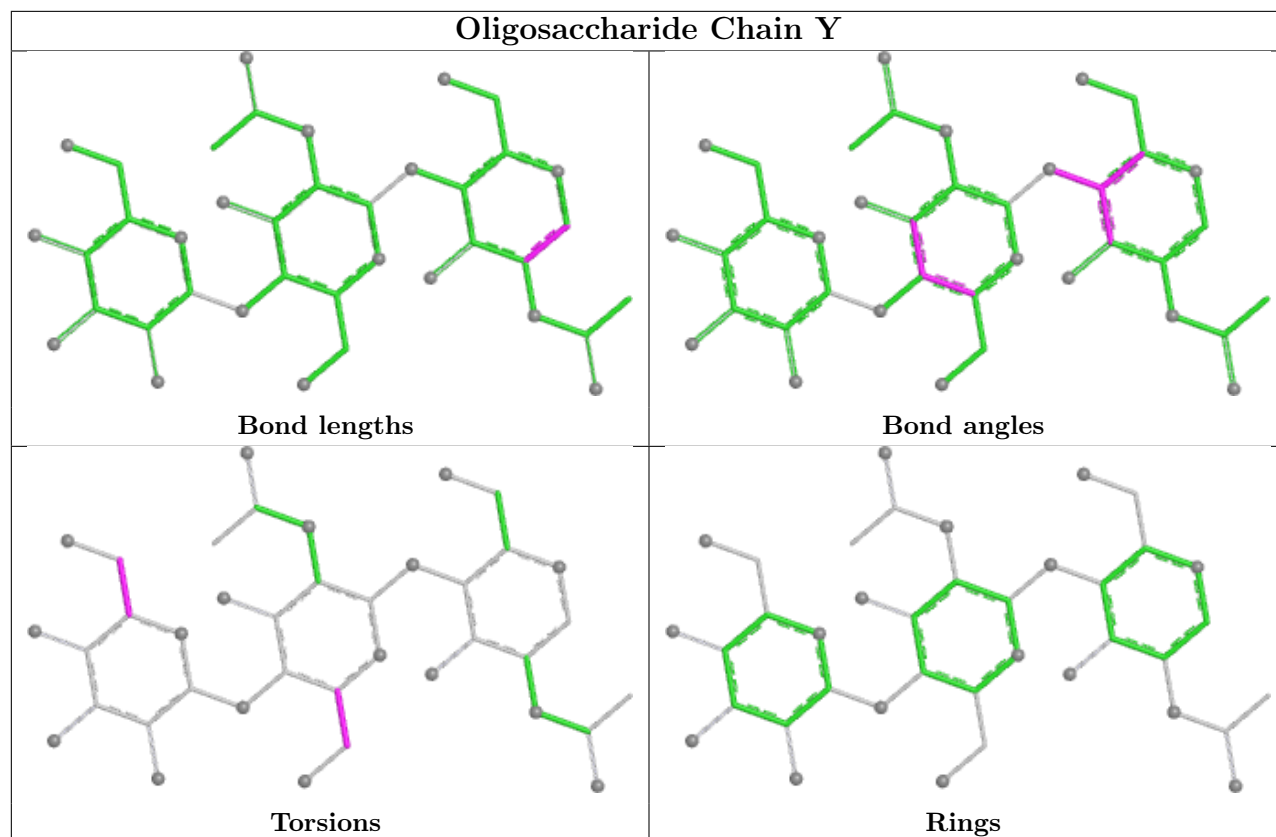


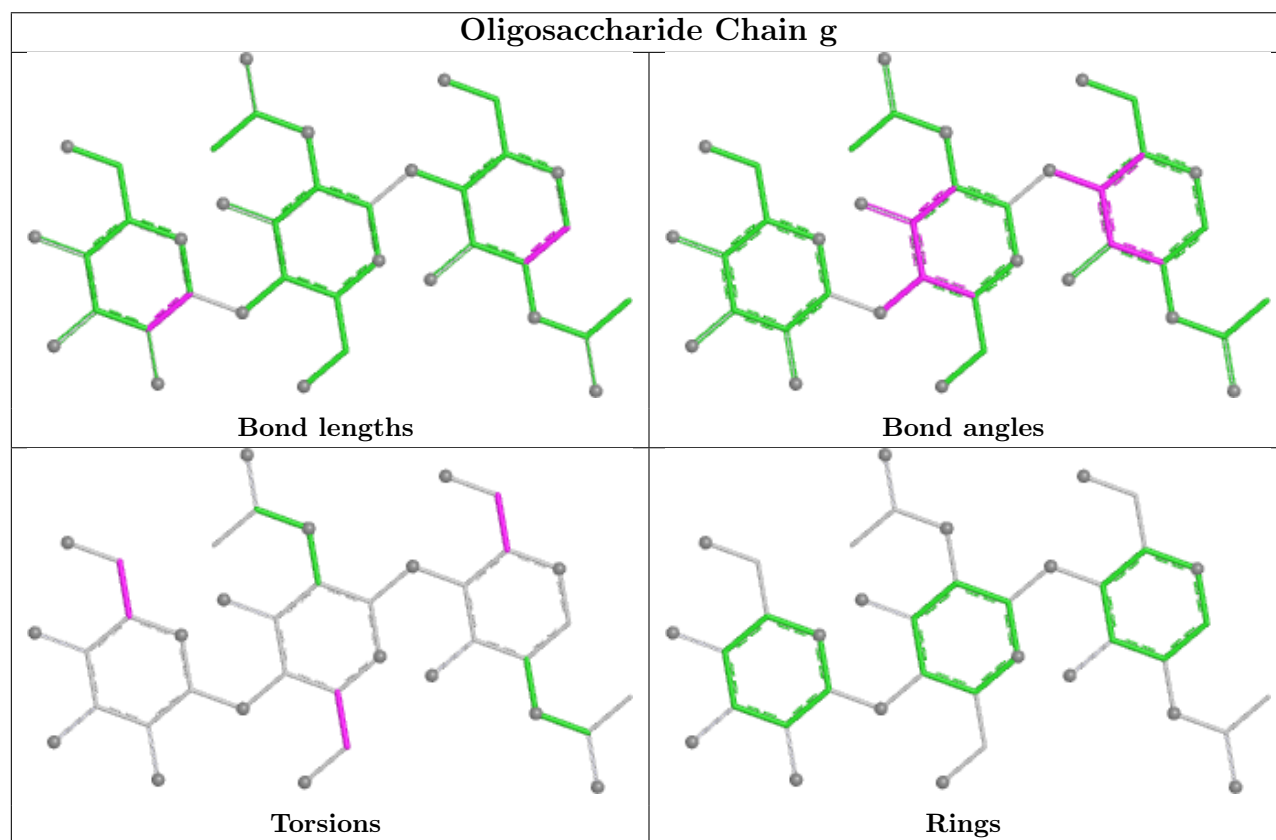
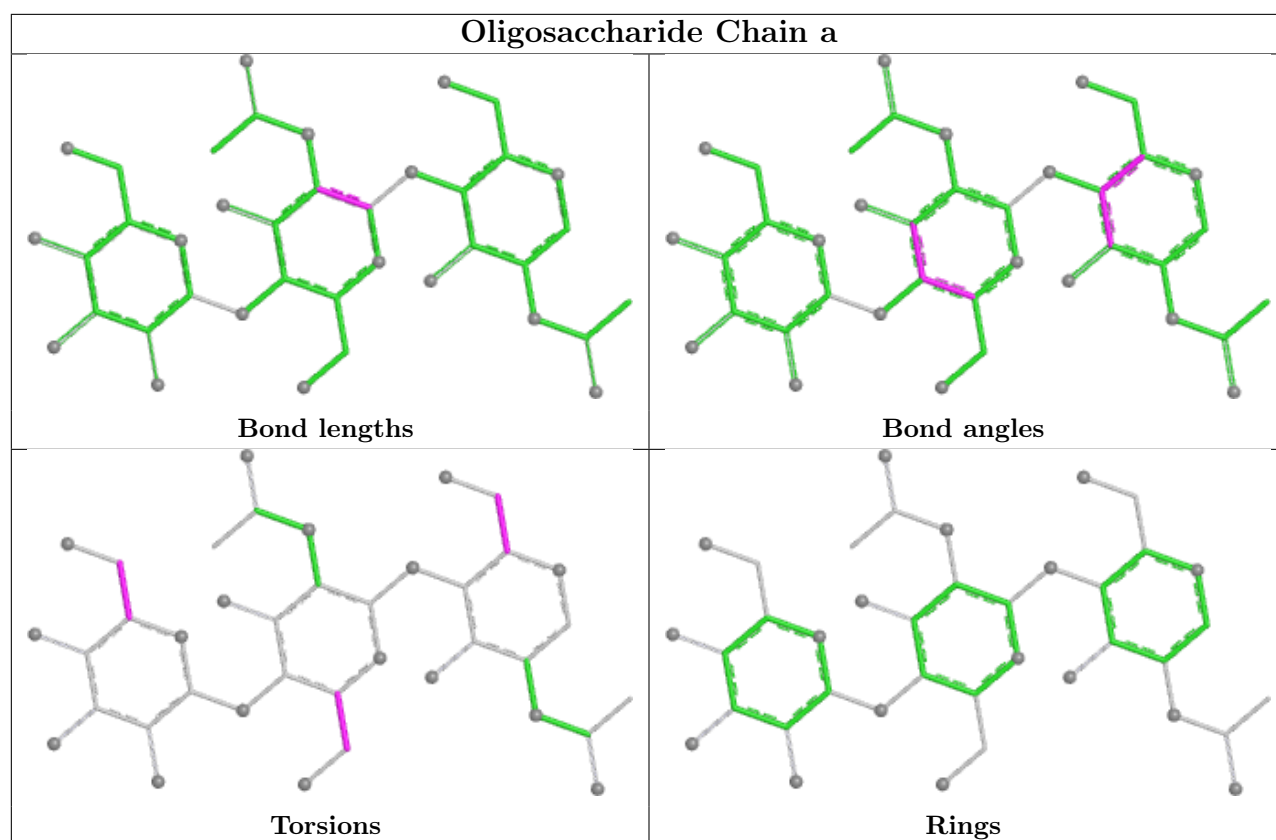


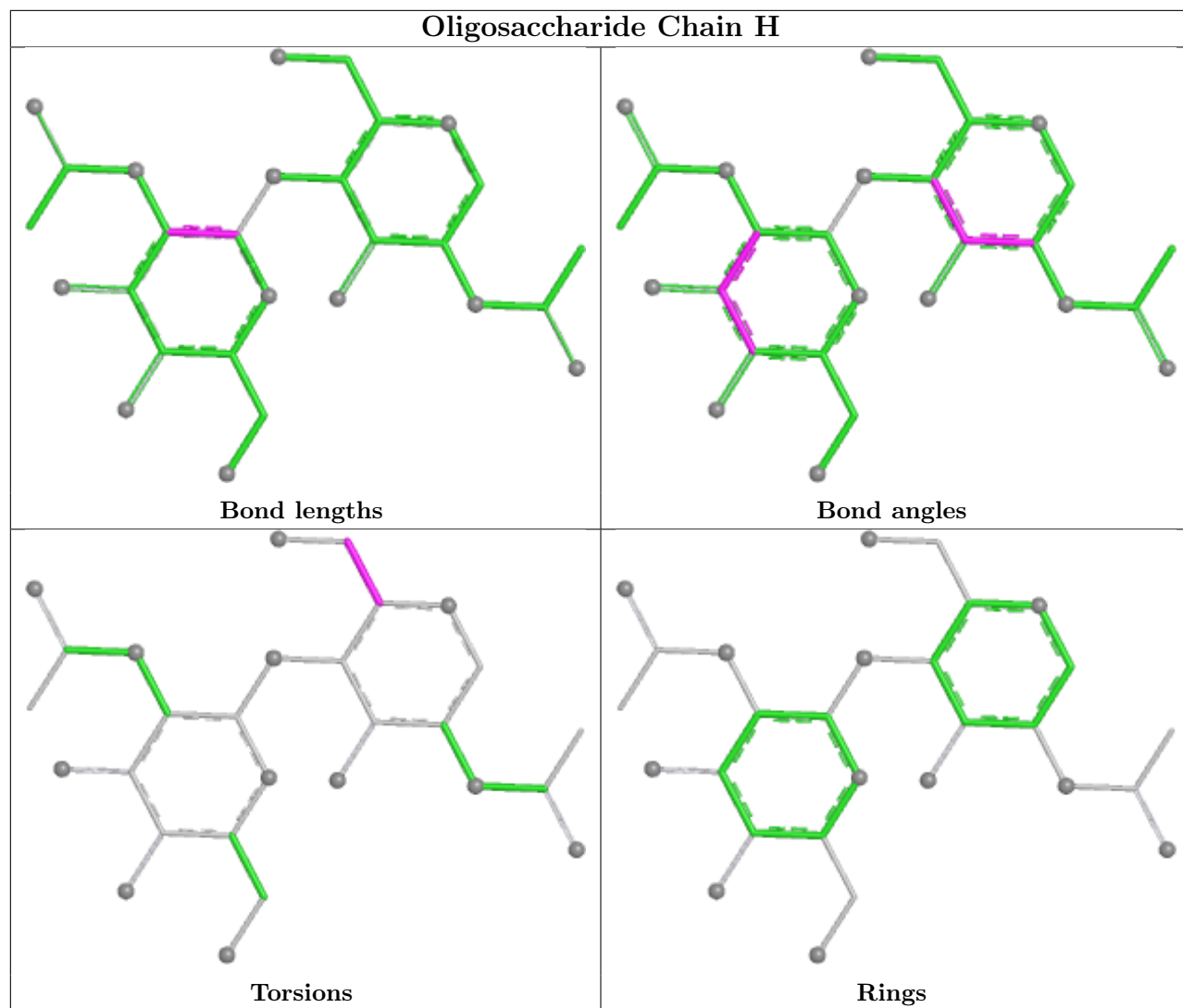


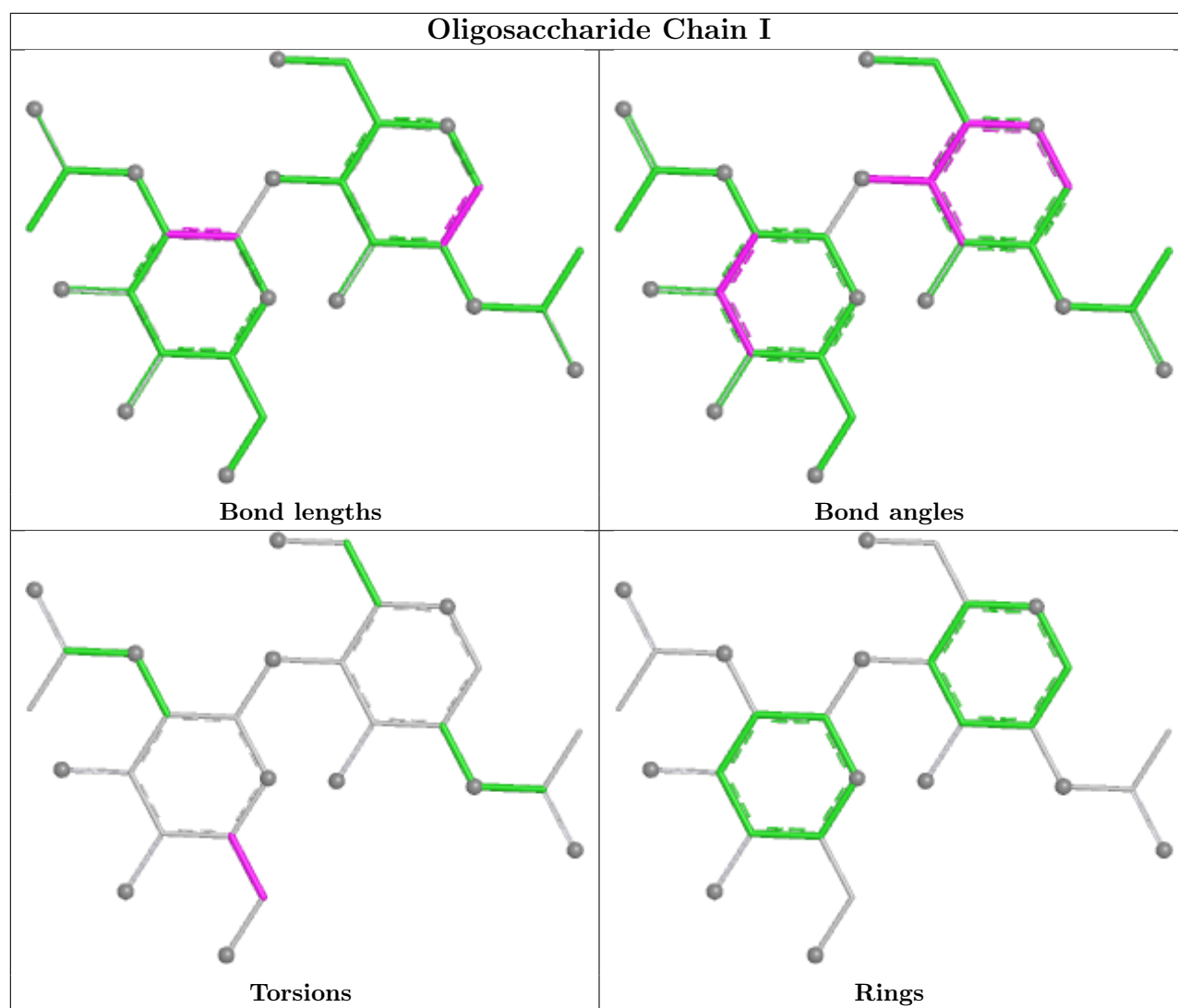


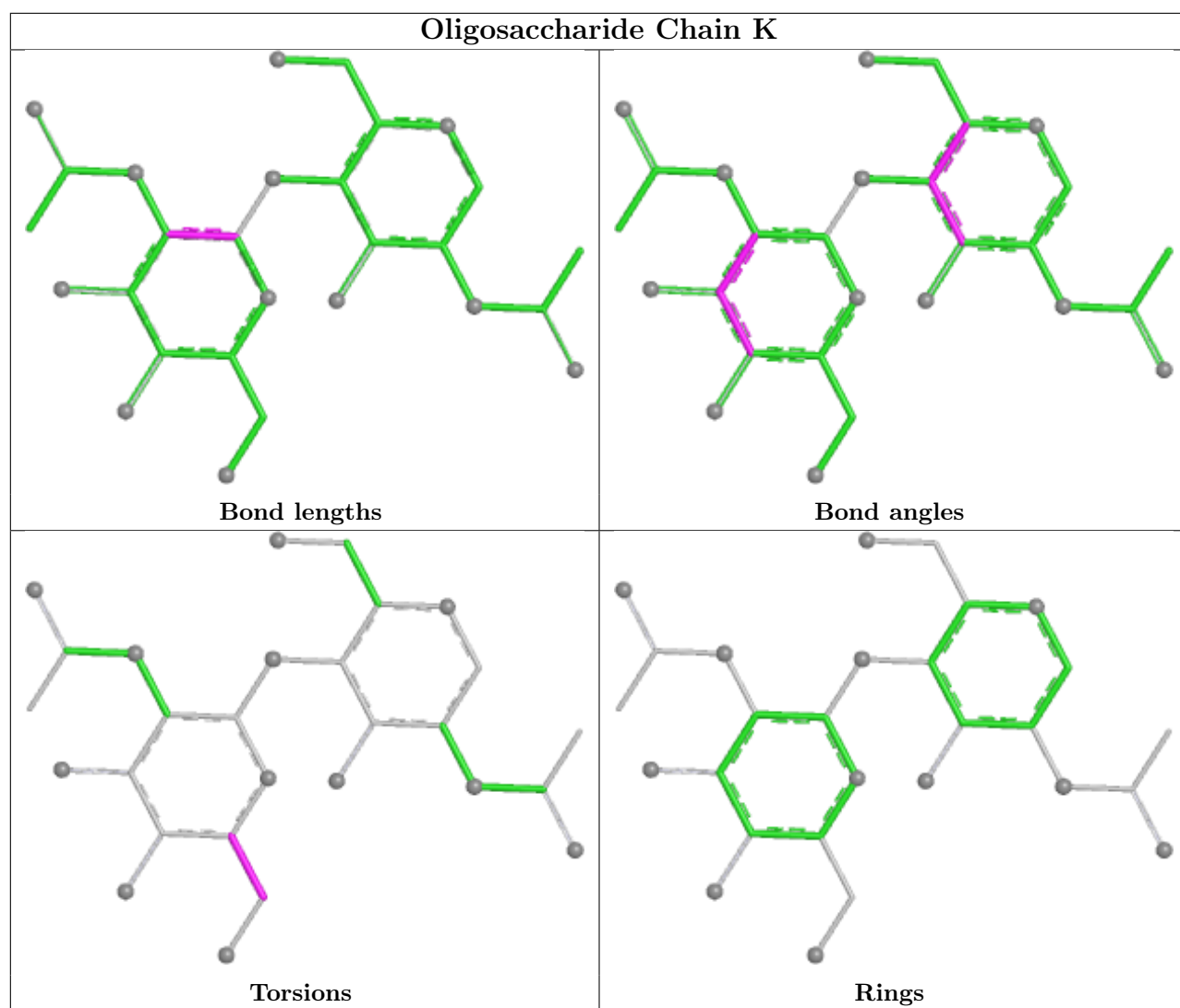


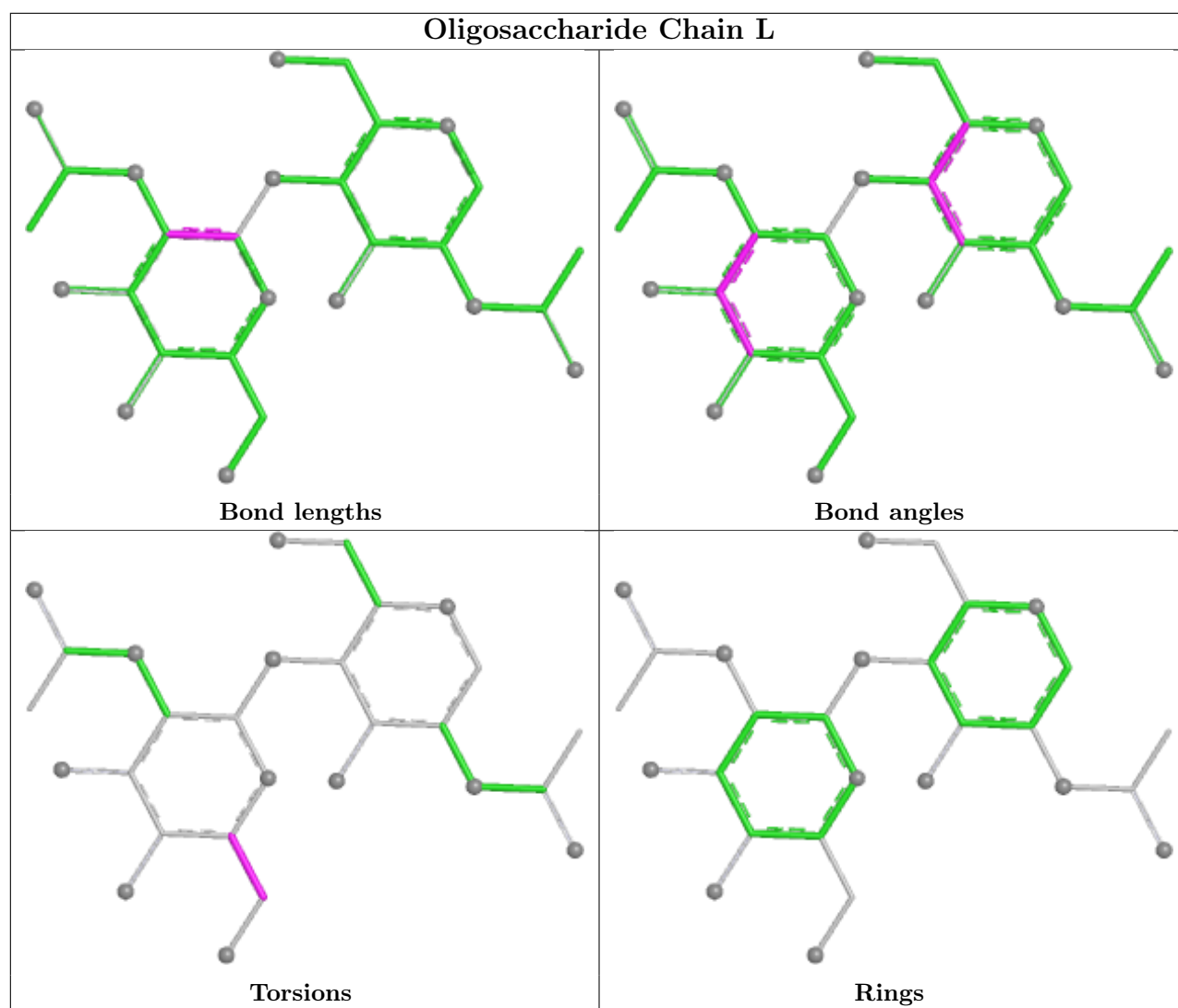


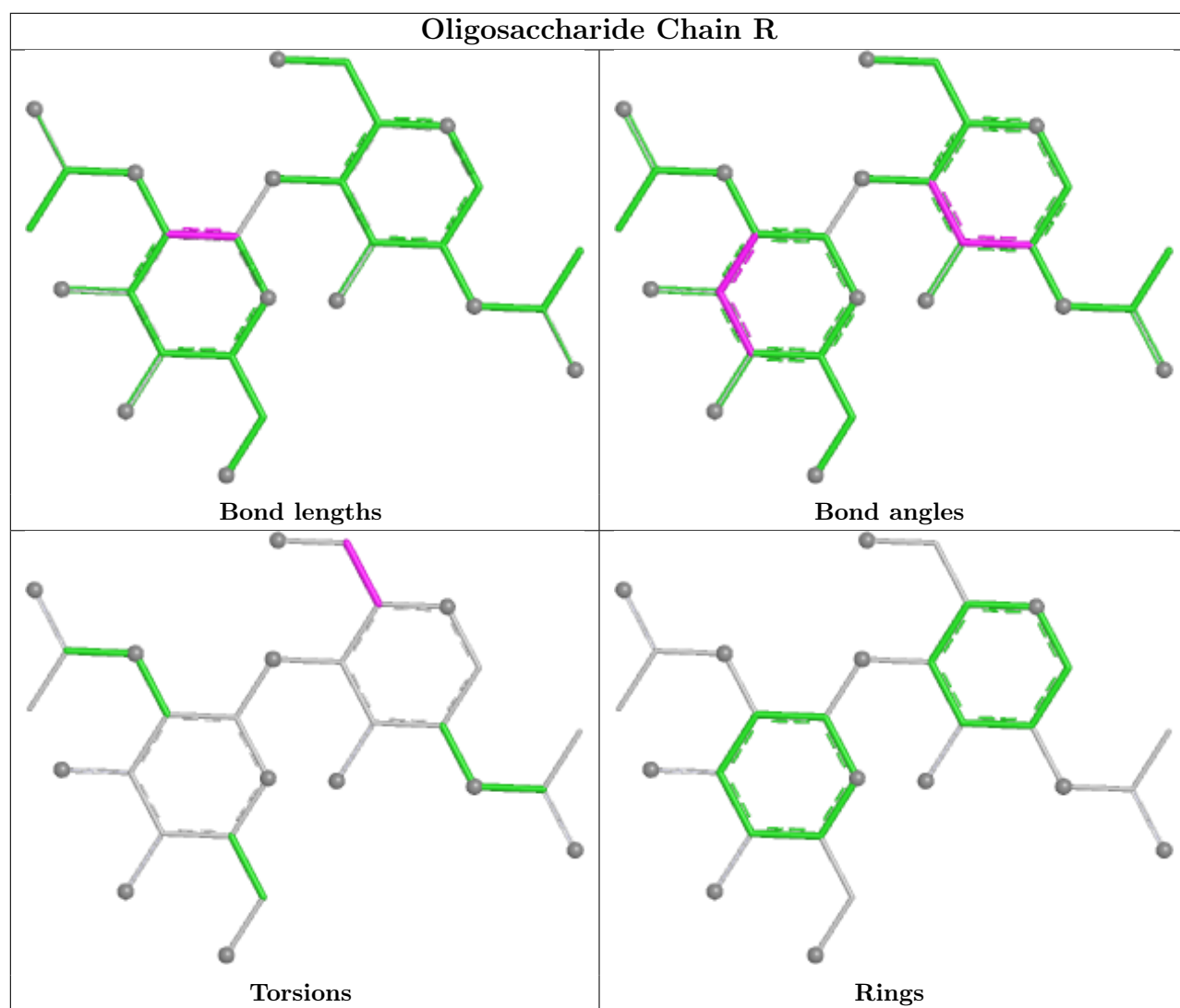


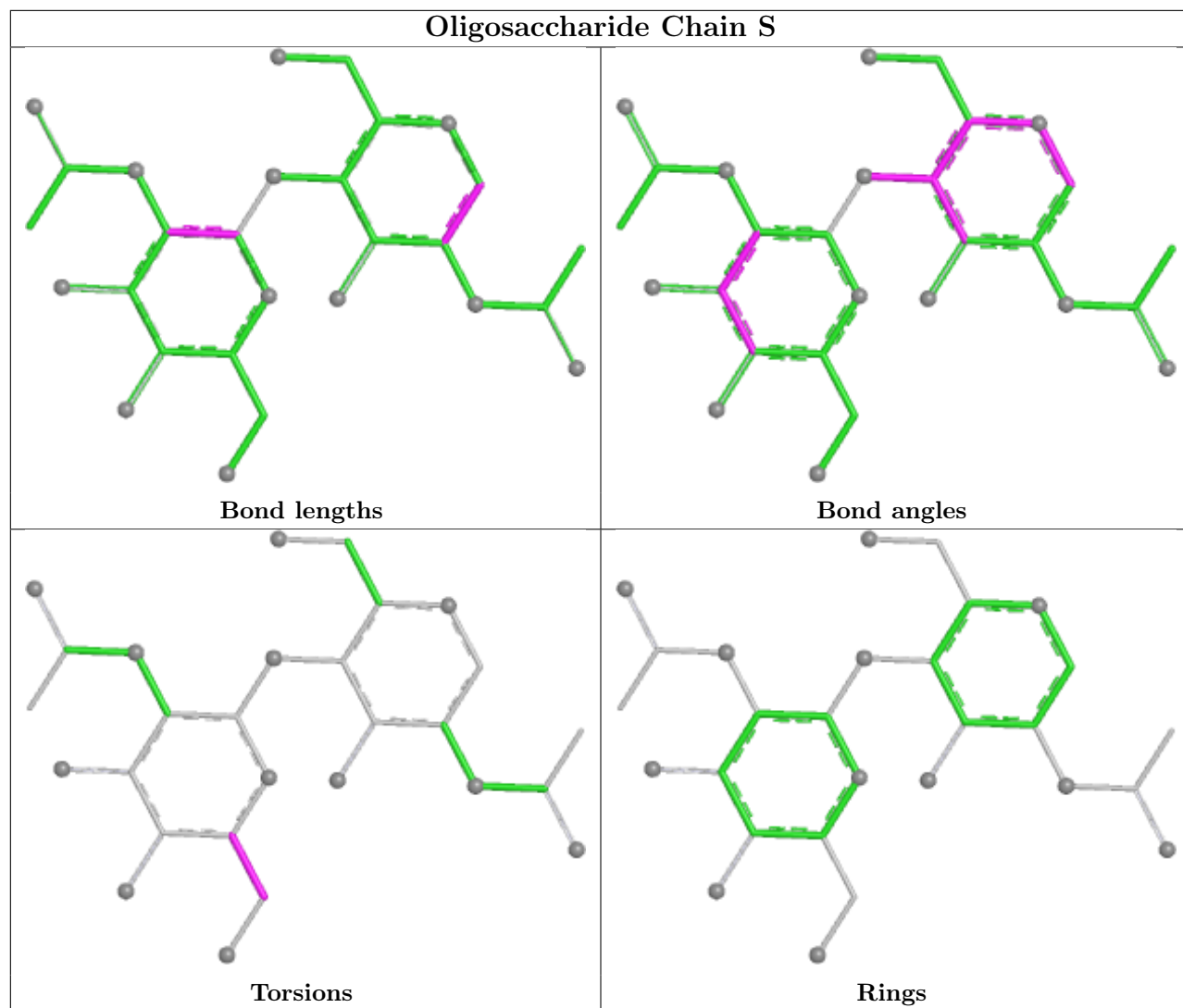


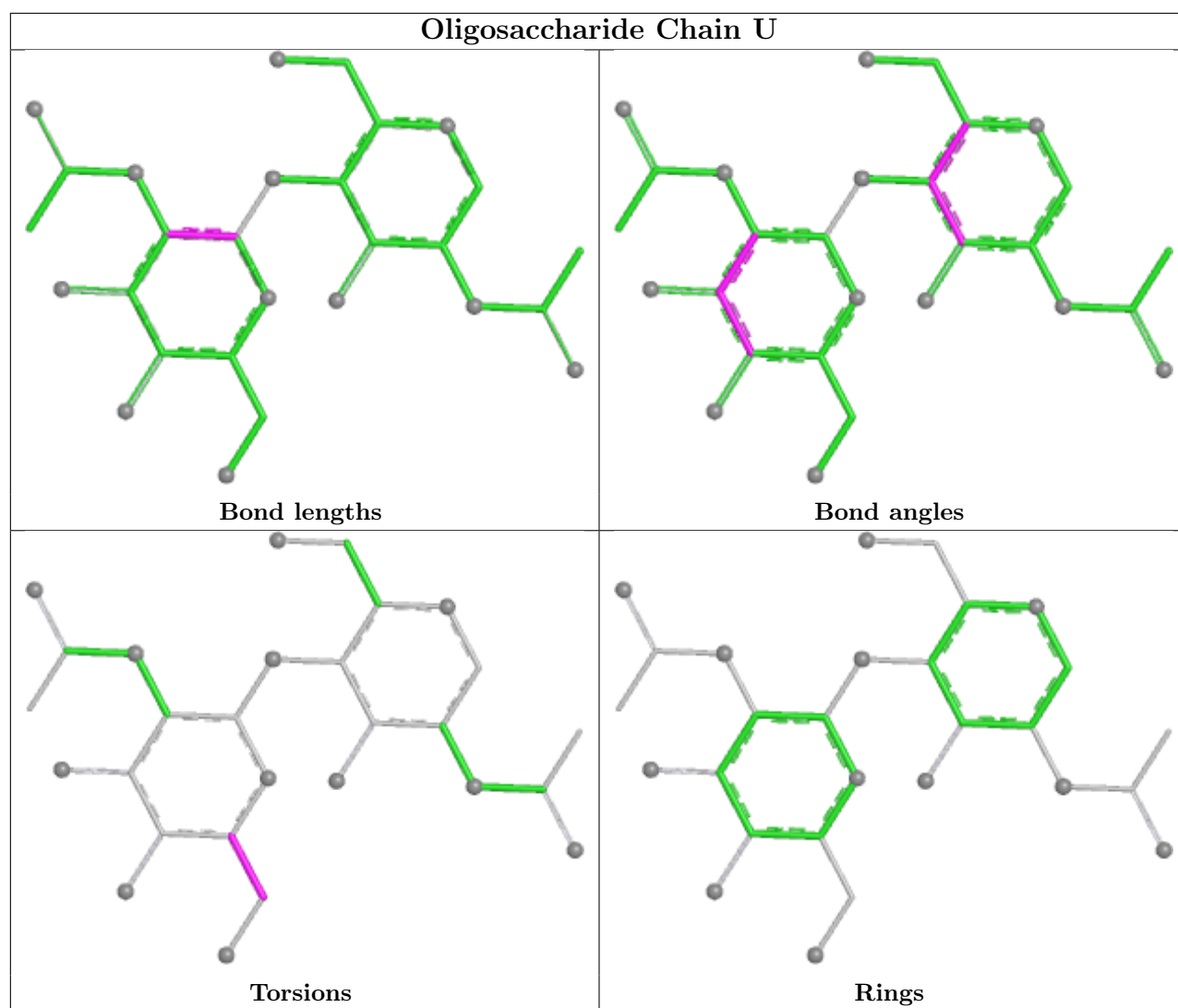


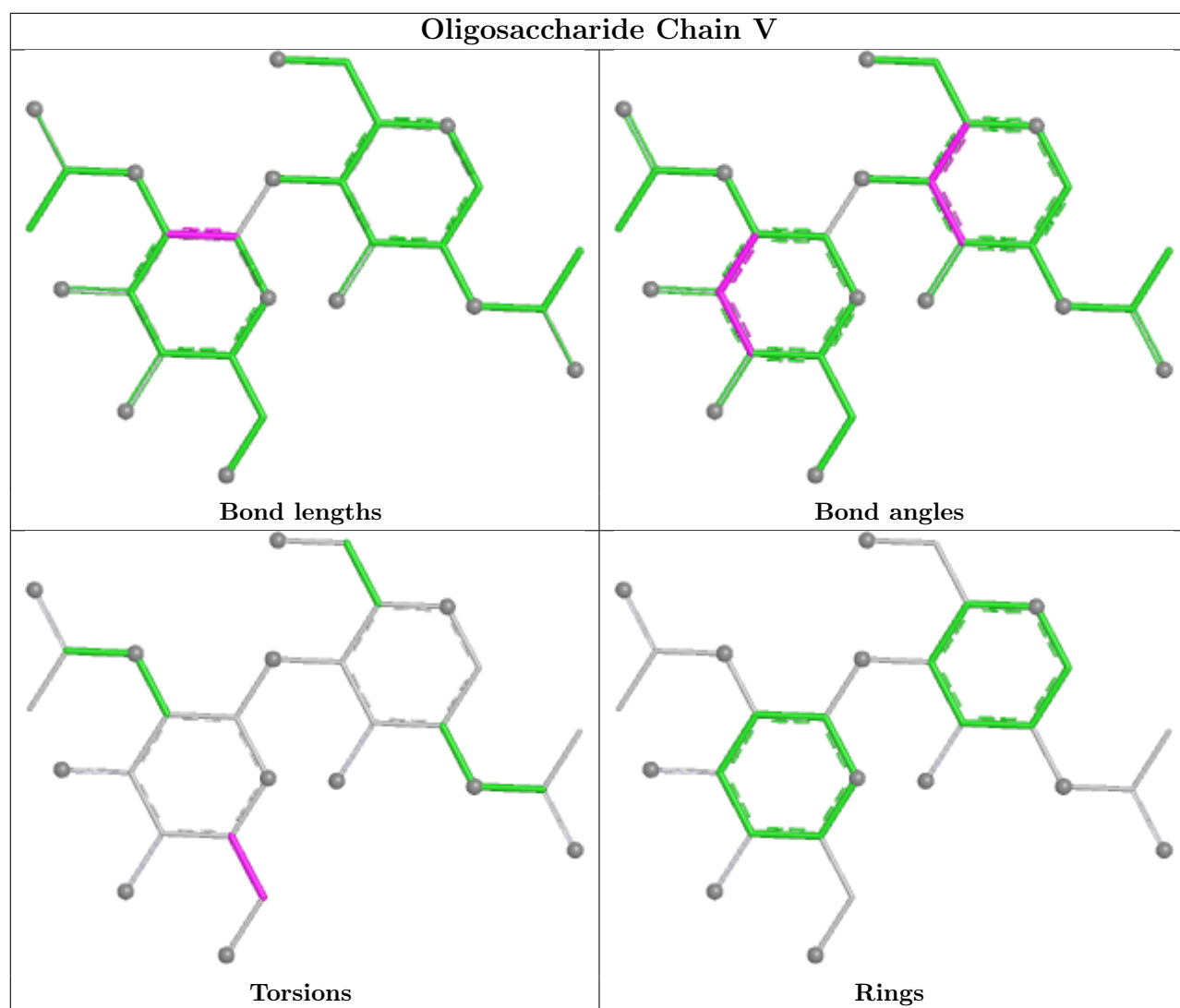


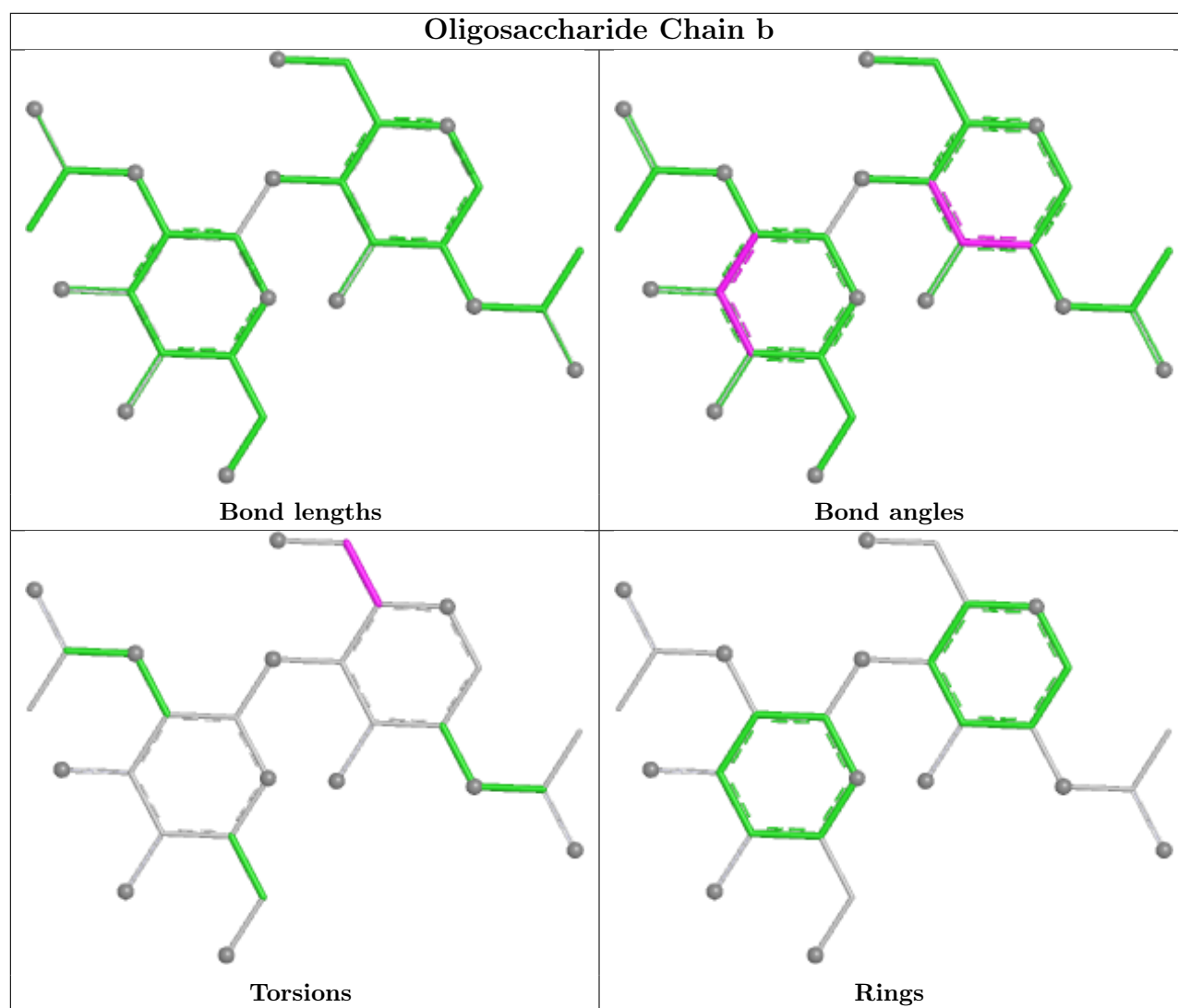


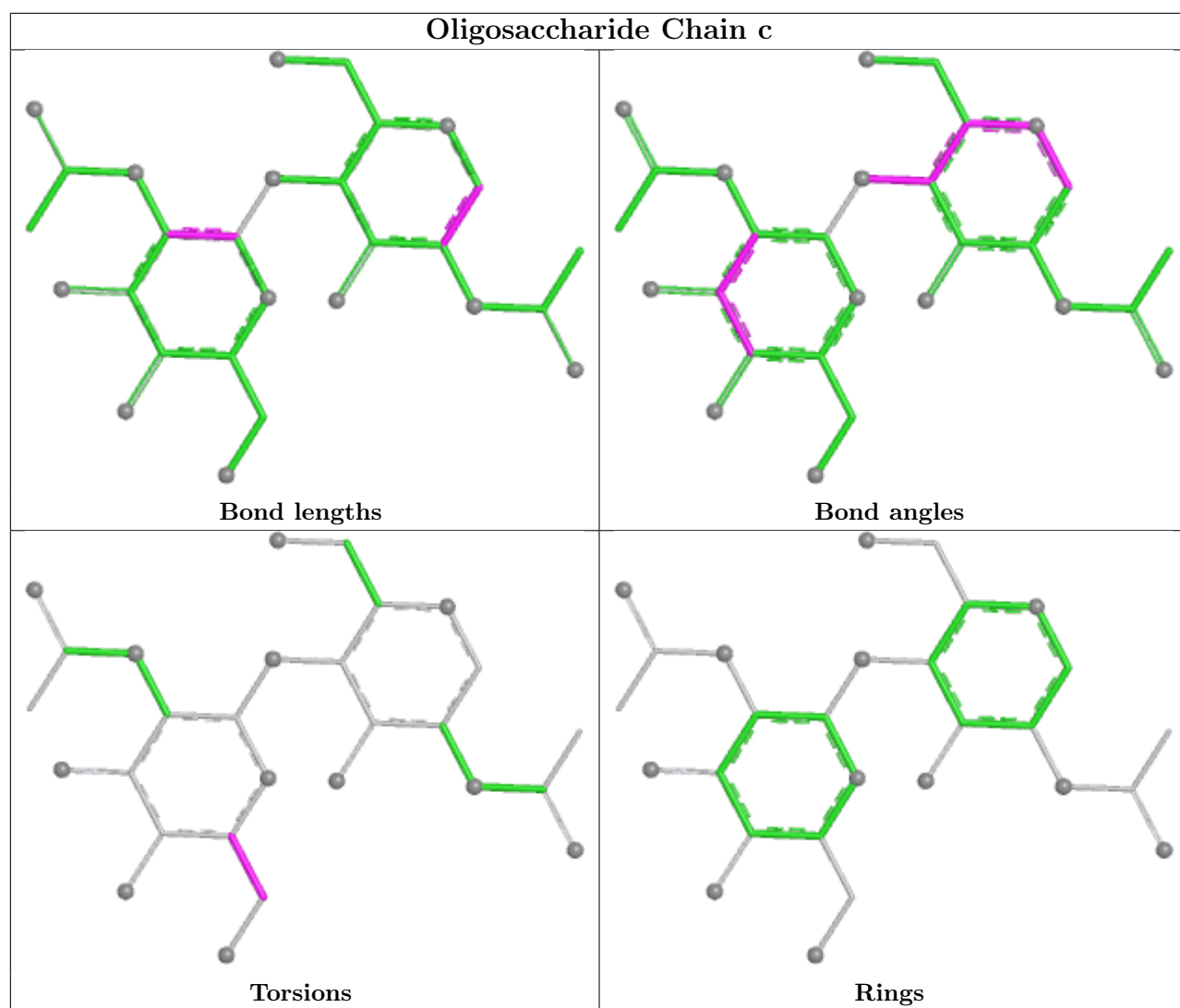


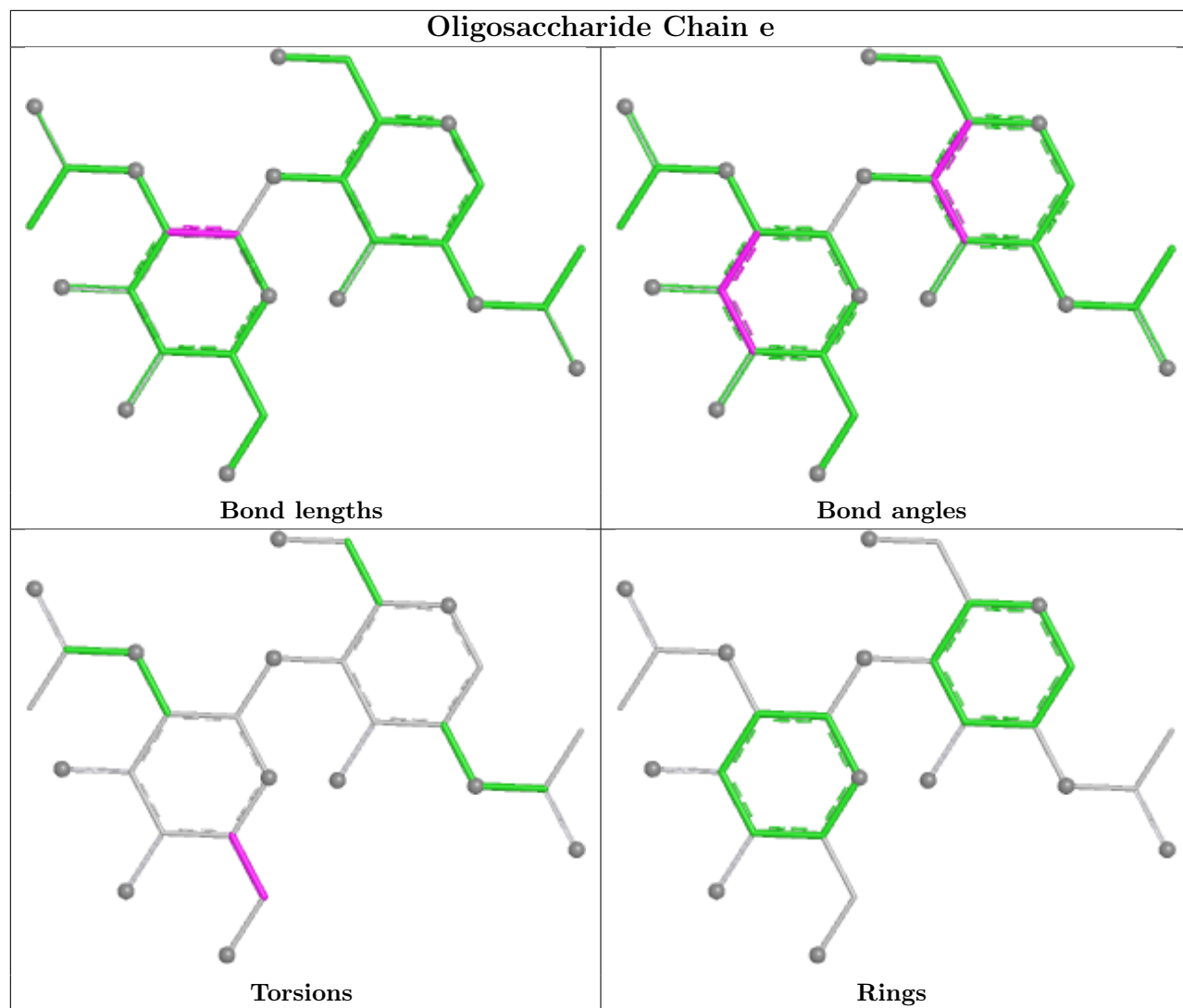


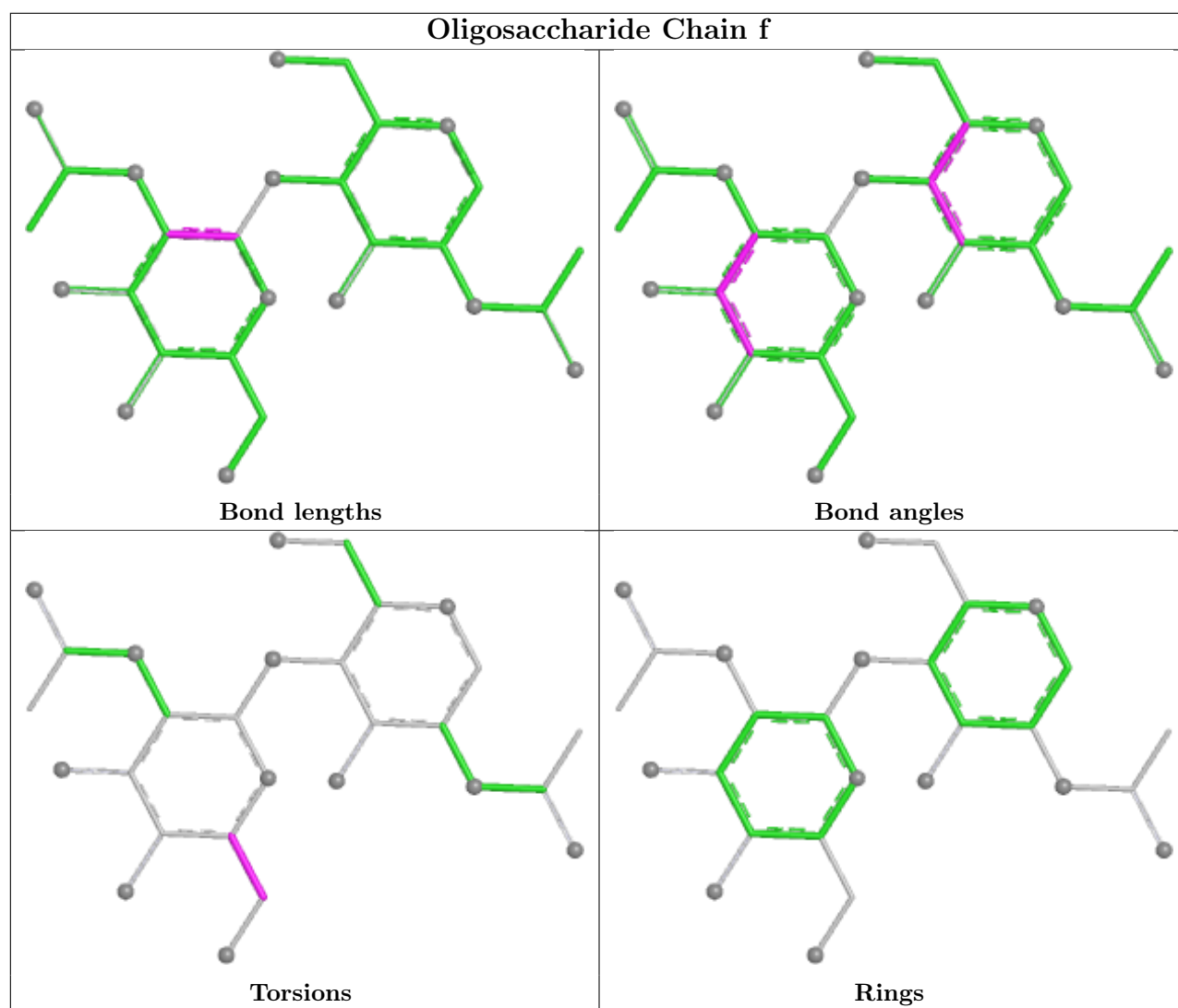


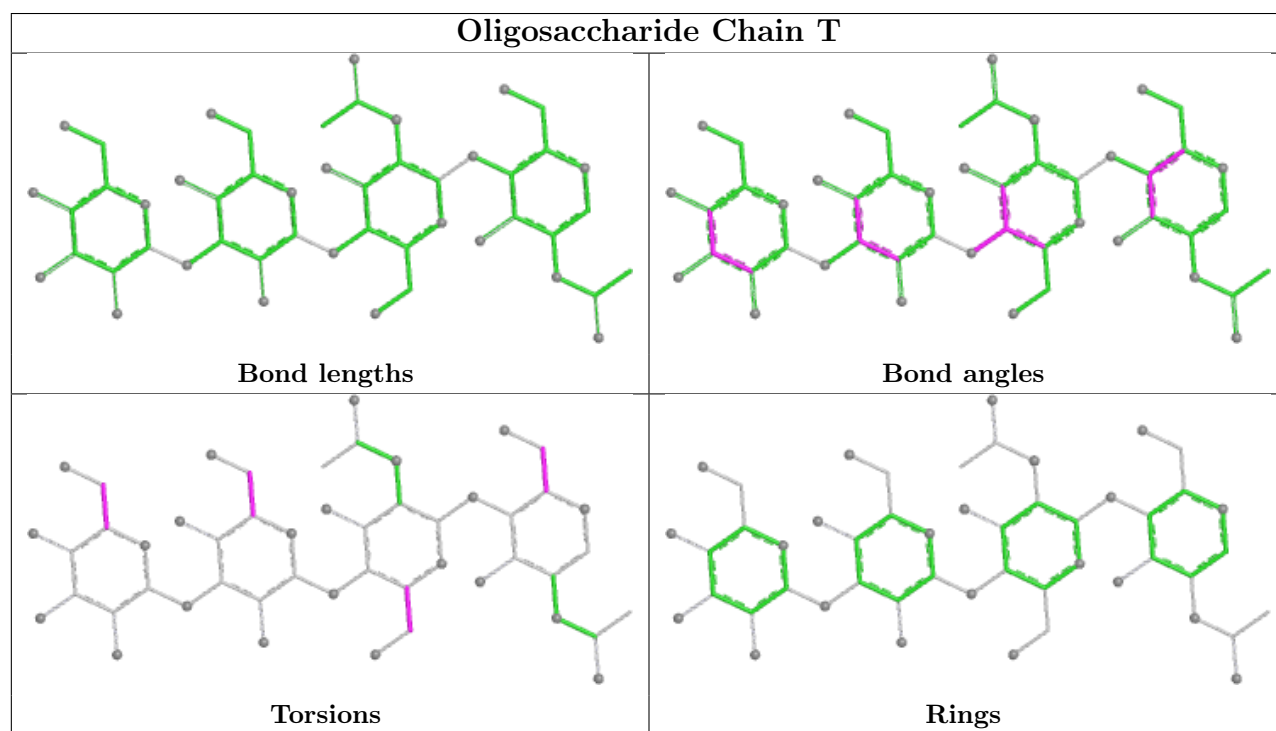
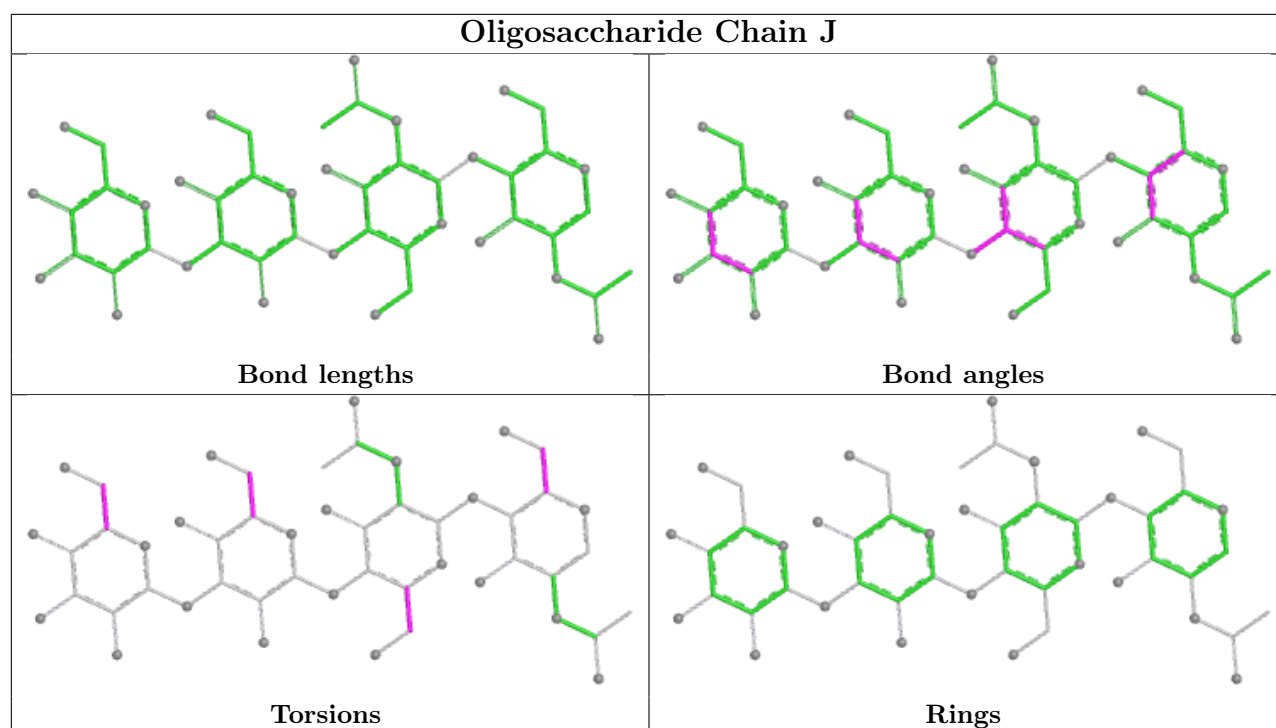


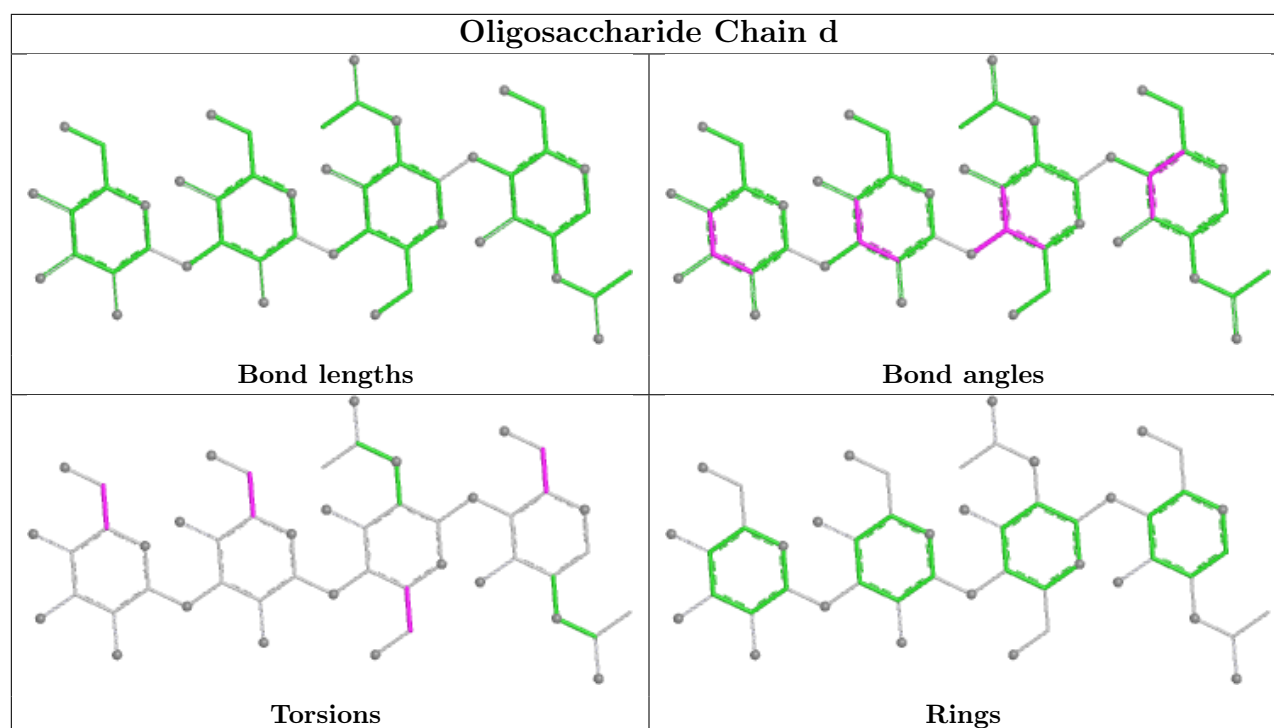












5.6 Ligand geometry [i](#)

15 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	NAG	B	1430	1	14,14,15	0.78	1 (7%)	17,19,21	0.87	1 (5%)
5	NAG	C	1431	1	14,14,15	0.81	1 (7%)	17,19,21	0.88	1 (5%)
5	NAG	A	1430	1	14,14,15	0.76	1 (7%)	17,19,21	0.87	1 (5%)
5	NAG	B	1428	1	14,14,15	0.82	1 (7%)	17,19,21	0.90	1 (5%)
5	NAG	B	1432	1	14,14,15	0.81	1 (7%)	17,19,21	1.04	1 (5%)
5	NAG	A	1429	1	14,14,15	0.73	1 (7%)	17,19,21	0.61	0
5	NAG	C	1428	1	14,14,15	0.81	1 (7%)	17,19,21	0.91	1 (5%)
5	NAG	C	1432	1	14,14,15	0.83	1 (7%)	17,19,21	1.04	1 (5%)
5	NAG	A	1431	1	14,14,15	0.81	1 (7%)	17,19,21	0.88	1 (5%)
5	NAG	B	1431	1	14,14,15	0.81	1 (7%)	17,19,21	0.88	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	A	1428	1	14,14,15	0.82	1 (7%)	17,19,21	0.91	1 (5%)
5	NAG	B	1429	1	14,14,15	0.73	1 (7%)	17,19,21	0.62	0
5	NAG	C	1429	1	14,14,15	0.73	1 (7%)	17,19,21	0.62	0
5	NAG	A	1432	1	14,14,15	0.81	1 (7%)	17,19,21	1.04	1 (5%)
5	NAG	C	1430	1	14,14,15	0.77	1 (7%)	17,19,21	0.87	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
5	NAG	B	1430	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1431	1	-	1/6/23/26	0/1/1/1
5	NAG	A	1430	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1428	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1432	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1429	1	-	1/6/23/26	0/1/1/1
5	NAG	C	1428	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1432	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1431	1	-	1/6/23/26	0/1/1/1
5	NAG	B	1431	1	-	1/6/23/26	0/1/1/1
5	NAG	A	1428	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1429	1	-	1/6/23/26	0/1/1/1
5	NAG	C	1429	1	-	1/6/23/26	0/1/1/1
5	NAG	A	1432	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1430	1	-	2/6/23/26	0/1/1/1

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1431	NAG	C1-C2	2.78	1.56	1.52
5	B	1431	NAG	C1-C2	2.78	1.56	1.52
5	C	1431	NAG	C1-C2	2.77	1.56	1.52
5	C	1432	NAG	C1-C2	2.55	1.55	1.52
5	A	1432	NAG	C1-C2	2.52	1.55	1.52
5	B	1432	NAG	C1-C2	2.49	1.55	1.52
5	B	1430	NAG	C1-C2	2.41	1.55	1.52
5	C	1429	NAG	C1-C2	2.39	1.55	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	1430	NAG	C1-C2	2.37	1.55	1.52
5	A	1430	NAG	C1-C2	2.36	1.55	1.52
5	B	1429	NAG	C1-C2	2.36	1.55	1.52
5	A	1429	NAG	C1-C2	2.35	1.55	1.52
5	B	1428	NAG	C1-C2	2.35	1.55	1.52
5	A	1428	NAG	C1-C2	2.35	1.55	1.52
5	C	1428	NAG	C1-C2	2.30	1.55	1.52

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	1432	NAG	C4-C3-C2	-3.43	106.00	111.02
5	A	1432	NAG	C4-C3-C2	-3.41	106.02	111.02
5	C	1432	NAG	C4-C3-C2	-3.40	106.03	111.02
5	B	1431	NAG	C4-C3-C2	-2.56	107.26	111.02
5	C	1431	NAG	C4-C3-C2	-2.55	107.28	111.02
5	A	1431	NAG	C4-C3-C2	-2.54	107.29	111.02
5	C	1428	NAG	C4-C3-C2	-2.11	107.92	111.02
5	A	1428	NAG	C4-C3-C2	-2.11	107.93	111.02
5	B	1428	NAG	C4-C3-C2	-2.09	107.96	111.02
5	A	1430	NAG	C4-C3-C2	-2.08	107.97	111.02
5	B	1430	NAG	C4-C3-C2	-2.07	107.98	111.02
5	C	1430	NAG	C4-C3-C2	-2.07	107.99	111.02

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1428	NAG	C4-C5-C6-O6
5	B	1428	NAG	C4-C5-C6-O6
5	C	1428	NAG	C4-C5-C6-O6
5	A	1430	NAG	C4-C5-C6-O6
5	B	1430	NAG	C4-C5-C6-O6
5	C	1430	NAG	C4-C5-C6-O6
5	A	1432	NAG	O5-C5-C6-O6
5	B	1432	NAG	O5-C5-C6-O6
5	C	1432	NAG	O5-C5-C6-O6
5	A	1428	NAG	O5-C5-C6-O6
5	B	1428	NAG	O5-C5-C6-O6
5	C	1428	NAG	O5-C5-C6-O6
5	A	1430	NAG	O5-C5-C6-O6
5	B	1430	NAG	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
5	C	1430	NAG	O5-C5-C6-O6
5	A	1429	NAG	O5-C5-C6-O6
5	B	1429	NAG	O5-C5-C6-O6
5	C	1429	NAG	O5-C5-C6-O6
5	A	1432	NAG	C4-C5-C6-O6
5	B	1432	NAG	C4-C5-C6-O6
5	C	1432	NAG	C4-C5-C6-O6
5	A	1431	NAG	O5-C5-C6-O6
5	B	1431	NAG	O5-C5-C6-O6
5	C	1431	NAG	O5-C5-C6-O6

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1429	NAG	1	0
5	B	1429	NAG	1	0
5	C	1429	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.

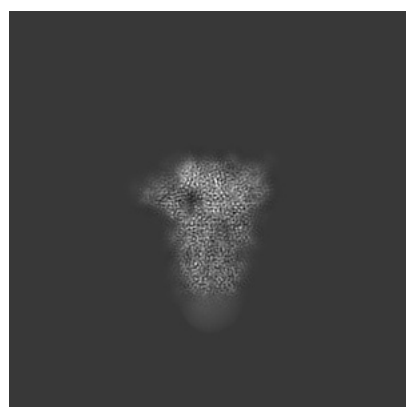
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20070. These allow visual inspection of the internal detail of the map and identification of artifacts.

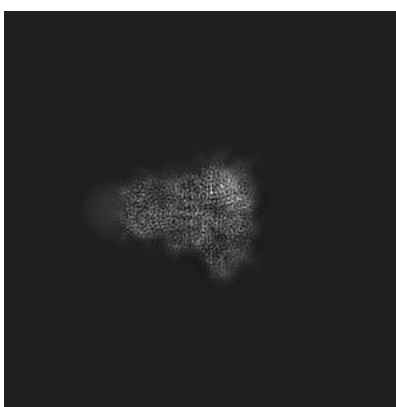
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

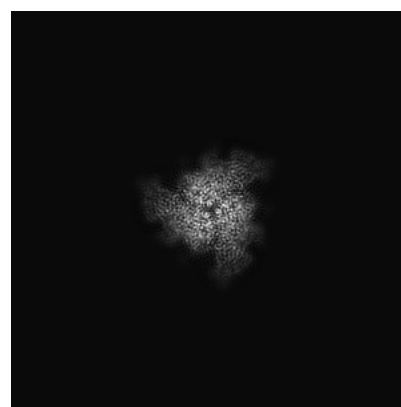
6.1.1 Primary map



X



Y



Z

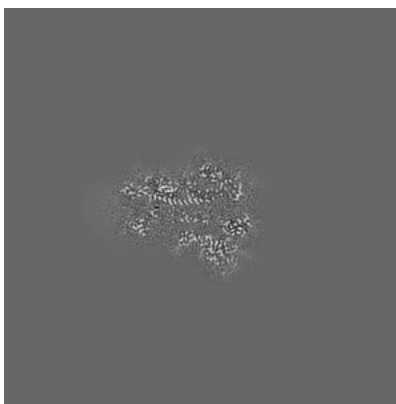
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

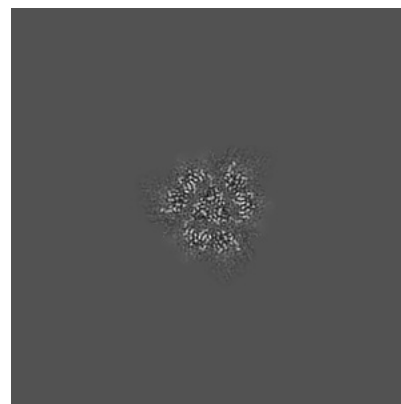
6.2.1 Primary map



X Index: 200



Y Index: 200



Z Index: 200

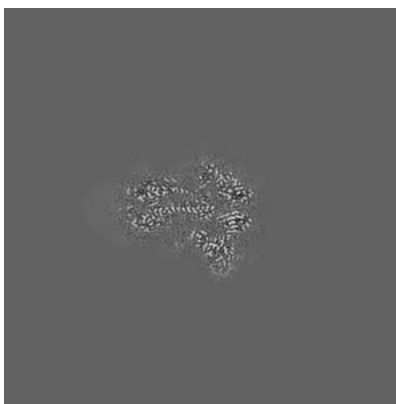
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

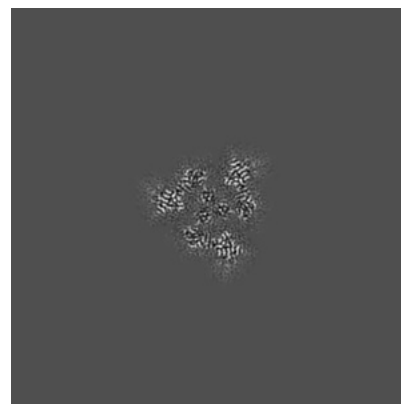
6.3.1 Primary map



X Index: 213



Y Index: 207

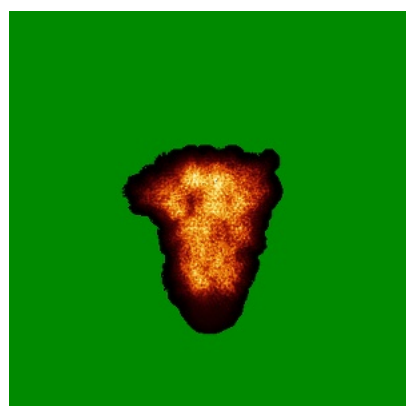


Z Index: 206

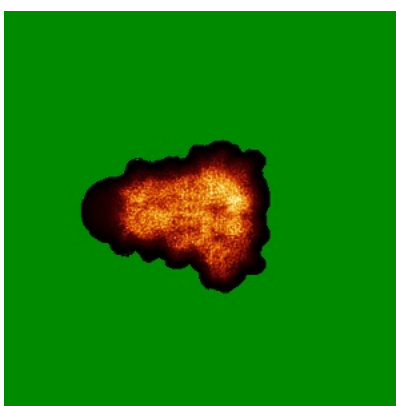
The images above show the largest variance slices of the map in three orthogonal directions.

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

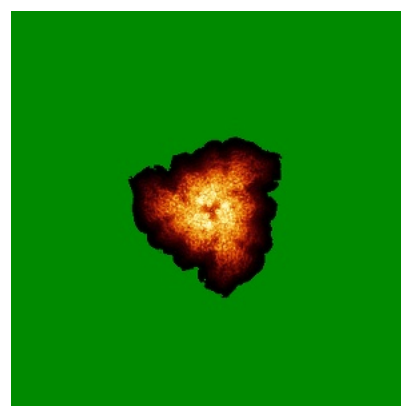
6.4.1 Primary map



X



Y



Z

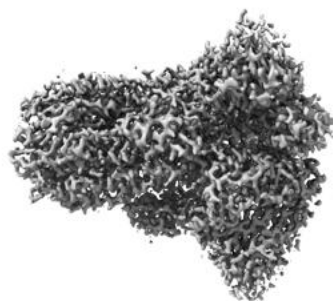
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

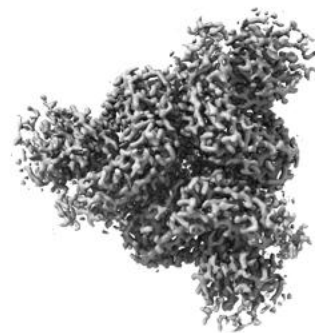
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

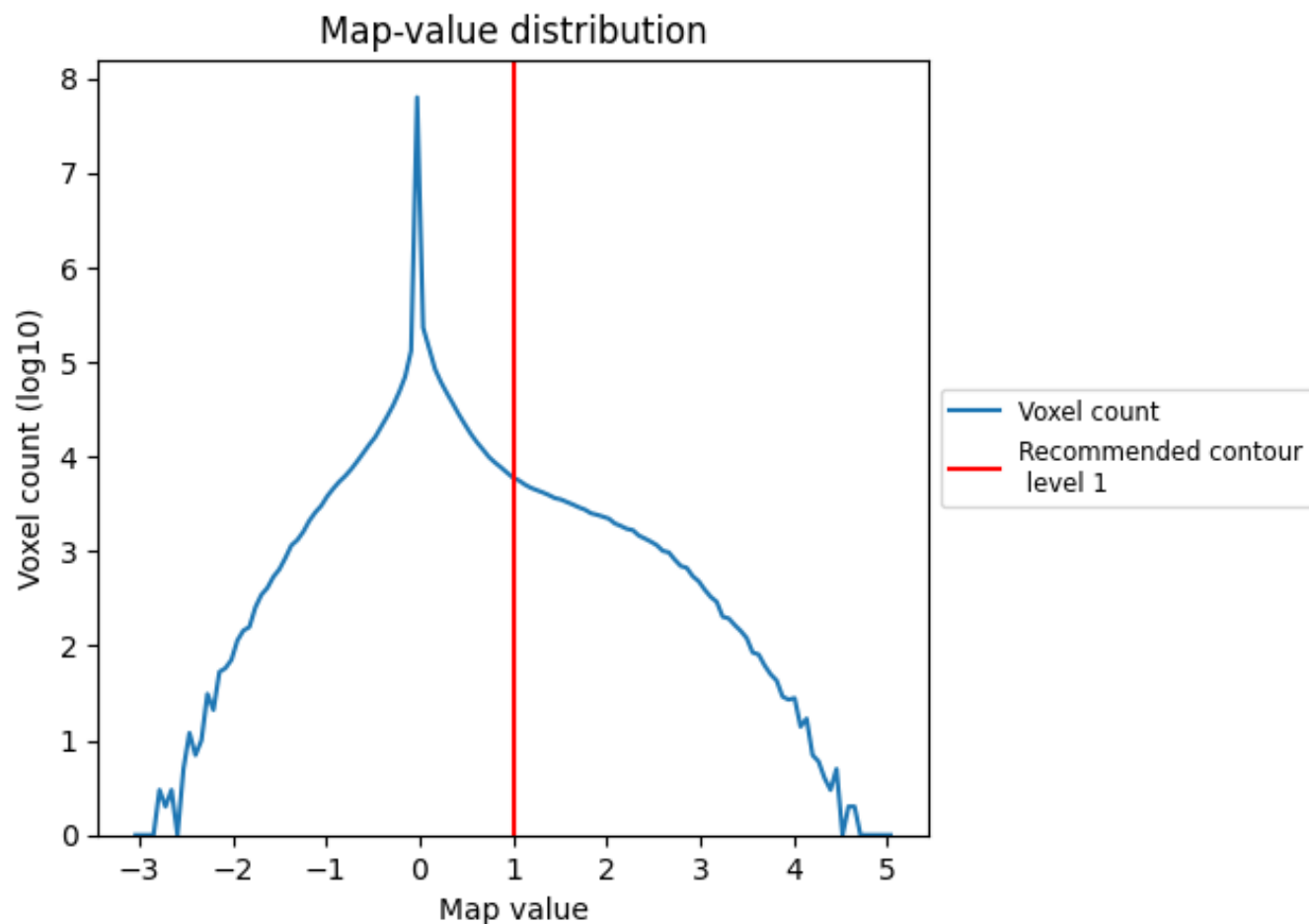
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

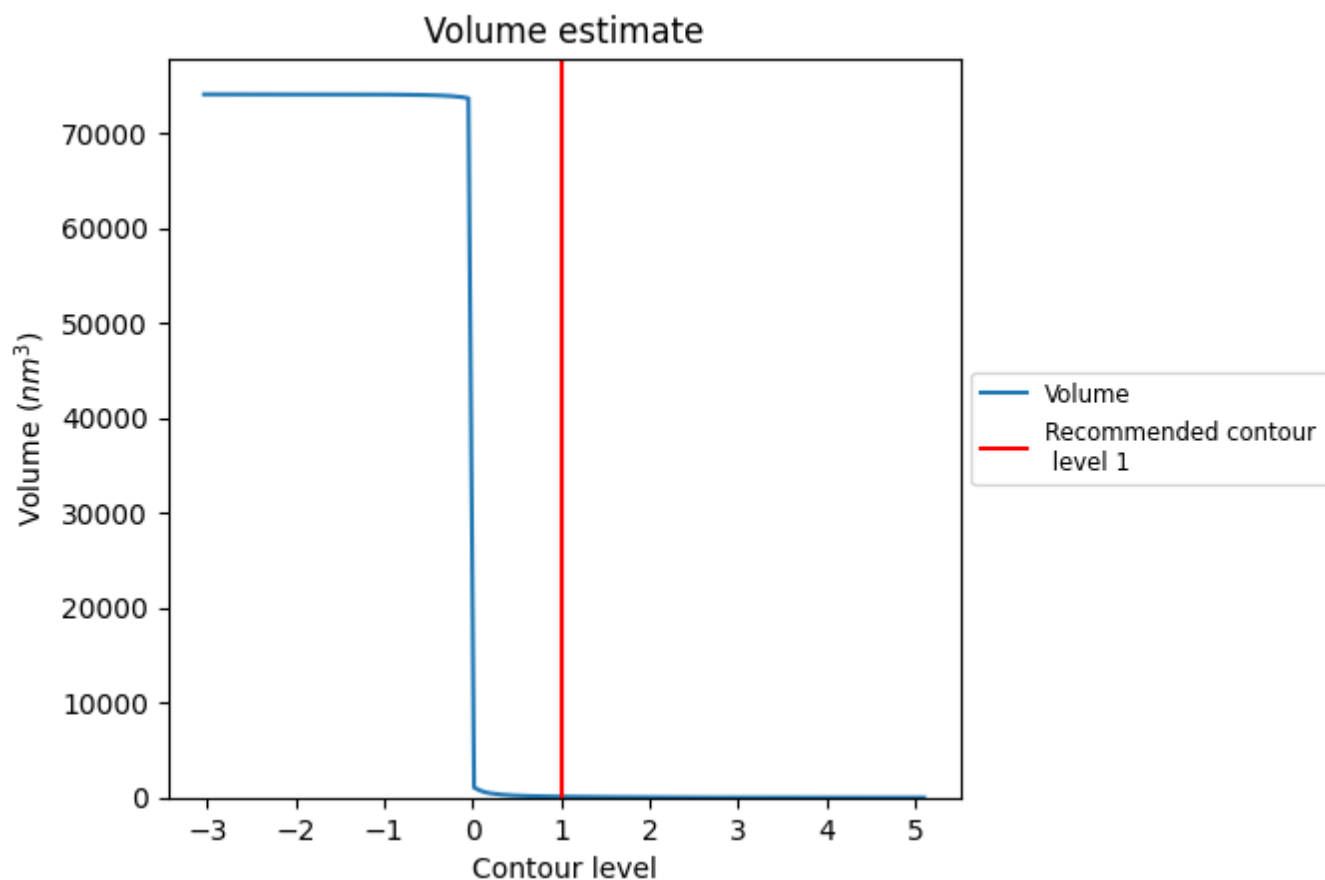
This section contains the results of statistical analysis of the map.

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.

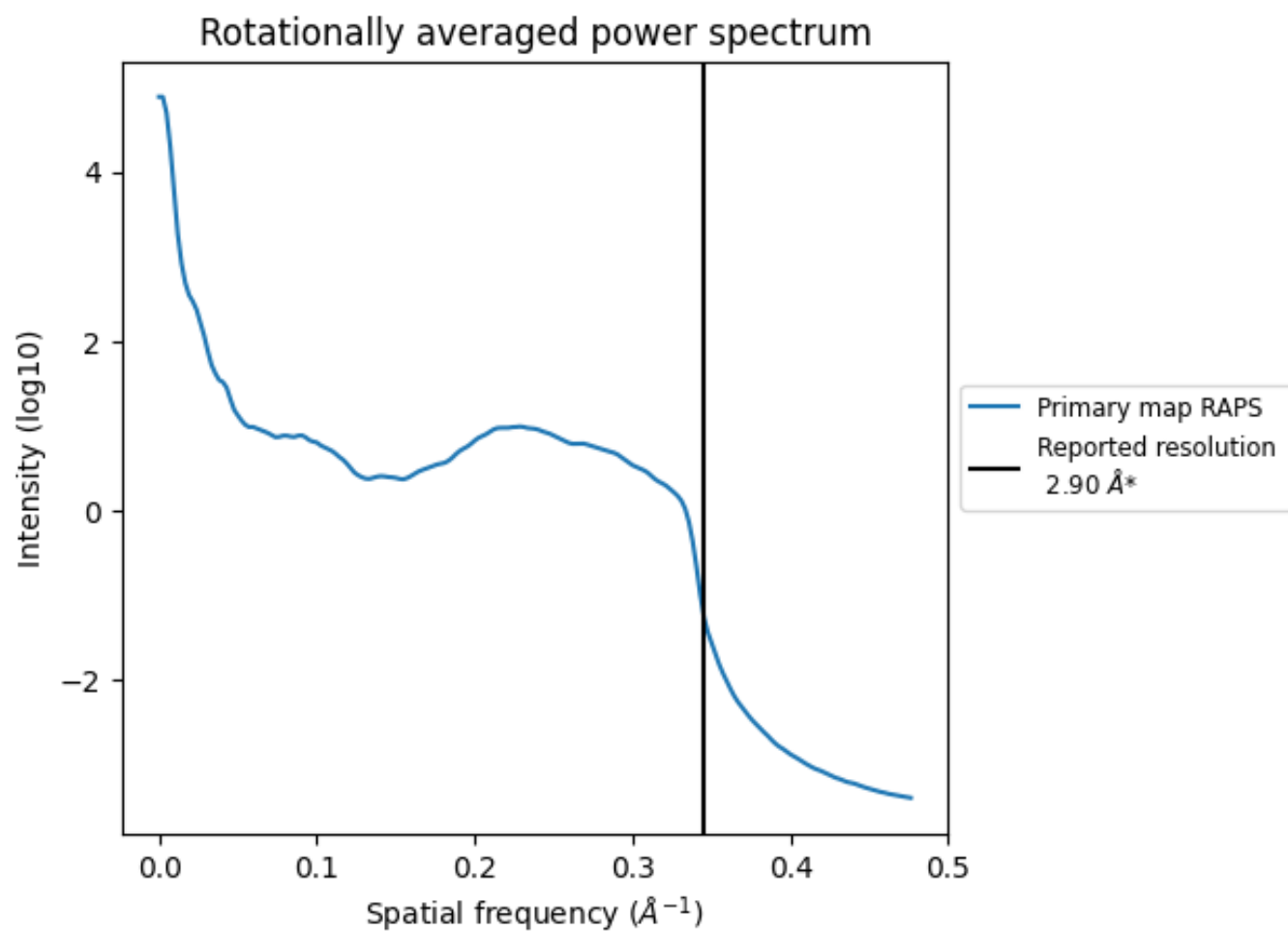
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 95 nm^3 ; this corresponds to an approximate mass of 86 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 0.345 Å⁻¹

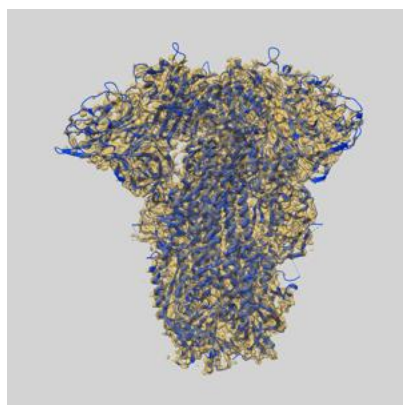
8 Fourier-Shell correlation ⓘ

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

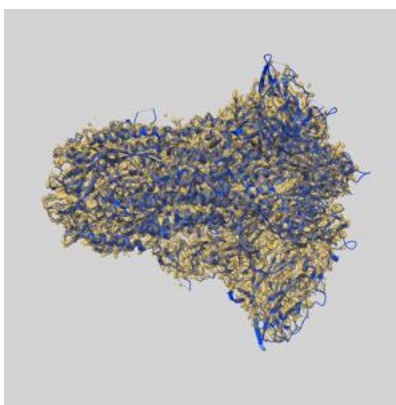
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20070 and PDB model 6OHW. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

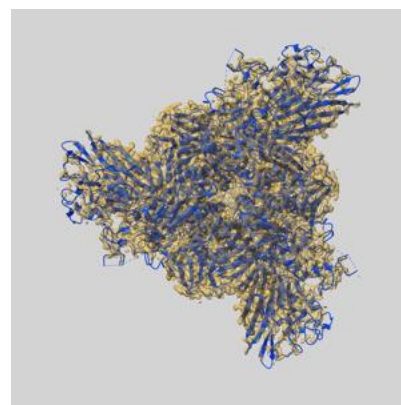
9.1 Map-model overlay [i](#)



X



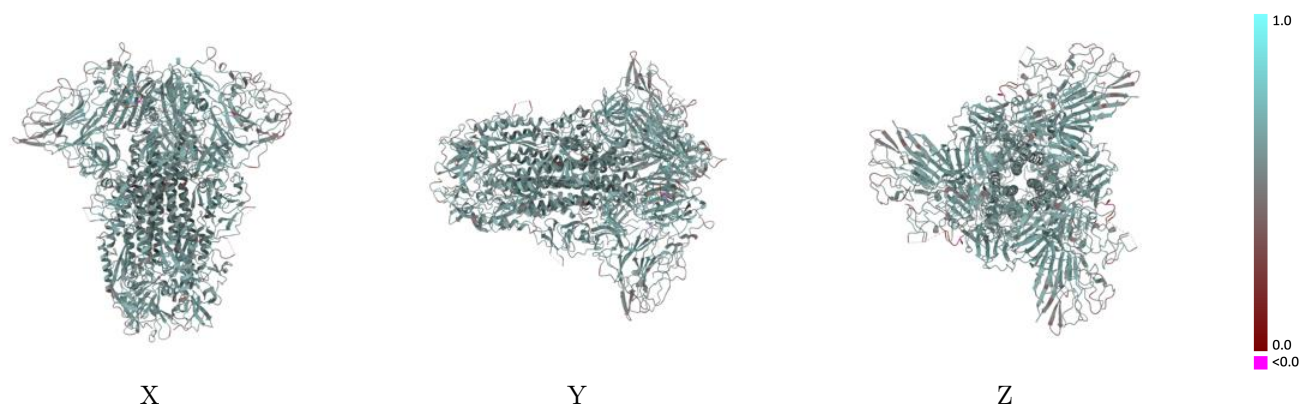
Y



Z

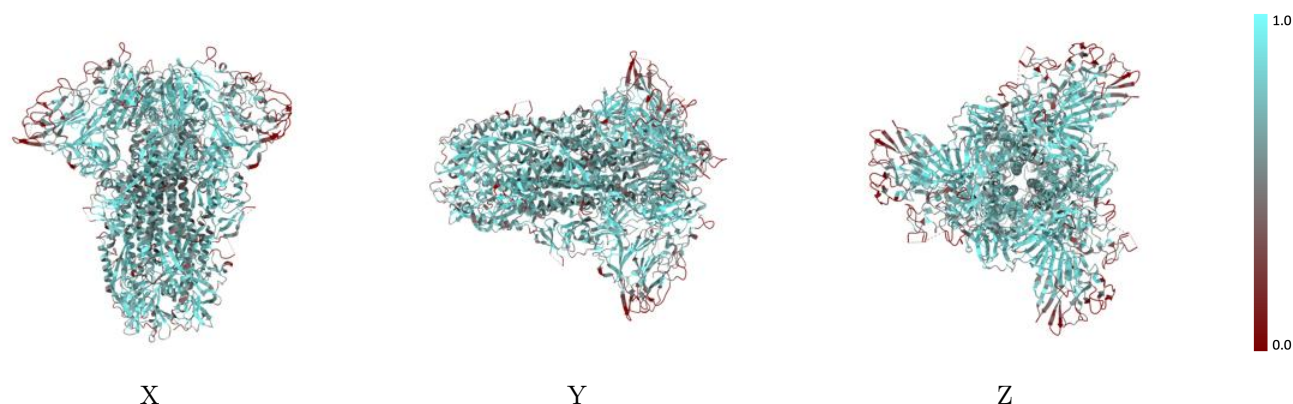
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



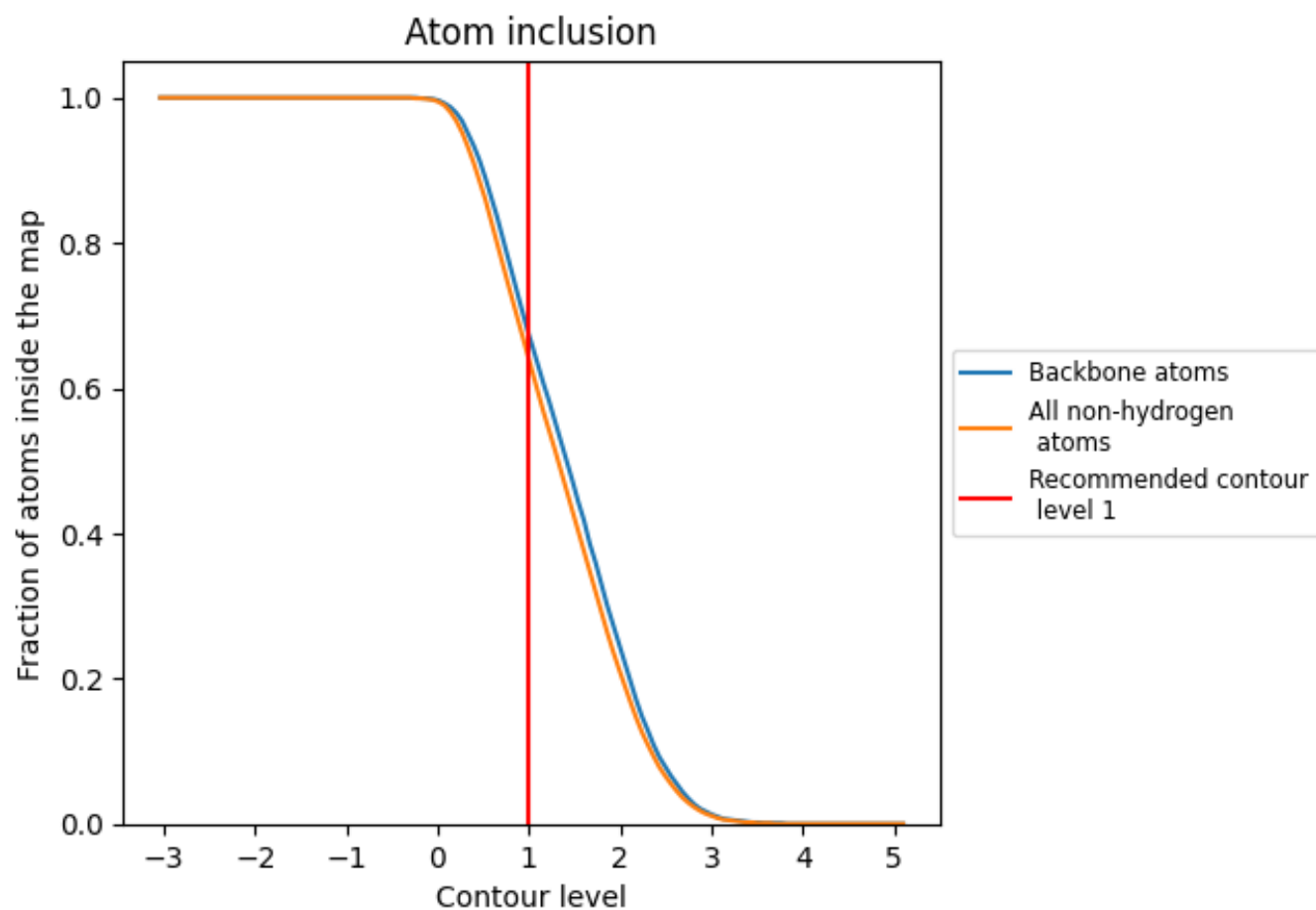
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1).





































































9.4 Atom inclusion [i](#)



At the recommended contour level, 67% of all backbone atoms, 64% 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 (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6390	 0.5610
A	 0.6660	 0.5700
B	 0.6640	 0.5710
C	 0.6640	 0.5710
D	 0.0000	 0.2880
E	 0.1280	 0.3660
F	 0.0000	 0.2480
G	 0.2310	 0.3990
H	 0.0000	 0.3140
I	 0.0000	 0.1820
J	 0.1600	 0.2640
K	 0.0000	 0.2850
L	 0.0360	 0.3020
M	 0.0260	 0.3230
N	 0.0000	 0.2850
O	 0.1540	 0.3720
P	 0.0260	 0.2510
Q	 0.2310	 0.3750
R	 0.0000	 0.3290
S	 0.0000	 0.1810
T	 0.1600	 0.2780
U	 0.0000	 0.3080
V	 0.0360	 0.3120
W	 0.0000	 0.3370
X	 0.0000	 0.2820
Y	 0.1540	 0.3730
Z	 0.0000	 0.2380
a	 0.2310	 0.3790
b	 0.0000	 0.3300
c	 0.0000	 0.1630
d	 0.1600	 0.2650
e	 0.0000	 0.2900
f	 0.0000	 0.3060
g	 0.0000	 0.3360

