



Full wwPDB EM Validation Report ⓘ

Nov 29, 2022 – 08:50 PM JST

PDB ID : 7X08
EMDB ID : EMD-32920
Title : S protein of SARS-CoV-2 in complex with 2G1
Authors : Guo, Y.Y.; Zhang, Y.Y.; Zhou, Q.
Deposited on : 2022-02-21
Resolution : 2.70 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:

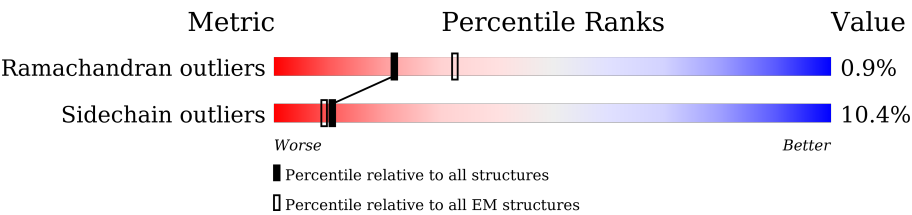
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.70 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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	1283	<div><div></div><div>77%9%14%</div></div>
1	B	1283	<div><div></div><div>77%9%14%</div></div>
1	C	1283	<div><div></div><div>77%9%14%</div></div>
2	H	452	<div><div>44%</div><div>44%53%</div></div>
2	I	452	<div><div>43%</div><div>44%53%</div></div>
2	J	452	<div><div>43%</div><div>44%53%</div></div>
3	L	216	<div><div>93%</div><div>87%10%..</div></div>
3	M	216	<div><div>95%</div><div>87%10%..</div></div>
3	N	216	<div><div>93%</div><div>87%10%..</div></div>

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Mol	Chain	Length	Quality of chain
4	D	2	100%
4	E	2	100%
4	F	2	50% 100%
4	G	2	50% 50%
4	K	2	50% 100%
4	O	2	100%
4	P	2	50% 50% 50%
4	Q	2	100% 100%
4	R	2	100%
4	S	2	50% 50% 50%
4	T	2	50% 100%
4	U	2	50% 50% 50%
4	V	2	50% 50% 50%
4	W	2	50% 50% 50%
4	X	2	50% 100%
4	Y	2	50% 50% 50%
4	Z	2	50% 50% 50%
4	a	2	50% 100%
4	b	2	50% 50% 50%
4	c	2	50% 100%
4	d	2	50% 50% 50%
4	e	2	50% 50% 50%
4	f	2	50% 100%
4	g	2	50% 50% 50%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 36396 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Spike glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1099	Total	C	N	O	S	0	0
			8595	5483	1436	1636	40		
1	B	1099	Total	C	N	O	S	0	0
			8595	5483	1436	1636	40		
1	C	1099	Total	C	N	O	S	0	0
			8595	5483	1436	1636	40		

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	817	PRO	PHE	engineered mutation	UNP P0DTC2
A	892	PRO	ALA	engineered mutation	UNP P0DTC2
A	899	PRO	ALA	engineered mutation	UNP P0DTC2
A	942	PRO	ALA	engineered mutation	UNP P0DTC2
A	986	PRO	LYS	engineered mutation	UNP P0DTC2
A	987	PRO	VAL	engineered mutation	UNP P0DTC2
A	1274	LEU	-	expression tag	UNP P0DTC2
A	1275	GLU	-	expression tag	UNP P0DTC2
A	1276	ASP	-	expression tag	UNP P0DTC2
A	1277	TYR	-	expression tag	UNP P0DTC2
A	1278	LYS	-	expression tag	UNP P0DTC2
A	1279	ASP	-	expression tag	UNP P0DTC2
A	1280	ASP	-	expression tag	UNP P0DTC2
A	1281	ASP	-	expression tag	UNP P0DTC2
A	1282	ASP	-	expression tag	UNP P0DTC2
A	1283	LYS	-	expression tag	UNP P0DTC2
B	817	PRO	PHE	engineered mutation	UNP P0DTC2
B	892	PRO	ALA	engineered mutation	UNP P0DTC2
B	899	PRO	ALA	engineered mutation	UNP P0DTC2
B	942	PRO	ALA	engineered mutation	UNP P0DTC2
B	986	PRO	LYS	engineered mutation	UNP P0DTC2
B	987	PRO	VAL	engineered mutation	UNP P0DTC2
B	1274	LEU	-	expression tag	UNP P0DTC2
B	1275	GLU	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1276	ASP	-	expression tag	UNP P0DTC2
B	1277	TYR	-	expression tag	UNP P0DTC2
B	1278	LYS	-	expression tag	UNP P0DTC2
B	1279	ASP	-	expression tag	UNP P0DTC2
B	1280	ASP	-	expression tag	UNP P0DTC2
B	1281	ASP	-	expression tag	UNP P0DTC2
B	1282	ASP	-	expression tag	UNP P0DTC2
B	1283	LYS	-	expression tag	UNP P0DTC2
C	817	PRO	PHE	engineered mutation	UNP P0DTC2
C	892	PRO	ALA	engineered mutation	UNP P0DTC2
C	899	PRO	ALA	engineered mutation	UNP P0DTC2
C	942	PRO	ALA	engineered mutation	UNP P0DTC2
C	986	PRO	LYS	engineered mutation	UNP P0DTC2
C	987	PRO	VAL	engineered mutation	UNP P0DTC2
C	1274	LEU	-	expression tag	UNP P0DTC2
C	1275	GLU	-	expression tag	UNP P0DTC2
C	1276	ASP	-	expression tag	UNP P0DTC2
C	1277	TYR	-	expression tag	UNP P0DTC2
C	1278	LYS	-	expression tag	UNP P0DTC2
C	1279	ASP	-	expression tag	UNP P0DTC2
C	1280	ASP	-	expression tag	UNP P0DTC2
C	1281	ASP	-	expression tag	UNP P0DTC2
C	1282	ASP	-	expression tag	UNP P0DTC2
C	1283	LYS	-	expression tag	UNP P0DTC2

- Molecule 2 is a protein called heavy chain of 2G1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	214	Total	C	N	O	S	0	0
			1603	1016	268	311	8		
2	I	214	Total	C	N	O	S	0	0
			1603	1016	268	311	8		
2	J	214	Total	C	N	O	S	0	0
			1603	1016	268	311	8		

- Molecule 3 is a protein called light chain of 2G1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L	211	Total	C	N	O	S	0	0
			1550	964	260	321	5		
3	M	211	Total	C	N	O	S	0	0
			1550	964	260	321	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	N	211	Total	C	N	O	S	0	0
			1550	964	260	321	5		

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



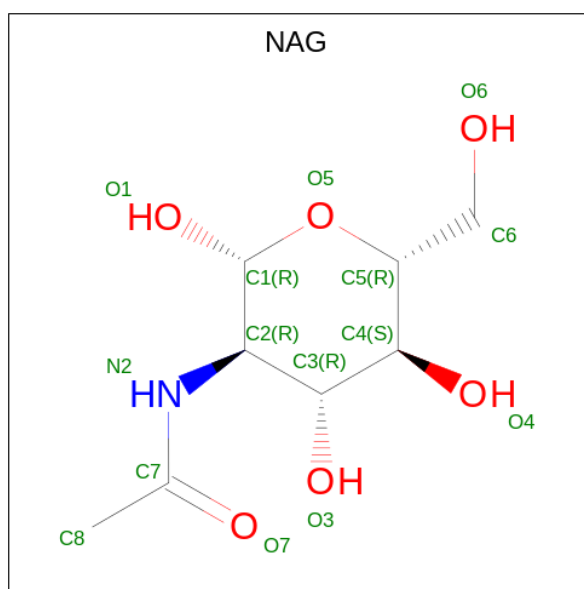
Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	2	Total	C	N	O		0	0
			28	16	2	10			
4	E	2	Total	C	N	O		0	0
			28	16	2	10			
4	F	2	Total	C	N	O		0	0
			28	16	2	10			
4	G	2	Total	C	N	O		0	0
			28	16	2	10			
4	K	2	Total	C	N	O		0	0
			28	16	2	10			
4	O	2	Total	C	N	O		0	0
			28	16	2	10			
4	P	2	Total	C	N	O		0	0
			28	16	2	10			
4	Q	2	Total	C	N	O		0	0
			28	16	2	10			
4	R	2	Total	C	N	O		0	0
			28	16	2	10			
4	S	2	Total	C	N	O		0	0
			28	16	2	10			
4	T	2	Total	C	N	O		0	0
			28	16	2	10			
4	U	2	Total	C	N	O		0	0
			28	16	2	10			
4	V	2	Total	C	N	O		0	0
			28	16	2	10			
4	W	2	Total	C	N	O		0	0
			28	16	2	10			
4	X	2	Total	C	N	O		0	0
			28	16	2	10			
4	Y	2	Total	C	N	O		0	0
			28	16	2	10			

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Mol	Chain	Residues	Atoms				AltConf	Trace
4	Z	2	Total	C	N	O	0	0
			28	16	2	10		
4	a	2	Total	C	N	O	0	0
			28	16	2	10		
4	b	2	Total	C	N	O	0	0
			28	16	2	10		
4	c	2	Total	C	N	O	0	0
			28	16	2	10		
4	d	2	Total	C	N	O	0	0
			28	16	2	10		
4	e	2	Total	C	N	O	0	0
			28	16	2	10		
4	f	2	Total	C	N	O	0	0
			28	16	2	10		
4	g	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
5	A	1	Total	C	N	O	0
			140	80	10	50	
5	A	1	Total	C	N	O	0
			140	80	10	50	
5	A	1	Total	C	N	O	0
			140	80	10	50	

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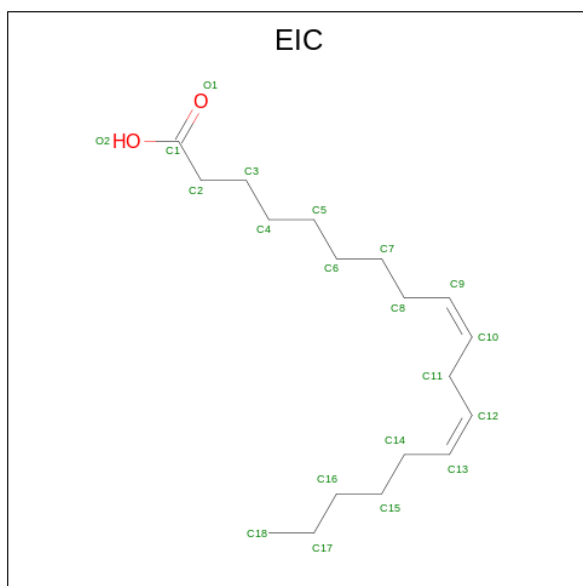
Mol	Chain	Residues	Atoms				AltConf
5	A	1	Total 140	C 80	N 10	O 50	0
5	A	1	Total 140	C 80	N 10	O 50	0
5	A	1	Total 140	C 80	N 10	O 50	0
5	A	1	Total 140	C 80	N 10	O 50	0
5	A	1	Total 140	C 80	N 10	O 50	0
5	A	1	Total 140	C 80	N 10	O 50	0
5	A	1	Total 140	C 80	N 10	O 50	0
5	B	1	Total 140	C 80	N 10	O 50	0
5	B	1	Total 140	C 80	N 10	O 50	0
5	B	1	Total 140	C 80	N 10	O 50	0
5	B	1	Total 140	C 80	N 10	O 50	0
5	B	1	Total 140	C 80	N 10	O 50	0
5	B	1	Total 140	C 80	N 10	O 50	0
5	B	1	Total 140	C 80	N 10	O 50	0
5	B	1	Total 140	C 80	N 10	O 50	0
5	B	1	Total 140	C 80	N 10	O 50	0
5	B	1	Total 140	C 80	N 10	O 50	0
5	C	1	Total 140	C 80	N 10	O 50	0
5	C	1	Total 140	C 80	N 10	O 50	0
5	C	1	Total 140	C 80	N 10	O 50	0
5	C	1	Total 140	C 80	N 10	O 50	0

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Mol	Chain	Residues	Atoms				AltConf
5	C	1	Total	C	N	O	0
			140	80	10	50	
5	C	1	Total	C	N	O	0
			140	80	10	50	
5	C	1	Total	C	N	O	0
			140	80	10	50	
5	C	1	Total	C	N	O	0
			140	80	10	50	
5	C	1	Total	C	N	O	0
			140	80	10	50	
5	C	1	Total	C	N	O	0
			140	80	10	50	

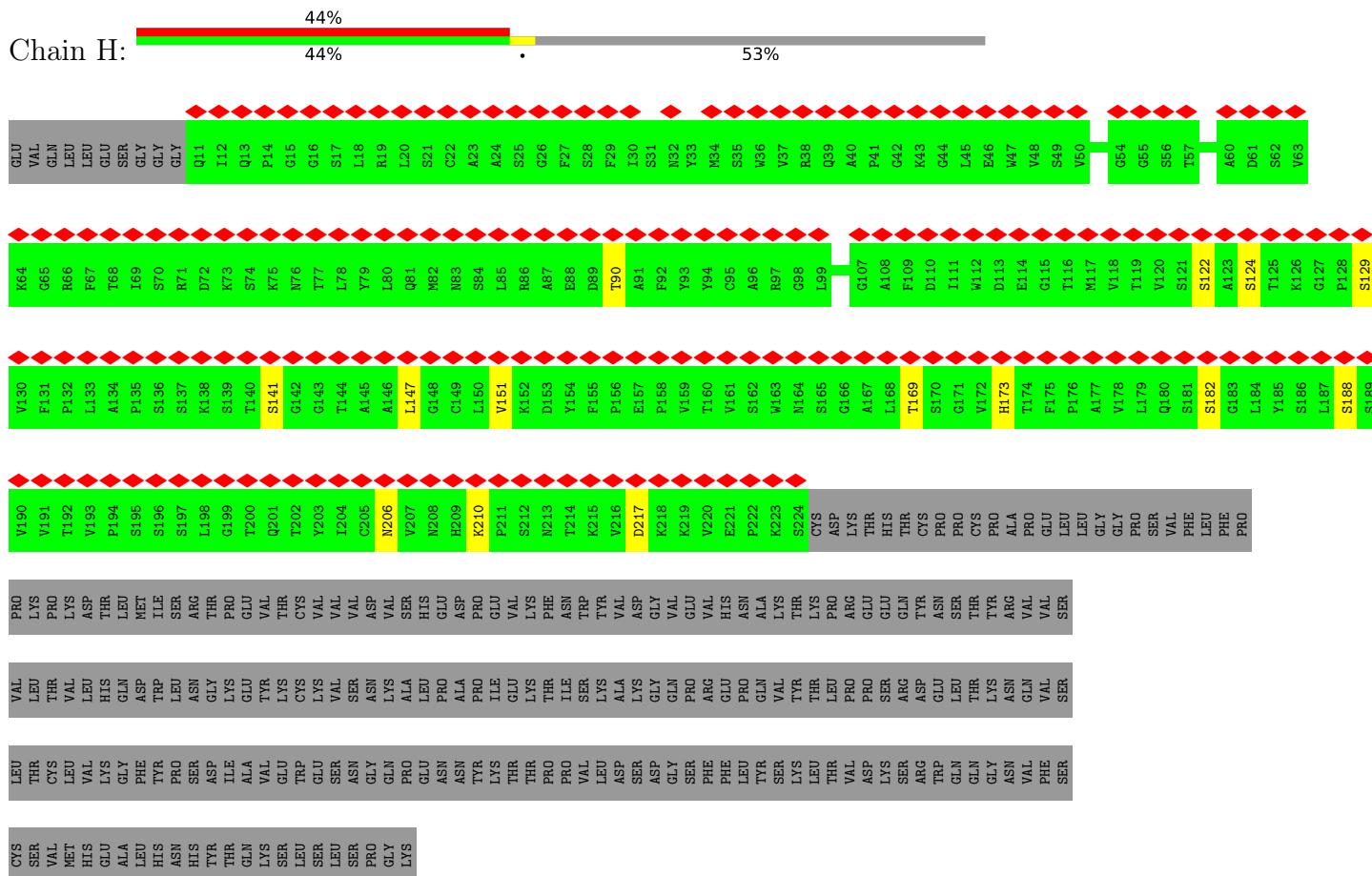
- Molecule 6 is LINOLEIC ACID (three-letter code: EIC) (formula: $C_{18}H_{32}O_2$) (labeled as "Ligand of Interest" by depositor).



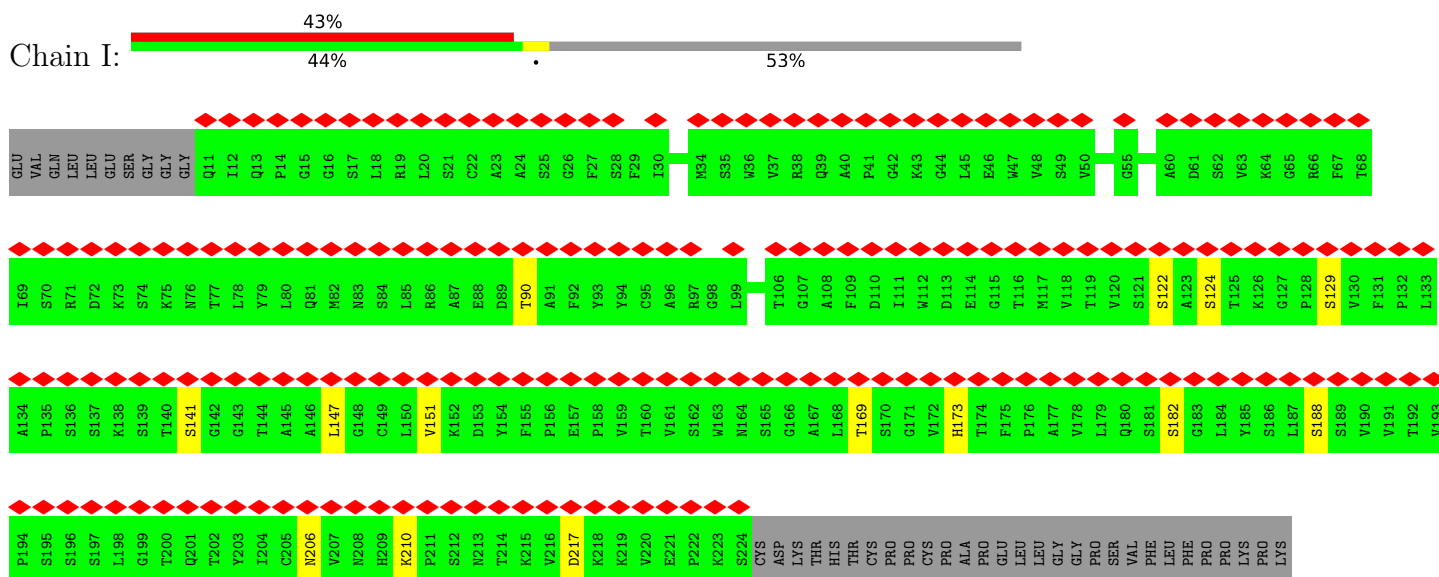
Mol	Chain	Residues	Atoms			AltConf
6	A	1	Total	C	O	0
			40	36	4	
6	A	1	Total	C	O	0
			40	36	4	
6	B	1	Total	C	O	0
			20	18	2	



- Molecule 2: heavy chain of 2G1

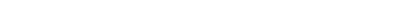


- Molecule 2: heavy chain of 2G1



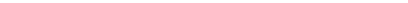
[illegible]

- Molecule 2: heavy chain of 2G1

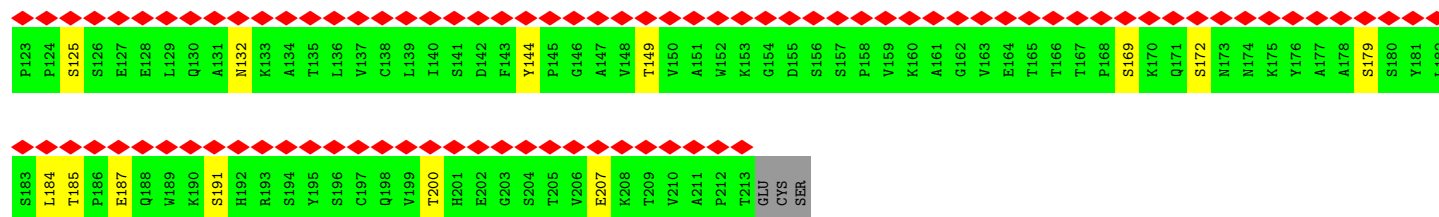
Chain J: 

VAL	GLU	GLN	LEU	GLU	SER	GLY	GLY	Q11	I12	Q13	P14	G15	G16	S17	L18	R19	L20	S21	C22	A23	A24	S25	G26	F27	S28	F29	I30	S31	N32	Y33	N34	S35	N36	V37	Q38	Q39	A40	P41	G42	K43	G44	L45	E46	W47	V48	S49	V50	S53	G54	G55	A60	D61	S62	V63	K64
GLU	VAL	GLN	LEU	GLU	SER	GLY	GLY	Q11	I12	Q13	P14	G15	G16	S17	L18	R19	L20	S21	C22	A23	A24	S25	G26	F27	S28	F29	I30	S31	N32	Y33	N34	S35	N36	V37	Q38	Q39	A40	P41	G42	K43	G44	L45	E46	W47	V48	S49	V50	S53	G54	G55	A60	D61	S62	V63	K64
GLU	VAL	GLN	LEU	GLU	SER	GLY	GLY	Q11	I12	Q13	P14	G15	G16	S17	L18	R19	L20	S21	C22	A23	A24	S25	G26	F27	S28	F29	I30	S31	N32	Y33	N34	S35	N36	V37	Q38	Q39	A40	P41	G42	K43	G44	L45	E46	W47	V48	S49	V50	S53	G54	G55	A60	D61	S62	V63	K64
GLU	VAL	GLN	LEU	GLU	SER	GLY	GLY	Q11	I12	Q13	P14	G15	G16	S17	L18	R19	L20	S21	C22	A23	A24	S25	G26	F27	S28	F29	I30	S31	N32	Y33	N34	S35	N36	V37	Q38	Q39	A40	P41	G42	K43	G44	L45	E46	W47	V48	S49	V50	S53	G54	G55	A60	D61	S62	V63	K64
GLU	VAL	GLN	LEU	GLU	SER	GLY	GLY	Q11	I12	Q13	P14	G15	G16	S17	L18	R19	L20	S21	C22	A23	A24	S25	G26	F27	S28	F29	I30	S31	N32	Y33	N34	S35	N36	V37	Q38	Q39	A40	P41	G42	K43	G44	L45	E46	W47	V48	S49	V50	S53	G54	G55	A60	D61	S62	V63	K64
GLU	VAL	GLN	LEU	GLU	SER	GLY	GLY	Q11	I12	Q13	P14	G15	G16	S17	L18	R19	L20	S21	C22	A23	A24	S25	G26	F27	S28	F29	I30	S31	N32	Y33	N34	S35	N36	V37	Q38	Q39	A40	P41	G42	K43	G44	L45	E46	W47	V48	S49	V50	S53	G54	G55	A60	D61	S62	V63	K64
GLU	VAL	GLN	LEU	GLU	SER	GLY	GLY	Q11	I12	Q13	P14	G15	G16	S17	L18	R19	L20	S21	C22	A23	A24	S25	G26	F27	S28	F29	I30	S31	N32	Y33	N34	S35	N36	V37	Q38	Q39	A40	P41	G42	K43	G44	L45	E46	W47	V48	S49	V50	S53	G54	G55	A60	D61	S62	V63	K64
GLU	VAL	GLN	LEU	GLU	SER	GLY	GLY	Q11	I12	Q13	P14	G15	G16	S17	L18	R19	L20	S21	C22	A23	A24	S25	G26	F27	S28	F29	I30	S31	N32	Y33	N34	S35	N36	V37	Q38	Q39	A40	P41	G42	K43	G44	L45	E46	W47	V48	S49	V50	S53	G54	G55	A60	D61	S62	V63	K64
GLU	VAL	GLN	LEU	GLU	SER	GLY	GLY	Q11	I12	Q13	P14	G15	G16	S17	L18	R19	L20	S21	C22	A23	A24	S25	G26	F27	S28	F29	I30	S31	N32	Y33	N34	S35	N36	V37	Q38	Q39	A40	P41	G42	K43	G44	L45	E46	W47	V48	S49	V50	S53	G54	G55	A60	D61	S62	V63	K64
GLU	VAL	GLN	LEU	GLU	SER	GLY	GLY	Q11	I12	Q13	P14	G15	G16	S17	L18	R19	L20	S21	C22	A23	A24	S25	G26	F27	S28	F29	I30	S31	N32	Y33	N34	S35	N36	V37	Q38	Q39	A40	P41	G42	K43	G44	L45	E46	W47	V48	S49	V50	S53	G54	G55	A60	D61	S62	V63	K64
GLU	VAL	GLN	LEU	GLU	SER	GLY	GLY	Q11	I12	Q13	P14	G15																																											

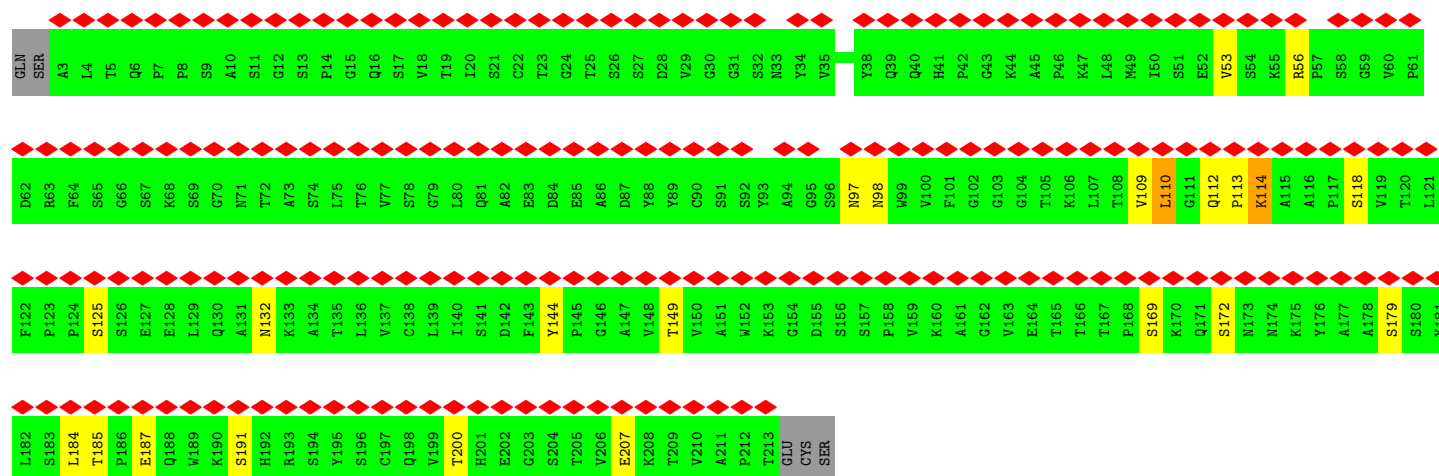
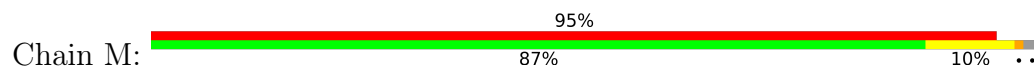
- Molecule 3: light chain of 2G1

Chain L:  93% 87% 10%

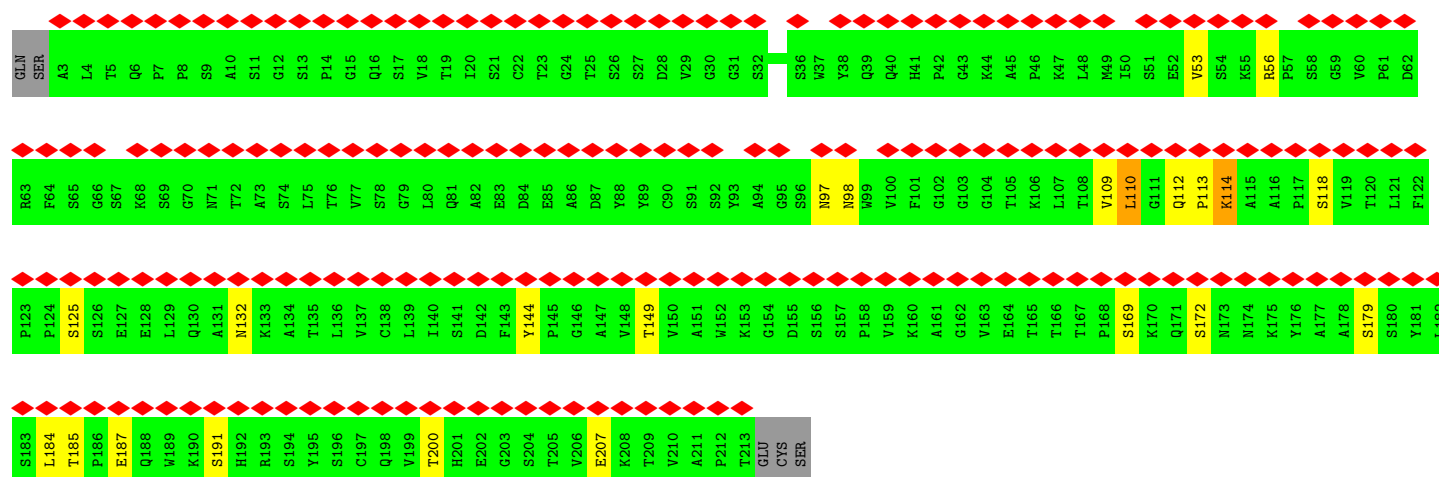
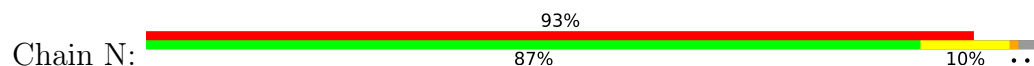
D62	R63	F64	S65	G66	P67	K68	S69	G70	M71	S74	L75	T76	V77	S78	G79	L80	Q81	A82	E83	D84	E85	A86	D87	V88	Y89	C90	S91	S92	Y93	A94	G95	S96	N97	N98	Y99	V100	F101	G102	G103	G104	T105	K106	L107	T108	V109	L110	G111	Q112	P113	K114	A115	A116	P117	S118	V119	T120	L121	L122
A3	L4	T5	P6	Q7	P8	S9	A10	S11	G12	S13	P14	G15	Q16	S17	V18	T19	S20	S21	C22	T23	G24	T25	S26	S27	V28	S29	G30	G31	S32	N33	Y34	V35	Y36	Y37	Y38	Q39	F40	H41	P42	G43	K44	A45	P46	K47	L48	W49	L50	S51	E52	Y53	S54	K55	Y56	P57	S58	G59	V60	P61



• Molecule 3: light chain of 2G1



• Molecule 3: light chain of 2G1



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





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

Chain E:  100%



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

Chain F:  50% 100%



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

Chain G:  50% 50%



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

Chain K:  50% 100%



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

Chain O:  100%



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

Chain P:  50% 50%



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



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



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



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



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



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





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



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



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



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



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



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



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



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



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



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



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



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	349830	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.225	Depositor
Minimum map value	-0.112	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.025	Depositor
Map size (Å)	313.056, 313.056, 313.056	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.087, 1.087, 1.087	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: EIC, NAG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.45	0/8797	0.52	0/11975
1	B	0.45	0/8797	0.51	0/11975
1	C	0.45	0/8797	0.51	0/11975
2	H	0.46	0/1641	0.58	0/2229
2	I	0.46	0/1641	0.58	0/2229
2	J	0.46	0/1641	0.58	0/2229
3	L	0.44	0/1589	0.56	0/2169
3	M	0.44	0/1589	0.56	0/2169
3	N	0.44	0/1589	0.56	0/2169
All	All	0.45	0/36081	0.53	0/49119

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	1089/1283 (85%)	1011 (93%)	72 (7%)	6 (1%)	25	50
1	B	1089/1283 (85%)	1011 (93%)	73 (7%)	5 (0%)	29	54
1	C	1089/1283 (85%)	1013 (93%)	71 (6%)	5 (0%)	29	54
2	H	212/452 (47%)	185 (87%)	26 (12%)	1 (0%)	29	54
2	I	212/452 (47%)	185 (87%)	26 (12%)	1 (0%)	29	54
2	J	212/452 (47%)	185 (87%)	26 (12%)	1 (0%)	29	54
3	L	209/216 (97%)	172 (82%)	29 (14%)	8 (4%)	3	7
3	M	209/216 (97%)	172 (82%)	29 (14%)	8 (4%)	3	7
3	N	209/216 (97%)	172 (82%)	29 (14%)	8 (4%)	3	7
All	All	4530/5853 (77%)	4106 (91%)	381 (8%)	43 (1%)	21	40

All (43) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	67	ALA
1	B	67	ALA
1	C	67	ALA
3	L	53	VAL
3	L	112	GLN
3	L	144	TYR
3	M	53	VAL
3	M	112	GLN
3	M	144	TYR
3	N	53	VAL
3	N	112	GLN
3	N	144	TYR
1	A	360	ASN
1	B	360	ASN
1	C	360	ASN
1	A	939	SER
1	B	939	SER
1	C	939	SER
2	H	124	SER
2	I	124	SER
2	J	124	SER
3	L	110	LEU
3	L	114	LYS

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Mol	Chain	Res	Type
3	M	109	VAL
3	M	110	LEU
3	M	114	LYS
3	N	110	LEU
3	N	114	LYS
1	A	936	ASP
1	B	936	ASP
1	C	936	ASP
3	L	109	VAL
3	N	109	VAL
1	A	515	PHE
3	L	98	ASN
3	L	113	PRO
3	M	98	ASN
3	M	113	PRO
3	N	98	ASN
3	N	113	PRO
1	A	251	PRO
1	B	251	PRO
1	C	251	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	959/1125 (85%)	851 (89%)	108 (11%)	6	13
1	B	959/1125 (85%)	854 (89%)	105 (11%)	6	14
1	C	959/1125 (85%)	852 (89%)	107 (11%)	6	13
2	H	180/398 (45%)	167 (93%)	13 (7%)	14	34
2	I	180/398 (45%)	167 (93%)	13 (7%)	14	34
2	J	180/398 (45%)	167 (93%)	13 (7%)	14	34
3	L	175/180 (97%)	158 (90%)	17 (10%)	8	19
3	M	175/180 (97%)	158 (90%)	17 (10%)	8	19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	N	175/180 (97%)	158 (90%)	17 (10%)	8	19
All	All	3942/5109 (77%)	3532 (90%)	410 (10%)	10	16

All (410) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	THR
1	A	31	SER
1	A	40	ASP
1	A	47	VAL
1	A	51	THR
1	A	53	ASP
1	A	66	HIS
1	A	79	PHE
1	A	94	SER
1	A	96	GLU
1	A	108	THR
1	A	118	LEU
1	A	124	THR
1	A	131	CYS
1	A	147	LYS
1	A	153	MET
1	A	156	GLU
1	A	162	SER
1	A	166	CYS
1	A	173	GLN
1	A	178	ASP
1	A	185	ASN
1	A	197	ILE
1	A	198	ASP
1	A	205	SER
1	A	208	THR
1	A	212	LEU
1	A	215	ASP
1	A	221	SER
1	A	247	SER
1	A	255	SER
1	A	259	THR
1	A	271	GLN
1	A	277	LEU
1	A	281	GLU
1	A	299	THR

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Mol	Chain	Res	Type
1	A	305	SER
1	A	317	ASN
1	A	325	SER
1	A	333	THR
1	A	342	PHE
1	A	355	ARG
1	A	357	ARG
1	A	359	SER
1	A	362	VAL
1	A	371	SER
1	A	373	SER
1	A	376	THR
1	A	386	LYS
1	A	389	ASP
1	A	421	TYR
1	A	459	SER
1	A	469	SER
1	A	477	SER
1	A	513	LEU
1	A	516	GLU
1	A	528	LYS
1	A	530	SER
1	A	531	THR
1	A	534	VAL
1	A	544	ASN
1	A	569	ILE
1	A	586	ASP
1	A	588	THR
1	A	590	CYS
1	A	599	THR
1	A	604	THR
1	A	606	ASN
1	A	614	ASP
1	A	617	CYS
1	A	638	THR
1	A	642	VAL
1	A	645	THR
1	A	657	ASN
1	A	675	GLN
1	A	676	THR
1	A	691	SER
1	A	708	SER

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Mol	Chain	Res	Type
1	A	710	ASN
1	A	719	THR
1	A	723	THR
1	A	726	ILE
1	A	730	SER
1	A	732	THR
1	A	735	SER
1	A	745	ASP
1	A	746	SER
1	A	761	THR
1	A	780	GLU
1	A	790	LYS
1	A	810	SER
1	A	814	LYS
1	A	881	THR
1	A	884	SER
1	A	886	TRP
1	A	962	LEU
1	A	964	LYS
1	A	974	SER
1	A	982	SER
1	A	991	VAL
1	A	1002	GLN
1	A	1030	SER
1	A	1092	GLU
1	A	1097	SER
1	A	1118	ASP
1	A	1128	VAL
1	A	1136	THR
1	A	1142	GLN
1	B	19	THR
1	B	31	SER
1	B	40	ASP
1	B	47	VAL
1	B	51	THR
1	B	53	ASP
1	B	66	HIS
1	B	94	SER
1	B	96	GLU
1	B	108	THR
1	B	118	LEU
1	B	124	THR

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Mol	Chain	Res	Type
1	B	131	CYS
1	B	147	LYS
1	B	156	GLU
1	B	162	SER
1	B	166	CYS
1	B	173	GLN
1	B	178	ASP
1	B	185	ASN
1	B	197	ILE
1	B	198	ASP
1	B	205	SER
1	B	208	THR
1	B	212	LEU
1	B	215	ASP
1	B	221	SER
1	B	247	SER
1	B	255	SER
1	B	259	THR
1	B	271	GLN
1	B	277	LEU
1	B	281	GLU
1	B	299	THR
1	B	305	SER
1	B	317	ASN
1	B	325	SER
1	B	333	THR
1	B	355	ARG
1	B	357	ARG
1	B	359	SER
1	B	362	VAL
1	B	373	SER
1	B	376	THR
1	B	386	LYS
1	B	389	ASP
1	B	421	TYR
1	B	459	SER
1	B	469	SER
1	B	477	SER
1	B	513	LEU
1	B	516	GLU
1	B	518	LEU
1	B	528	LYS

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Mol	Chain	Res	Type
1	B	530	SER
1	B	531	THR
1	B	534	VAL
1	B	544	ASN
1	B	569	ILE
1	B	586	ASP
1	B	588	THR
1	B	590	CYS
1	B	599	THR
1	B	604	THR
1	B	606	ASN
1	B	614	ASP
1	B	617	CYS
1	B	638	THR
1	B	642	VAL
1	B	645	THR
1	B	657	ASN
1	B	675	GLN
1	B	676	THR
1	B	691	SER
1	B	708	SER
1	B	710	ASN
1	B	719	THR
1	B	723	THR
1	B	726	ILE
1	B	730	SER
1	B	732	THR
1	B	735	SER
1	B	745	ASP
1	B	746	SER
1	B	761	THR
1	B	780	GLU
1	B	790	LYS
1	B	810	SER
1	B	814	LYS
1	B	881	THR
1	B	884	SER
1	B	886	TRP
1	B	962	LEU
1	B	964	LYS
1	B	974	SER
1	B	982	SER

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Mol	Chain	Res	Type
1	B	991	VAL
1	B	1002	GLN
1	B	1030	SER
1	B	1092	GLU
1	B	1097	SER
1	B	1118	ASP
1	B	1128	VAL
1	B	1136	THR
1	B	1142	GLN
1	C	19	THR
1	C	31	SER
1	C	40	ASP
1	C	47	VAL
1	C	51	THR
1	C	53	ASP
1	C	66	HIS
1	C	79	PHE
1	C	94	SER
1	C	96	GLU
1	C	108	THR
1	C	118	LEU
1	C	124	THR
1	C	131	CYS
1	C	147	LYS
1	C	156	GLU
1	C	162	SER
1	C	166	CYS
1	C	173	GLN
1	C	178	ASP
1	C	185	ASN
1	C	197	ILE
1	C	198	ASP
1	C	205	SER
1	C	208	THR
1	C	212	LEU
1	C	215	ASP
1	C	221	SER
1	C	247	SER
1	C	255	SER
1	C	259	THR
1	C	271	GLN
1	C	277	LEU

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Mol	Chain	Res	Type
1	C	281	GLU
1	C	299	THR
1	C	305	SER
1	C	317	ASN
1	C	325	SER
1	C	333	THR
1	C	355	ARG
1	C	357	ARG
1	C	359	SER
1	C	362	VAL
1	C	371	SER
1	C	373	SER
1	C	376	THR
1	C	386	LYS
1	C	389	ASP
1	C	421	TYR
1	C	459	SER
1	C	469	SER
1	C	477	SER
1	C	513	LEU
1	C	516	GLU
1	C	518	LEU
1	C	530	SER
1	C	531	THR
1	C	534	VAL
1	C	544	ASN
1	C	569	ILE
1	C	586	ASP
1	C	588	THR
1	C	590	CYS
1	C	599	THR
1	C	604	THR
1	C	606	ASN
1	C	614	ASP
1	C	617	CYS
1	C	638	THR
1	C	642	VAL
1	C	645	THR
1	C	657	ASN
1	C	675	GLN
1	C	676	THR
1	C	691	SER

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Mol	Chain	Res	Type
1	C	708	SER
1	C	710	ASN
1	C	719	THR
1	C	723	THR
1	C	726	ILE
1	C	730	SER
1	C	732	THR
1	C	735	SER
1	C	745	ASP
1	C	746	SER
1	C	761	THR
1	C	780	GLU
1	C	790	LYS
1	C	810	SER
1	C	814	LYS
1	C	881	THR
1	C	884	SER
1	C	886	TRP
1	C	894	LEU
1	C	962	LEU
1	C	964	LYS
1	C	974	SER
1	C	982	SER
1	C	991	VAL
1	C	1002	GLN
1	C	1030	SER
1	C	1092	GLU
1	C	1097	SER
1	C	1118	ASP
1	C	1128	VAL
1	C	1136	THR
1	C	1142	GLN
2	H	90	THR
2	H	122	SER
2	H	129	SER
2	H	141	SER
2	H	147	LEU
2	H	151	VAL
2	H	169	THR
2	H	173	HIS
2	H	182	SER
2	H	188	SER

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Mol	Chain	Res	Type
2	H	206	ASN
2	H	210	LYS
2	H	217	ASP
3	L	56	ARG
3	L	97	ASN
3	L	110	LEU
3	L	114	LYS
3	L	118	SER
3	L	125	SER
3	L	132	ASN
3	L	149	THR
3	L	169	SER
3	L	172	SER
3	L	179	SER
3	L	184	LEU
3	L	185	THR
3	L	187	GLU
3	L	191	SER
3	L	200	THR
3	L	207	GLU
2	I	90	THR
2	I	122	SER
2	I	129	SER
2	I	141	SER
2	I	147	LEU
2	I	151	VAL
2	I	169	THR
2	I	173	HIS
2	I	182	SER
2	I	188	SER
2	I	206	ASN
2	I	210	LYS
2	I	217	ASP
3	M	56	ARG
3	M	97	ASN
3	M	110	LEU
3	M	114	LYS
3	M	118	SER
3	M	125	SER
3	M	132	ASN
3	M	149	THR
3	M	169	SER

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Mol	Chain	Res	Type
3	M	172	SER
3	M	179	SER
3	M	184	LEU
3	M	185	THR
3	M	187	GLU
3	M	191	SER
3	M	200	THR
3	M	207	GLU
2	J	90	THR
2	J	122	SER
2	J	129	SER
2	J	141	SER
2	J	147	LEU
2	J	151	VAL
2	J	169	THR
2	J	173	HIS
2	J	182	SER
2	J	188	SER
2	J	206	ASN
2	J	210	LYS
2	J	217	ASP
3	N	56	ARG
3	N	97	ASN
3	N	110	LEU
3	N	114	LYS
3	N	118	SER
3	N	125	SER
3	N	132	ASN
3	N	149	THR
3	N	169	SER
3	N	172	SER
3	N	179	SER
3	N	184	LEU
3	N	185	THR
3	N	187	GLU
3	N	191	SER
3	N	200	THR
3	N	207	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (102) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	66	HIS
1	A	69	HIS
1	A	183	GLN
1	A	188	ASN
1	A	207	HIS
1	A	239	GLN
1	A	314	GLN
1	A	317	ASN
1	A	414	GLN
1	A	422	ASN
1	A	450	ASN
1	A	532	ASN
1	A	544	ASN
1	A	556	ASN
1	A	564	GLN
1	A	606	ASN
1	A	613	GLN
1	A	675	GLN
1	A	710	ASN
1	A	751	ASN
1	A	804	GLN
1	A	856	ASN
1	A	919	ASN
1	A	925	ASN
1	A	1023	ASN
1	A	1036	GLN
1	A	1054	GLN
1	A	1064	HIS
1	A	1125	ASN
1	B	66	HIS
1	B	69	HIS
1	B	183	GLN
1	B	188	ASN
1	B	207	HIS
1	B	239	GLN
1	B	314	GLN
1	B	317	ASN
1	B	414	GLN
1	B	422	ASN
1	B	450	ASN
1	B	532	ASN
1	B	544	ASN
1	B	556	ASN

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Mol	Chain	Res	Type
1	B	564	GLN
1	B	606	ASN
1	B	613	GLN
1	B	675	GLN
1	B	710	ASN
1	B	751	ASN
1	B	804	GLN
1	B	856	ASN
1	B	919	ASN
1	B	925	ASN
1	B	1023	ASN
1	B	1036	GLN
1	B	1054	GLN
1	B	1064	HIS
1	B	1125	ASN
1	C	66	HIS
1	C	69	HIS
1	C	183	GLN
1	C	188	ASN
1	C	207	HIS
1	C	239	GLN
1	C	314	GLN
1	C	317	ASN
1	C	414	GLN
1	C	422	ASN
1	C	450	ASN
1	C	532	ASN
1	C	544	ASN
1	C	556	ASN
1	C	564	GLN
1	C	606	ASN
1	C	613	GLN
1	C	675	GLN
1	C	710	ASN
1	C	751	ASN
1	C	804	GLN
1	C	856	ASN
1	C	919	ASN
1	C	925	ASN
1	C	1023	ASN
1	C	1036	GLN
1	C	1054	GLN

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Mol	Chain	Res	Type
1	C	1064	HIS
1	C	1125	ASN
2	H	81	GLN
3	L	6	GLN
3	L	40	GLN
3	L	98	ASN
3	L	198	GLN
2	I	81	GLN
3	M	6	GLN
3	M	40	GLN
3	M	98	ASN
3	M	198	GLN
2	J	81	GLN
3	N	6	GLN
3	N	40	GLN
3	N	98	ASN
3	N	198	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

48 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	D	1	1,4	14,14,15	1.16	1 (7%)	17,19,21	0.60	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	D	2	4	14,14,15	2.27	2 (14%)	17,19,21	0.98	2 (11%)
4	NAG	E	1	1,4	14,14,15	0.31	0	17,19,21	0.62	0
4	NAG	E	2	4	14,14,15	0.53	0	17,19,21	0.47	0
4	NAG	F	1	1,4	14,14,15	0.70	1 (7%)	17,19,21	0.69	0
4	NAG	F	2	4	14,14,15	0.41	0	17,19,21	1.40	3 (17%)
4	NAG	G	1	1,4	14,14,15	0.72	1 (7%)	17,19,21	0.67	0
4	NAG	G	2	4	14,14,15	0.29	0	17,19,21	0.65	0
4	NAG	K	1	1,4	14,14,15	1.16	1 (7%)	17,19,21	0.61	0
4	NAG	K	2	4	14,14,15	2.27	2 (14%)	17,19,21	0.97	2 (11%)
4	NAG	O	1	1,4	14,14,15	0.31	0	17,19,21	0.62	0
4	NAG	O	2	4	14,14,15	0.53	0	17,19,21	0.47	0
4	NAG	P	1	1,4	14,14,15	0.72	1 (7%)	17,19,21	0.67	0
4	NAG	P	2	4	14,14,15	0.29	0	17,19,21	0.65	0
4	NAG	Q	1	1,4	14,14,15	1.14	1 (7%)	17,19,21	0.61	0
4	NAG	Q	2	4	14,14,15	2.27	2 (14%)	17,19,21	0.98	2 (11%)
4	NAG	R	1	1,4	14,14,15	0.30	0	17,19,21	0.61	0
4	NAG	R	2	4	14,14,15	0.51	0	17,19,21	0.48	0
4	NAG	S	1	1,4	14,14,15	0.71	1 (7%)	17,19,21	0.67	0
4	NAG	S	2	4	14,14,15	0.31	0	17,19,21	0.65	0
4	NAG	T	1	1,4	14,14,15	0.41	0	17,19,21	1.16	2 (11%)
4	NAG	T	2	4	14,14,15	0.40	0	17,19,21	1.16	2 (11%)
4	NAG	U	1	1,4	14,14,15	0.29	0	17,19,21	0.63	0
4	NAG	U	2	4	14,14,15	0.40	0	17,19,21	1.16	2 (11%)
4	NAG	V	1	1,4	14,14,15	0.37	0	17,19,21	0.72	0
4	NAG	V	2	4	14,14,15	0.31	0	17,19,21	1.31	2 (11%)
4	NAG	W	1	1,4	14,14,15	0.24	0	17,19,21	0.68	1 (5%)
4	NAG	W	2	4	14,14,15	0.17	0	17,19,21	0.47	0
4	NAG	X	1	1,4	14,14,15	0.41	0	17,19,21	1.16	2 (11%)
4	NAG	X	2	4	14,14,15	0.41	0	17,19,21	1.18	2 (11%)
4	NAG	Y	1	1,4	14,14,15	0.29	0	17,19,21	0.63	0
4	NAG	Y	2	4	14,14,15	0.41	0	17,19,21	1.16	1 (5%)
4	NAG	Z	1	1,4	14,14,15	0.36	0	17,19,21	0.72	0
4	NAG	Z	2	4	14,14,15	0.29	0	17,19,21	1.32	2 (11%)
4	NAG	a	1	1,4	14,14,15	0.71	1 (7%)	17,19,21	0.70	0
4	NAG	a	2	4	14,14,15	0.40	0	17,19,21	1.41	3 (17%)
4	NAG	b	1	1,4	14,14,15	0.25	0	17,19,21	0.69	1 (5%)
4	NAG	b	2	4	14,14,15	0.16	0	17,19,21	0.47	0
4	NAG	c	1	1,4	14,14,15	0.41	0	17,19,21	1.17	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	c	2	4	14,14,15	0.42	0	17,19,21	1.18	2 (11%)
4	NAG	d	1	1,4	14,14,15	0.28	0	17,19,21	0.62	0
4	NAG	d	2	4	14,14,15	0.42	0	17,19,21	1.16	2 (11%)
4	NAG	e	1	1,4	14,14,15	0.36	0	17,19,21	0.73	0
4	NAG	e	2	4	14,14,15	0.29	0	17,19,21	1.32	2 (11%)
4	NAG	f	1	1,4	14,14,15	0.70	1 (7%)	17,19,21	0.69	0
4	NAG	f	2	4	14,14,15	0.41	0	17,19,21	1.41	3 (17%)
4	NAG	g	1	1,4	14,14,15	0.25	0	17,19,21	0.67	1 (5%)
4	NAG	g	2	4	14,14,15	0.16	0	17,19,21	0.46	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
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	NAG	E	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	E	2	4	-	2/6/23/26	0/1/1/1
4	NAG	F	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	F	2	4	-	5/6/23/26	0/1/1/1
4	NAG	G	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	G	2	4	-	3/6/23/26	0/1/1/1
4	NAG	K	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	K	2	4	-	2/6/23/26	0/1/1/1
4	NAG	O	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	O	2	4	-	2/6/23/26	0/1/1/1
4	NAG	P	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	P	2	4	-	3/6/23/26	0/1/1/1
4	NAG	Q	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	Q	2	4	-	2/6/23/26	0/1/1/1
4	NAG	R	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	R	2	4	-	2/6/23/26	0/1/1/1
4	NAG	S	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	S	2	4	-	3/6/23/26	0/1/1/1
4	NAG	T	1	1,4	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	T	2	4	-	0/6/23/26	0/1/1/1
4	NAG	U	1	1,4	-	6/6/23/26	0/1/1/1
4	NAG	U	2	4	-	0/6/23/26	0/1/1/1
4	NAG	V	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	V	2	4	-	3/6/23/26	0/1/1/1
4	NAG	W	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	W	2	4	-	0/6/23/26	0/1/1/1
4	NAG	X	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	X	2	4	-	0/6/23/26	0/1/1/1
4	NAG	Y	1	1,4	-	6/6/23/26	0/1/1/1
4	NAG	Y	2	4	-	0/6/23/26	0/1/1/1
4	NAG	Z	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	Z	2	4	-	3/6/23/26	0/1/1/1
4	NAG	a	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	a	2	4	-	5/6/23/26	0/1/1/1
4	NAG	b	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	b	2	4	-	0/6/23/26	0/1/1/1
4	NAG	c	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	c	2	4	-	0/6/23/26	0/1/1/1
4	NAG	d	1	1,4	-	6/6/23/26	0/1/1/1
4	NAG	d	2	4	-	0/6/23/26	0/1/1/1
4	NAG	e	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	e	2	4	-	3/6/23/26	0/1/1/1
4	NAG	f	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	f	2	4	-	5/6/23/26	0/1/1/1
4	NAG	g	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	g	2	4	-	0/6/23/26	0/1/1/1

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	K	2	NAG	O5-C1	-7.18	1.32	1.43
4	D	2	NAG	O5-C1	-7.17	1.32	1.43
4	Q	2	NAG	O5-C1	-7.12	1.32	1.43
4	Q	2	NAG	C1-C2	-4.47	1.45	1.52
4	K	2	NAG	C1-C2	-4.42	1.45	1.52
4	D	2	NAG	C1-C2	-4.41	1.45	1.52
4	K	1	NAG	O5-C1	-4.25	1.36	1.43
4	D	1	NAG	O5-C1	-4.23	1.37	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	Q	1	NAG	O5-C1	-4.19	1.37	1.43
4	G	1	NAG	O5-C1	-2.62	1.39	1.43
4	P	1	NAG	O5-C1	-2.61	1.39	1.43
4	S	1	NAG	O5-C1	-2.57	1.39	1.43
4	a	1	NAG	O5-C1	-2.39	1.39	1.43
4	F	1	NAG	O5-C1	-2.36	1.39	1.43
4	f	1	NAG	O5-C1	-2.35	1.40	1.43

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	f	2	NAG	C2-N2-C7	4.48	129.28	122.90
4	a	2	NAG	C2-N2-C7	4.43	129.22	122.90
4	F	2	NAG	C2-N2-C7	4.42	129.20	122.90
4	Z	2	NAG	C2-N2-C7	4.28	128.99	122.90
4	e	2	NAG	C2-N2-C7	4.28	128.99	122.90
4	V	2	NAG	C2-N2-C7	4.26	128.96	122.90
4	K	2	NAG	C1-C2-N2	2.53	114.81	110.49
4	D	2	NAG	C1-C2-N2	2.52	114.80	110.49
4	Q	2	NAG	C1-O5-C5	2.52	115.60	112.19
4	Q	2	NAG	C1-C2-N2	2.50	114.76	110.49
4	D	2	NAG	C1-O5-C5	2.48	115.56	112.19
4	K	2	NAG	C1-O5-C5	2.45	115.51	112.19
4	e	2	NAG	C1-C2-N2	2.40	114.58	110.49
4	c	1	NAG	C8-C7-N2	2.37	120.11	116.10
4	a	2	NAG	C1-C2-N2	2.36	114.52	110.49
4	V	2	NAG	C1-C2-N2	2.36	114.51	110.49
4	F	2	NAG	C1-C2-N2	2.35	114.50	110.49
4	X	2	NAG	C8-C7-N2	2.35	120.07	116.10
4	c	2	NAG	C8-C7-N2	2.34	120.06	116.10
4	Z	2	NAG	C1-C2-N2	2.34	114.48	110.49
4	U	2	NAG	C8-C7-N2	2.33	120.04	116.10
4	f	2	NAG	C1-C2-N2	2.33	114.46	110.49
4	X	1	NAG	C8-C7-N2	2.32	120.03	116.10
4	d	2	NAG	C8-C7-N2	2.31	120.02	116.10
4	Y	2	NAG	C8-C7-N2	2.31	120.01	116.10
4	T	1	NAG	C8-C7-N2	2.30	120.00	116.10
4	T	2	NAG	C8-C7-N2	2.30	120.00	116.10
4	b	1	NAG	C1-O5-C5	2.10	115.04	112.19
4	F	2	NAG	C1-O5-C5	2.09	115.03	112.19
4	a	2	NAG	C1-O5-C5	2.09	115.02	112.19
4	W	1	NAG	C1-O5-C5	2.08	115.00	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	f	2	NAG	C1-O5-C5	2.07	115.00	112.19
4	T	1	NAG	C2-N2-C7	-2.04	120.00	122.90
4	X	2	NAG	C2-N2-C7	-2.03	120.01	122.90
4	g	1	NAG	C1-O5-C5	2.03	114.95	112.19
4	c	2	NAG	C2-N2-C7	-2.03	120.01	122.90
4	T	2	NAG	C2-N2-C7	-2.03	120.02	122.90
4	d	2	NAG	C2-N2-C7	-2.01	120.04	122.90
4	X	1	NAG	C2-N2-C7	-2.01	120.04	122.90
4	U	2	NAG	C2-N2-C7	-2.00	120.05	122.90

There are no chirality outliers.

All (93) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	U	1	NAG	O5-C5-C6-O6
4	Y	1	NAG	O5-C5-C6-O6
4	d	1	NAG	O5-C5-C6-O6
4	D	2	NAG	O5-C5-C6-O6
4	K	2	NAG	O5-C5-C6-O6
4	Q	2	NAG	O5-C5-C6-O6
4	G	1	NAG	O5-C5-C6-O6
4	P	1	NAG	O5-C5-C6-O6
4	S	1	NAG	O5-C5-C6-O6
4	U	1	NAG	C8-C7-N2-C2
4	Y	1	NAG	C8-C7-N2-C2
4	d	1	NAG	C8-C7-N2-C2
4	G	1	NAG	C4-C5-C6-O6
4	P	1	NAG	C4-C5-C6-O6
4	S	1	NAG	C4-C5-C6-O6
4	U	1	NAG	C4-C5-C6-O6
4	Y	1	NAG	C4-C5-C6-O6
4	d	1	NAG	C4-C5-C6-O6
4	U	1	NAG	C1-C2-N2-C7
4	Y	1	NAG	C1-C2-N2-C7
4	d	1	NAG	C1-C2-N2-C7
4	D	2	NAG	C4-C5-C6-O6
4	K	2	NAG	C4-C5-C6-O6
4	Q	2	NAG	C4-C5-C6-O6
4	F	2	NAG	C8-C7-N2-C2
4	F	2	NAG	O7-C7-N2-C2
4	U	1	NAG	O7-C7-N2-C2
4	V	2	NAG	C8-C7-N2-C2

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Mol	Chain	Res	Type	Atoms
4	V	2	NAG	O7-C7-N2-C2
4	Y	1	NAG	O7-C7-N2-C2
4	Z	2	NAG	C8-C7-N2-C2
4	Z	2	NAG	O7-C7-N2-C2
4	a	2	NAG	C8-C7-N2-C2
4	a	2	NAG	O7-C7-N2-C2
4	d	1	NAG	O7-C7-N2-C2
4	e	2	NAG	C8-C7-N2-C2
4	e	2	NAG	O7-C7-N2-C2
4	f	2	NAG	C8-C7-N2-C2
4	f	2	NAG	O7-C7-N2-C2
4	F	1	NAG	C4-C5-C6-O6
4	a	1	NAG	C4-C5-C6-O6
4	f	1	NAG	C4-C5-C6-O6
4	V	1	NAG	C4-C5-C6-O6
4	Z	1	NAG	C4-C5-C6-O6
4	e	1	NAG	C4-C5-C6-O6
4	G	2	NAG	O5-C5-C6-O6
4	P	2	NAG	O5-C5-C6-O6
4	S	2	NAG	O5-C5-C6-O6
4	V	1	NAG	O5-C5-C6-O6
4	Z	1	NAG	O5-C5-C6-O6
4	e	1	NAG	O5-C5-C6-O6
4	F	1	NAG	O5-C5-C6-O6
4	a	1	NAG	O5-C5-C6-O6
4	f	1	NAG	O5-C5-C6-O6
4	G	2	NAG	C4-C5-C6-O6
4	P	2	NAG	C4-C5-C6-O6
4	S	2	NAG	C4-C5-C6-O6
4	W	1	NAG	C4-C5-C6-O6
4	b	1	NAG	C4-C5-C6-O6
4	g	1	NAG	C4-C5-C6-O6
4	W	1	NAG	O5-C5-C6-O6
4	g	1	NAG	O5-C5-C6-O6
4	b	1	NAG	O5-C5-C6-O6
4	U	1	NAG	C3-C2-N2-C7
4	Y	1	NAG	C3-C2-N2-C7
4	d	1	NAG	C3-C2-N2-C7
4	E	2	NAG	O5-C5-C6-O6
4	O	2	NAG	O5-C5-C6-O6
4	E	2	NAG	C4-C5-C6-O6
4	R	2	NAG	C4-C5-C6-O6

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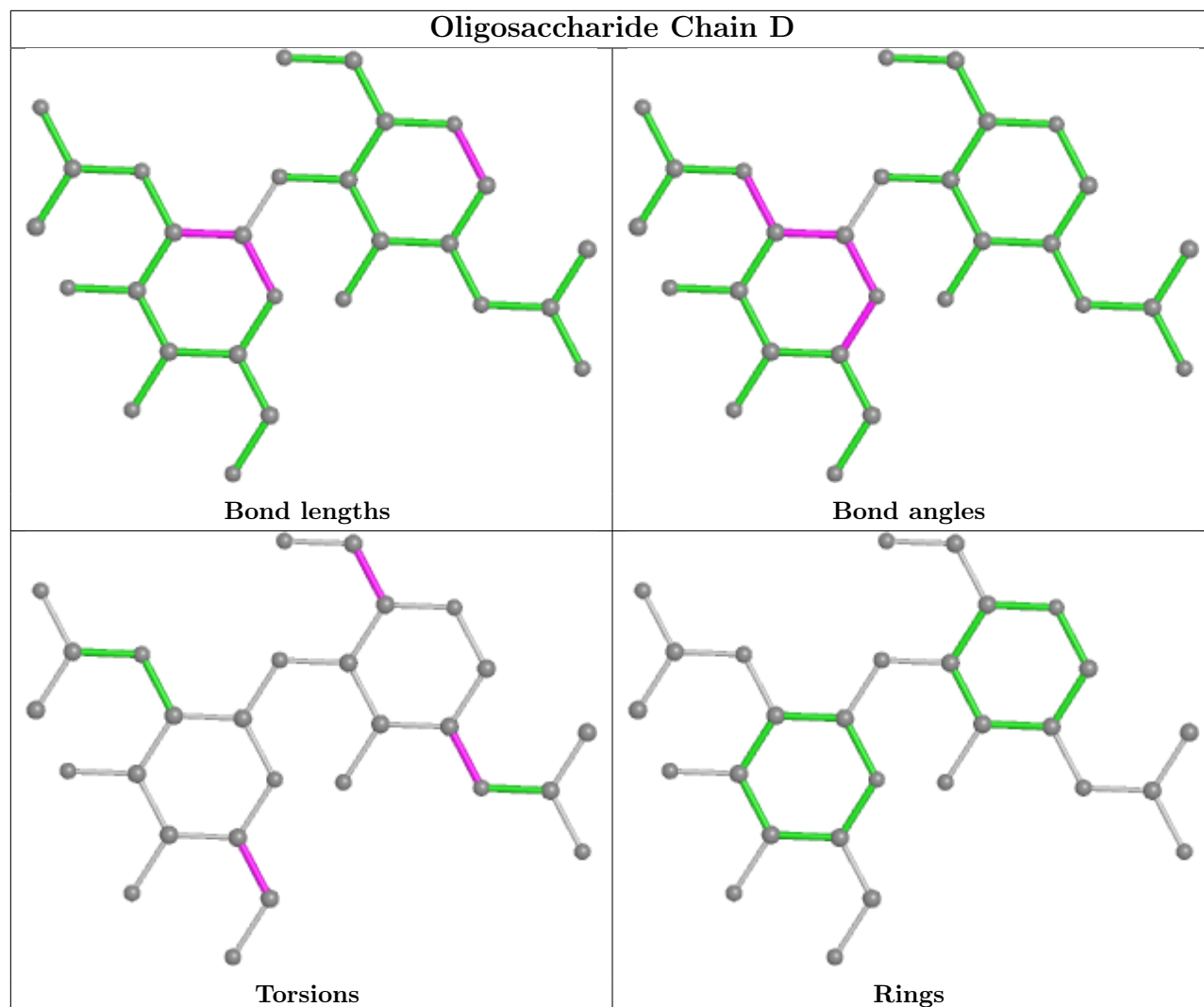
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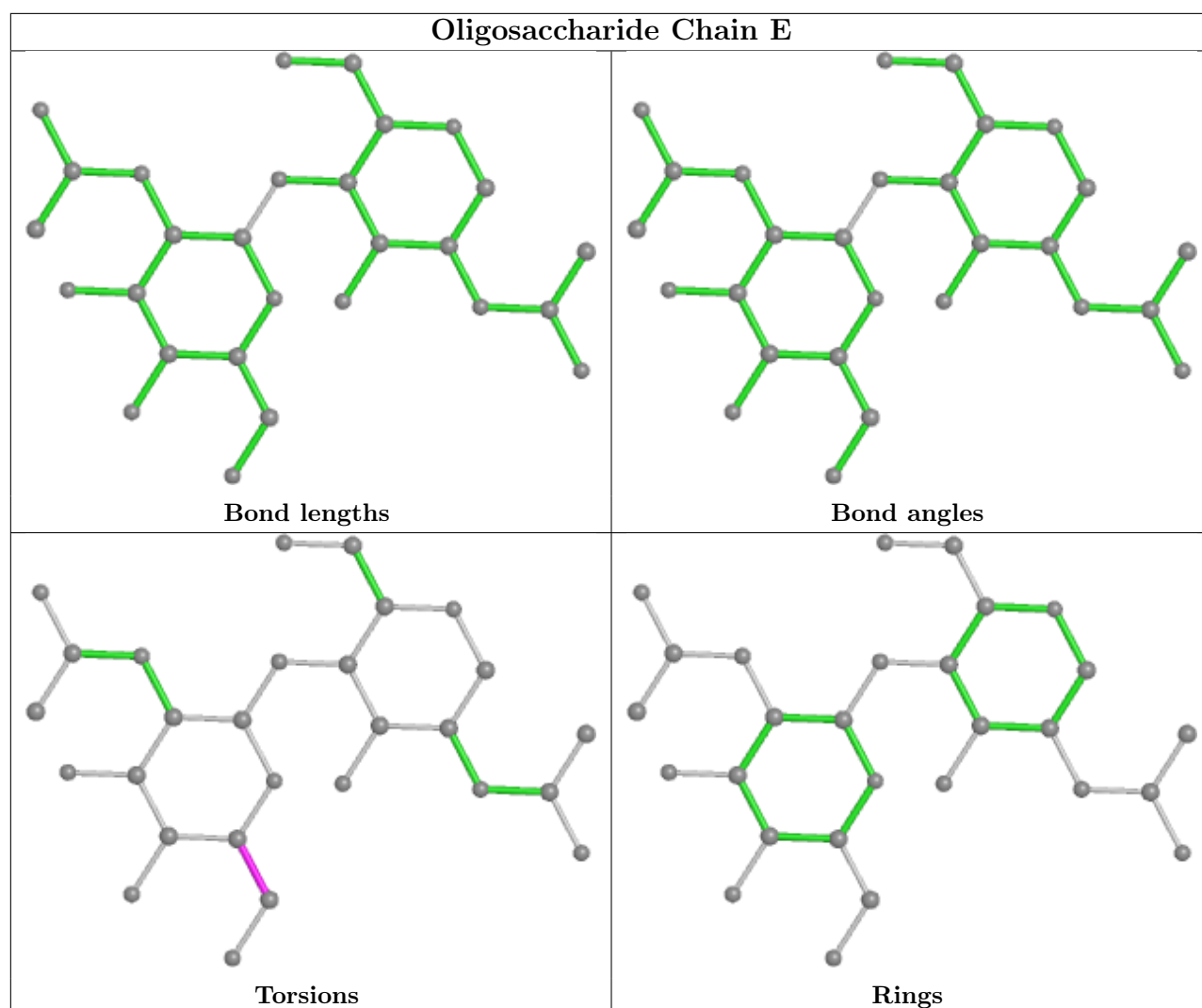
Mol	Chain	Res	Type	Atoms
4	R	2	NAG	O5-C5-C6-O6
4	O	2	NAG	C4-C5-C6-O6
4	G	2	NAG	C3-C2-N2-C7
4	P	2	NAG	C3-C2-N2-C7
4	S	2	NAG	C3-C2-N2-C7
4	a	2	NAG	C4-C5-C6-O6
4	Q	1	NAG	O5-C5-C6-O6
4	F	2	NAG	C4-C5-C6-O6
4	f	2	NAG	C4-C5-C6-O6
4	D	1	NAG	O5-C5-C6-O6
4	K	1	NAG	O5-C5-C6-O6
4	F	2	NAG	O5-C5-C6-O6
4	f	2	NAG	O5-C5-C6-O6
4	a	2	NAG	O5-C5-C6-O6
4	Q	1	NAG	C1-C2-N2-C7
4	D	1	NAG	C1-C2-N2-C7
4	K	1	NAG	C1-C2-N2-C7
4	F	2	NAG	C3-C2-N2-C7
4	V	2	NAG	C3-C2-N2-C7
4	Z	2	NAG	C3-C2-N2-C7
4	a	2	NAG	C3-C2-N2-C7
4	e	2	NAG	C3-C2-N2-C7
4	f	2	NAG	C3-C2-N2-C7

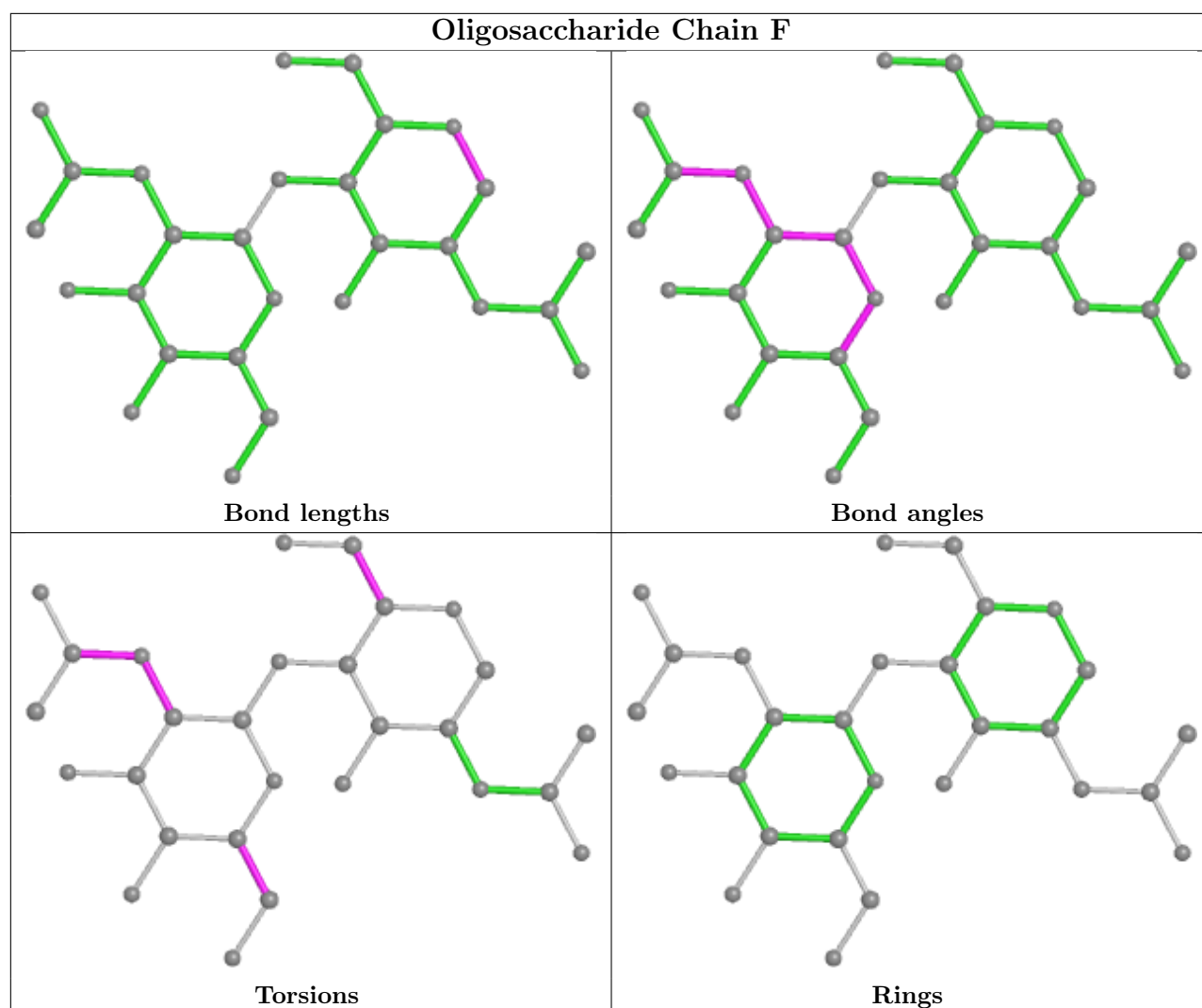
There are no ring outliers.

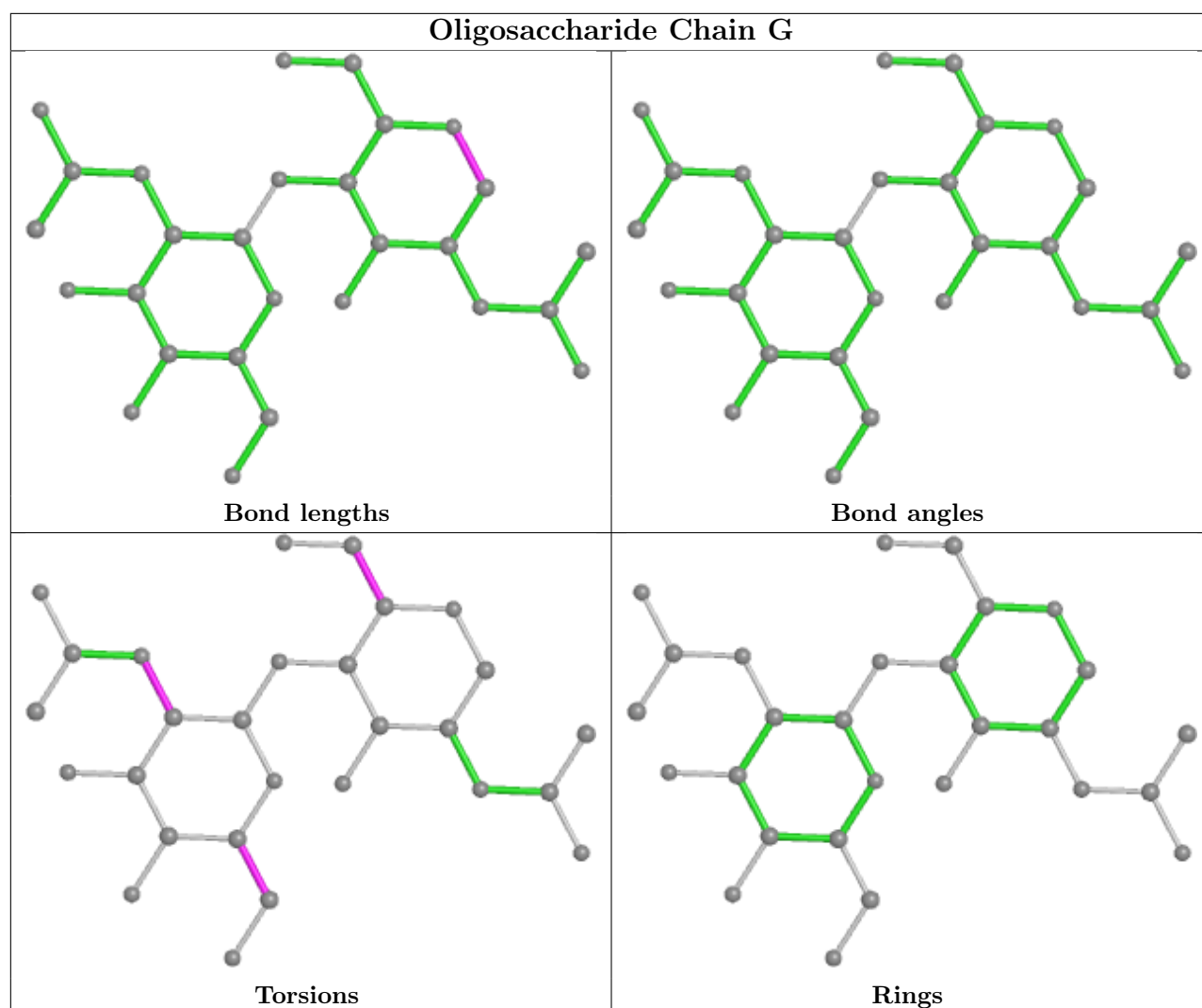
No monomer is involved in short contacts.

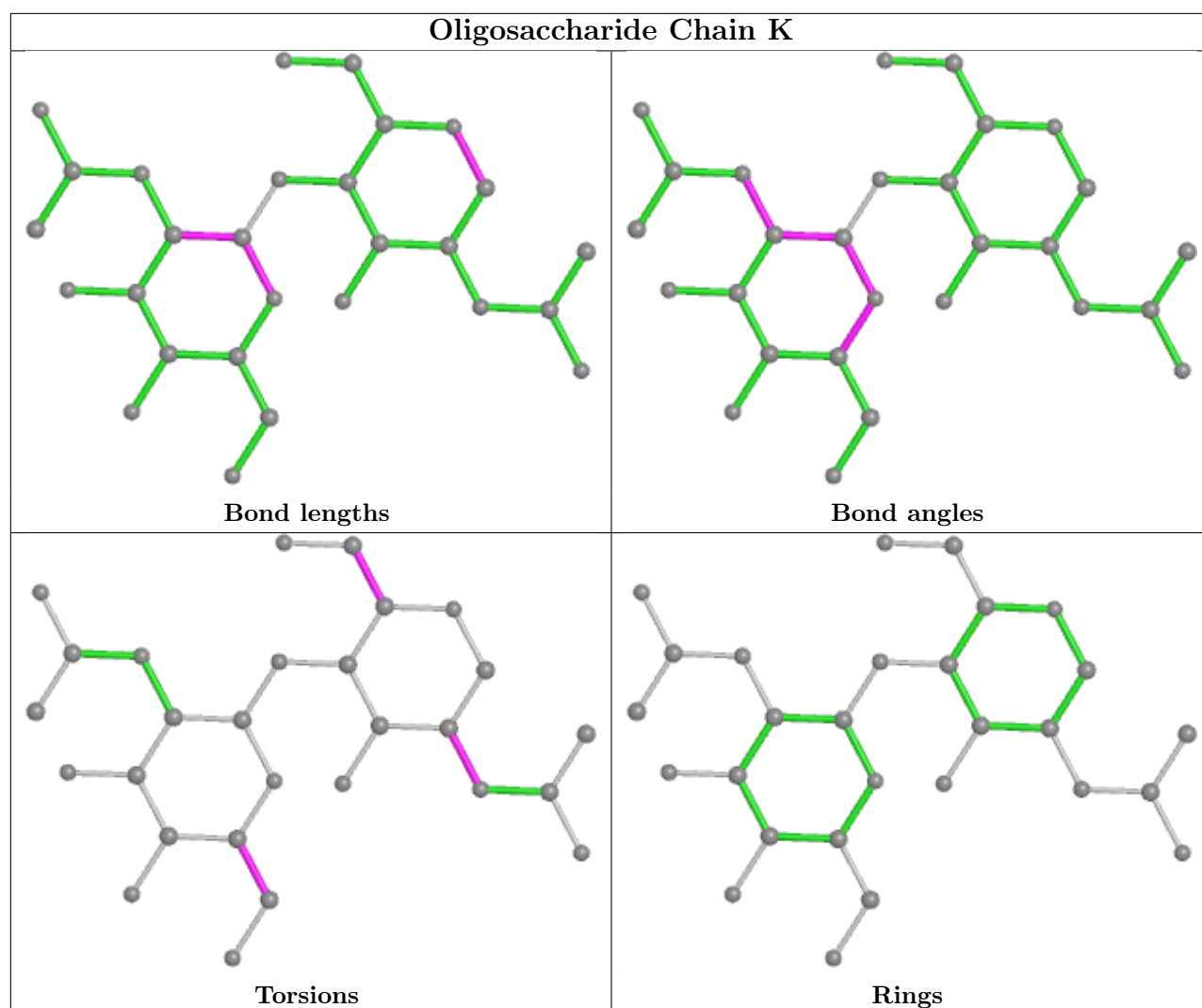
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

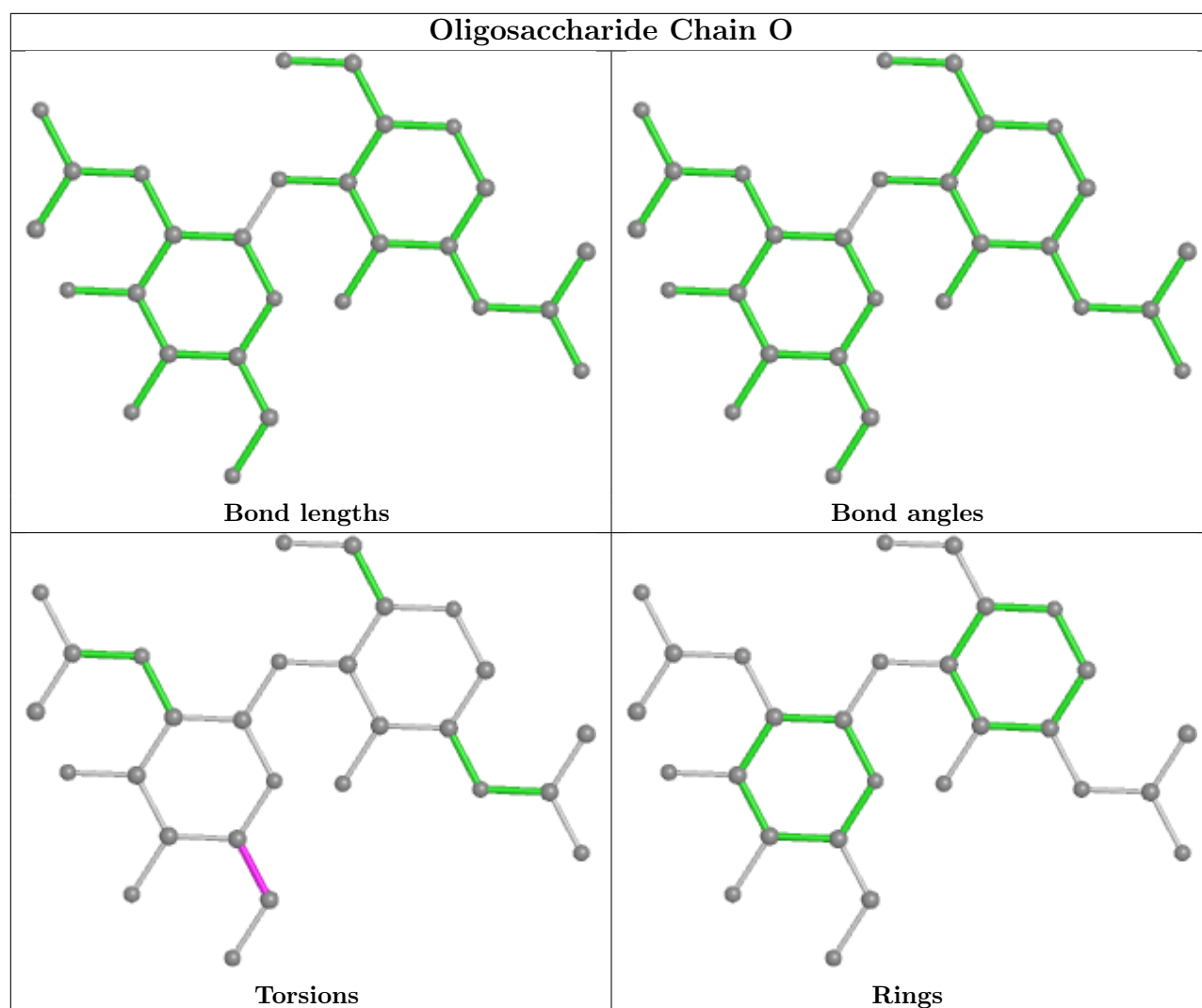


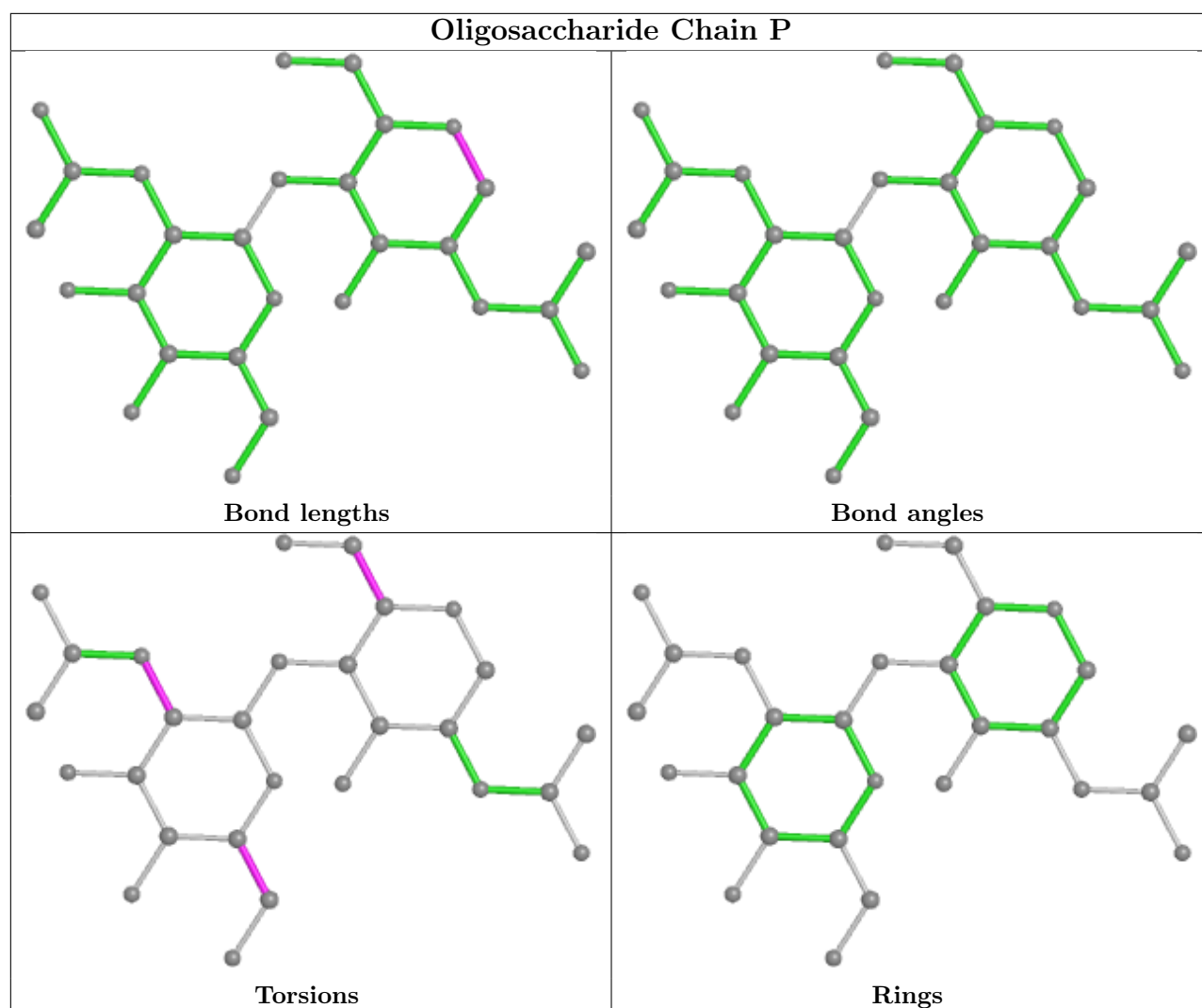


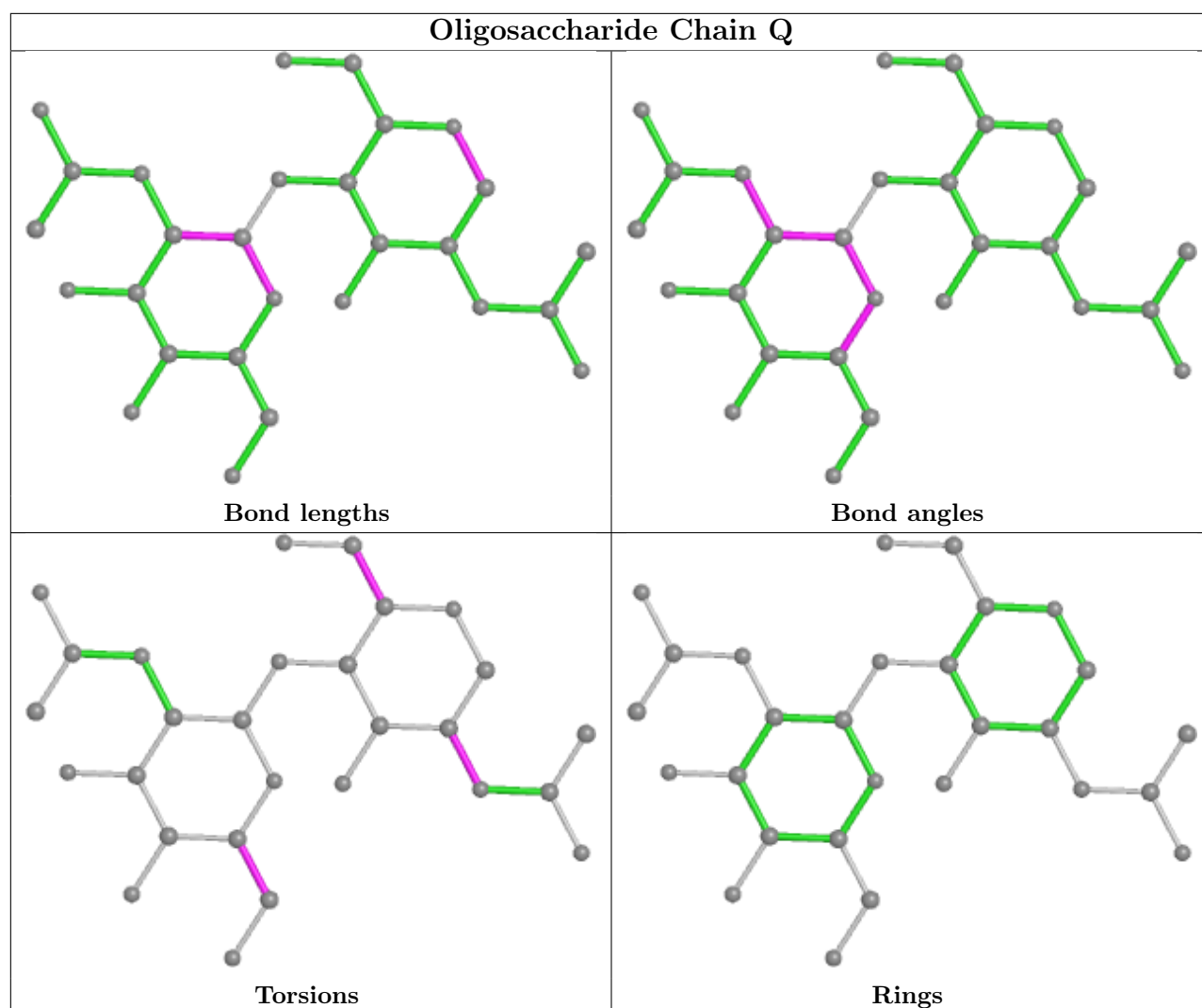


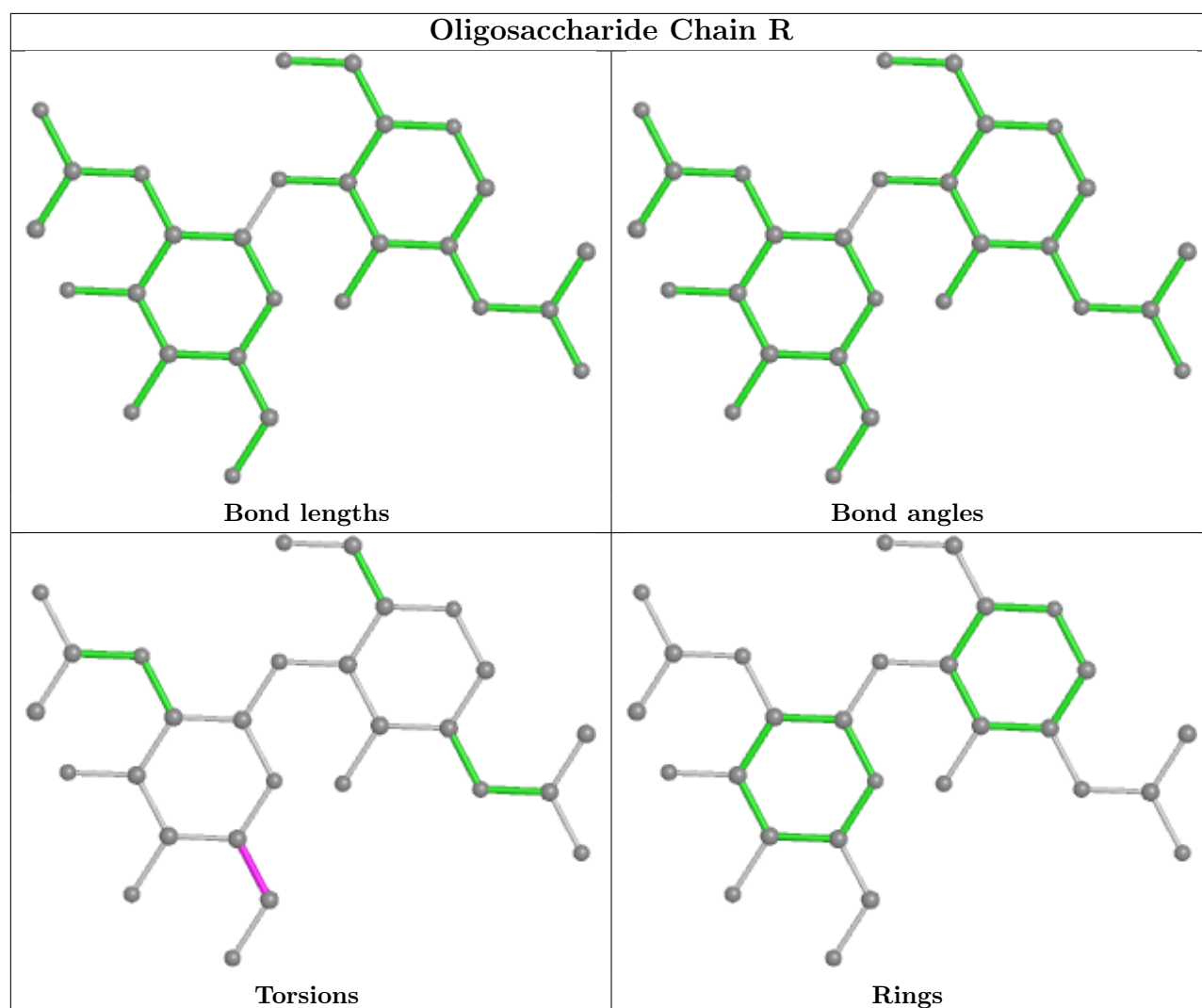


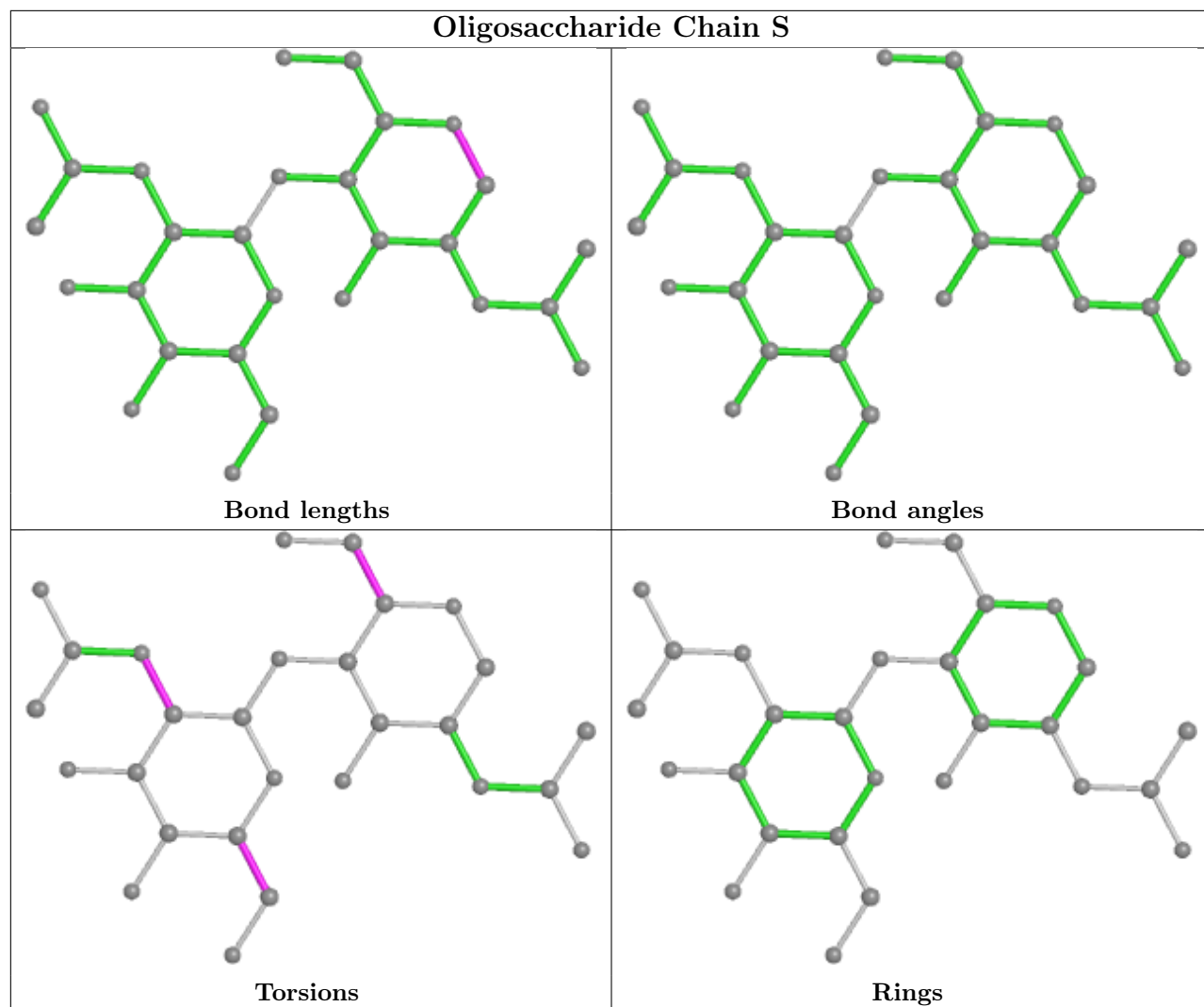


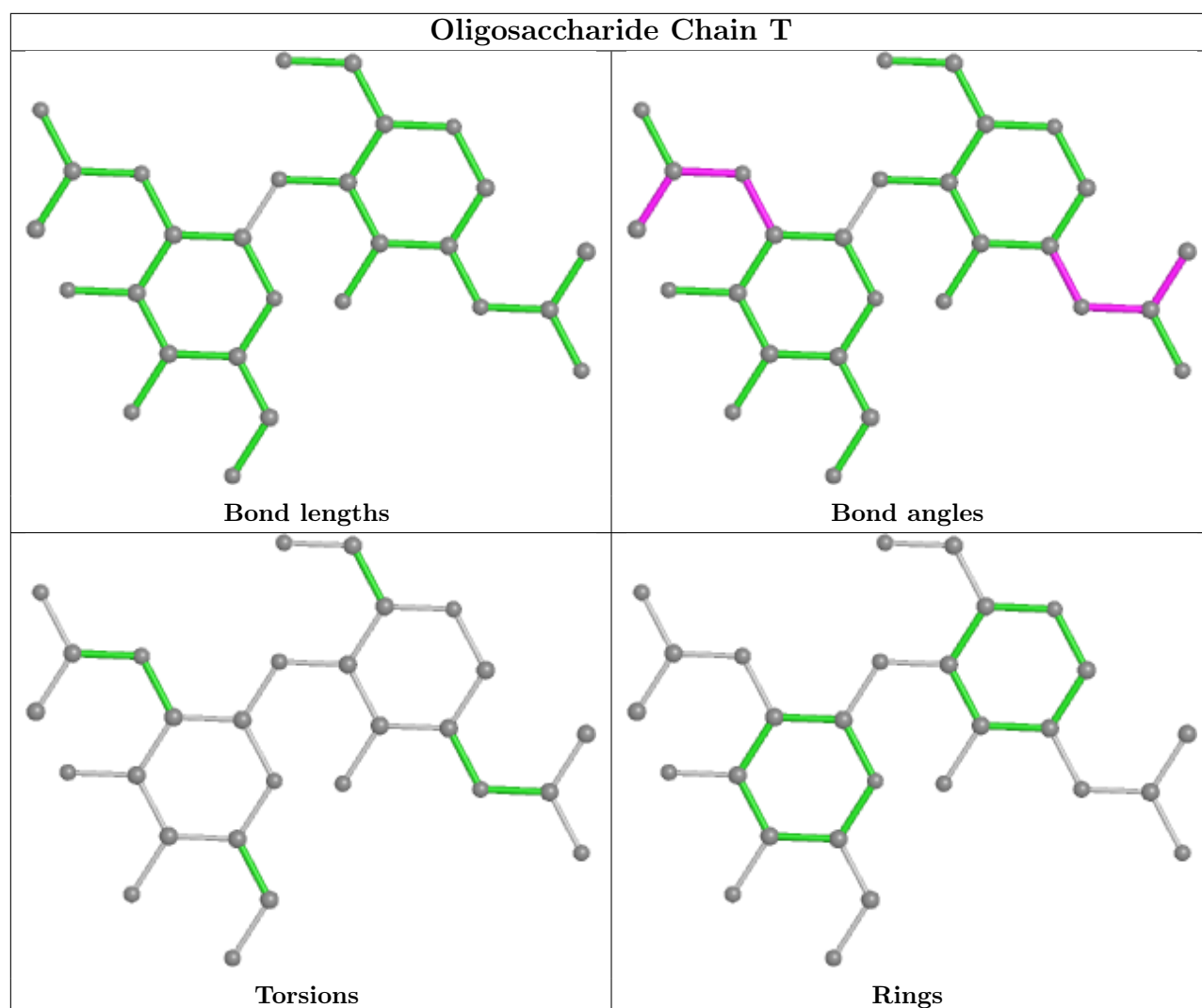


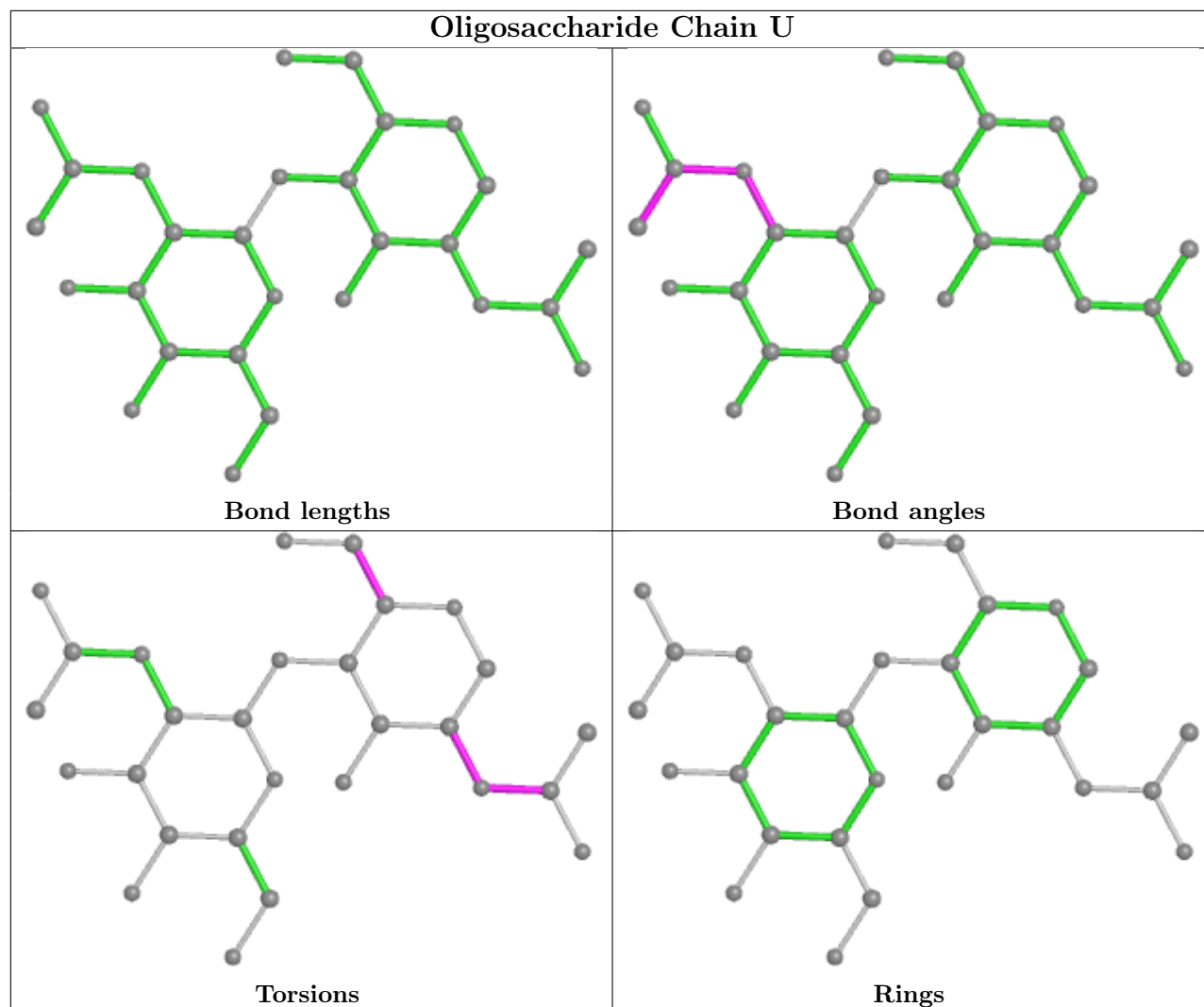


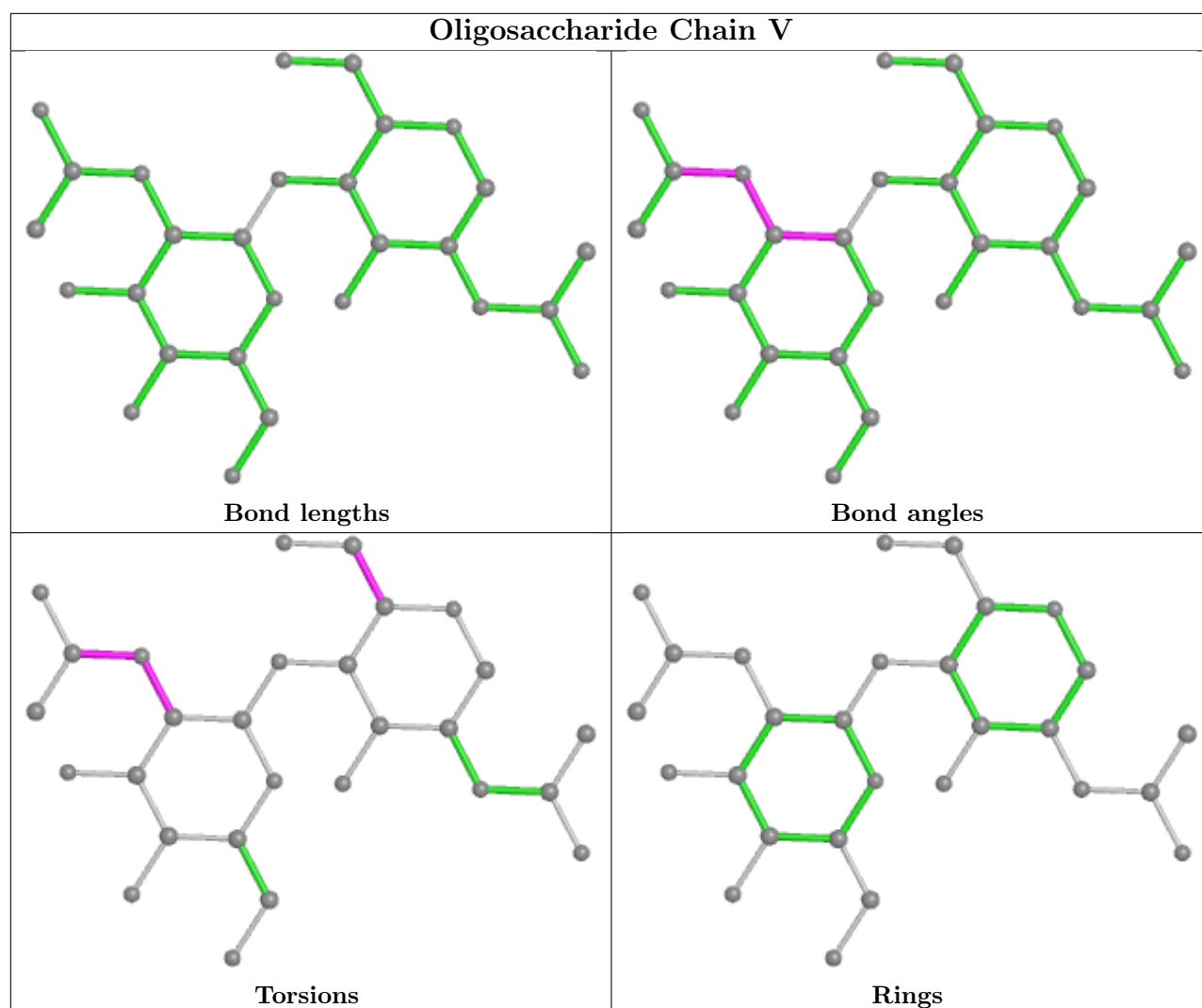


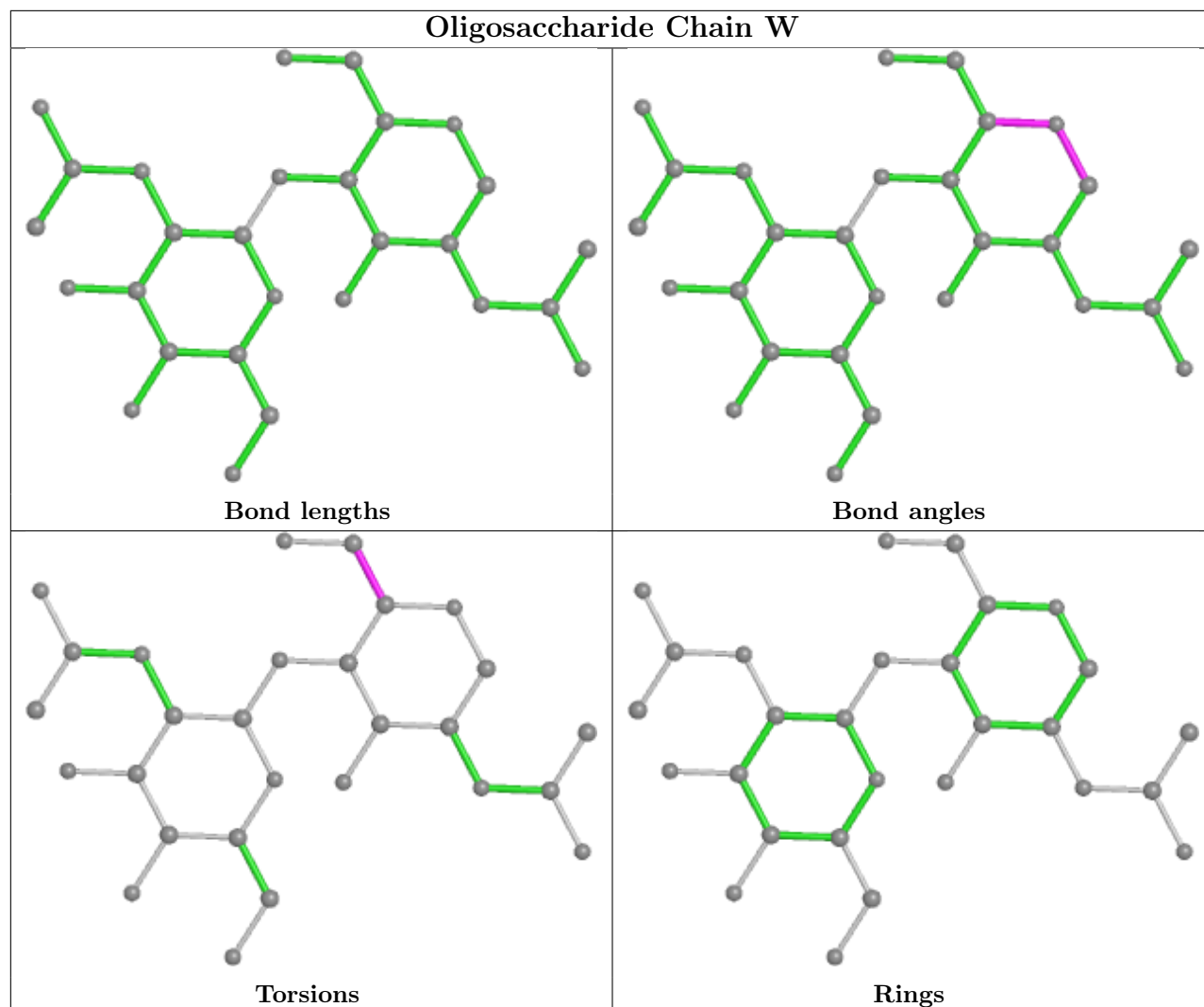


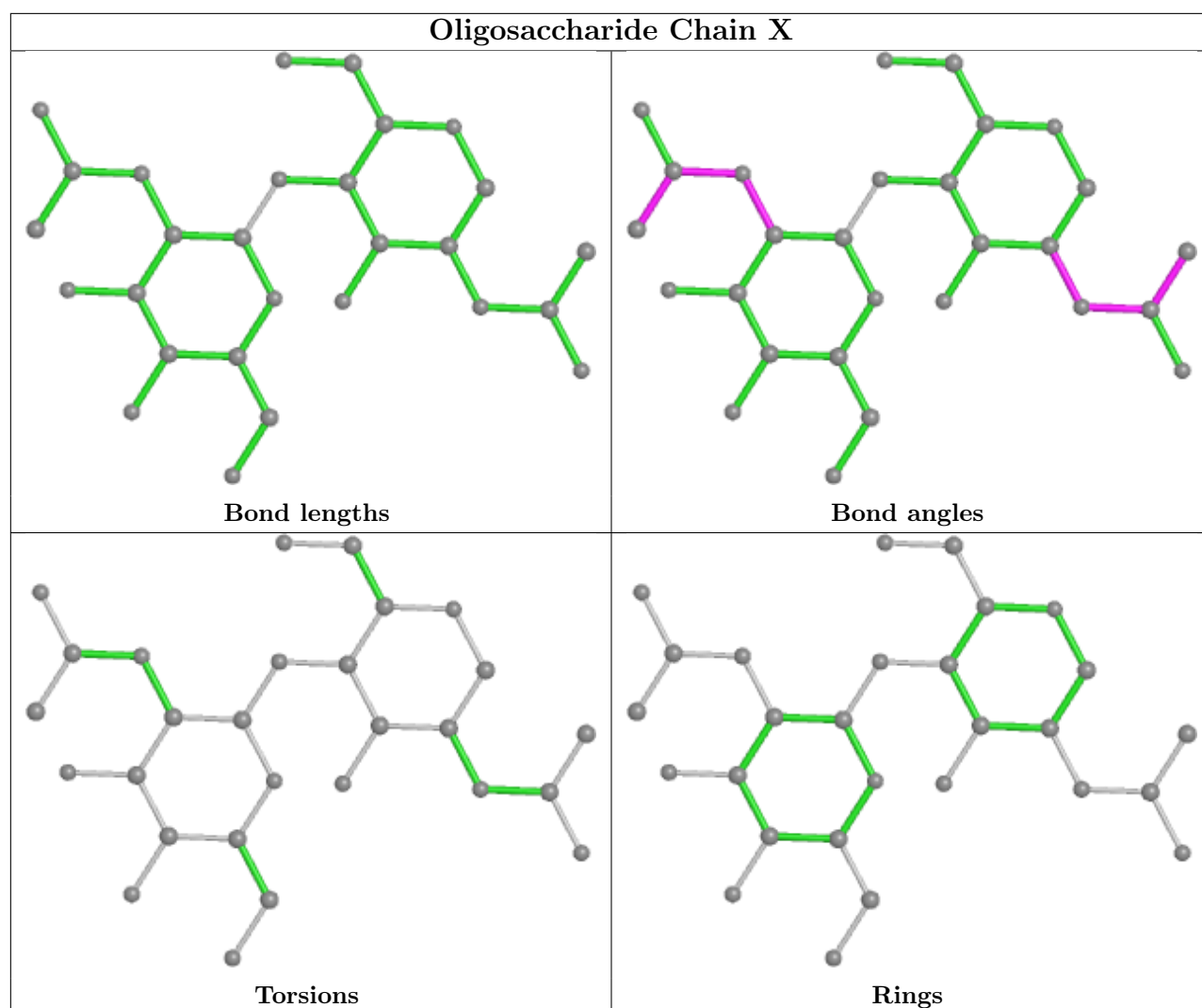


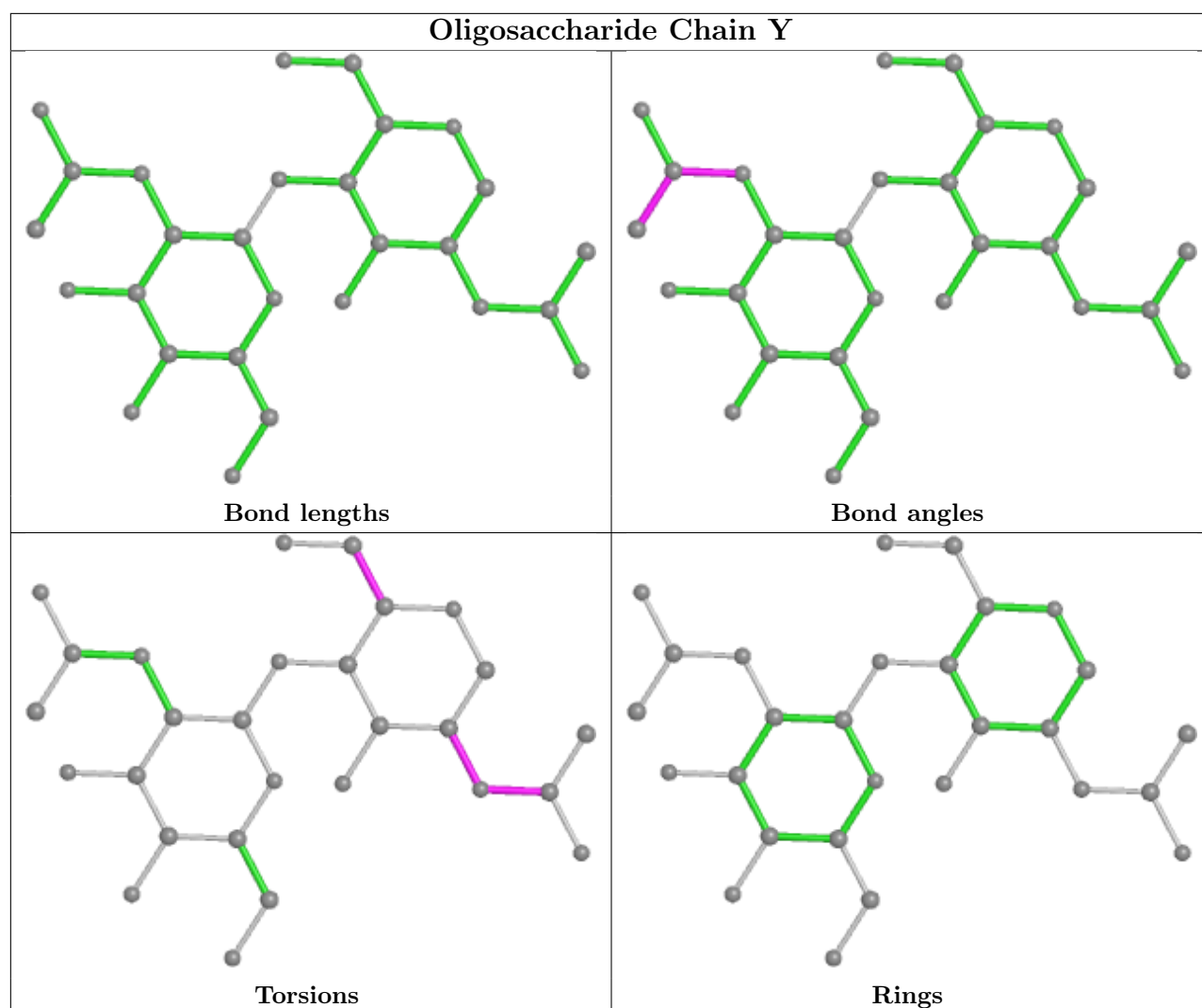


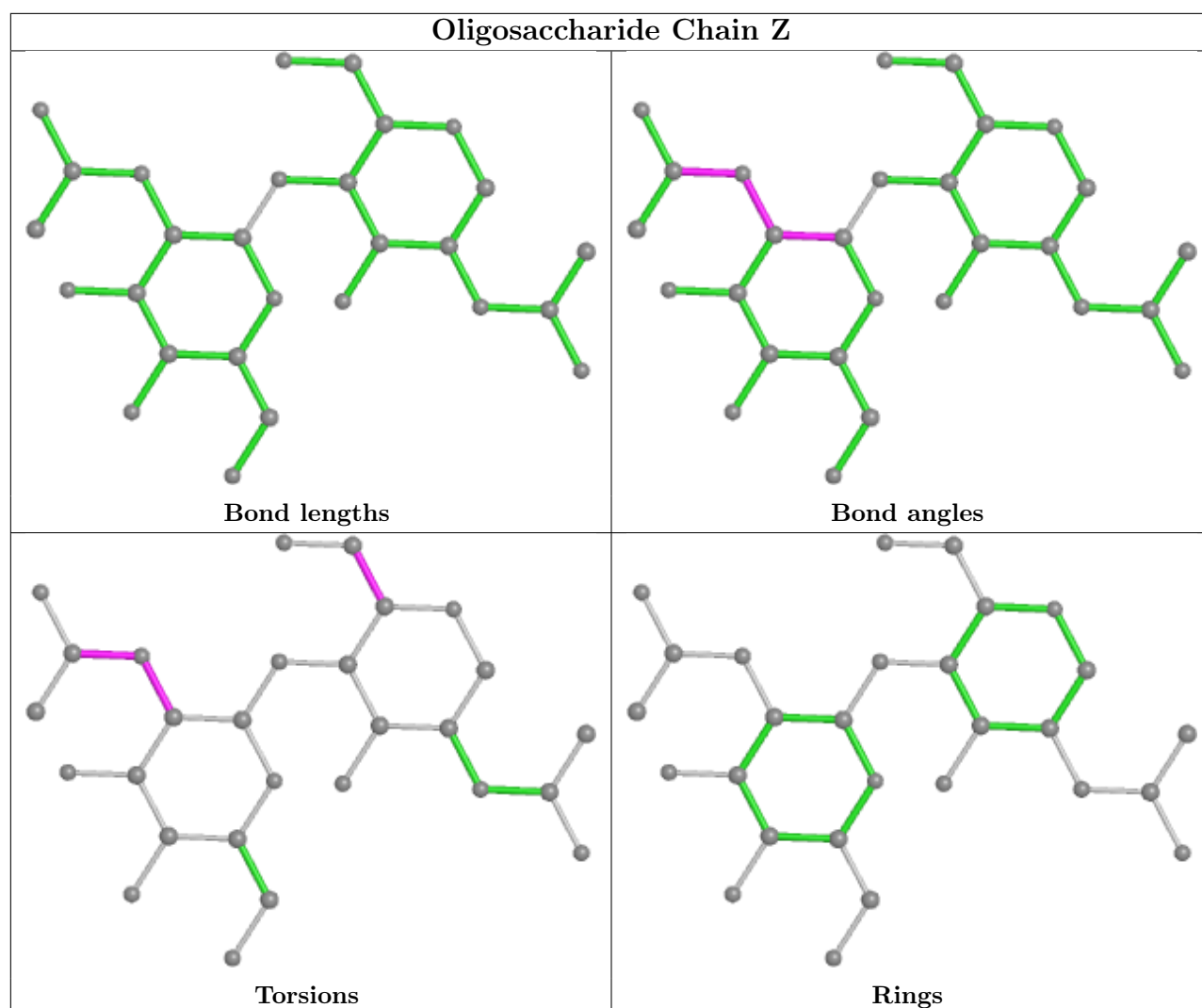


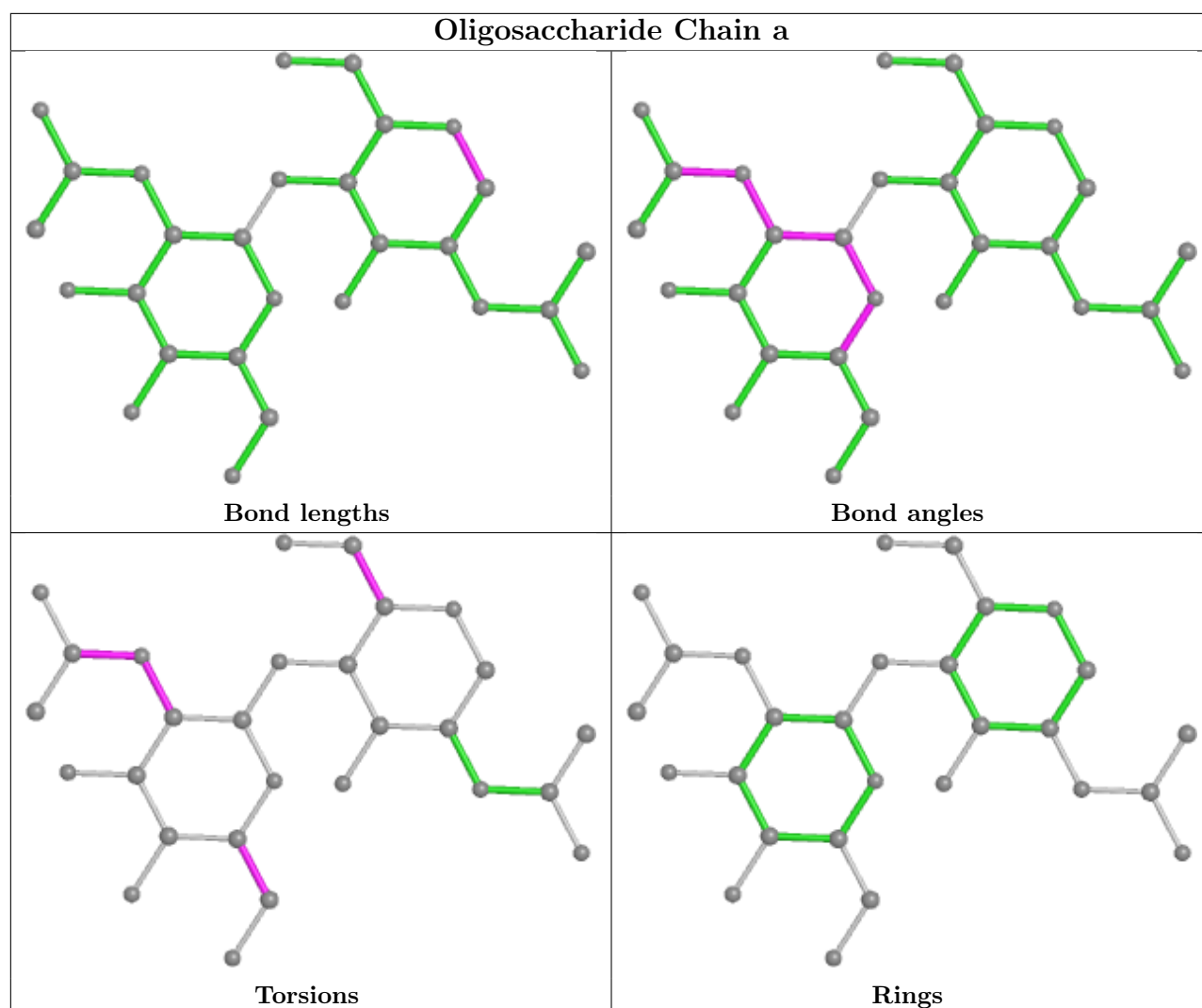


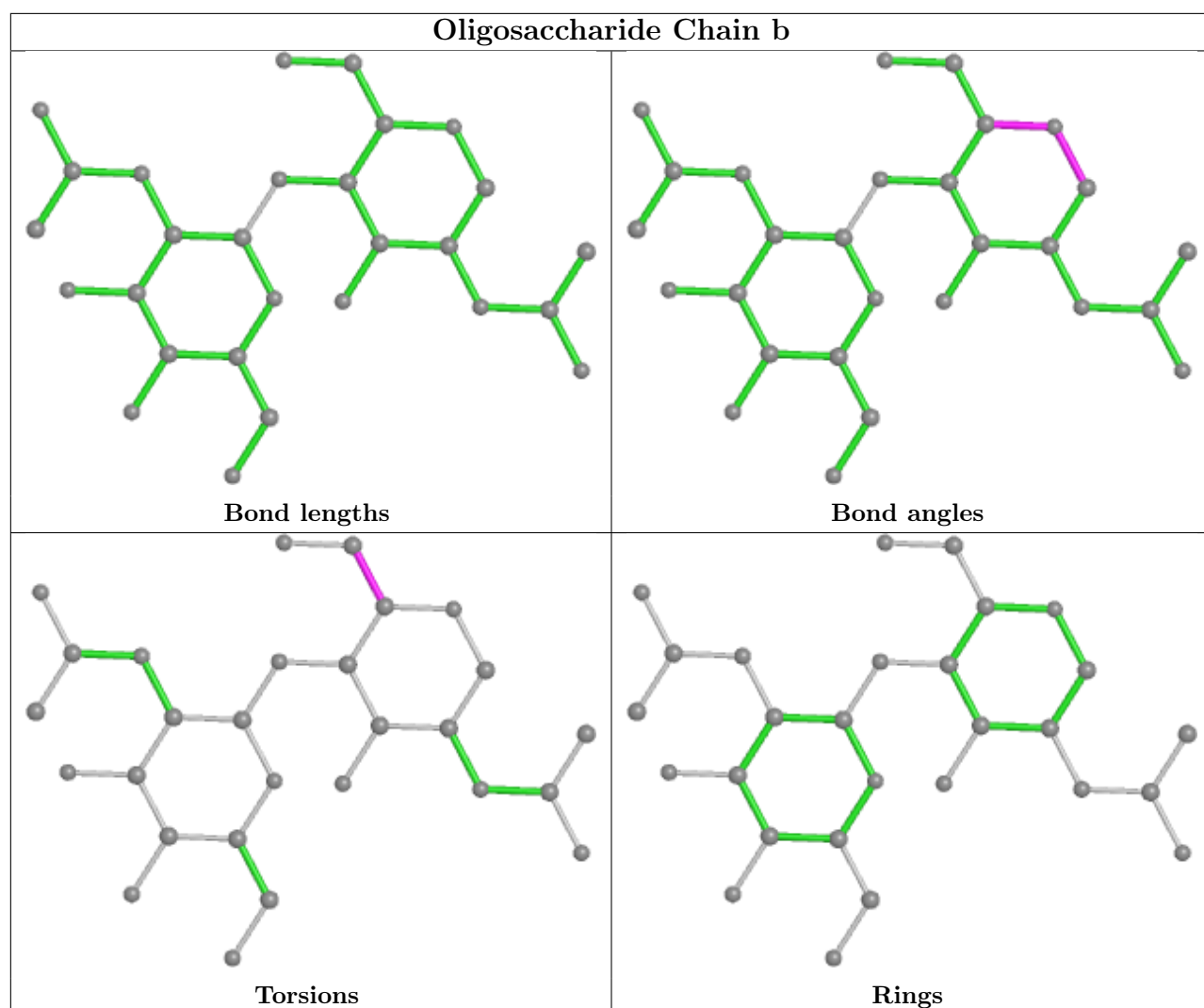


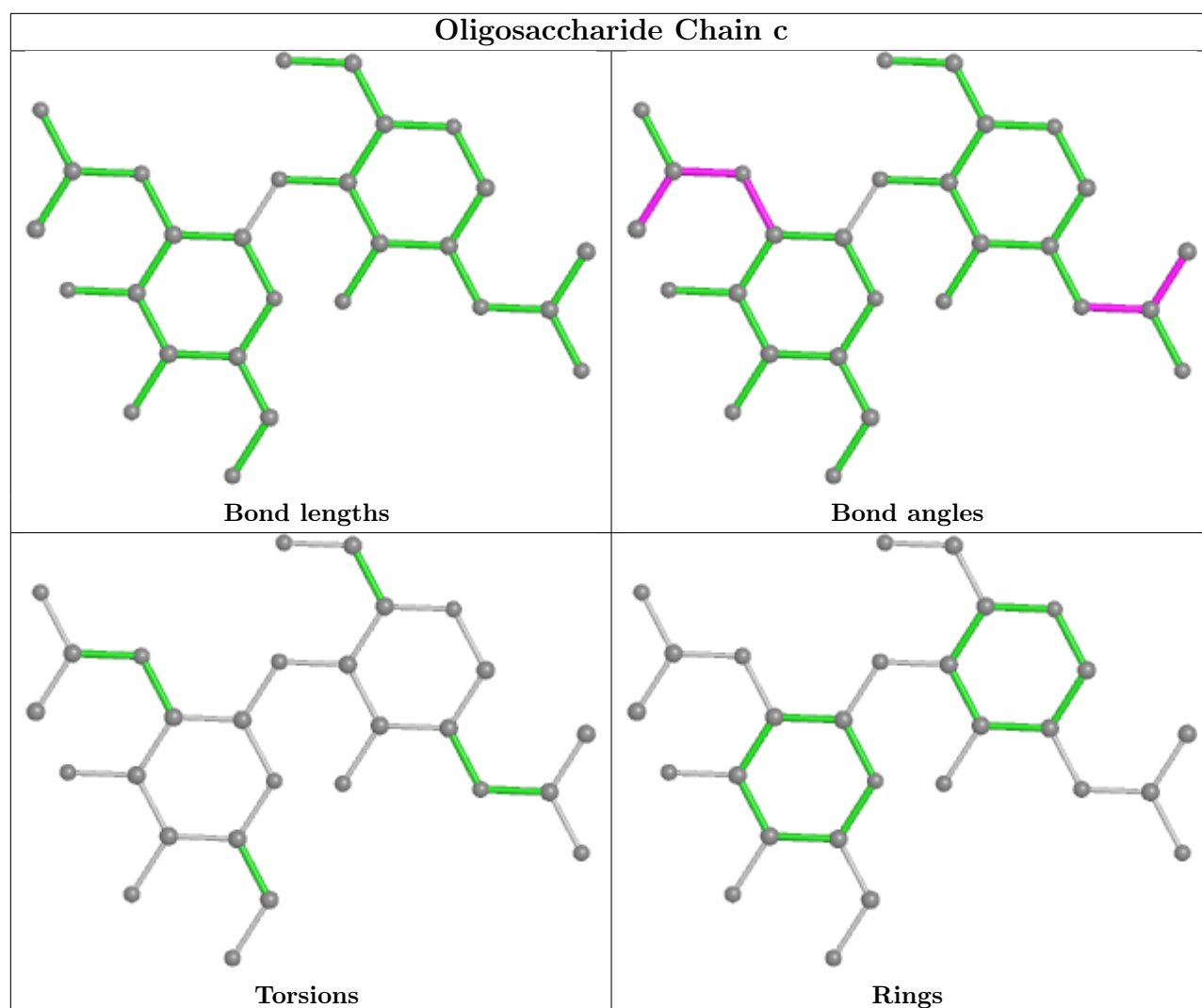


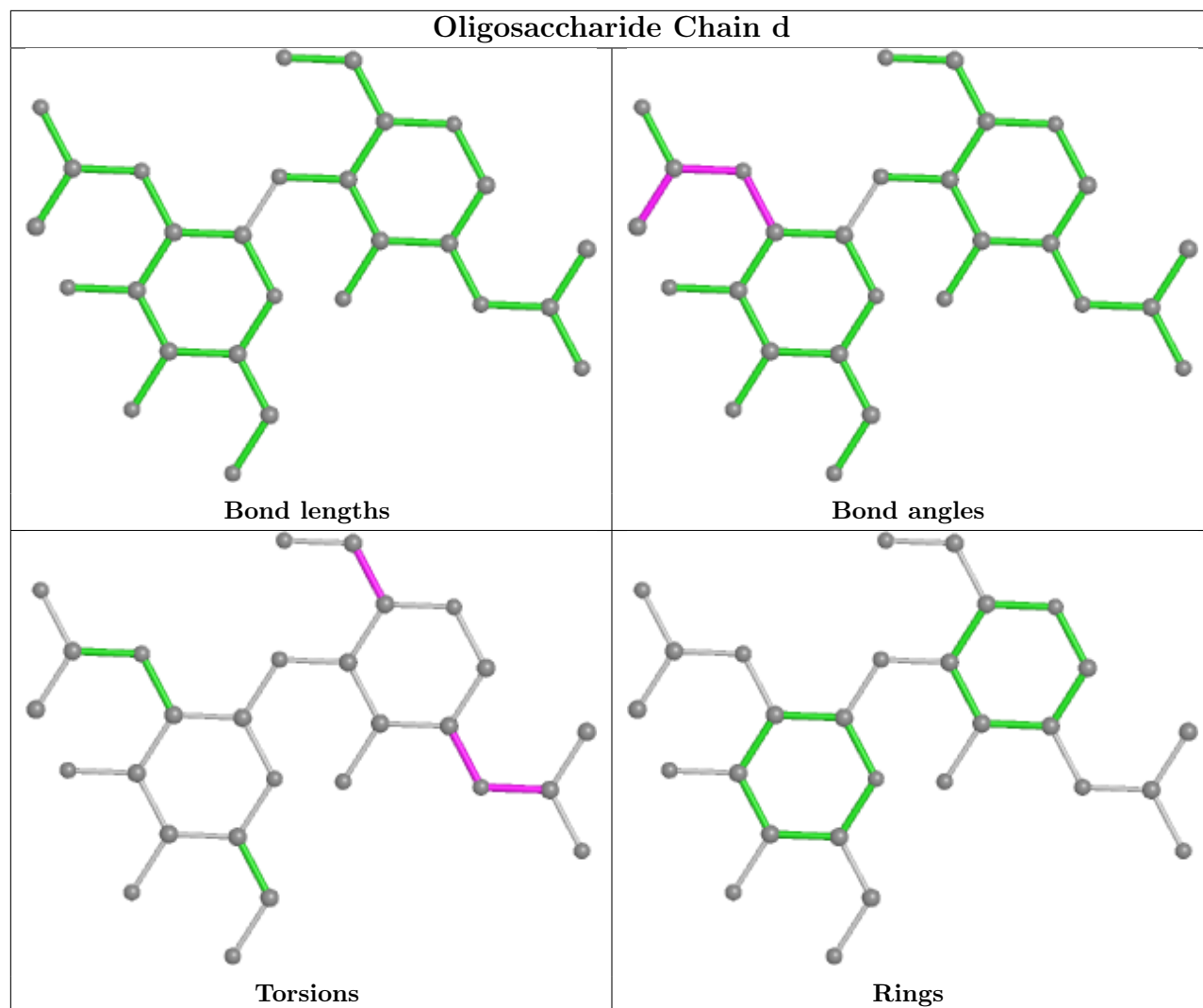


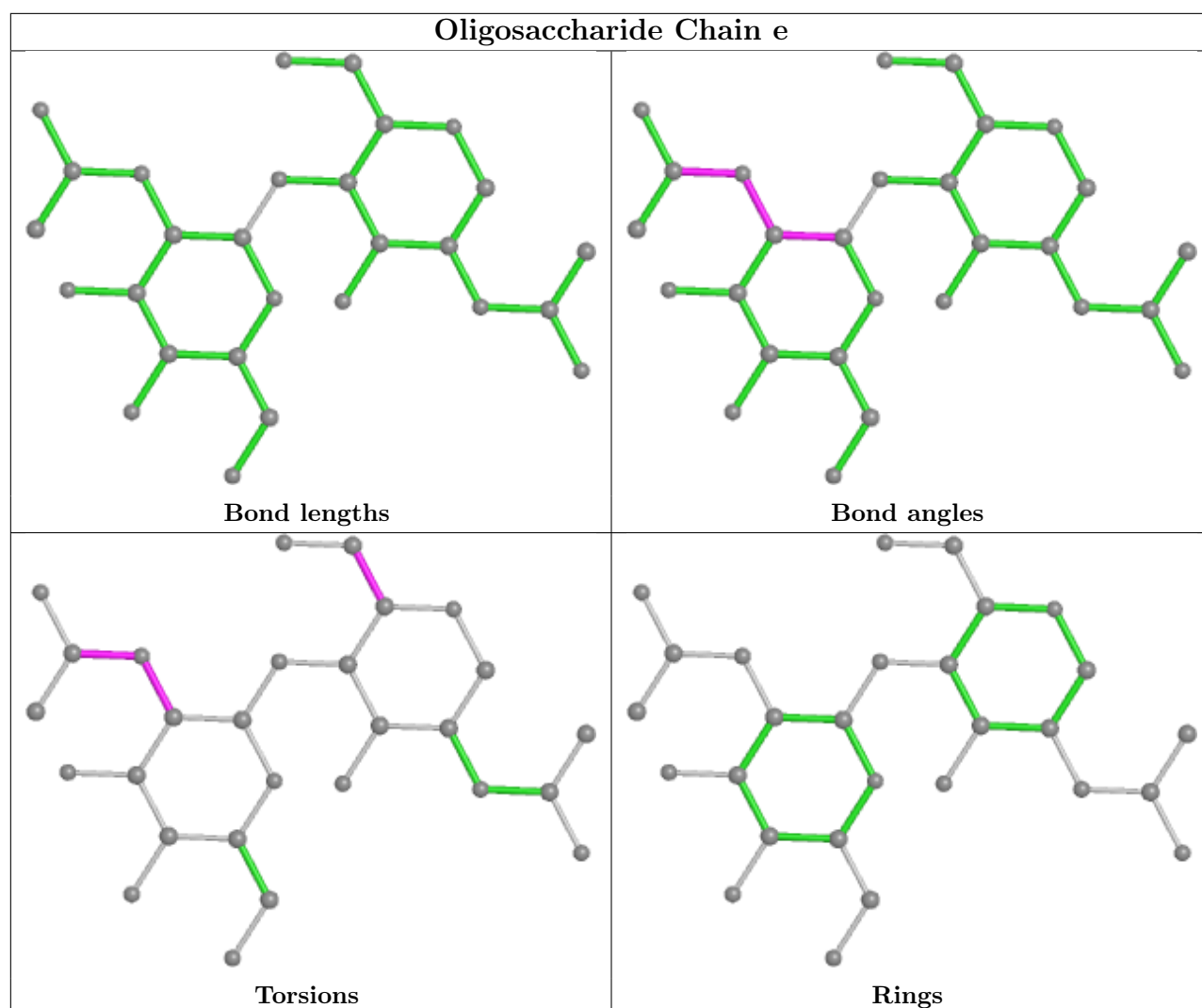


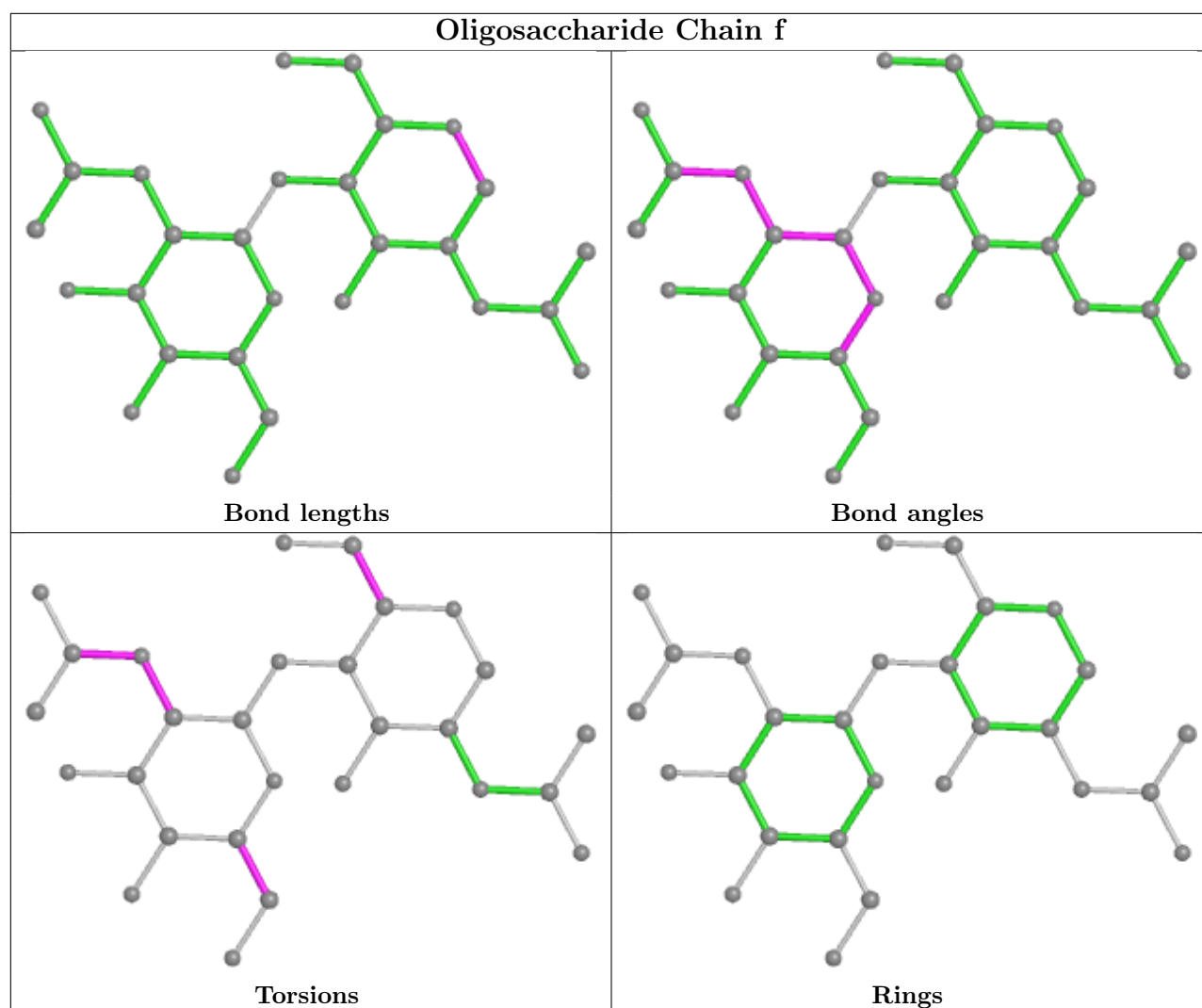


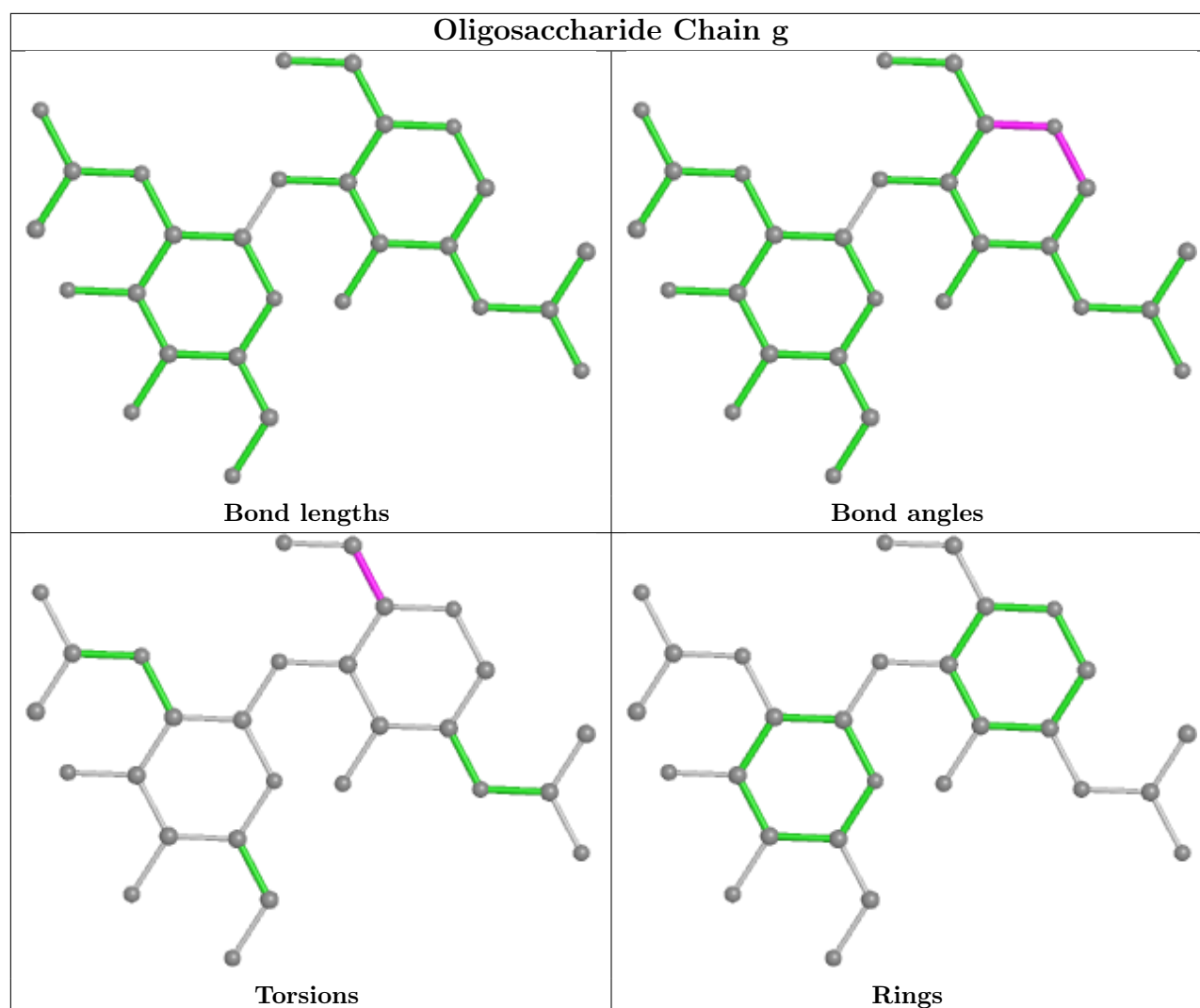












5.6 Ligand geometry [i](#)

33 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	NAG	C	1403	1	14,14,15	0.21	0	17,19,21	0.38	0
5	NAG	A	1407	1	14,14,15	0.75	1 (7%)	17,19,21	0.59	0
5	NAG	B	1404	1	14,14,15	0.46	0	17,19,21	0.61	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	A	1414	1	14,14,15	0.51	0	17,19,21	0.35	0
5	NAG	A	1408	1	14,14,15	0.29	0	17,19,21	0.62	0
5	NAG	C	1407	1	14,14,15	0.74	0	17,19,21	0.59	0
6	EIC	A	1419	-	19,19,19	0.55	0	19,19,19	0.99	0
5	NAG	A	1413	1	14,14,15	0.28	0	17,19,21	0.62	0
5	NAG	B	1409	1	14,14,15	0.83	1 (7%)	17,19,21	0.57	0
5	NAG	B	1414	1	14,14,15	0.53	0	17,19,21	0.36	0
5	NAG	B	1408	1	14,14,15	0.29	0	17,19,21	0.62	0
5	NAG	C	1408	1	14,14,15	0.29	0	17,19,21	0.63	0
5	NAG	C	1414	1	14,14,15	0.51	0	17,19,21	0.35	0
5	NAG	C	1409	1	14,14,15	0.40	0	17,19,21	1.16	2 (11%)
5	NAG	A	1410	1	14,14,15	0.63	0	17,19,21	0.74	1 (5%)
6	EIC	A	1420	-	19,19,19	0.57	0	19,19,19	0.96	0
5	NAG	C	1413	1	14,14,15	0.28	0	17,19,21	0.62	0
5	NAG	C	1410	1	14,14,15	0.61	0	17,19,21	0.74	1 (5%)
5	NAG	B	1406	1	14,14,15	0.31	0	17,19,21	0.40	0
5	NAG	B	1413	1	14,14,15	0.30	0	17,19,21	0.61	0
5	NAG	B	1403	1	14,14,15	0.19	0	17,19,21	0.38	0
5	NAG	B	1407	1	14,14,15	0.75	1 (7%)	17,19,21	0.60	0
5	NAG	A	1405	1	14,14,15	0.41	0	17,19,21	1.17	2 (11%)
5	NAG	A	1409	1	14,14,15	0.86	1 (7%)	17,19,21	0.55	0
5	NAG	A	1406	1	14,14,15	0.29	0	17,19,21	0.40	0
5	NAG	C	1405	1	14,14,15	0.41	0	17,19,21	1.17	2 (11%)
5	NAG	A	1404	1	14,14,15	0.46	0	17,19,21	0.62	0
5	NAG	B	1410	1	14,14,15	0.61	0	17,19,21	0.75	1 (5%)
5	NAG	C	1404	1	14,14,15	0.47	0	17,19,21	0.63	0
5	NAG	B	1405	1	14,14,15	0.41	0	17,19,21	1.18	2 (11%)
5	NAG	C	1406	1	14,14,15	0.31	0	17,19,21	0.39	0
5	NAG	A	1403	1	14,14,15	0.21	0	17,19,21	0.38	0
6	EIC	B	1421	-	19,19,19	0.57	0	19,19,19	0.96	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
5	NAG	C	1403	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1407	1	-	4/6/23/26	0/1/1/1
5	NAG	B	1404	1	-	3/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	A	1414	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1408	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1407	1	-	4/6/23/26	0/1/1/1
6	EIC	A	1419	-	-	11/17/17/17	-
5	NAG	A	1413	1	-	4/6/23/26	0/1/1/1
5	NAG	B	1409	1	-	1/6/23/26	0/1/1/1
5	NAG	B	1414	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1408	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1408	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1414	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1409	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1410	1	-	2/6/23/26	0/1/1/1
6	EIC	A	1420	-	-	7/17/17/17	-
5	NAG	C	1413	1	-	4/6/23/26	0/1/1/1
5	NAG	C	1410	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1406	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1413	1	-	4/6/23/26	0/1/1/1
5	NAG	B	1403	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1407	1	-	4/6/23/26	0/1/1/1
5	NAG	A	1405	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1409	1	-	1/6/23/26	0/1/1/1
5	NAG	A	1406	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1405	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1404	1	-	3/6/23/26	0/1/1/1
5	NAG	B	1410	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1404	1	-	4/6/23/26	0/1/1/1
5	NAG	B	1405	1	-	0/6/23/26	0/1/1/1
5	NAG	C	1406	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1403	1	-	2/6/23/26	0/1/1/1
6	EIC	B	1421	-	-	6/17/17/17	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1409	NAG	O5-C1	-2.84	1.39	1.43
5	B	1409	NAG	O5-C1	-2.70	1.39	1.43
5	A	1407	NAG	C1-C2	2.03	1.55	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	1407	NAG	C1-C2	2.02	1.55	1.52

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	1405	NAG	C8-C7-N2	2.32	120.02	116.10
5	C	1409	NAG	C8-C7-N2	2.32	120.02	116.10
5	B	1405	NAG	C8-C7-N2	2.30	120.00	116.10
5	A	1405	NAG	C8-C7-N2	2.29	119.98	116.10
5	B	1410	NAG	C1-O5-C5	2.25	115.23	112.19
5	A	1410	NAG	C1-O5-C5	2.23	115.21	112.19
5	C	1410	NAG	C1-O5-C5	2.20	115.17	112.19
5	A	1405	NAG	C2-N2-C7	-2.04	120.00	122.90
5	B	1405	NAG	C2-N2-C7	-2.04	120.00	122.90
5	C	1405	NAG	C2-N2-C7	-2.03	120.01	122.90
5	C	1409	NAG	C2-N2-C7	-2.01	120.04	122.90

There are no chirality outliers.

All (90) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1408	NAG	C8-C7-N2-C2
5	A	1408	NAG	O7-C7-N2-C2
5	A	1413	NAG	C8-C7-N2-C2
5	A	1413	NAG	O7-C7-N2-C2
5	B	1408	NAG	C8-C7-N2-C2
5	B	1408	NAG	O7-C7-N2-C2
5	B	1413	NAG	C8-C7-N2-C2
5	B	1413	NAG	O7-C7-N2-C2
5	C	1408	NAG	C8-C7-N2-C2
5	C	1408	NAG	O7-C7-N2-C2
5	C	1413	NAG	C8-C7-N2-C2
5	C	1413	NAG	O7-C7-N2-C2
5	B	1404	NAG	C4-C5-C6-O6
5	C	1404	NAG	C4-C5-C6-O6
5	A	1404	NAG	C4-C5-C6-O6
5	B	1407	NAG	O5-C5-C6-O6
5	C	1407	NAG	O5-C5-C6-O6
5	A	1407	NAG	O5-C5-C6-O6
5	A	1404	NAG	O5-C5-C6-O6
5	B	1404	NAG	O5-C5-C6-O6
5	C	1404	NAG	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
5	A	1407	NAG	C1-C2-N2-C7
5	B	1407	NAG	C1-C2-N2-C7
5	C	1407	NAG	C1-C2-N2-C7
5	A	1403	NAG	O5-C5-C6-O6
5	B	1403	NAG	O5-C5-C6-O6
5	C	1403	NAG	O5-C5-C6-O6
5	A	1414	NAG	C4-C5-C6-O6
5	B	1414	NAG	C4-C5-C6-O6
5	C	1414	NAG	C4-C5-C6-O6
5	A	1414	NAG	O5-C5-C6-O6
5	B	1414	NAG	O5-C5-C6-O6
5	C	1414	NAG	O5-C5-C6-O6
5	A	1410	NAG	O5-C5-C6-O6
5	B	1410	NAG	O5-C5-C6-O6
5	C	1410	NAG	O5-C5-C6-O6
6	A	1419	EIC	C1-C2-C3-C4
5	A	1413	NAG	O5-C5-C6-O6
5	B	1413	NAG	O5-C5-C6-O6
5	C	1413	NAG	O5-C5-C6-O6
5	B	1410	NAG	C4-C5-C6-O6
5	A	1410	NAG	C4-C5-C6-O6
5	C	1410	NAG	C4-C5-C6-O6
5	A	1407	NAG	C4-C5-C6-O6
5	B	1407	NAG	C4-C5-C6-O6
5	C	1407	NAG	C4-C5-C6-O6
5	B	1413	NAG	C1-C2-N2-C7
5	C	1413	NAG	C1-C2-N2-C7
5	A	1406	NAG	O5-C5-C6-O6
5	B	1406	NAG	O5-C5-C6-O6
5	C	1406	NAG	O5-C5-C6-O6
6	B	1421	EIC	C4-C5-C6-C7
5	A	1413	NAG	C1-C2-N2-C7
5	A	1406	NAG	C4-C5-C6-O6
6	A	1419	EIC	C5-C6-C7-C8
5	B	1406	NAG	C4-C5-C6-O6
5	C	1406	NAG	C4-C5-C6-O6
6	A	1419	EIC	C13-C14-C15-C16
6	A	1419	EIC	C14-C15-C16-C17
6	A	1419	EIC	C15-C16-C17-C18
6	A	1419	EIC	C6-C7-C8-C9
6	B	1421	EIC	C2-C3-C4-C5
6	A	1420	EIC	C4-C5-C6-C7

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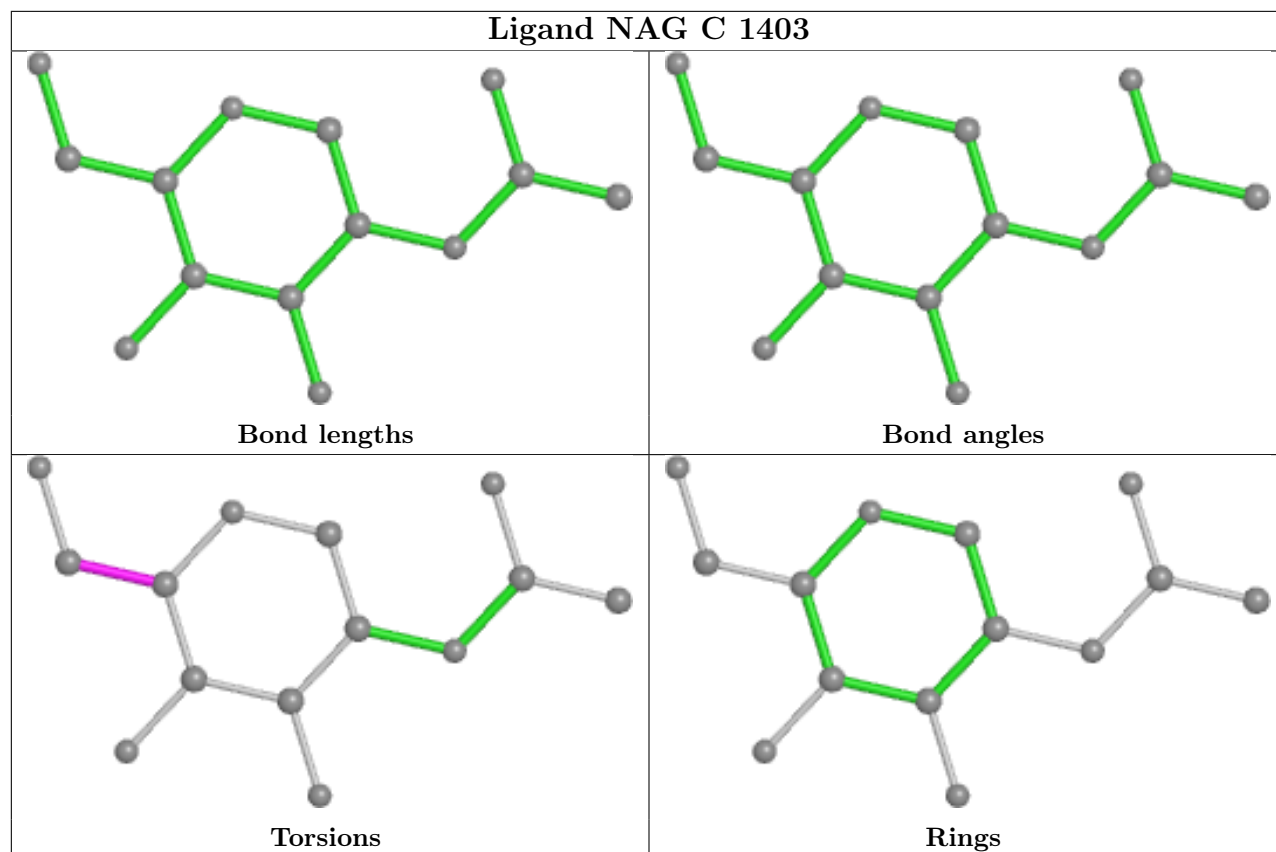
Mol	Chain	Res	Type	Atoms
6	A	1419	EIC	C10-C11-C12-C13
6	A	1420	EIC	C10-C11-C12-C13
5	A	1404	NAG	C1-C2-N2-C7
5	B	1404	NAG	C1-C2-N2-C7
5	C	1404	NAG	C1-C2-N2-C7
6	B	1421	EIC	C5-C6-C7-C8
5	B	1403	NAG	C4-C5-C6-O6
5	C	1403	NAG	C4-C5-C6-O6
5	A	1403	NAG	C4-C5-C6-O6
6	A	1420	EIC	C15-C16-C17-C18
6	B	1421	EIC	O1-C1-C2-C3
6	A	1419	EIC	C9-C10-C11-C12
6	A	1420	EIC	C7-C8-C9-C10
6	B	1421	EIC	O2-C1-C2-C3
6	A	1419	EIC	C4-C5-C6-C7
5	A	1409	NAG	C4-C5-C6-O6
5	B	1409	NAG	C4-C5-C6-O6
6	A	1420	EIC	O1-C1-C2-C3
6	A	1420	EIC	O2-C1-C2-C3
6	B	1421	EIC	C7-C8-C9-C10
6	A	1420	EIC	C14-C15-C16-C17
5	A	1407	NAG	C3-C2-N2-C7
5	B	1407	NAG	C3-C2-N2-C7
5	C	1404	NAG	C3-C2-N2-C7
5	C	1407	NAG	C3-C2-N2-C7
6	A	1419	EIC	C7-C8-C9-C10
6	A	1419	EIC	C12-C13-C14-C15

There are no ring outliers.

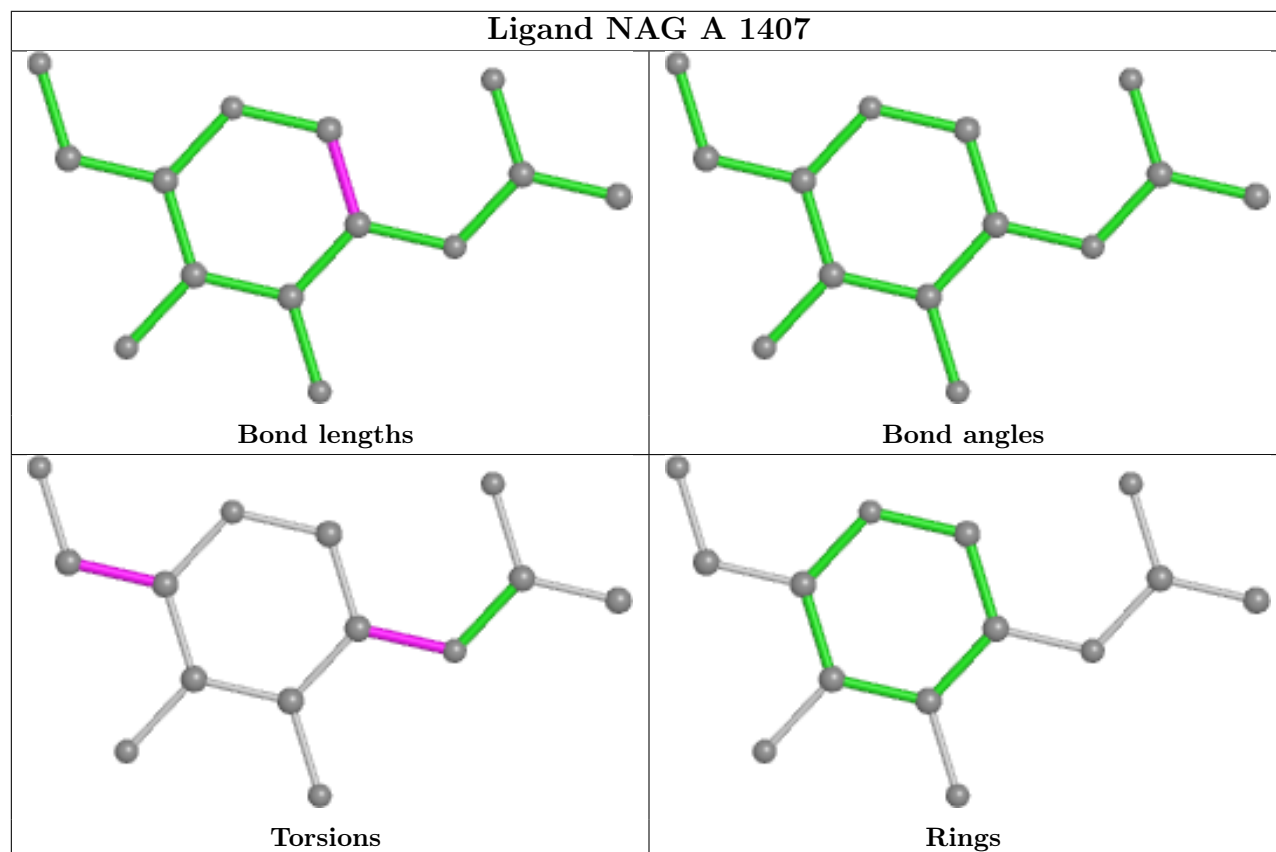
No monomer is involved in short contacts.

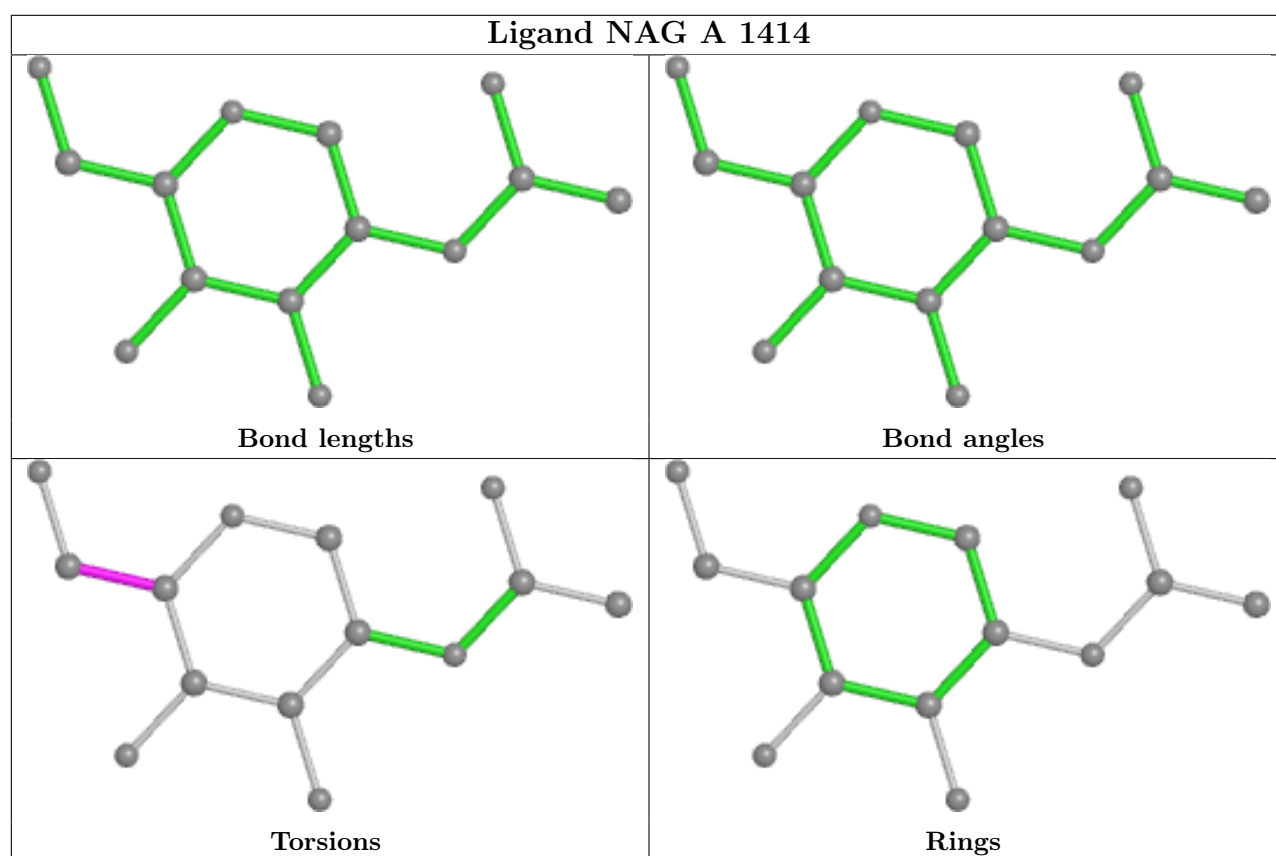
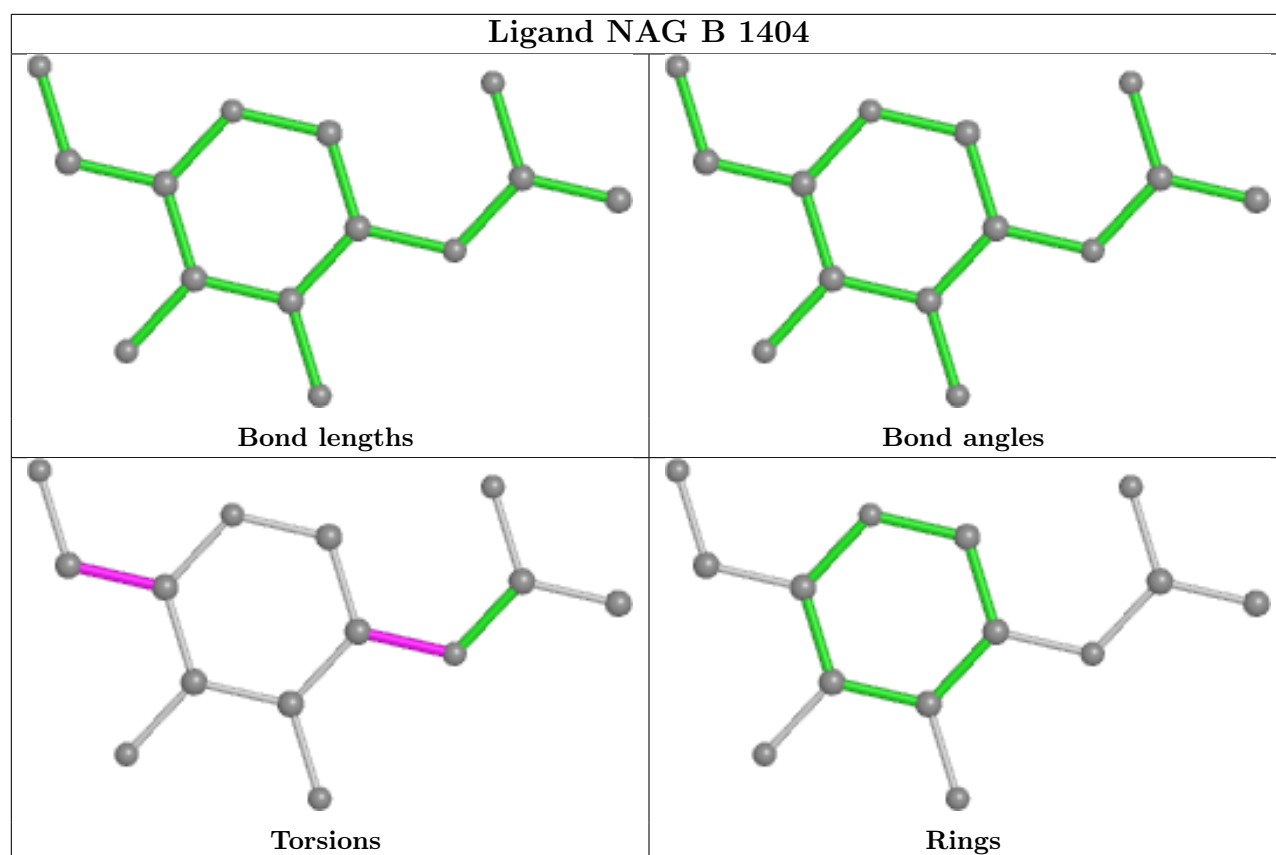
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

Ligand NAG C 1403

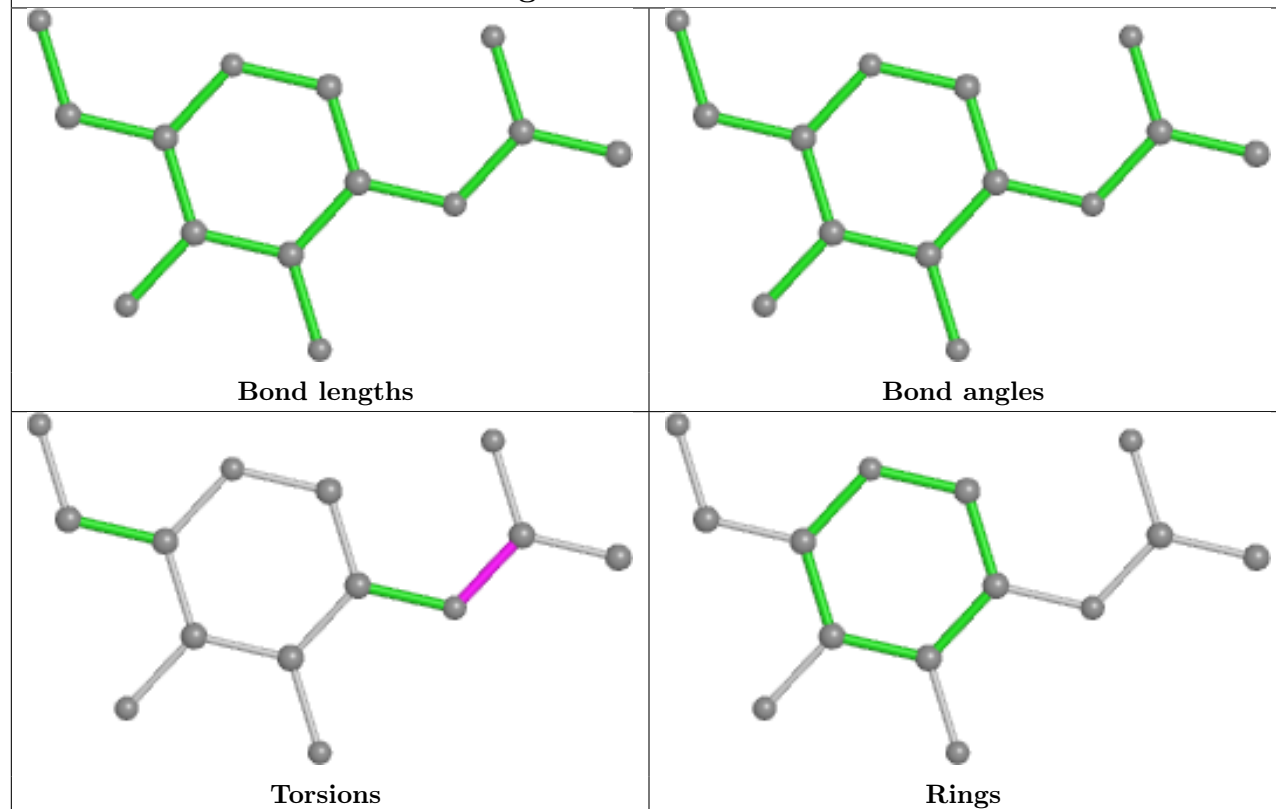


Ligand NAG A 1407

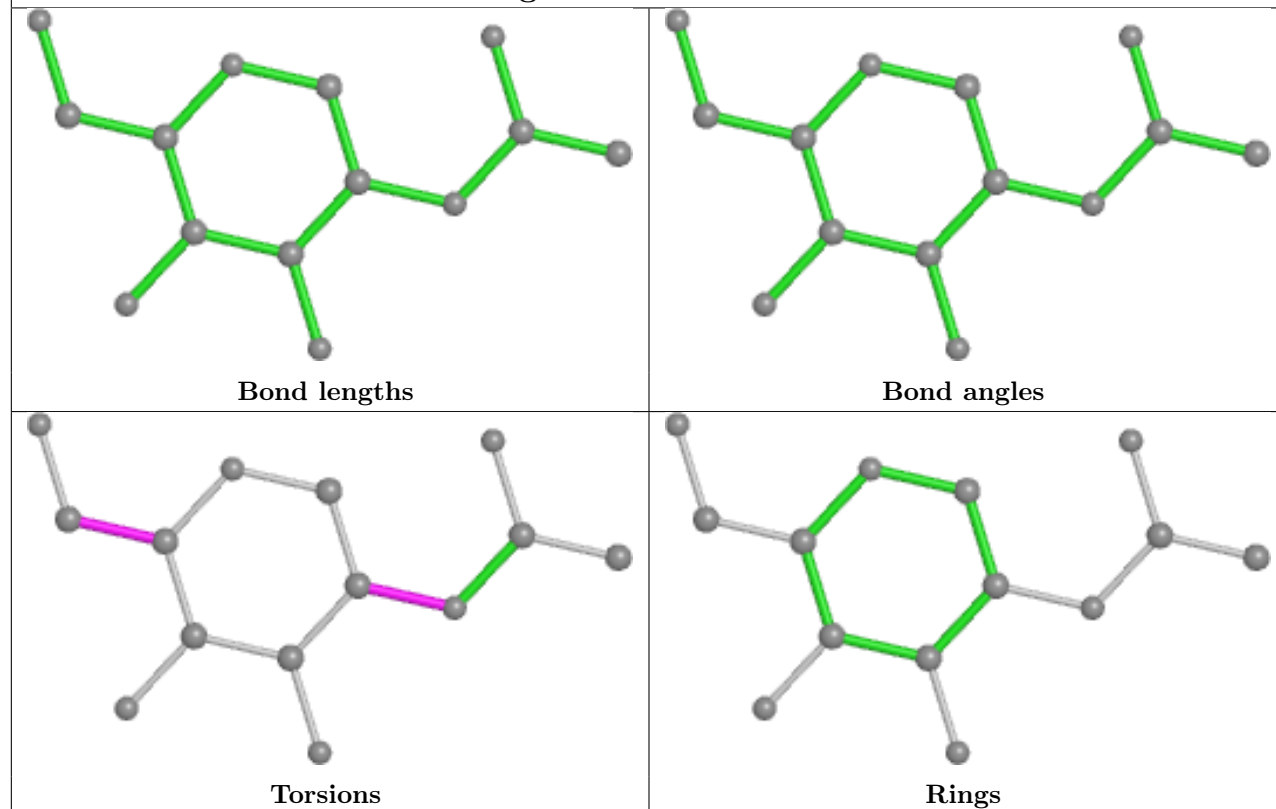


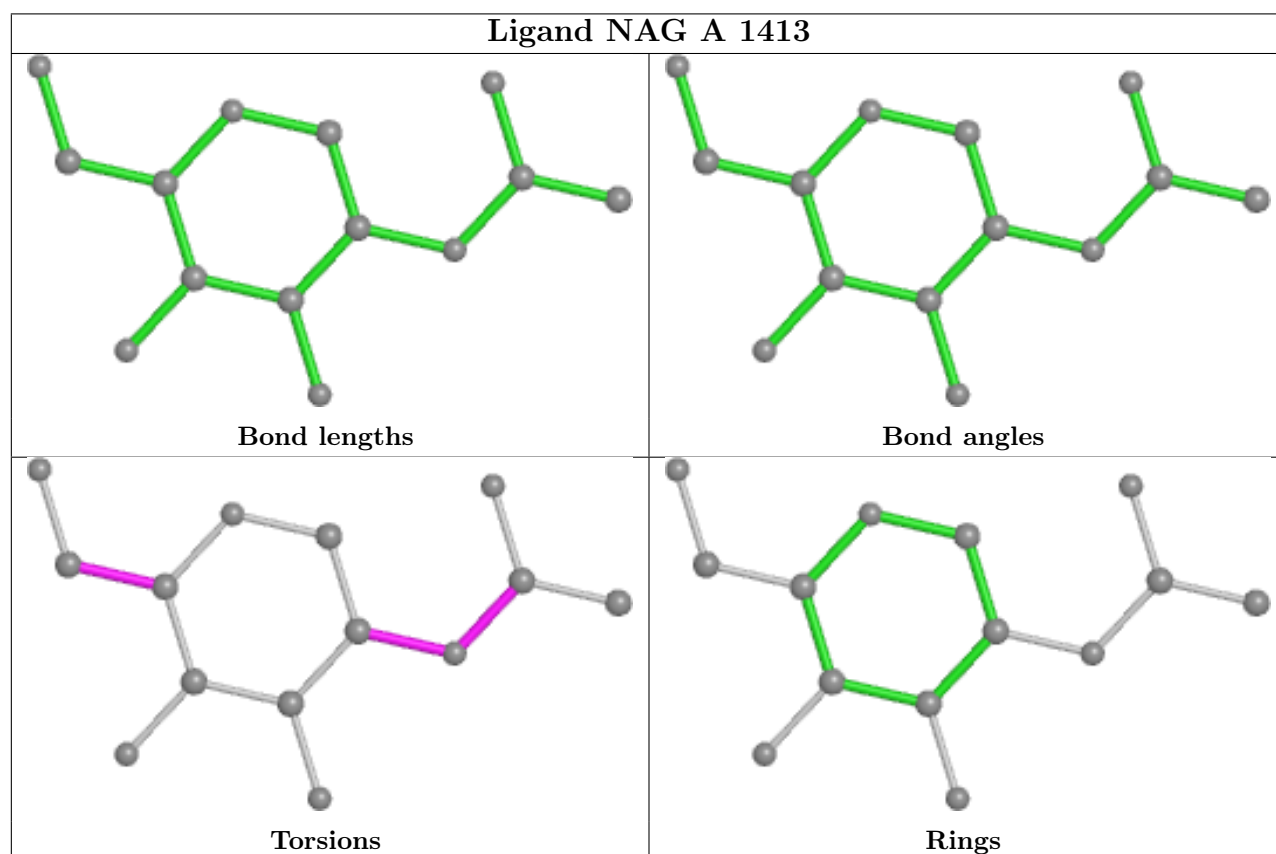
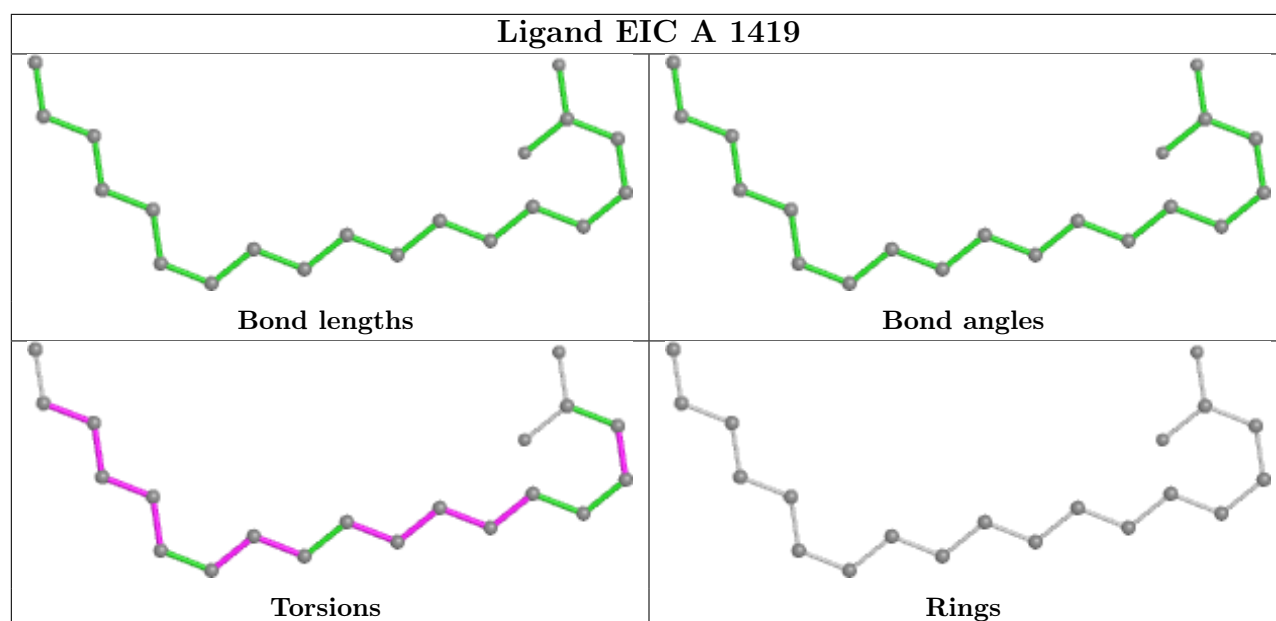


Ligand NAG A 1408

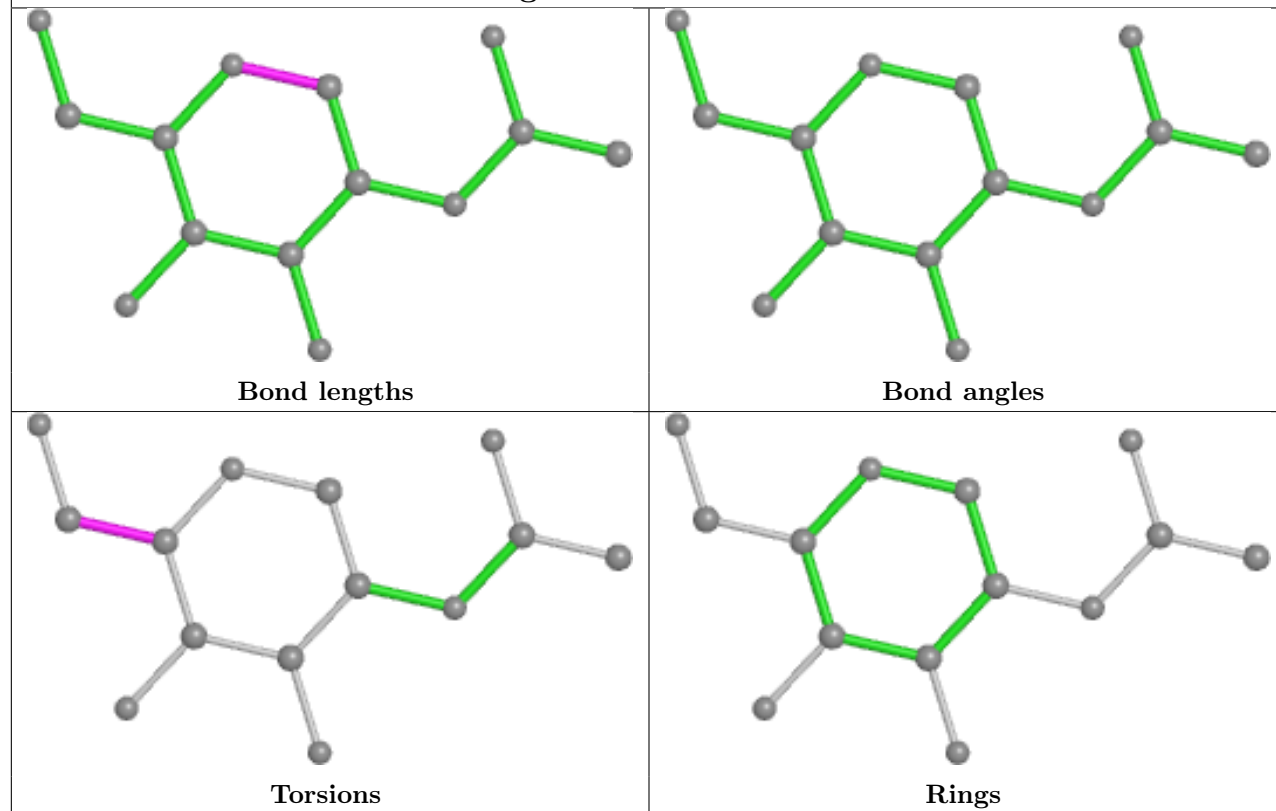


Ligand NAG C 1407

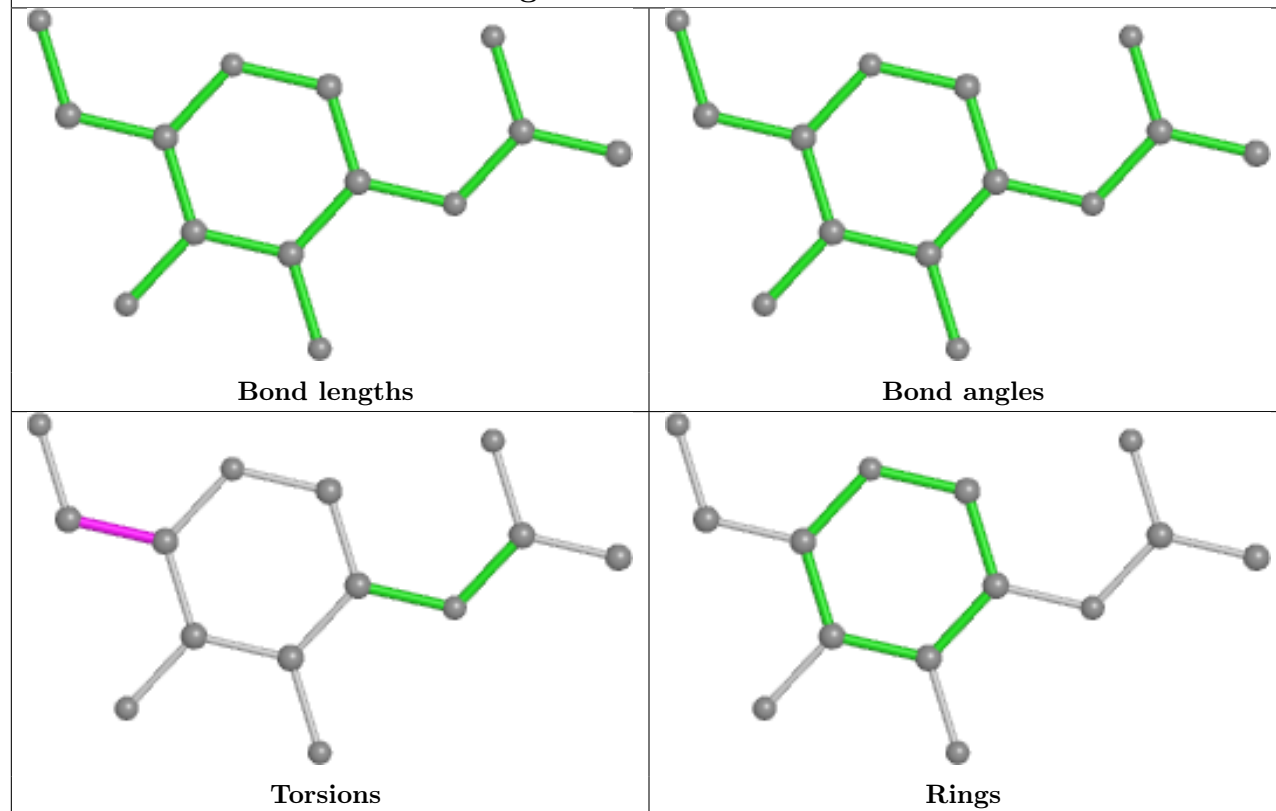


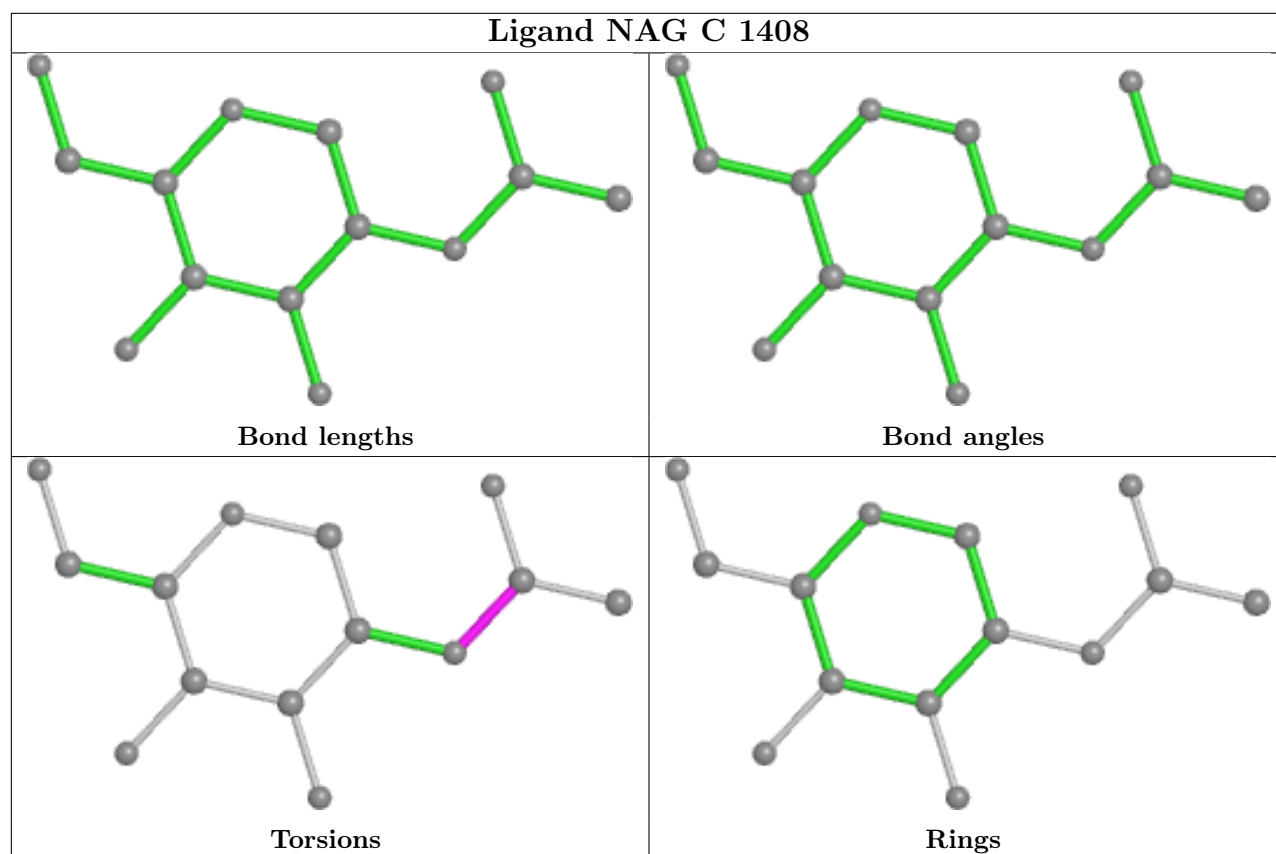
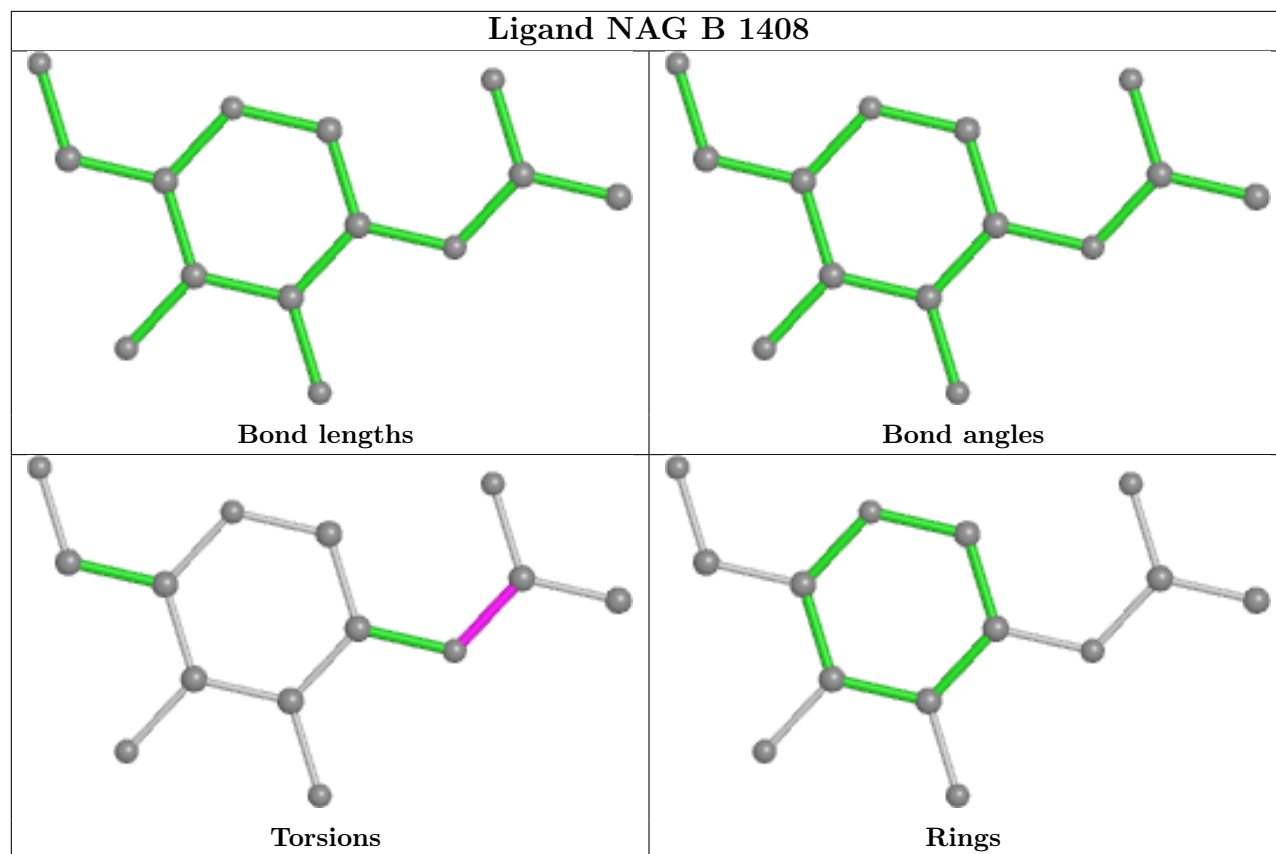


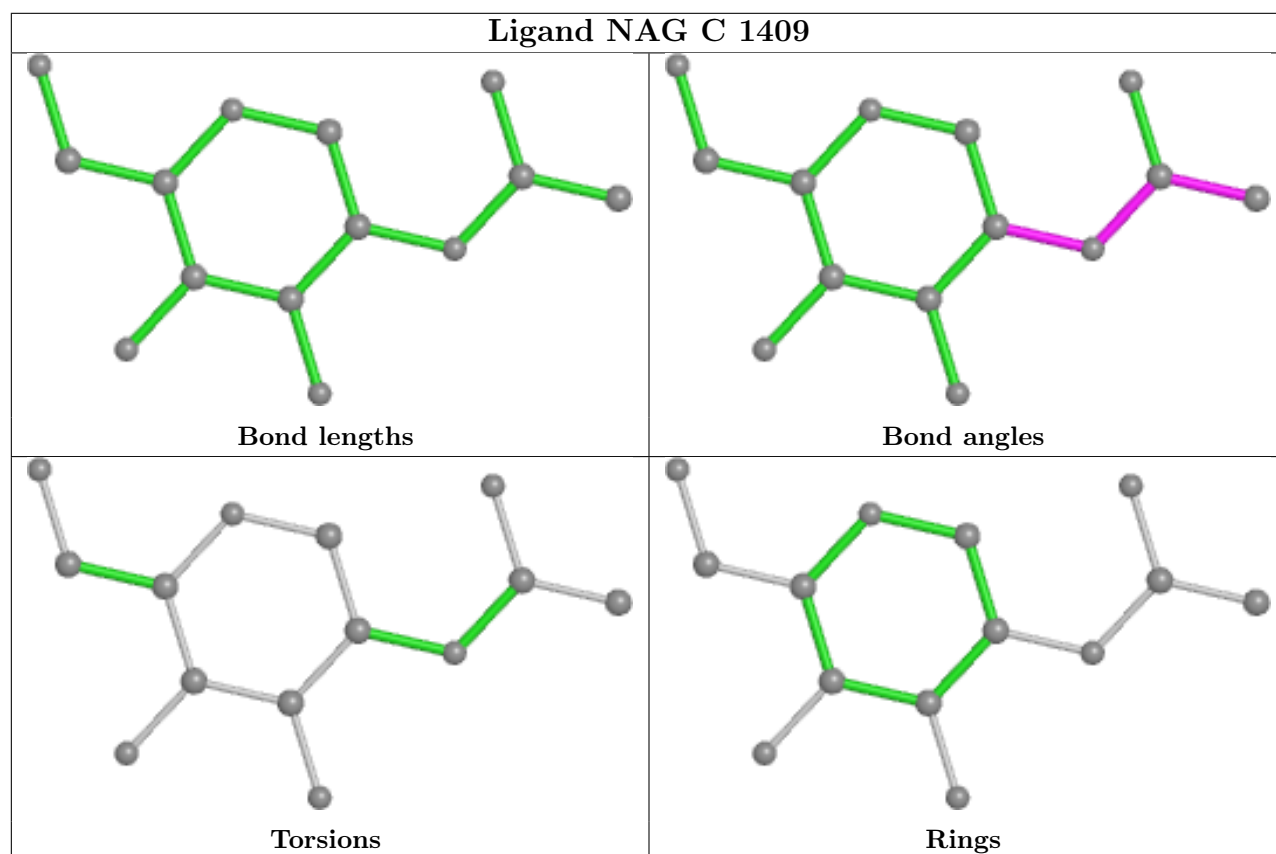
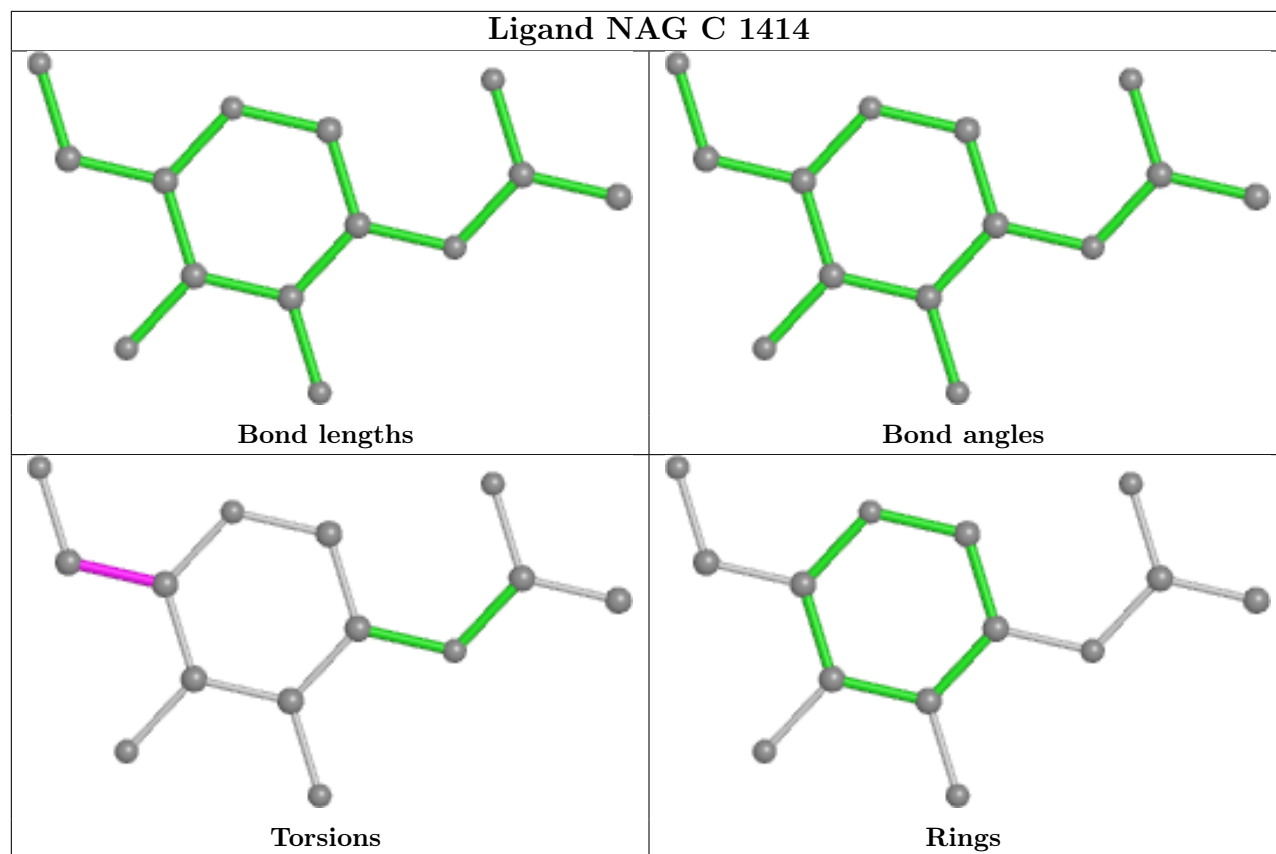
Ligand NAG B 1409

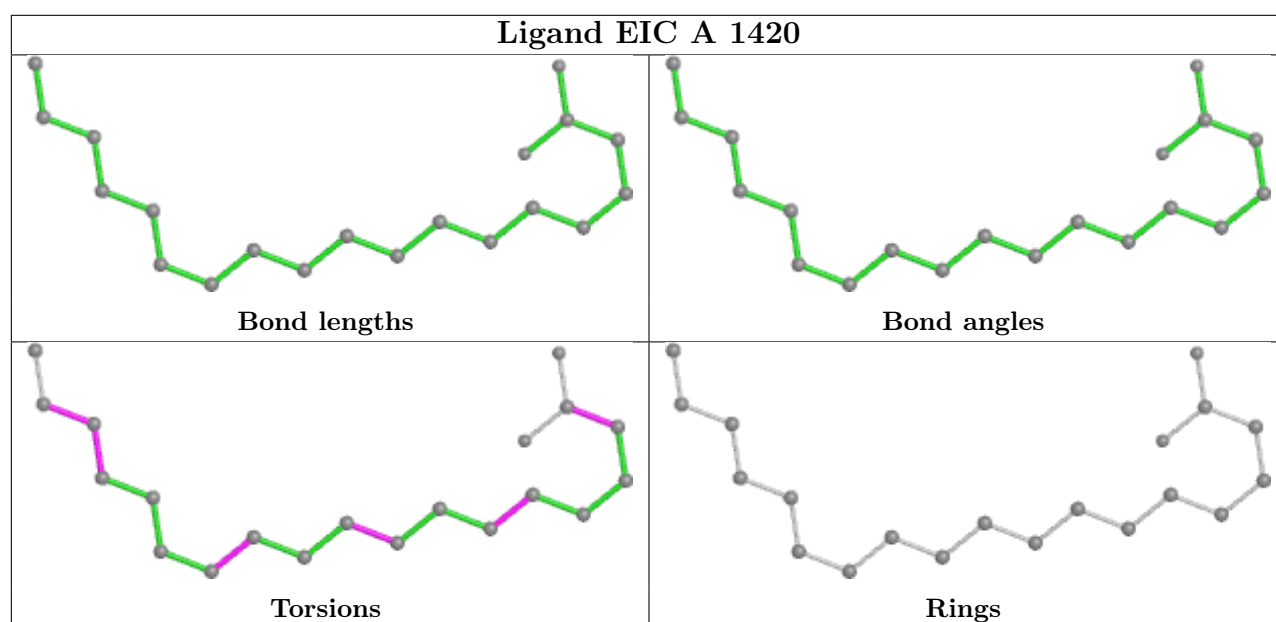
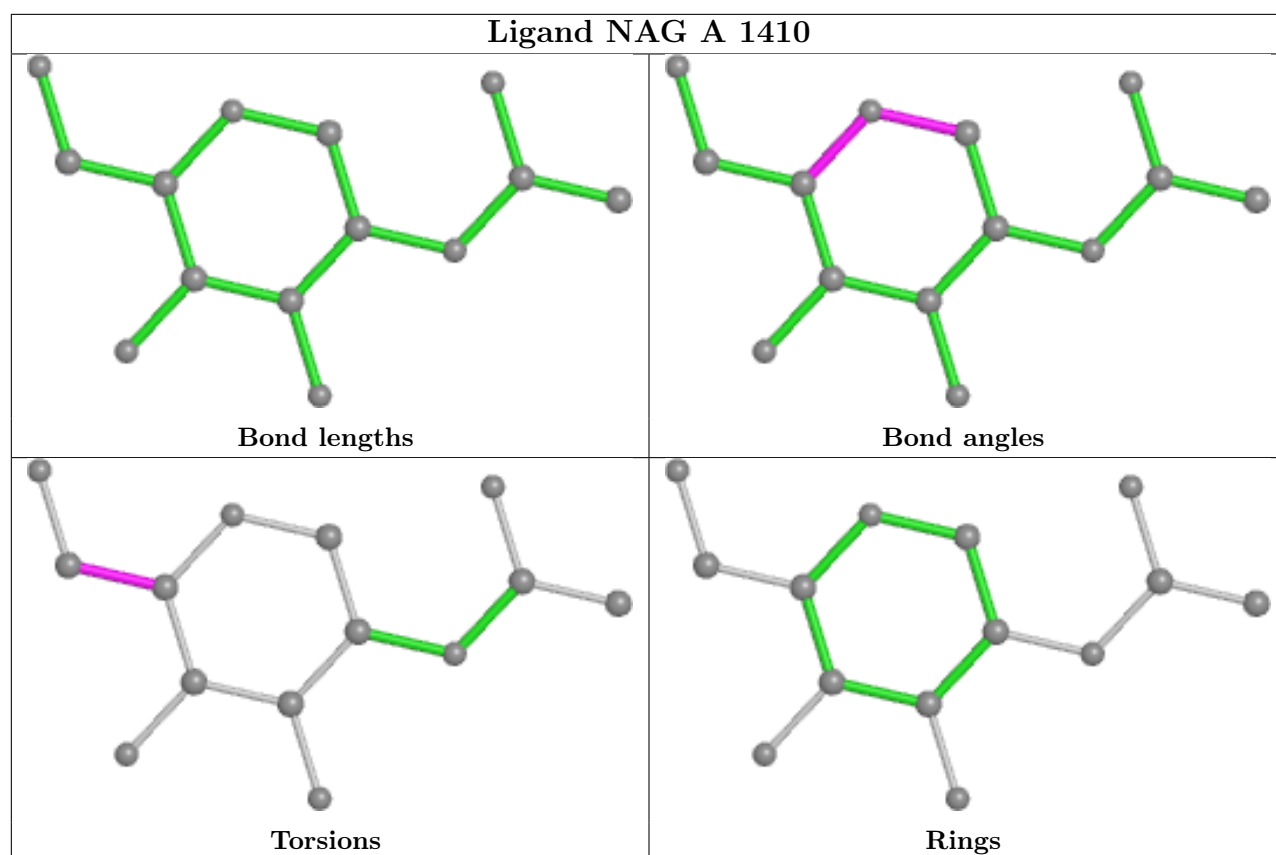


Ligand NAG B 1414

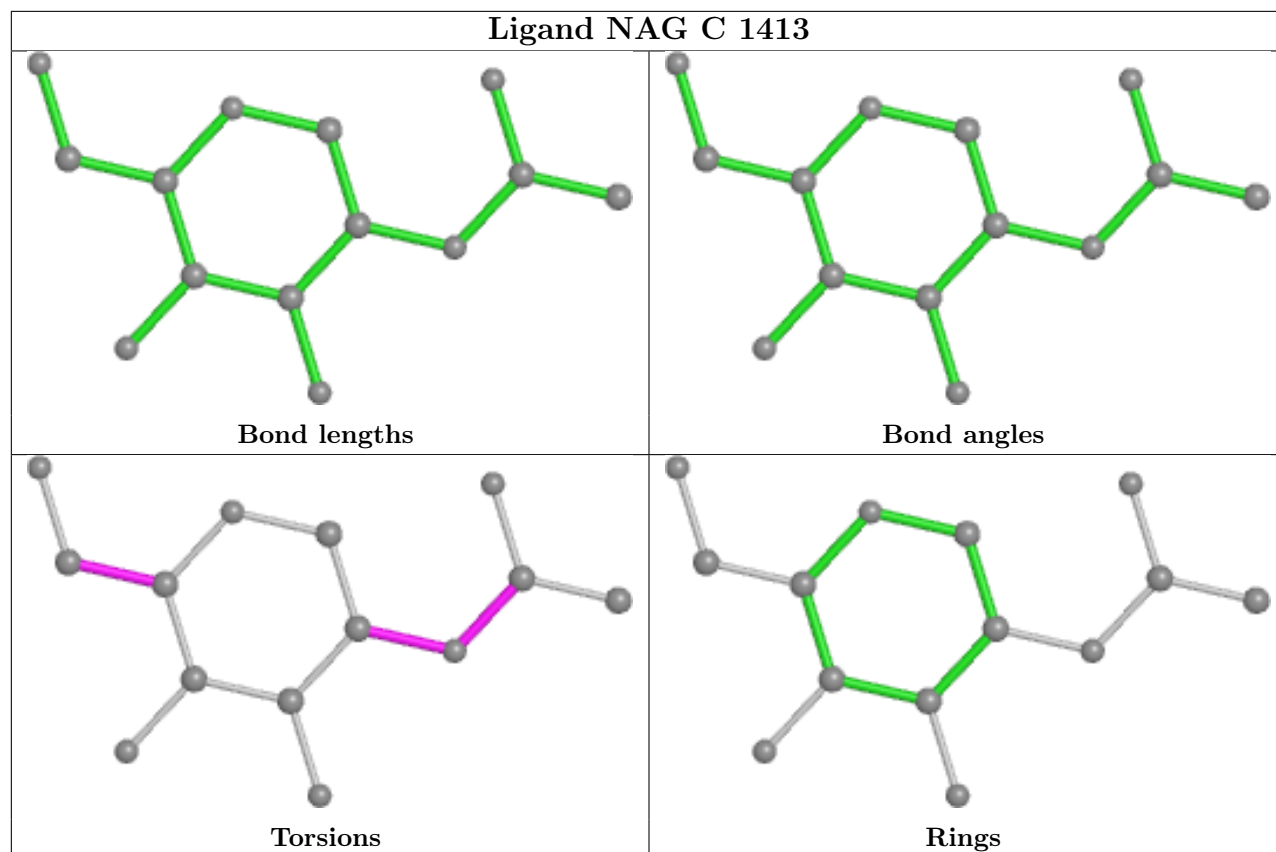




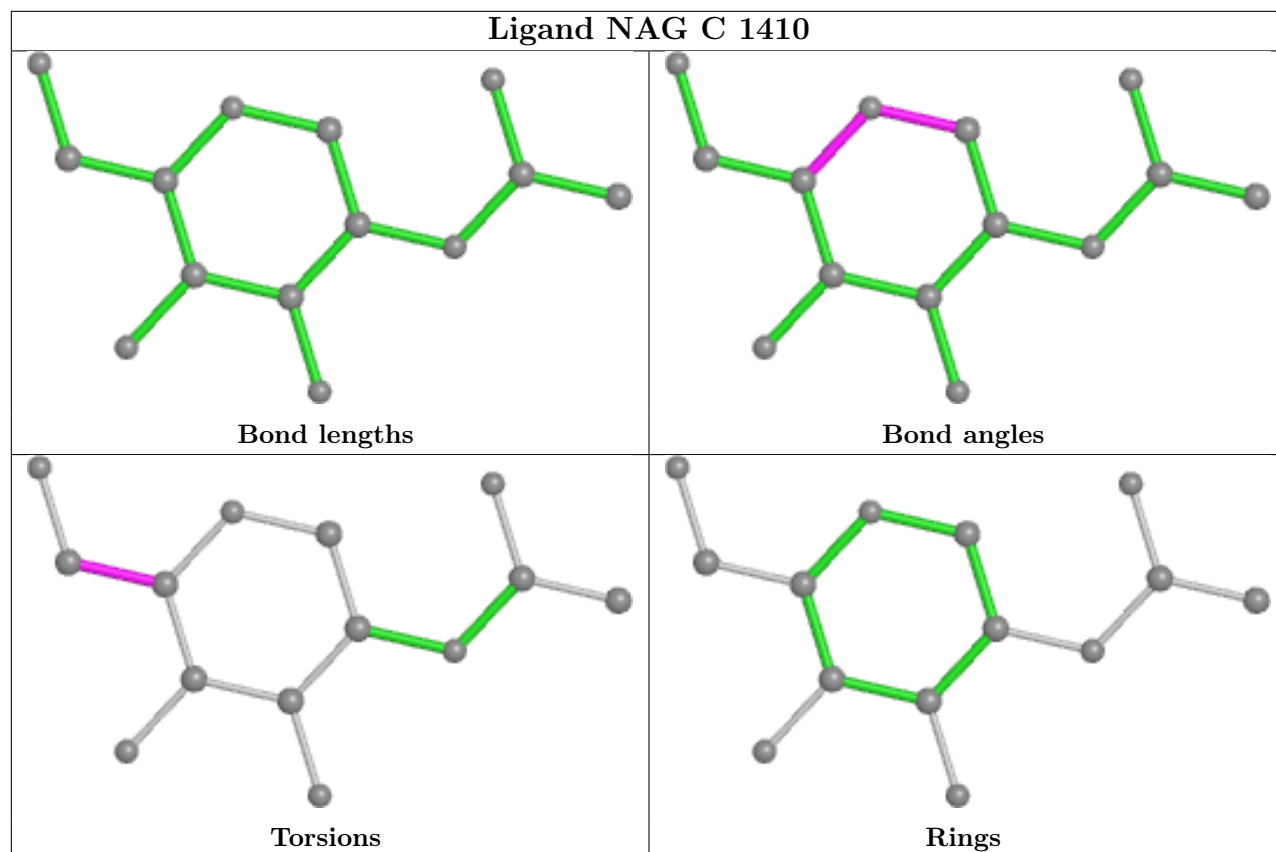


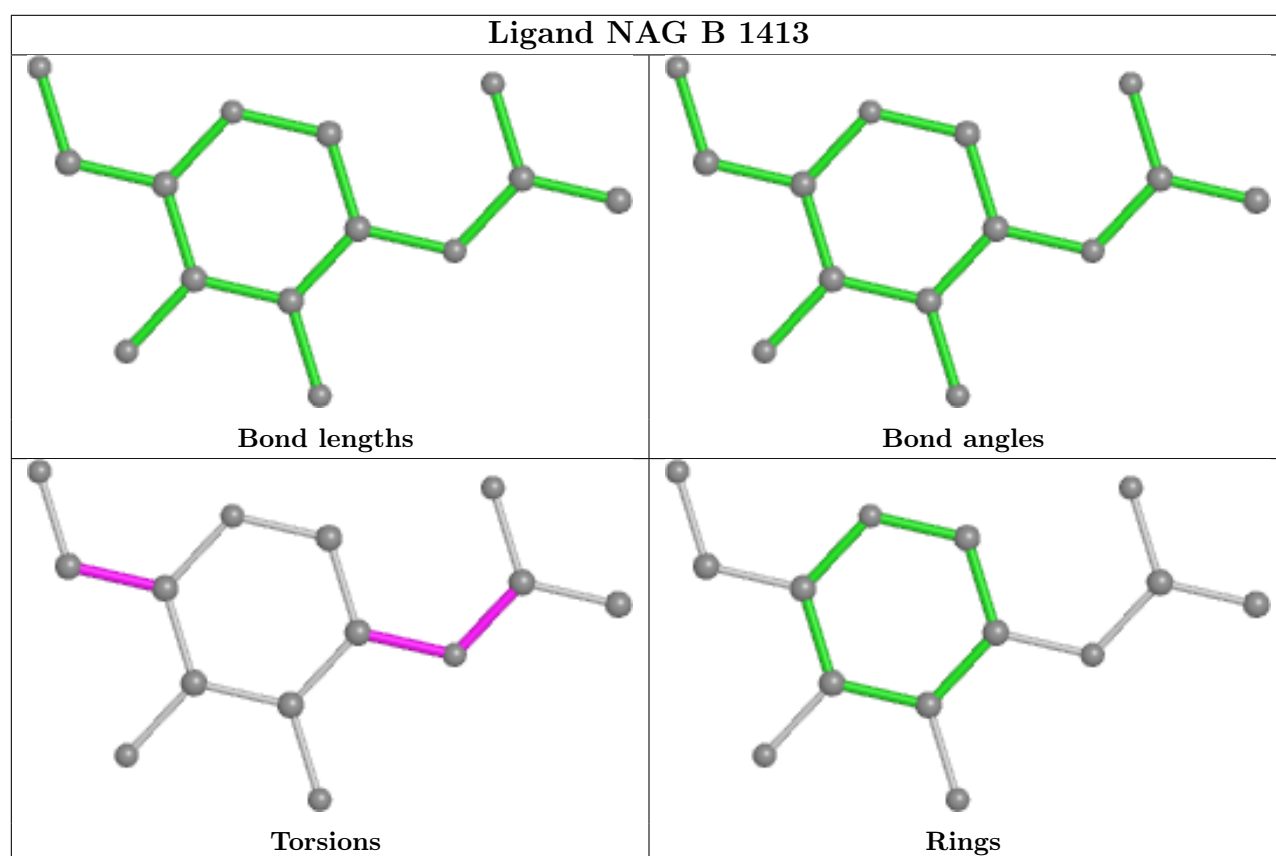
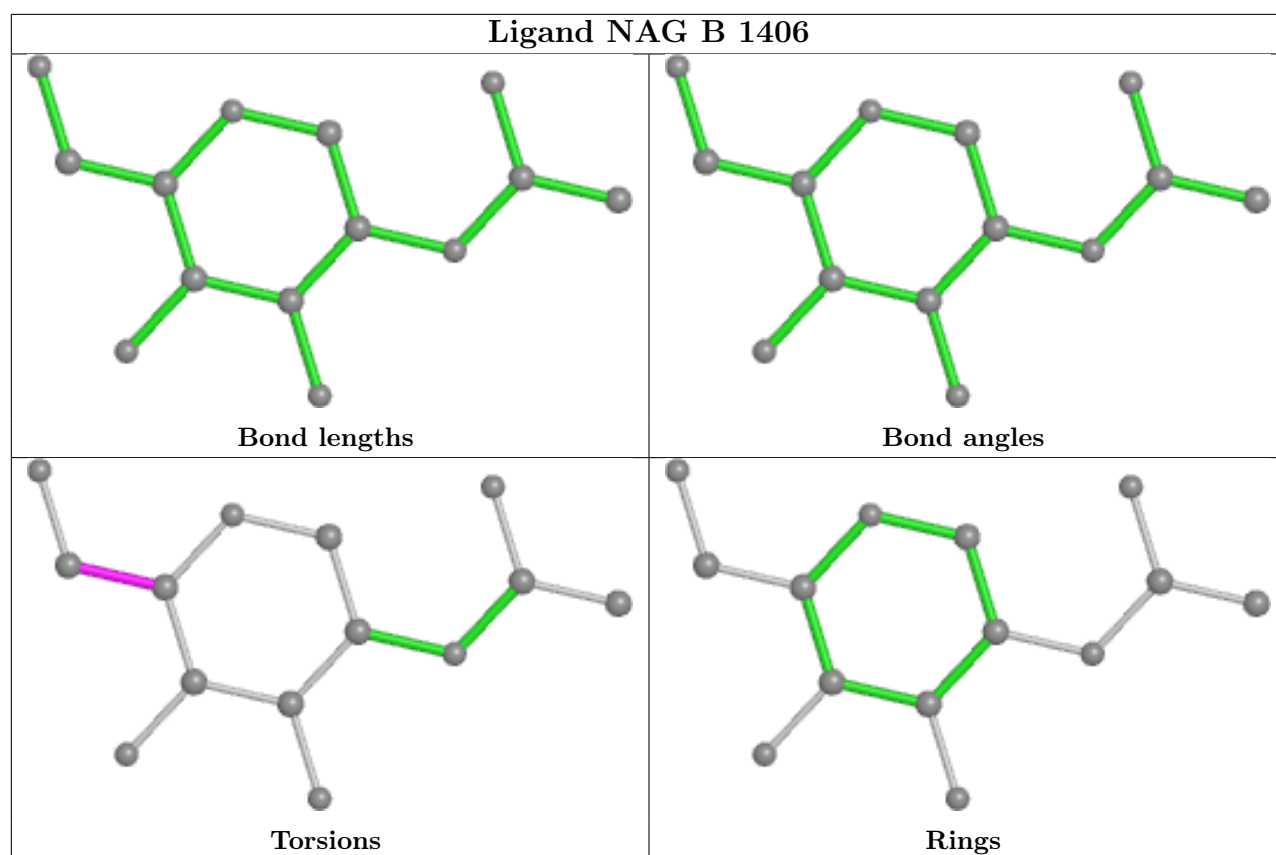


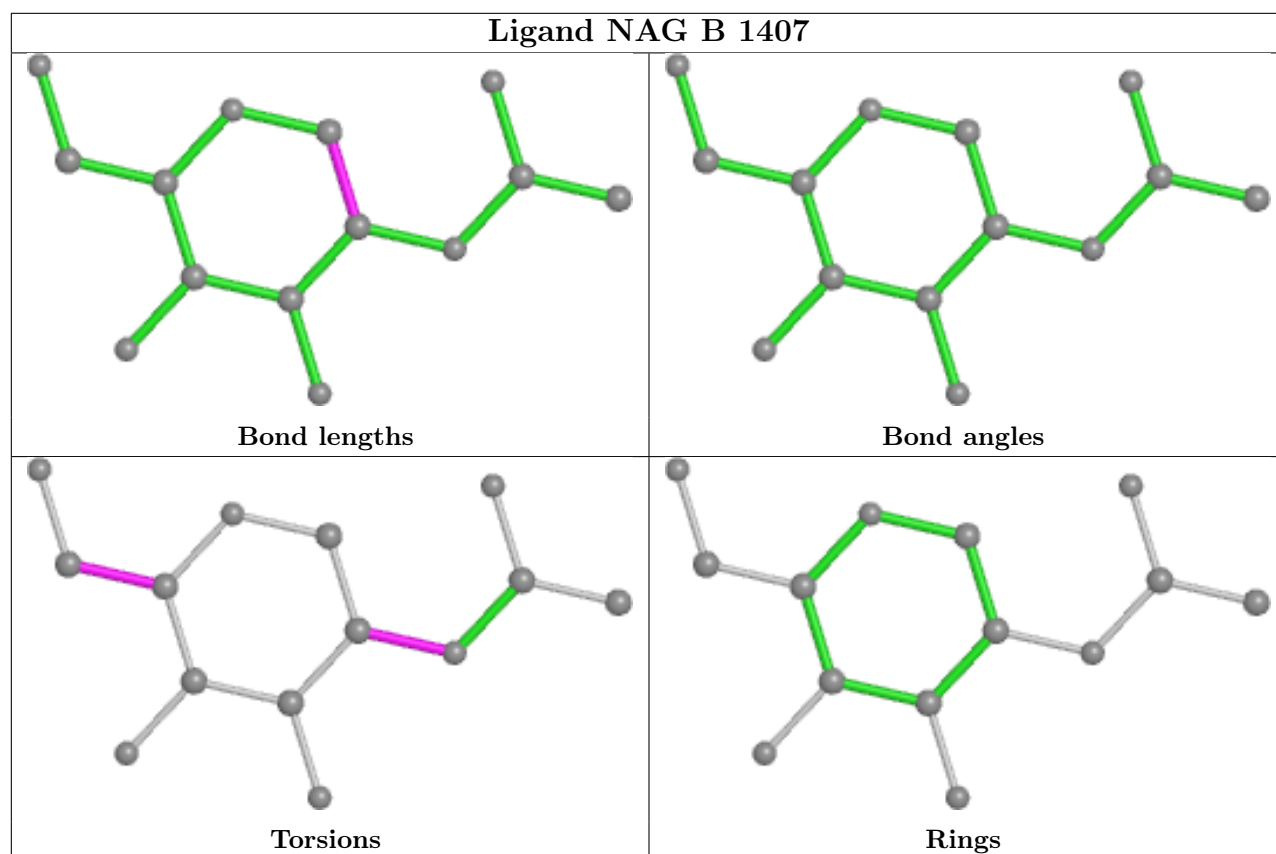
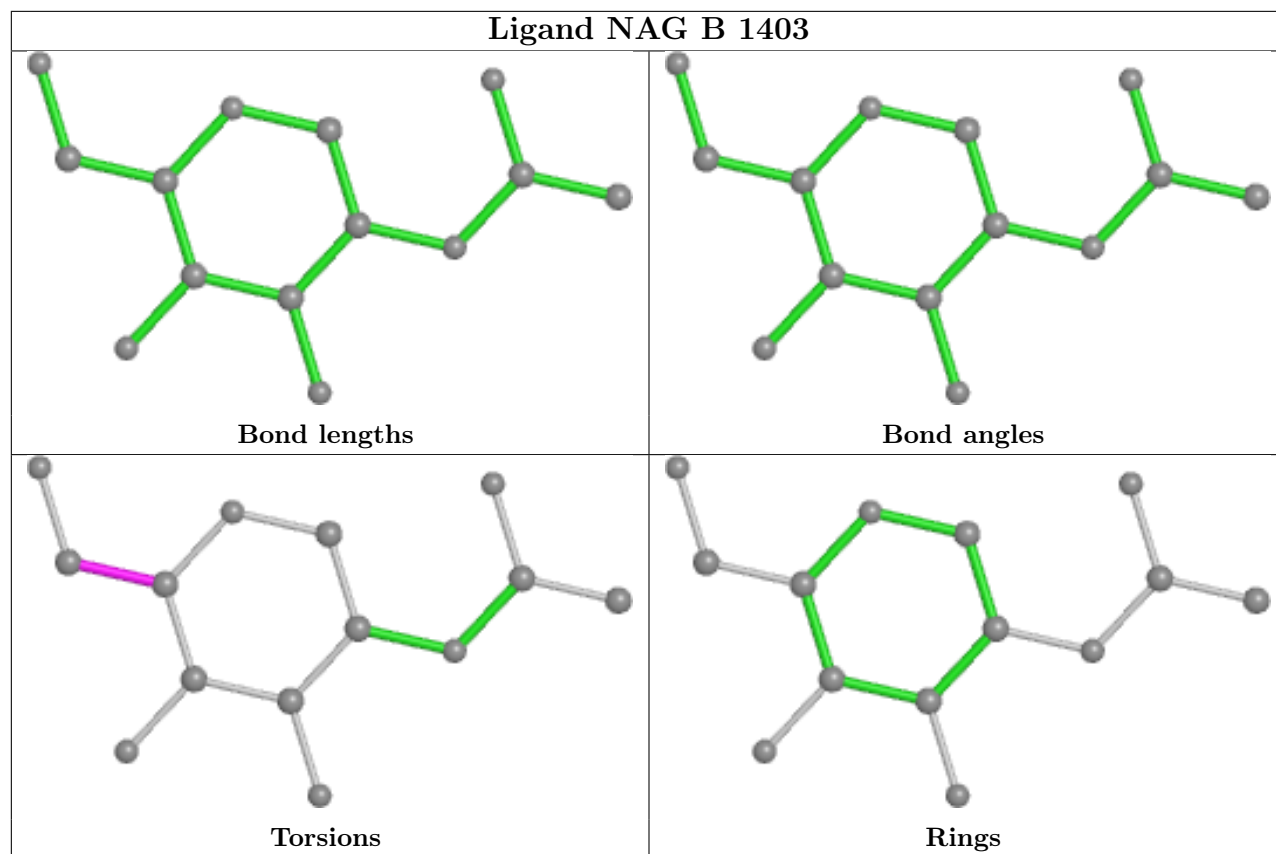
Ligand NAG C 1413



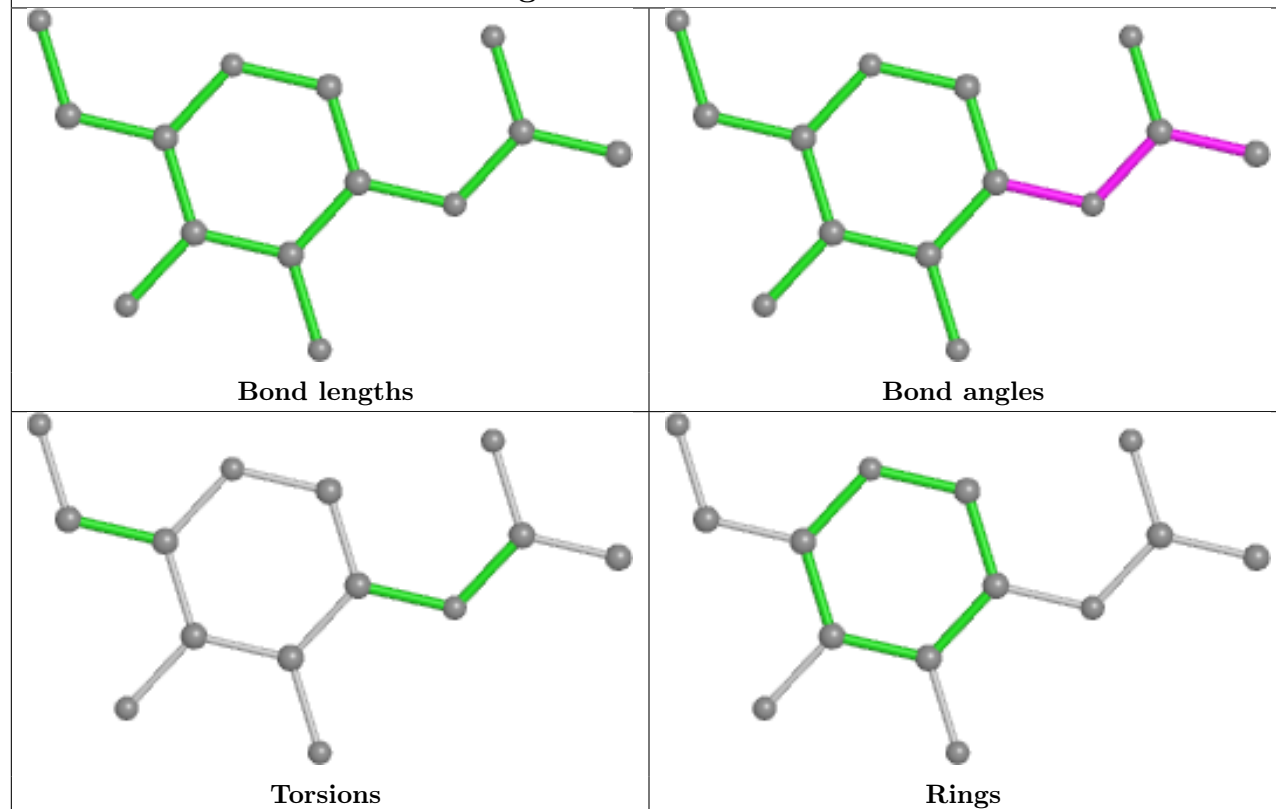
Ligand NAG C 1410



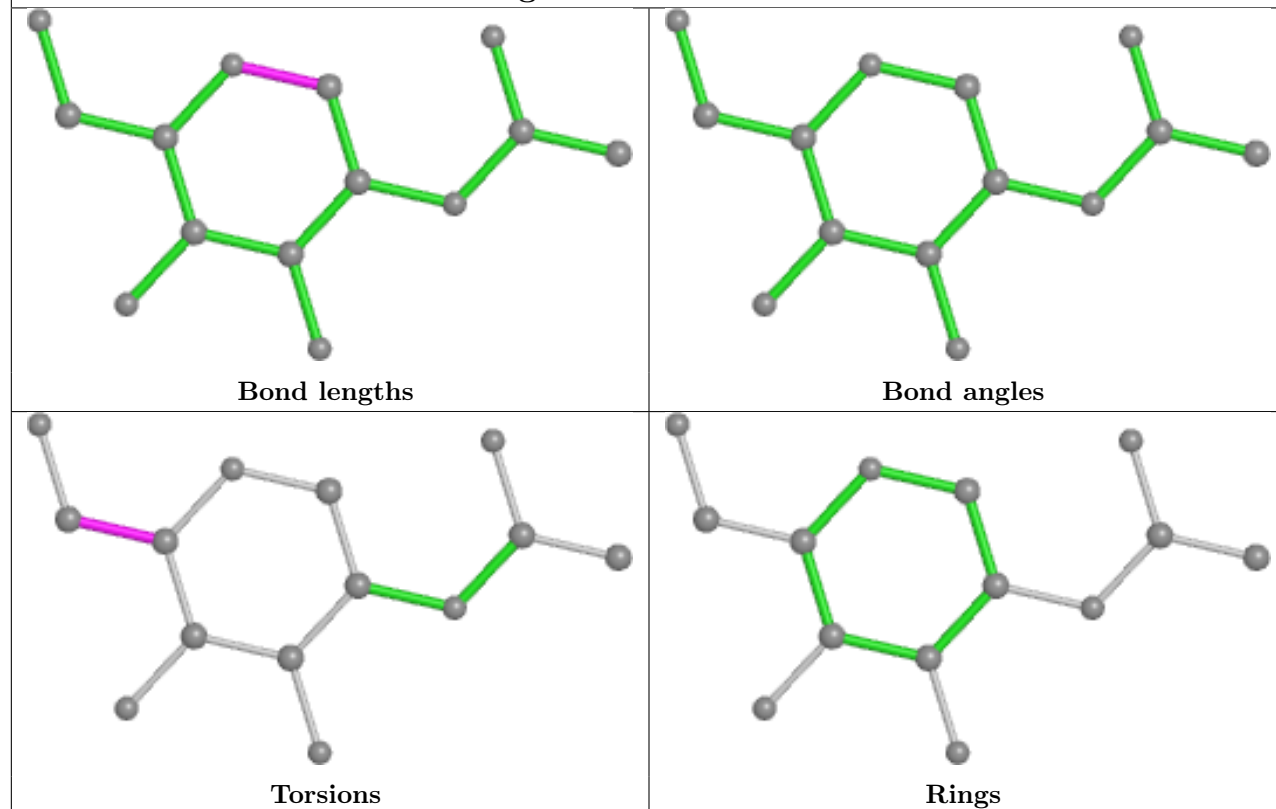




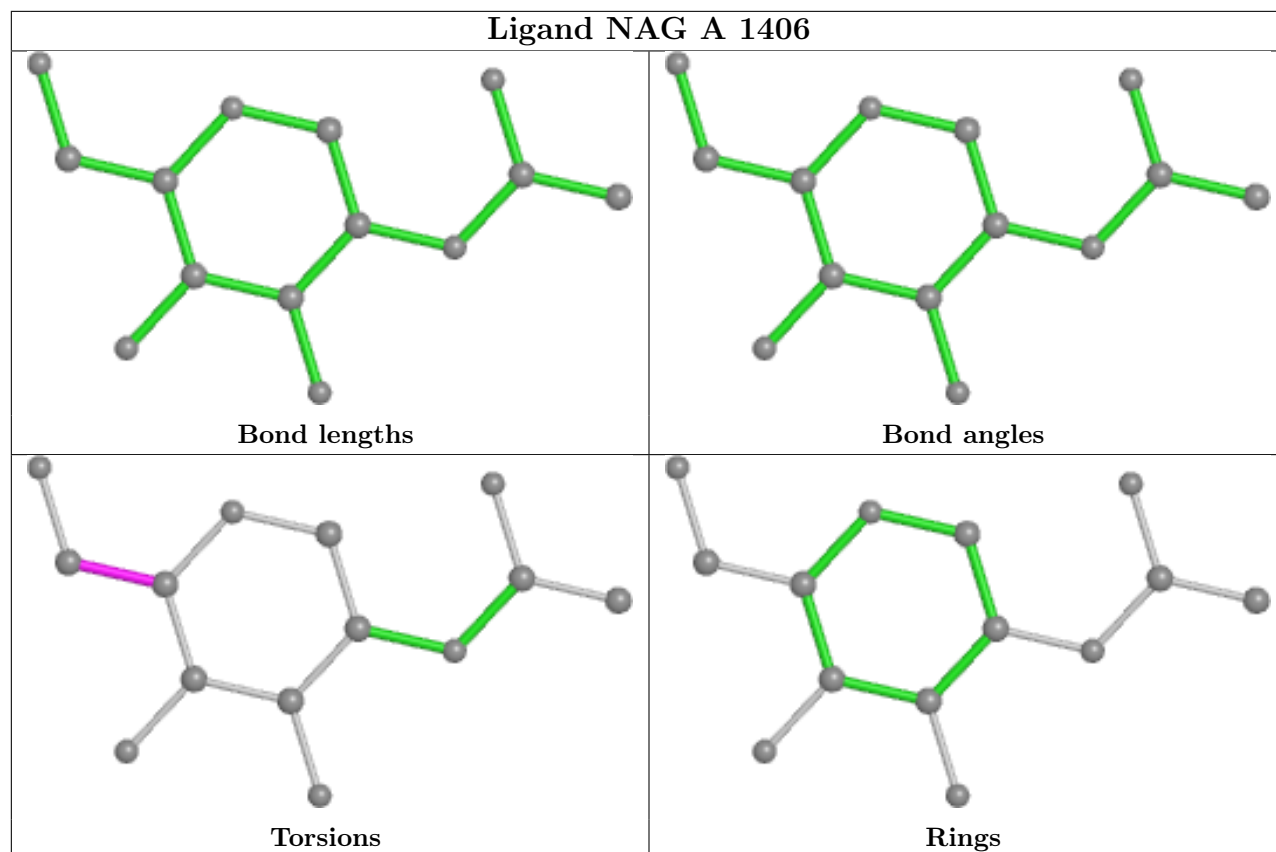
Ligand NAG A 1405



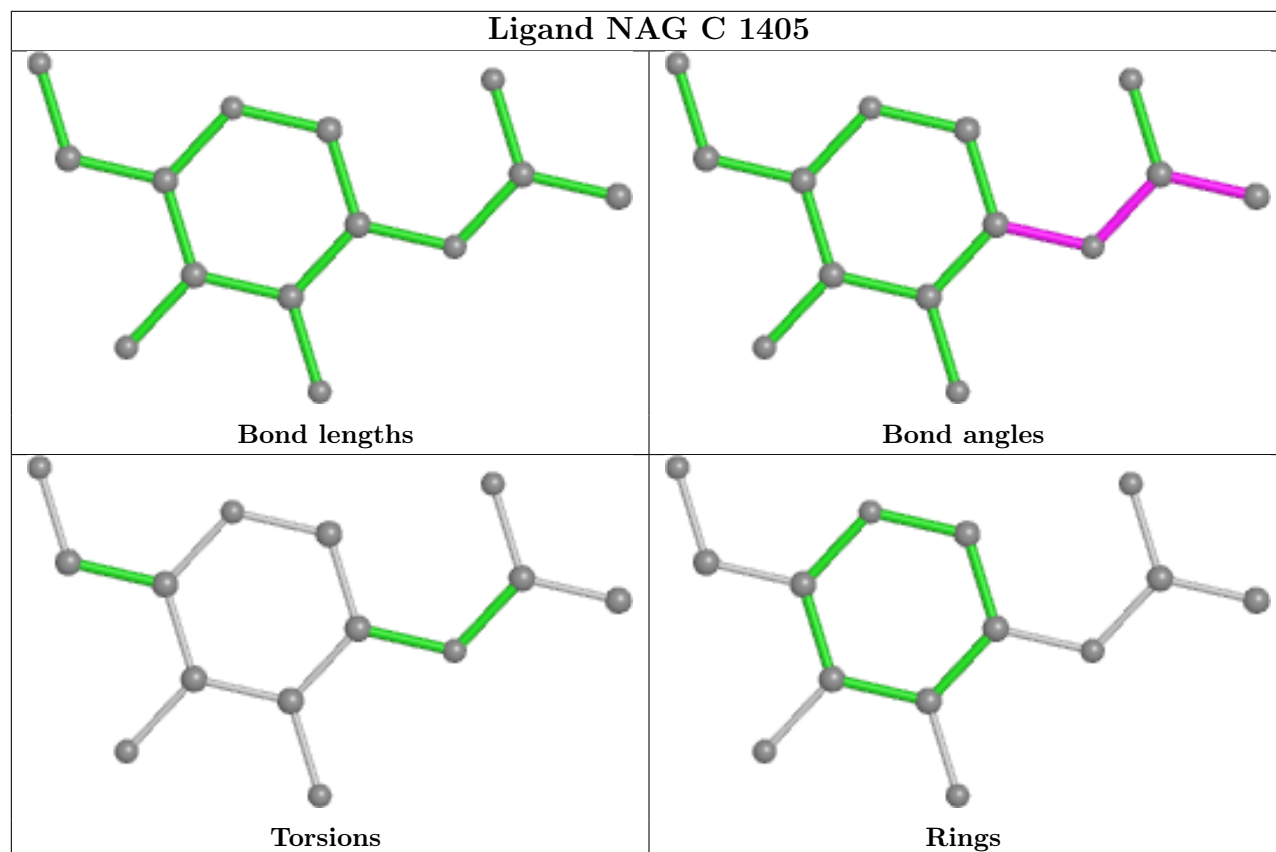
Ligand NAG A 1409



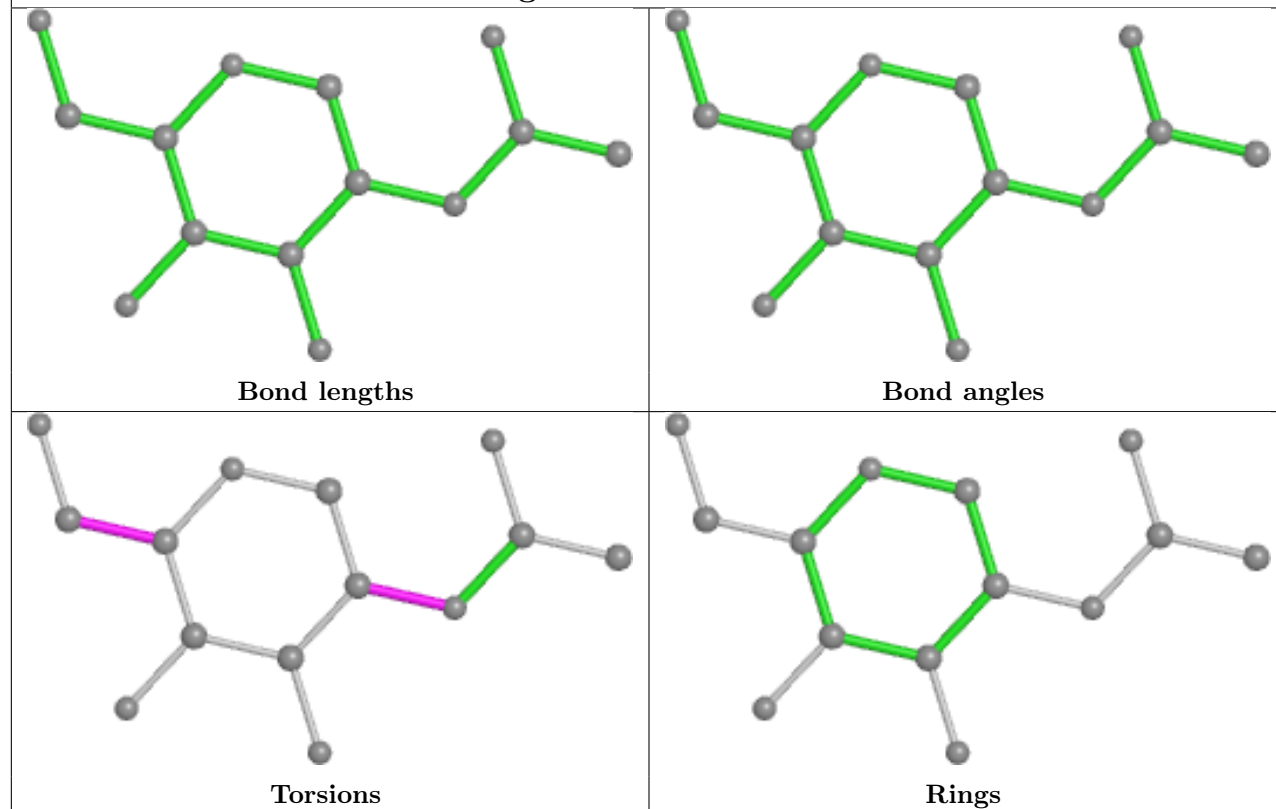
Ligand NAG A 1406



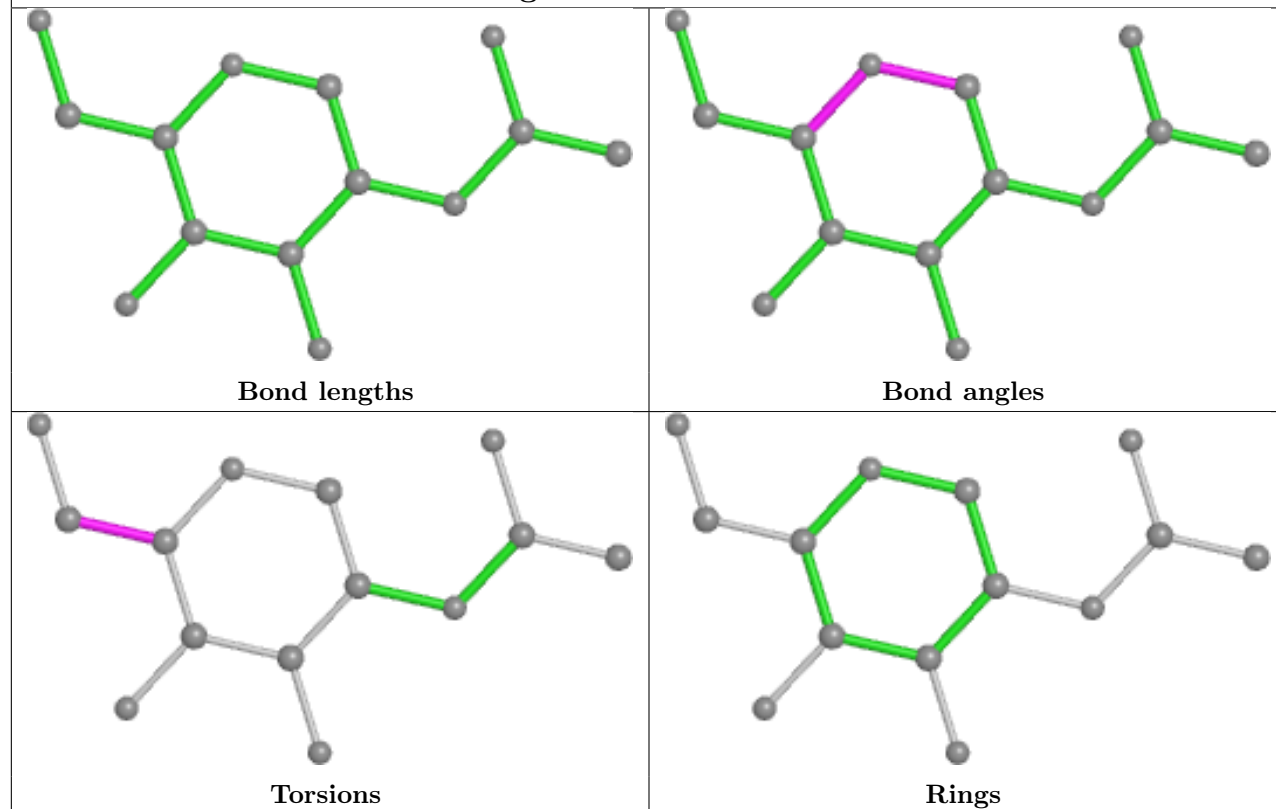
Ligand NAG C 1405

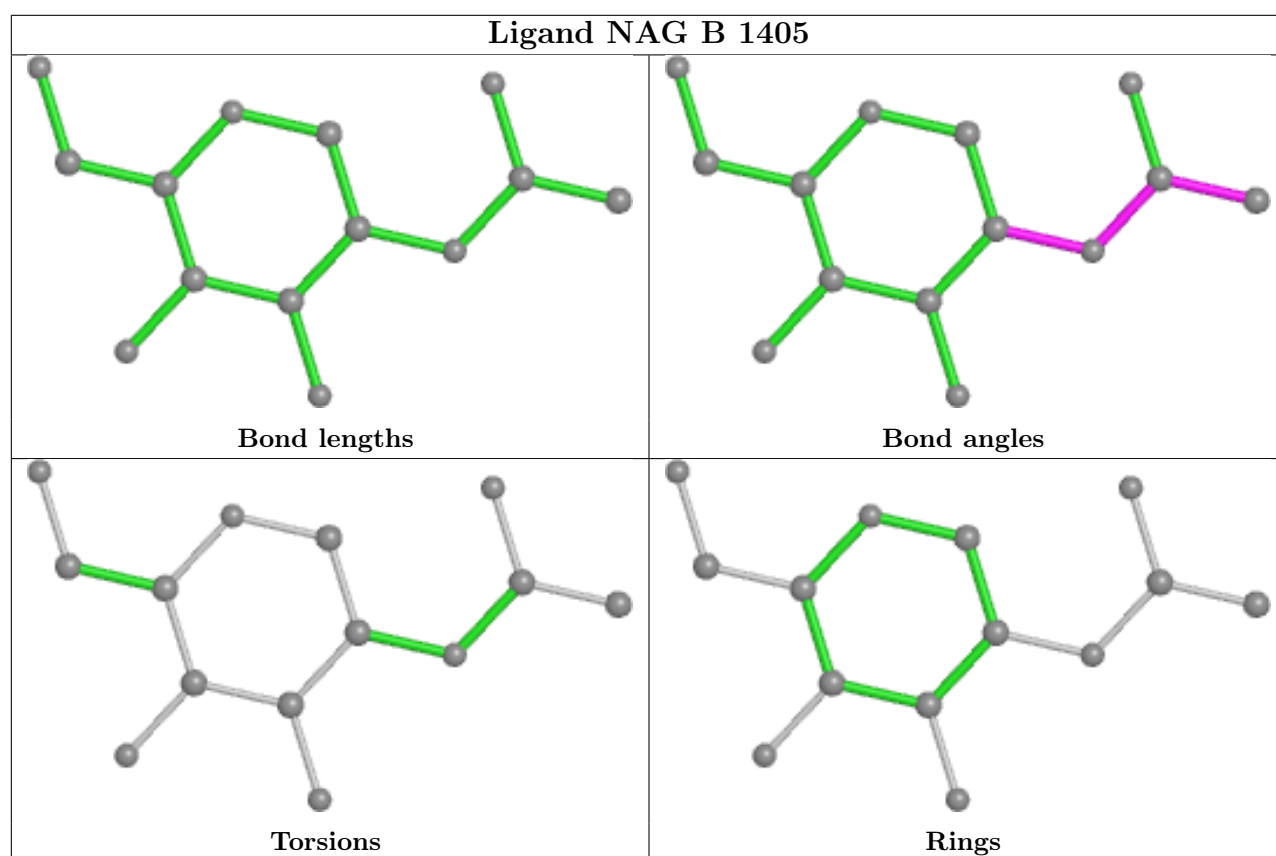
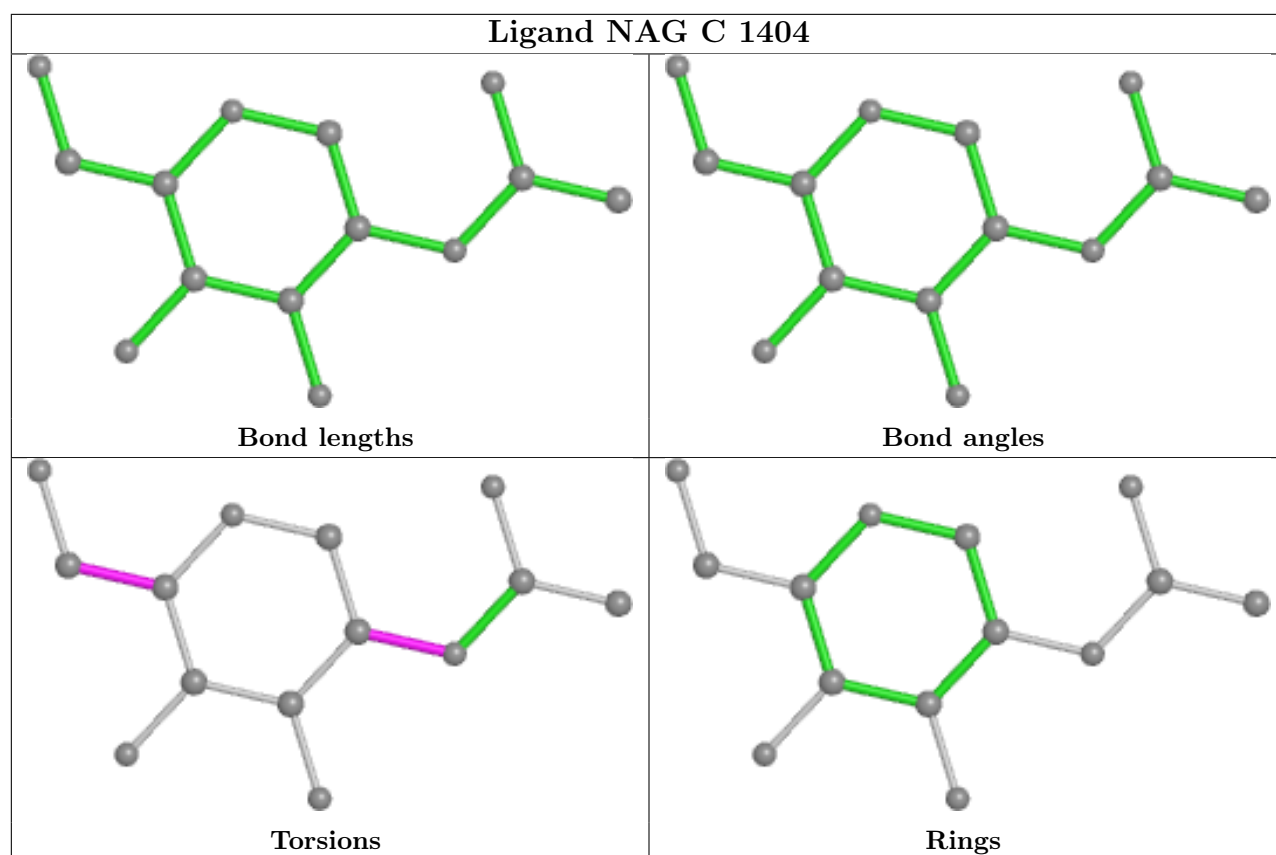


Ligand NAG A 1404

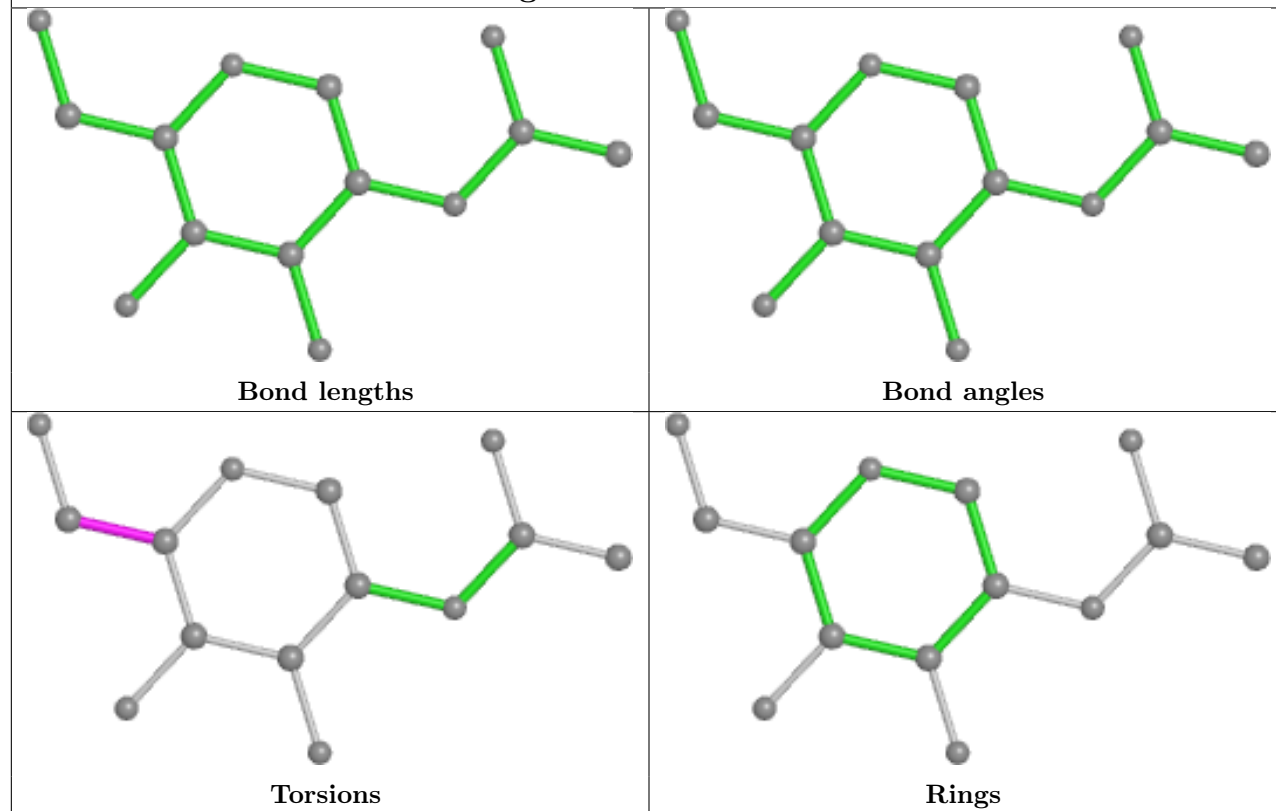


Ligand NAG B 1410

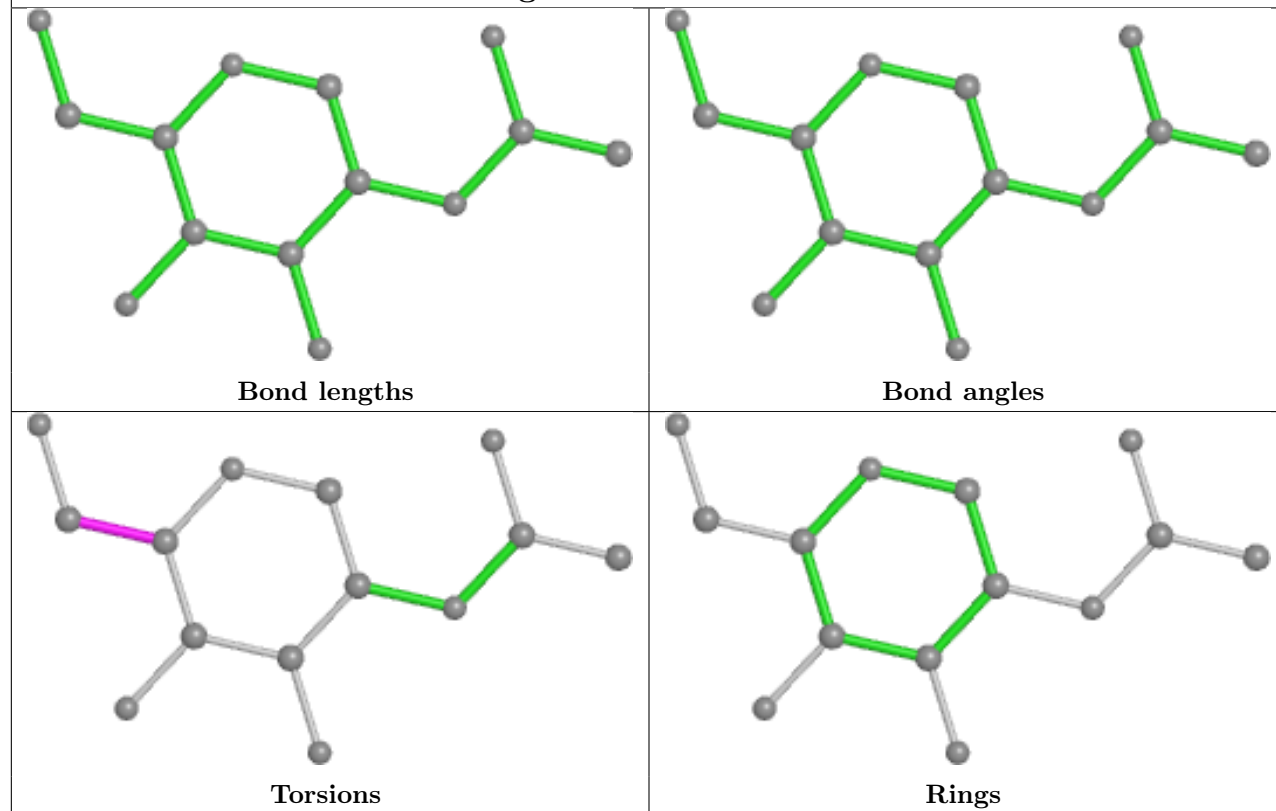


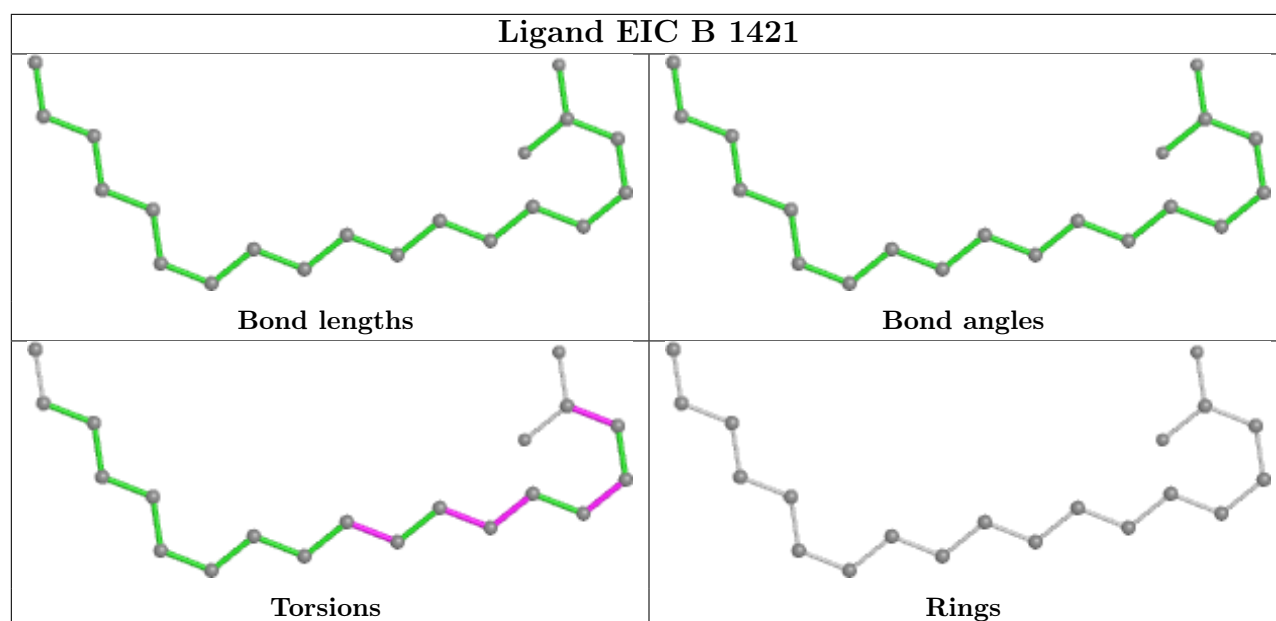


Ligand NAG C 1406



Ligand NAG A 1403





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.

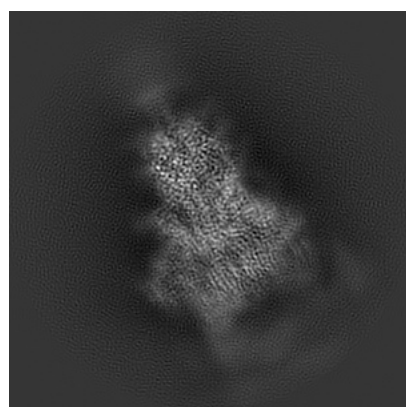
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32920. These allow visual inspection of the internal detail of the map and identification of artifacts.

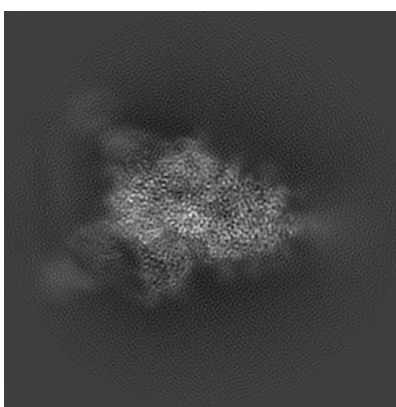
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

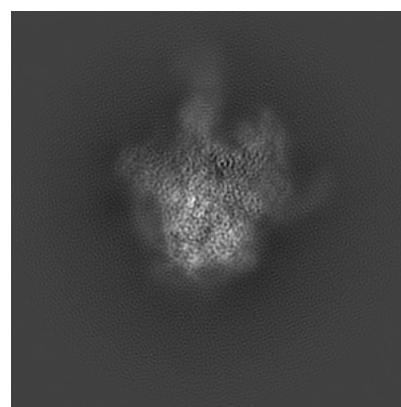
6.1.1 Primary map



X



Y

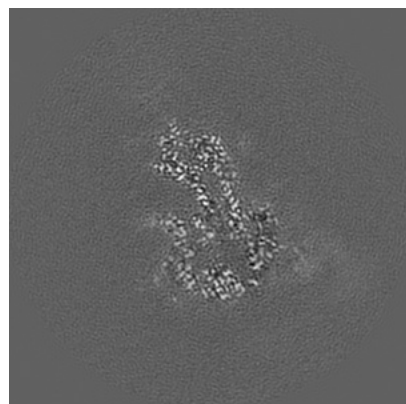


Z

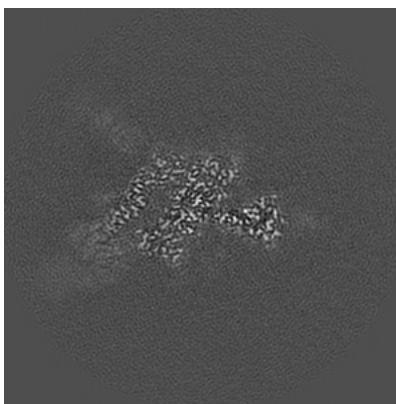
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

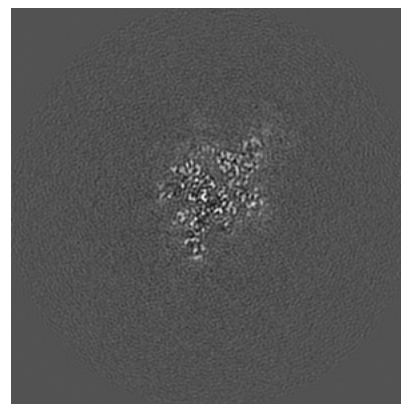
6.2.1 Primary map



X Index: 144



Y Index: 144

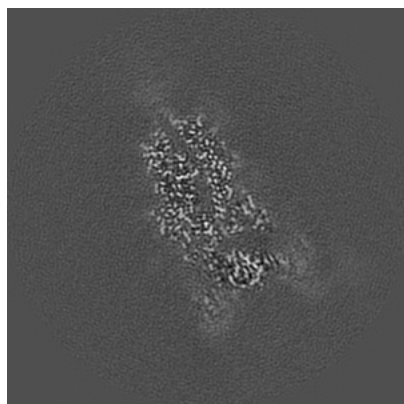


Z Index: 144

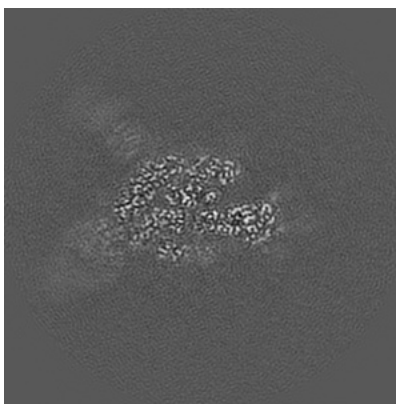
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

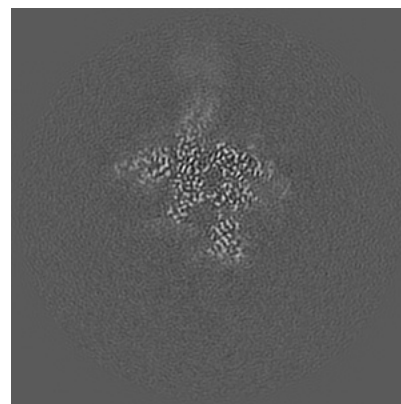
6.3.1 Primary map



X Index: 129



Y Index: 149

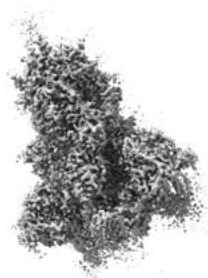


Z Index: 102

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

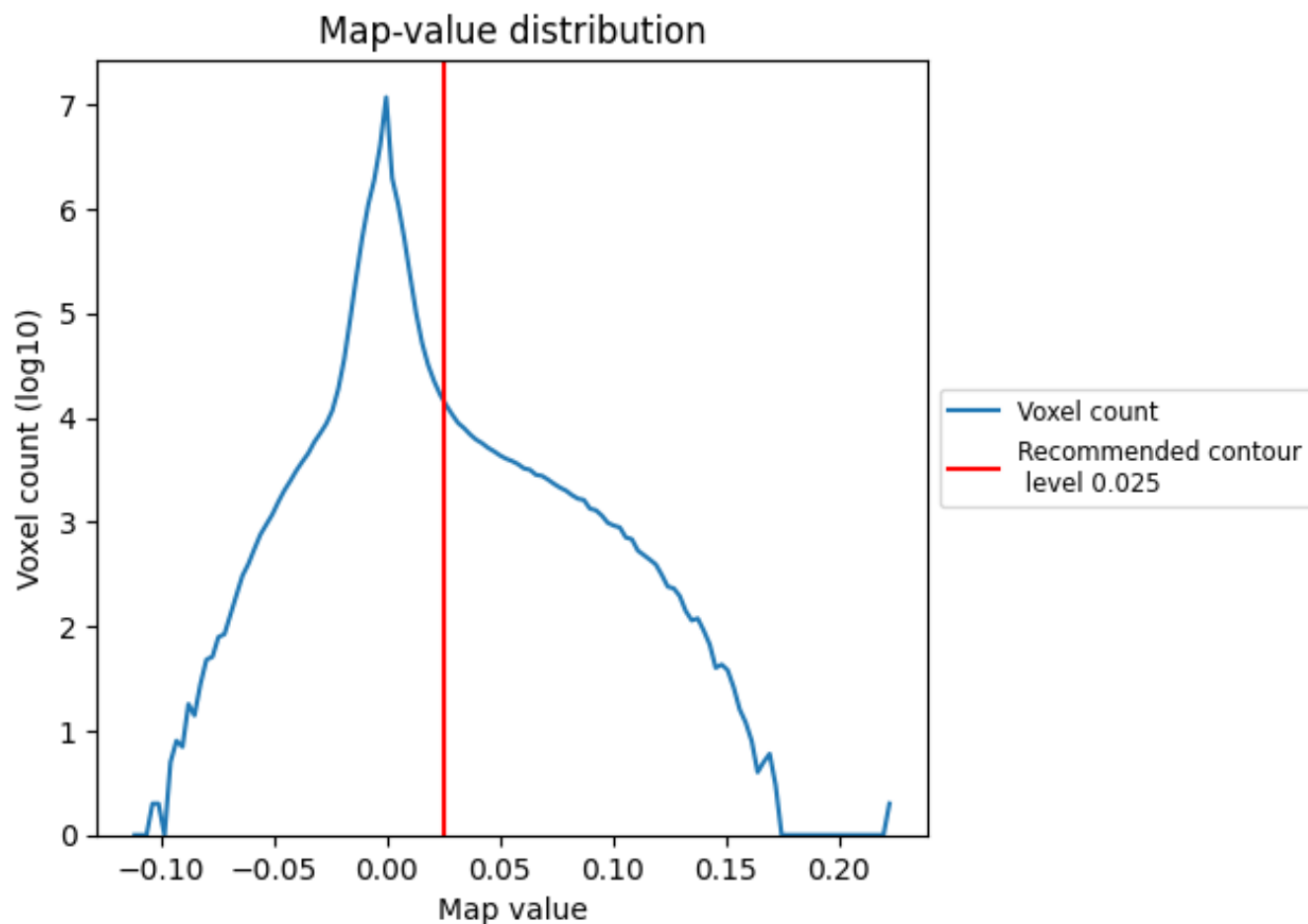
6.5 Mask visualisation

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

7 Map analysis [i](#)

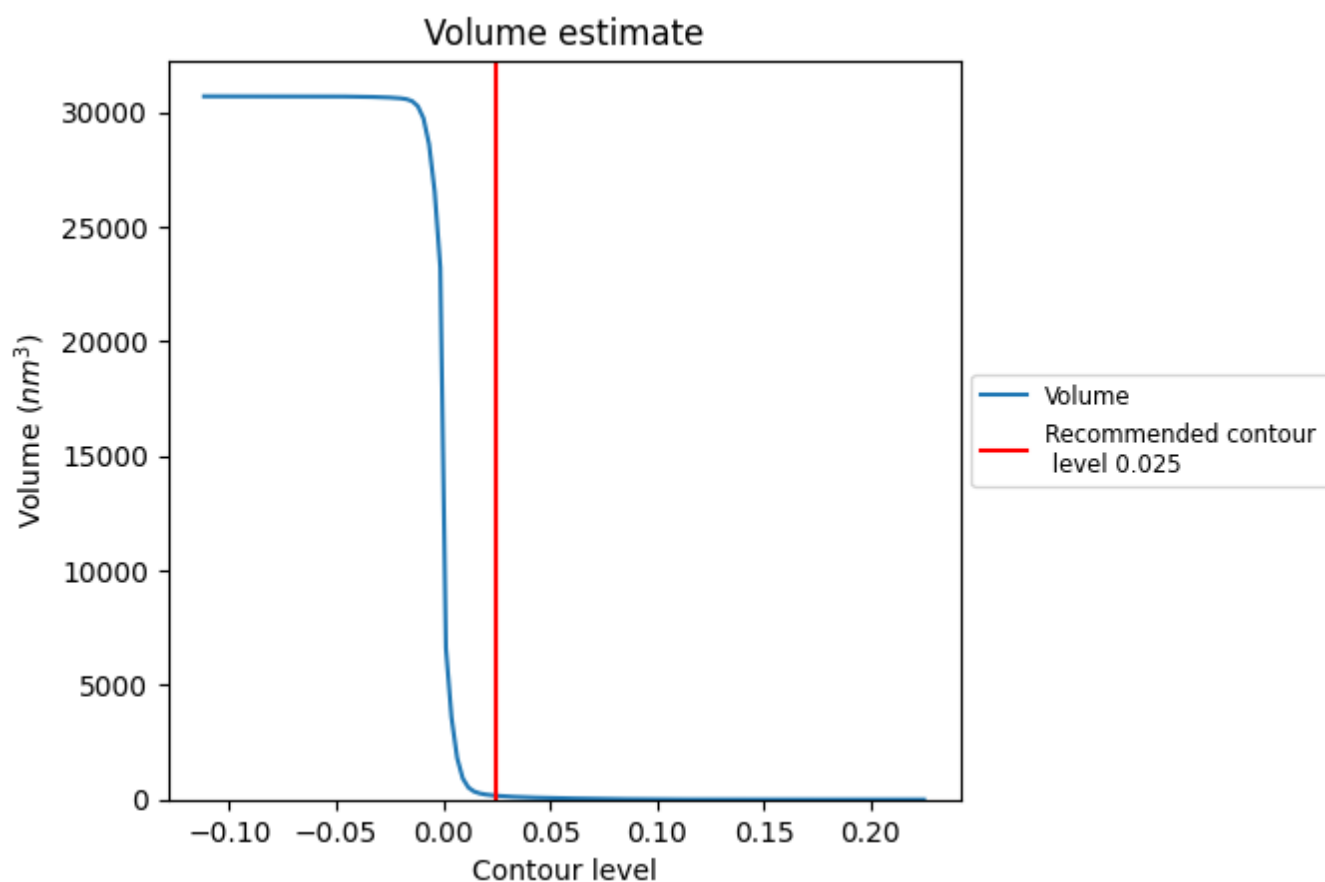
This section contains the results of statistical analysis of the map.

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.

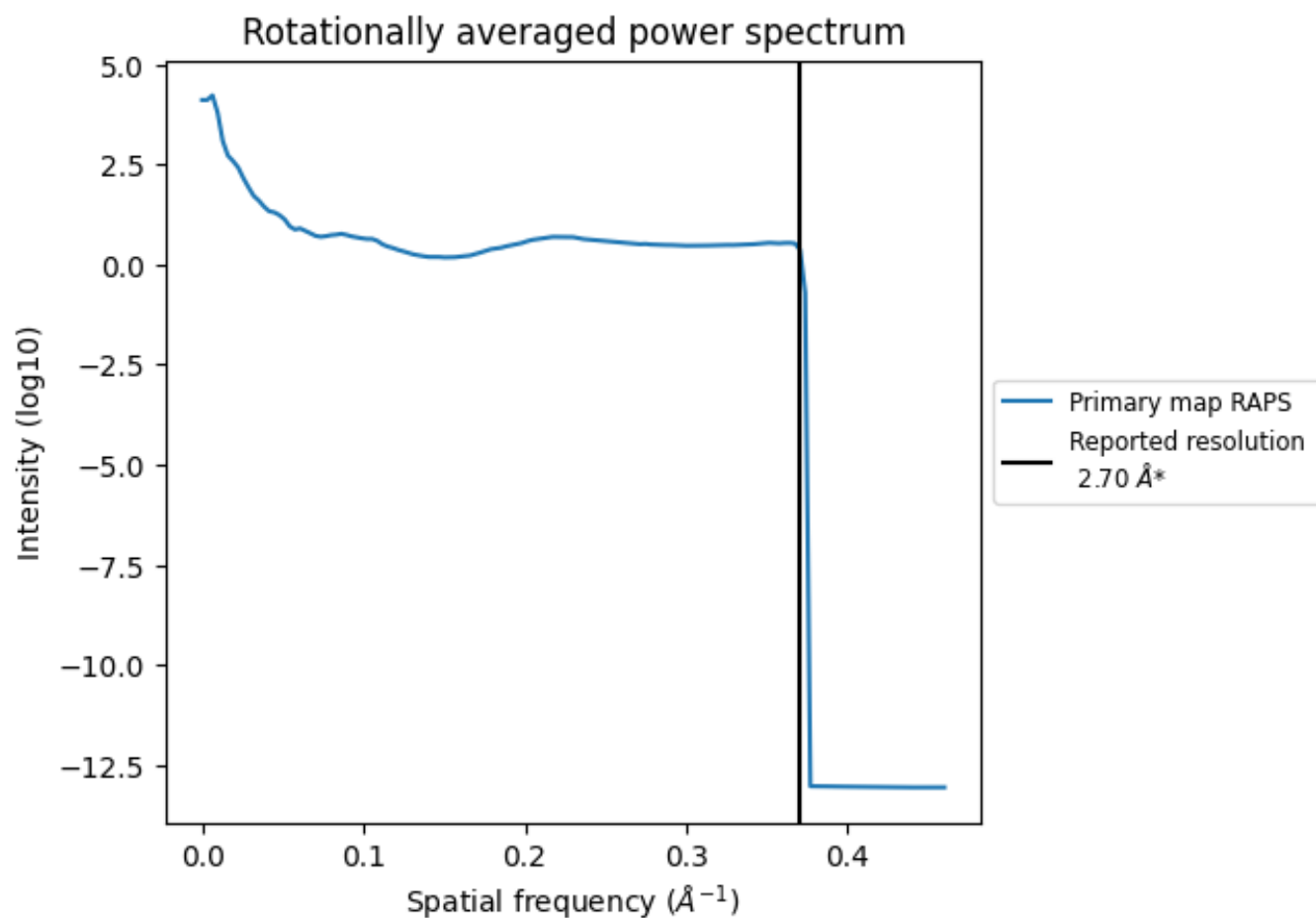
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 166 nm³; this corresponds to an approximate mass of 150 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 0.370 Å⁻¹

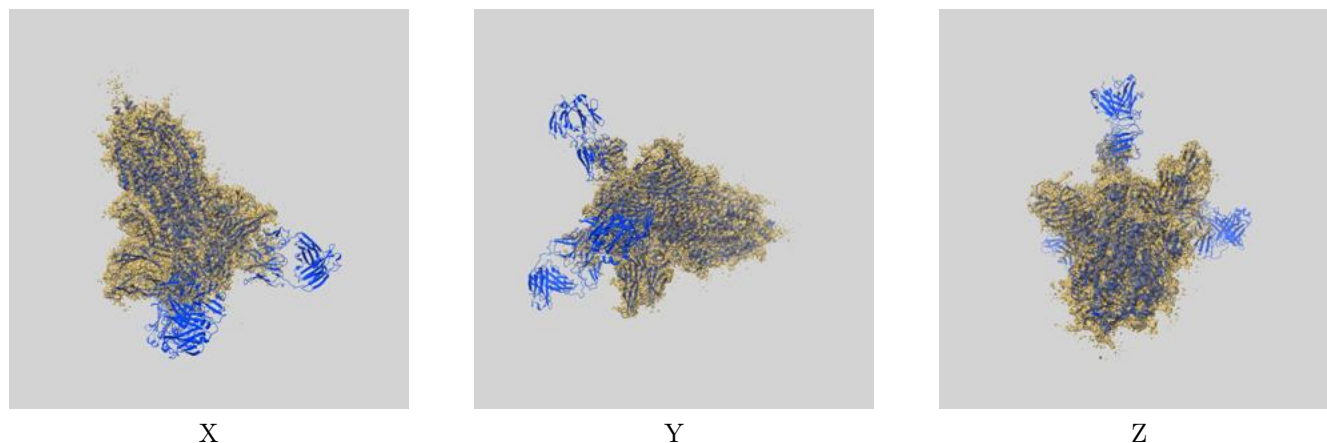
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

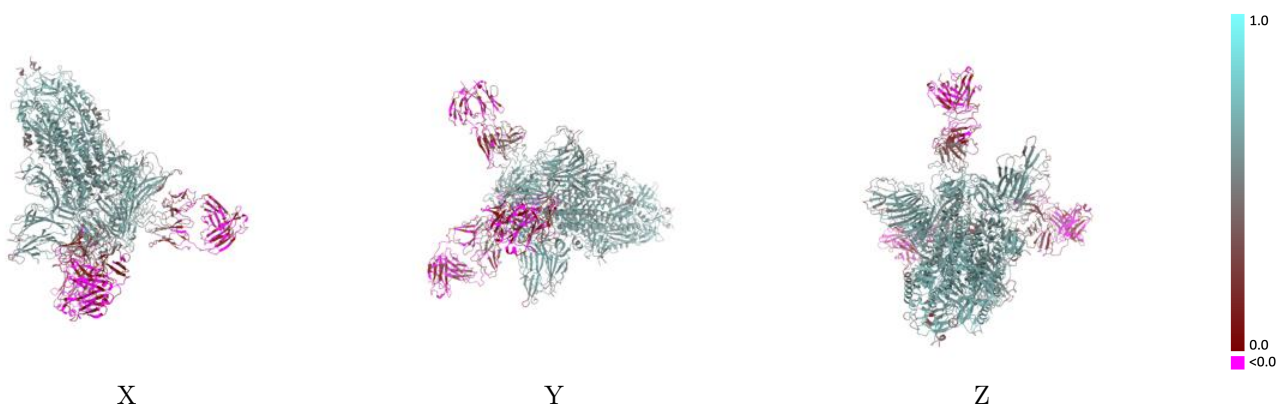
This section contains information regarding the fit between EMDB map EMD-32920 and PDB model 7X08. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

9.1 Map-model overlay [i](#)



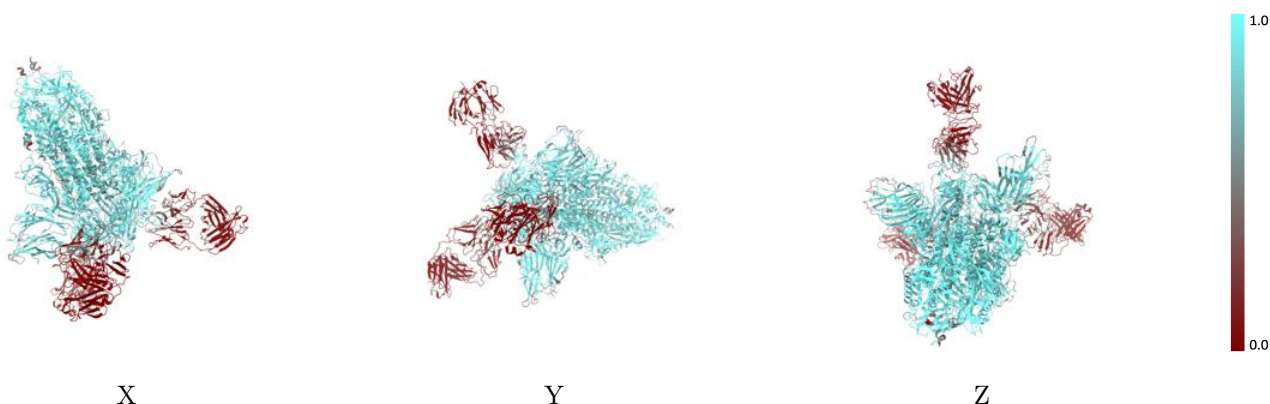
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



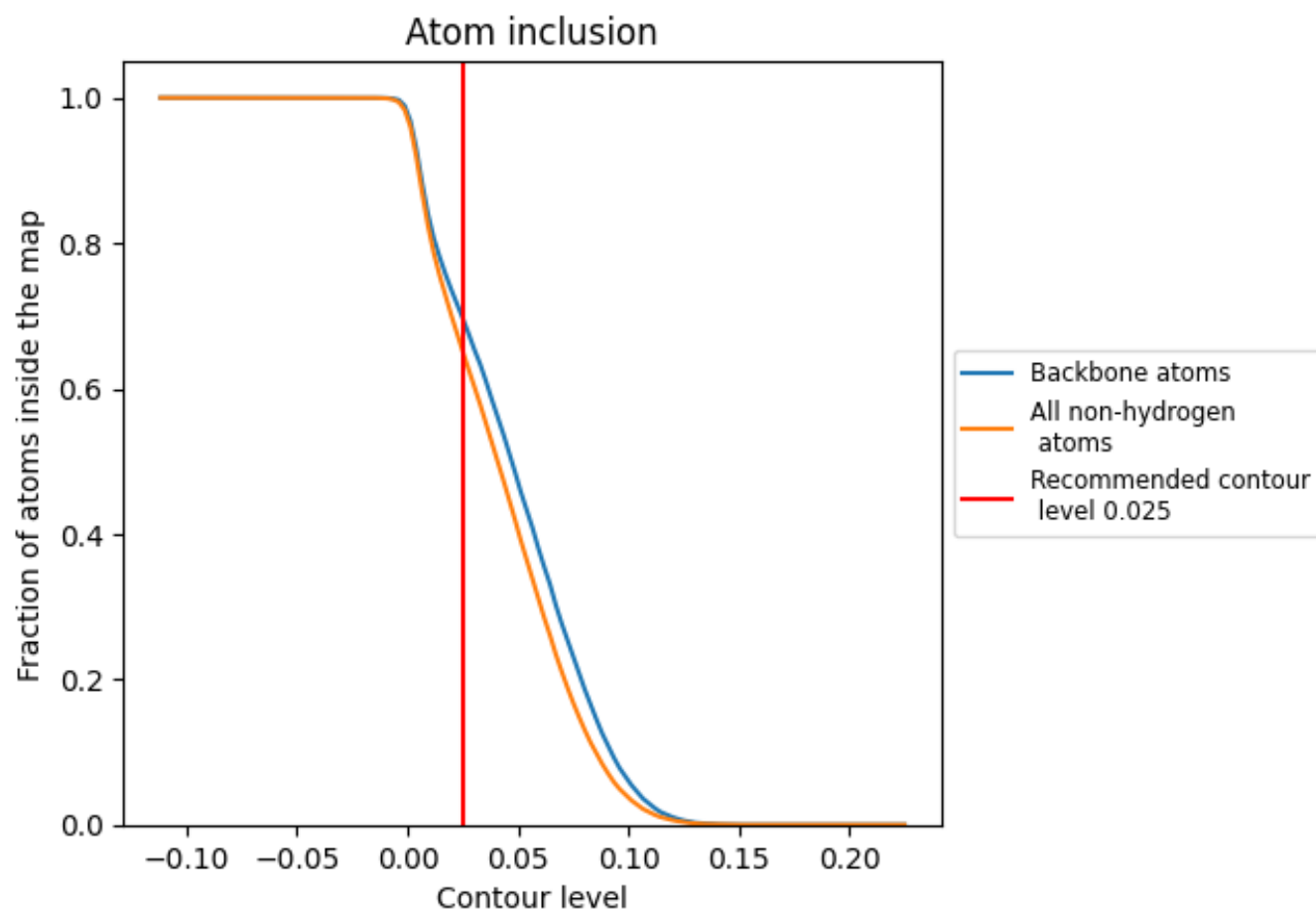
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.025).





































































9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 65% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6509	 0.4580
A	 0.8589	 0.5880
B	 0.8695	 0.5880
C	 0.8694	 0.5860
D	 0.2500	 0.2500
E	 0.6071	 0.4790
F	 0.3214	 0.5030
G	 0.5357	 0.4310
H	 0.0780	 0.1200
I	 0.0920	 0.1100
J	 0.0863	 0.1060
K	 0.2500	 0.2200
L	 0.0686	 0.1070
M	 0.0470	 0.1040
N	 0.0607	 0.0970
O	 0.6071	 0.4680
P	 0.4643	 0.3490
Q	 0.1429	 0.1630
R	 0.7143	 0.5060
S	 0.4643	 0.4080
T	 0.2857	 0.2750
U	 0.2857	 0.1200
V	 0.3929	 0.3170
W	 0.4286	 0.3570
X	 0.2500	 0.2390
Y	 0.4286	 0.3580
Z	 0.5357	 0.4500
a	 0.3214	 0.3630
b	 0.4286	 0.3930
c	 0.2857	 0.2180
d	 0.3214	 0.2290
e	 0.5714	 0.3330
f	 0.2500	 0.3990
g	 0.4286	 0.3100

