



## wwPDB EM Validation Summary Report ⓘ

May 7, 2026 – 12:27 PM EDT

PDB ID : 9DHW / pdb\_00009dhw  
EMDB ID : EMD-46884  
Title : Q23.MD39 in Complex with Fabs from antibodies CH01 iGL and 35O22  
Authors : Lin, Z.J.; Cui, J.; Du, J.; Habib, R.; Kulp, D.; Pallesen, J.  
Deposited on : 2024-09-04  
Resolution : 3.35 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](mailto: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>.

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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  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
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

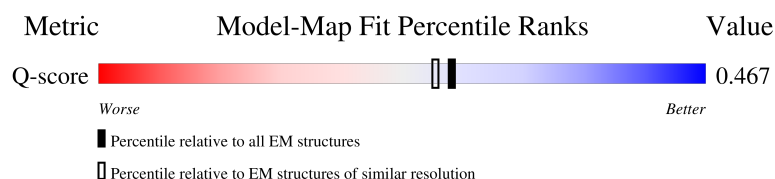
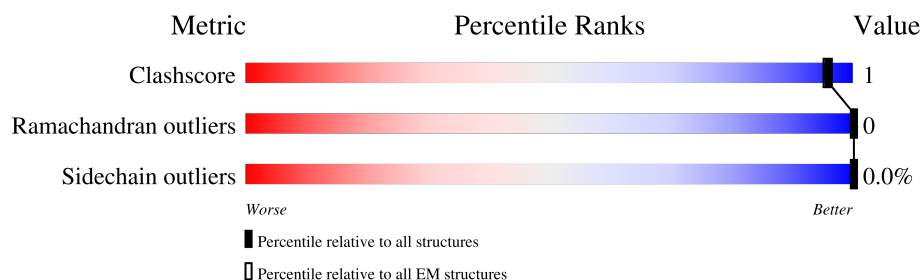
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.35 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.








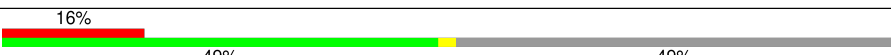
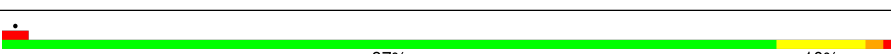
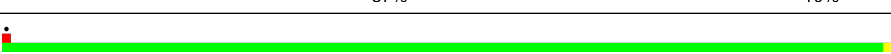
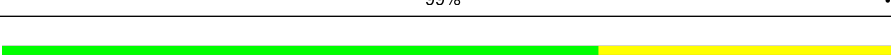

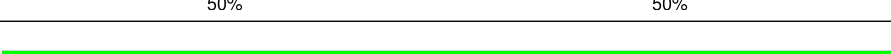
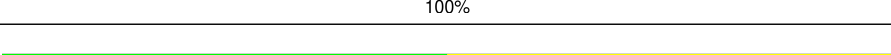
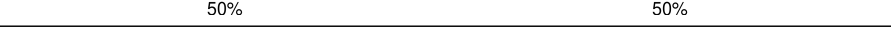

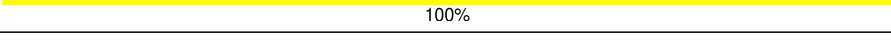

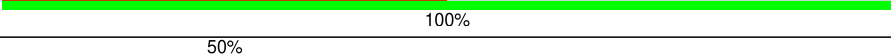
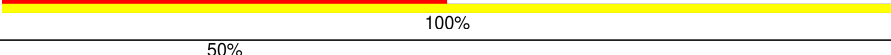

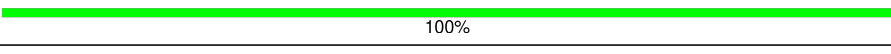



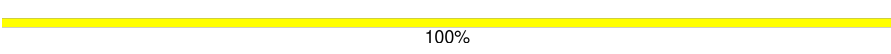
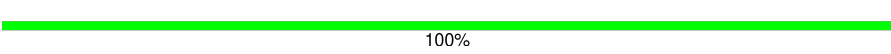
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14390 ( 2.85 - 3.85 )

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  $\geq 3$ , 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	467	91% 6%
1	C	467	90% 5%
1	G	467	90% 6%
2	B	153	82% 18%

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Mol	Chain	Length	Quality of chain
2	D	153	
2	I	153	
3	E	243	
3	H	243	
4	F	216	
4	L	216	
5	M	108	
6	N	133	
7	J	6	
8	K	2	
8	P	2	
8	R	2	
8	X	2	
8	Y	2	
8	Z	2	
8	a	2	
8	c	2	
8	d	2	
8	e	2	
8	i	2	
8	j	2	
8	k	2	
8	l	2	
8	m	2	
8	n	2	

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Mol	Chain	Length	Quality of chain
9	O	7	
10	Q	3	
10	S	3	
10	U	3	
10	h	3	
11	T	2	
12	V	5	
13	W	5	
13	g	5	
14	b	8	
15	f	4	

## 2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 20383 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 Q23.MD39 Surface protein gp120.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	441	Total	C	N	O	S	0	0
			3495	2205	614	650	26		
1	C	442	Total	C	N	O	S	0	0
			3504	2211	616	651	26		
1	G	440	Total	C	N	O	S	0	0
			3486	2200	613	647	26		

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	106	GLU	THR	engineered mutation	UNP O55774
A	271	ILE	THR	engineered mutation	UNP O55774
A	304	VAL	ARG	engineered mutation	UNP O55774
A	319	TYR	ALA	engineered mutation	UNP O55774
A	363	GLN	ASN	engineered mutation	UNP O55774
A	473	SER	GLY	engineered mutation	UNP O55774
A	501	CYS	ALA	engineered mutation	UNP O55774
C	106	GLU	THR	engineered mutation	UNP O55774
C	271	ILE	THR	engineered mutation	UNP O55774
C	304	VAL	ARG	engineered mutation	UNP O55774
C	319	TYR	ALA	engineered mutation	UNP O55774
C	363	GLN	ASN	engineered mutation	UNP O55774
C	473	SER	GLY	engineered mutation	UNP O55774
C	501	CYS	ALA	engineered mutation	UNP O55774
G	106	GLU	THR	engineered mutation	UNP O55774
G	271	ILE	THR	engineered mutation	UNP O55774
G	304	VAL	ARG	engineered mutation	UNP O55774
G	319	TYR	ALA	engineered mutation	UNP O55774
G	363	GLN	ASN	engineered mutation	UNP O55774
G	473	SER	GLY	engineered mutation	UNP O55774
G	501	CYS	ALA	engineered mutation	UNP O55774

- Molecule 2 is a protein called Q23.MD39 Transmembrane protein gp41.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	126	Total	C	N	O	S	0	0
			1012	639	175	193	5		
2	D	120	Total	C	N	O	S	0	0
			973	614	169	185	5		
2	I	117	Total	C	N	O	S	0	0
			946	598	166	177	5		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	519	SER	PHE	engineered mutation	UNP O55774
B	533	ALA	THR	engineered mutation	UNP O55774
B	559	PRO	ILE	engineered mutation	UNP O55774
B	561	PRO	ALA	engineered mutation	UNP O55774
B	568	ASP	LEU	engineered mutation	UNP O55774
B	570	HIS	VAL	engineered mutation	UNP O55774
B	585	HIS	ARG	engineered mutation	UNP O55774
B	605	CYS	THR	engineered mutation	UNP O55774
D	519	SER	PHE	engineered mutation	UNP O55774
D	533	ALA	THR	engineered mutation	UNP O55774
D	559	PRO	ILE	engineered mutation	UNP O55774
D	561	PRO	ALA	engineered mutation	UNP O55774
D	568	ASP	LEU	engineered mutation	UNP O55774
D	570	HIS	VAL	engineered mutation	UNP O55774
D	585	HIS	ARG	engineered mutation	UNP O55774
D	605	CYS	THR	engineered mutation	UNP O55774
I	519	SER	PHE	engineered mutation	UNP O55774
I	533	ALA	THR	engineered mutation	UNP O55774
I	559	PRO	ILE	engineered mutation	UNP O55774
I	561	PRO	ALA	engineered mutation	UNP O55774
I	568	ASP	LEU	engineered mutation	UNP O55774
I	570	HIS	VAL	engineered mutation	UNP O55774
I	585	HIS	ARG	engineered mutation	UNP O55774
I	605	CYS	THR	engineered mutation	UNP O55774

- Molecule 3 is a protein called 35O22 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	130	Total	C	N	O	S	0	0
			1015	649	171	190	5		
3	H	130	Total	C	N	O	S	0	0
			1015	649	171	190	5		

- Molecule 4 is a protein called 35O22 Fab Light Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	110	Total	C	N	O	S	0	0
			836	525	138	167	6		
4	L	110	Total	C	N	O	S	0	0
			836	525	138	167	6		

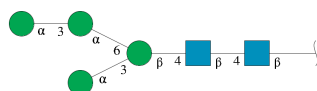
- Molecule 5 is a protein called CH01 iGL Fab Light Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	M	108	Total	C	N	O	S	0	0
			822	516	138	166	2		

- Molecule 6 is a protein called CH01 iGL Fab Heavy Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	N	133	Total	C	N	O	S	0	0
			1026	643	178	201	4		

- Molecule 7 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[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
7	J	6	Total	C	N	O	0	0
			72	40	2	30		

- Molecule 8 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



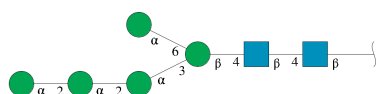
Mol	Chain	Residues	Atoms				AltConf	Trace
8	K	2	Total	C	N	O	0	0
			28	16	2	10		

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Mol	Chain	Residues	Atoms				AltConf	Trace
8	P	2	Total	C	N	O	0	0
			28	16	2	10		
8	R	2	Total	C	N	O	0	0
			28	16	2	10		
8	X	2	Total	C	N	O	0	0
			28	16	2	10		
8	Y	2	Total	C	N	O	0	0
			28	16	2	10		
8	Z	2	Total	C	N	O	0	0
			28	16	2	10		
8	a	2	Total	C	N	O	0	0
			28	16	2	10		
8	c	2	Total	C	N	O	0	0
			28	16	2	10		
8	d	2	Total	C	N	O	0	0
			28	16	2	10		
8	e	2	Total	C	N	O	0	0
			28	16	2	10		
8	i	2	Total	C	N	O	0	0
			28	16	2	10		
8	j	2	Total	C	N	O	0	0
			28	16	2	10		
8	k	2	Total	C	N	O	0	0
			28	16	2	10		
8	l	2	Total	C	N	O	0	0
			28	16	2	10		
8	m	2	Total	C	N	O	0	0
			28	16	2	10		
8	n	2	Total	C	N	O	0	0
			28	16	2	10		

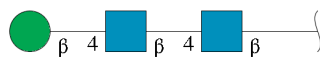
- Molecule 9 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
9	O	7	Total	C	N	O	0	0
			83	46	2	35		



- Molecule 10 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.



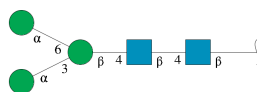
Mol	Chain	Residues	Atoms				AltConf	Trace
10	Q	3	Total	C	N	O	0	0
			39	22	2	15		
10	S	3	Total	C	N	O	0	0
			39	22	2	15		
10	U	3	Total	C	N	O	0	0
			39	22	2	15		
10	h	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 11 is an oligosaccharide called alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose.



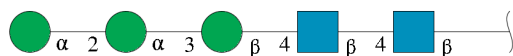
Mol	Chain	Residues	Atoms				AltConf	Trace
11	T	2	Total	C	N	O	0	0
			24	14	1	9		

- Molecule 12 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



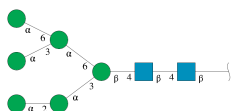
Mol	Chain	Residues	Atoms				AltConf	Trace
12	V	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 13 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-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.



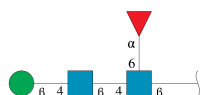
Mol	Chain	Residues	Atoms				AltConf	Trace
13	W	5	Total	C	N	O	0	0
			61	34	2	25		
13	g	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 14 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



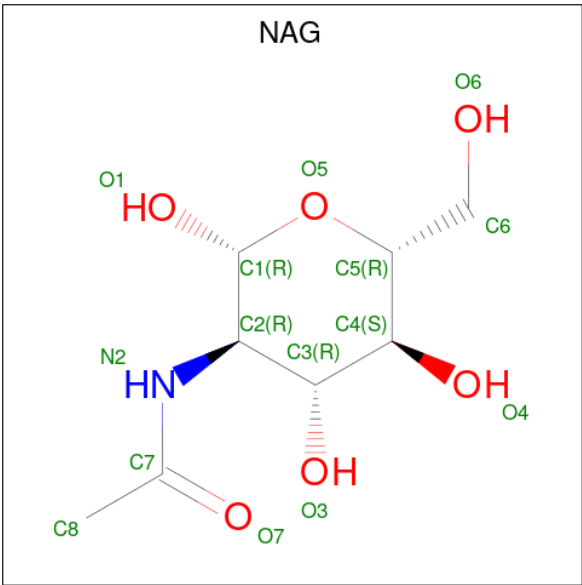
Mol	Chain	Residues	Atoms				AltConf	Trace
14	b	8	Total	C	N	O	0	0
			94	52	2	40		

- Molecule 15 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
15	f	4	Total	C	N	O	0	0
			49	28	2	19		

- Molecule 16 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>) (labeled as "Ligand of Interest" by depositor).



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

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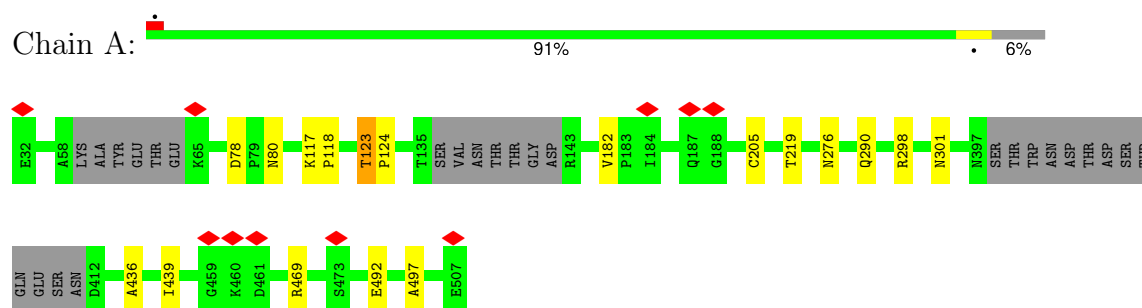
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Mol	Chain	Residues	Atoms				AltConf
16	D	1	Total	C	N	O	0
			14	8	1	5	
16	G	1	Total	C	N	O	0
			14	8	1	5	
16	G	1	Total	C	N	O	0
			14	8	1	5	
16	G	1	Total	C	N	O	0
			14	8	1	5	
16	G	1	Total	C	N	O	0
			14	8	1	5	
16	G	1	Total	C	N	O	0
			14	8	1	5	
16	G	1	Total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

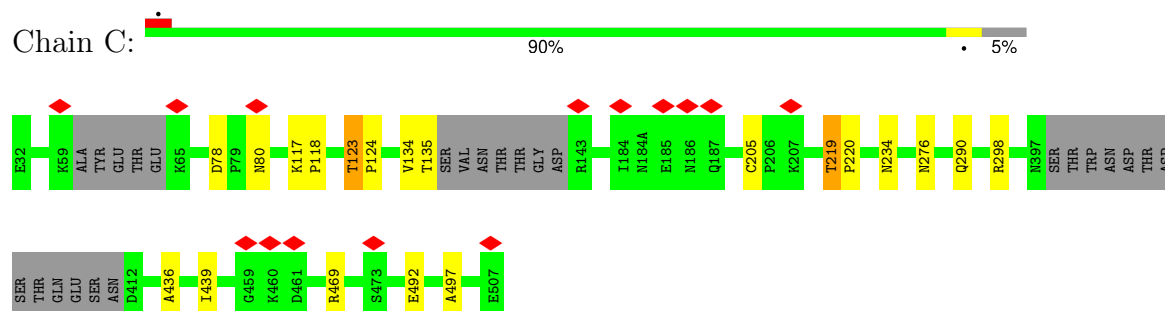
### 3 Residue-property plots [i](#)

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

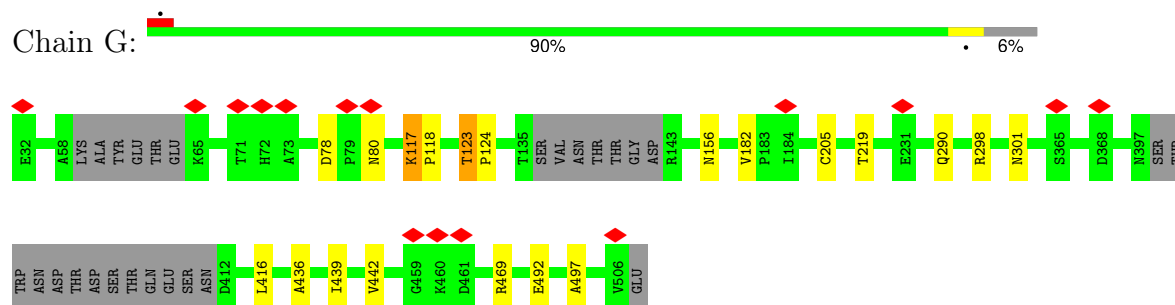
- Molecule 1: Q23.MD39 Surface protein gp120



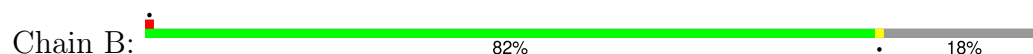
- Molecule 1: Q23.MD39 Surface protein gp120

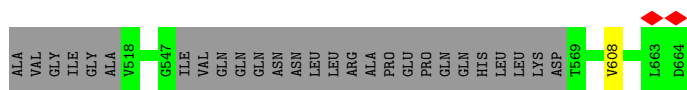


- Molecule 1: Q23.MD39 Surface protein gp120

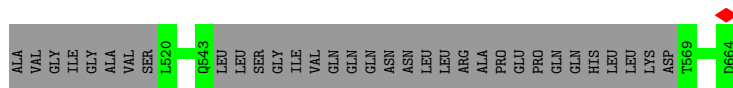
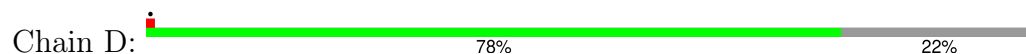


- Molecule 2: Q23.MD39 Transmembrane protein gp41

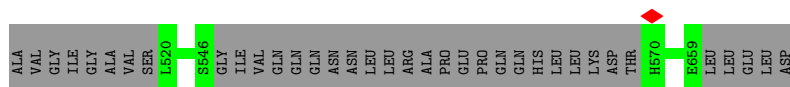




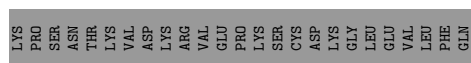
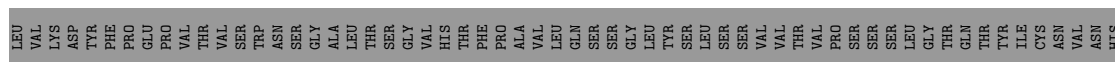
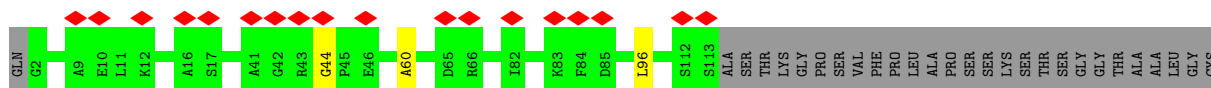
- Molecule 2: Q23.MD39 Transmembrane protein gp41



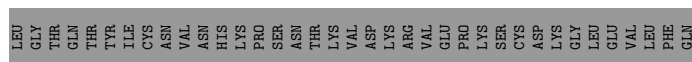
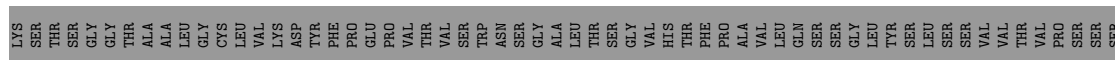
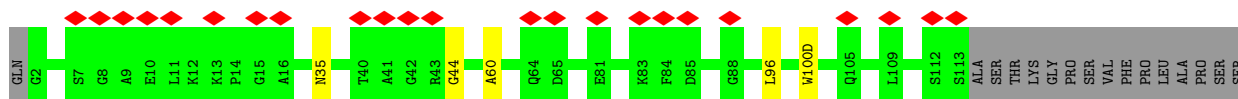
- Molecule 2: Q23.MD39 Transmembrane protein gp41



- Molecule 3: 35O22 Fab Heavy Chain

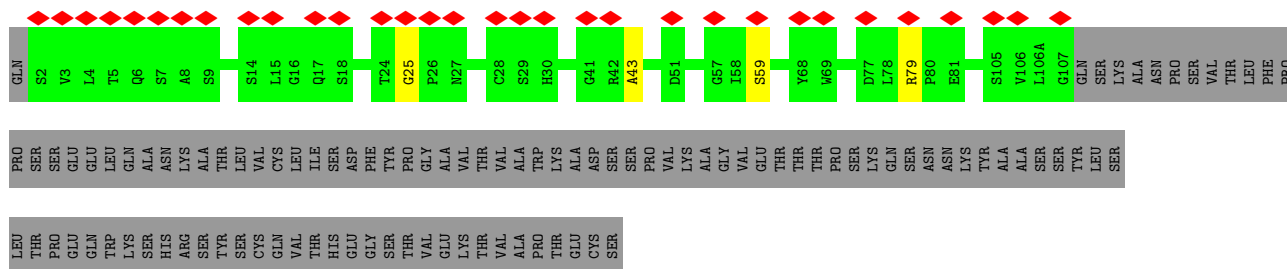


- Molecule 3: 35O22 Fab Heavy Chain

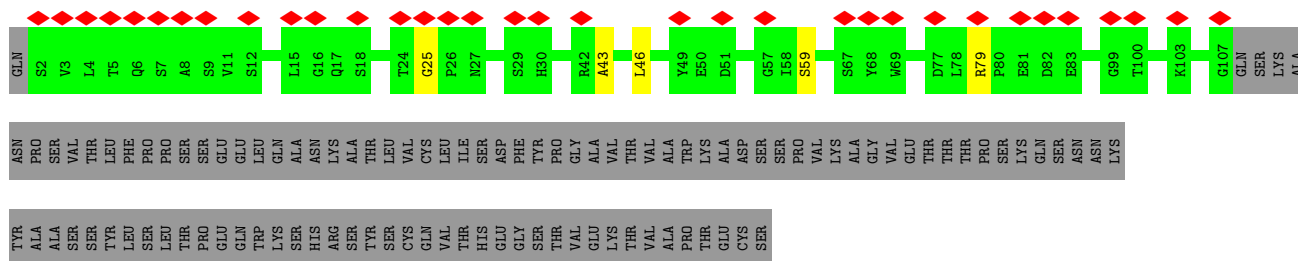


- Molecule 4: 35O22 Fab Light Chain





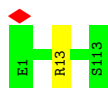
- Molecule 4: 35O22 Fab Light Chain



- Molecule 5: CH01 iGL Fab Light Chain



- Molecule 6: CH01 iGL Fab Heavy Chain



- Molecule 7:  $\alpha$ -D-mannopyranose-(1-3)- $\alpha$ -D-mannopyranose-(1-6)-[ $\alpha$ -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 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose





- Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P:



- Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain R:



- Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain X:



- Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Y:



- Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Z:



- Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain a:





- Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain l:  100%

NAG1  
NAG2

- Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain m:  100%

NAG1  
NAG2


- Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain n:  100%

NAG1  
NAG2

- Molecule 9: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain O:  57% 86% 14%

  
NAG1  
NAG2  
BMA3  
MAN4  
MAN5  
MAN6  
MAN7

- Molecule 10: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Q:  100%

NAG1  
NAG2  
BMA3

- Molecule 10: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain S:  33% 100%

  
NAG1  
NAG2  
BMA3

- Molecule 10: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain U:  33% 100%



- Molecule 10: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain h:  67% 33%



- Molecule 11: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain T:  100%



- Molecule 12: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain V:  100%




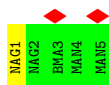
- Molecule 13: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain W:  20% 100%

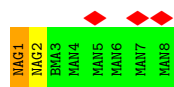
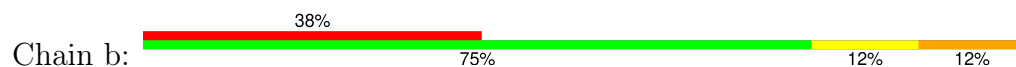


- Molecule 13: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain g:  40% 80% 20%



- Molecule 14:  $\alpha$ -D-mannopyranose-(1-2)- $\alpha$ -D-mannopyranose-(1-3)-[ $\alpha$ -D-mannopyranose-(1-3)-[ $\alpha$ -D-mannopyranose-(1-6)] $\alpha$ -D-mannopyranose-(1-6)] $\beta$ -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- $\beta$ -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- $\beta$ -D-glucopyranose



- Molecule 15:  $\beta$ -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



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	71949	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	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)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	3.315	Depositor
Minimum map value	-1.707	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.079	Depositor
Recommended contour level	0.46	Depositor
Map size ( $\text{\AA}$ )	358.36002, 358.36002, 358.36002	wwPDB
Map dimensions	340, 340, 340	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.054, 1.054, 1.054	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MAN, 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	0.65	0/3569	0.95	26/4847 (0.5%)
1	C	0.64	0/3578	0.94	24/4858 (0.5%)
1	G	0.63	0/3560	0.94	30/4835 (0.6%)
2	B	0.69	0/1031	0.67	2/1396 (0.1%)
2	D	0.66	0/992	0.66	0/1343
2	I	0.60	0/965	0.65	0/1307
3	E	0.65	0/1043	0.90	5/1416 (0.4%)
3	H	0.62	0/1043	0.89	5/1416 (0.4%)
4	F	0.58	0/860	1.03	8/1175 (0.7%)
4	L	0.58	0/860	1.03	8/1175 (0.7%)
5	M	0.71	0/841	1.26	9/1140 (0.8%)
6	N	0.67	0/1052	0.82	2/1425 (0.1%)
All	All	0.64	0/19394	0.92	119/26333 (0.5%)

There are no bond length outliers.

The worst 5 of 119 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	M	91	TYR	CB-CA-C	-12.23	86.23	109.72
4	L	59	SER	CA-C-N	7.78	127.50	119.56
4	L	59	SER	C-N-CA	7.78	127.50	119.56
1	C	492	GLU	CA-C-N	7.73	127.44	119.56
1	C	492	GLU	C-N-CA	7.73	127.44	119.56

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	3495	0	3439	5	0
1	C	3504	0	3453	7	0
1	G	3486	0	3433	5	0
2	B	1012	0	986	0	0
2	D	973	0	942	0	0
2	I	946	0	922	0	0
3	E	1015	0	985	0	0
3	H	1015	0	985	1	0
4	F	836	0	785	0	0
4	L	836	0	785	1	0
5	M	822	0	797	7	0
6	N	1026	0	956	0	0
7	J	72	0	61	0	0
8	K	28	0	25	0	0
8	P	28	0	25	0	0
8	R	28	0	25	3	0
8	X	28	0	25	0	0
8	Y	28	0	25	0	0
8	Z	28	0	25	0	0
8	a	28	0	25	0	0
8	c	28	0	25	0	0
8	d	28	0	25	0	0
8	e	28	0	25	0	0
8	i	28	0	25	0	0
8	j	28	0	25	0	0
8	k	28	0	25	0	0
8	l	28	0	25	0	0
8	m	28	0	25	0	0
8	n	28	0	25	0	0
9	O	83	0	70	1	0
10	Q	39	0	34	0	0
10	S	39	0	34	0	0
10	U	39	0	34	0	0
10	h	39	0	34	0	0
11	T	24	0	22	0	0
12	V	61	0	52	0	0
13	W	61	0	52	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	g	61	0	52	0	0
14	b	94	0	79	3	0
15	f	49	0	43	4	0
16	A	112	0	104	1	0
16	B	28	0	26	0	0
16	C	42	0	39	0	0
16	D	28	0	26	0	0
16	G	98	0	91	1	0
All	All	20383	0	19721	37	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.

The worst 5 of 37 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)
14:b:1:NAG:O6	14:b:2:NAG:N2	2.19	0.75
15:f:2:NAG:O7	15:f:2:NAG:C3	2.36	0.74
8:R:2:NAG:O7	8:R:2:NAG:C3	2.36	0.73
1:G:442:VAL:H	16:G:603:NAG:H82	1.61	0.66
15:f:2:NAG:O7	15:f:2:NAG:O3	2.15	0.64

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	433/467 (93%)	429 (99%)	4 (1%)	0	100	100
1	C	434/467 (93%)	427 (98%)	7 (2%)	0	100	100
1	G	432/467 (92%)	426 (99%)	6 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	122/153 (80%)	122 (100%)	0	0	100	100
2	D	116/153 (76%)	116 (100%)	0	0	100	100
2	I	113/153 (74%)	113 (100%)	0	0	100	100
3	E	128/243 (53%)	127 (99%)	1 (1%)	0	100	100
3	H	128/243 (53%)	127 (99%)	1 (1%)	0	100	100
4	F	108/216 (50%)	106 (98%)	2 (2%)	0	100	100
4	L	108/216 (50%)	107 (99%)	1 (1%)	0	100	100
5	M	106/108 (98%)	106 (100%)	0	0	100	100
6	N	131/133 (98%)	130 (99%)	1 (1%)	0	100	100
All	All	2359/3019 (78%)	2336 (99%)	23 (1%)	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	395/419 (94%)	395 (100%)	0	100	100
1	C	396/419 (94%)	396 (100%)	0	100	100
1	G	394/419 (94%)	394 (100%)	0	100	100
2	B	110/132 (83%)	110 (100%)	0	100	100
2	D	105/132 (80%)	105 (100%)	0	100	100
2	I	102/132 (77%)	102 (100%)	0	100	100
3	E	108/206 (52%)	108 (100%)	0	100	100
3	H	108/206 (52%)	108 (100%)	0	100	100
4	F	96/189 (51%)	96 (100%)	0	100	100
4	L	96/189 (51%)	96 (100%)	0	100	100
5	M	90/90 (100%)	89 (99%)	1 (1%)	65	73
6	N	105/105 (100%)	105 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	2105/2638 (80%)	2104 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	M	91	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	374	HIS
2	I	570	HIS
6	N	82(A)	ASN
2	I	575	GLN
2	D	570	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 ⓘ

86 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	$\# Z  > 2$
7	NAG	J	1	7,1	14,14,15	0.39	0	17,19,21	2.16	2 (11%)
7	NAG	J	2	7	14,14,15	0.38	0	17,19,21	0.49	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
7	BMA	J	3	7	11,11,12	0.55	0	15,15,17	0.51	0
7	MAN	J	4	7	11,11,12	0.42	0	15,15,17	1.20	3 (20%)
7	MAN	J	5	7	11,11,12	0.28	0	15,15,17	0.58	0
7	MAN	J	6	7	11,11,12	0.34	0	15,15,17	0.61	0
8	NAG	K	1	8,1	14,14,15	0.39	0	17,19,21	0.88	1 (5%)
8	NAG	K	2	8	14,14,15	0.38	0	17,19,21	0.52	0
9	NAG	O	1	9,1	14,14,15	0.37	0	17,19,21	0.60	0
9	NAG	O	2	9	14,14,15	0.38	0	17,19,21	0.49	0
9	BMA	O	3	9	11,11,12	0.35	0	15,15,17	0.59	0
9	MAN	O	4	9	11,11,12	0.36	0	15,15,17	0.50	0
9	MAN	O	5	9	11,11,12	0.30	0	15,15,17	0.47	0
9	MAN	O	6	9	11,11,12	0.33	0	15,15,17	0.54	0
9	MAN	O	7	9	11,11,12	0.31	0	15,15,17	0.52	0
8	NAG	P	1	8,1	14,14,15	0.38	0	17,19,21	0.65	0
8	NAG	P	2	8	14,14,15	0.38	0	17,19,21	0.44	0
10	NAG	Q	1	10,1	14,14,15	0.39	0	17,19,21	0.53	0
10	NAG	Q	2	10	14,14,15	0.38	0	17,19,21	0.44	0
10	BMA	Q	3	10	11,11,12	0.31	0	15,15,17	0.54	0
8	NAG	R	1	8,1	14,14,15	0.38	0	17,19,21	0.73	0
8	NAG	R	2	8	14,14,15	0.39	0	17,19,21	0.52	0
10	NAG	S	1	10,1	14,14,15	0.40	0	17,19,21	0.49	0
10	NAG	S	2	10	14,14,15	0.40	0	17,19,21	0.51	0
10	BMA	S	3	10	11,11,12	0.31	0	15,15,17	0.50	0
11	NAG	T	1	2,11	14,14,15	0.41	0	17,19,21	0.67	0
11	FUC	T	2	11	10,10,11	0.39	0	14,14,16	0.43	0
10	NAG	U	1	10,1	14,14,15	0.35	0	17,19,21	0.59	0
10	NAG	U	2	10	14,14,15	0.37	0	17,19,21	0.51	0
10	BMA	U	3	10	11,11,12	0.27	0	15,15,17	0.54	0
12	NAG	V	1	12,1	14,14,15	0.41	0	17,19,21	0.81	0
12	NAG	V	2	12	14,14,15	0.40	0	17,19,21	0.56	0
12	BMA	V	3	12	11,11,12	0.39	0	15,15,17	0.49	0
12	MAN	V	4	12	11,11,12	0.33	0	15,15,17	0.56	0
12	MAN	V	5	12	11,11,12	0.28	0	15,15,17	0.51	0
13	NAG	W	1	13,1	14,14,15	0.39	0	17,19,21	0.61	0
13	NAG	W	2	13	14,14,15	0.37	0	17,19,21	0.46	0
13	BMA	W	3	13	11,11,12	0.37	0	15,15,17	0.46	0
13	MAN	W	4	13	11,11,12	0.26	0	15,15,17	0.59	0
13	MAN	W	5	13	11,11,12	0.27	0	15,15,17	0.53	0
8	NAG	X	1	8,1	14,14,15	0.40	0	17,19,21	0.71	0
8	NAG	X	2	8	14,14,15	0.39	0	17,19,21	1.25	2 (11%)
8	NAG	Y	1	8,1	14,14,15	0.38	0	17,19,21	0.64	1 (5%)
8	NAG	Y	2	8	14,14,15	0.37	0	17,19,21	1.76	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
8	NAG	Z	1	8,1	14,14,15	0.39	0	17,19,21	0.76	1 (5%)
8	NAG	Z	2	8	14,14,15	0.37	0	17,19,21	0.44	0
8	NAG	a	1	8,1	14,14,15	0.37	0	17,19,21	0.75	0
8	NAG	a	2	8	14,14,15	0.38	0	17,19,21	0.47	0
14	NAG	b	1	14,1	14,14,15	0.41	0	17,19,21	0.83	1 (5%)
14	NAG	b	2	14	14,14,15	0.37	0	17,19,21	0.55	0
14	BMA	b	3	14	11,11,12	0.47	0	15,15,17	0.54	0
14	MAN	b	4	14	11,11,12	0.33	0	15,15,17	0.50	0
14	MAN	b	5	14	11,11,12	0.30	0	15,15,17	0.57	0
14	MAN	b	6	14	11,11,12	0.31	0	15,15,17	0.61	0
14	MAN	b	7	14	11,11,12	0.30	0	15,15,17	0.54	0
14	MAN	b	8	14	11,11,12	0.35	0	15,15,17	0.50	0
8	NAG	c	1	8,1	14,14,15	0.35	0	17,19,21	0.93	1 (5%)
8	NAG	c	2	8	14,14,15	0.37	0	17,19,21	1.64	1 (5%)
8	NAG	d	1	8,1	14,14,15	0.39	0	17,19,21	0.64	0
8	NAG	d	2	8	14,14,15	0.40	0	17,19,21	1.92	2 (11%)
8	NAG	e	1	8,1	14,14,15	0.37	0	17,19,21	0.62	0
8	NAG	e	2	8	14,14,15	0.39	0	17,19,21	0.55	0
15	NAG	f	1	2,15	14,14,15	0.43	0	17,19,21	1.12	1 (5%)
15	NAG	f	2	15	14,14,15	0.41	0	17,19,21	0.68	0
15	BMA	f	3	15	11,11,12	0.28	0	15,15,17	0.46	0
15	FUC	f	4	15	10,10,11	0.43	0	14,14,16	0.34	0
13	NAG	g	1	13,1	14,14,15	0.37	0	17,19,21	1.98	2 (11%)
13	NAG	g	2	13	14,14,15	0.40	0	17,19,21	0.45	0
13	BMA	g	3	13	11,11,12	0.41	0	15,15,17	0.58	0
13	MAN	g	4	13	11,11,12	0.30	0	15,15,17	0.54	0
13	MAN	g	5	13	11,11,12	0.33	0	15,15,17	0.55	0
10	NAG	h	1	10,1	14,14,15	0.42	0	17,19,21	1.66	4 (23%)
10	NAG	h	2	10	14,14,15	0.38	0	17,19,21	0.52	0
10	BMA	h	3	10	11,11,12	0.26	0	15,15,17	0.50	0
8	NAG	i	1	8,1	14,14,15	0.38	0	17,19,21	0.91	1 (5%)
8	NAG	i	2	8	14,14,15	0.38	0	17,19,21	0.77	0
8	NAG	j	1	8,1	14,14,15	0.38	0	17,19,21	0.69	0
8	NAG	j	2	8	14,14,15	0.37	0	17,19,21	1.63	2 (11%)
8	NAG	k	1	8,1	14,14,15	0.36	0	17,19,21	1.77	1 (5%)
8	NAG	k	2	8	14,14,15	0.38	0	17,19,21	0.52	0
8	NAG	l	1	8,1	14,14,15	0.37	0	17,19,21	0.66	1 (5%)
8	NAG	l	2	8	14,14,15	0.38	0	17,19,21	1.31	2 (11%)
8	NAG	m	1	8,1	14,14,15	0.38	0	17,19,21	0.47	0
8	NAG	m	2	8	14,14,15	0.38	0	17,19,21	0.51	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
8	NAG	n	1	8,1	14,14,15	0.39	0	17,19,21	0.57	0
8	NAG	n	2	8	14,14,15	0.38	0	17,19,21	0.47	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
7	NAG	J	1	7,1	-	0/6/23/26	0/1/1/1
7	NAG	J	2	7	-	1/6/23/26	0/1/1/1
7	BMA	J	3	7	-	2/2/19/22	0/1/1/1
7	MAN	J	4	7	-	1/2/19/22	0/1/1/1
7	MAN	J	5	7	-	0/2/19/22	0/1/1/1
7	MAN	J	6	7	-	0/2/19/22	0/1/1/1
8	NAG	K	1	8,1	-	0/6/23/26	0/1/1/1
8	NAG	K	2	8	-	0/6/23/26	0/1/1/1
9	NAG	O	1	9,1	-	0/6/23/26	0/1/1/1
9	NAG	O	2	9	-	0/6/23/26	0/1/1/1
9	BMA	O	3	9	-	0/2/19/22	0/1/1/1
9	MAN	O	4	9	-	0/2/19/22	0/1/1/1
9	MAN	O	5	9	-	0/2/19/22	0/1/1/1
9	MAN	O	6	9	-	0/2/19/22	0/1/1/1
9	MAN	O	7	9	-	0/2/19/22	0/1/1/1
8	NAG	P	1	8,1	-	0/6/23/26	0/1/1/1
8	NAG	P	2	8	-	1/6/23/26	0/1/1/1
10	NAG	Q	1	10,1	-	0/6/23/26	0/1/1/1
10	NAG	Q	2	10	-	1/6/23/26	0/1/1/1
10	BMA	Q	3	10	-	1/2/19/22	0/1/1/1
8	NAG	R	1	8,1	-	1/6/23/26	0/1/1/1
8	NAG	R	2	8	-	2/6/23/26	0/1/1/1
10	NAG	S	1	10,1	-	0/6/23/26	0/1/1/1
10	NAG	S	2	10	-	0/6/23/26	0/1/1/1
10	BMA	S	3	10	-	0/2/19/22	0/1/1/1
11	NAG	T	1	2,11	-	0/6/23/26	0/1/1/1
11	FUC	T	2	11	-	-	0/1/1/1
10	NAG	U	1	10,1	-	0/6/23/26	0/1/1/1
10	NAG	U	2	10	-	0/6/23/26	0/1/1/1
10	BMA	U	3	10	-	1/2/19/22	0/1/1/1
12	NAG	V	1	12,1	-	0/6/23/26	0/1/1/1
12	NAG	V	2	12	-	0/6/23/26	0/1/1/1
12	BMA	V	3	12	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	MAN	V	4	12	-	1/2/19/22	0/1/1/1
12	MAN	V	5	12	-	0/2/19/22	0/1/1/1
13	NAG	W	1	13,1	-	0/6/23/26	0/1/1/1
13	NAG	W	2	13	-	0/6/23/26	0/1/1/1
13	BMA	W	3	13	-	1/2/19/22	0/1/1/1
13	MAN	W	4	13	-	1/2/19/22	0/1/1/1
13	MAN	W	5	13	-	1/2/19/22	0/1/1/1
8	NAG	X	1	8,1	-	0/6/23/26	0/1/1/1
8	NAG	X	2	8	-	1/6/23/26	0/1/1/1
8	NAG	Y	1	8,1	-	0/6/23/26	0/1/1/1
8	NAG	Y	2	8	-	0/6/23/26	0/1/1/1
8	NAG	Z	1	8,1	-	0/6/23/26	0/1/1/1
8	NAG	Z	2	8	-	0/6/23/26	0/1/1/1
8	NAG	a	1	8,1	-	0/6/23/26	0/1/1/1
8	NAG	a	2	8	-	0/6/23/26	0/1/1/1
14	NAG	b	1	14,1	-	1/6/23/26	0/1/1/1
14	NAG	b	2	14	-	0/6/23/26	0/1/1/1
14	BMA	b	3	14	-	0/2/19/22	0/1/1/1
14	MAN	b	4	14	-	0/2/19/22	0/1/1/1
14	MAN	b	5	14	-	0/2/19/22	0/1/1/1
14	MAN	b	6	14	-	0/2/19/22	0/1/1/1
14	MAN	b	7	14	-	1/2/19/22	0/1/1/1
14	MAN	b	8	14	-	0/2/19/22	0/1/1/1
8	NAG	c	1	8,1	-	0/6/23/26	0/1/1/1
8	NAG	c	2	8	-	0/6/23/26	0/1/1/1
8	NAG	d	1	8,1	-	0/6/23/26	0/1/1/1
8	NAG	d	2	8	-	0/6/23/26	0/1/1/1
8	NAG	e	1	8,1	-	0/6/23/26	0/1/1/1
8	NAG	e	2	8	-	1/6/23/26	0/1/1/1
15	NAG	f	1	2,15	-	0/6/23/26	0/1/1/1
15	NAG	f	2	15	-	1/6/23/26	0/1/1/1
15	BMA	f	3	15	-	1/2/19/22	0/1/1/1
15	FUC	f	4	15	-	-	0/1/1/1
13	NAG	g	1	13,1	-	0/6/23/26	0/1/1/1
13	NAG	g	2	13	-	0/6/23/26	0/1/1/1
13	BMA	g	3	13	-	1/2/19/22	0/1/1/1
13	MAN	g	4	13	-	0/2/19/22	0/1/1/1
13	MAN	g	5	13	-	0/2/19/22	0/1/1/1
10	NAG	h	1	10,1	-	0/6/23/26	0/1/1/1
10	NAG	h	2	10	-	0/6/23/26	0/1/1/1
10	BMA	h	3	10	-	0/2/19/22	0/1/1/1
8	NAG	i	1	8,1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	NAG	i	2	8	-	1/6/23/26	0/1/1/1
8	NAG	j	1	8,1	-	0/6/23/26	0/1/1/1
8	NAG	j	2	8	-	1/6/23/26	0/1/1/1
8	NAG	k	1	8,1	-	1/6/23/26	0/1/1/1
8	NAG	k	2	8	-	0/6/23/26	0/1/1/1
8	NAG	l	1	8,1	-	0/6/23/26	0/1/1/1
8	NAG	l	2	8	-	1/6/23/26	0/1/1/1
8	NAG	m	1	8,1	-	0/6/23/26	0/1/1/1
8	NAG	m	2	8	-	1/6/23/26	0/1/1/1
8	NAG	n	1	8,1	-	0/6/23/26	0/1/1/1
8	NAG	n	2	8	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	J	1	NAG	C2-N2-C7	7.28	132.65	122.90
8	k	1	NAG	C2-N2-C7	6.84	132.07	122.90
8	Y	2	NAG	C2-N2-C7	6.81	132.03	122.90
13	g	1	NAG	C2-N2-C7	6.70	131.88	122.90
8	c	2	NAG	C2-N2-C7	5.96	130.89	122.90

There are no chirality outliers.

5 of 28 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	R	2	NAG	C3-C2-N2-C7
15	f	2	NAG	C3-C2-N2-C7
7	J	3	BMA	O5-C5-C6-O6
13	W	3	BMA	O5-C5-C6-O6
13	W	4	MAN	O5-C5-C6-O6

There are no ring outliers.

6 monomers are involved in 11 short contacts:

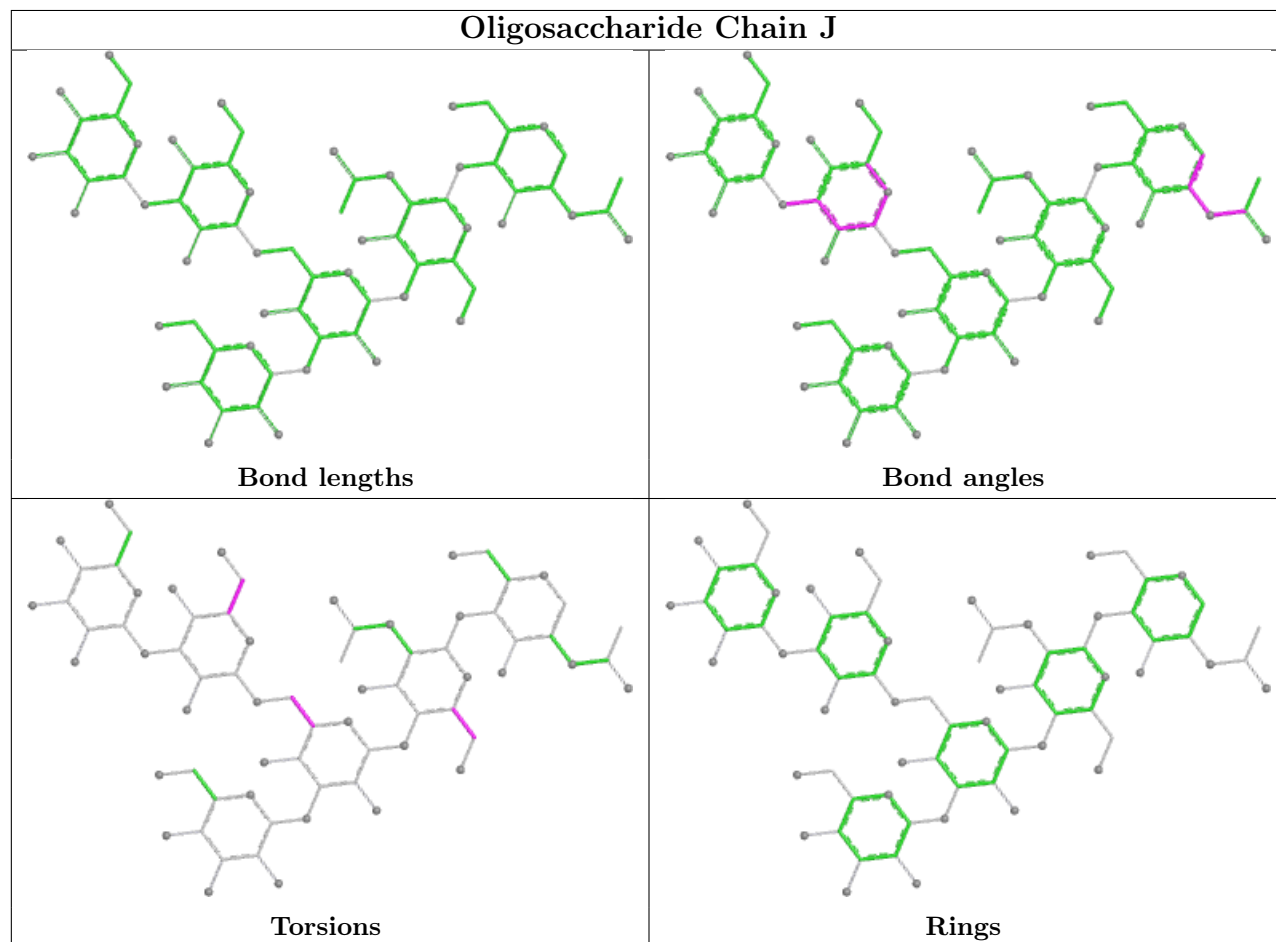
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	O	1	NAG	1	0
15	f	1	NAG	1	0
14	b	2	NAG	3	0
14	b	1	NAG	3	0
8	R	2	NAG	3	0

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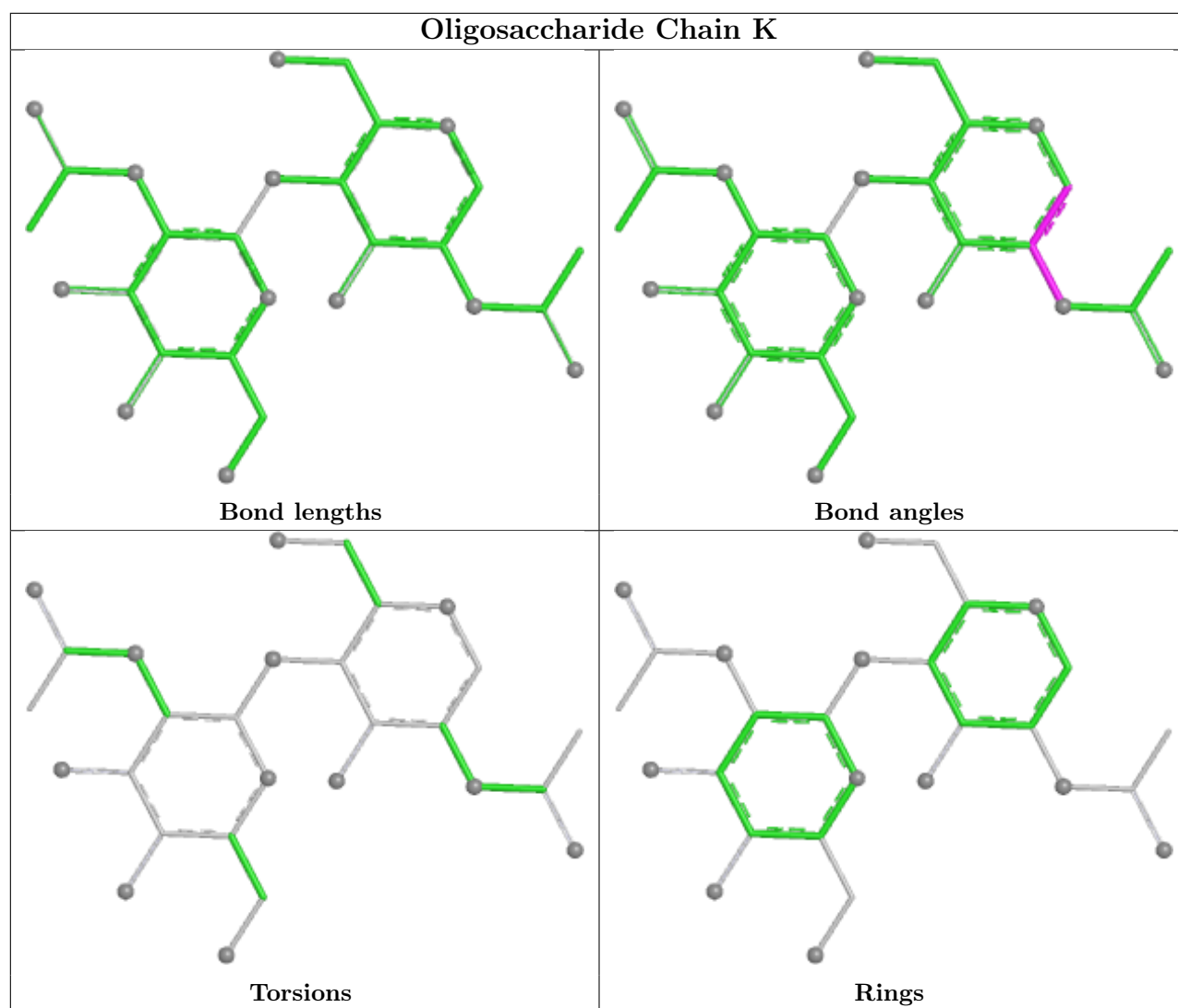
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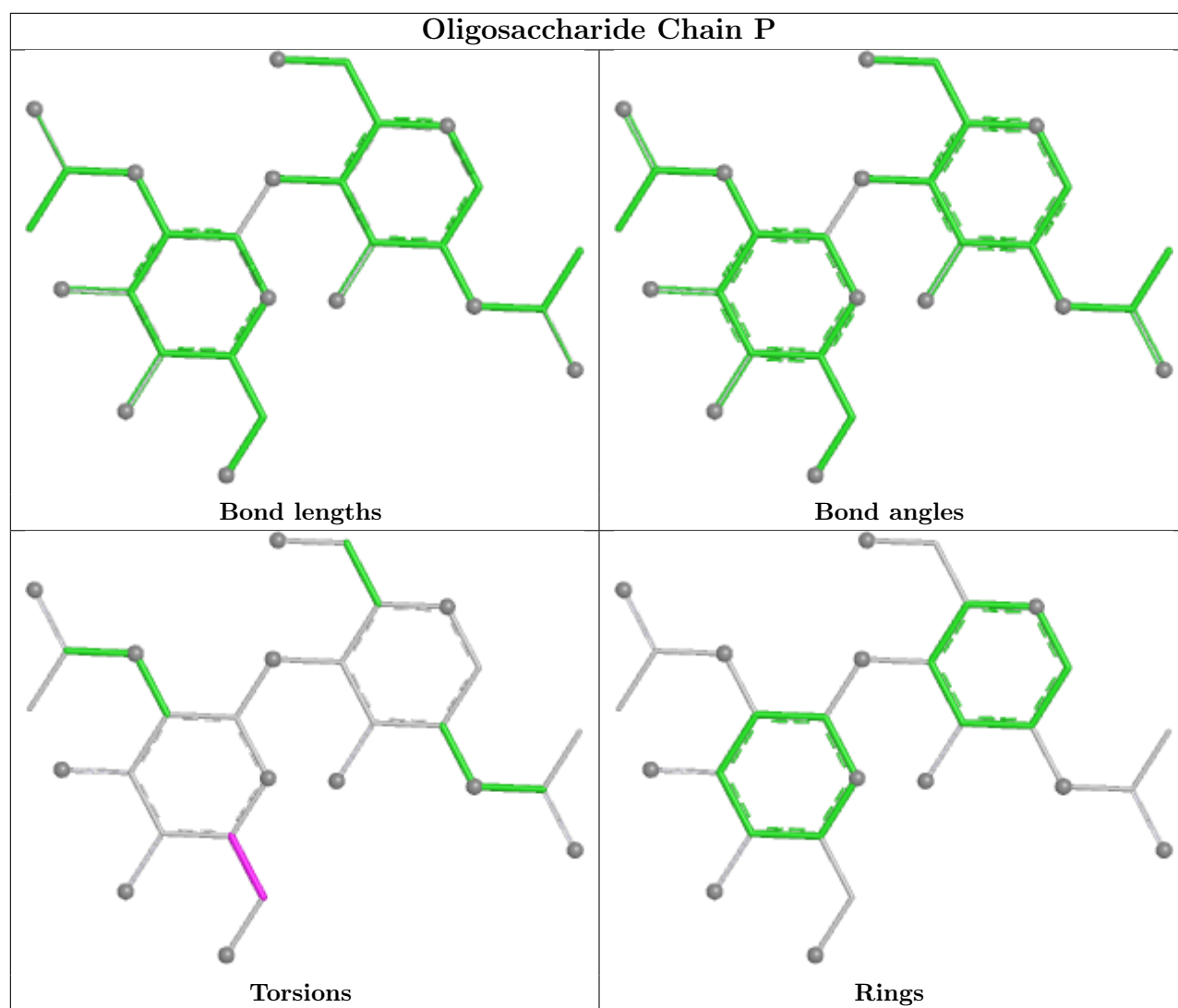
Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	f	2	NAG	4	0

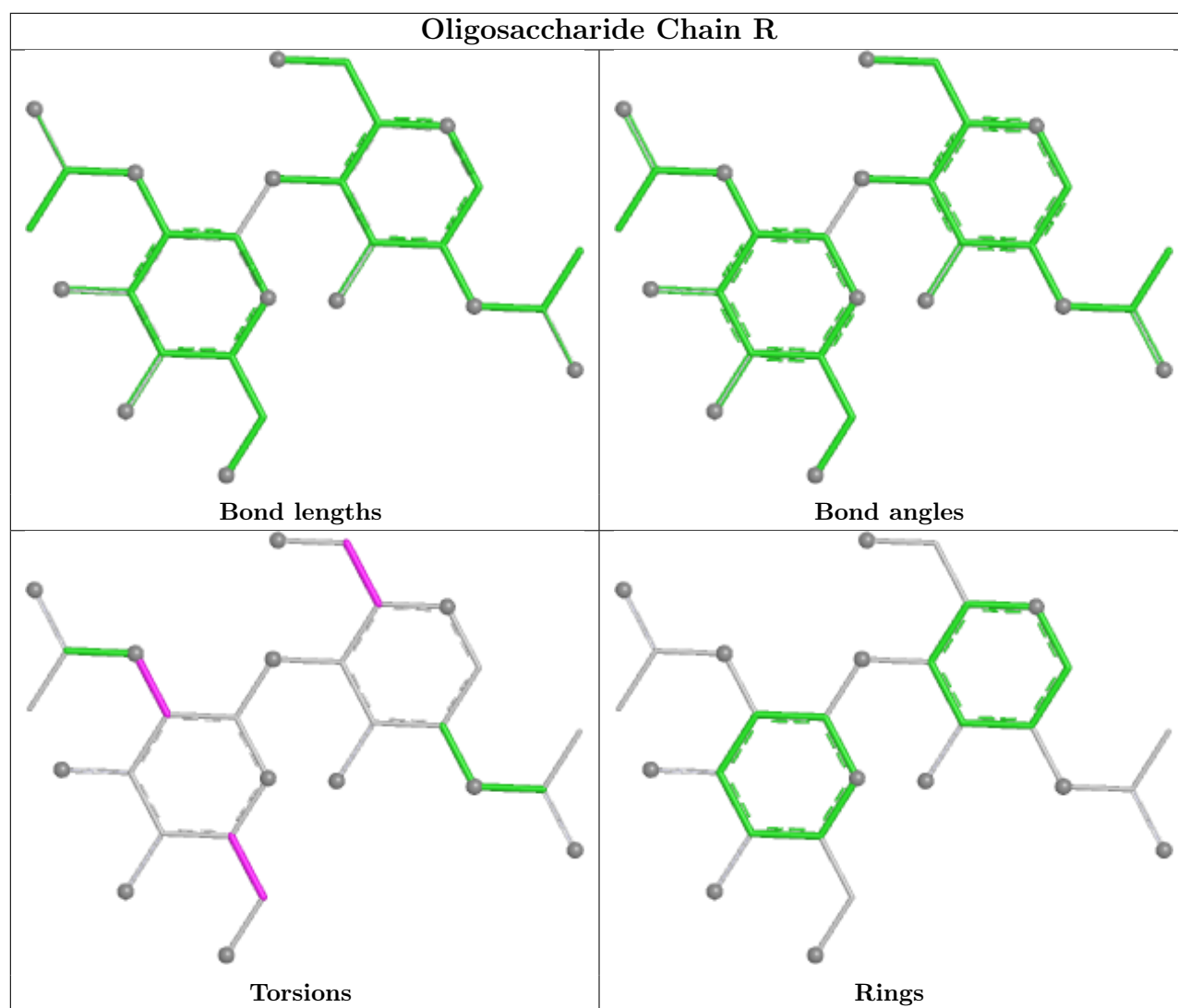
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

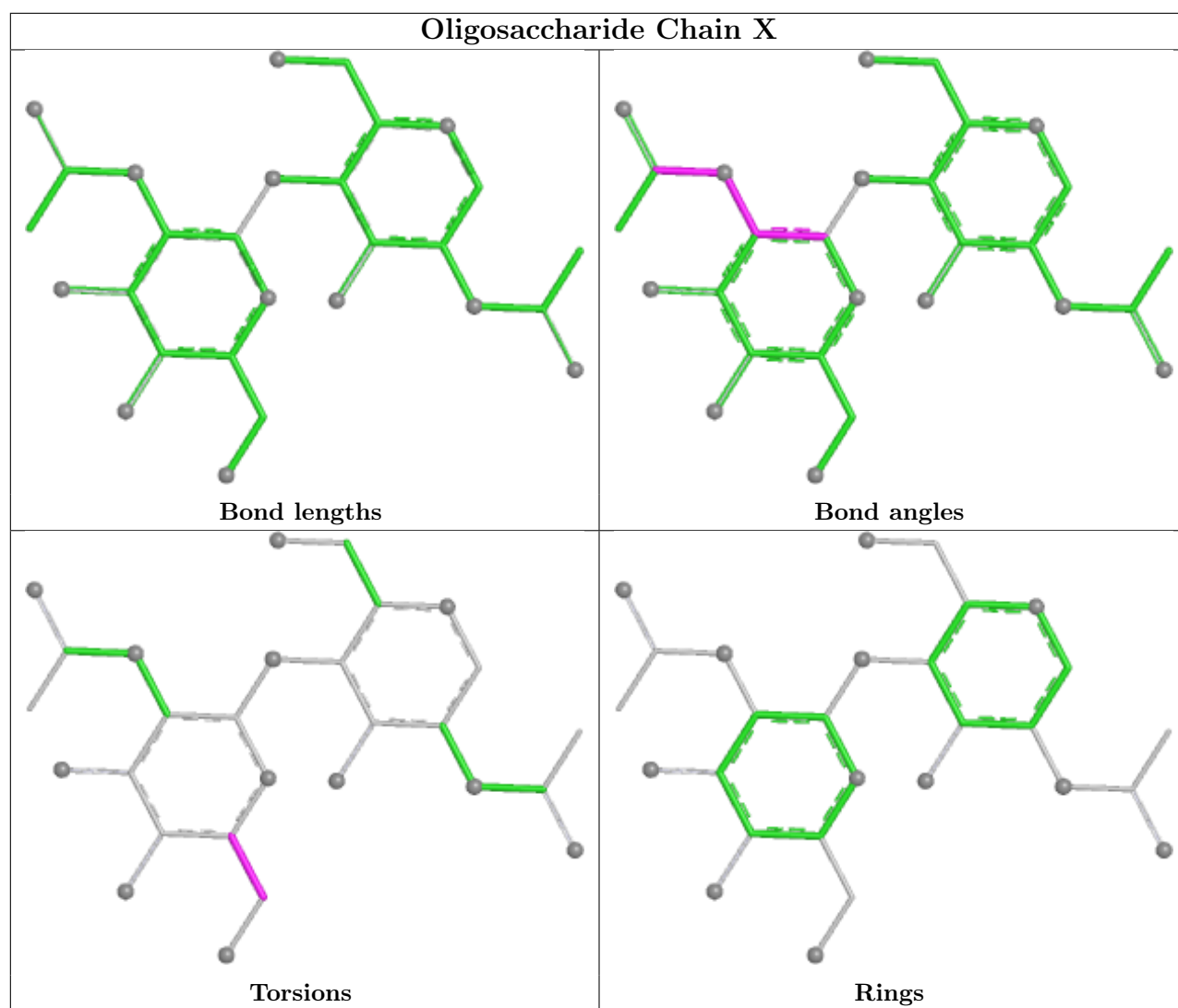


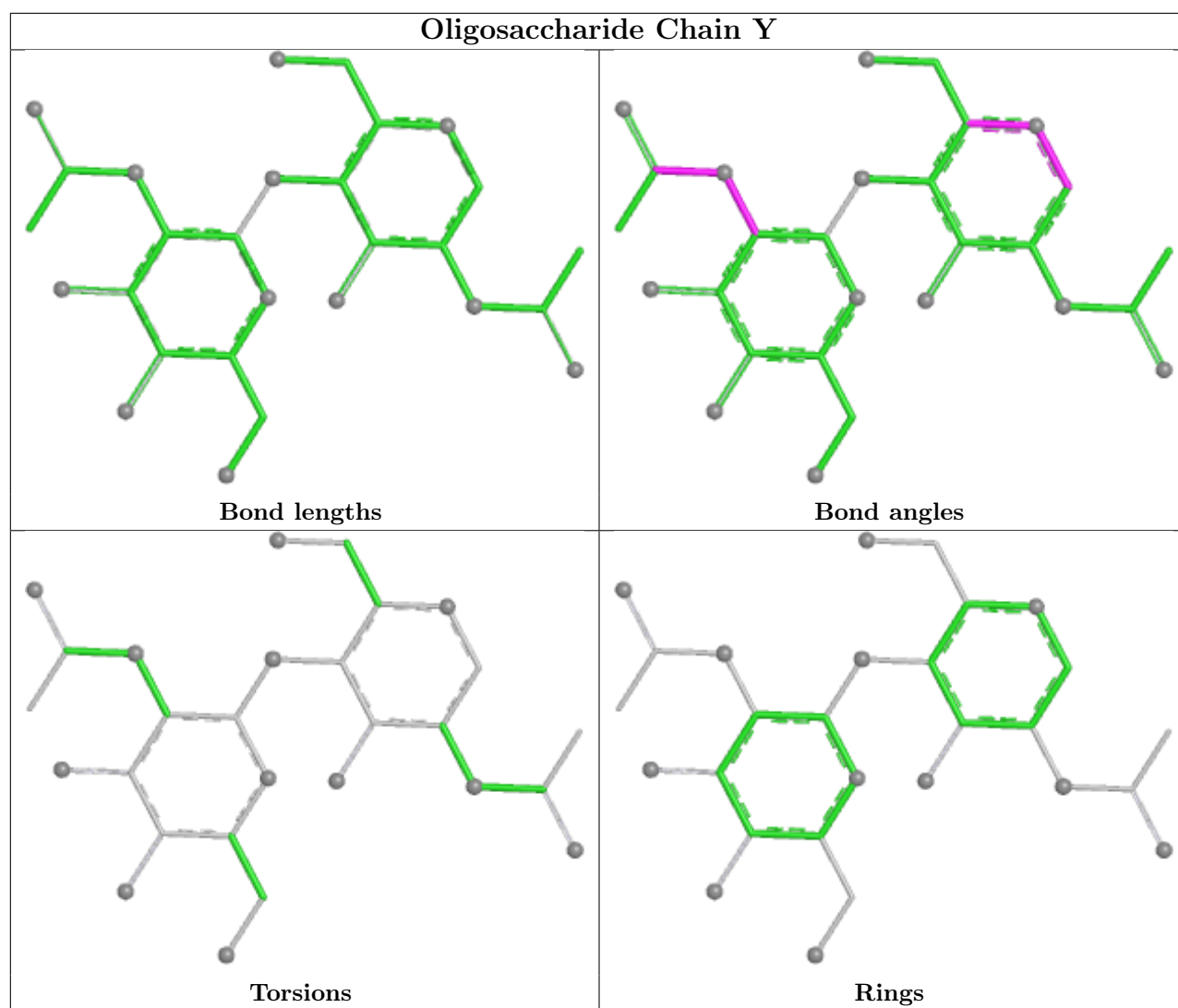


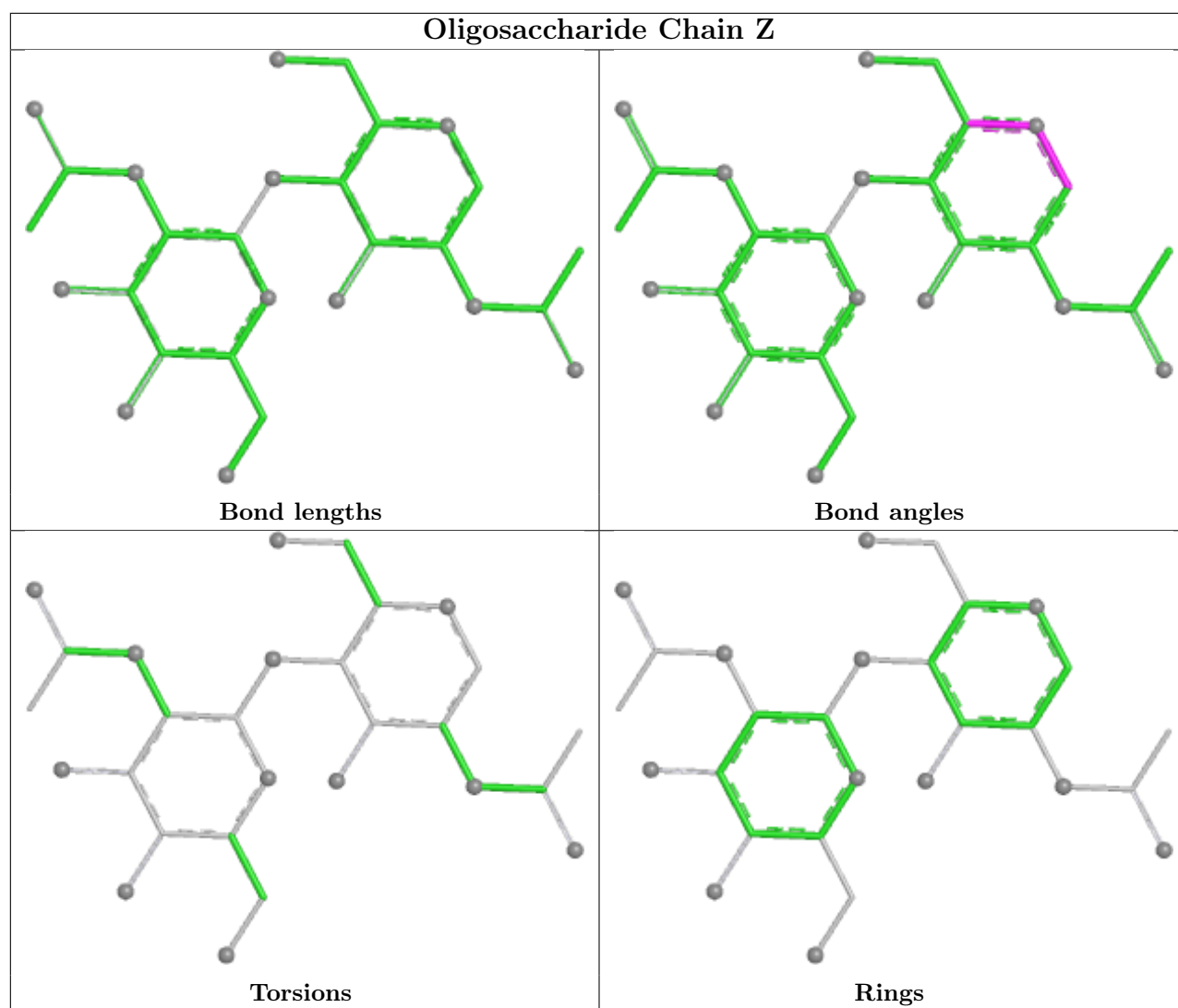


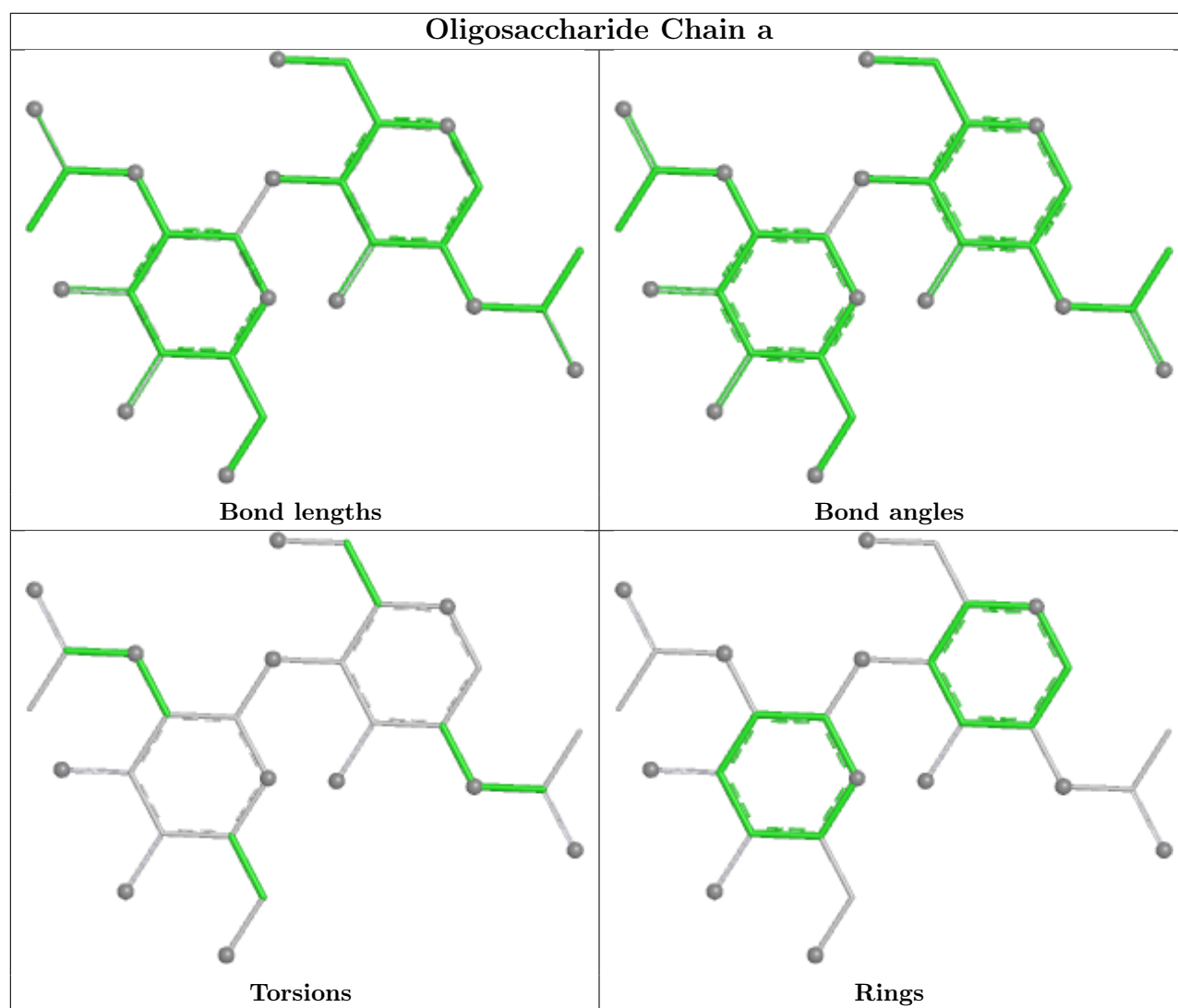


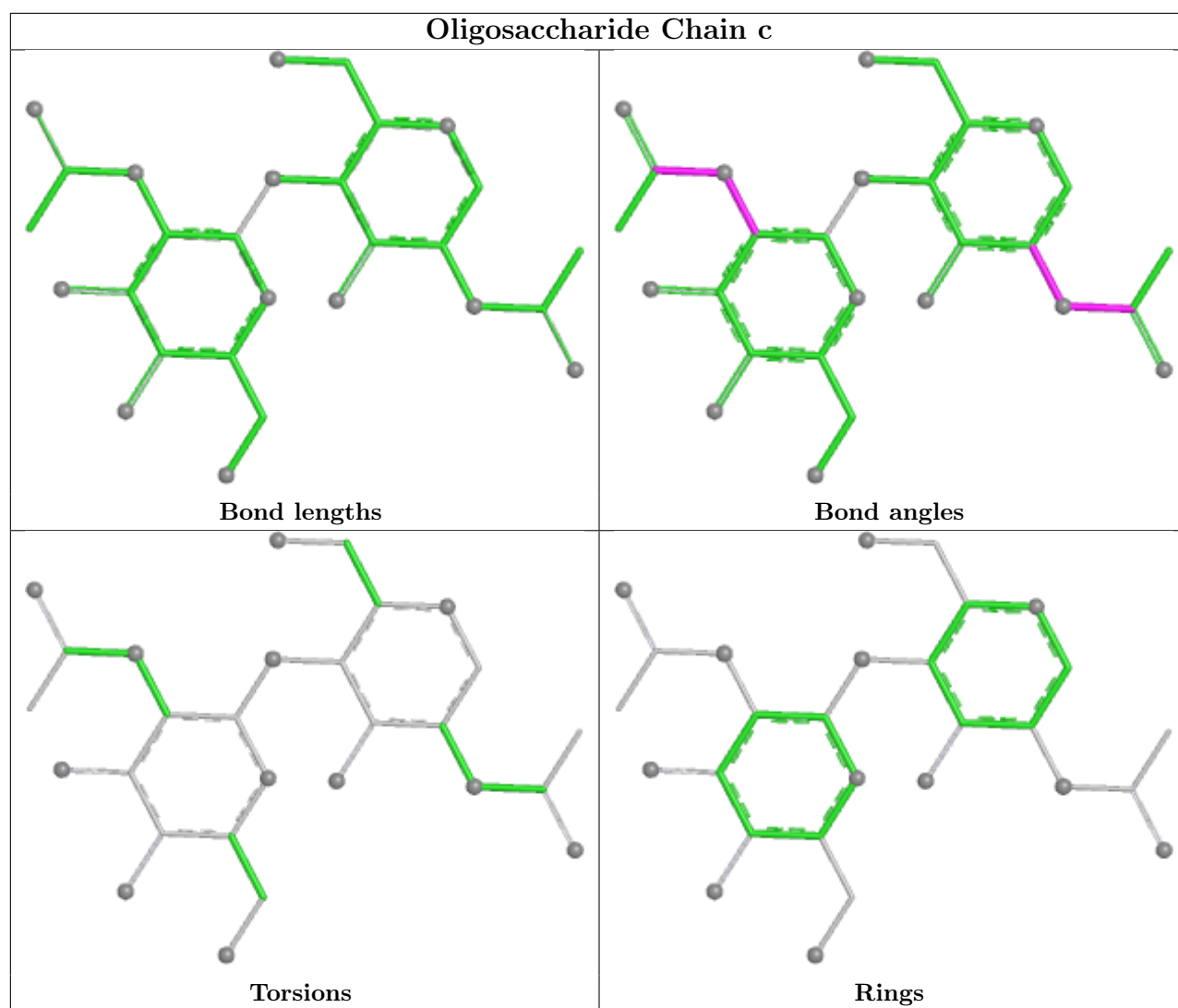




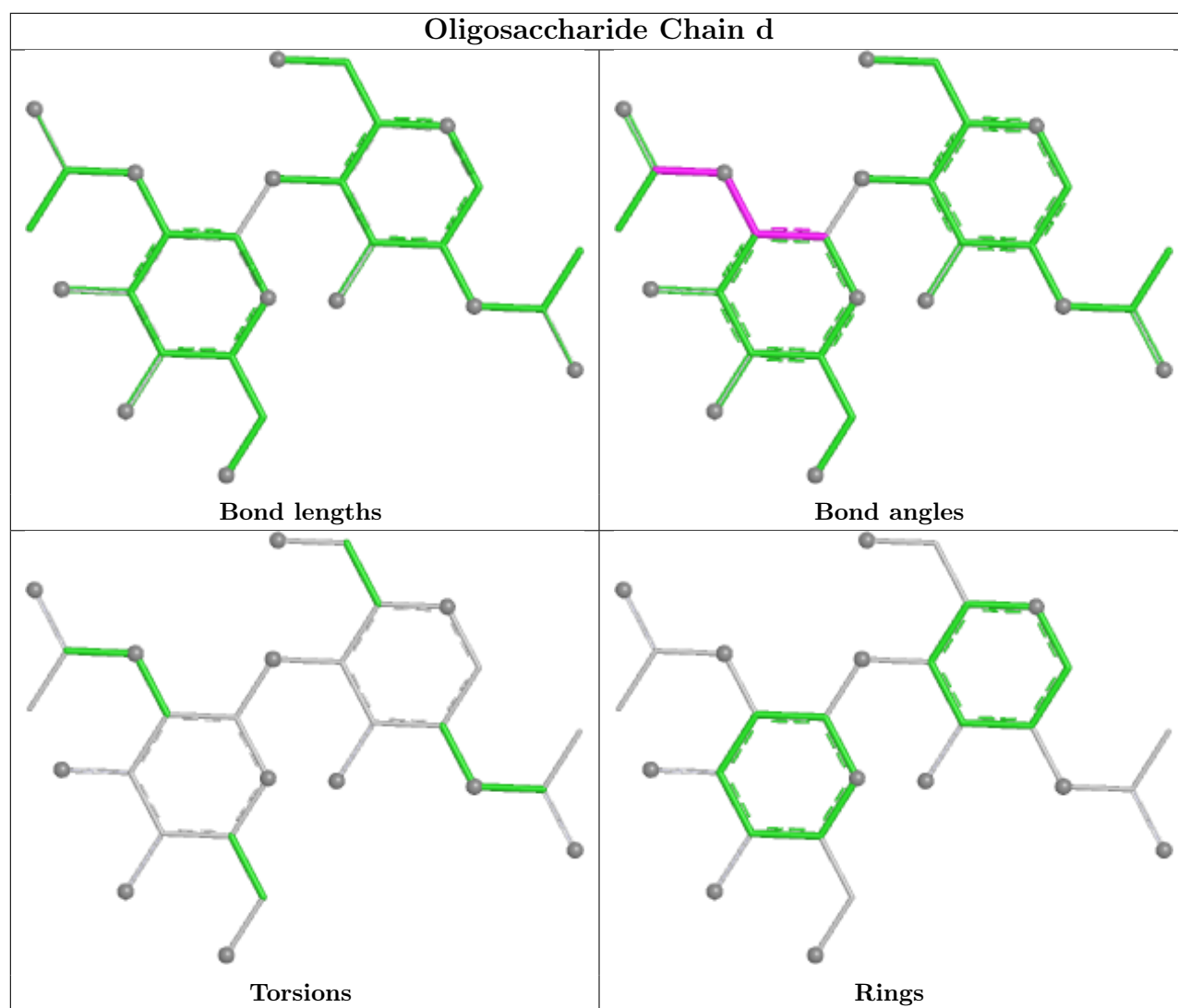


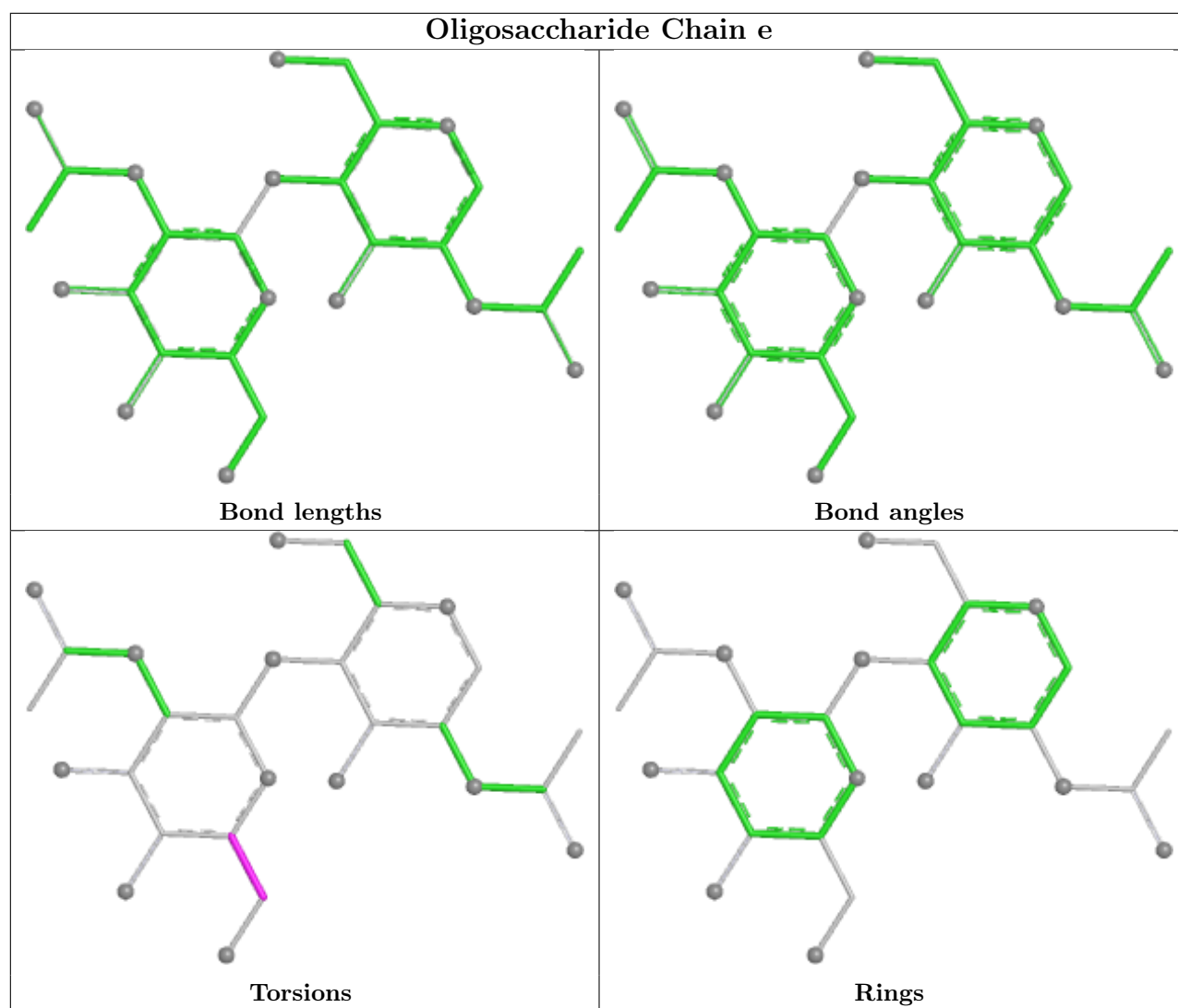


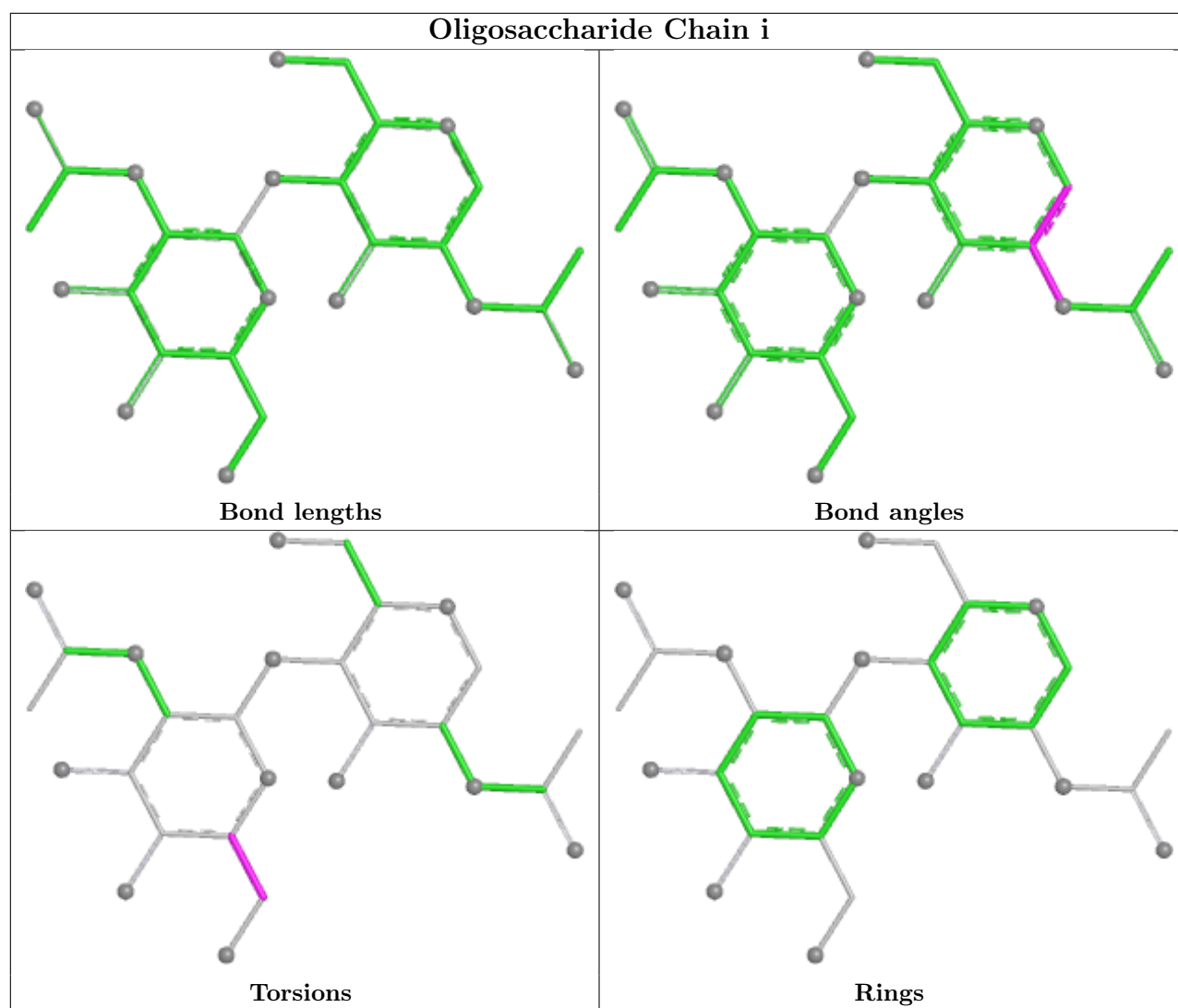


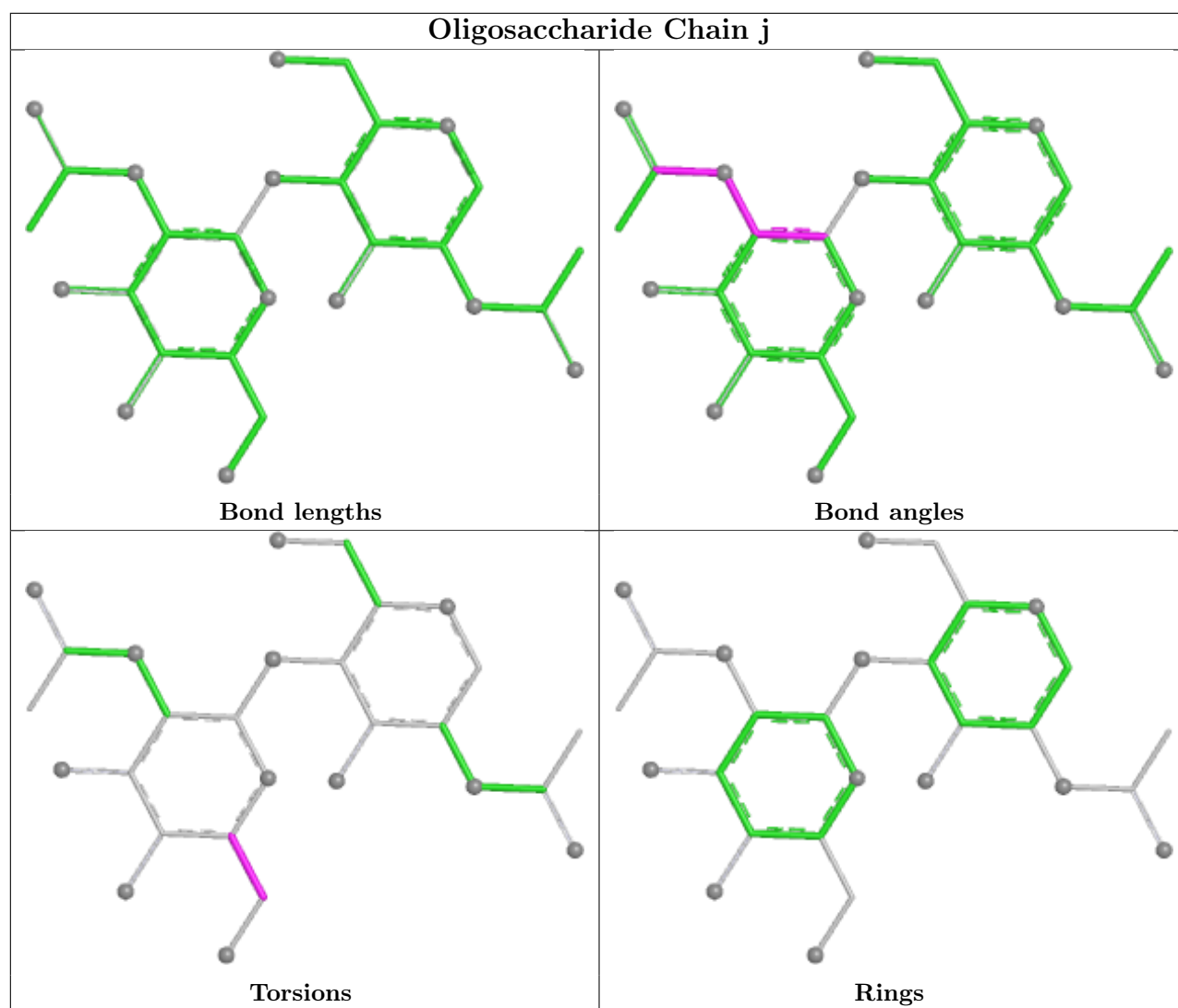


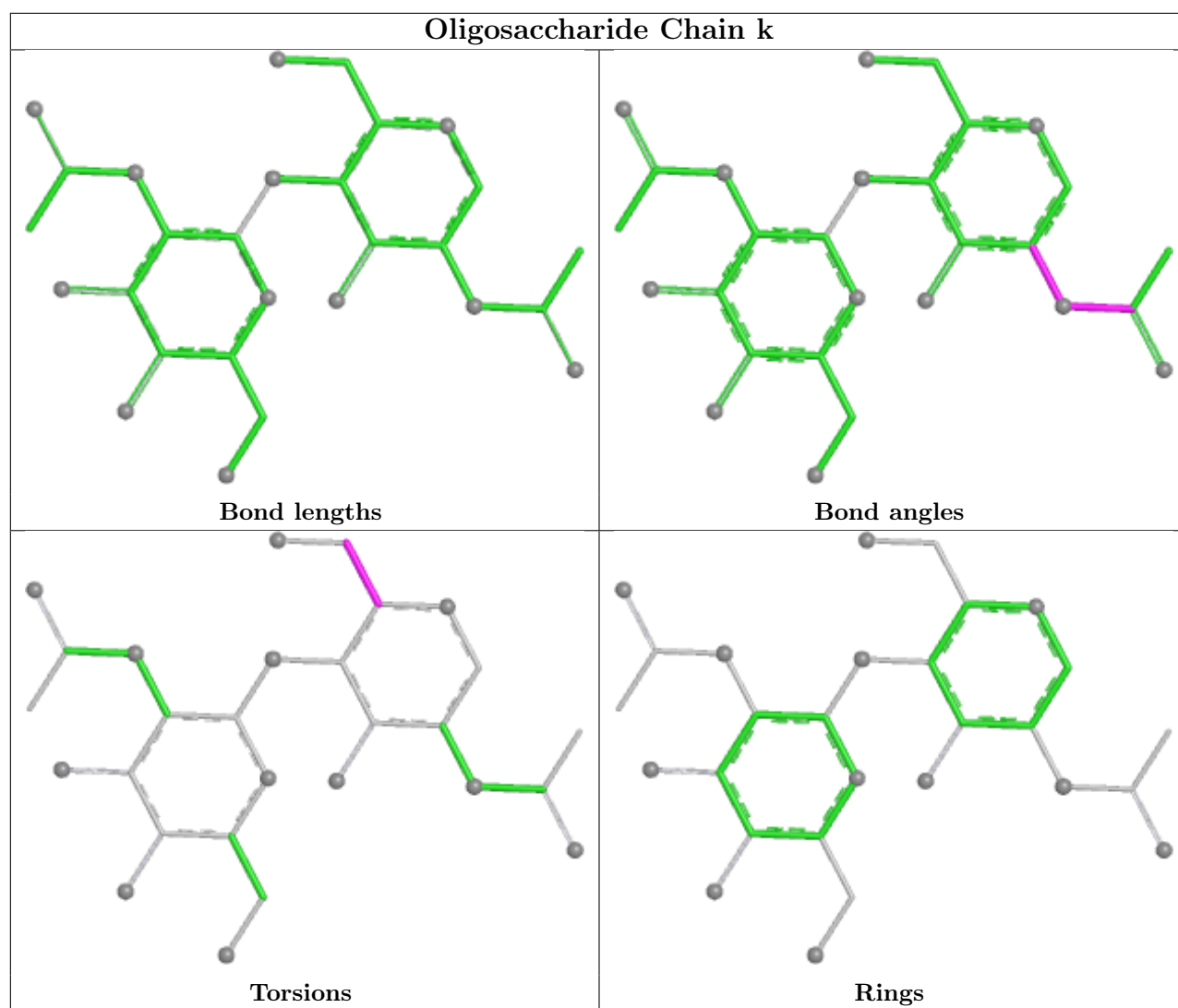


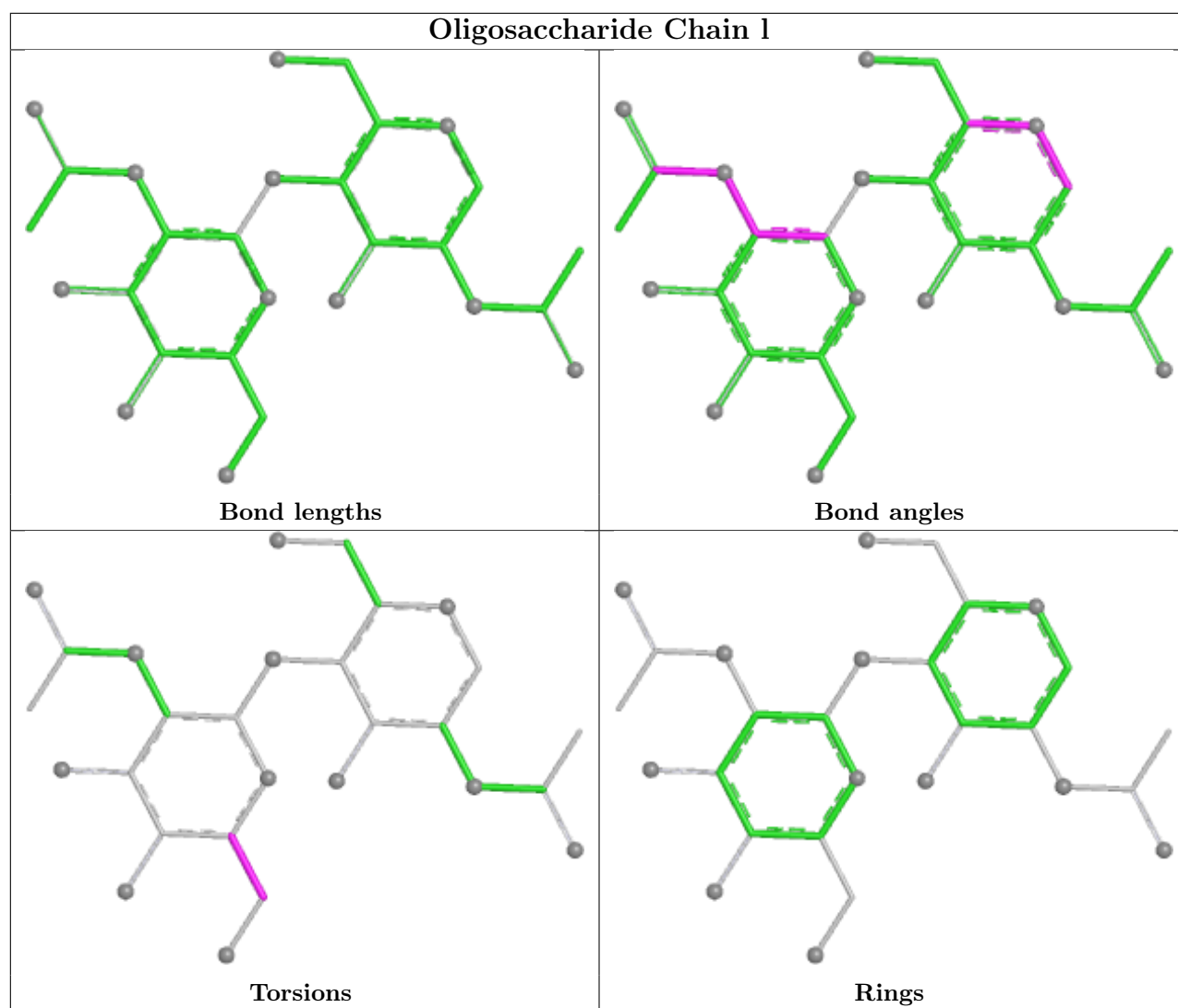


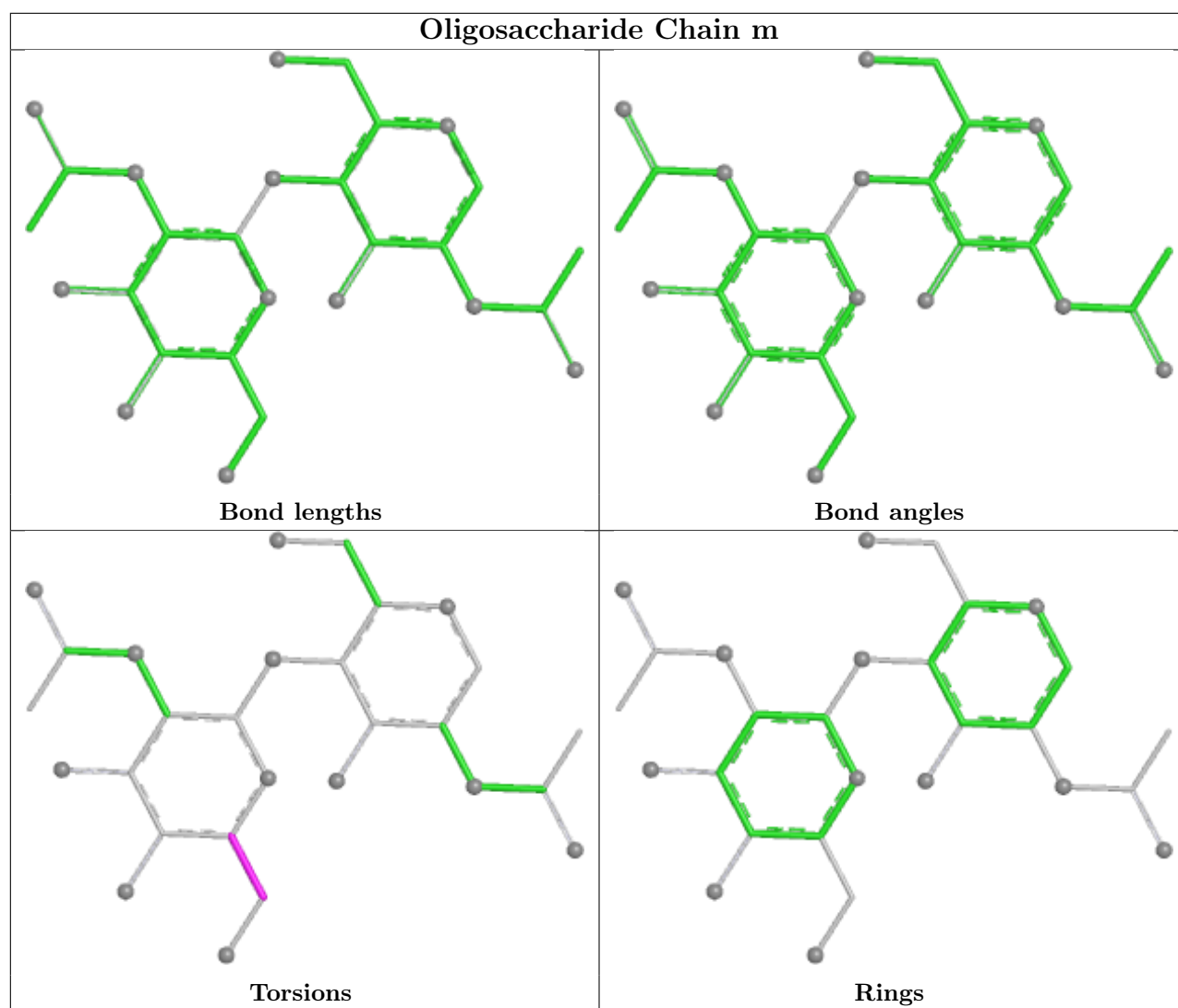


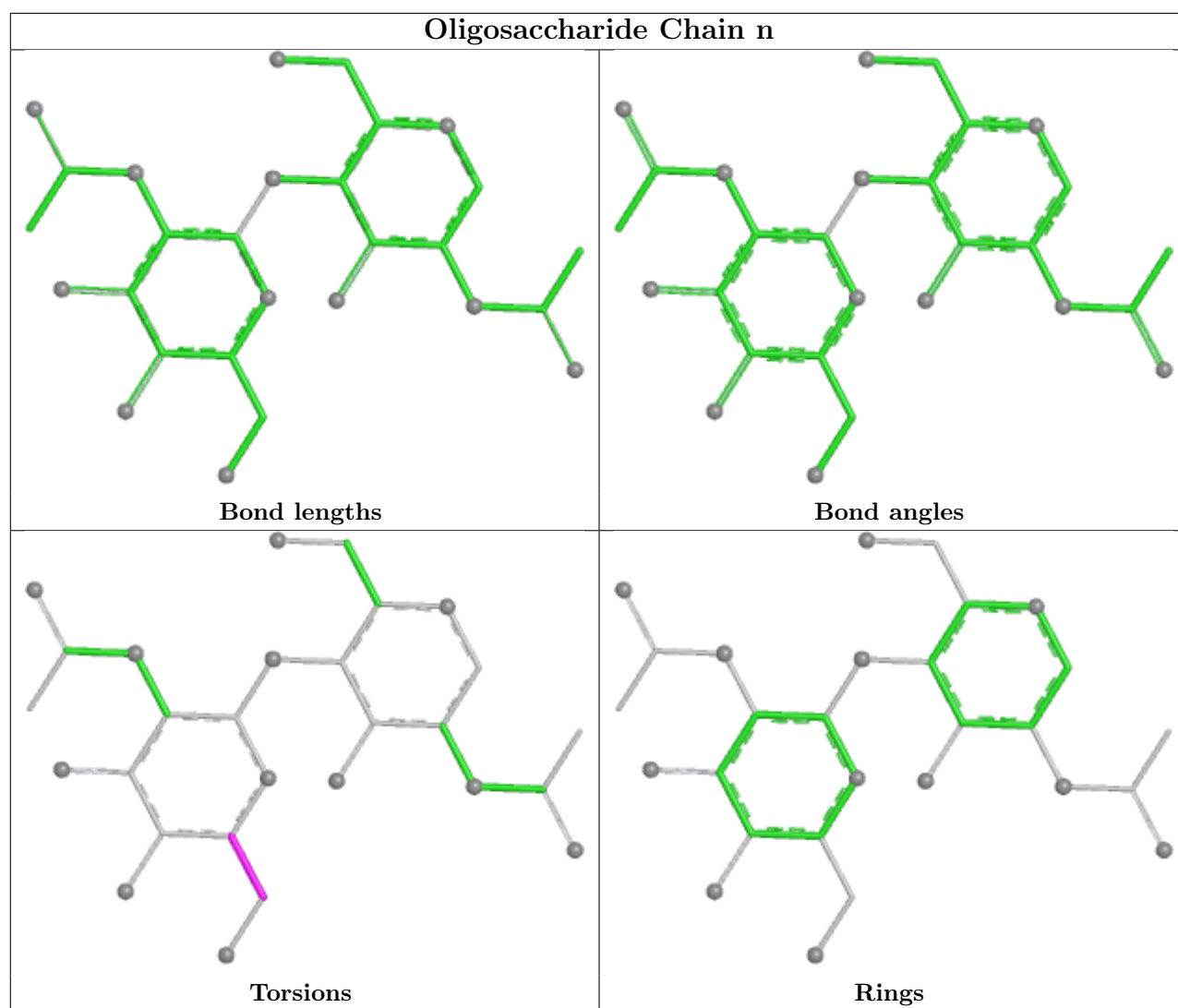




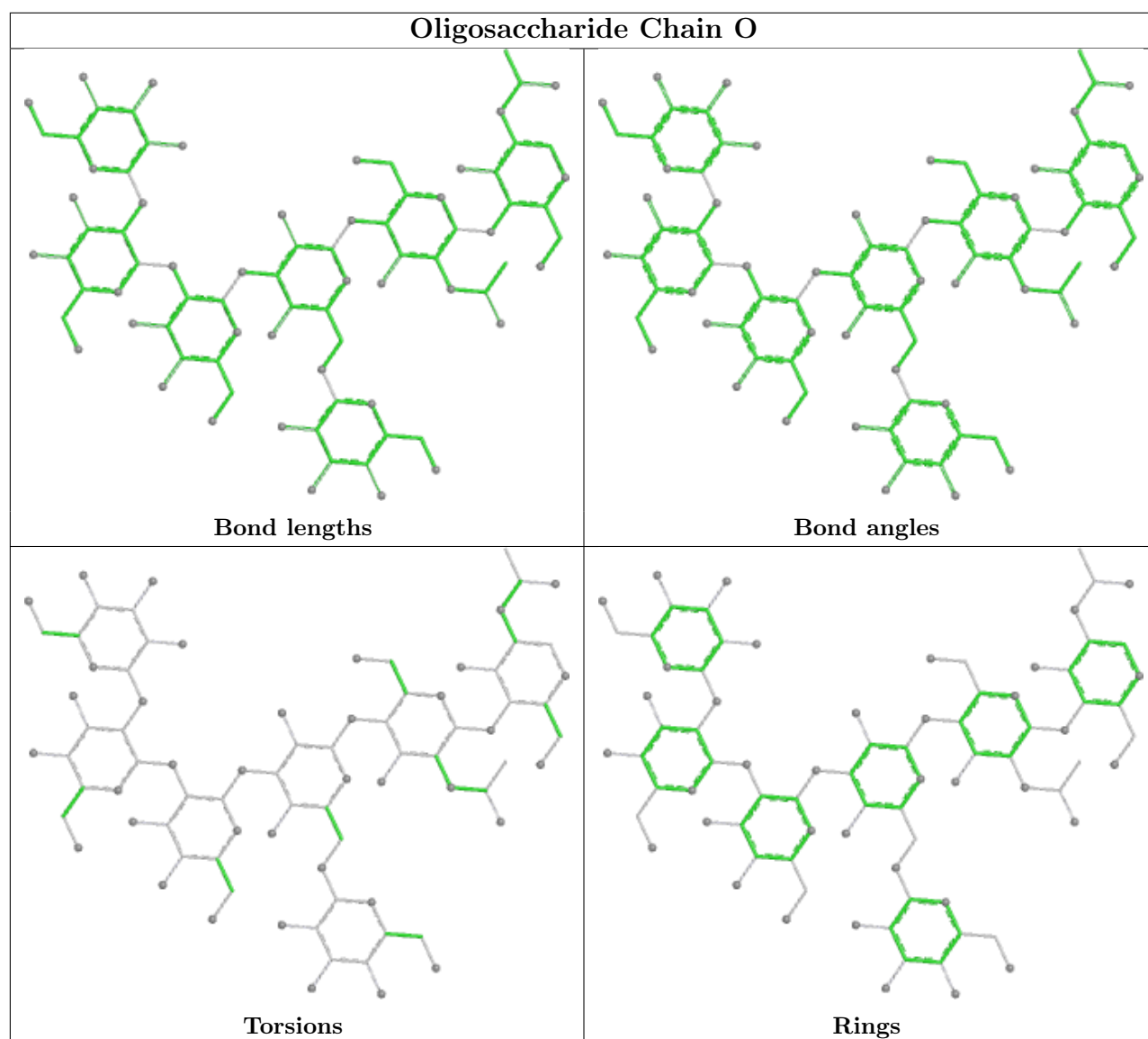


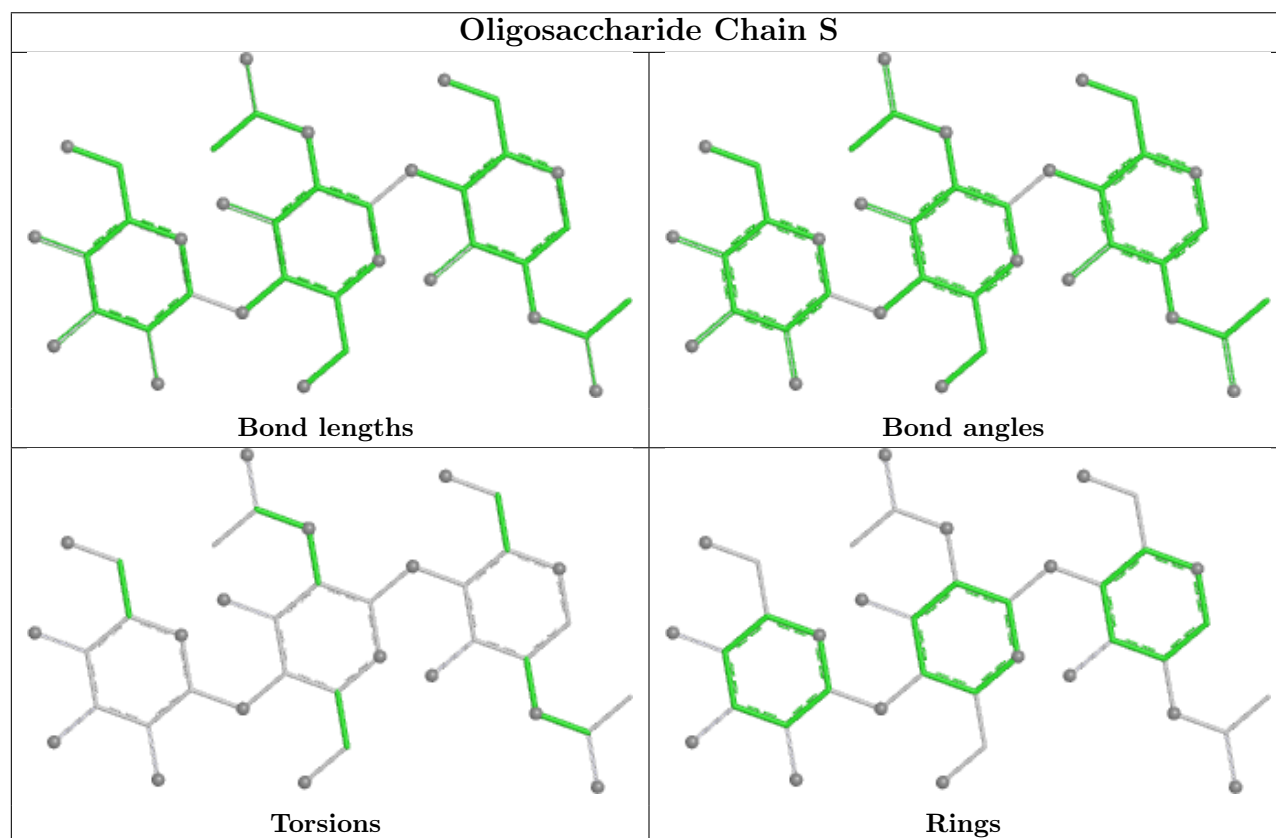
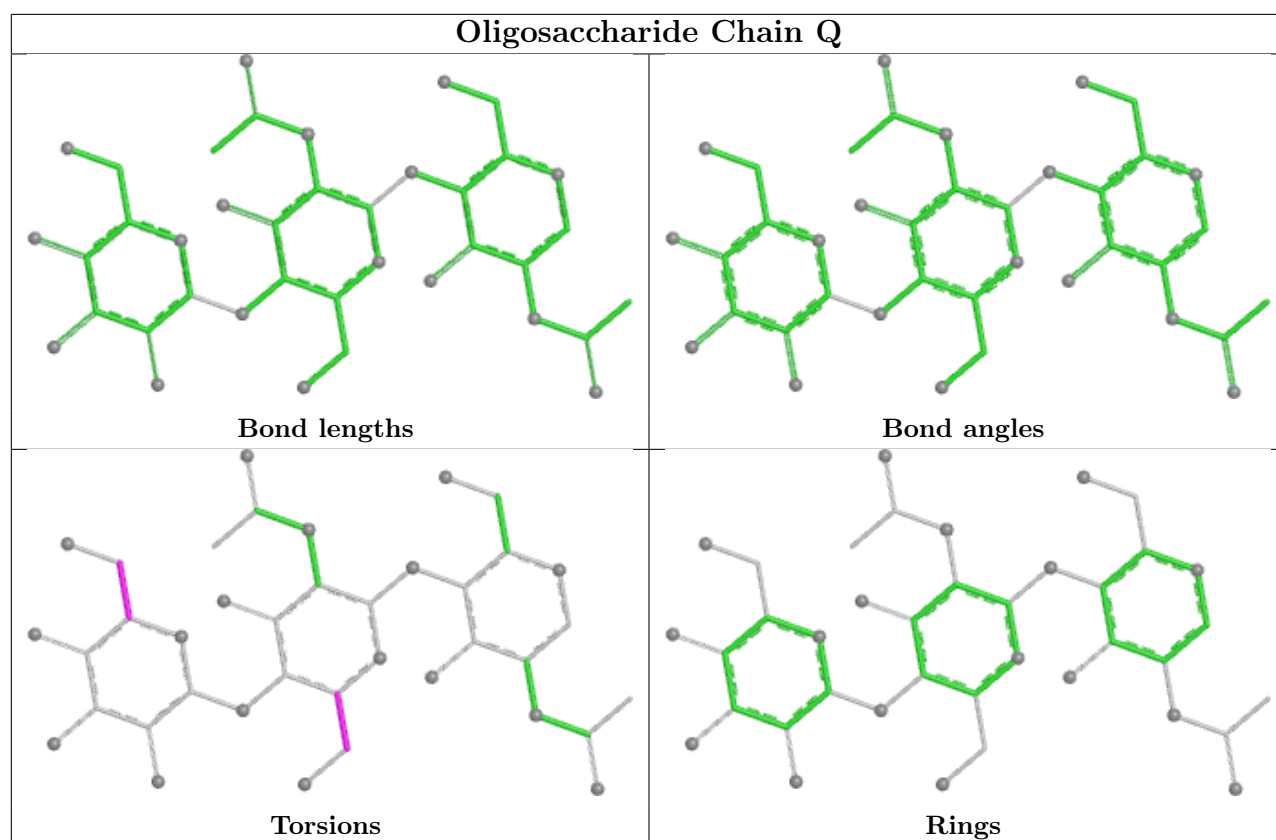


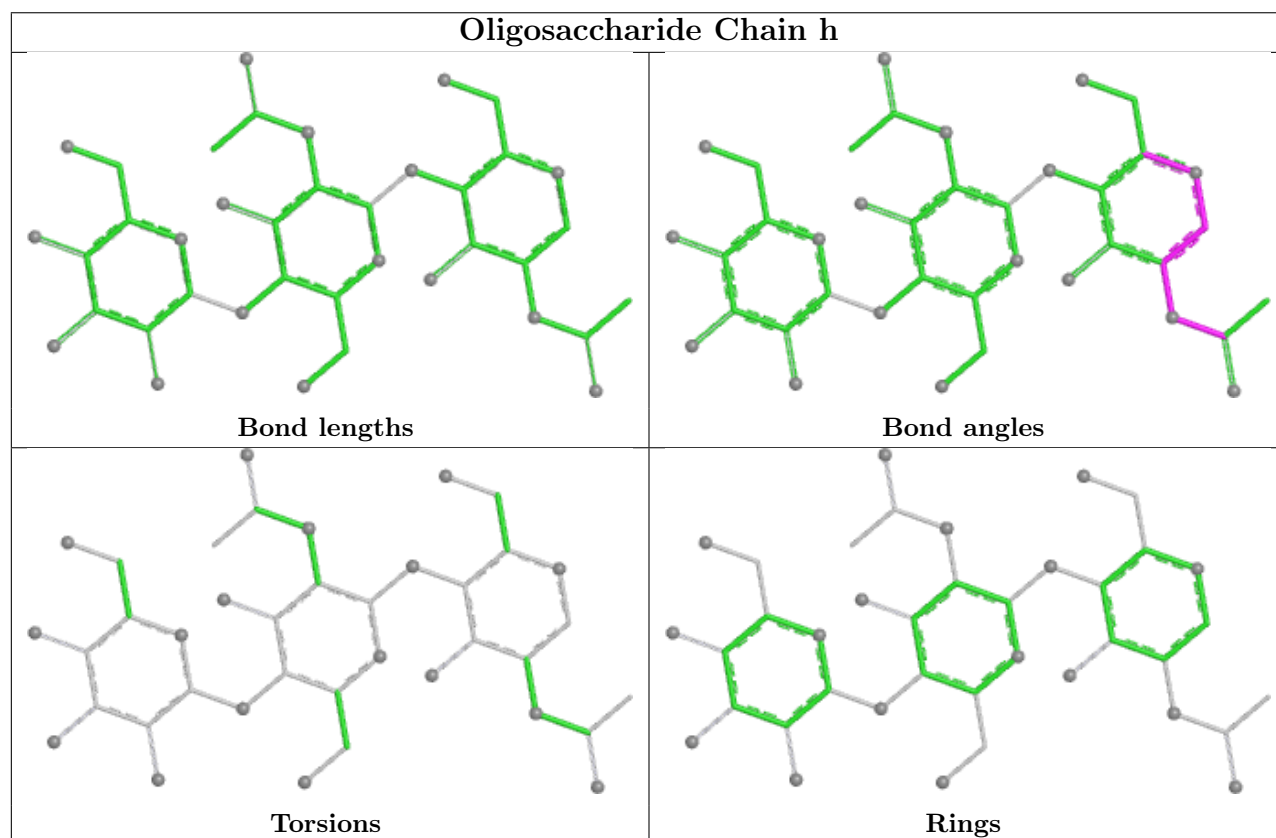
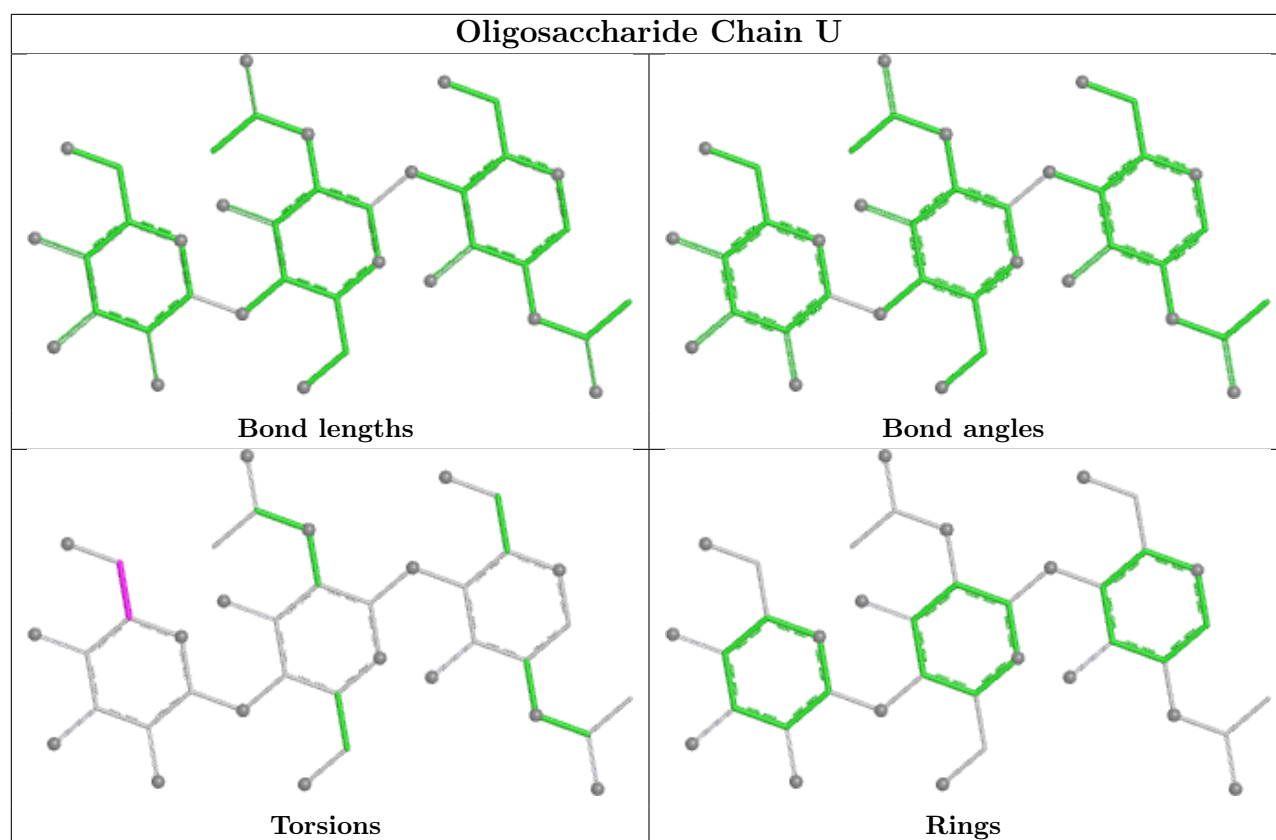


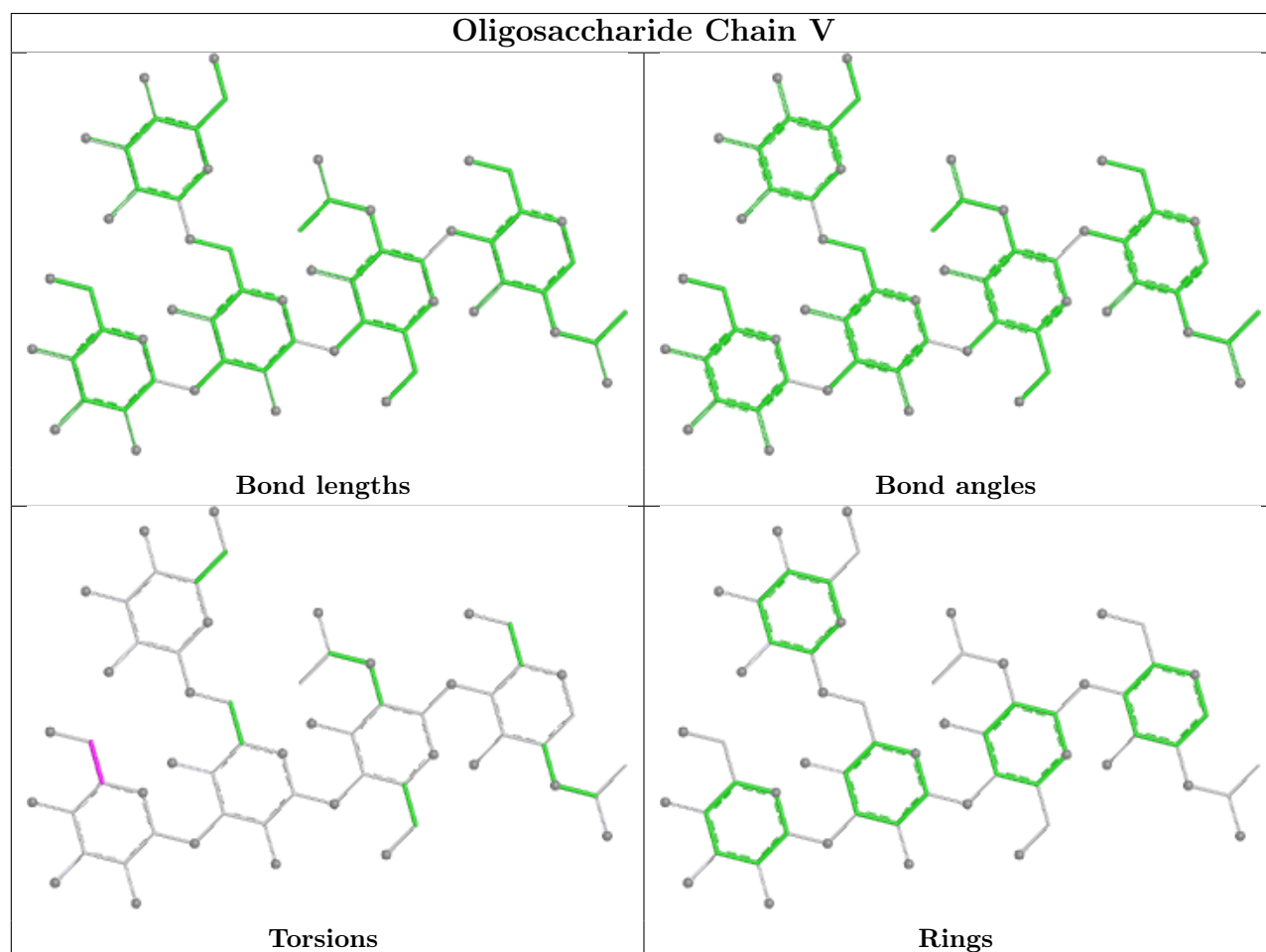
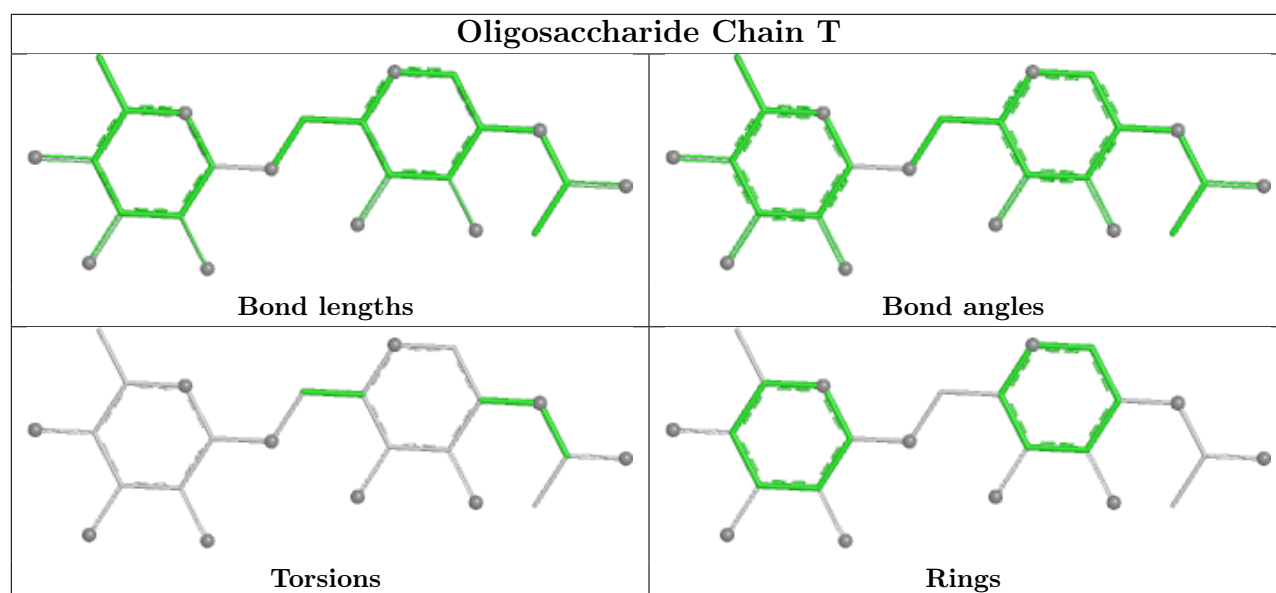


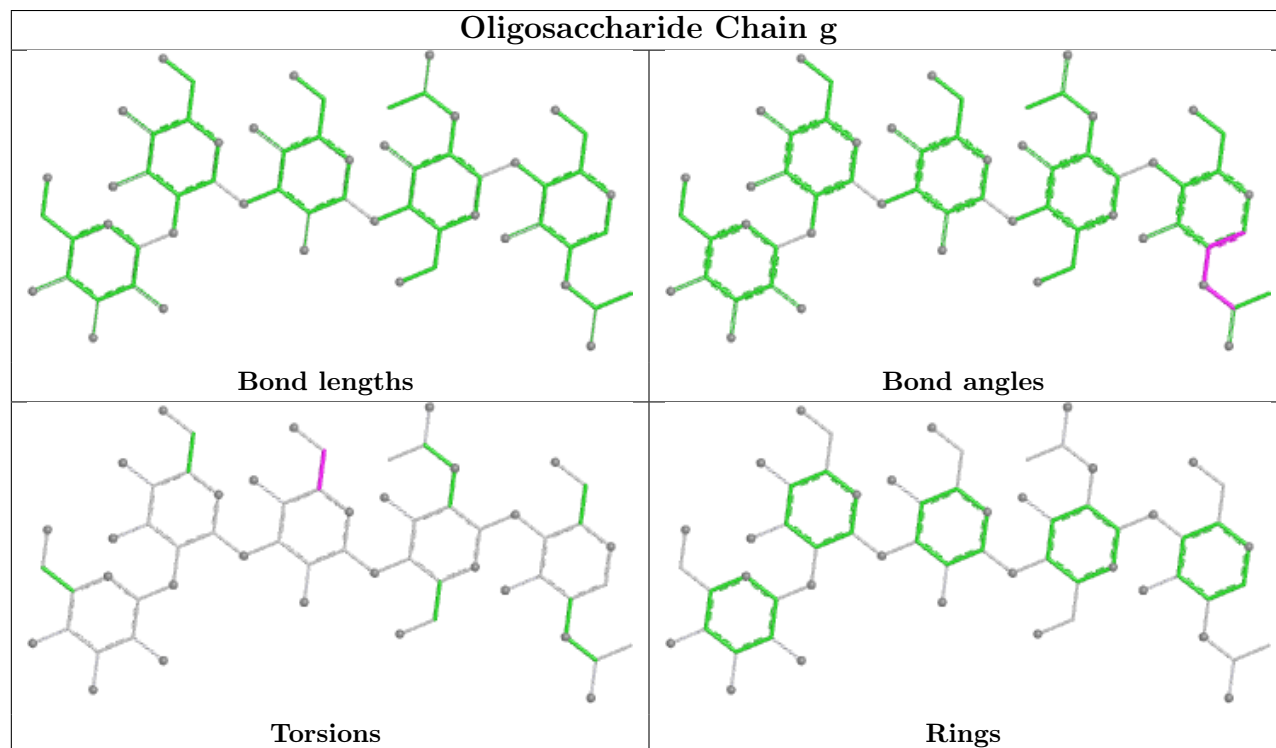
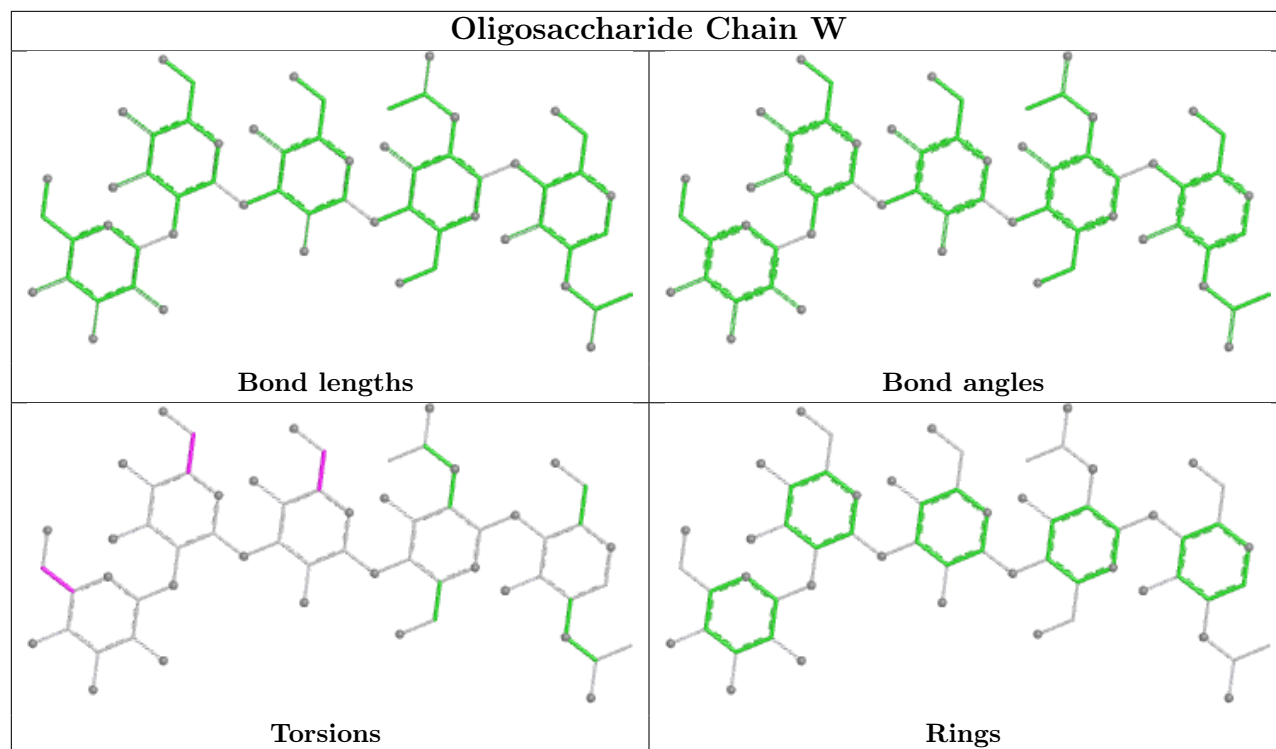


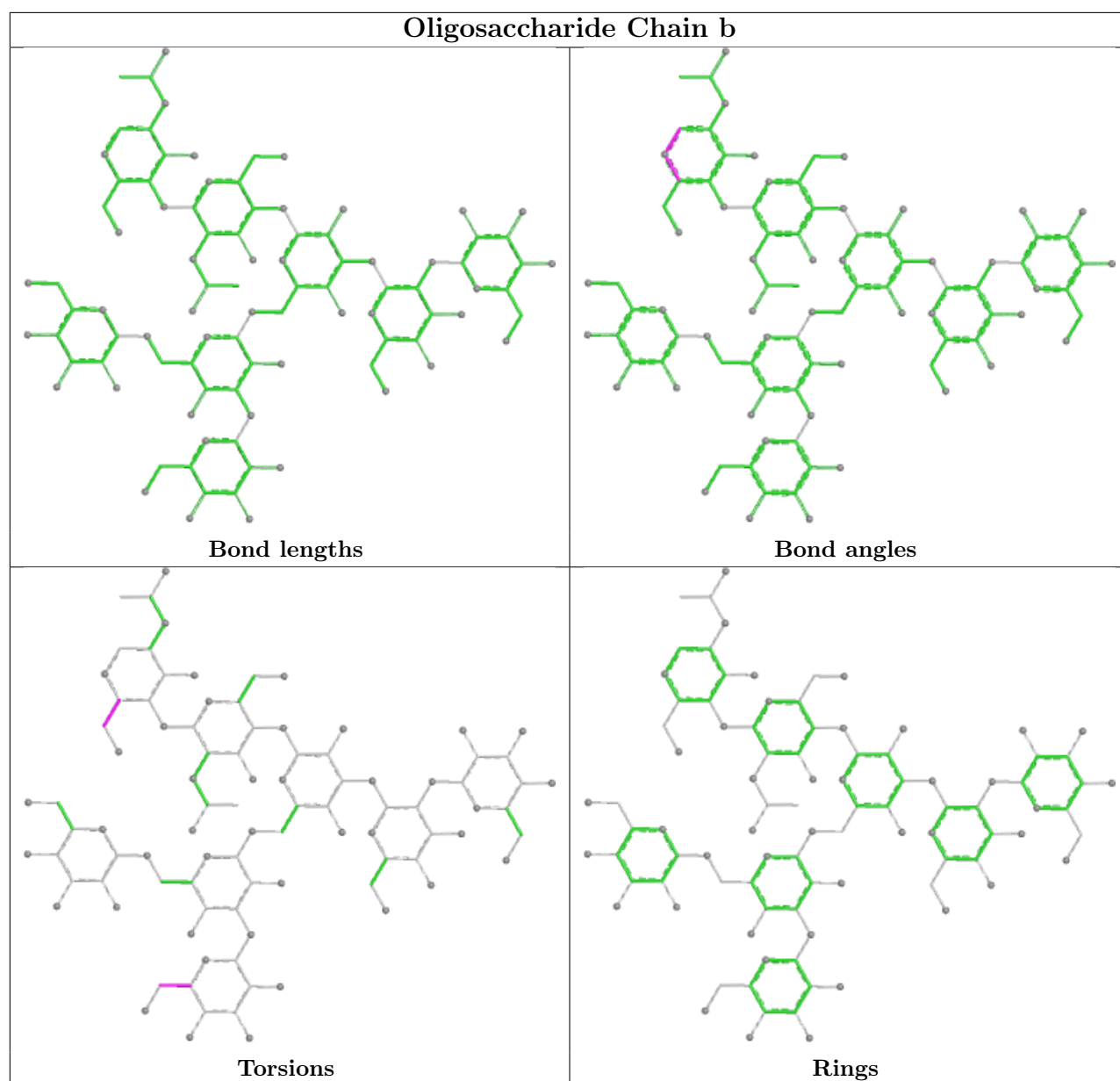


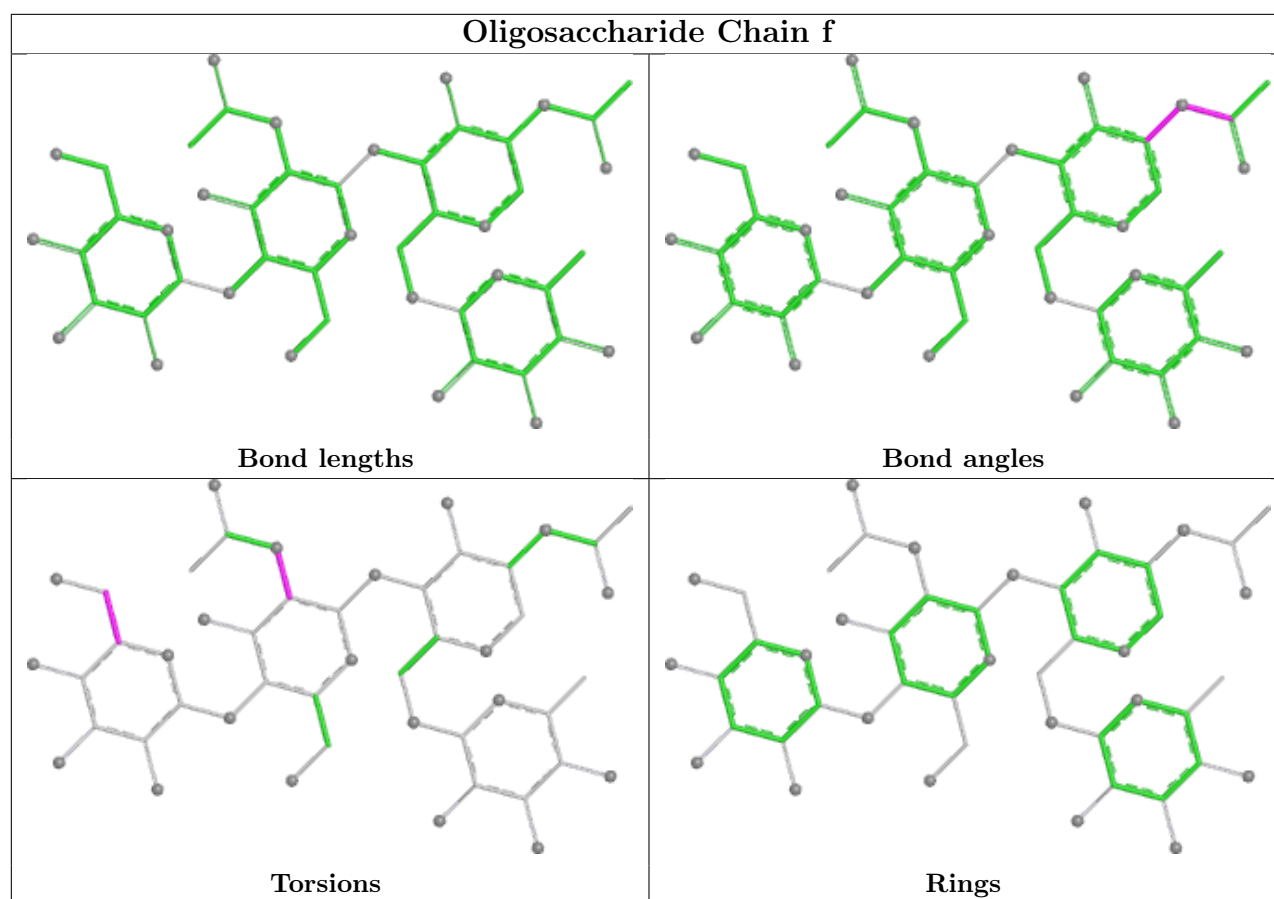












## 5.6 Ligand geometry [i](#)

22 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	$\# Z  > 2$
16	NAG	A	607	1	14,14,15	0.39	0	17,19,21	0.69	1 (5%)
16	NAG	A	604	1	14,14,15	0.39	0	17,19,21	0.64	0
16	NAG	G	605	1	14,14,15	0.39	0	17,19,21	0.63	0
16	NAG	C	603	1	14,14,15	0.40	0	17,19,21	0.95	1 (5%)
16	NAG	A	608	1	14,14,15	0.39	0	17,19,21	0.68	0
16	NAG	C	601	1	14,14,15	0.39	0	17,19,21	0.50	0
16	NAG	A	601	1	14,14,15	0.40	0	17,19,21	0.74	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
16	NAG	B	702	2	14,14,15	0.38	0	17,19,21	0.54	0
16	NAG	D	702	2	14,14,15	0.37	0	17,19,21	0.43	0
16	NAG	G	607	1	14,14,15	0.38	0	17,19,21	0.50	0
16	NAG	A	603	1	14,14,15	0.40	0	17,19,21	0.82	1 (5%)
16	NAG	B	701	2	14,14,15	0.38	0	17,19,21	0.65	0
16	NAG	C	602	1	14,14,15	0.39	0	17,19,21	0.78	1 (5%)
16	NAG	A	605	1	14,14,15	0.37	0	17,19,21	0.48	0
16	NAG	G	604	1	14,14,15	0.37	0	17,19,21	0.58	0
16	NAG	G	606	1	14,14,15	0.38	0	17,19,21	0.60	0
16	NAG	G	603	1	14,14,15	0.38	0	17,19,21	0.70	0
16	NAG	D	701	2	14,14,15	0.36	0	17,19,21	0.49	0
16	NAG	A	606	1	14,14,15	0.38	0	17,19,21	0.47	0
16	NAG	A	602	1	14,14,15	0.38	0	17,19,21	0.50	0
16	NAG	G	602	1	14,14,15	0.39	0	17,19,21	0.51	0
16	NAG	G	601	1	14,14,15	0.38	0	17,19,21	1.88	2 (11%)

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
16	NAG	A	607	1	-	0/6/23/26	0/1/1/1
16	NAG	A	604	1	-	0/6/23/26	0/1/1/1
16	NAG	G	605	1	-	1/6/23/26	0/1/1/1
16	NAG	C	603	1	-	0/6/23/26	0/1/1/1
16	NAG	A	608	1	-	1/6/23/26	0/1/1/1
16	NAG	C	601	1	-	0/6/23/26	0/1/1/1
16	NAG	A	601	1	-	1/6/23/26	0/1/1/1
16	NAG	B	702	2	-	0/6/23/26	0/1/1/1
16	NAG	D	702	2	-	0/6/23/26	0/1/1/1
16	NAG	G	607	1	-	0/6/23/26	0/1/1/1
16	NAG	A	603	1	-	1/6/23/26	0/1/1/1
16	NAG	B	701	2	-	0/6/23/26	0/1/1/1
16	NAG	C	602	1	-	0/6/23/26	0/1/1/1
16	NAG	A	605	1	-	0/6/23/26	0/1/1/1
16	NAG	G	604	1	-	1/6/23/26	0/1/1/1
16	NAG	G	606	1	-	0/6/23/26	0/1/1/1
16	NAG	G	603	1	-	0/6/23/26	0/1/1/1
16	NAG	D	701	2	-	1/6/23/26	0/1/1/1
16	NAG	A	606	1	-	0/6/23/26	0/1/1/1
16	NAG	A	602	1	-	1/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
16	NAG	G	602	1	-	1/6/23/26	0/1/1/1
16	NAG	G	601	1	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	G	601	NAG	C2-N2-C7	7.02	132.31	122.90
16	C	603	NAG	C1-C2-N2	2.80	114.85	110.43
16	A	607	NAG	C1-O5-C5	2.38	115.38	112.19
16	C	602	NAG	C2-N2-C7	2.35	126.05	122.90
16	A	603	NAG	C1-C2-N2	2.34	114.12	110.43

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
16	A	603	NAG	O5-C5-C6-O6
16	A	608	NAG	O5-C5-C6-O6
16	G	601	NAG	O5-C5-C6-O6
16	A	602	NAG	O5-C5-C6-O6
16	G	604	NAG	O5-C5-C6-O6

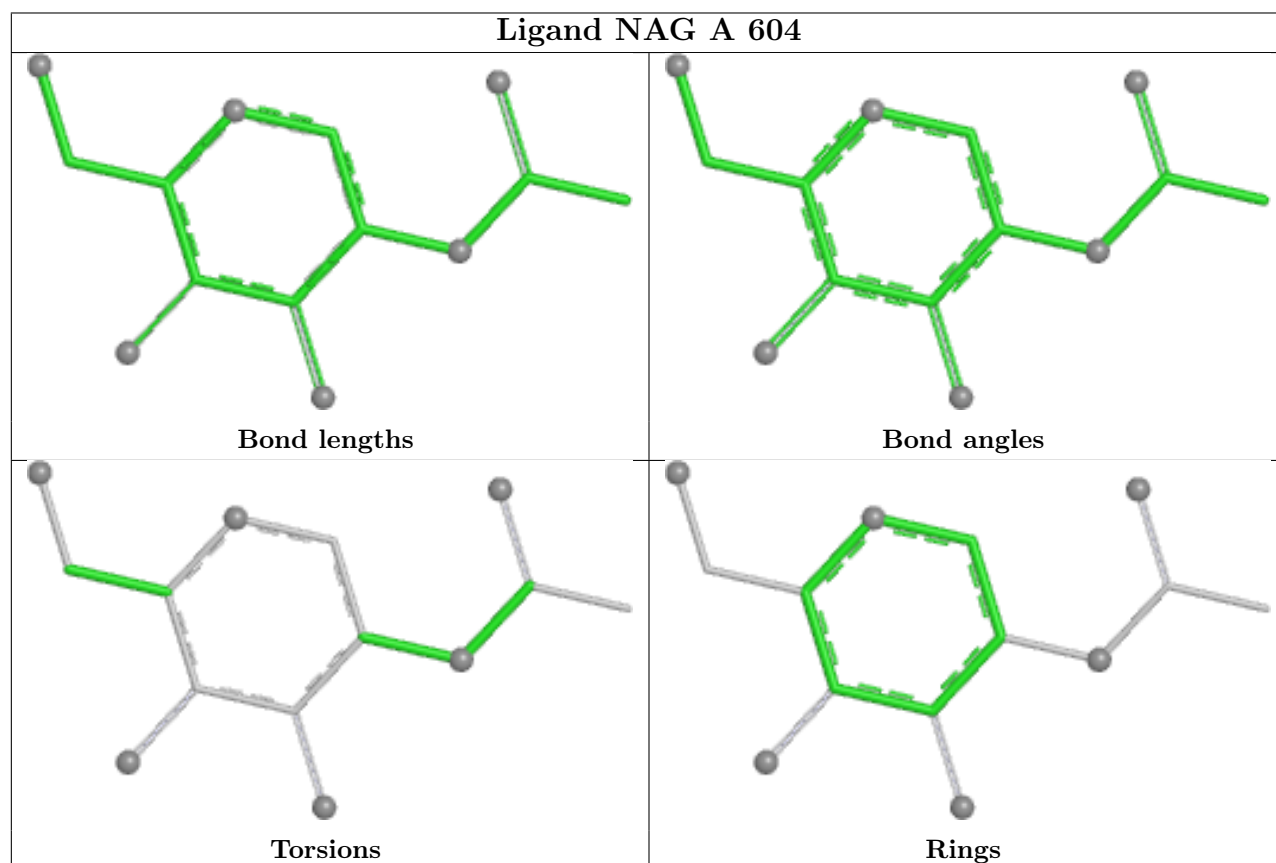
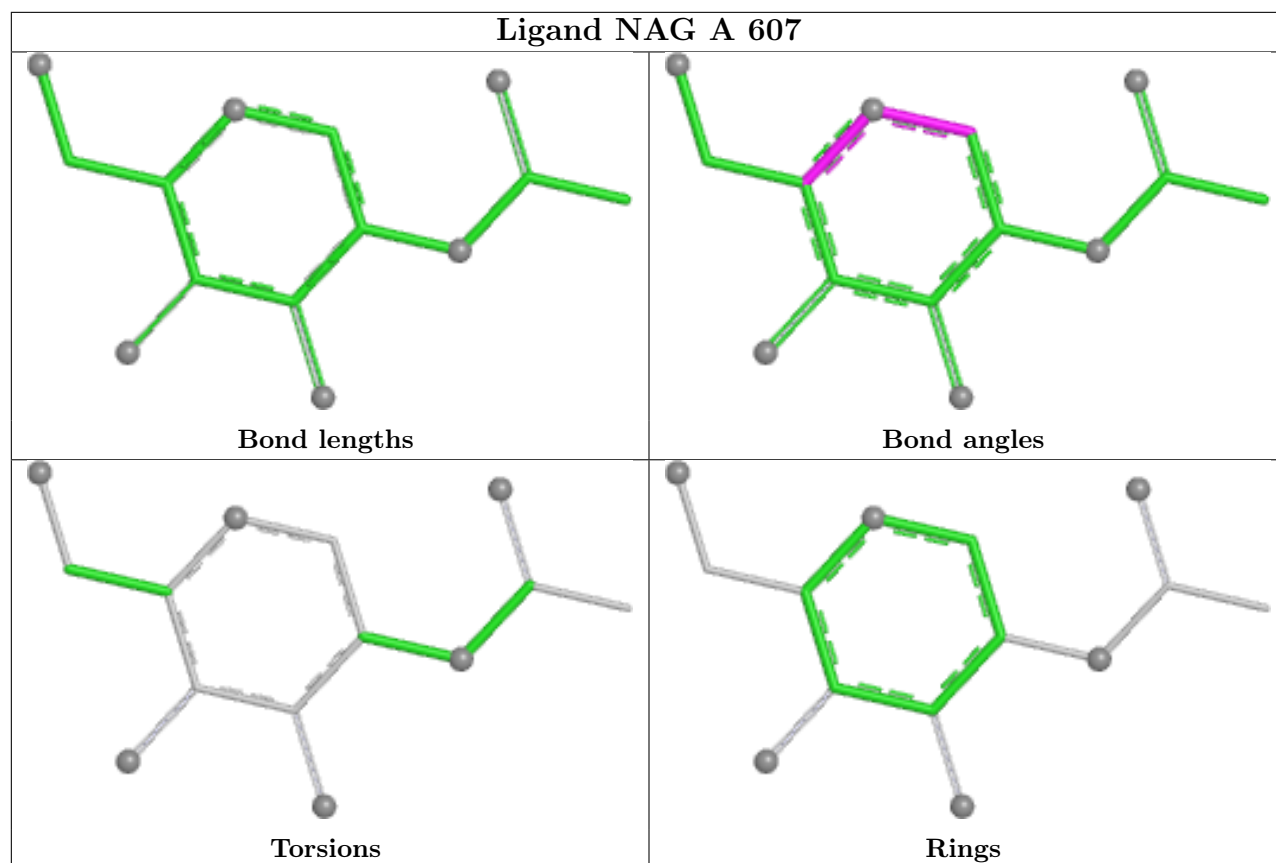
There are no ring outliers.

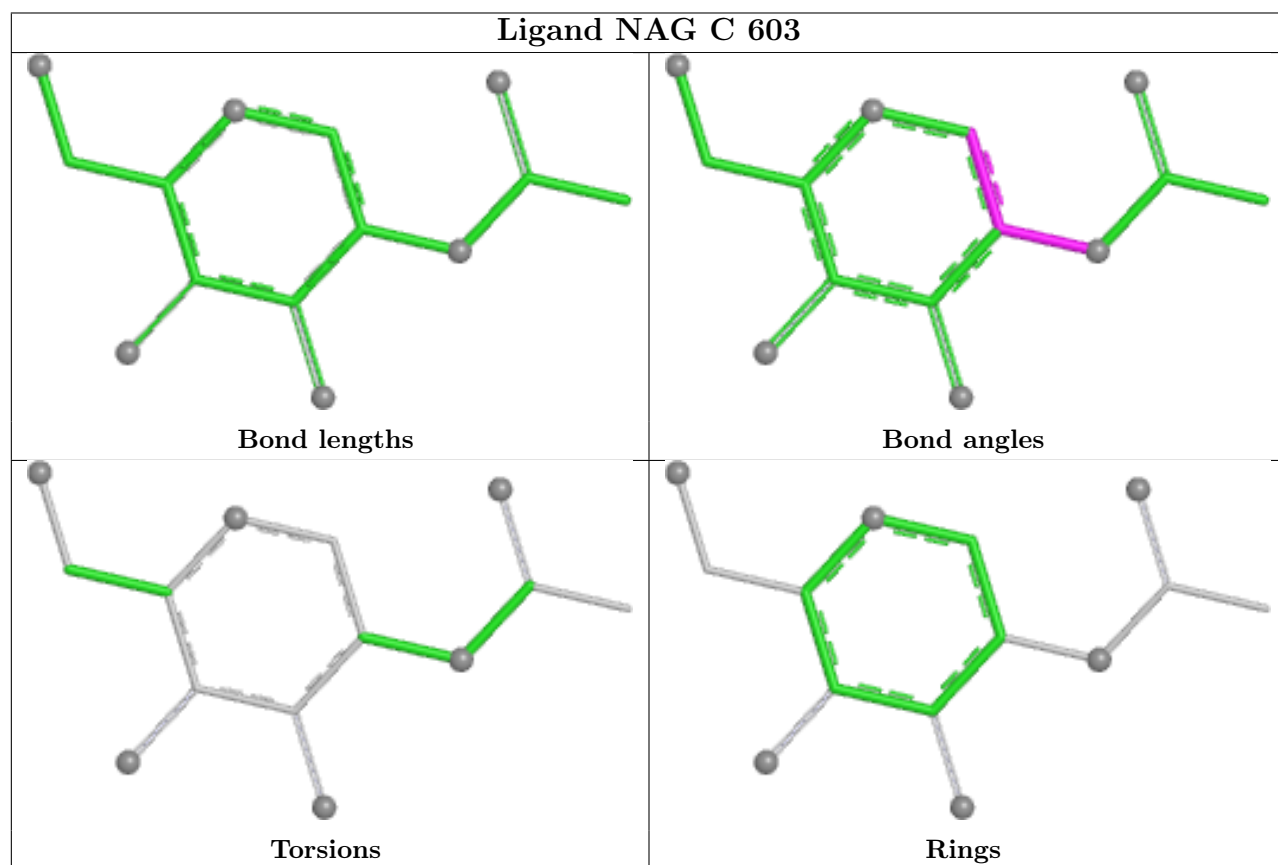
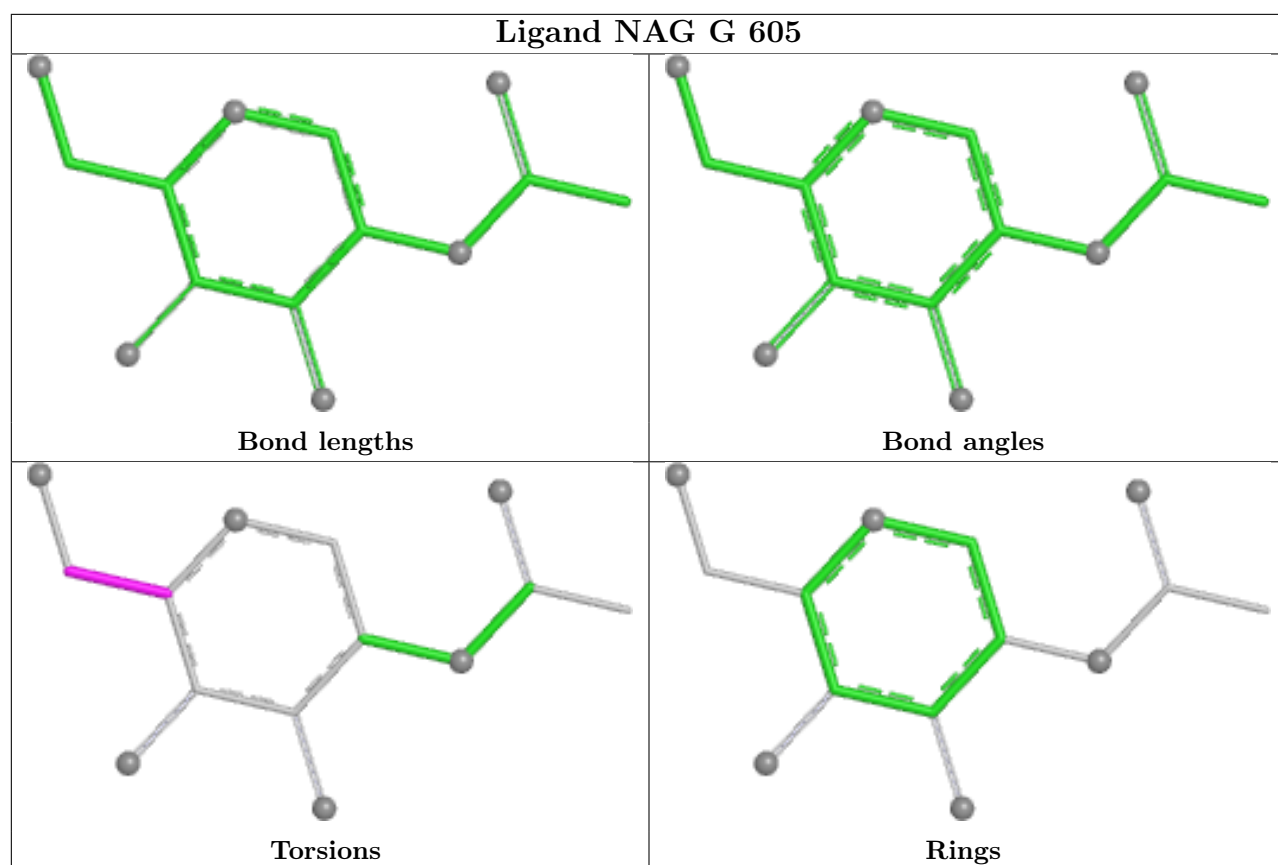
2 monomers are involved in 2 short contacts:

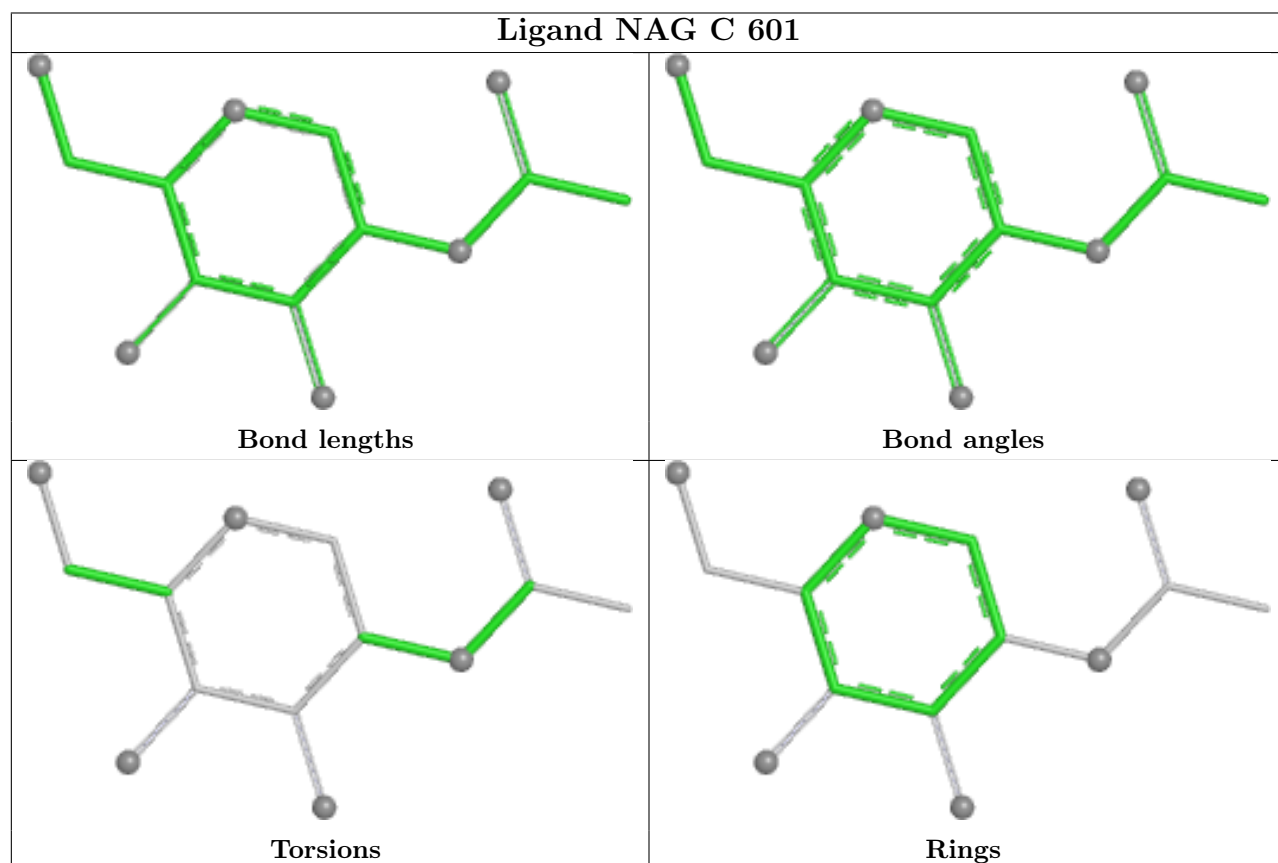
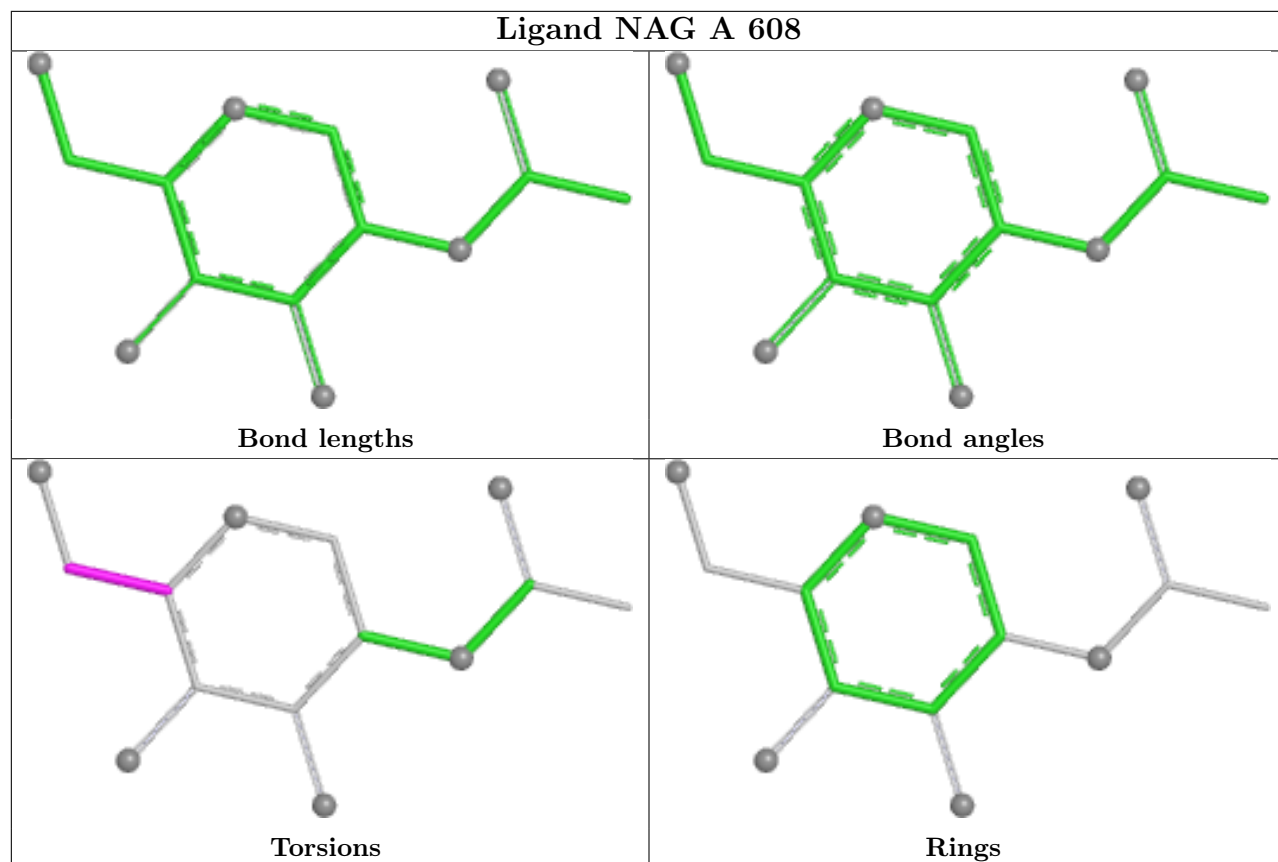
Mol	Chain	Res	Type	Clashes	Symm-Clashes
16	A	604	NAG	1	0
16	G	603	NAG	1	0

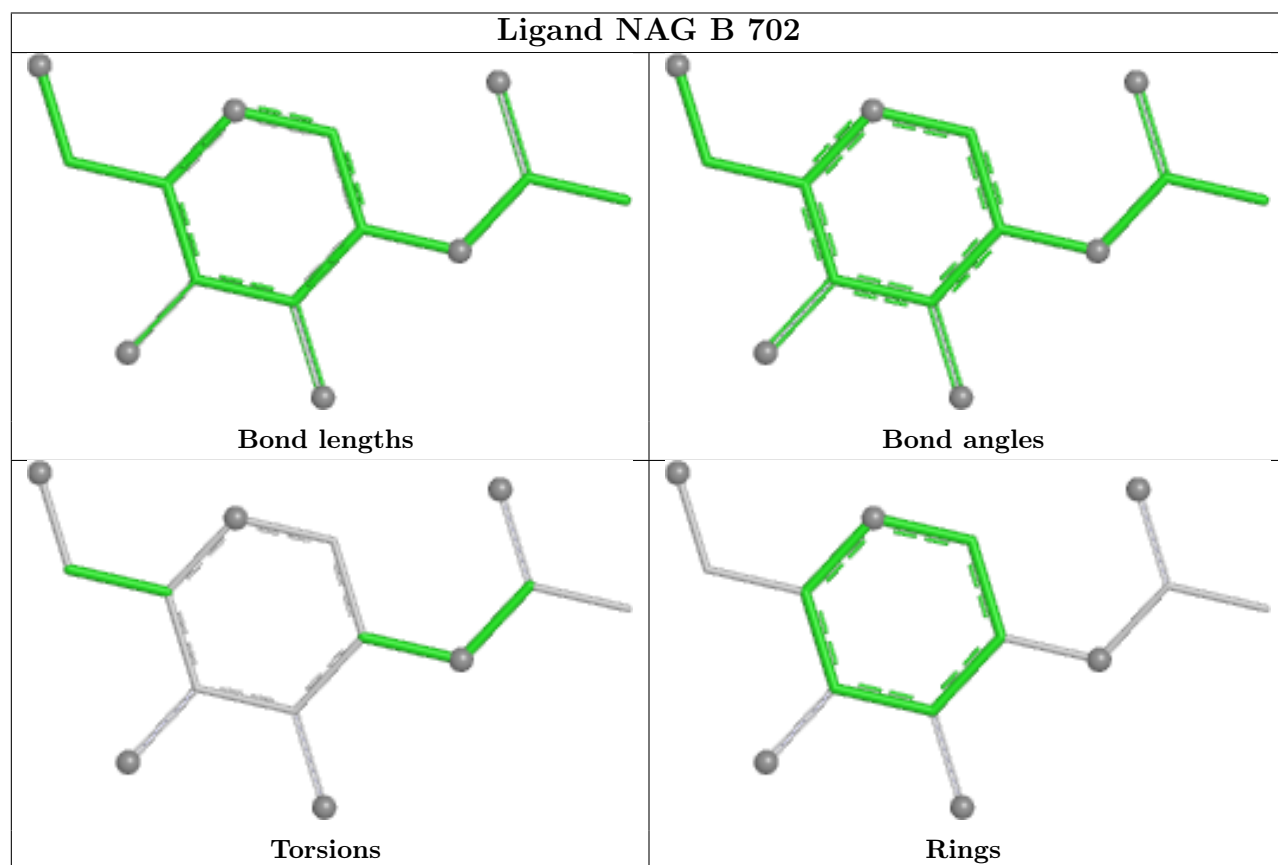
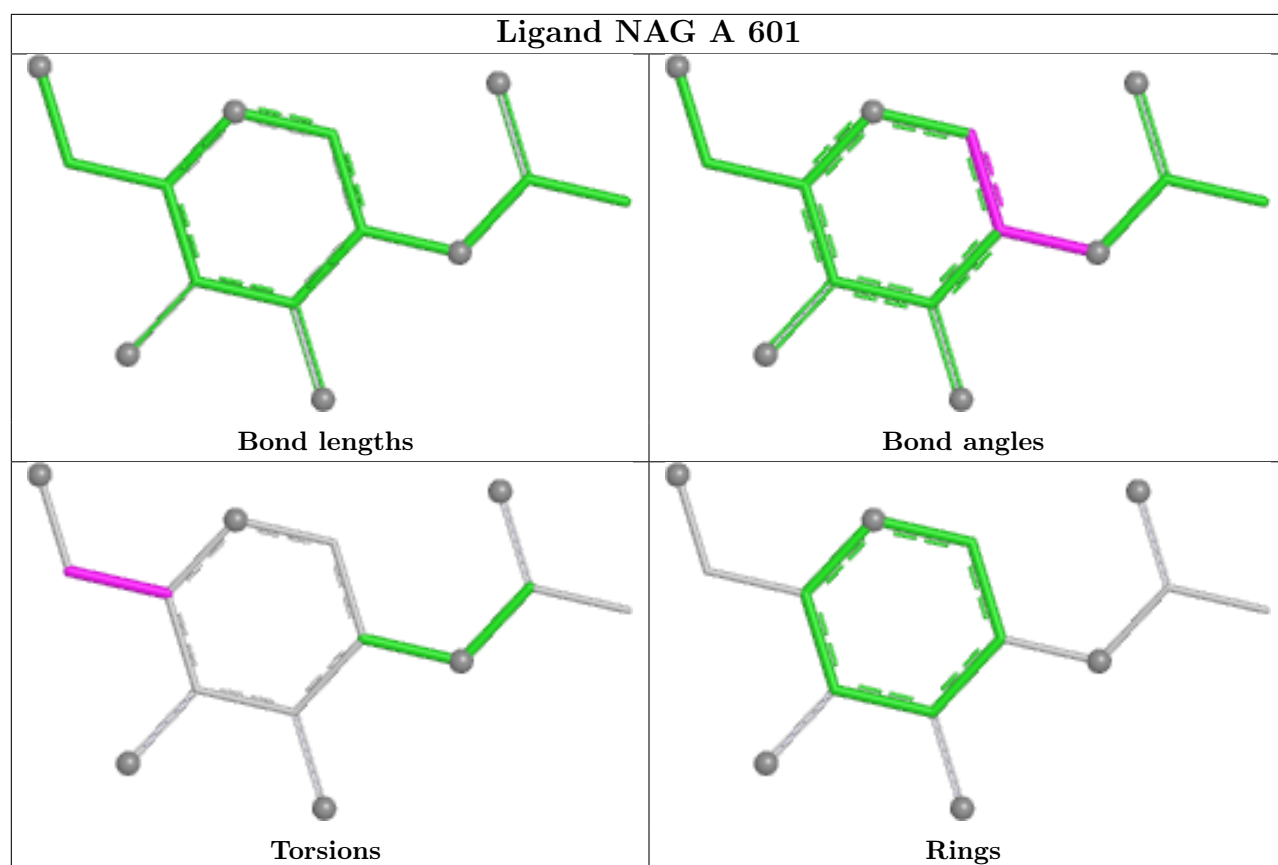
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient

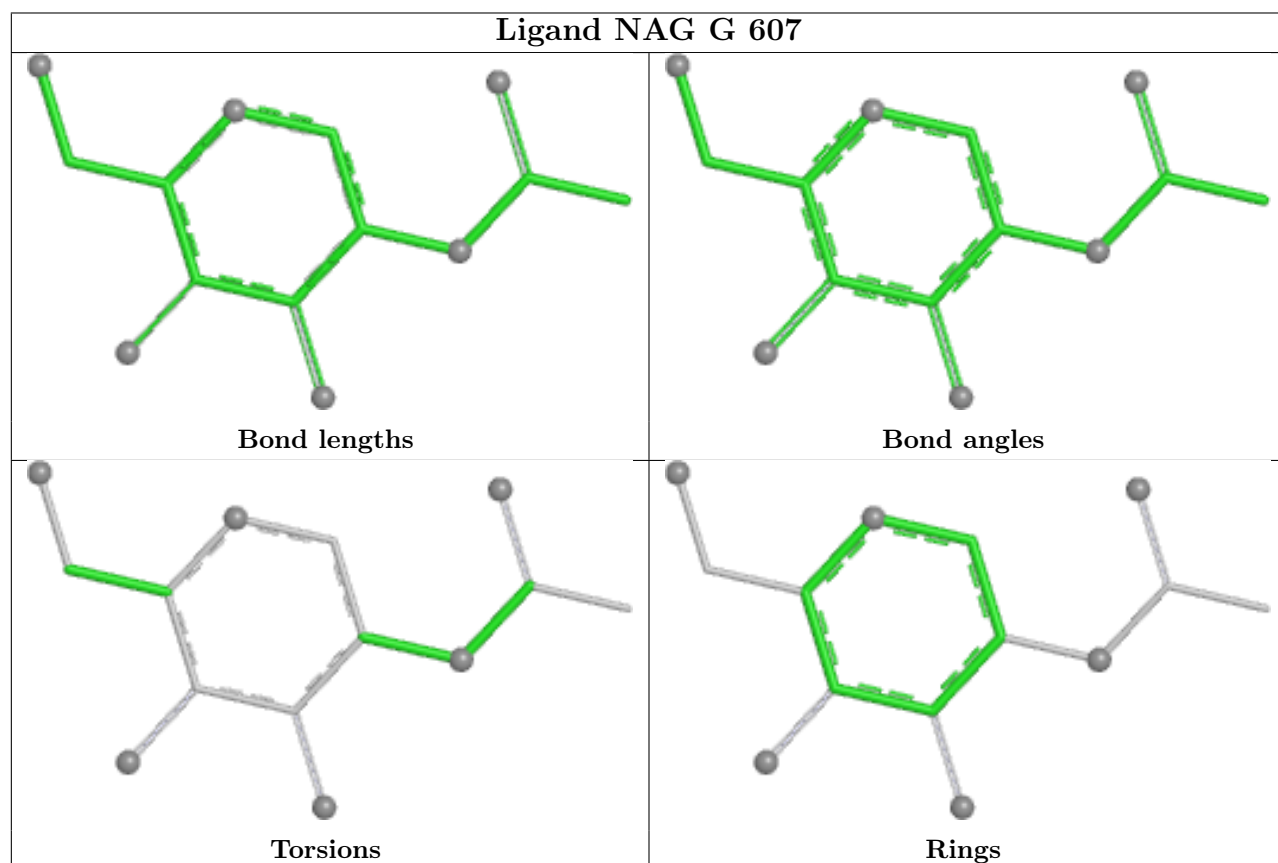
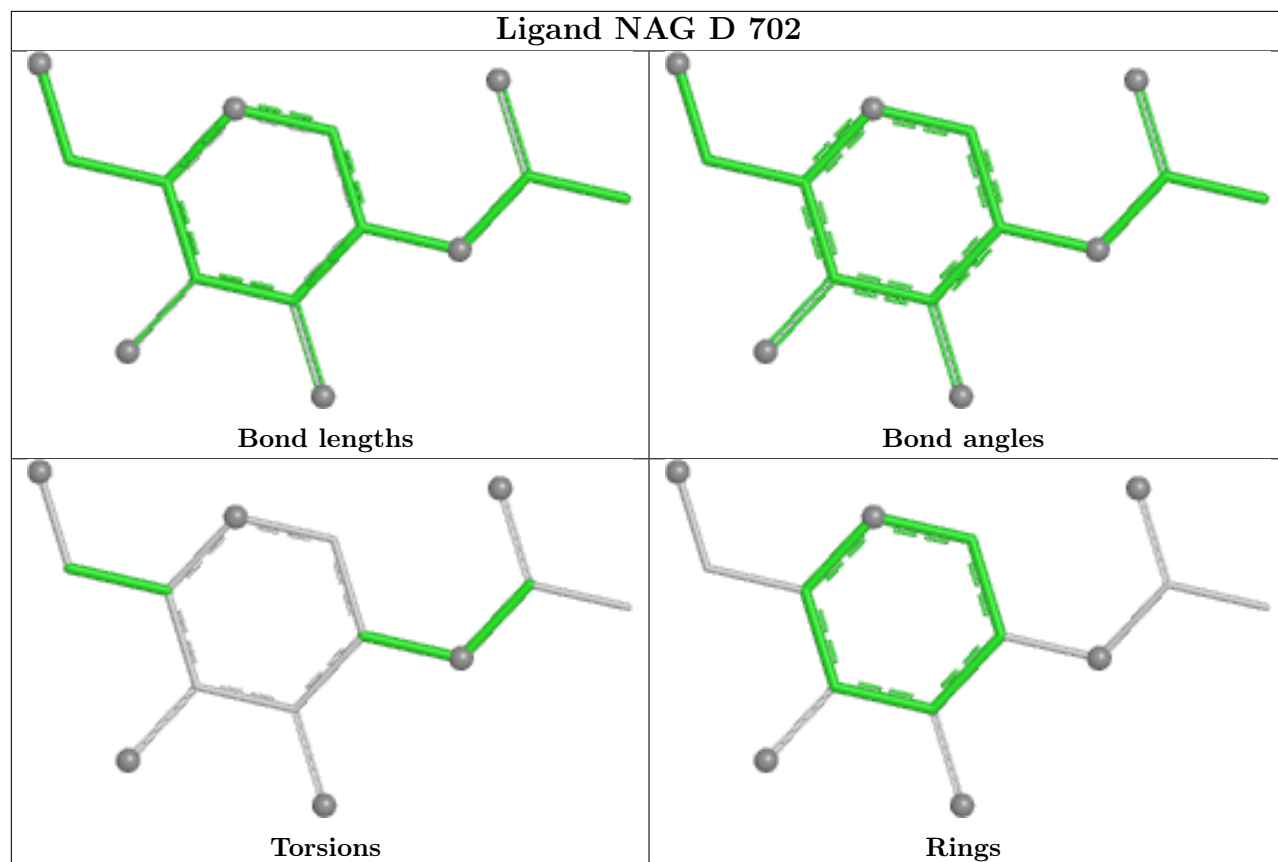
equivalents in the CSD to analyse the geometry.

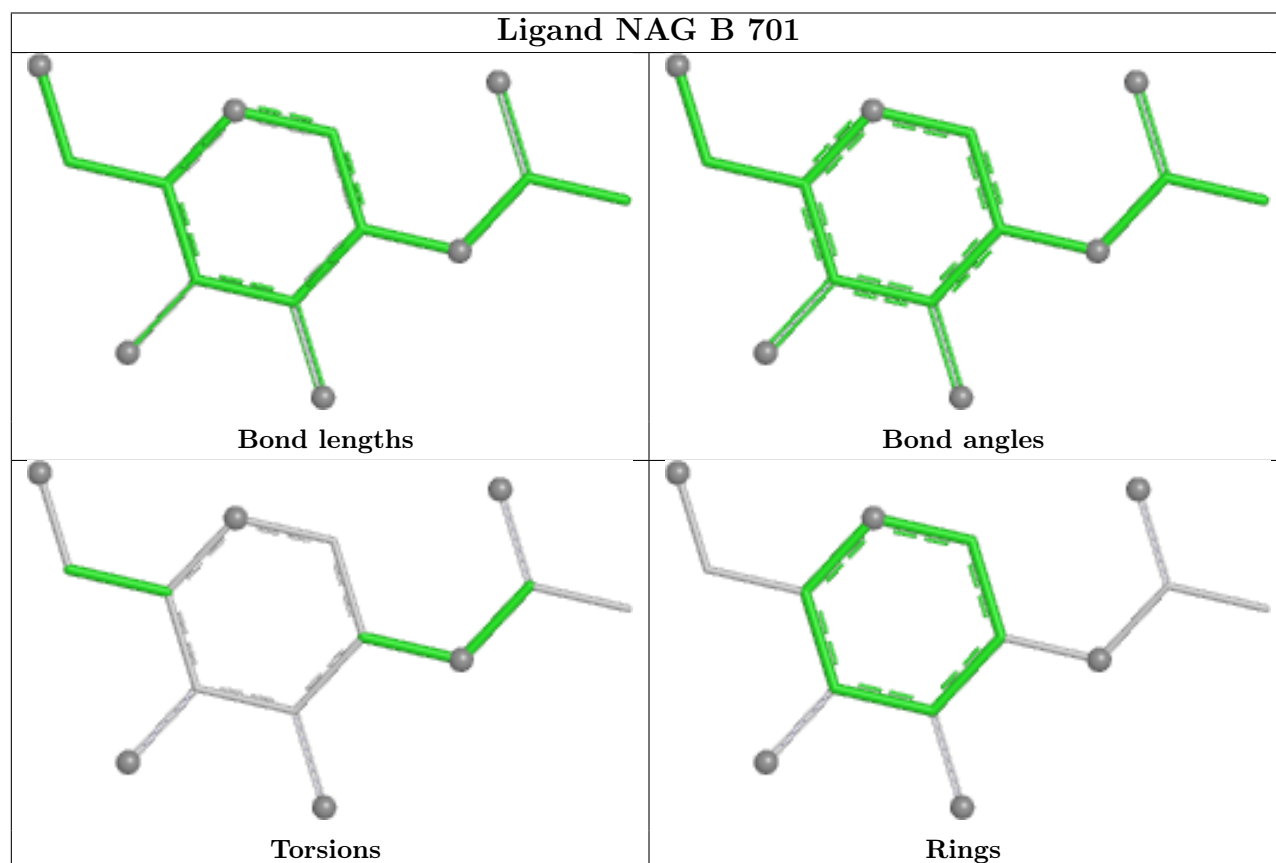
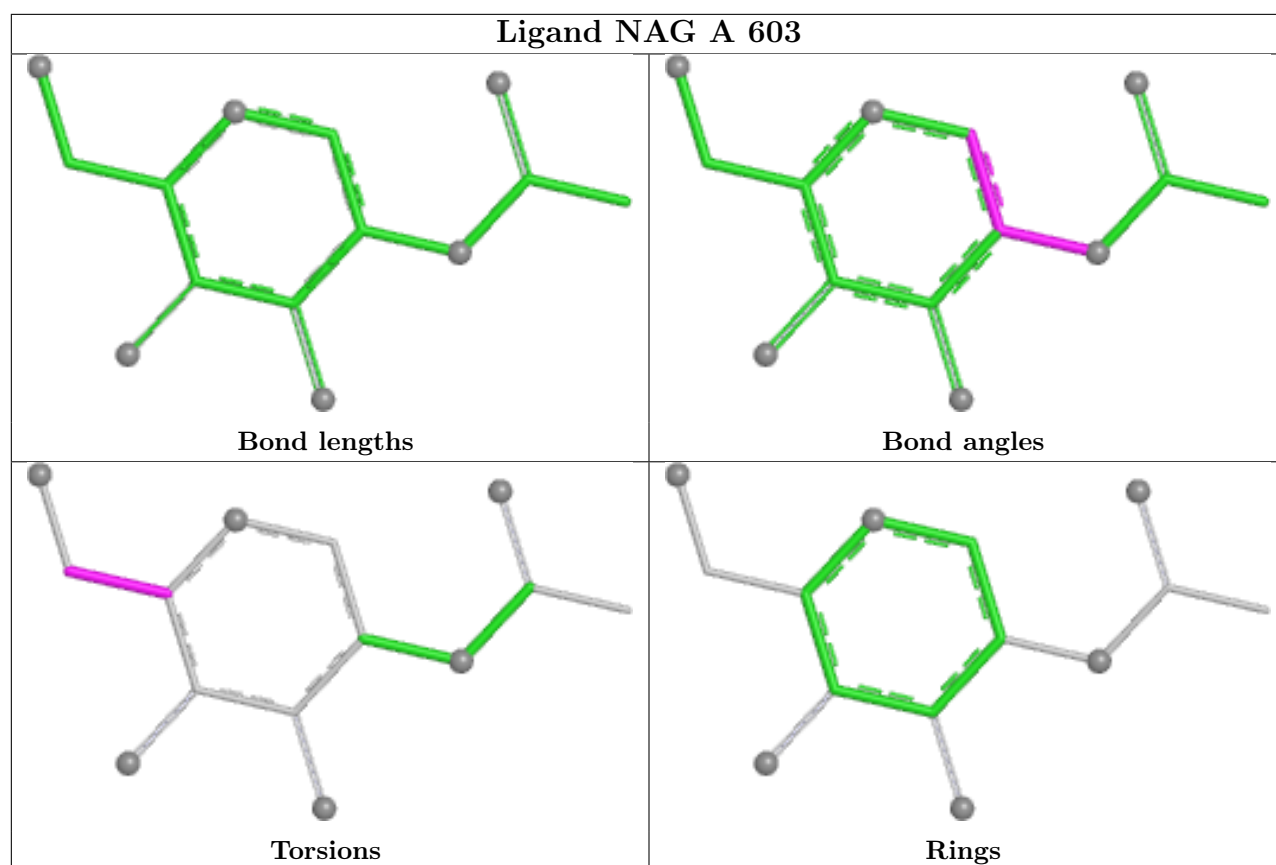


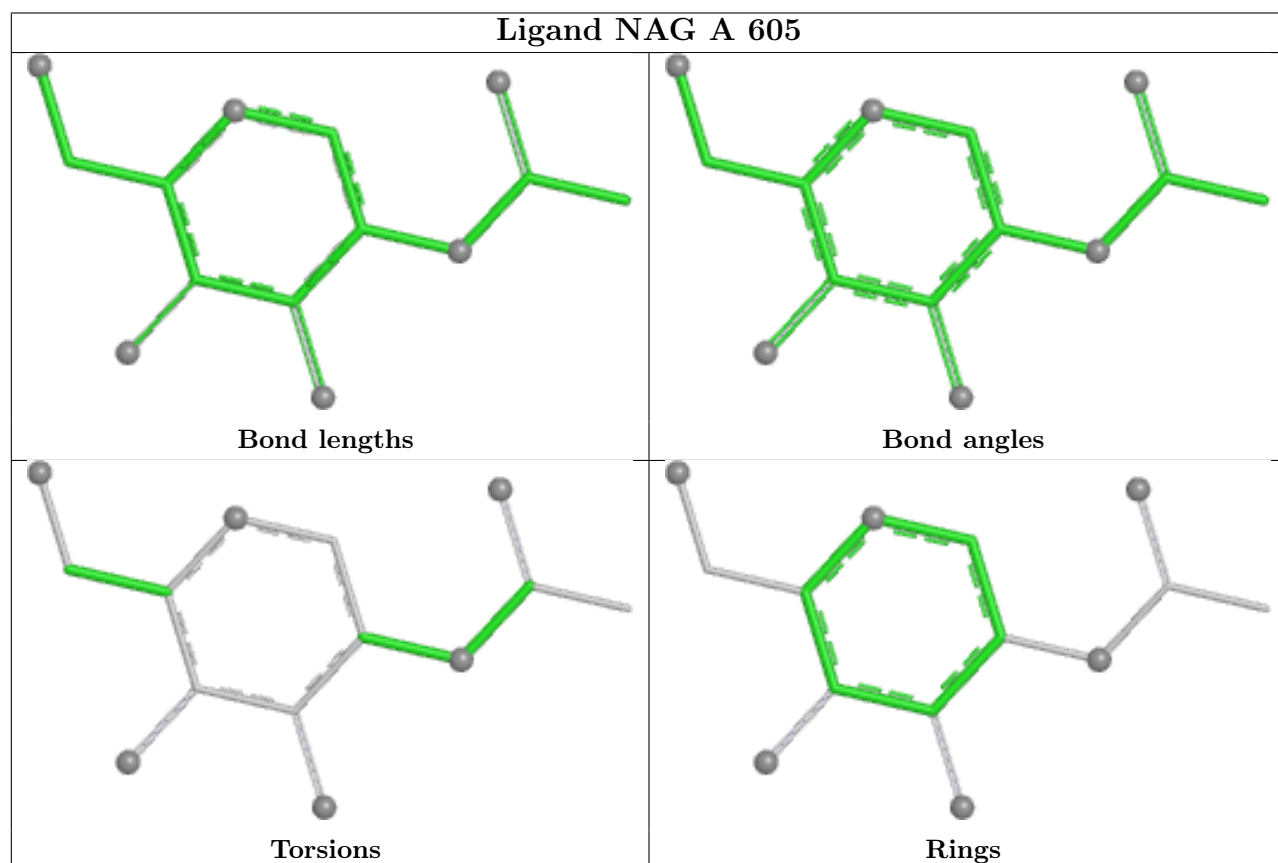
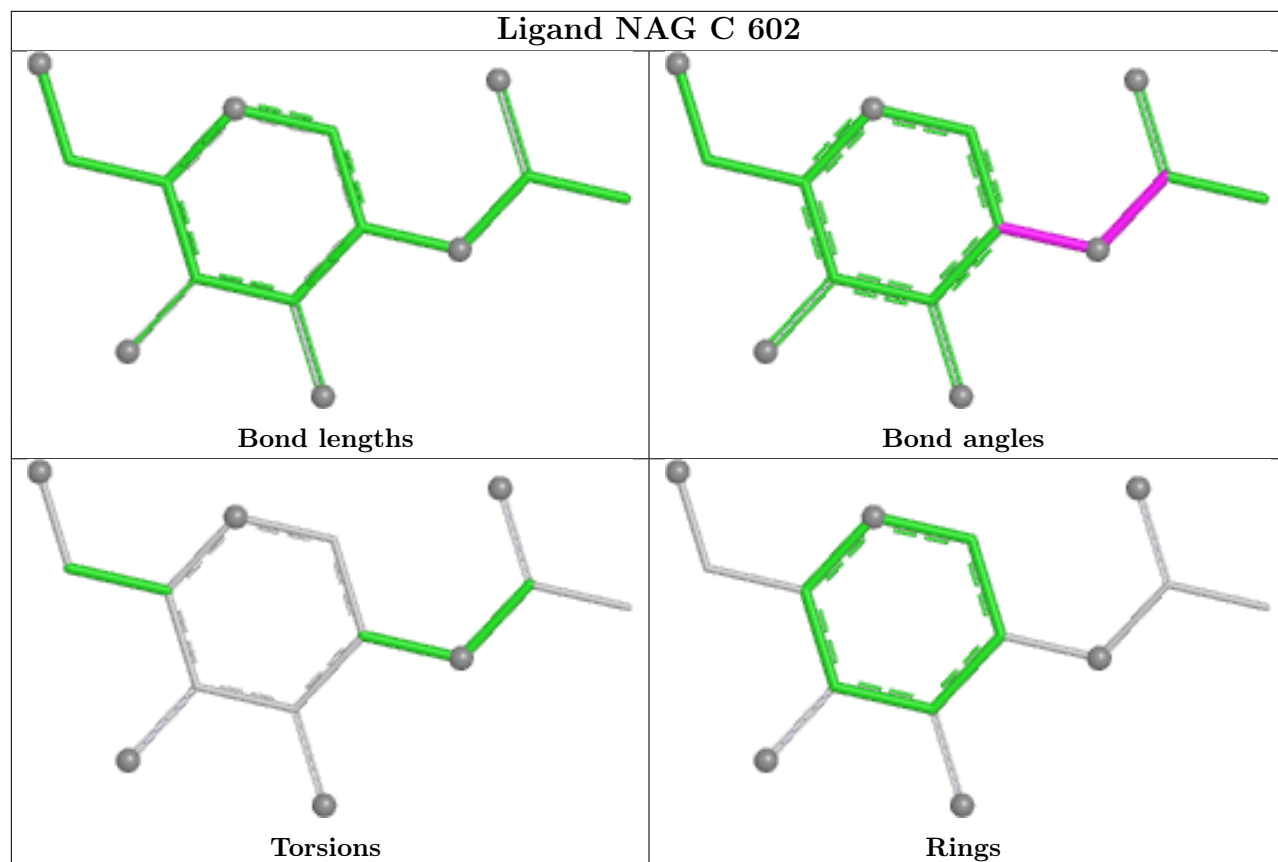




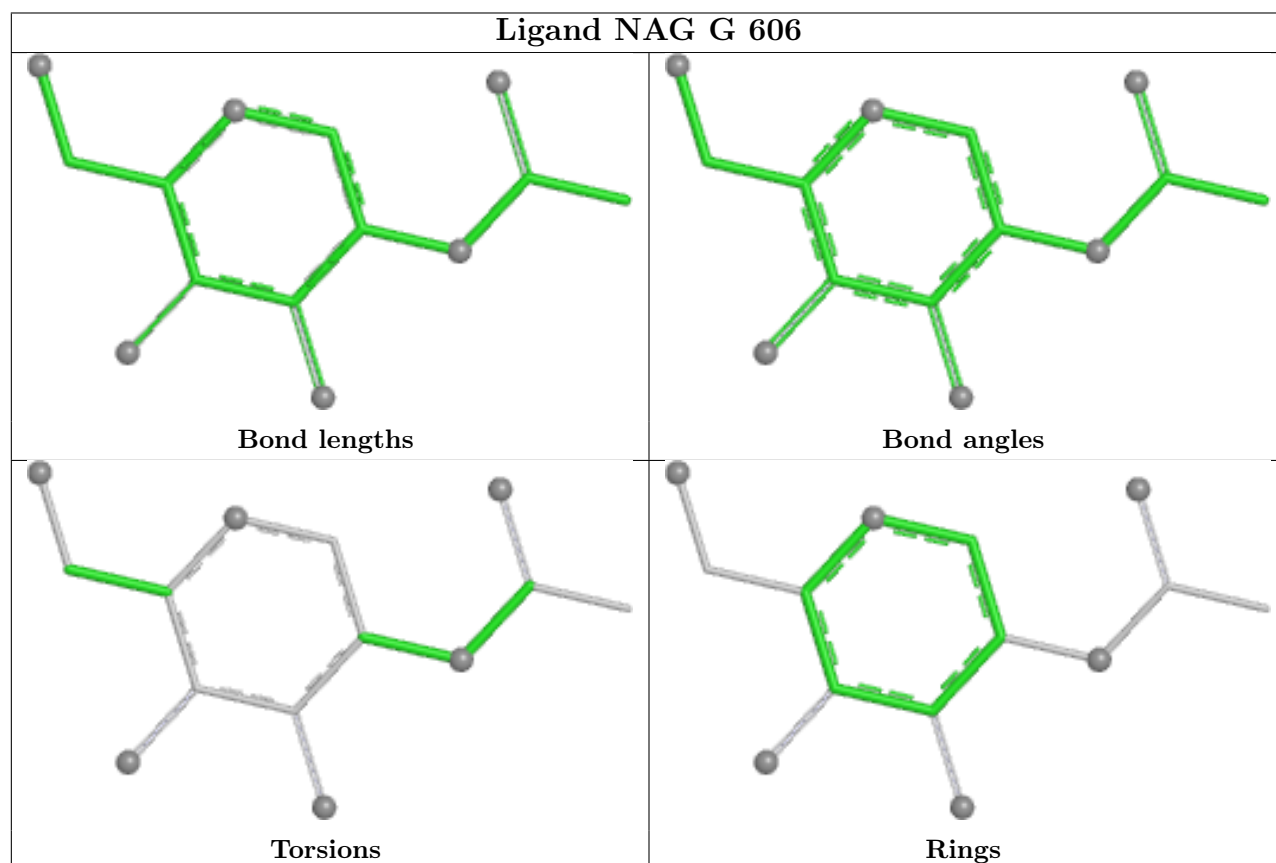
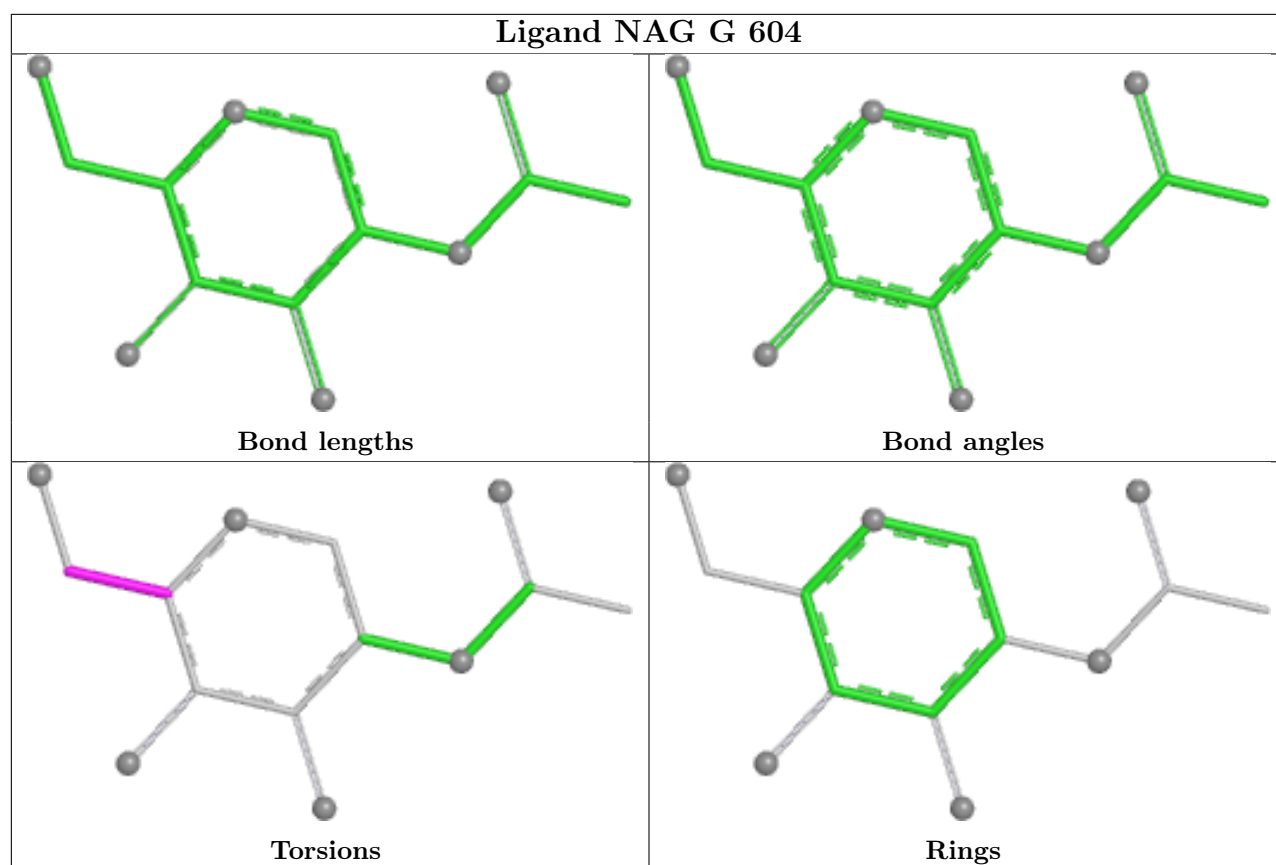


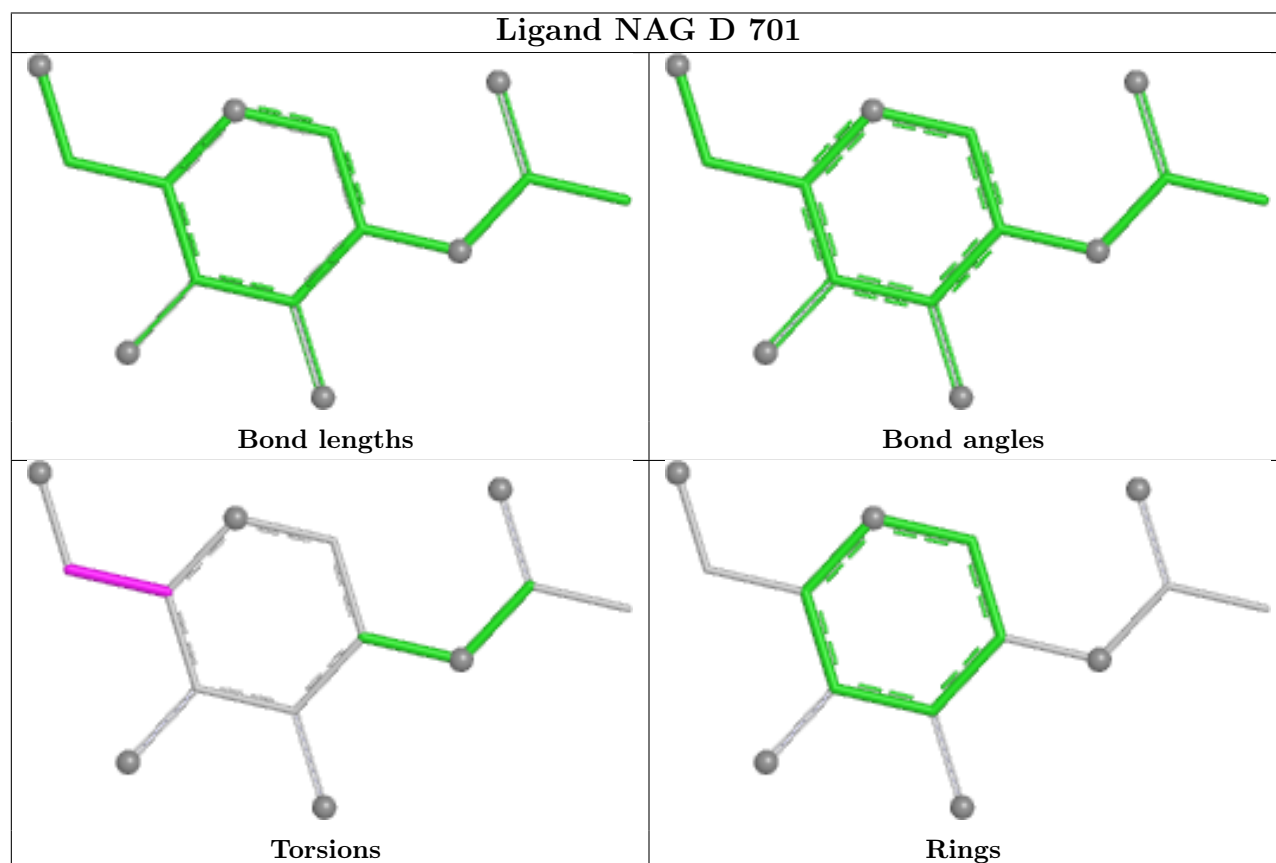
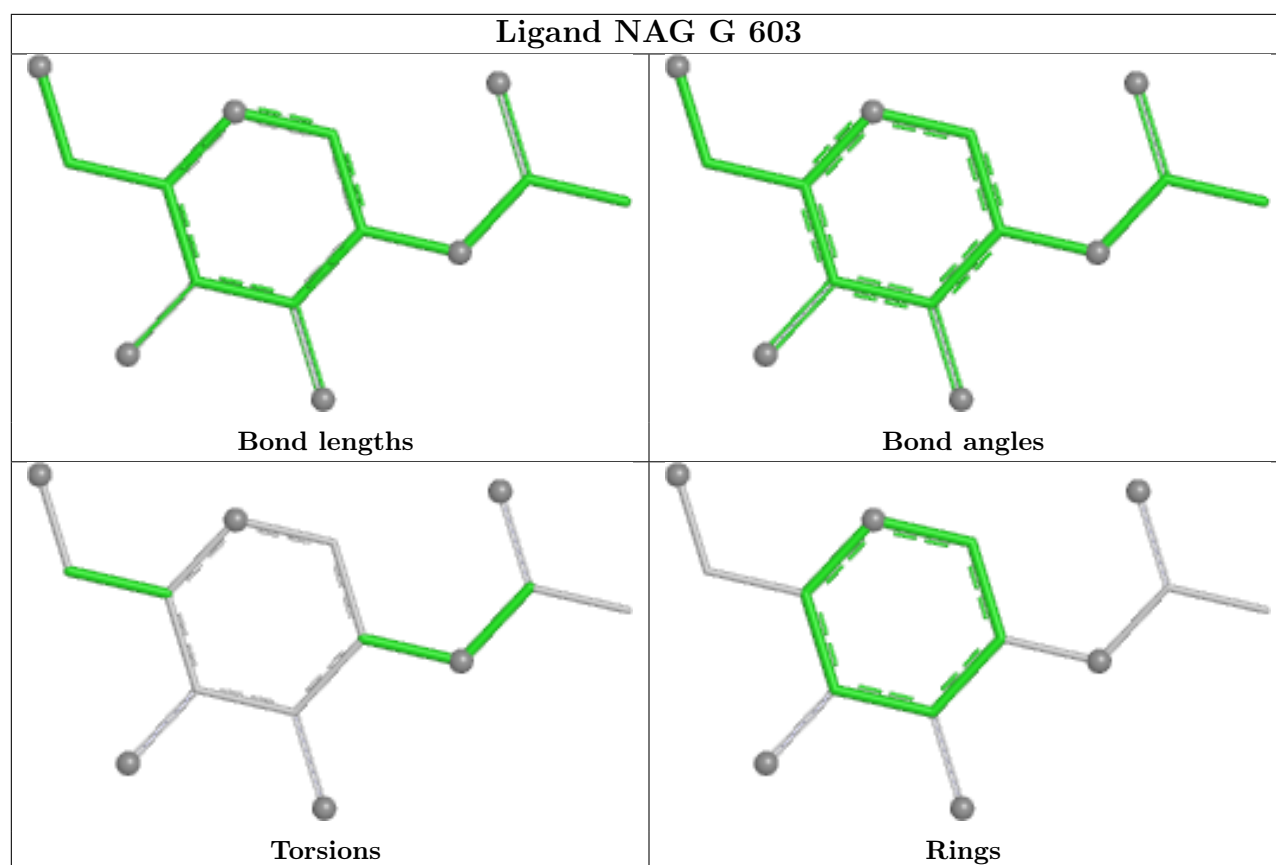


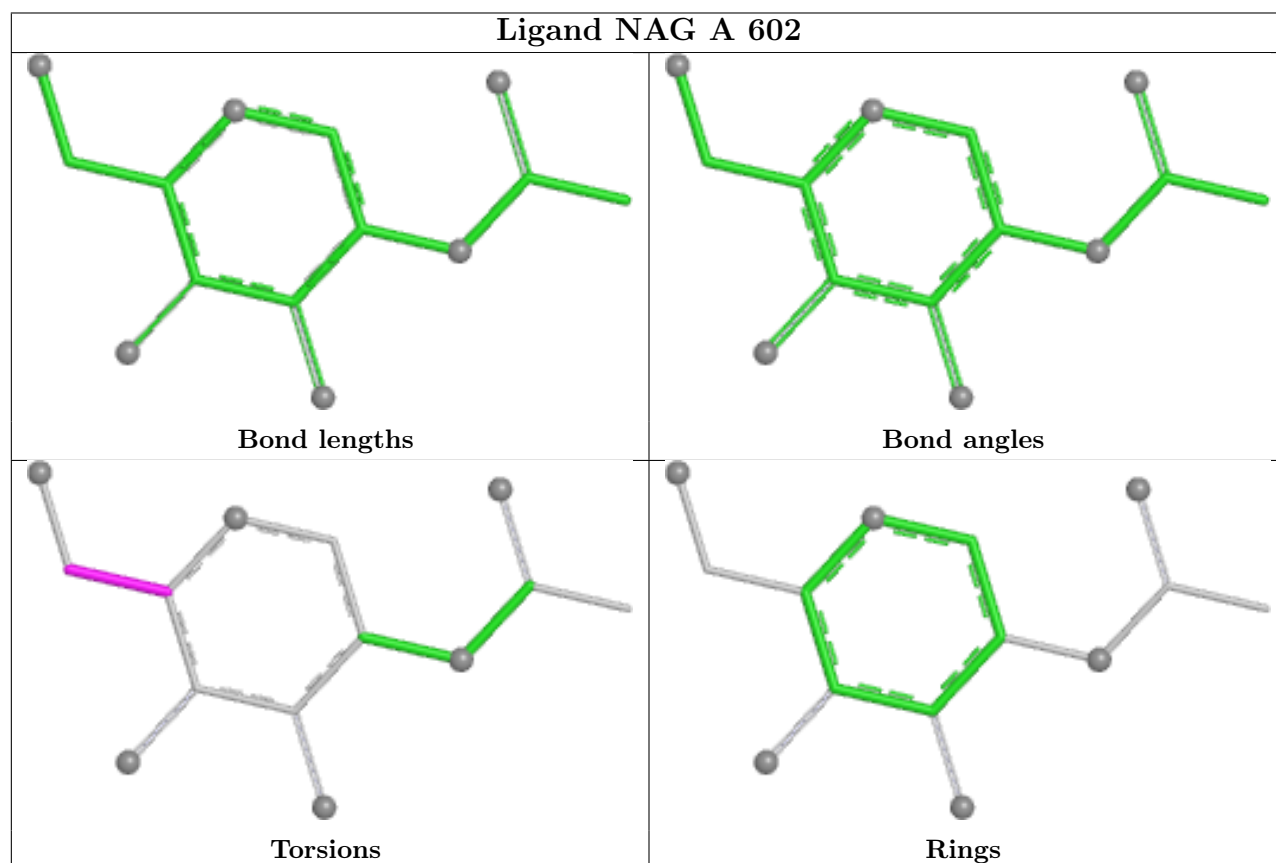
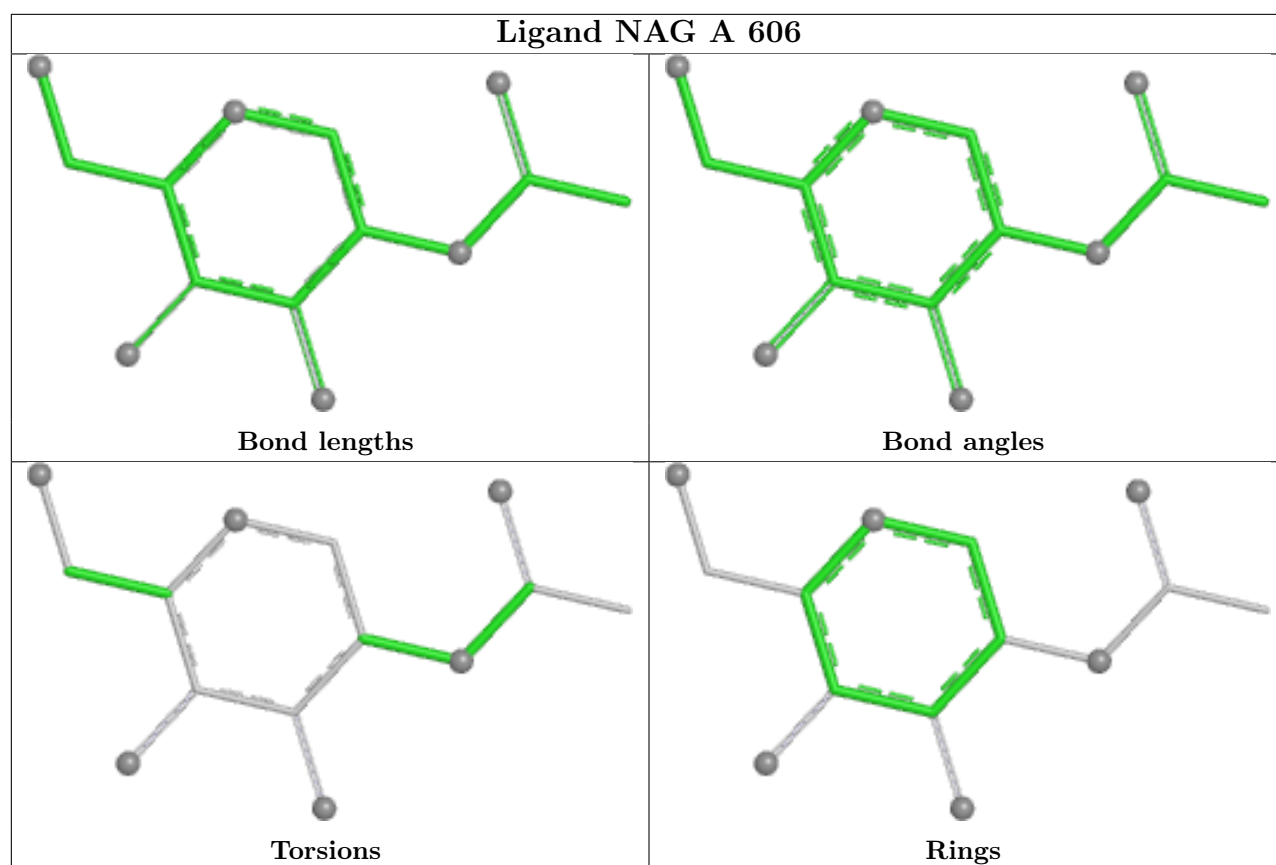


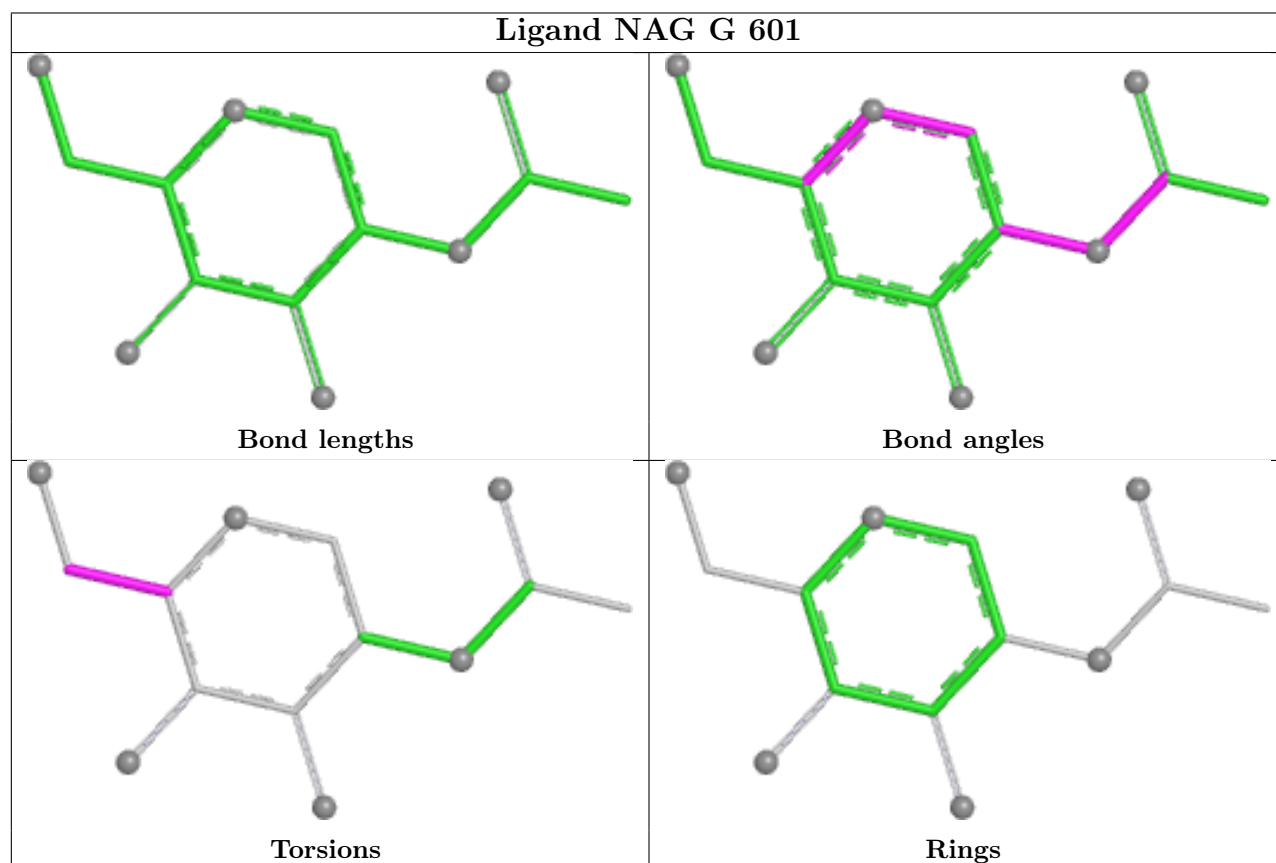
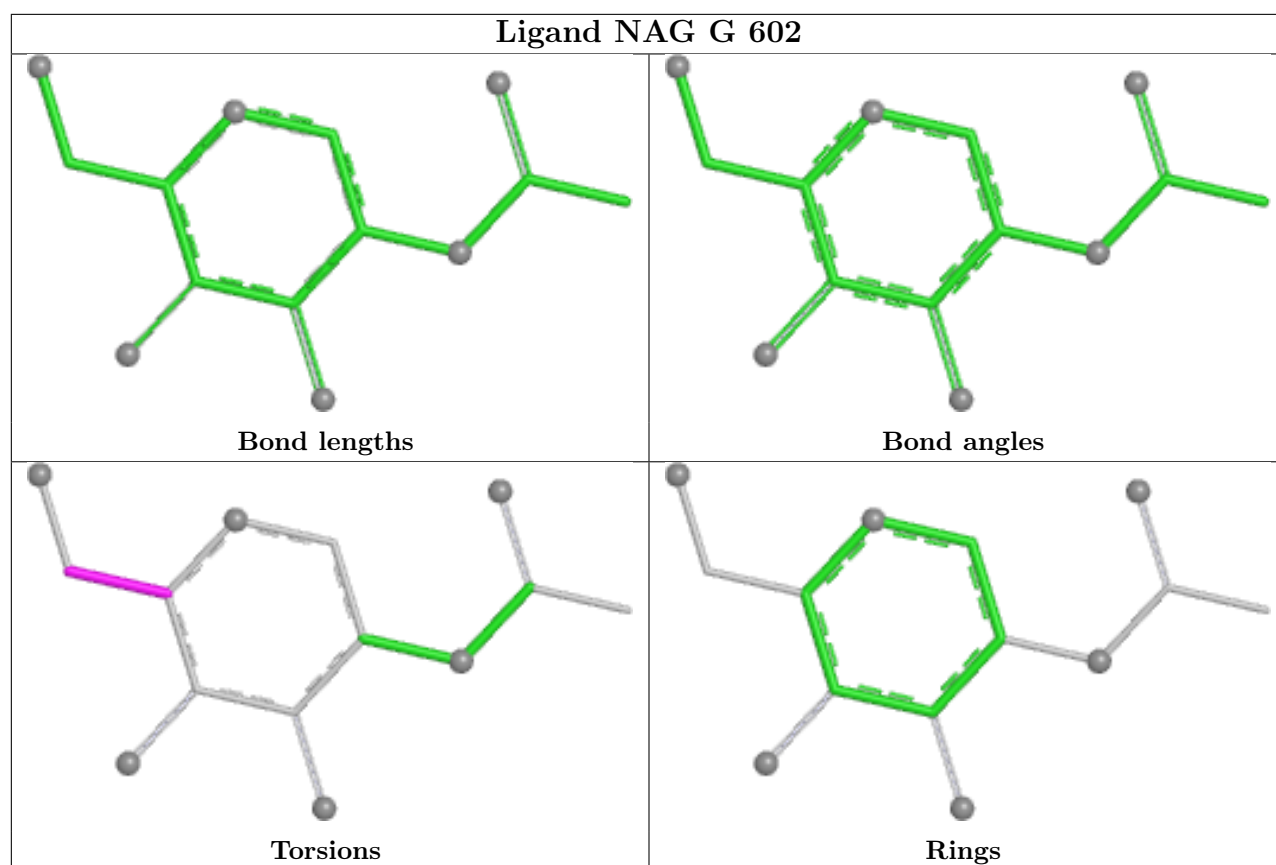












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

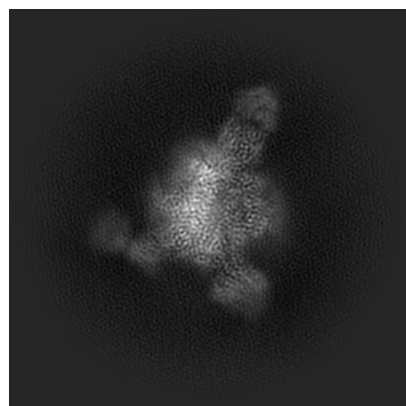
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-46884. These allow visual inspection of the internal detail of the map and identification of artifacts.

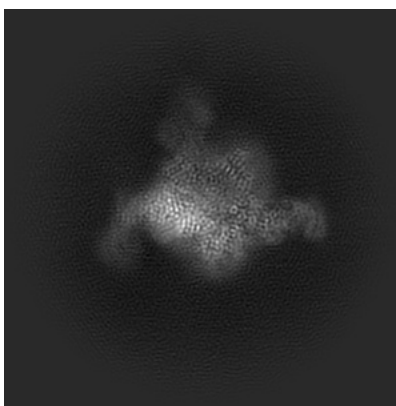
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

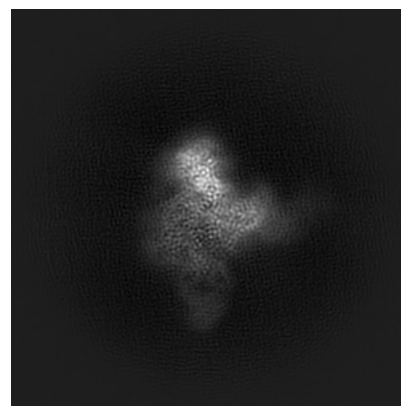
#### 6.1.1 Primary map



X

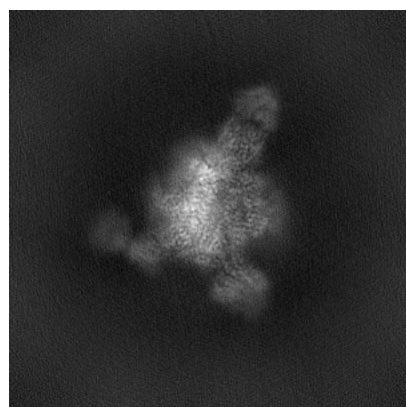


Y

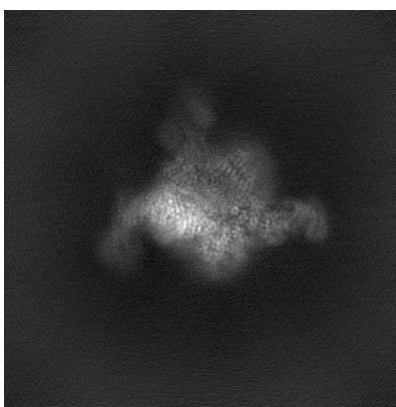


Z

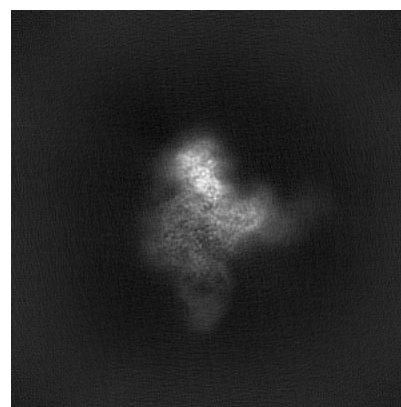
#### 6.1.2 Raw map



X



Y

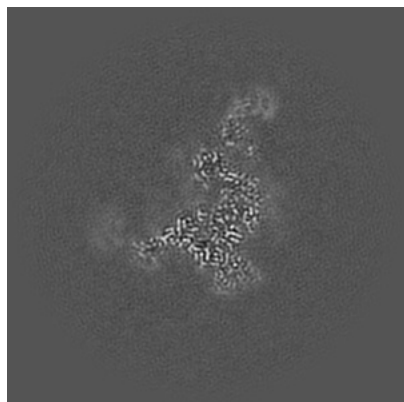


Z

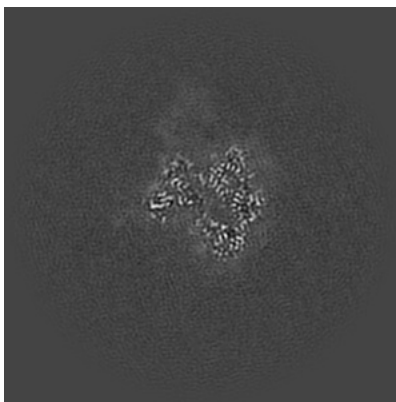
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

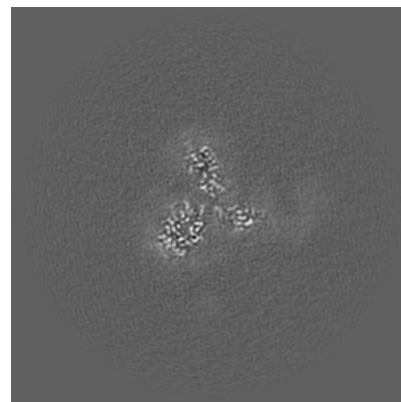
### 6.2.1 Primary map



X Index: 170

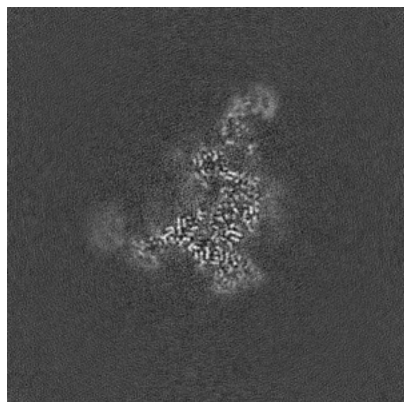


Y Index: 170

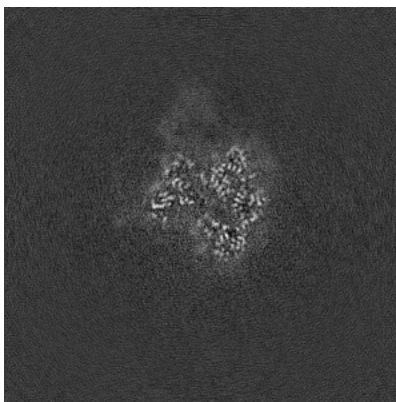


Z Index: 170

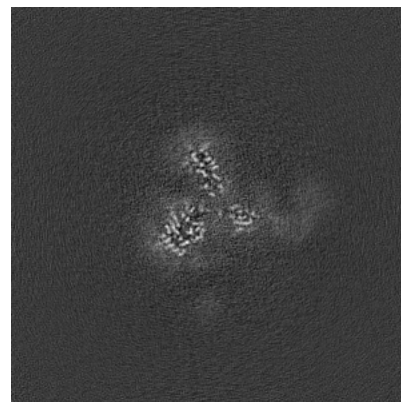
### 6.2.2 Raw map



X Index: 170



Y Index: 170



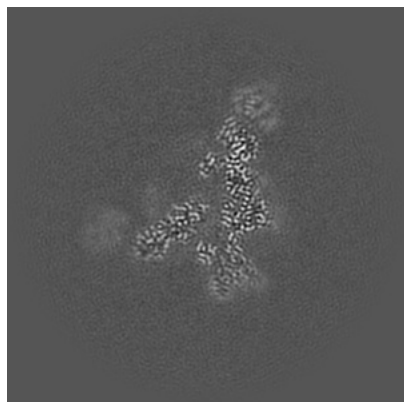
Z Index: 170

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

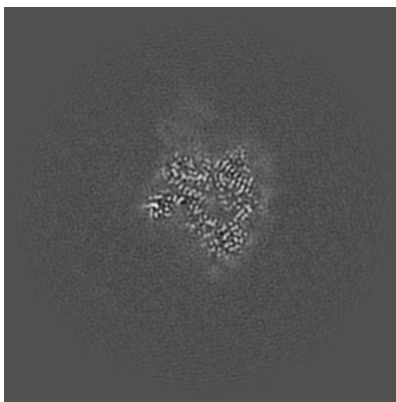


## 6.3 Largest variance slices [i](#)

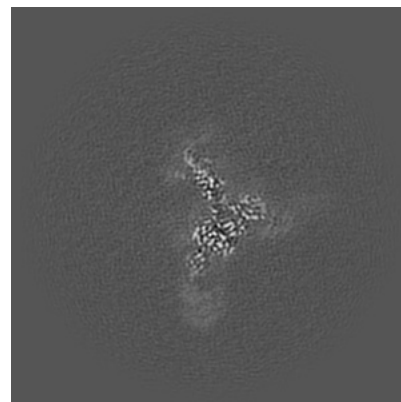
### 6.3.1 Primary map



X Index: 162

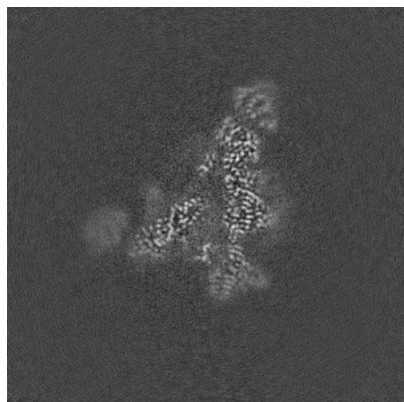


Y Index: 165

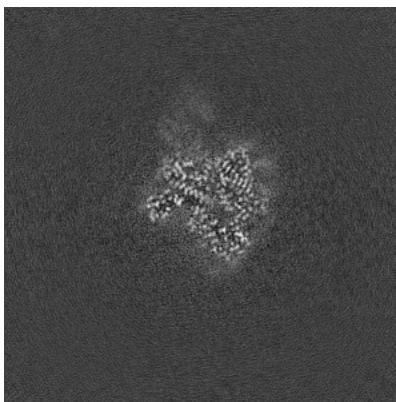


Z Index: 147

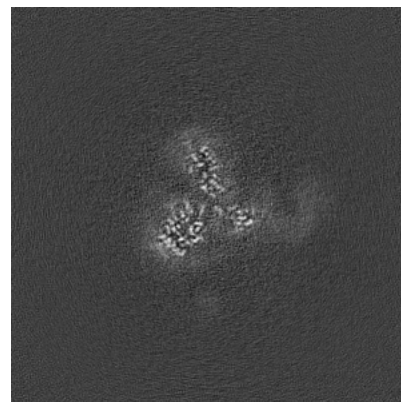
### 6.3.2 Raw map



X Index: 160



Y Index: 166



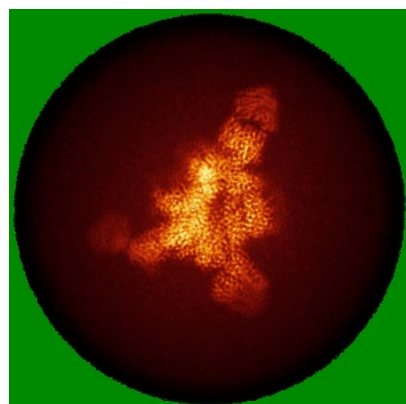
Z Index: 171

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

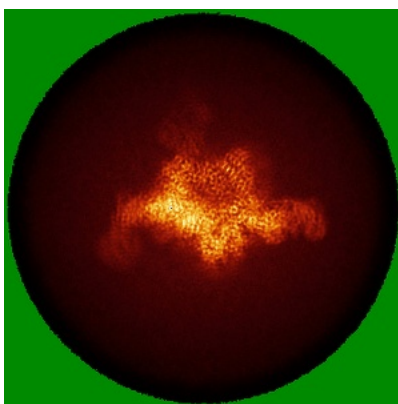


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

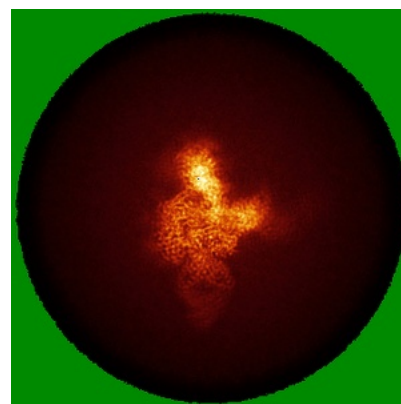
### 6.4.1 Primary map



X

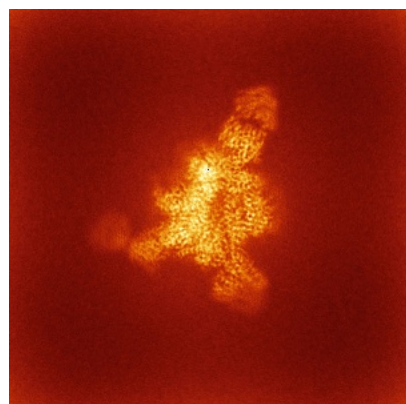


Y

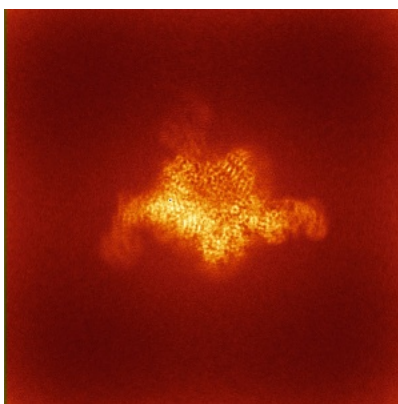


Z

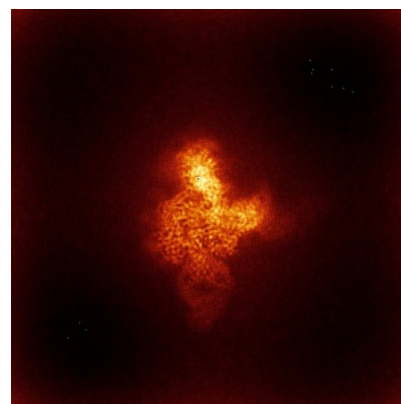
### 6.4.2 Raw map



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.

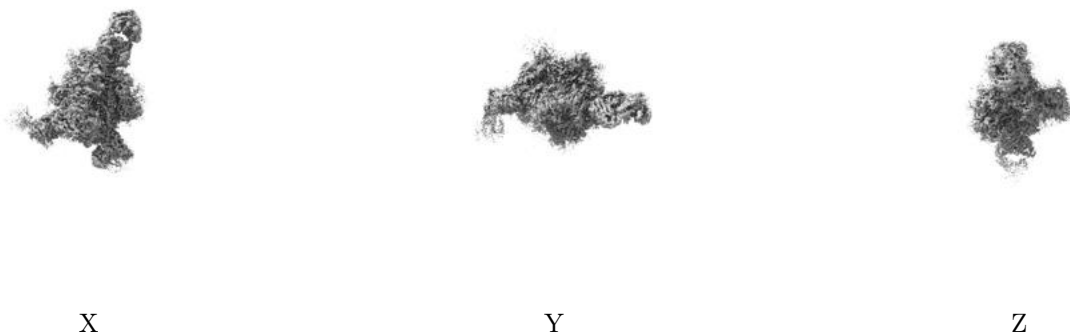
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.46. 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.

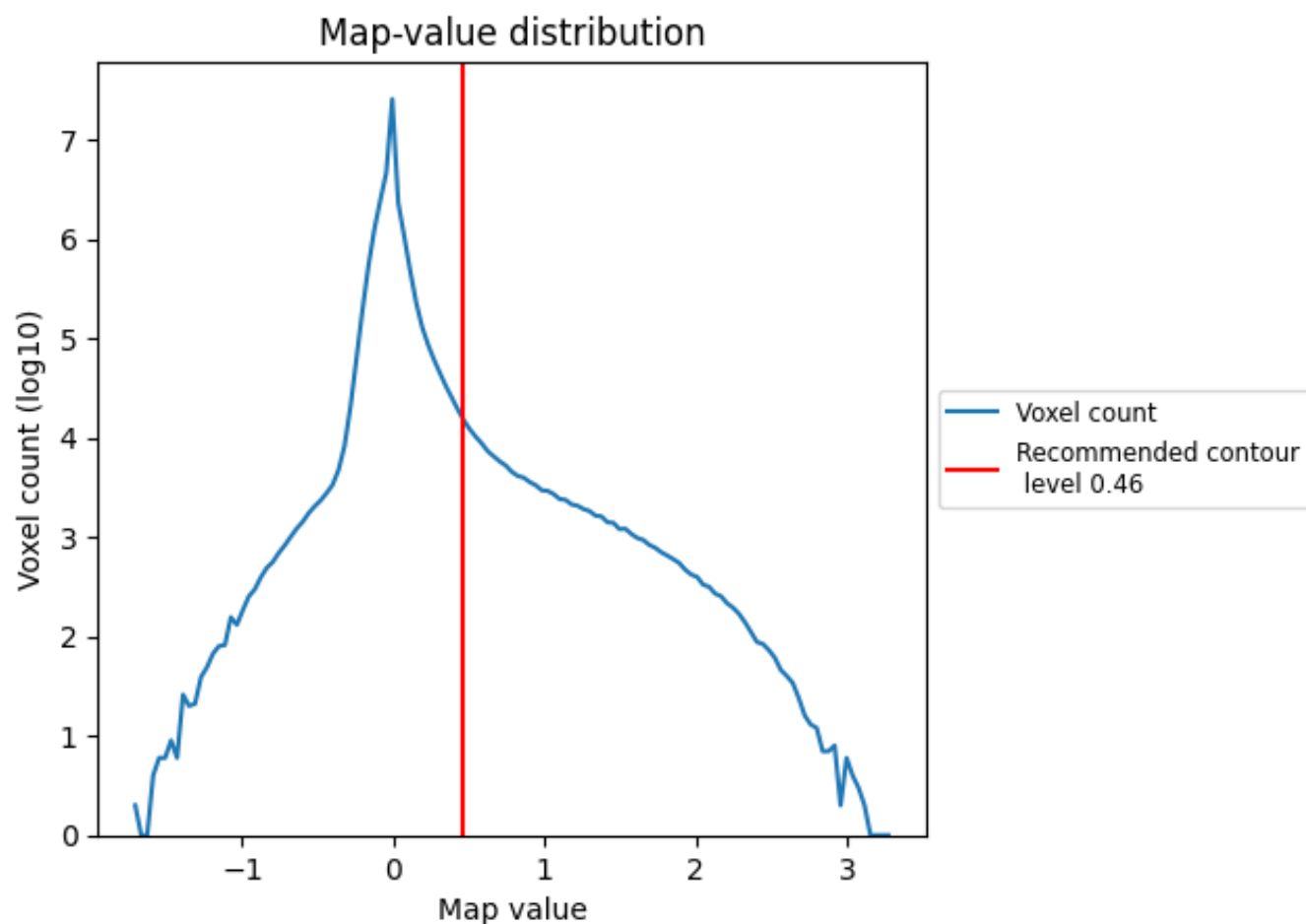
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

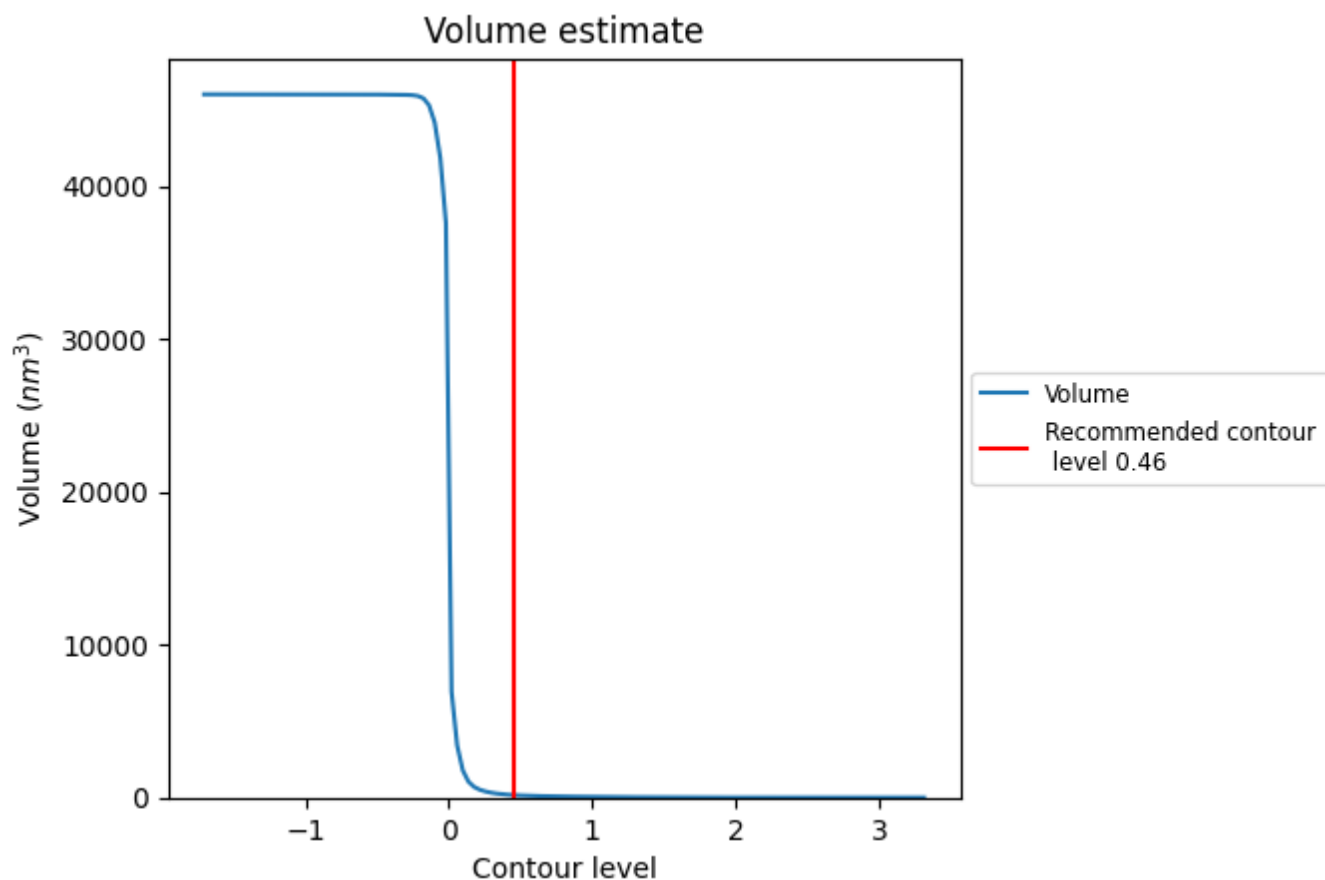
This section contains the results of statistical analysis of the map.

### 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.

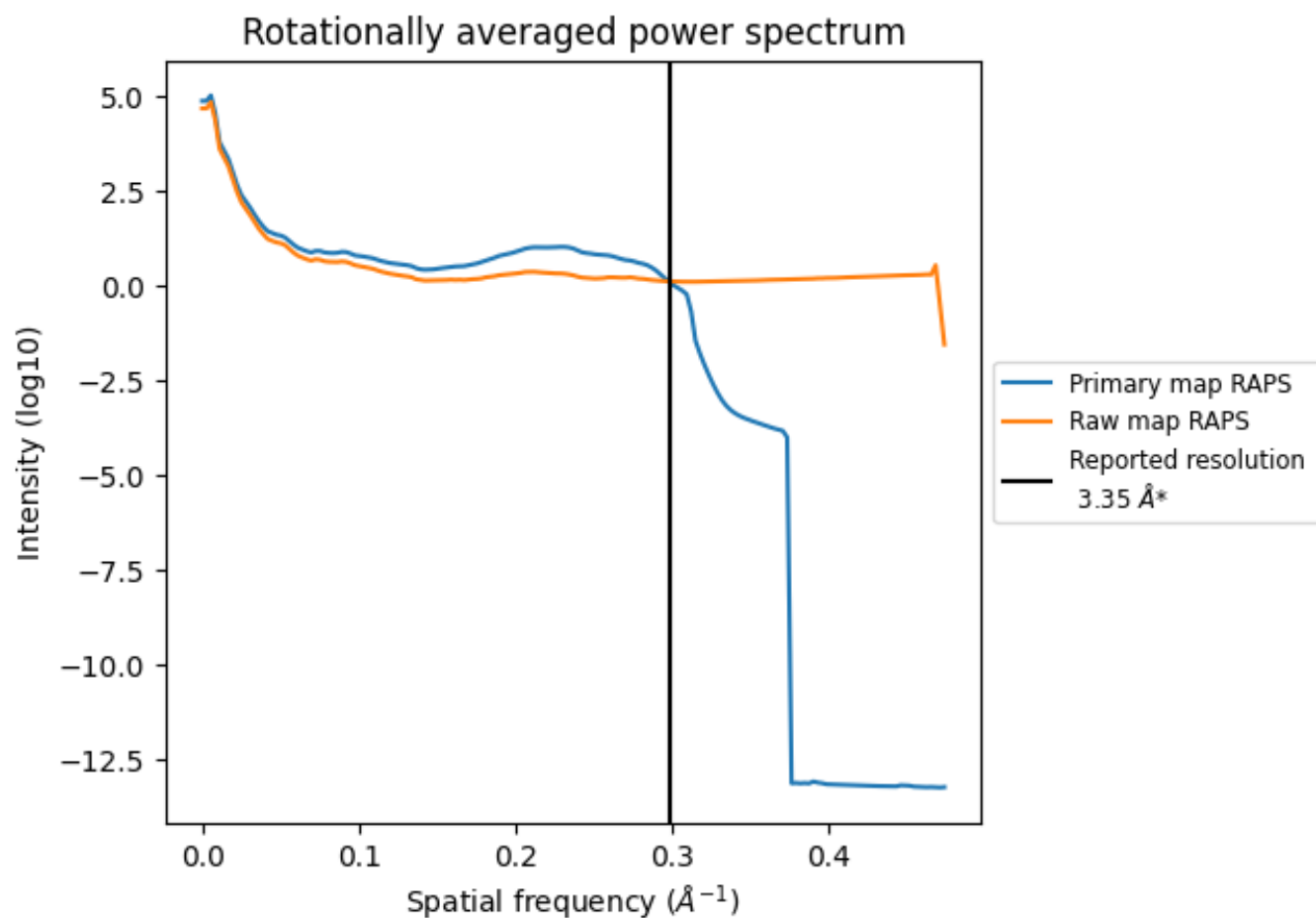
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 157 nm<sup>3</sup>; this corresponds to an approximate mass of 142 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 ⓘ

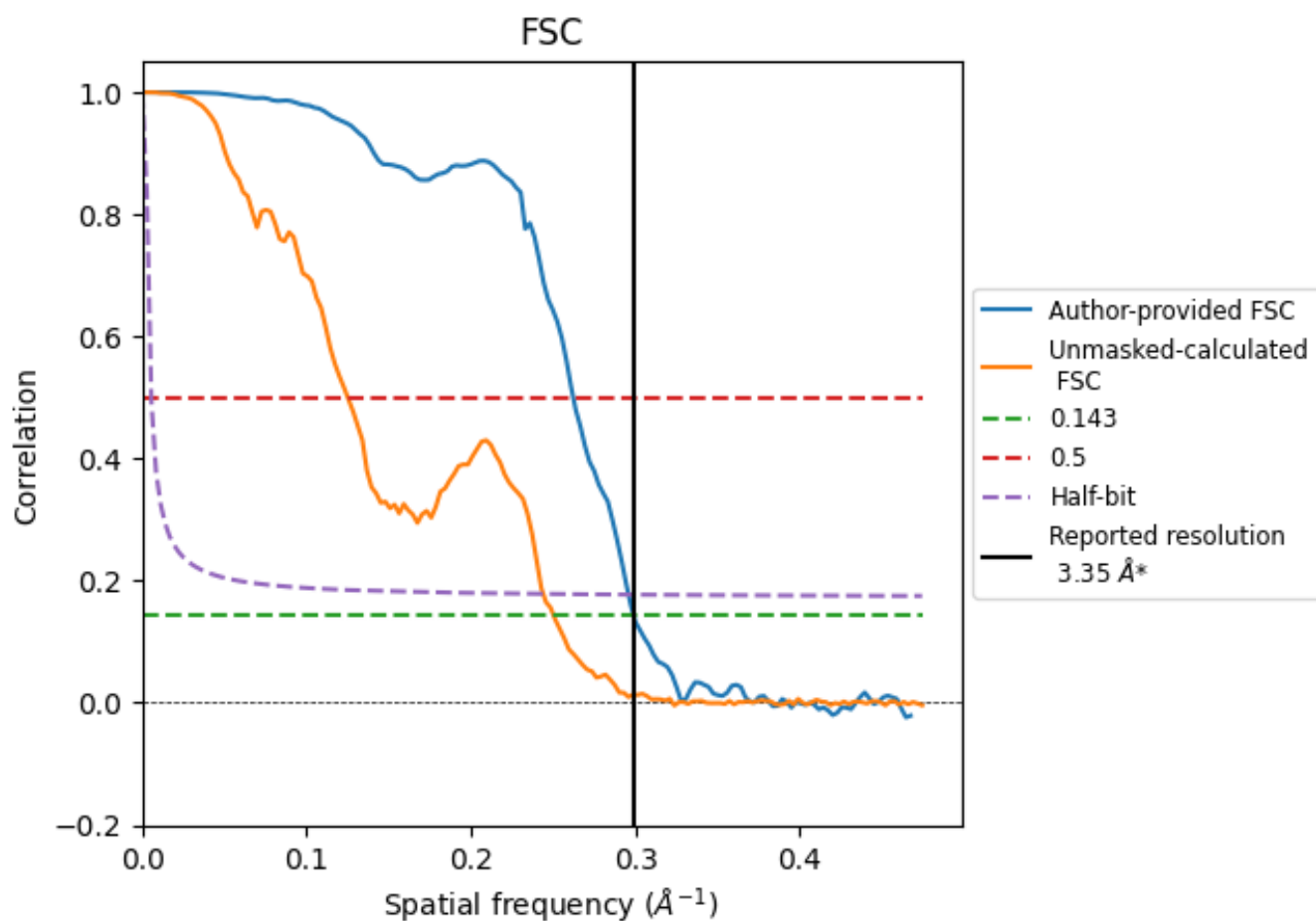


\*Reported resolution corresponds to spatial frequency of 0.299 Å<sup>-1</sup>

## 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 0.299  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

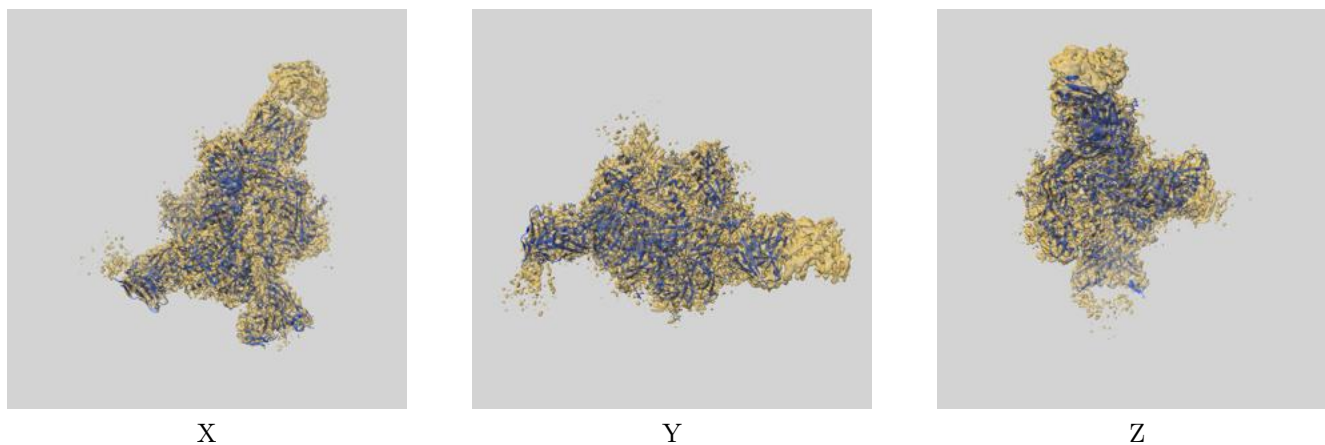
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.35	-	-
Author-provided FSC curve	3.35	3.81	3.38
Unmasked-calculated*	4.00	8.00	4.10

\*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 4.00 differs from the reported value 3.35 by more than 10 %

## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-46884 and PDB model 9DHW. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

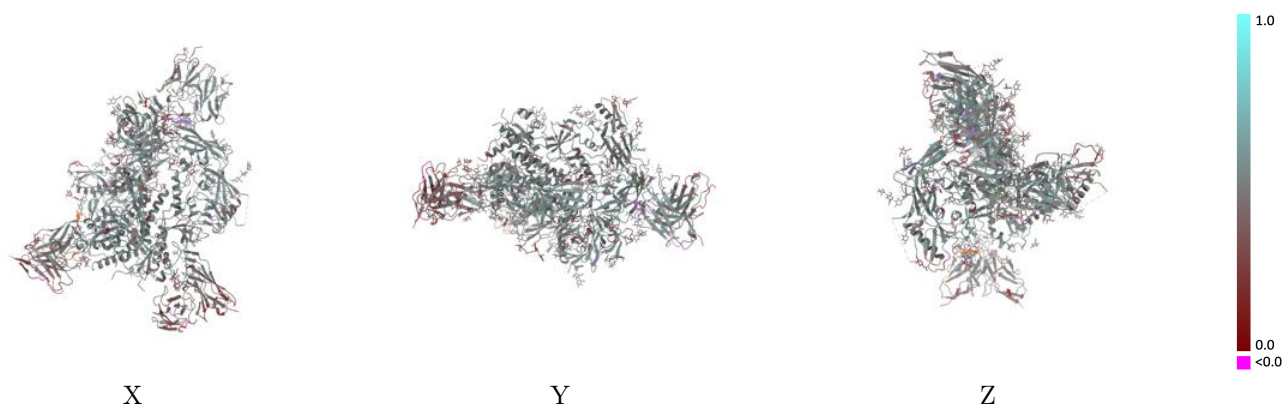
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.46 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.

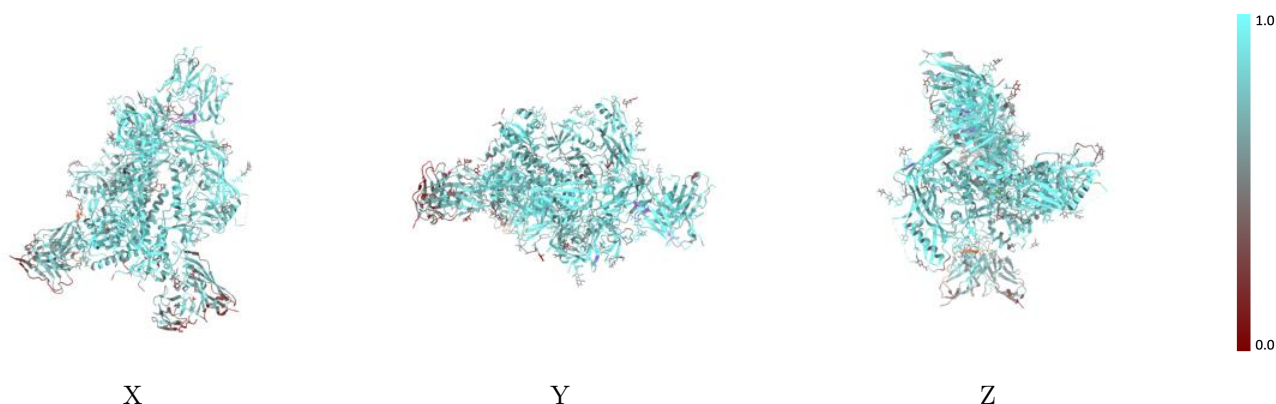


## 9.2 Q-score mapped to coordinate model [i](#)



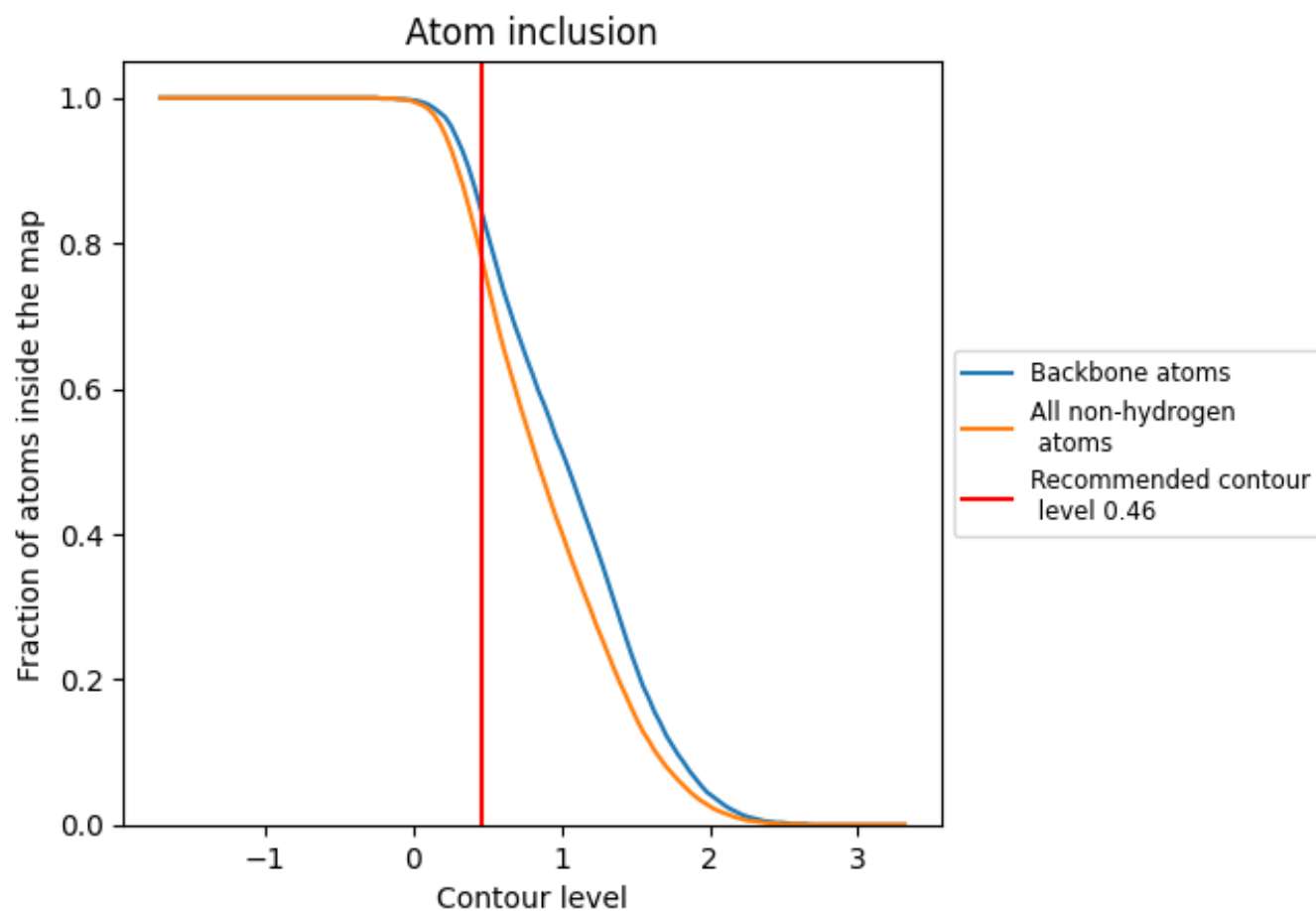
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.46).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 78% 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 (0.46) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7800	 0.4670
A	 0.8360	 0.4980
B	 0.8390	 0.5110
C	 0.8470	 0.5030
D	 0.8260	 0.5030
E	 0.6770	 0.4390
F	 0.5230	 0.3460
G	 0.8110	 0.4730
H	 0.6580	 0.3980
I	 0.8360	 0.4920
J	 0.7640	 0.4550
K	 0.6790	 0.4160
L	 0.5300	 0.3250
M	 0.8220	 0.4490
N	 0.8440	 0.4950
O	 0.5660	 0.4020
P	 0.6430	 0.3860
Q	 0.6920	 0.4640
R	 0.7140	 0.4110
S	 0.5900	 0.3570
T	 0.6250	 0.3670
U	 0.6670	 0.4490
V	 0.9020	 0.4940
W	 0.7210	 0.4630
X	 0.6070	 0.3290
Y	 0.5710	 0.4110
Z	 0.6430	 0.3890
a	 0.4290	 0.4330
b	 0.5850	 0.4030
c	 0.3210	 0.2560
d	 0.5360	 0.3530
e	 0.6430	 0.4170
f	 0.4900	 0.4110
g	 0.6070	 0.4130
h	 0.6670	 0.4440



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Chain	Atom inclusion	Q-score
i	 0.6070	 0.4280
j	 0.7860	 0.4970
k	 0.3570	 0.2880
l	 0.8570	 0.4690
m	 0.7140	 0.4240
n	 0.7860	 0.4230