



wwPDB EM Validation Summary Report ⓘ

Oct 26, 2025 – 04:27 AM JST

PDB ID : 9KR8 / pdb_00009kr8
EMDB ID : EMD-62522
Title : Overall structure of HKU5 S protein in closed conformation
Authors : Zhang, Y.Y.; Xia, L.Y.; Zhou, Q.
Deposited on : 2024-11-27
Resolution : 2.39 Å(reported)

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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:

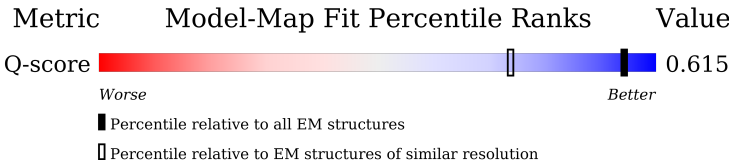
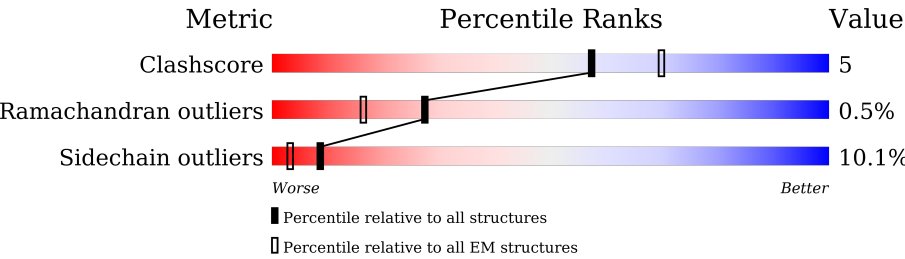
EMDB validation analysis : 0.0.1.dev129
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive 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) : 2.46

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 2.39 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.



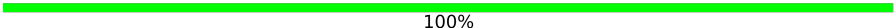

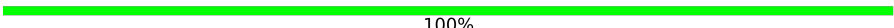








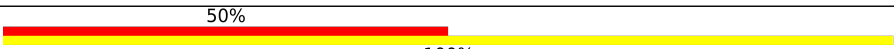
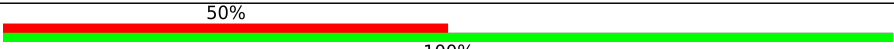





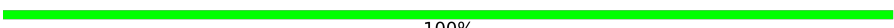



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
Q-score	-	25397	4884 (1.90 - 2.89)

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	1352	<div> <div>9%</div> <div>73%</div> <div>12%</div> <div>•</div> <div>14%</div> </div>
1	B	1352	<div> <div>8%</div> <div>72%</div> <div>13%</div> <div>•</div> <div>14%</div> </div>
1	C	1352	<div> <div>9%</div> <div>70%</div> <div>14%</div> <div>•</div> <div>14%</div> </div>
2	D	2	<div> <div>50%</div> <div>50%</div> </div>
2	E	2	<div> <div>50%</div> <div>50%</div> </div>

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Mol	Chain	Length	Quality of chain
2	F	2	 100%
2	G	2	 50% 100%
2	H	2	 100%
2	I	2	 50% 50%
2	J	2	 50% 100%
2	K	2	 50% 50%
2	L	2	 50% 50%
2	M	2	 50% 100%
2	N	2	 50% 50%
2	O	2	 50% 50%
2	P	2	 100%
2	Q	2	 50% 100%
2	R	2	 50% 100%
2	S	2	 50% 50%
2	T	2	 50% 50%
2	U	2	 50% 100%
2	V	2	 50% 50%
2	W	2	 50% 50%
2	X	2	 100%
2	Y	2	 50% 50%
2	Z	2	 50% 100%
2	a	2	 50% 50%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	PLM	A	3001	-	-	X	-
3	PLM	B	2002	-	-	X	-
3	PLM	C	2002	-	-	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 28356 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	1163	Total	C	N	O	S	0	0
			9036	5737	1490	1759	50		
1	B	1163	Total	C	N	O	S	0	0
			9036	5737	1490	1759	50		
1	C	1163	Total	C	N	O	S	0	0
			9036	5737	1490	1759	50		

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



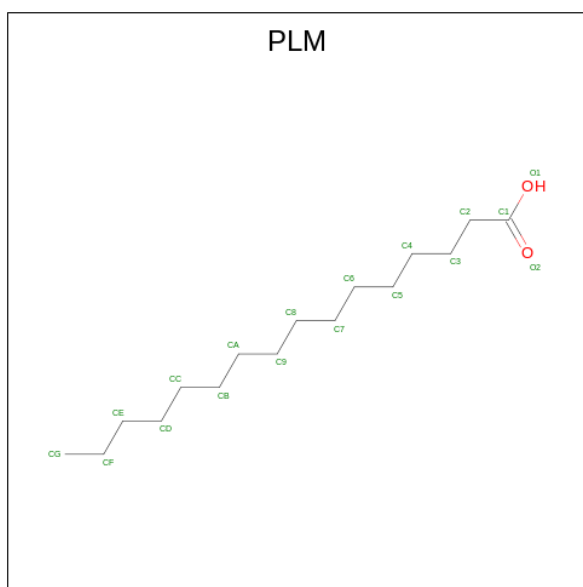
Mol	Chain	Residues	Atoms				AltConf	Trace
2	D	2	Total	C	N	O	0	0
			28	16	2	10		
2	E	2	Total	C	N	O	0	0
			28	16	2	10		
2	F	2	Total	C	N	O	0	0
			28	16	2	10		
2	G	2	Total	C	N	O	0	0
			28	16	2	10		
2	H	2	Total	C	N	O	0	0
			28	16	2	10		
2	I	2	Total	C	N	O	0	0
			28	16	2	10		
2	J	2	Total	C	N	O	0	0
			28	16	2	10		
2	K	2	Total	C	N	O	0	0
			28	16	2	10		
2	L	2	Total	C	N	O	0	0
			28	16	2	10		

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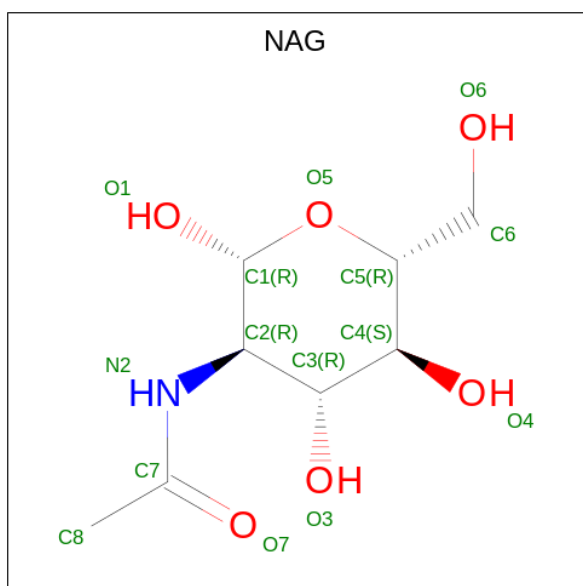
Mol	Chain	Residues	Atoms				AltConf	Trace
2	M	2	Total	C	N	O	0	0
			28	16	2	10		
2	N	2	Total	C	N	O	0	0
			28	16	2	10		
2	O	2	Total	C	N	O	0	0
			28	16	2	10		
2	P	2	Total	C	N	O	0	0
			28	16	2	10		
2	Q	2	Total	C	N	O	0	0
			28	16	2	10		
2	R	2	Total	C	N	O	0	0
			28	16	2	10		
2	S	2	Total	C	N	O	0	0
			28	16	2	10		
2	T	2	Total	C	N	O	0	0
			28	16	2	10		
2	U	2	Total	C	N	O	0	0
			28	16	2	10		
2	V	2	Total	C	N	O	0	0
			28	16	2	10		
2	W	2	Total	C	N	O	0	0
			28	16	2	10		
2	X	2	Total	C	N	O	0	0
			28	16	2	10		
2	Y	2	Total	C	N	O	0	0
			28	16	2	10		
2	Z	2	Total	C	N	O	0	0
			28	16	2	10		
2	a	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 3 is PALMITIC ACID (CCD ID: PLM) (formula: $C_{16}H_{32}O_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
3	A	1	Total	C	O	0
			18	16	2	
3	B	1	Total	C	O	0
			18	16	2	
3	C	1	Total	C	O	0
			18	16	2	

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$) (labeled as "Ligand of Interest" by depositor).



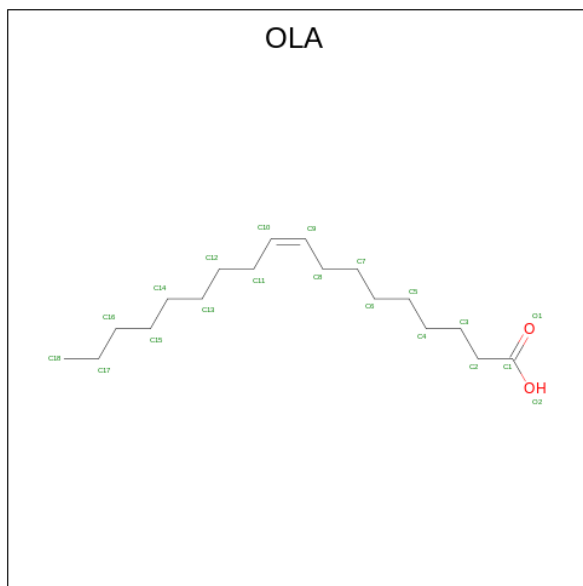
Mol	Chain	Residues	Atoms				AltConf
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4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

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

- Molecule 5 is OLEIC ACID (CCD ID: OLA) (formula: $C_{18}H_{34}O_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
5	A	1	Total 20	C 18	O 2	0
5	B	1	Total 20	C 18	O 2	0
5	C	1	Total 20	C 18	O 2	0

MET	ILE	ARG	SER	VAL	LEU	VAL	LEU	MET	CYS	SER	LEU	THR	ILE	GLY	ASN	LEU	ARG	GLN	GLY	SER	VAL	ASP	MET	GLY	HIS	ASN	GLY	THR	GLY	SER	CYS	LEU	ASP	SER	GLN	V39	Q40	P41	D42	Y43	F44	E45	S46	V47	H48	T49	T50	W51	N67	G68	K69	N73	P83	F84
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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

Chain F:  100%



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

Chain G:  50%
100%



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

Chain H:  100%



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

Chain I:  50%
50% 50%



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

Chain J:  50%
100%



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

Chain K:  50% 50%



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

Chain L:  50% 50%



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

Chain M:  50% 100%



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

Chain N:  50% 50%



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

Chain O:  50% 50%



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

Chain P:  100%



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

Chain Q:  50% 100%



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



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



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



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



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



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



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

Chain X:  100%



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

Chain Y:  50%
 50%



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

Chain Z:  50%
 100%



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

Chain a:  50%
 50%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	801468	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	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	6.394	Depositor
Minimum map value	-4.198	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.168	Depositor
Recommended contour level	0.6	Depositor
Map size (\AA)	347.84, 347.84, 347.84	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.087, 1.087, 1.087	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PLM, OLA, 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	0.36	0/9255	0.66	10/12610 (0.1%)
1	B	0.36	0/9255	0.65	10/12610 (0.1%)
1	C	0.35	0/9255	0.61	8/12610 (0.1%)
All	All	0.36	0/27765	0.64	28/37830 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	6
1	B	0	3
1	C	0	3
All	All	0	12

There are no bond length outliers.

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	497	THR	N-CA-C	9.19	122.65	108.96
1	A	497	THR	CA-C-N	8.75	136.97	122.54
1	A	497	THR	C-N-CA	8.75	136.97	122.54
1	B	494	GLN	N-CA-C	6.96	119.72	111.71
1	A	495	ASN	N-CA-C	6.90	121.99	113.50

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	137	THR	Peptide
1	A	164	THR	Peptide
1	A	173	LEU	Peptide
1	A	201	GLN	Peptide
1	A	382	PHE	Mainchain

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	9036	0	8676	78	0
1	B	9036	0	8676	93	0
1	C	9036	0	8676	93	0
2	D	28	0	25	0	0
2	E	28	0	25	1	0
2	F	28	0	25	0	0
2	G	28	0	25	0	0
2	H	28	0	25	0	0
2	I	28	0	25	0	0
2	J	28	0	25	0	0
2	K	28	0	25	0	0
2	L	28	0	25	0	0
2	M	28	0	25	0	0
2	N	28	0	25	0	0
2	O	28	0	25	0	0
2	P	28	0	25	0	0
2	Q	28	0	25	0	0
2	R	28	0	25	0	0
2	S	28	0	25	0	0
2	T	28	0	25	0	0
2	U	28	0	25	0	0
2	V	28	0	25	1	0
2	W	28	0	25	0	0
2	X	28	0	25	0	0
2	Y	28	0	25	0	0
2	Z	28	0	25	0	0
2	a	28	0	25	0	0
3	A	18	0	31	15	0
3	B	18	0	31	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	18	0	31	16	0
4	A	154	0	143	5	0
4	B	154	0	143	3	0
4	C	154	0	143	1	0
5	A	20	0	33	1	0
5	B	20	0	33	1	0
5	C	20	0	33	1	0
All	All	28356	0	27249	255	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 5.

The worst 5 of 255 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:494:GLN:NE2	4:A:3007:NAG:H82	1.43	1.28
1:C:403:PRO:HD3	3:C:2002:PLM:CB	1.68	1.21
1:B:403:PRO:HD3	3:B:2002:PLM:CB	1.73	1.19
1:B:403:PRO:HD3	3:B:2002:PLM:HB1	1.27	1.11
1:A:494:GLN:HE22	4:A:3007:NAG:C8	1.62	1.10

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	1157/1352 (86%)	1082 (94%)	69 (6%)	6 (0%)	25	38
1	B	1157/1352 (86%)	1086 (94%)	64 (6%)	7 (1%)	22	33
1	C	1157/1352 (86%)	1077 (93%)	74 (6%)	6 (0%)	25	38
All	All	3471/4056 (86%)	3245 (94%)	207 (6%)	19 (0%)	27	38

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	383	ILE
1	A	853	GLN
1	A	854	ASN
1	B	383	ILE
1	B	853	GLN

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	1004/1174 (86%)	903 (90%)	101 (10%)	6	9
1	B	1004/1174 (86%)	910 (91%)	94 (9%)	7	11
1	C	1004/1174 (86%)	894 (89%)	110 (11%)	5	7
All	All	3012/3522 (86%)	2707 (90%)	305 (10%)	9	9

5 of 305 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	390	GLU
1	C	1058	VAL
1	C	494	GLN
1	C	795	THR
1	C	1182	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 95 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1129	ASN
1	C	504	ASN
1	B	1154	ASN
1	C	141	GLN
1	C	755	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	$\# Z > 2$
2	NAG	D	1	1,2	14,14,15	0.34	0	17,19,21	0.67	1 (5%)
2	NAG	D	2	2	14,14,15	0.32	0	17,19,21	0.48	0
2	NAG	E	1	1,2	14,14,15	0.21	0	17,19,21	0.64	0
2	NAG	E	2	2	14,14,15	0.36	0	17,19,21	0.59	0
2	NAG	F	1	1,2	14,14,15	0.40	0	17,19,21	0.61	0
2	NAG	F	2	2	14,14,15	0.40	0	17,19,21	0.56	0
2	NAG	G	1	1,2	14,14,15	0.27	0	17,19,21	0.54	0
2	NAG	G	2	2	14,14,15	0.31	0	17,19,21	0.55	0
2	NAG	H	1	1,2	14,14,15	0.33	0	17,19,21	0.62	0
2	NAG	H	2	2	14,14,15	0.21	0	17,19,21	0.50	0
2	NAG	I	1	1,2	14,14,15	0.31	0	17,19,21	0.68	1 (5%)
2	NAG	I	2	2	14,14,15	0.41	0	17,19,21	0.57	0
2	NAG	J	1	1,2	14,14,15	0.26	0	17,19,21	0.37	0
2	NAG	J	2	2	14,14,15	0.39	0	17,19,21	0.58	0
2	NAG	K	1	1,2	14,14,15	0.24	0	17,19,21	0.50	0
2	NAG	K	2	2	14,14,15	0.27	0	17,19,21	0.82	1 (5%)
2	NAG	L	1	1,2	14,14,15	0.81	1 (7%)	17,19,21	0.91	1 (5%)
2	NAG	L	2	2	14,14,15	0.42	0	17,19,21	0.38	0
2	NAG	M	1	1,2	14,14,15	0.21	0	17,19,21	0.57	0
2	NAG	M	2	2	14,14,15	0.42	0	17,19,21	0.58	0
2	NAG	N	1	1,2	14,14,15	0.46	0	17,19,21	0.69	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	N	2	2	14,14,15	0.40	0	17,19,21	0.54	0
2	NAG	O	1	1,2	14,14,15	0.32	0	17,19,21	0.64	1 (5%)
2	NAG	O	2	2	14,14,15	0.41	0	17,19,21	0.52	0
2	NAG	P	1	1,2	14,14,15	0.47	0	17,19,21	0.63	0
2	NAG	P	2	2	14,14,15	0.26	0	17,19,21	0.59	0
2	NAG	Q	1	1,2	14,14,15	0.42	0	17,19,21	0.81	1 (5%)
2	NAG	Q	2	2	14,14,15	0.36	0	17,19,21	0.60	1 (5%)
2	NAG	R	1	1,2	14,14,15	0.25	0	17,19,21	0.57	0
2	NAG	R	2	2	14,14,15	0.26	0	17,19,21	0.59	0
2	NAG	S	1	1,2	14,14,15	0.41	0	17,19,21	0.61	0
2	NAG	S	2	2	14,14,15	0.33	0	17,19,21	0.63	1 (5%)
2	NAG	T	1	1,2	14,14,15	0.37	0	17,19,21	0.78	1 (5%)
2	NAG	T	2	2	14,14,15	0.40	0	17,19,21	0.37	0
2	NAG	U	1	1,2	14,14,15	0.28	0	17,19,21	0.50	0
2	NAG	U	2	2	14,14,15	0.30	0	17,19,21	0.57	0
2	NAG	V	1	1,2	14,14,15	0.56	0	17,19,21	0.58	0
2	NAG	V	2	2	14,14,15	0.46	0	17,19,21	0.60	0
2	NAG	W	1	1,2	14,14,15	0.34	0	17,19,21	0.69	1 (5%)
2	NAG	W	2	2	14,14,15	0.30	0	17,19,21	0.58	0
2	NAG	X	1	1,2	14,14,15	0.29	0	17,19,21	0.66	0
2	NAG	X	2	2	14,14,15	0.29	0	17,19,21	0.51	0
2	NAG	Y	1	1,2	14,14,15	0.26	0	17,19,21	0.62	1 (5%)
2	NAG	Y	2	2	14,14,15	0.25	0	17,19,21	0.60	0
2	NAG	Z	1	1,2	14,14,15	0.37	0	17,19,21	0.50	0
2	NAG	Z	2	2	14,14,15	0.38	0	17,19,21	0.54	0
2	NAG	a	1	1,2	14,14,15	0.25	0	17,19,21	0.54	0
2	NAG	a	2	2	14,14,15	0.22	0	17,19,21	0.68	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	D	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	D	2	2	-	1/6/23/26	0/1/1/1
2	NAG	E	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	E	2	2	-	2/6/23/26	0/1/1/1
2	NAG	F	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	F	2	2	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	G	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	G	2	2	-	2/6/23/26	0/1/1/1
2	NAG	H	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	H	2	2	-	2/6/23/26	0/1/1/1
2	NAG	I	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	I	2	2	-	2/6/23/26	0/1/1/1
2	NAG	J	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	J	2	2	-	2/6/23/26	0/1/1/1
2	NAG	K	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	K	2	2	-	2/6/23/26	0/1/1/1
2	NAG	L	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	L	2	2	-	1/6/23/26	0/1/1/1
2	NAG	M	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	M	2	2	-	2/6/23/26	0/1/1/1
2	NAG	N	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	N	2	2	-	2/6/23/26	0/1/1/1
2	NAG	O	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	O	2	2	-	2/6/23/26	0/1/1/1
2	NAG	P	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	P	2	2	-	2/6/23/26	0/1/1/1
2	NAG	Q	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	Q	2	2	-	0/6/23/26	0/1/1/1
2	NAG	R	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	R	2	2	-	2/6/23/26	0/1/1/1
2	NAG	S	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	S	2	2	-	0/6/23/26	0/1/1/1
2	NAG	T	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	T	2	2	-	2/6/23/26	0/1/1/1
2	NAG	U	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	U	2	2	-	2/6/23/26	0/1/1/1
2	NAG	V	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	V	2	2	-	0/6/23/26	0/1/1/1
2	NAG	W	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	W	2	2	-	0/6/23/26	0/1/1/1
2	NAG	X	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	X	2	2	-	0/6/23/26	0/1/1/1
2	NAG	Y	1	1,2	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	Y	2	2	-	0/6/23/26	0/1/1/1
2	NAG	Z	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	Z	2	2	-	2/6/23/26	0/1/1/1
2	NAG	a	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	a	2	2	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	1	NAG	O5-C1	-2.86	1.39	1.43

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Q	1	NAG	C1-O5-C5	3.07	116.35	112.19
2	K	2	NAG	C1-O5-C5	3.00	116.26	112.19
2	L	1	NAG	C1-O5-C5	2.63	115.76	112.19
2	T	1	NAG	C1-O5-C5	2.58	115.68	112.19
2	a	2	NAG	C1-O5-C5	2.46	115.52	112.19

There are no chirality outliers.

5 of 68 torsion outliers are listed below:

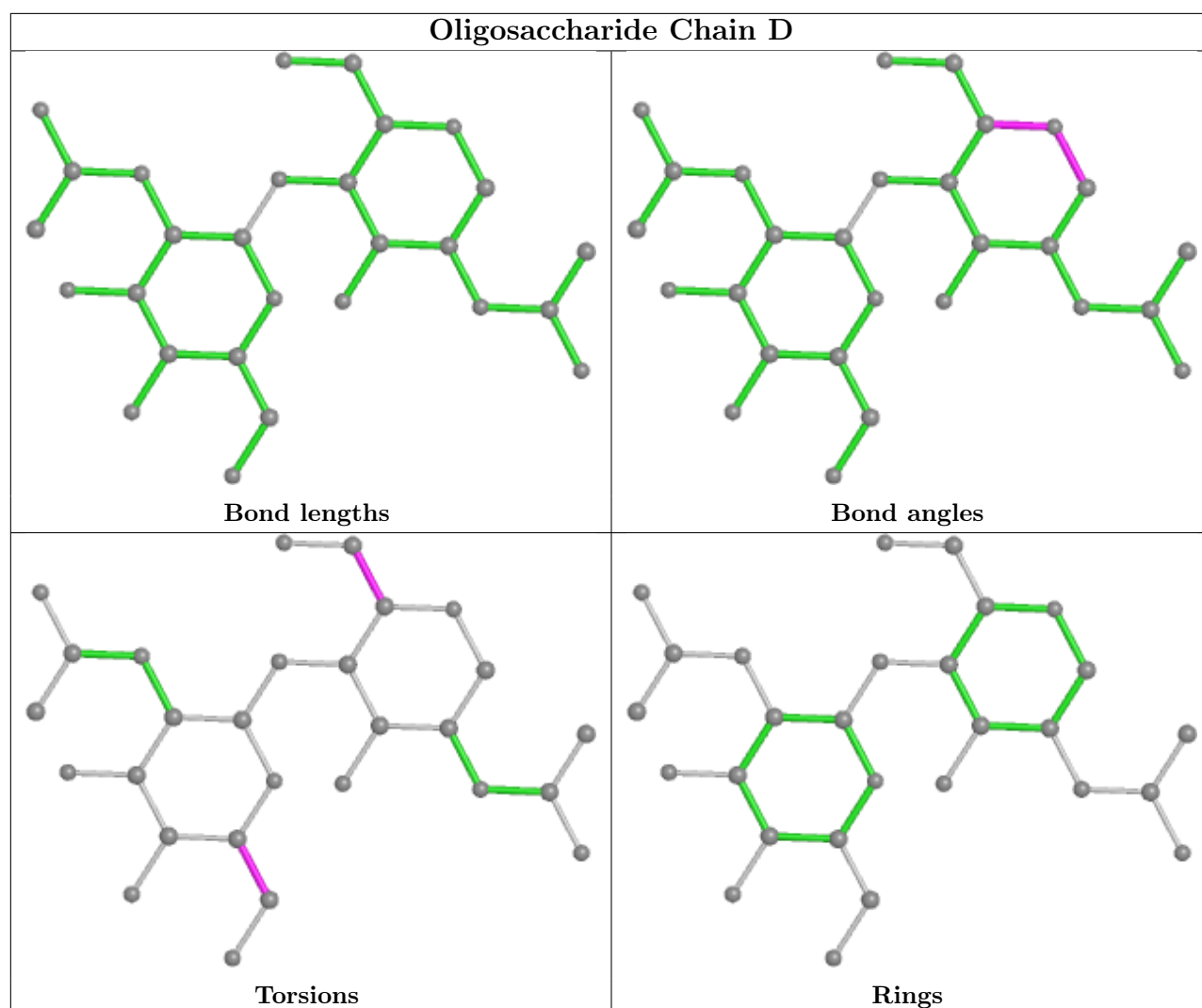
Mol	Chain	Res	Type	Atoms
2	H	2	NAG	O5-C5-C6-O6
2	P	2	NAG	O5-C5-C6-O6
2	F	1	NAG	O5-C5-C6-O6
2	S	1	NAG	O5-C5-C6-O6
2	J	2	NAG	O5-C5-C6-O6

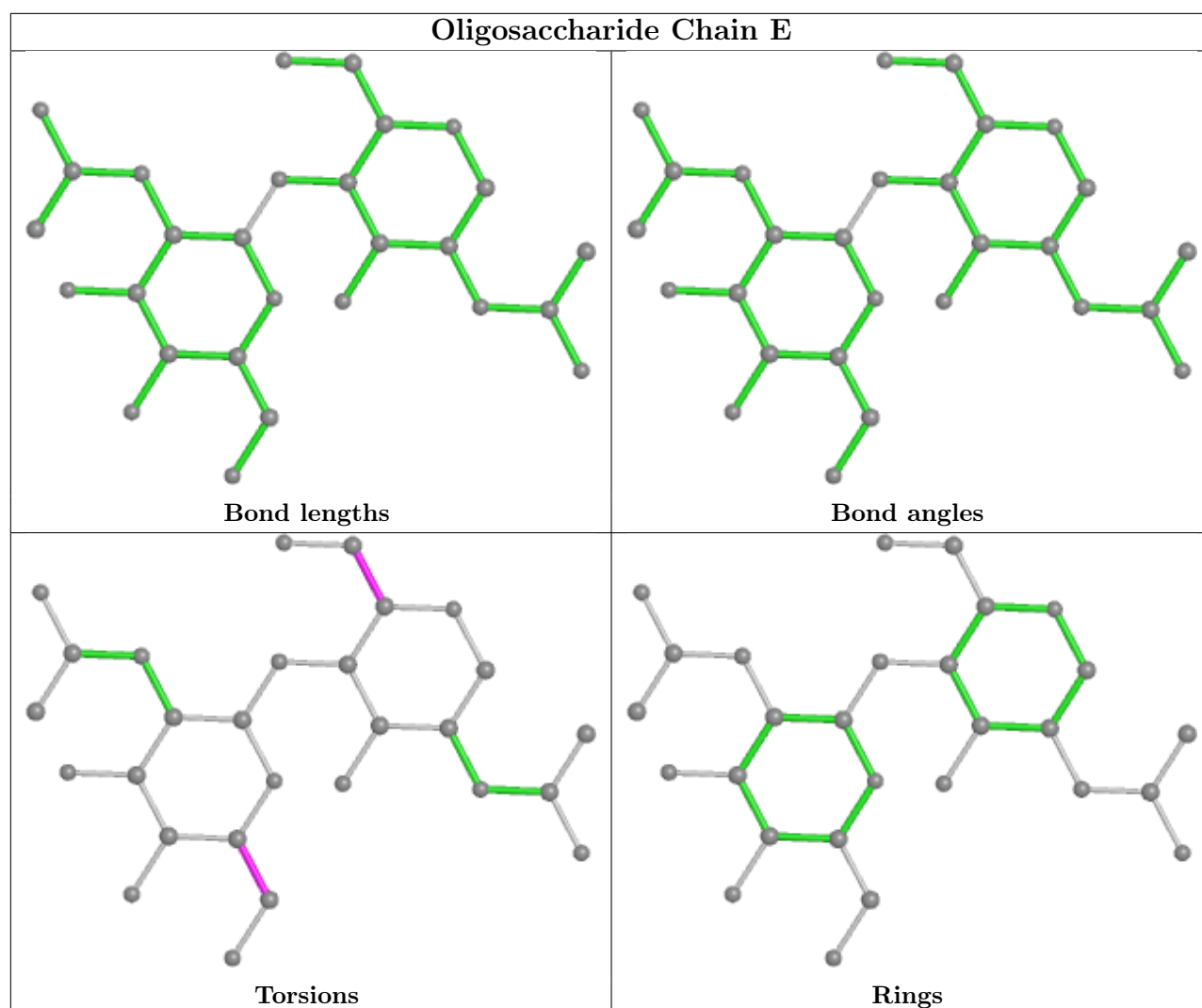
There are no ring outliers.

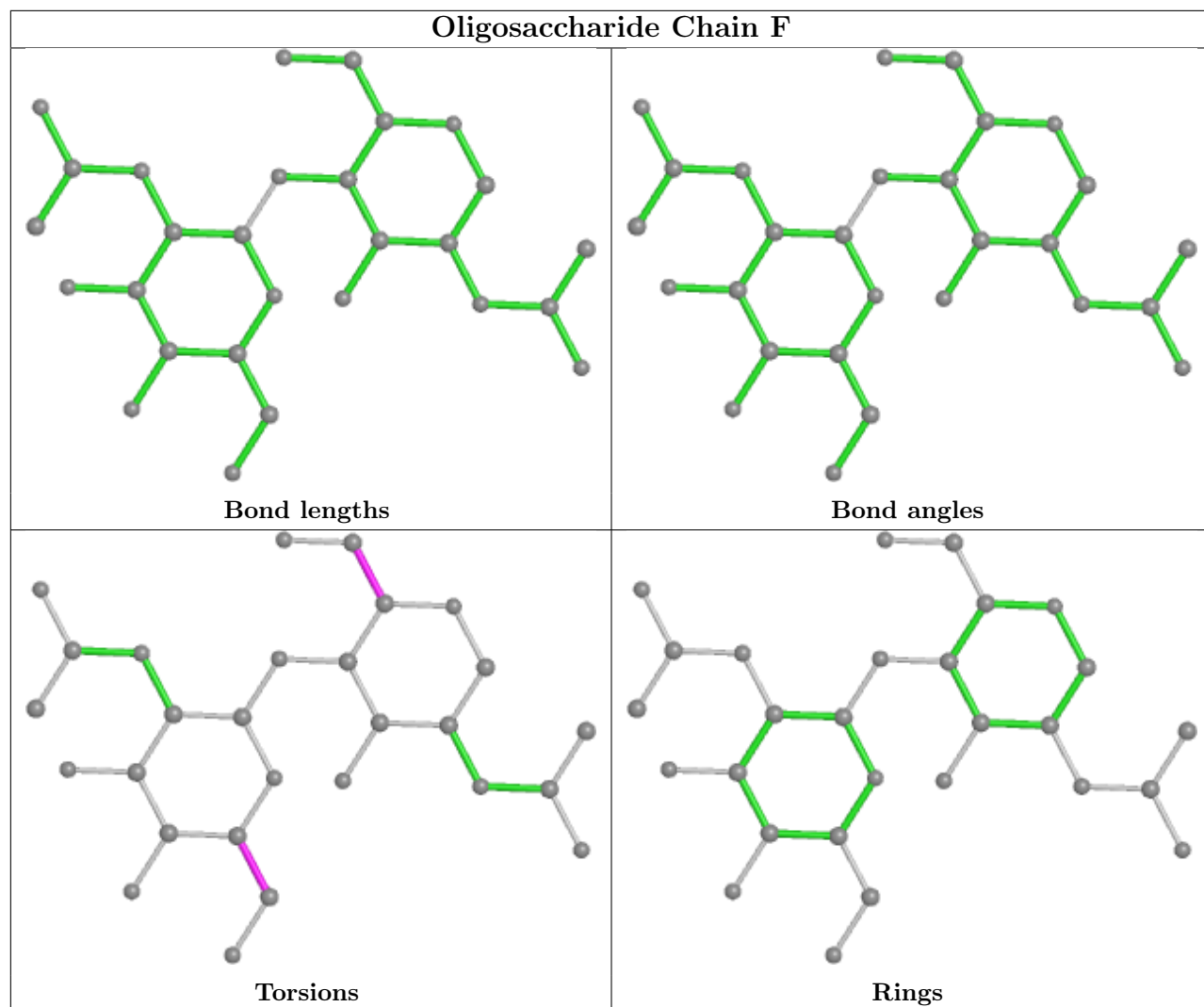
2 monomers are involved in 2 short contacts:

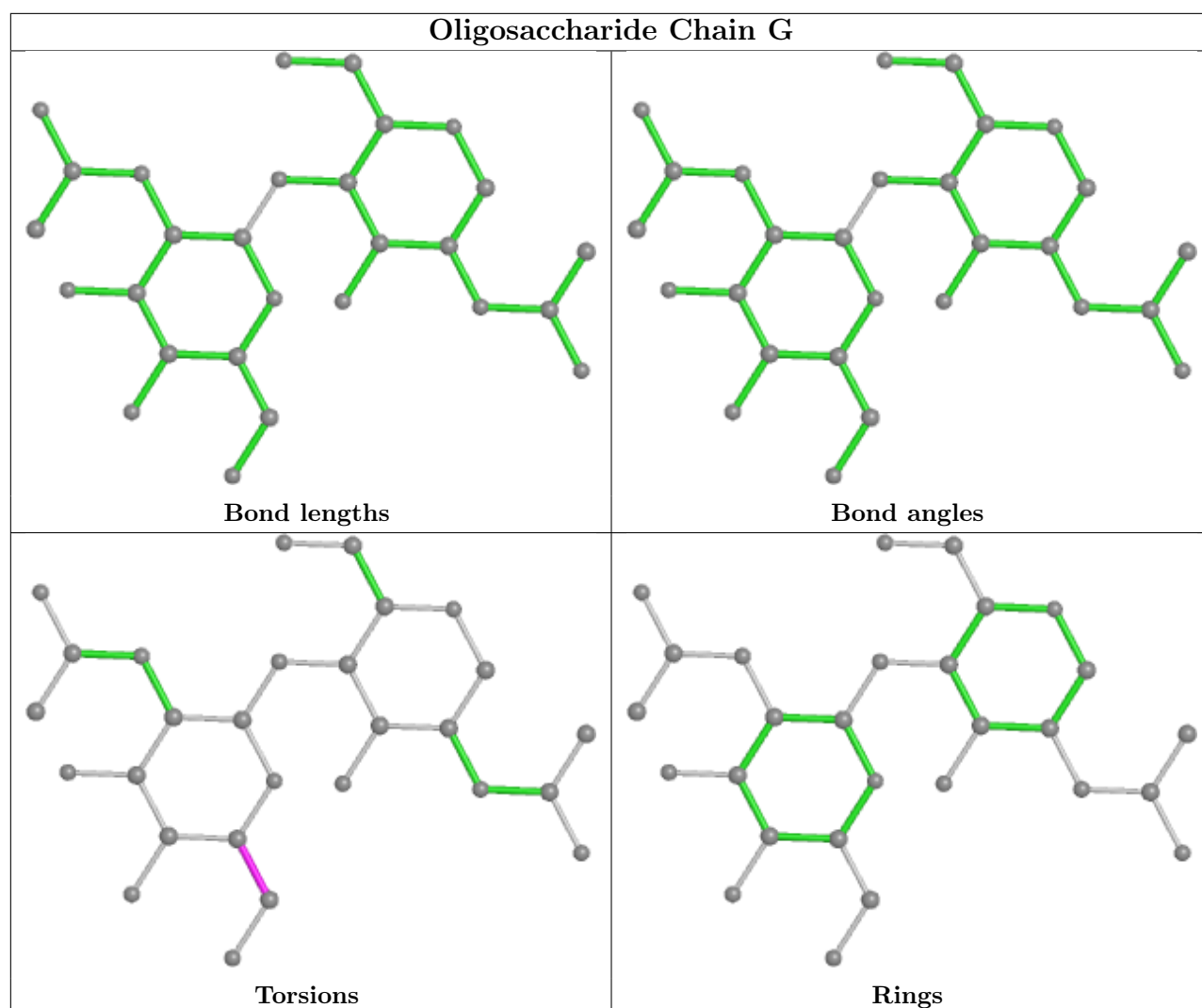
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	V	1	NAG	1	0
2	E	2	NAG	1	0

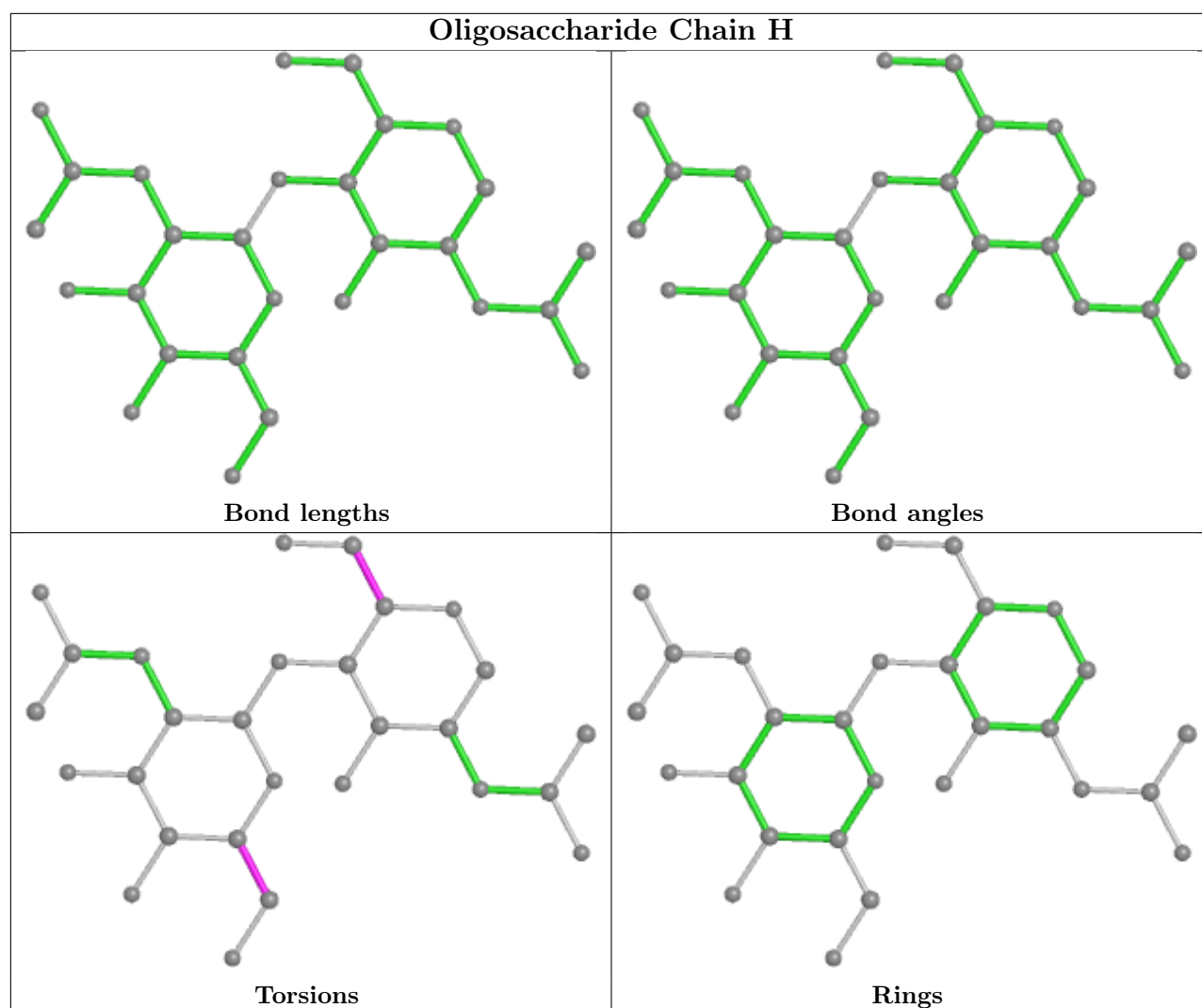
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

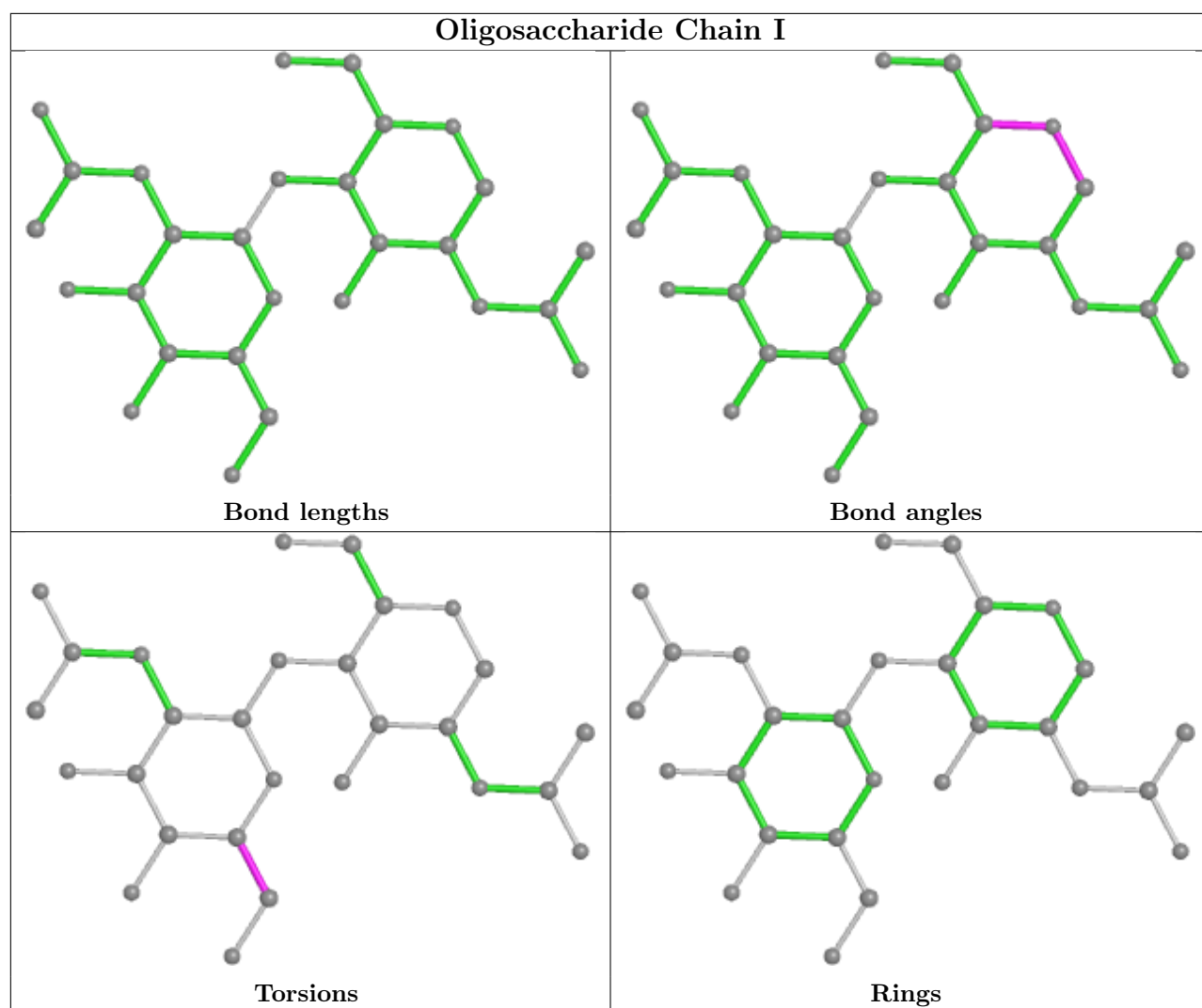


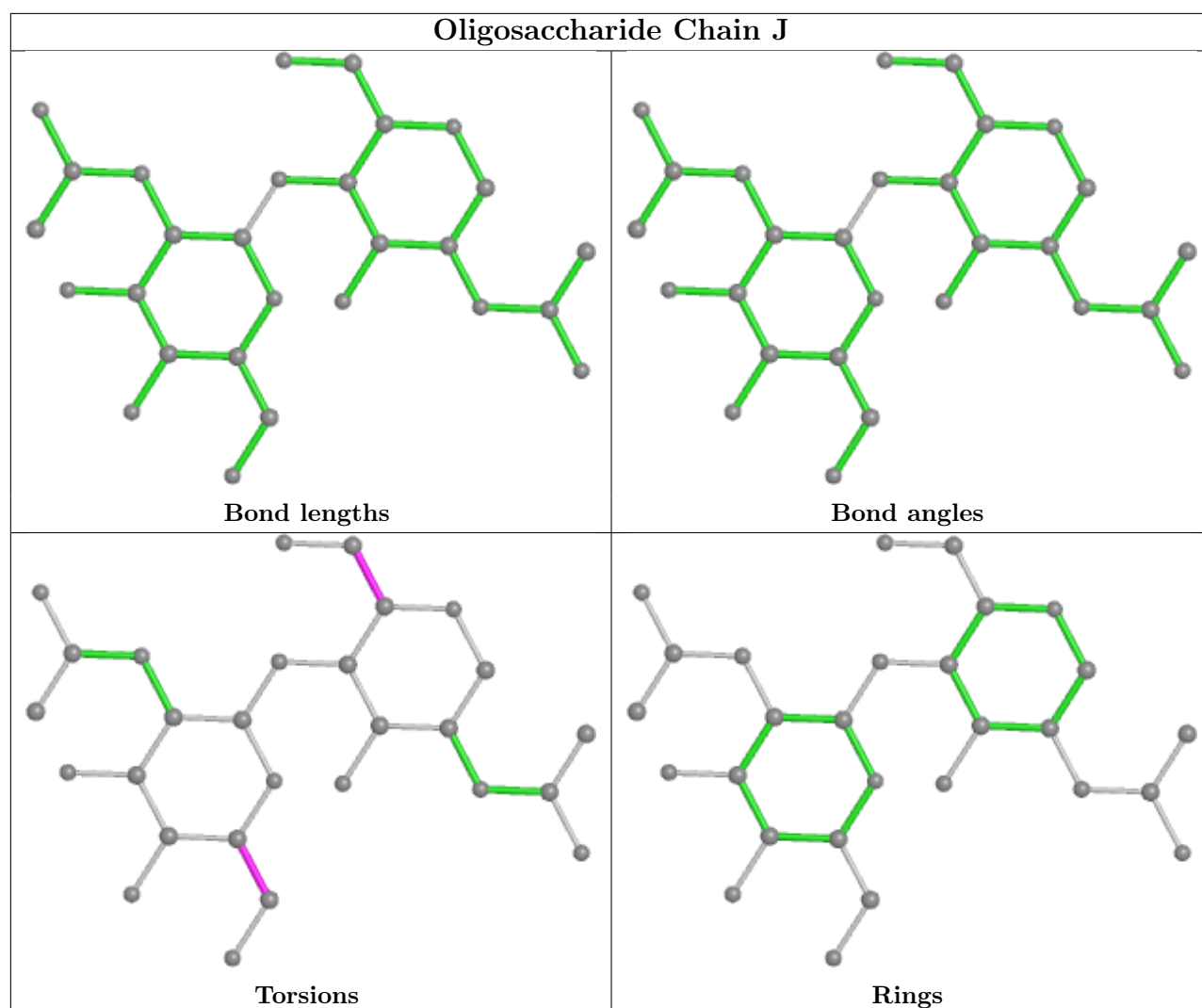


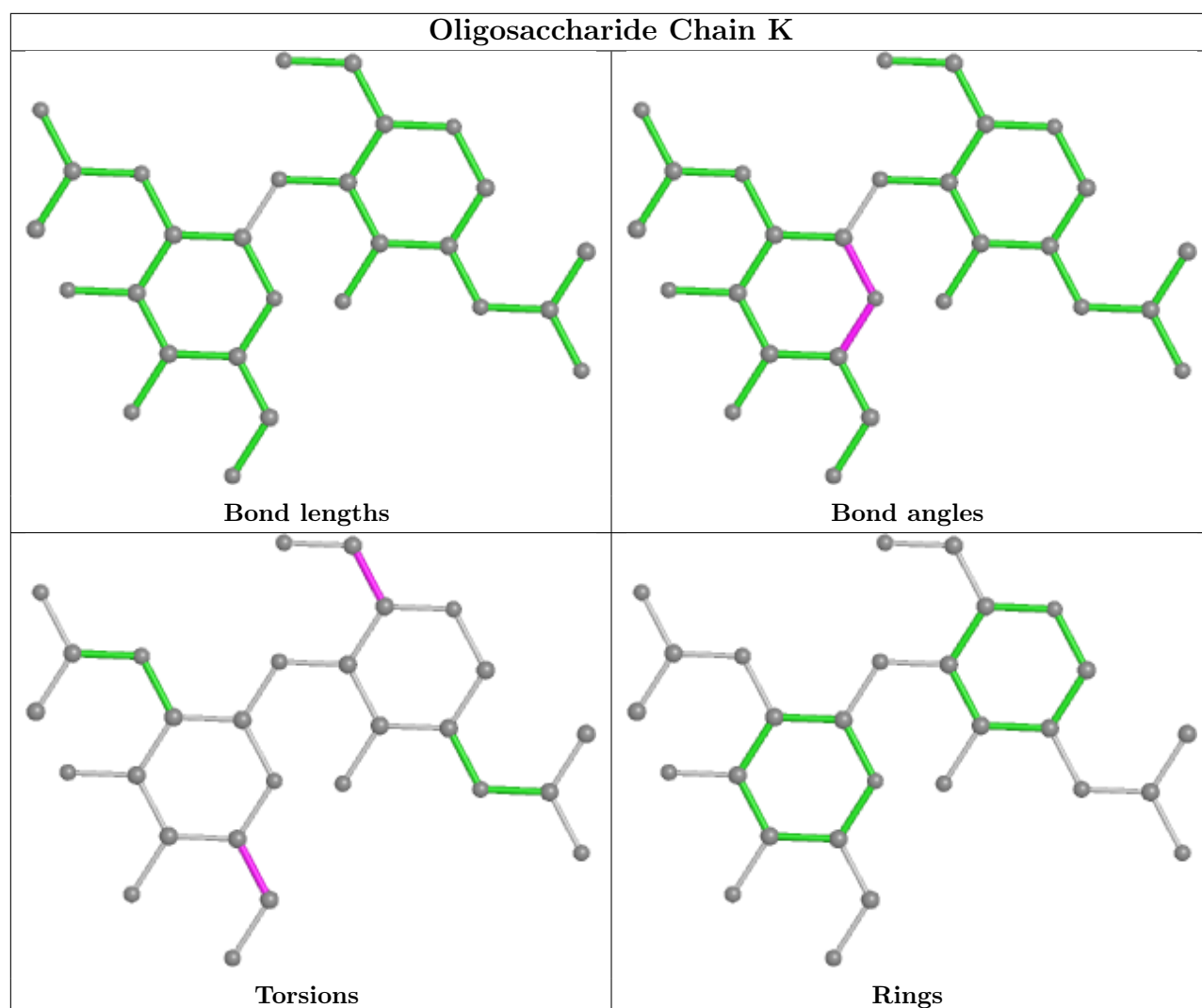


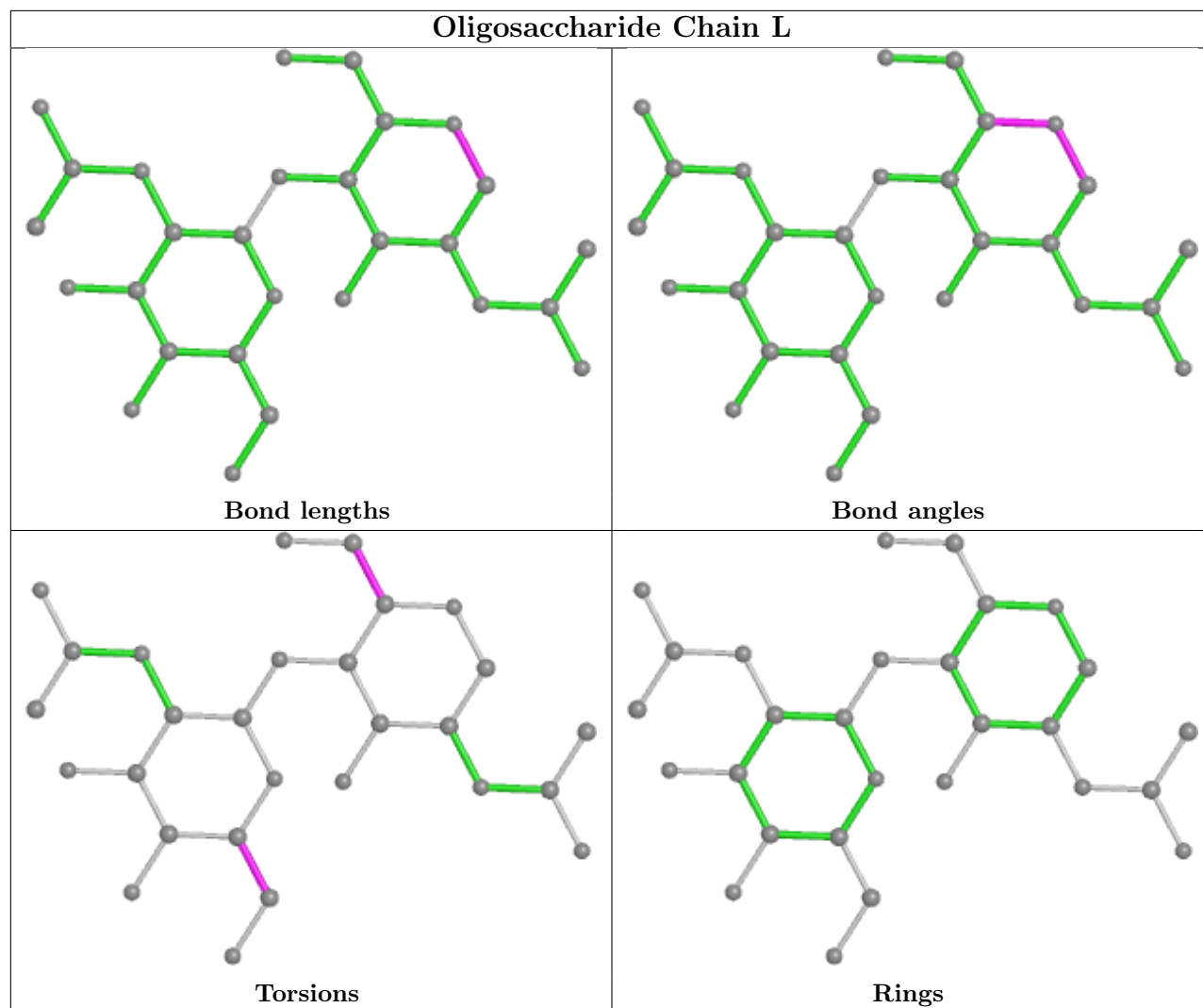


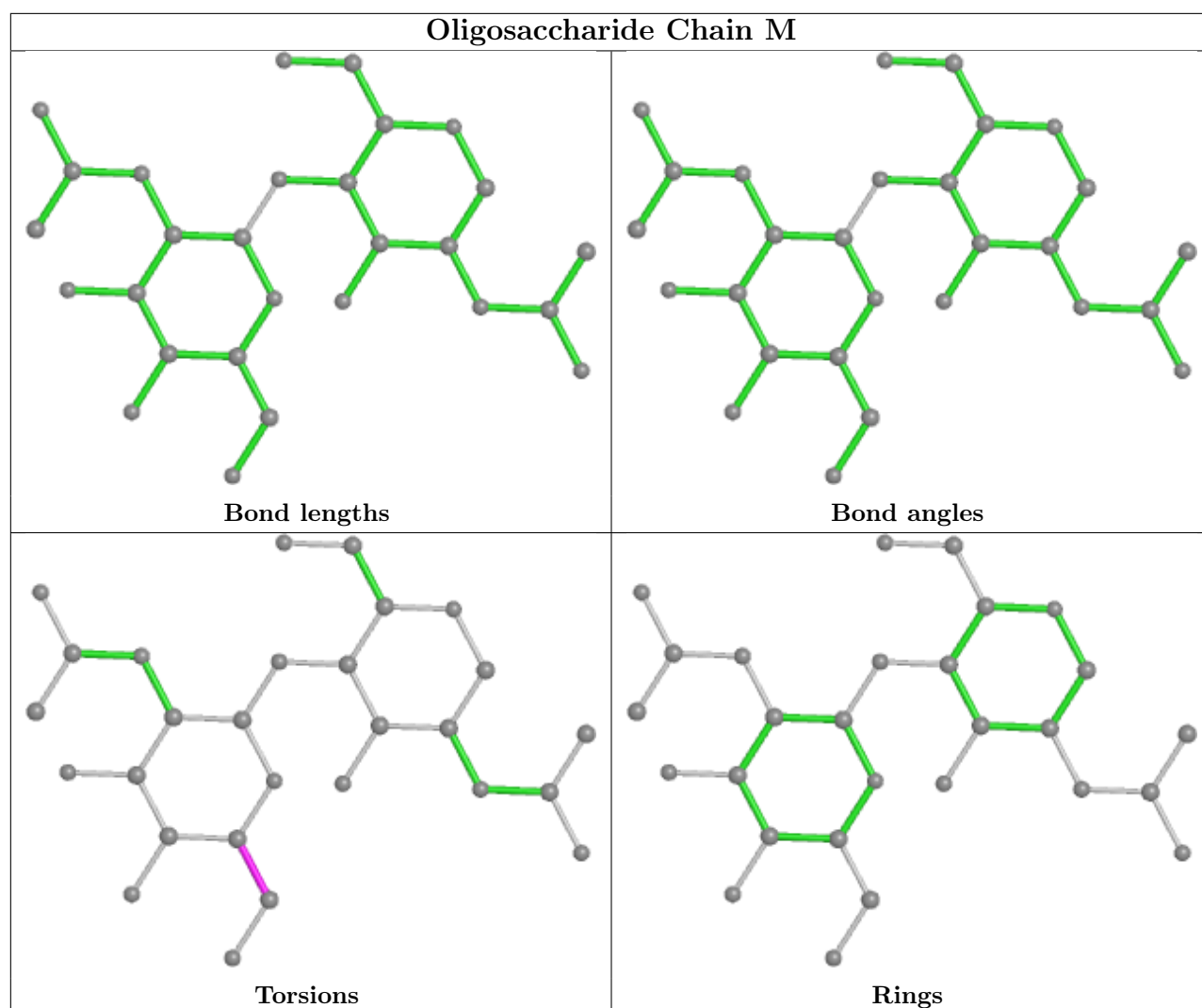


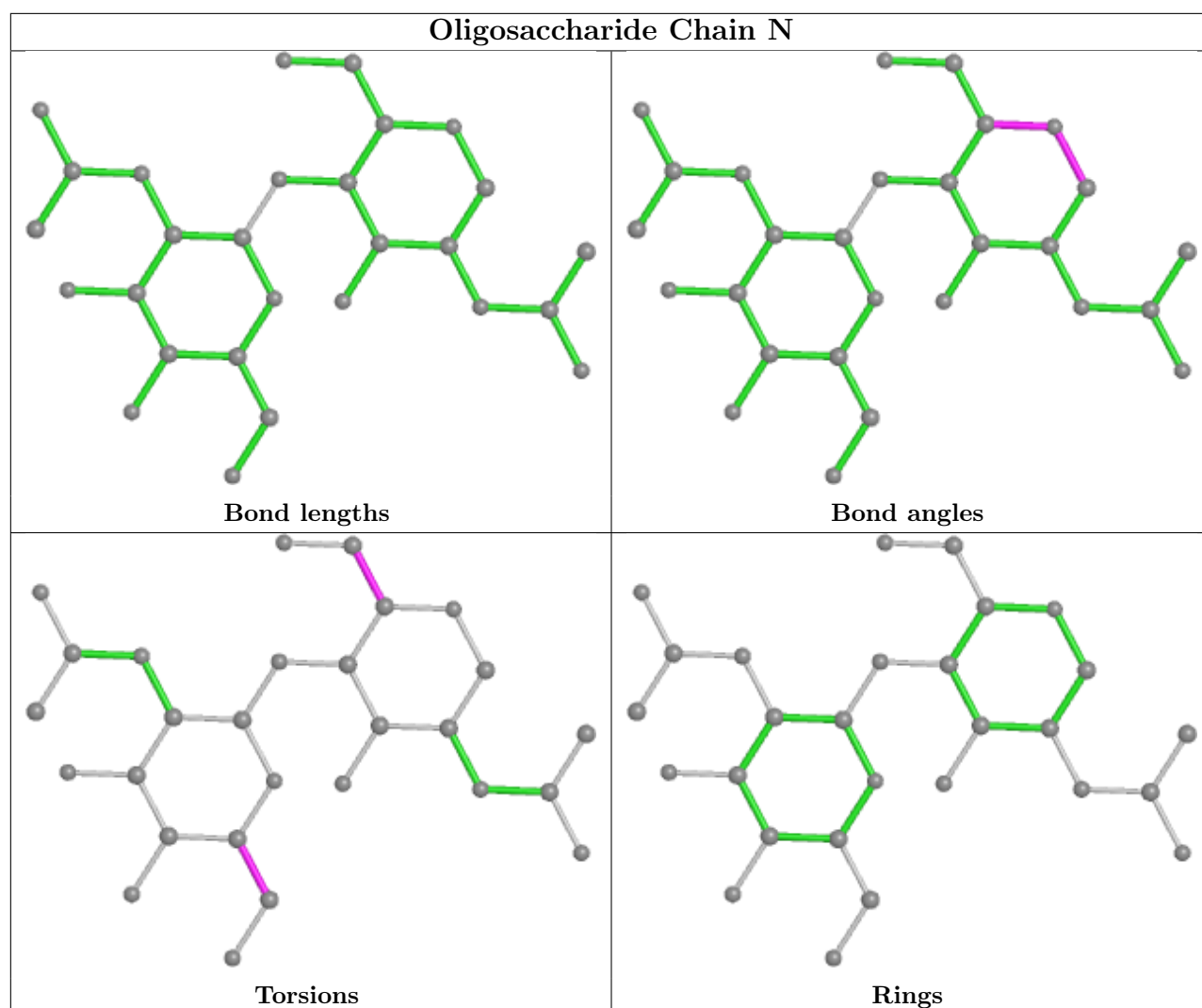


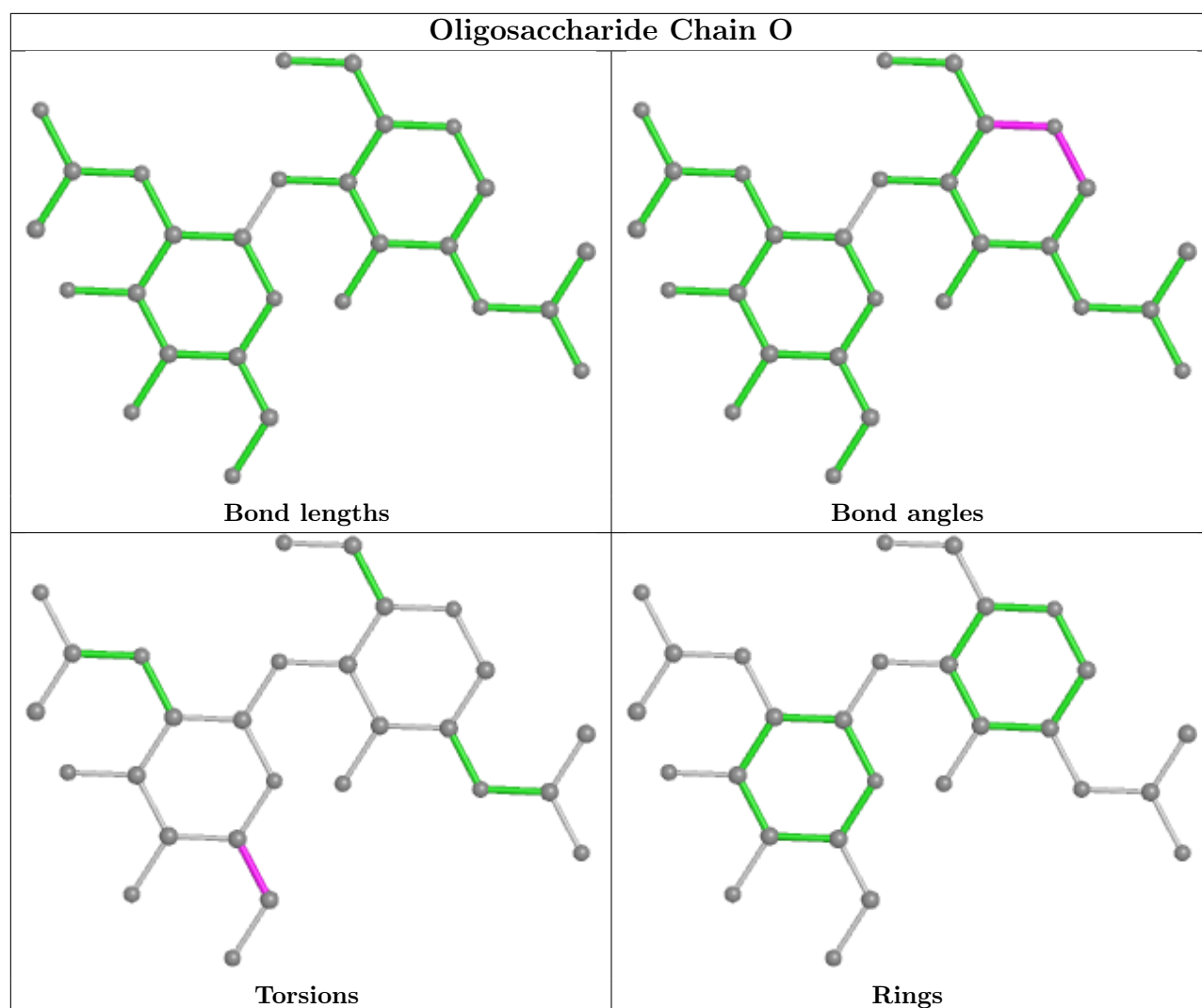


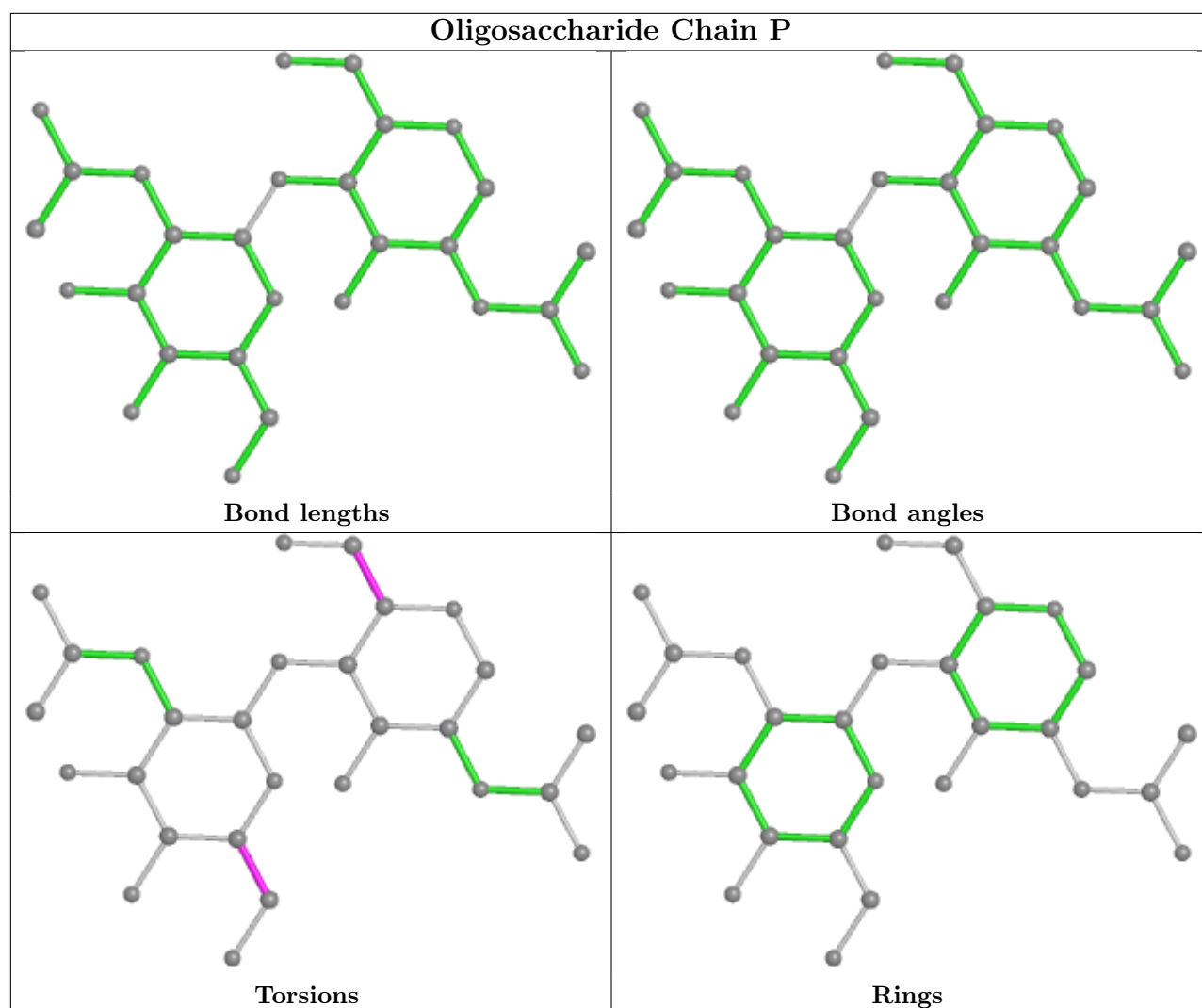


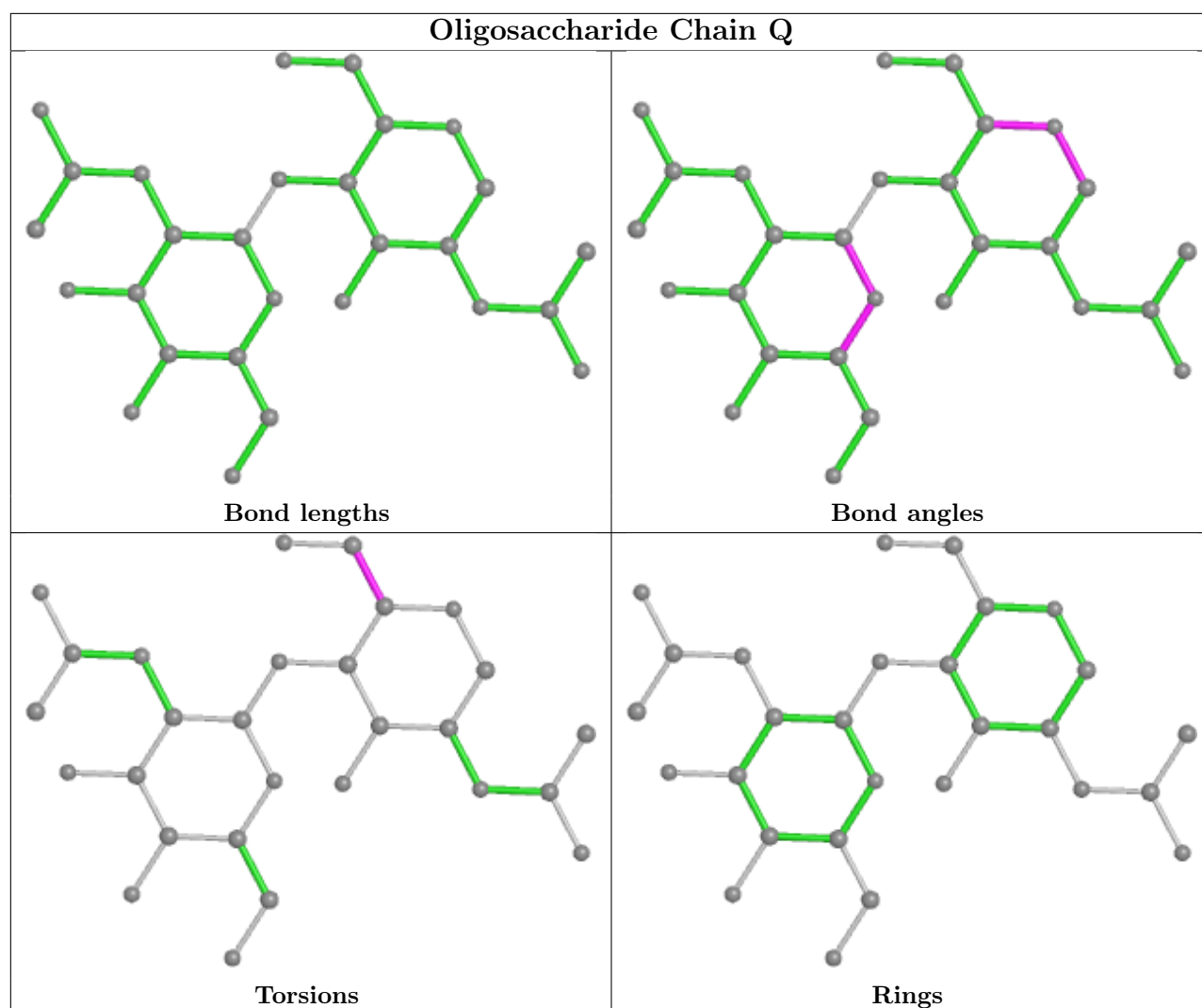


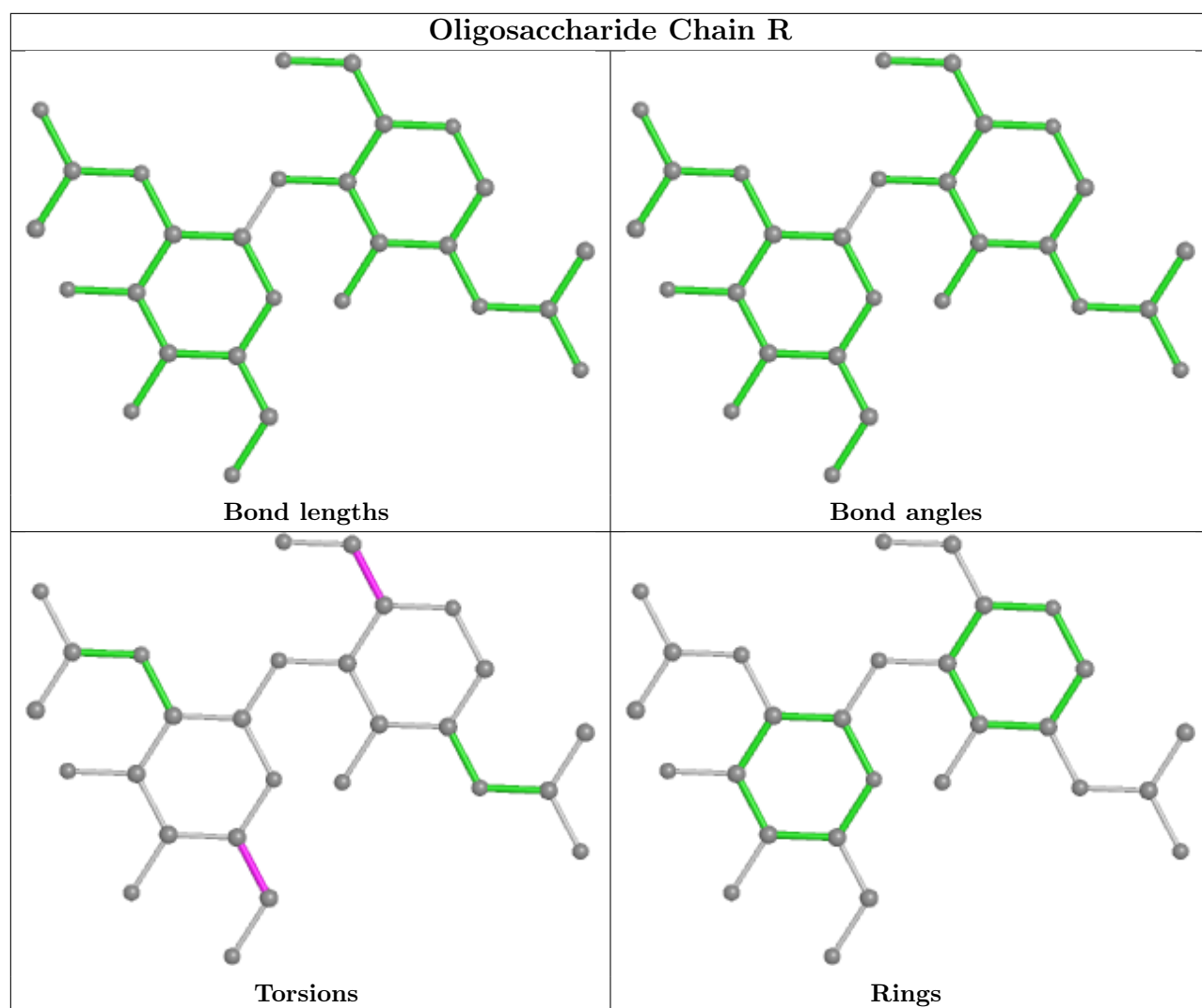


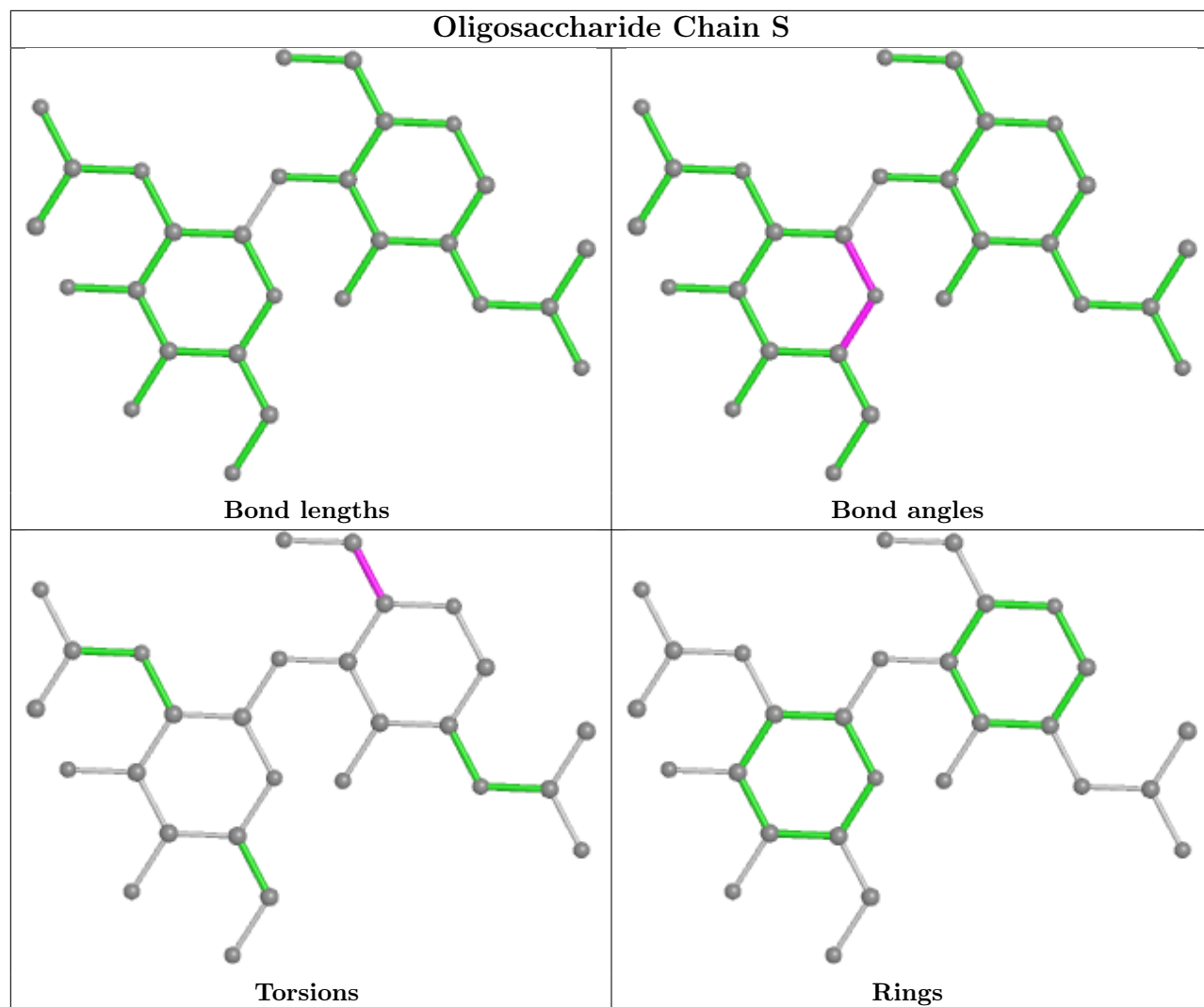


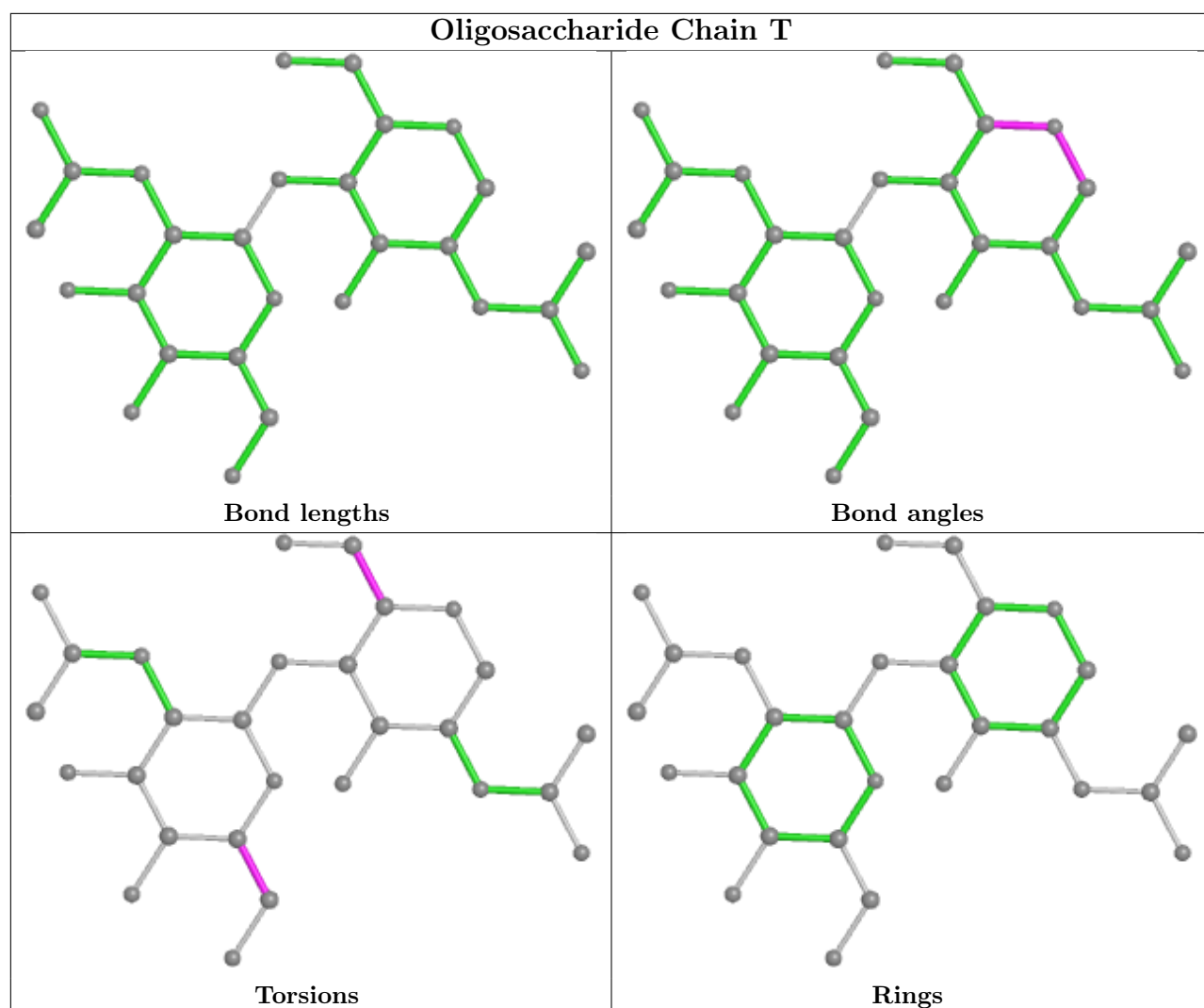


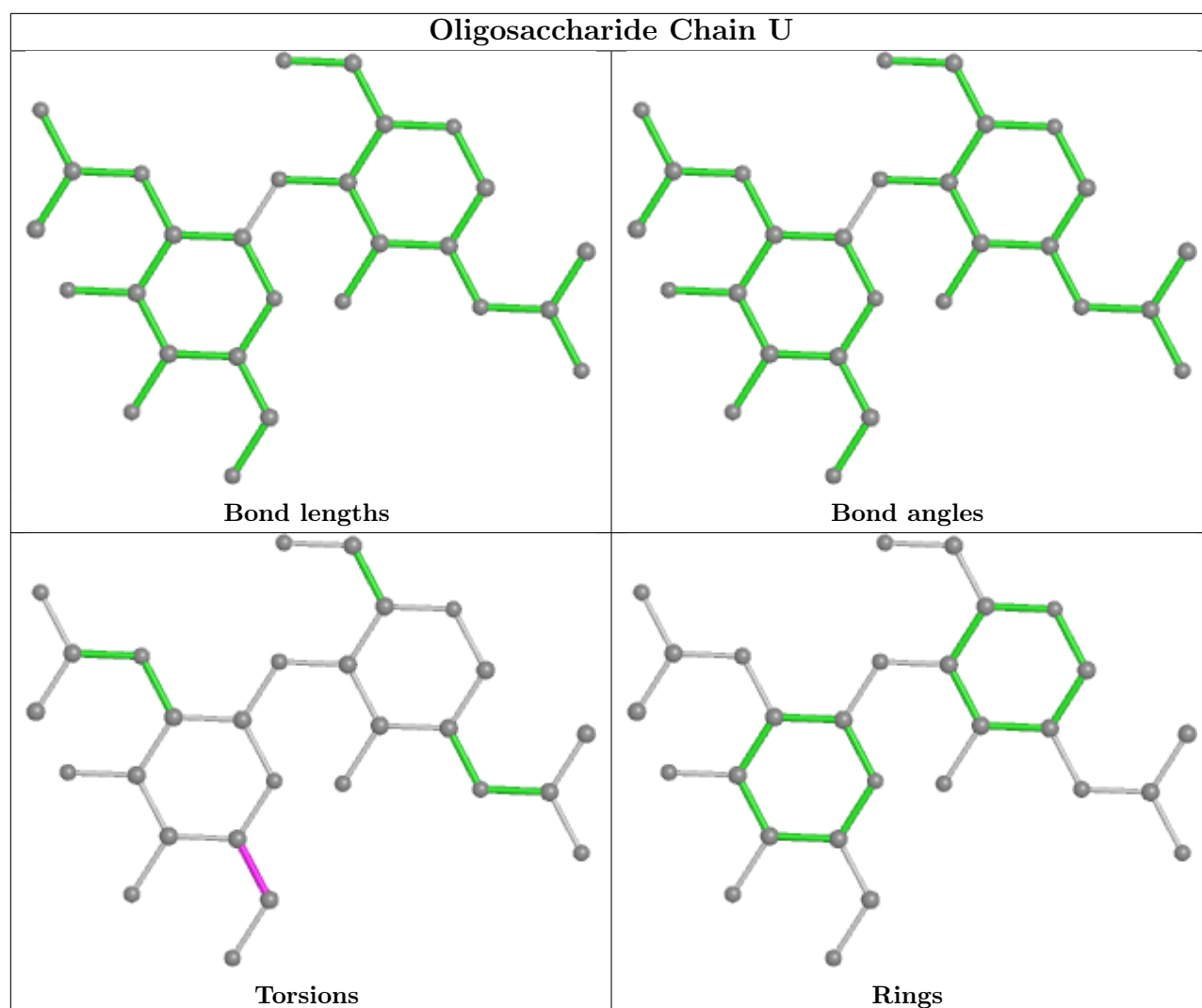


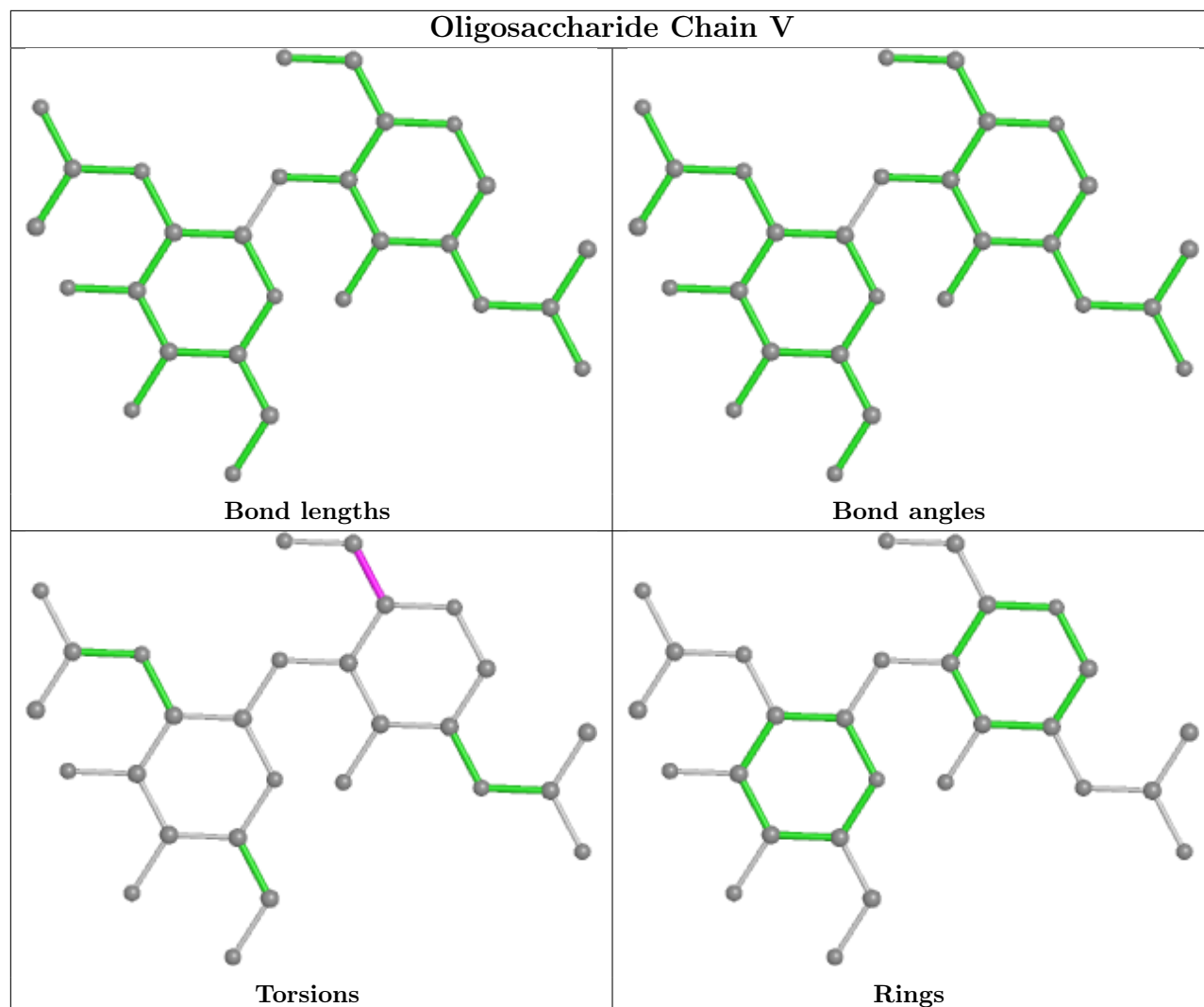


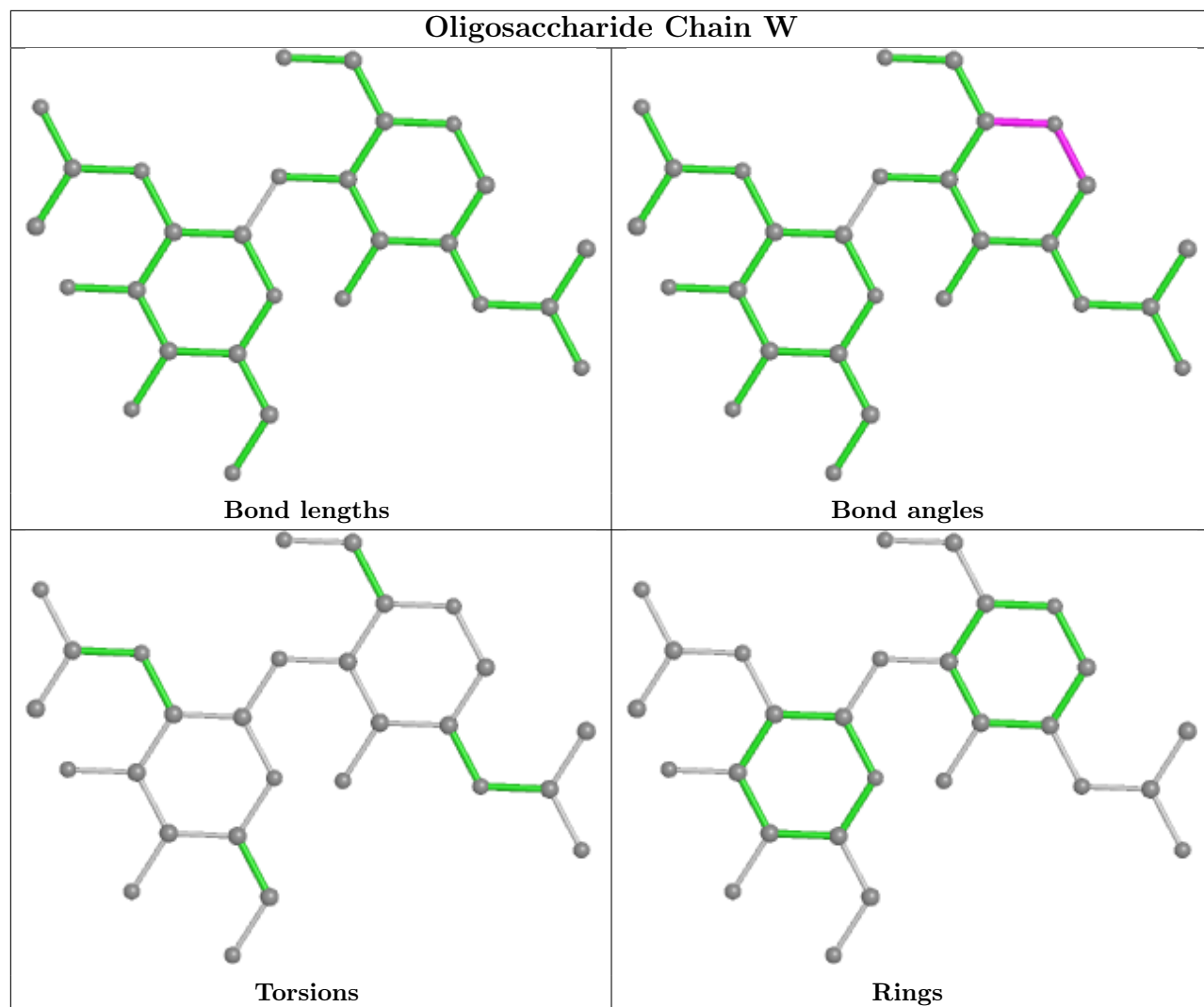


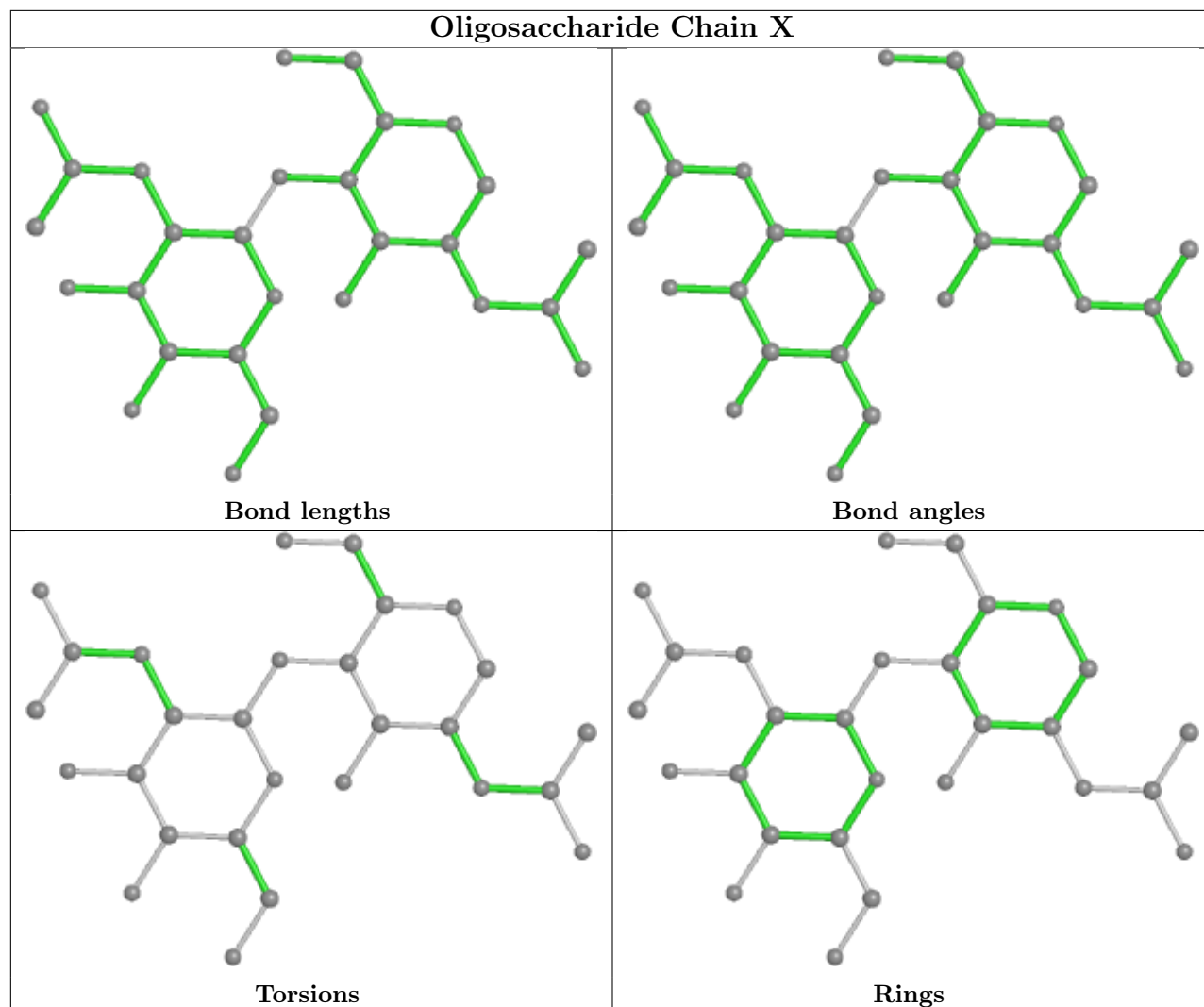


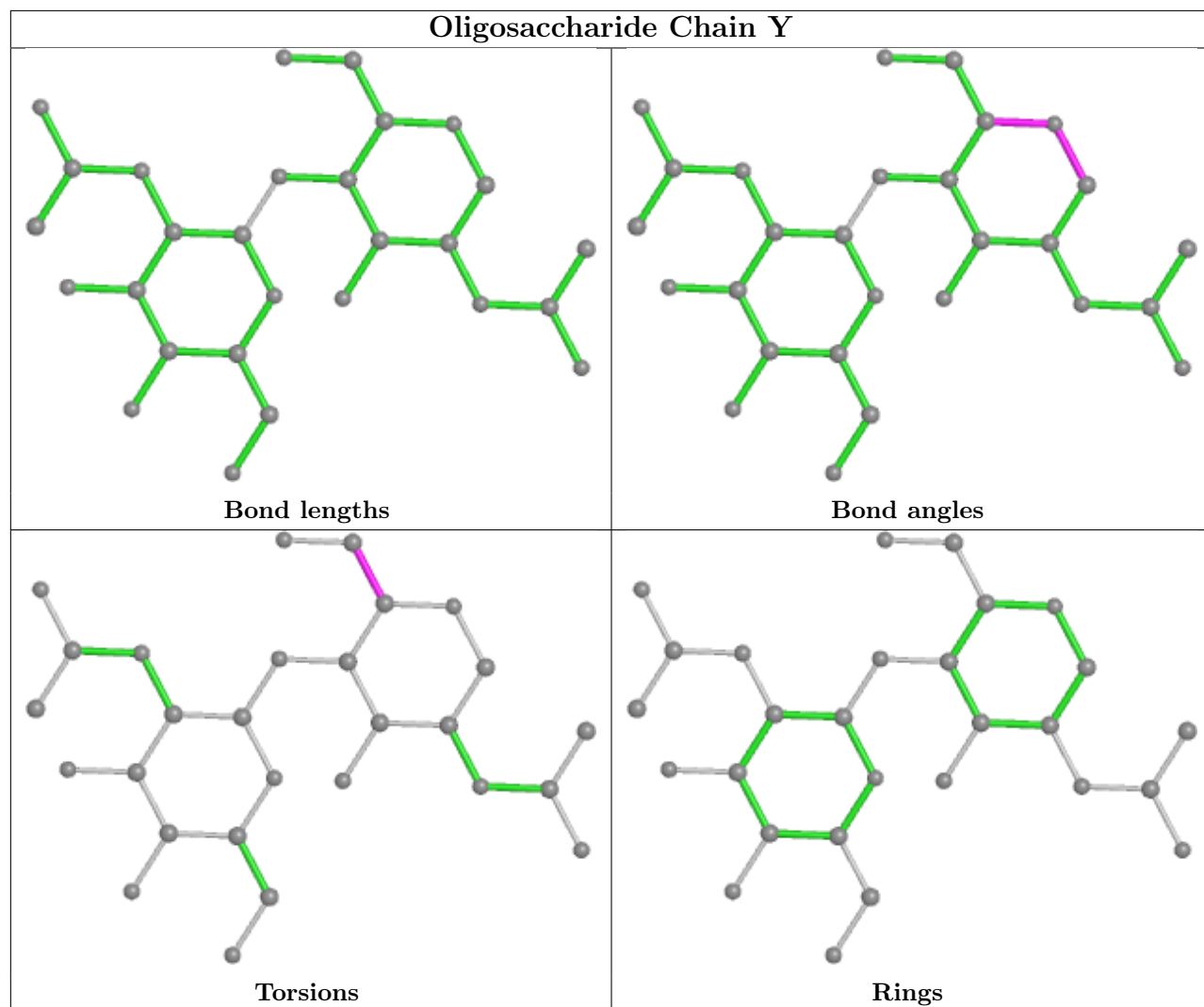


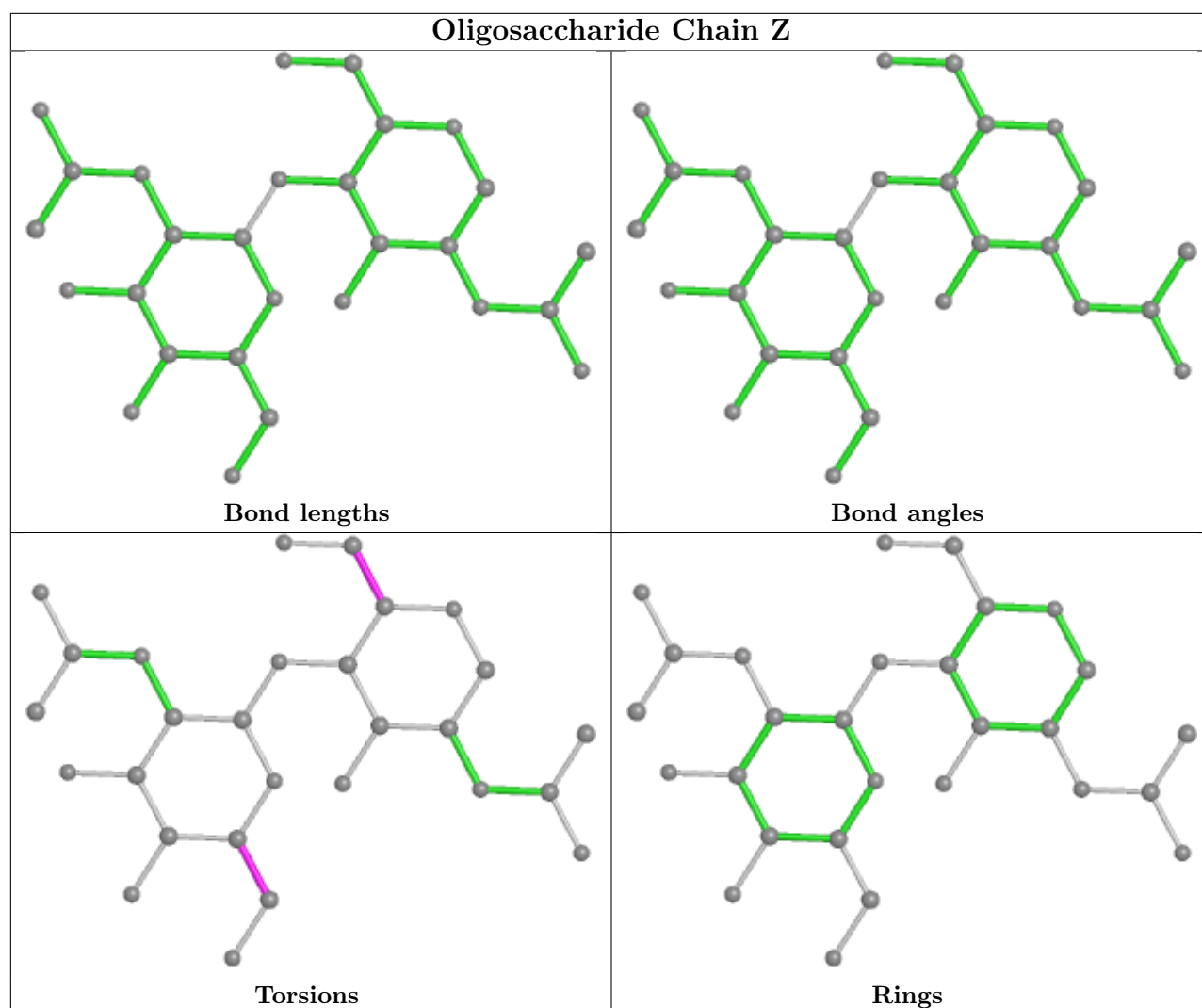


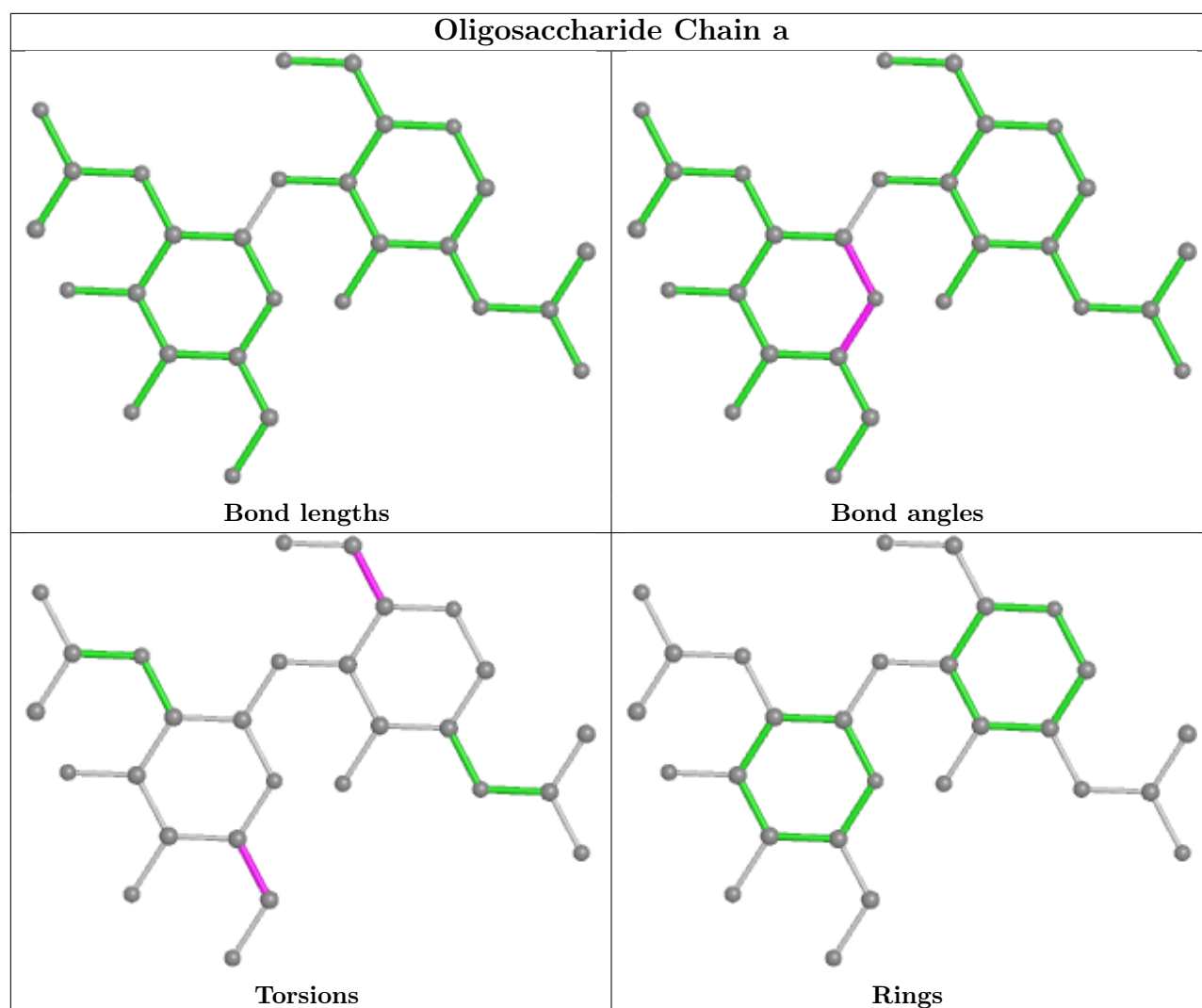












5.6 Ligand geometry [i](#)

39 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	$\# Z > 2$
4	NAG	C	2005	1	14,14,15	0.40	0	17,19,21	0.49	0
4	NAG	A	3003	1	14,14,15	0.58	0	17,19,21	0.51	0
3	PLM	C	2002	-	17,17,17	0.50	0	17,17,17	0.88	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	PLM	A	3001	-	17,17,17	0.59	1 (5%)	17,17,17	1.07	2 (11%)
4	NAG	B	2004	1	14,14,15	0.55	0	17,19,21	0.52	0
4	NAG	B	2011	1	14,14,15	0.37	0	17,19,21	0.61	1 (5%)
4	NAG	A	3006	1	14,14,15	0.35	0	17,19,21	0.50	0
4	NAG	C	2004	1	14,14,15	0.42	0	17,19,21	0.52	0
5	OLA	A	3013	-	19,19,19	0.44	0	19,19,19	1.02	1 (5%)
4	NAG	C	2011	1	14,14,15	0.40	0	17,19,21	0.70	1 (5%)
4	NAG	C	2007	1	14,14,15	0.34	0	17,19,21	0.72	1 (5%)
4	NAG	A	3007	1	14,14,15	0.30	0	17,19,21	0.54	0
4	NAG	A	3008	1	14,14,15	0.34	0	17,19,21	0.42	0
4	NAG	A	3004	1	14,14,15	0.32	0	17,19,21	0.51	0
4	NAG	B	2012	1	14,14,15	0.33	0	17,19,21	0.54	0
4	NAG	C	2006	1	14,14,15	0.34	0	17,19,21	0.45	0
4	NAG	B	2013	1	14,14,15	0.38	0	17,19,21	0.63	1 (5%)
4	NAG	B	2008	1	14,14,15	0.28	0	17,19,21	0.47	0
4	NAG	B	2006	1	14,14,15	0.45	0	17,19,21	0.50	0
4	NAG	B	2005	1	14,14,15	0.54	0	17,19,21	0.52	0
3	PLM	B	2002	-	17,17,17	0.50	0	17,17,17	0.88	0
4	NAG	A	3010	1	14,14,15	0.30	0	17,19,21	0.72	1 (5%)
4	NAG	C	2008	1	14,14,15	0.41	0	17,19,21	1.16	1 (5%)
4	NAG	A	3009	1	14,14,15	0.48	0	17,19,21	0.56	0
4	NAG	A	3002	1	14,14,15	0.30	0	17,19,21	0.53	0
4	NAG	B	2007	1	14,14,15	0.24	0	17,19,21	0.50	0
4	NAG	A	3011	1	14,14,15	0.48	0	17,19,21	0.55	0
4	NAG	A	3012	1	14,14,15	0.54	0	17,19,21	0.51	0
5	OLA	C	2001	-	19,19,19	0.40	0	19,19,19	0.95	0
4	NAG	A	3005	1	14,14,15	0.42	0	17,19,21	0.50	0
5	OLA	B	2001	-	19,19,19	0.40	0	19,19,19	1.10	1 (5%)
4	NAG	C	2013	1	14,14,15	0.33	0	17,19,21	0.67	1 (5%)
4	NAG	B	2010	1	14,14,15	0.39	0	17,19,21	0.50	0
4	NAG	B	2003	1	14,14,15	0.37	0	17,19,21	0.63	1 (5%)
4	NAG	C	2012	1	14,14,15	0.46	0	17,19,21	0.64	1 (5%)
4	NAG	C	2010	1	14,14,15	0.30	0	17,19,21	0.44	0
4	NAG	C	2009	1	14,14,15	0.48	0	17,19,21	0.41	0
4	NAG	B	2009	1	14,14,15	0.26	0	17,19,21	0.44	0
4	NAG	C	2003	1	14,14,15	0.34	0	17,19,21	0.69	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.

'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	C	2005	1	-	2/6/23/26	0/1/1/1
4	NAG	A	3003	1	-	2/6/23/26	0/1/1/1
3	PLM	C	2002	-	-	9/15/15/15	-
3	PLM	A	3001	-	-	9/15/15/15	-
4	NAG	B	2004	1	-	2/6/23/26	0/1/1/1
4	NAG	B	2011	1	-	2/6/23/26	0/1/1/1
4	NAG	A	3006	1	-	0/6/23/26	0/1/1/1
4	NAG	C	2004	1	-	2/6/23/26	0/1/1/1
5	OLA	A	3013	-	-	11/17/17/17	-
4	NAG	C	2011	1	-	2/6/23/26	0/1/1/1
4	NAG	C	2007	1	-	2/6/23/26	0/1/1/1
4	NAG	A	3007	1	-	1/6/23/26	0/1/1/1
4	NAG	A	3008	1	-	0/6/23/26	0/1/1/1
4	NAG	A	3004	1	-	0/6/23/26	0/1/1/1
4	NAG	B	2012	1	-	1/6/23/26	0/1/1/1
4	NAG	C	2006	1	-	2/6/23/26	0/1/1/1
4	NAG	B	2013	1	-	2/6/23/26	0/1/1/1
4	NAG	B	2008	1	-	0/6/23/26	0/1/1/1
4	NAG	B	2006	1	-	2/6/23/26	0/1/1/1
4	NAG	B	2005	1	-	2/6/23/26	0/1/1/1
3	PLM	B	2002	-	-	9/15/15/15	-
4	NAG	A	3010	1	-	2/6/23/26	0/1/1/1
4	NAG	C	2008	1	-	0/6/23/26	0/1/1/1
4	NAG	A	3009	1	-	2/6/23/26	0/1/1/1
4	NAG	A	3002	1	-	2/6/23/26	0/1/1/1
4	NAG	B	2007	1	-	2/6/23/26	0/1/1/1
4	NAG	A	3011	1	-	2/6/23/26	0/1/1/1
4	NAG	A	3012	1	-	1/6/23/26	0/1/1/1
5	OLA	C	2001	-	-	10/17/17/17	-
4	NAG	A	3005	1	-	1/6/23/26	0/1/1/1
5	OLA	B	2001	-	-	12/17/17/17	-
4	NAG	C	2013	1	-	2/6/23/26	0/1/1/1
4	NAG	B	2010	1	-	2/6/23/26	0/1/1/1
4	NAG	B	2003	1	-	2/6/23/26	0/1/1/1
4	NAG	C	2012	1	-	2/6/23/26	0/1/1/1
4	NAG	C	2010	1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	C	2009	1	-	2/6/23/26	0/1/1/1
4	NAG	B	2009	1	-	2/6/23/26	0/1/1/1
4	NAG	C	2003	1	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	3001	PLM	O1-C1	-2.17	1.23	1.30

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	3001	PLM	O1-C1-O2	-2.72	116.51	123.30
5	B	2001	OLA	C3-C2-C1	-2.68	107.73	114.47
4	C	2007	NAG	C1-O5-C5	2.67	115.81	112.19
4	A	3010	NAG	C1-O5-C5	2.57	115.68	112.19
5	A	3013	OLA	C3-C2-C1	-2.53	108.08	114.47

There are no chirality outliers.

5 of 112 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	3003	NAG	O5-C5-C6-O6
4	B	2004	NAG	O5-C5-C6-O6
4	B	2005	NAG	O5-C5-C6-O6
4	A	3002	NAG	O5-C5-C6-O6
4	A	3010	NAG	O5-C5-C6-O6

There are no ring outliers.

11 monomers are involved in 66 short contacts:

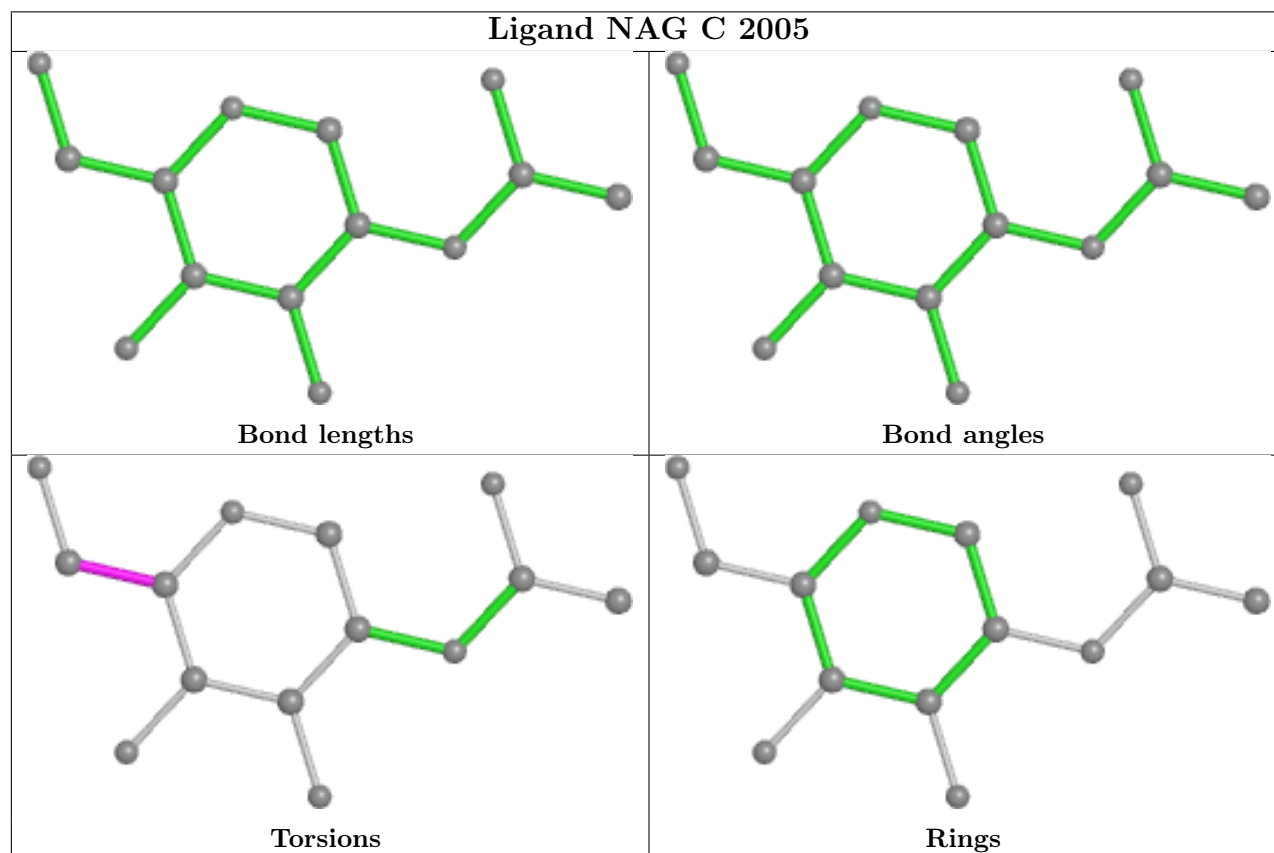
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	2002	PLM	16	0
3	A	3001	PLM	15	0
5	A	3013	OLA	1	0
4	A	3007	NAG	4	0
4	B	2008	NAG	2	0
3	B	2002	PLM	23	0
4	A	3002	NAG	1	0
5	C	2001	OLA	1	0

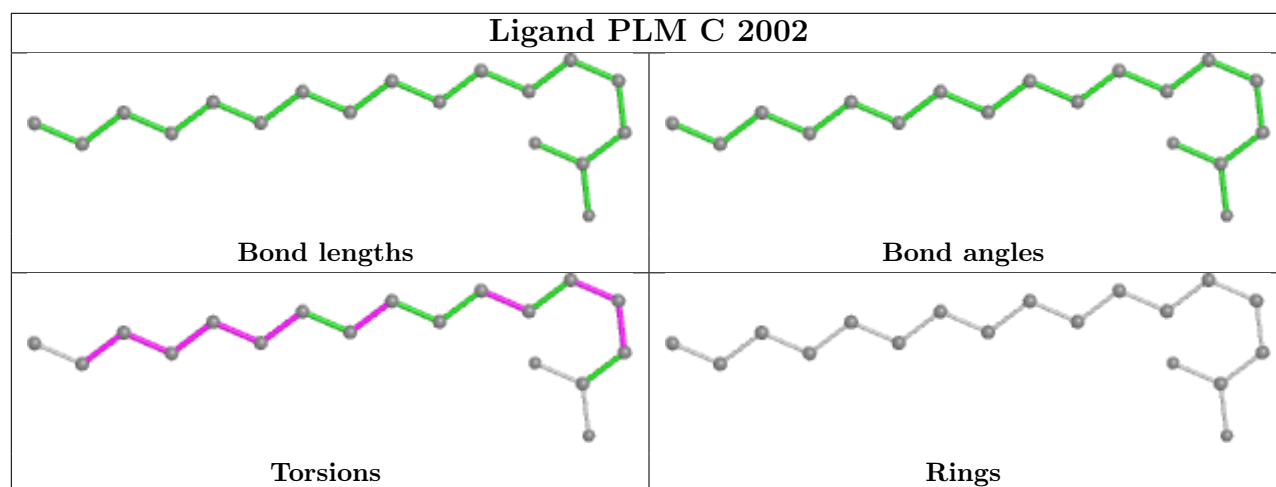
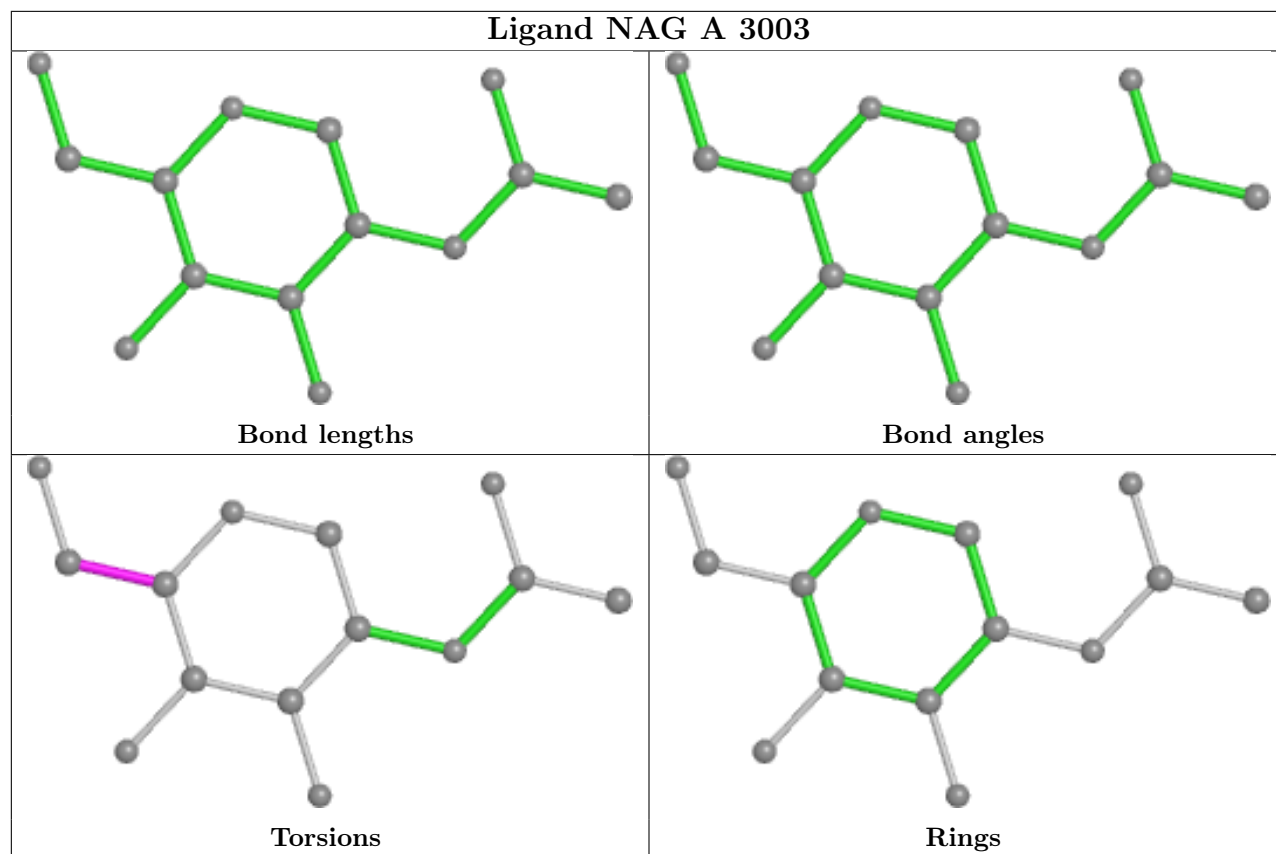
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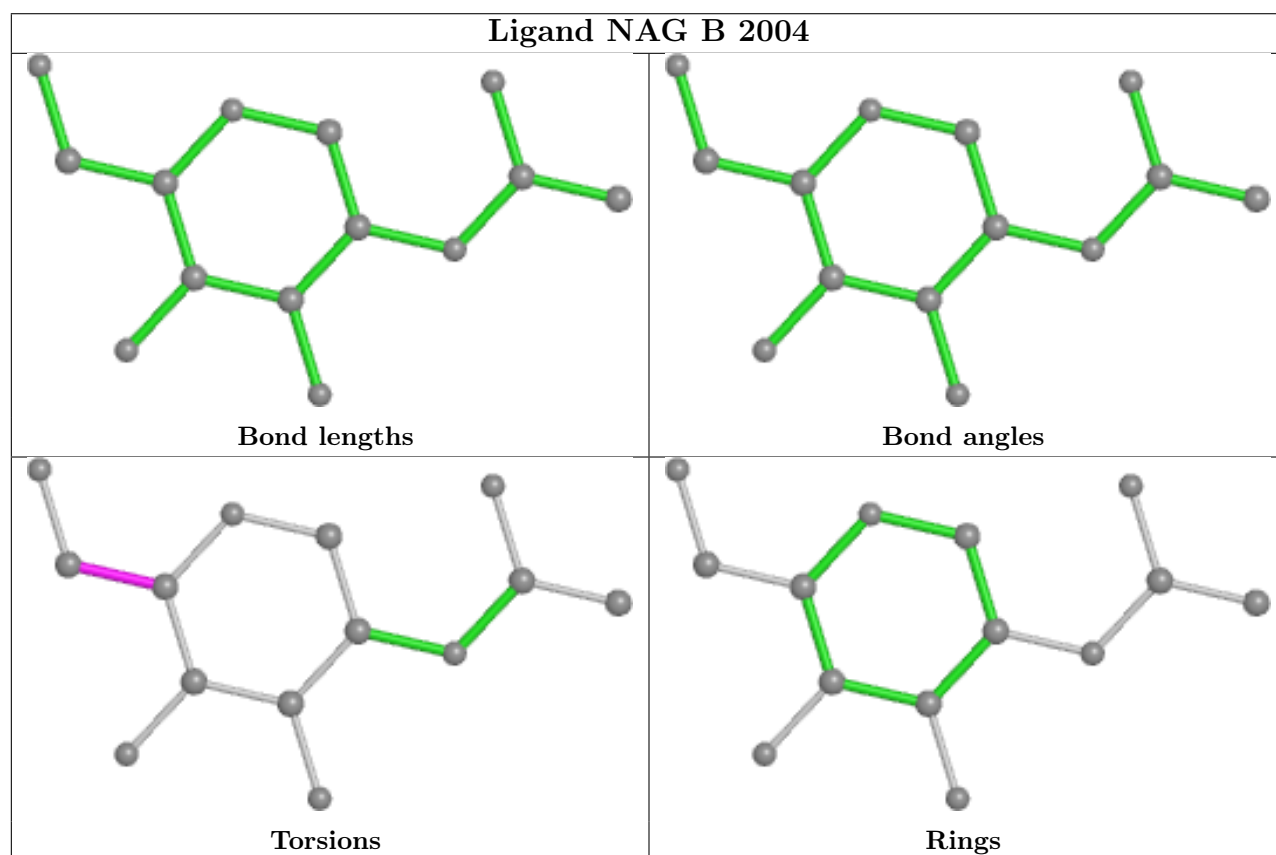
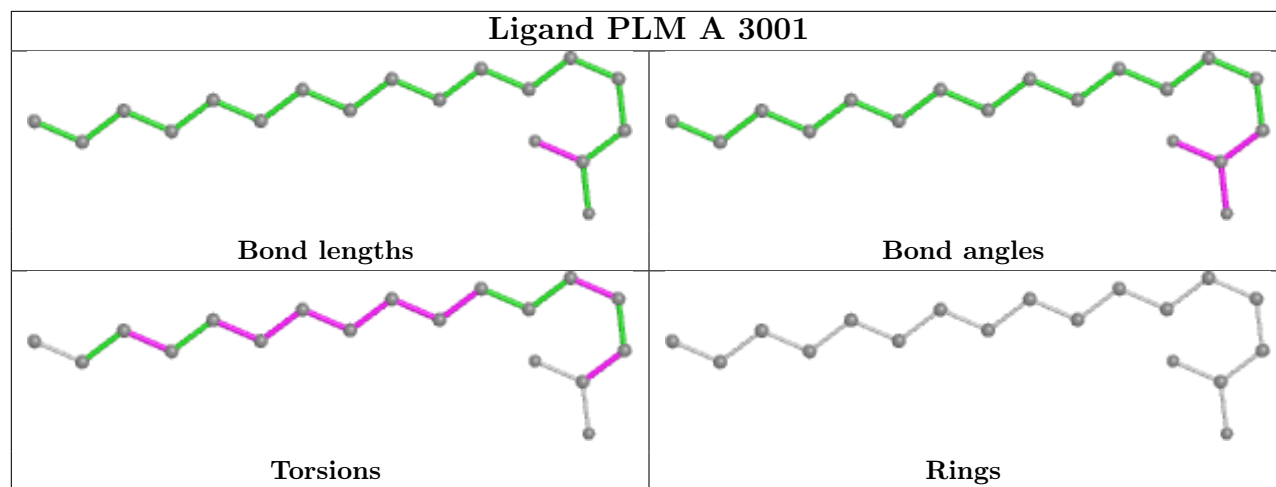
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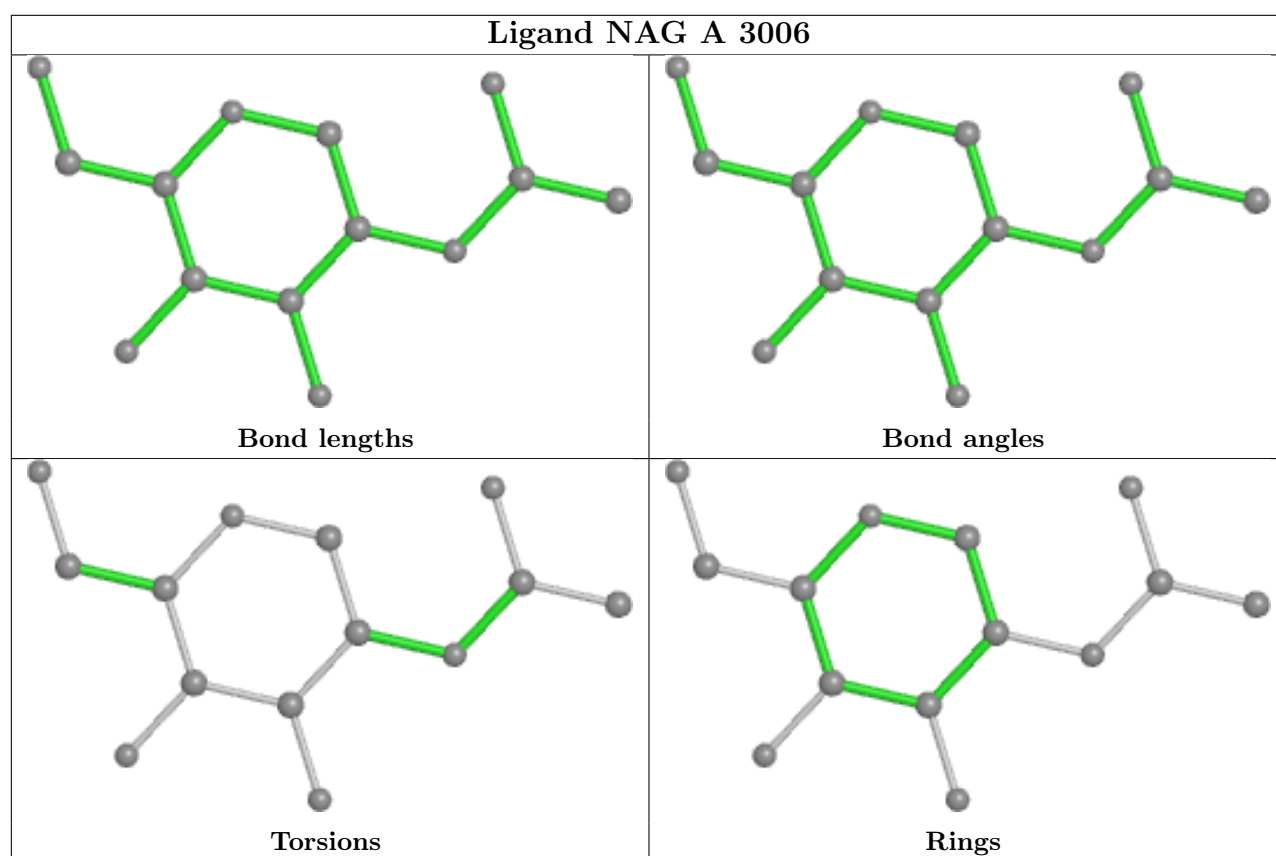
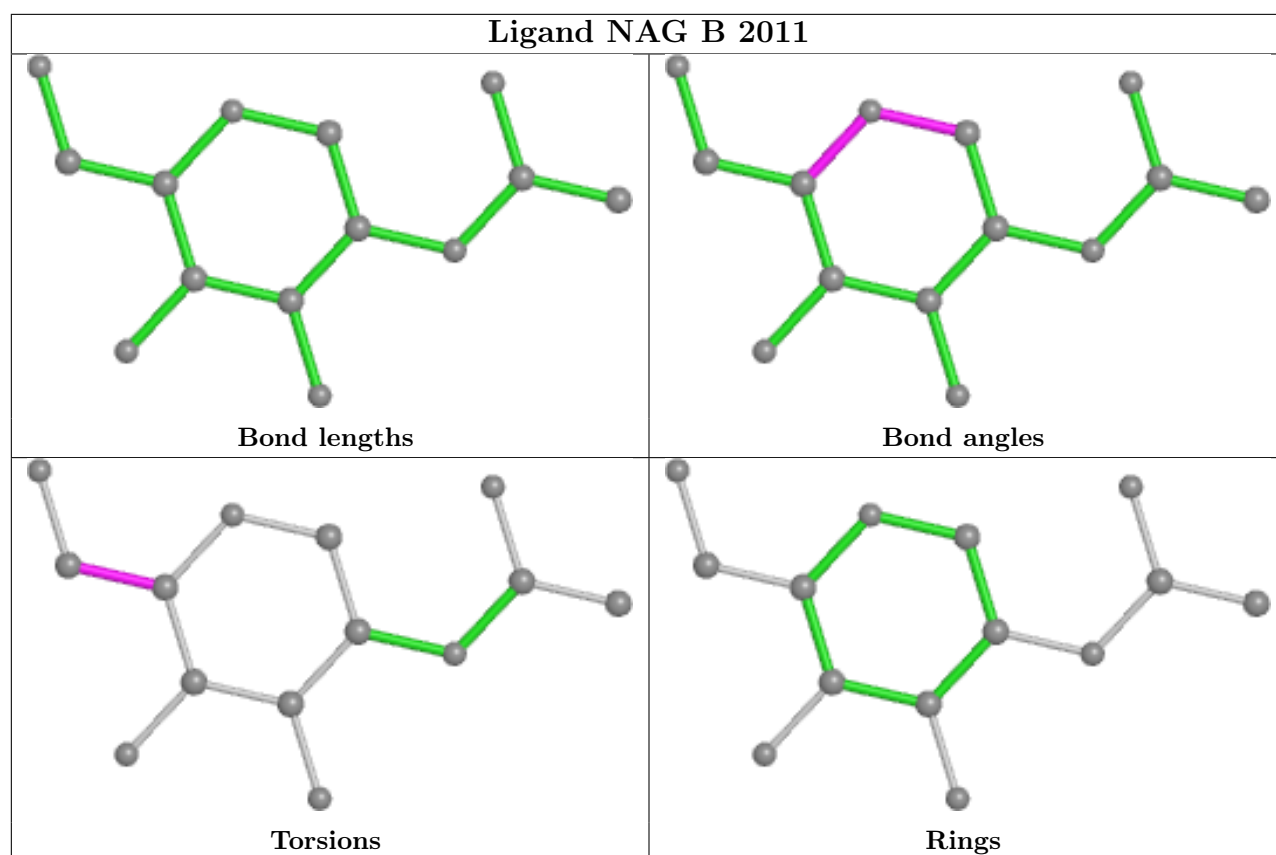
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	2001	OLA	1	0
4	B	2003	NAG	1	0
4	C	2003	NAG	1	0

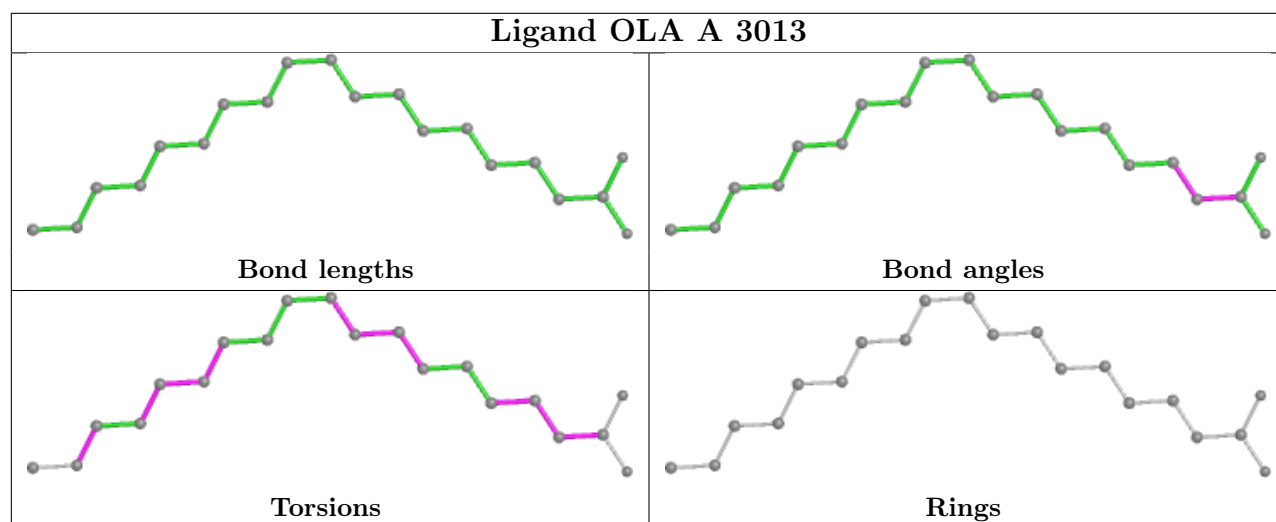
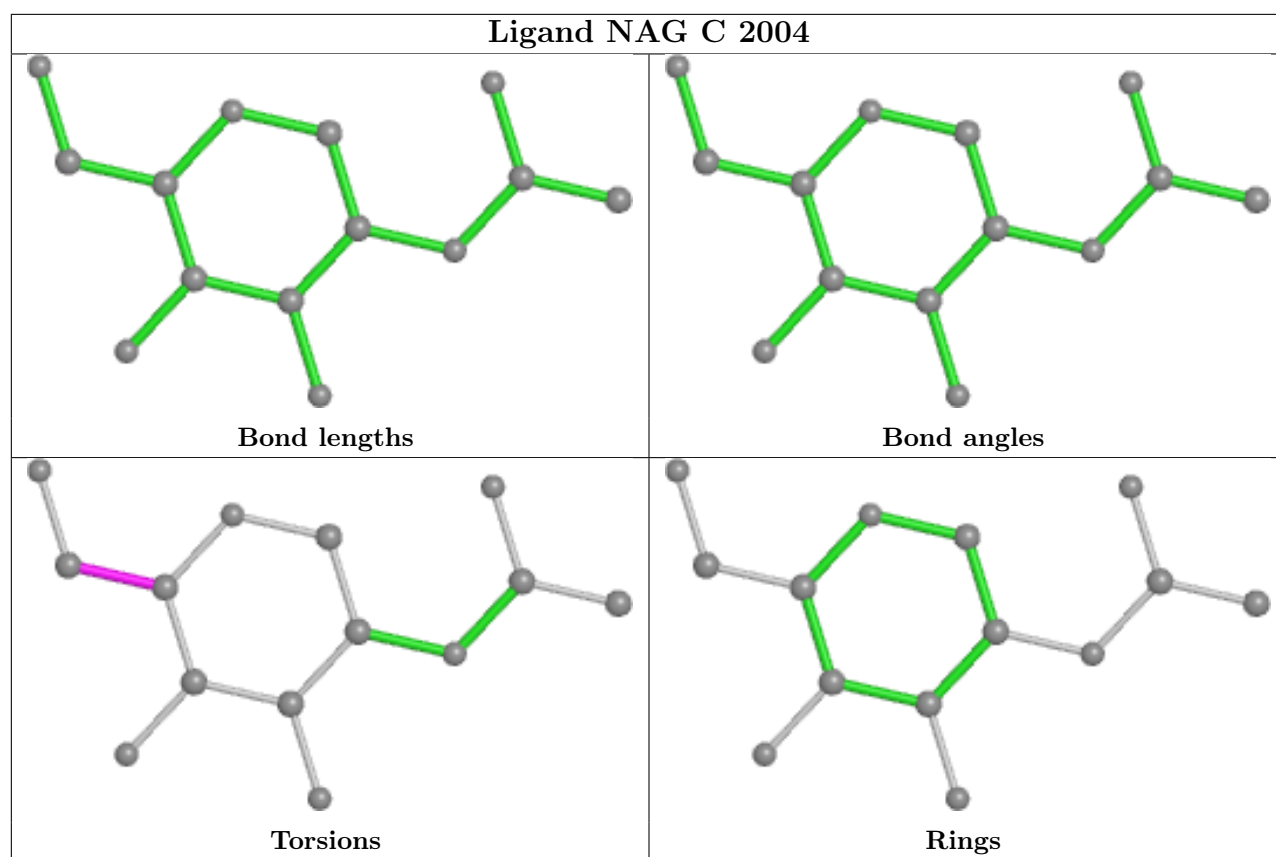
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

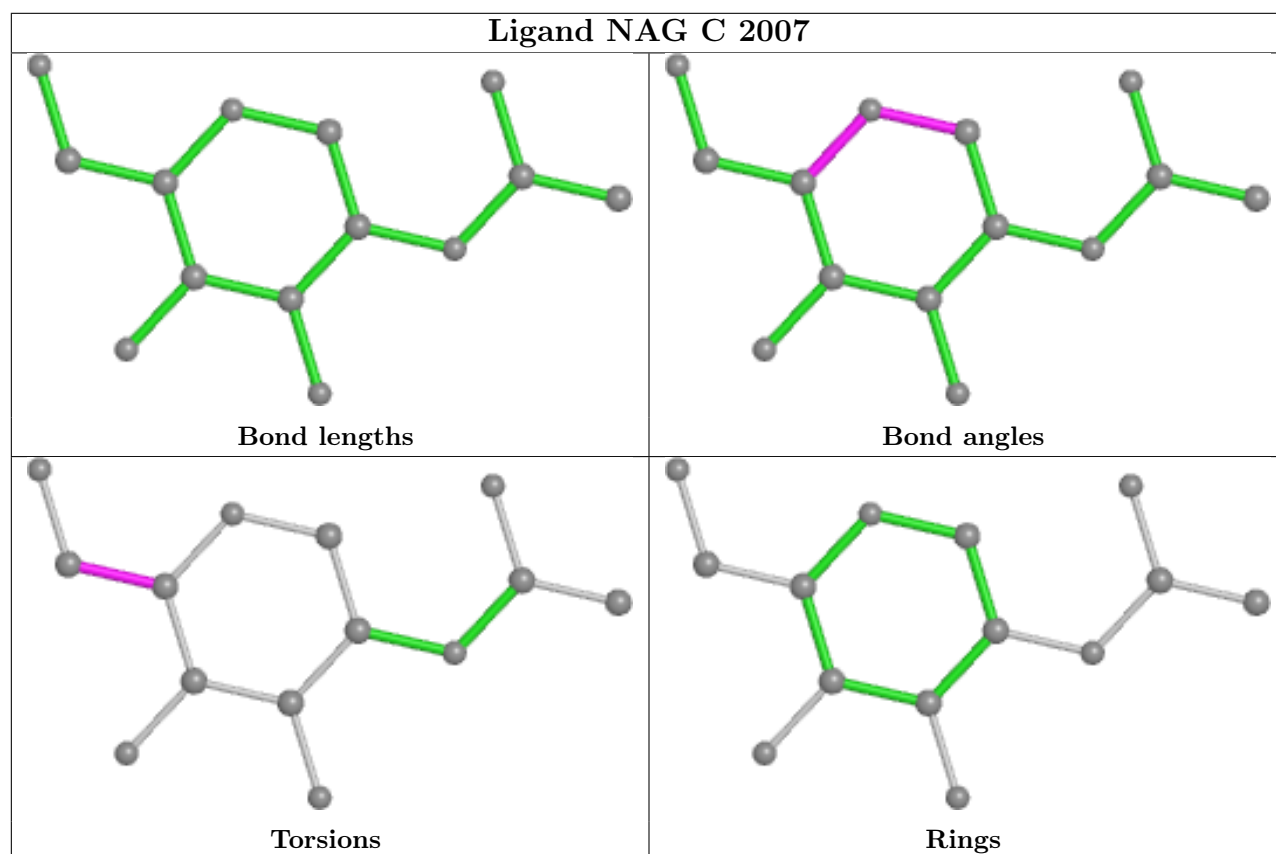
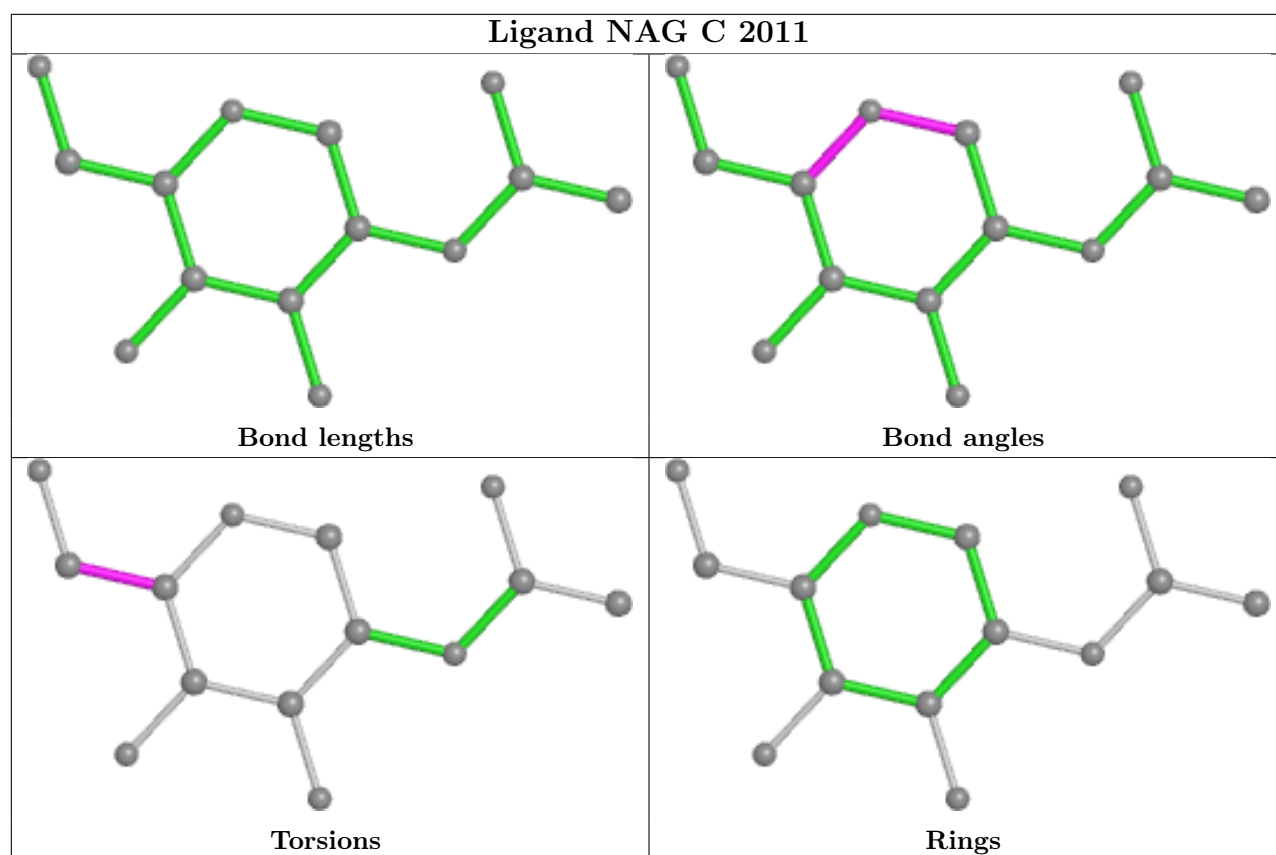




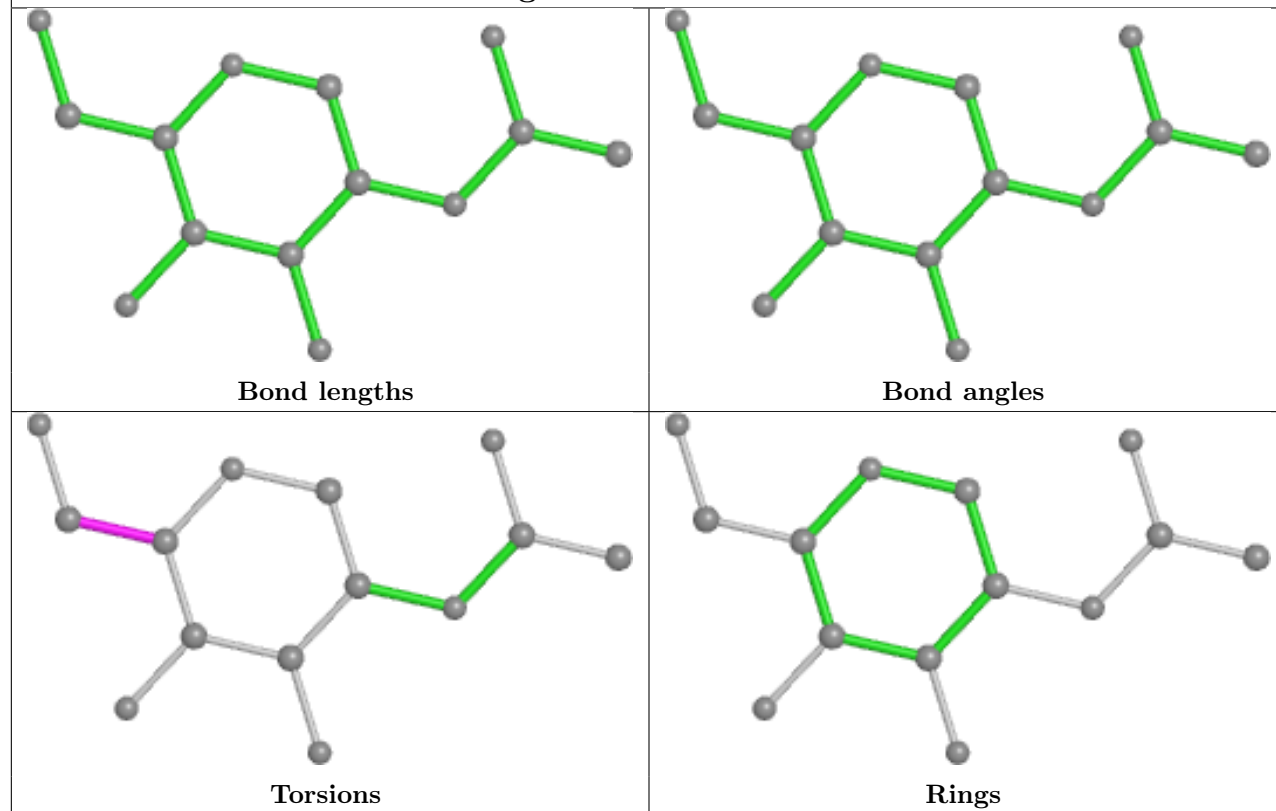




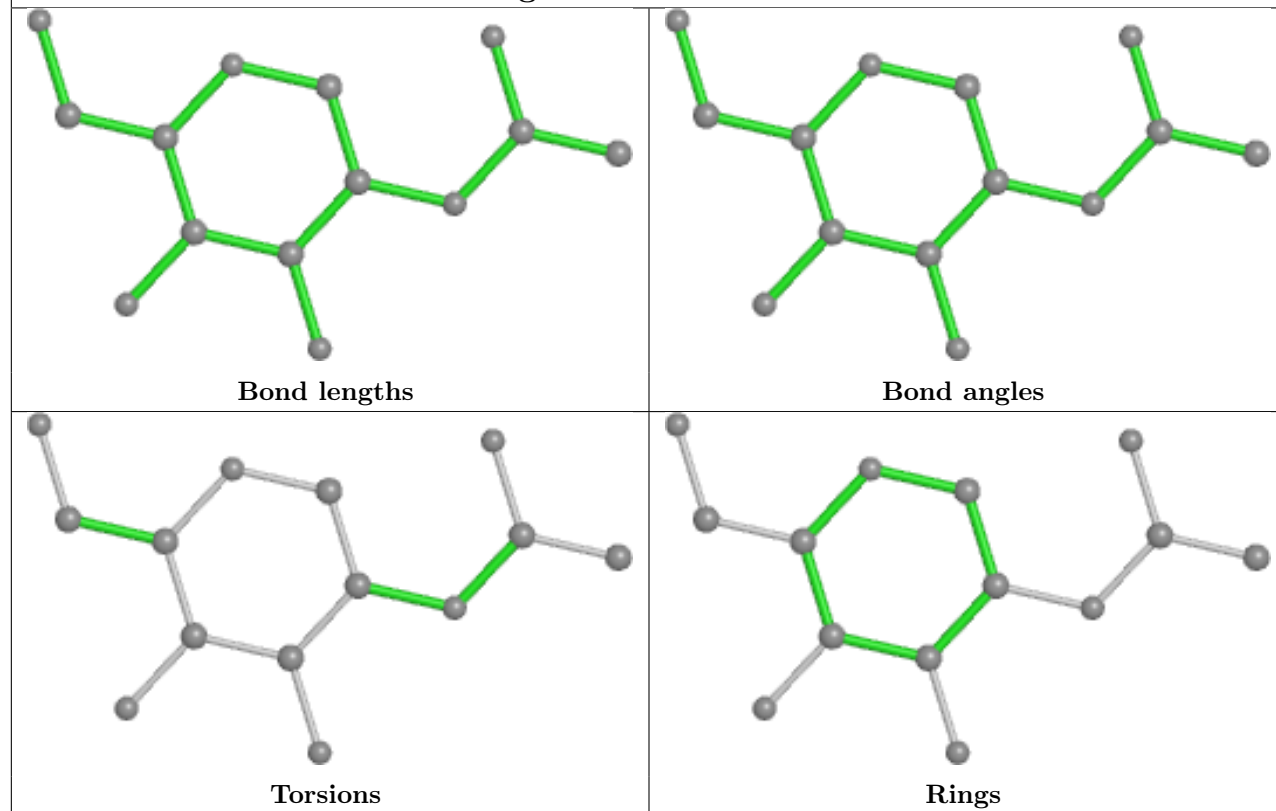


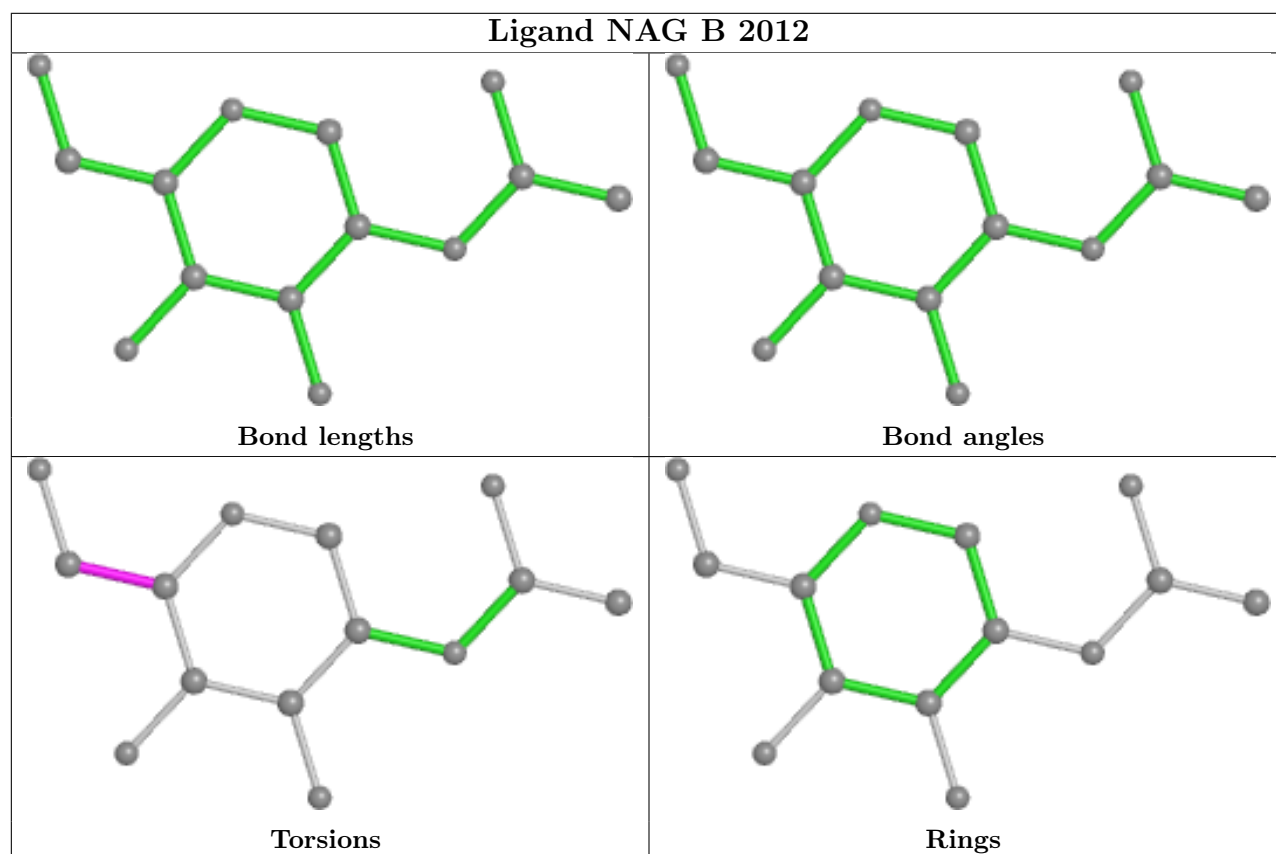
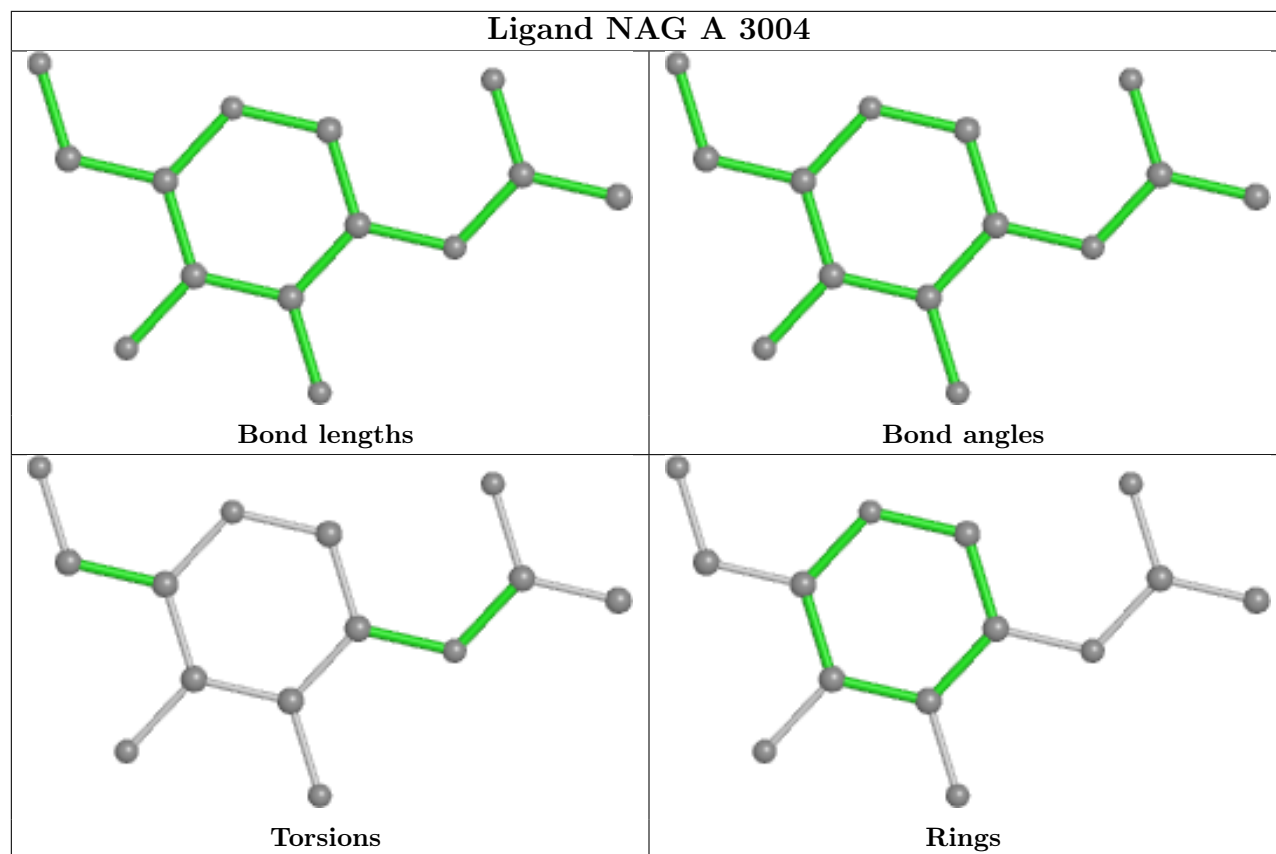


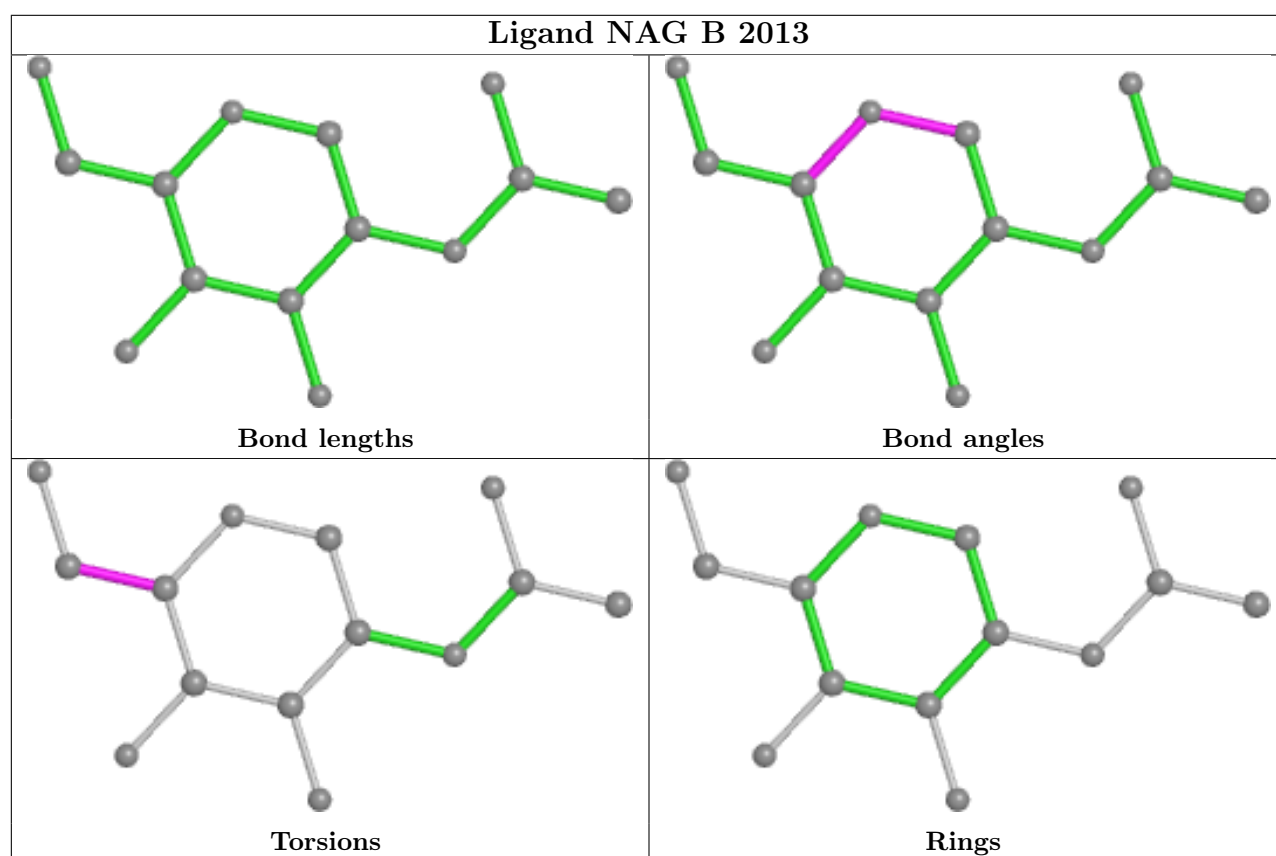
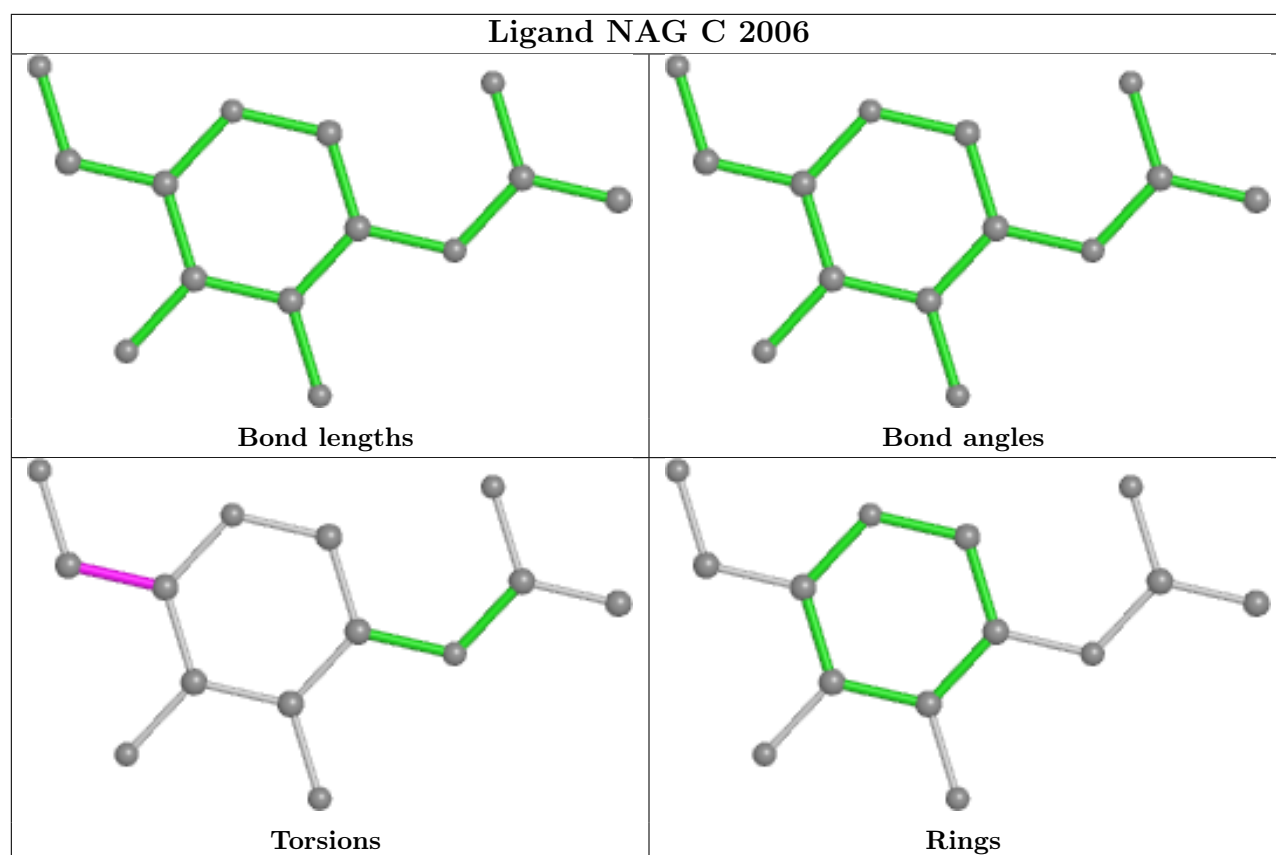
Ligand NAG A 3007

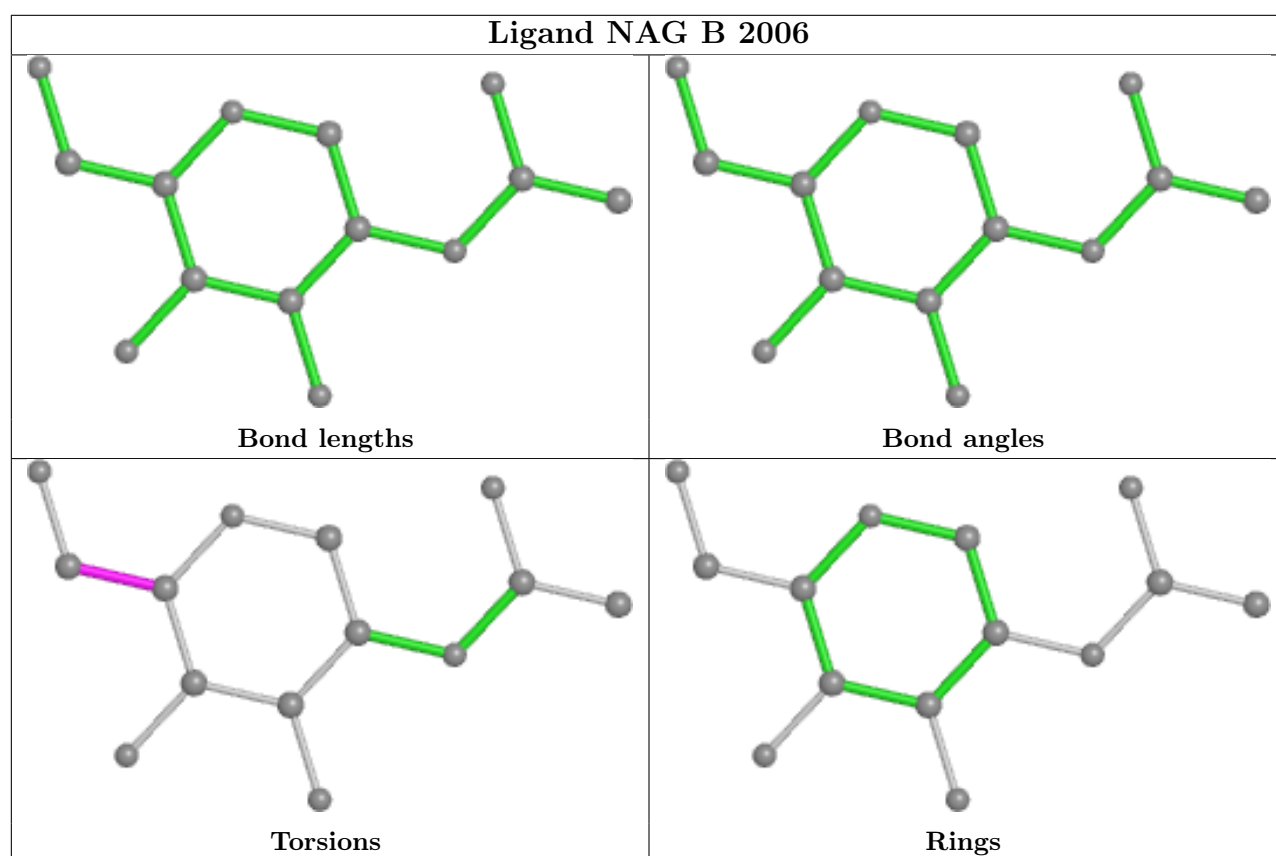
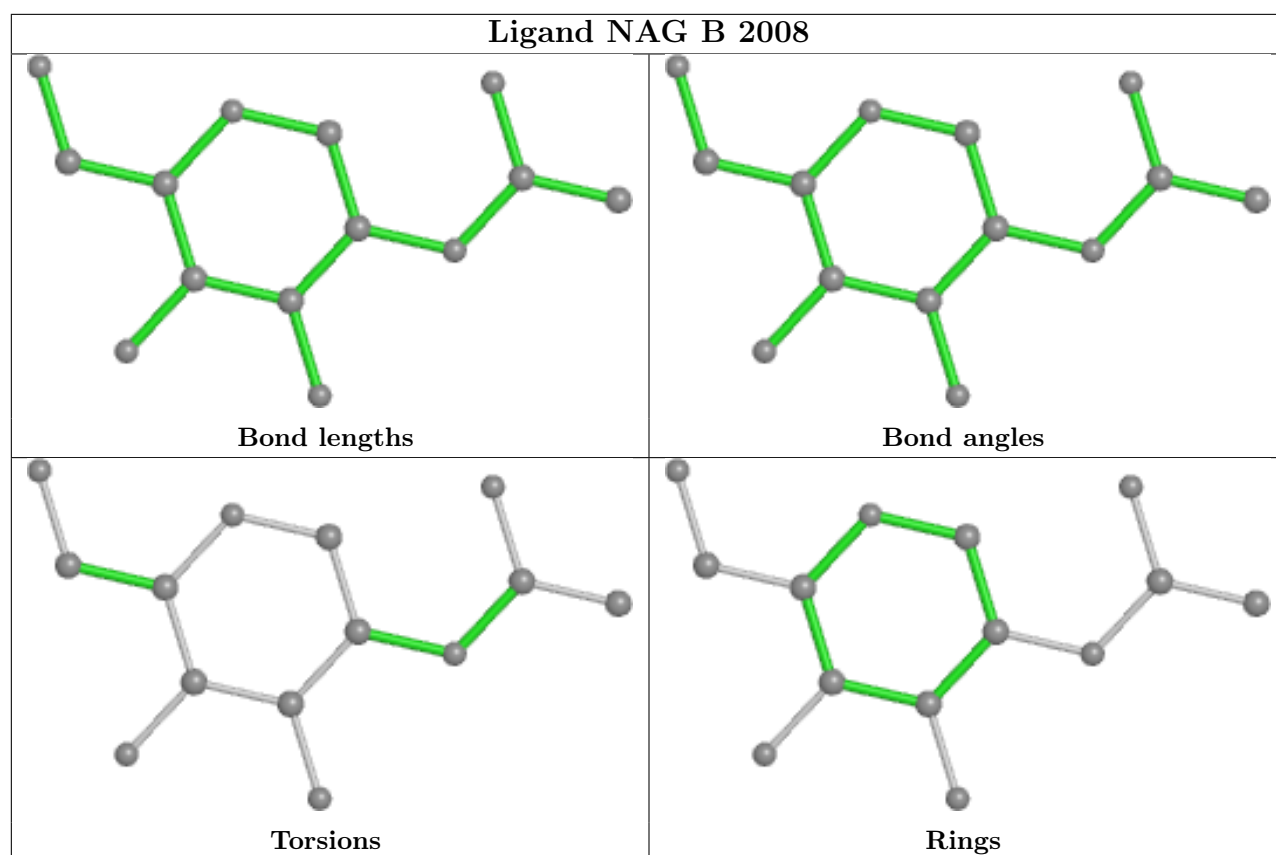


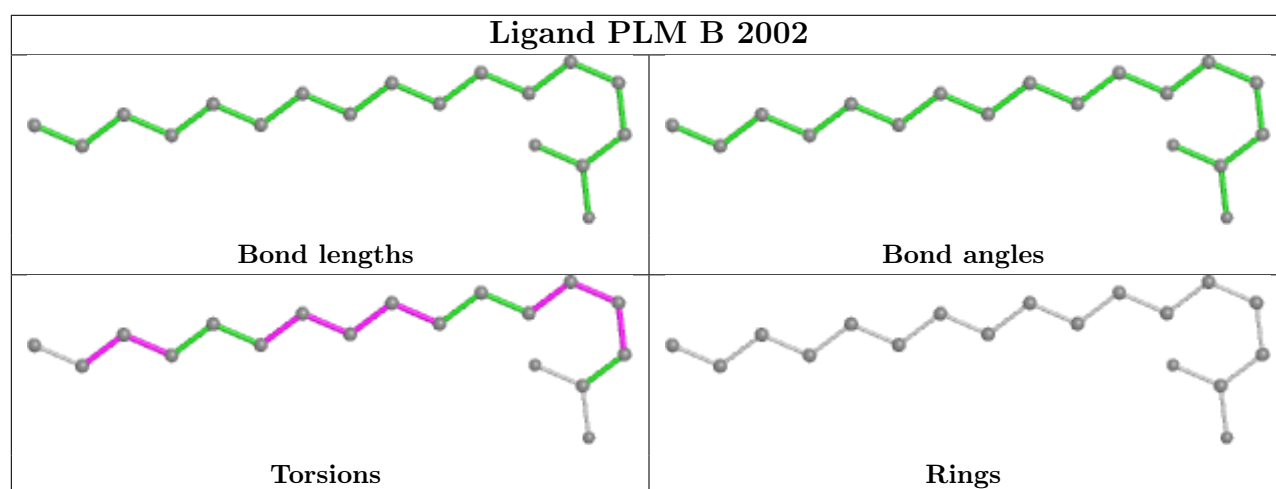
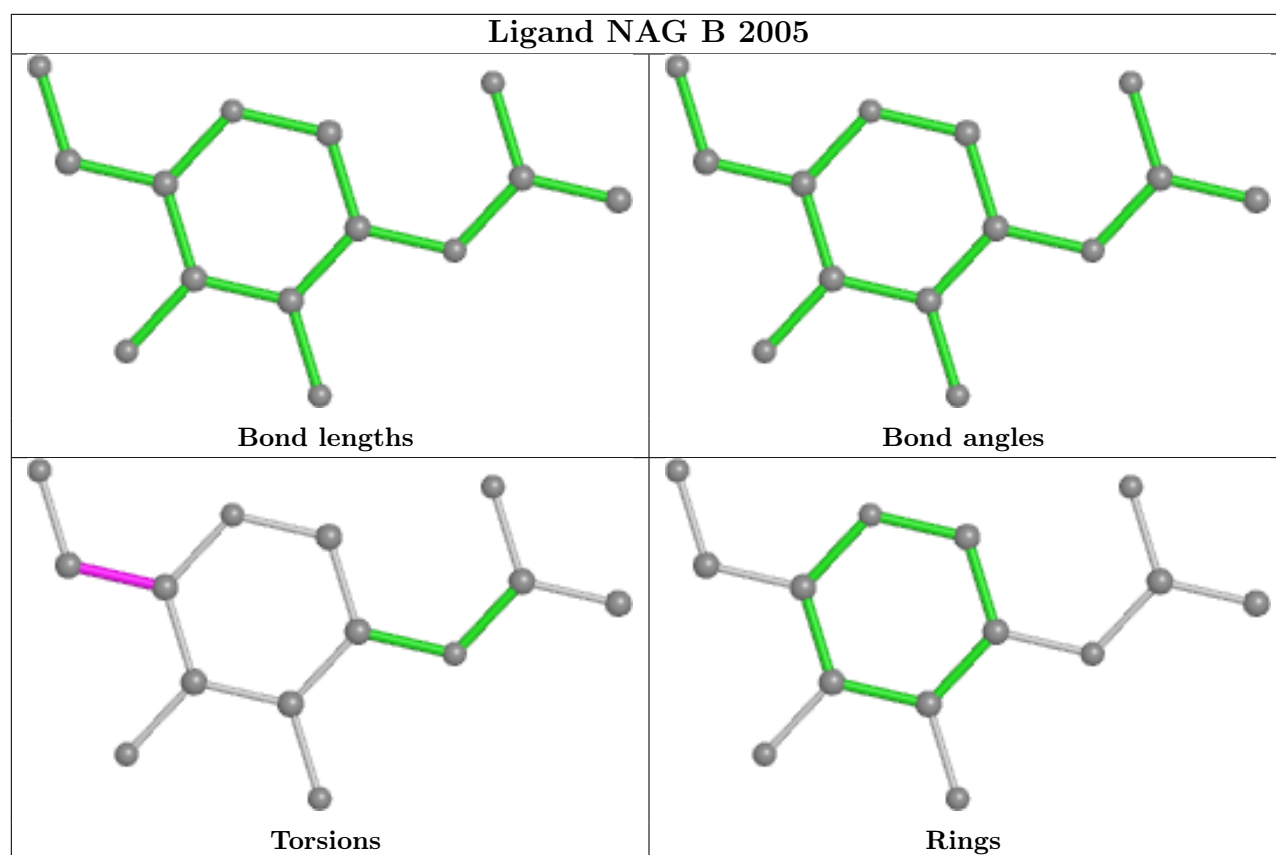
Ligand NAG A 3008

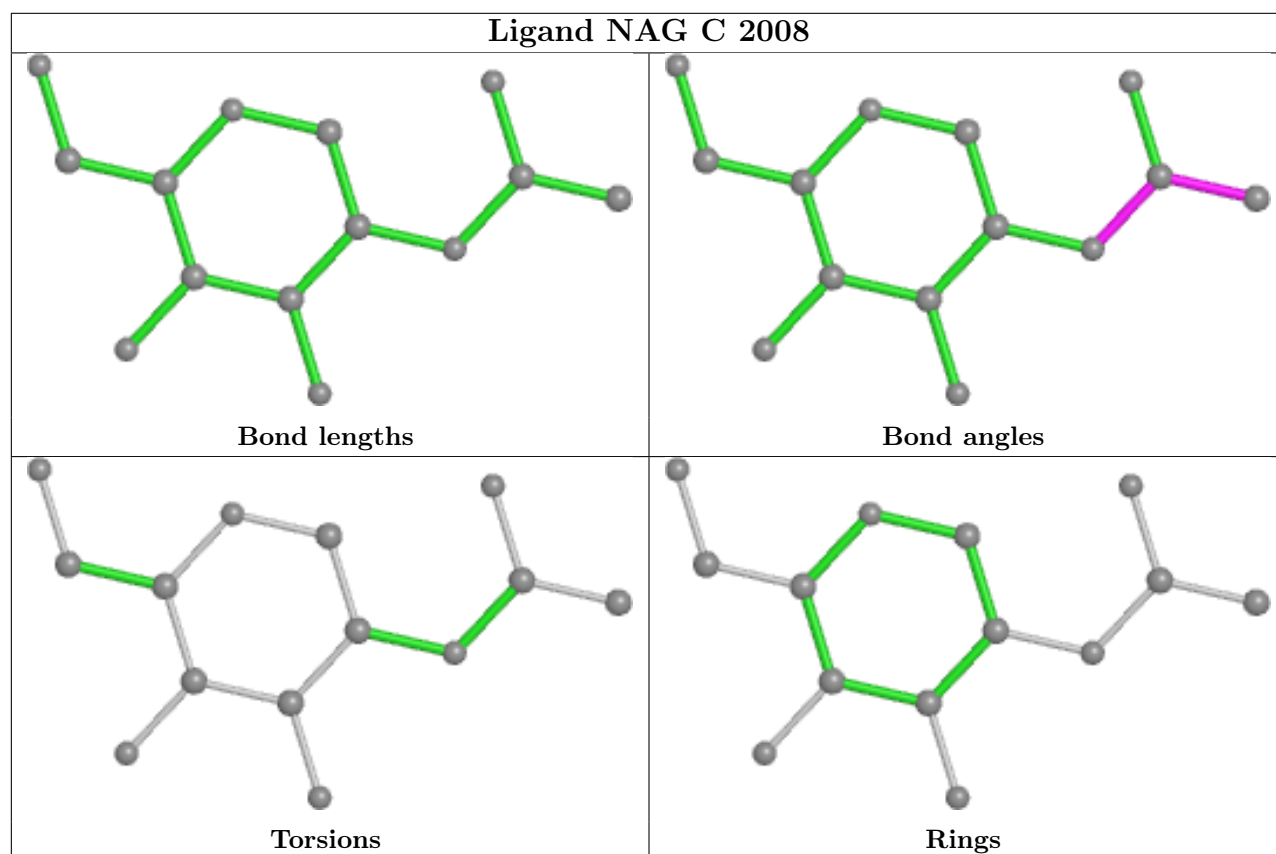
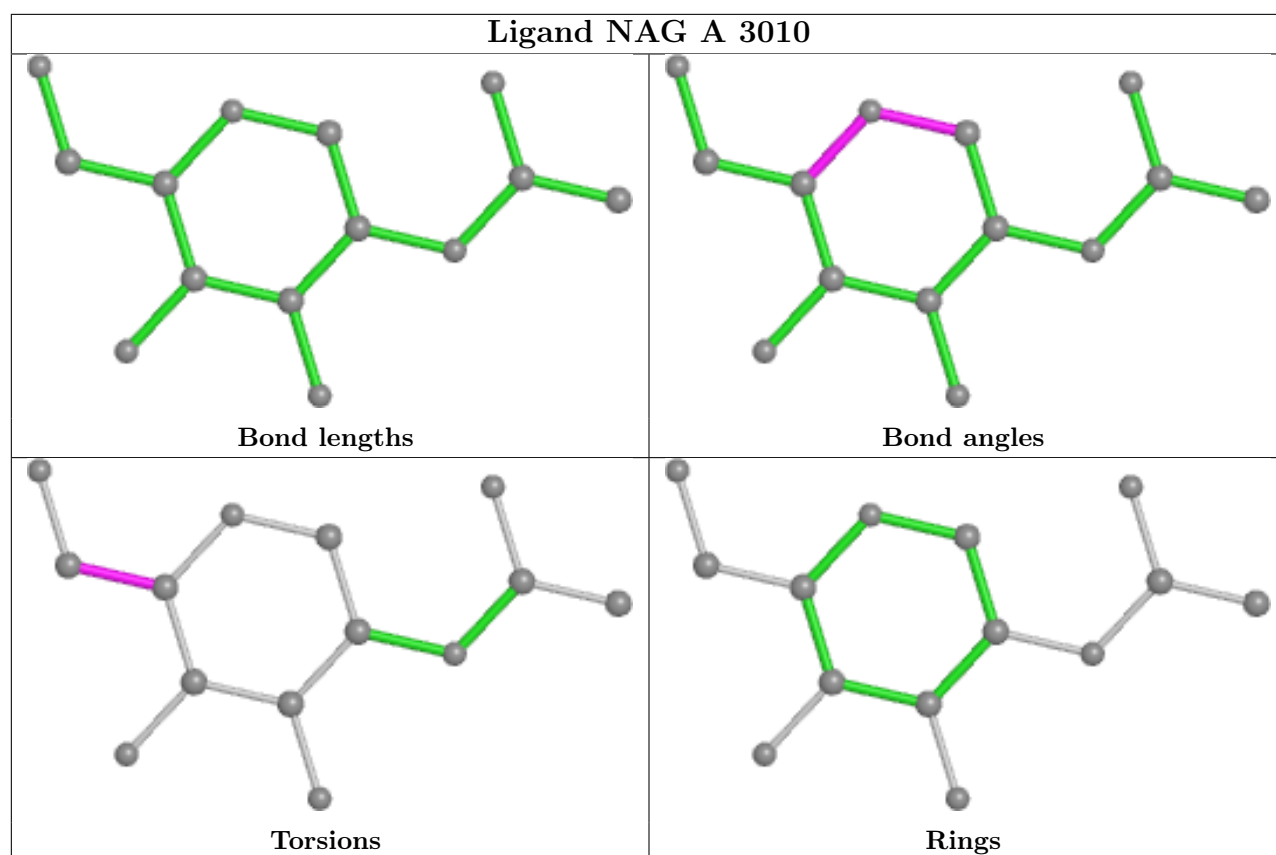


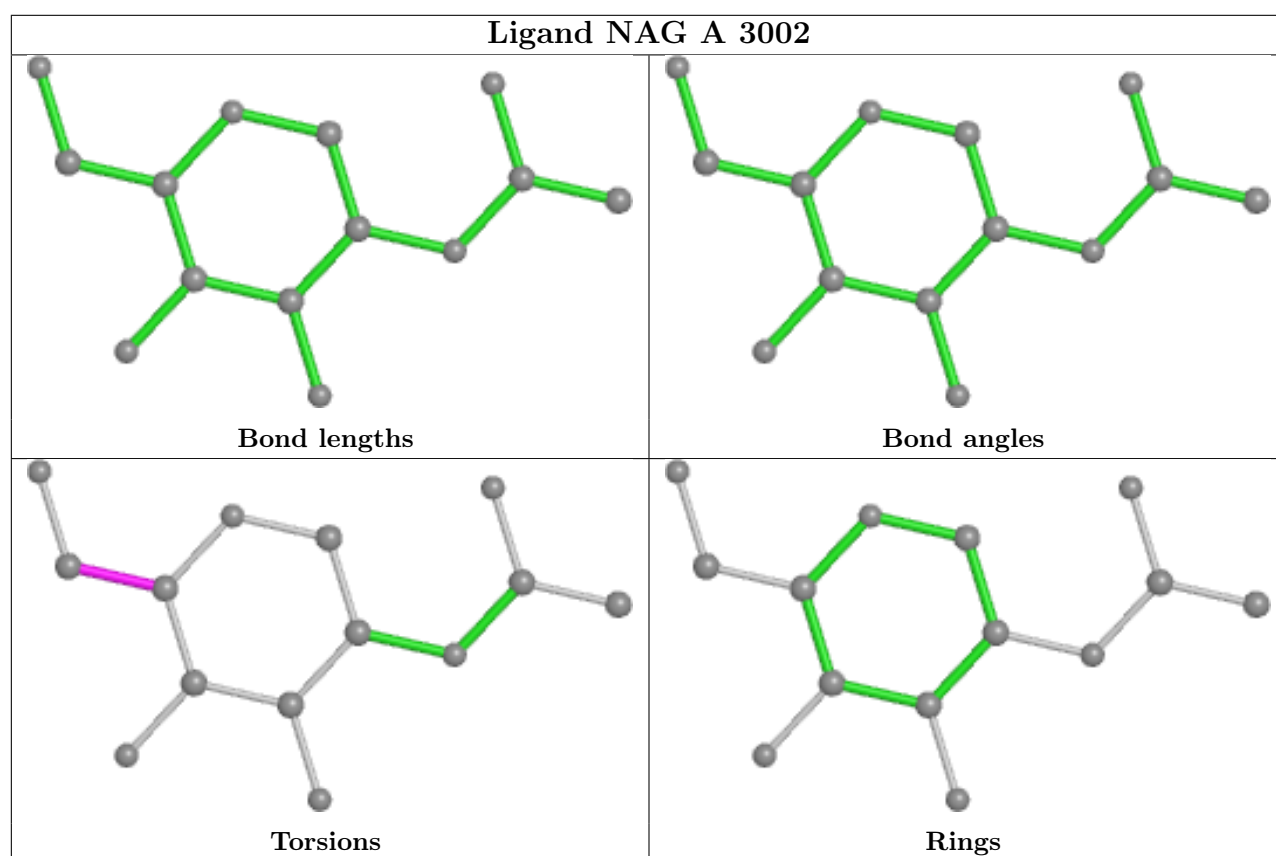
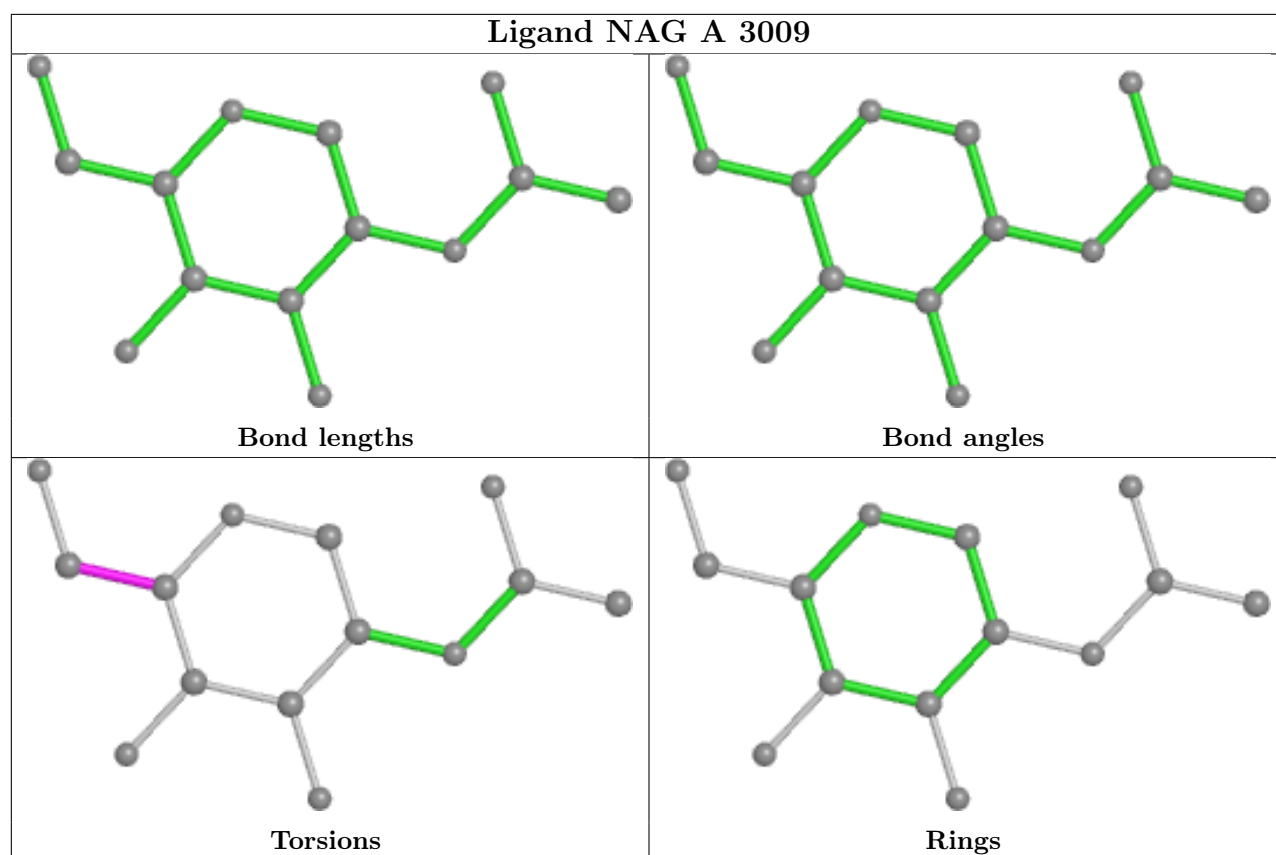


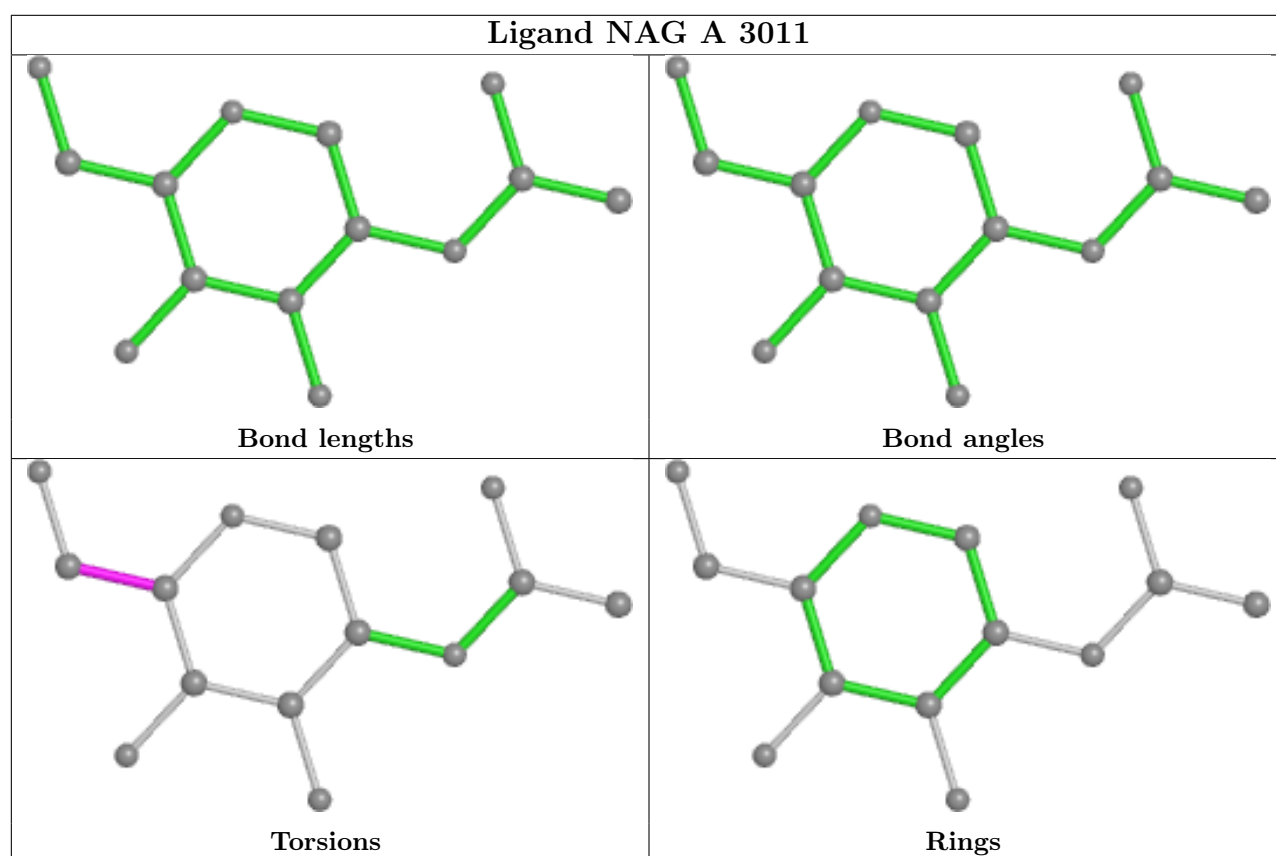
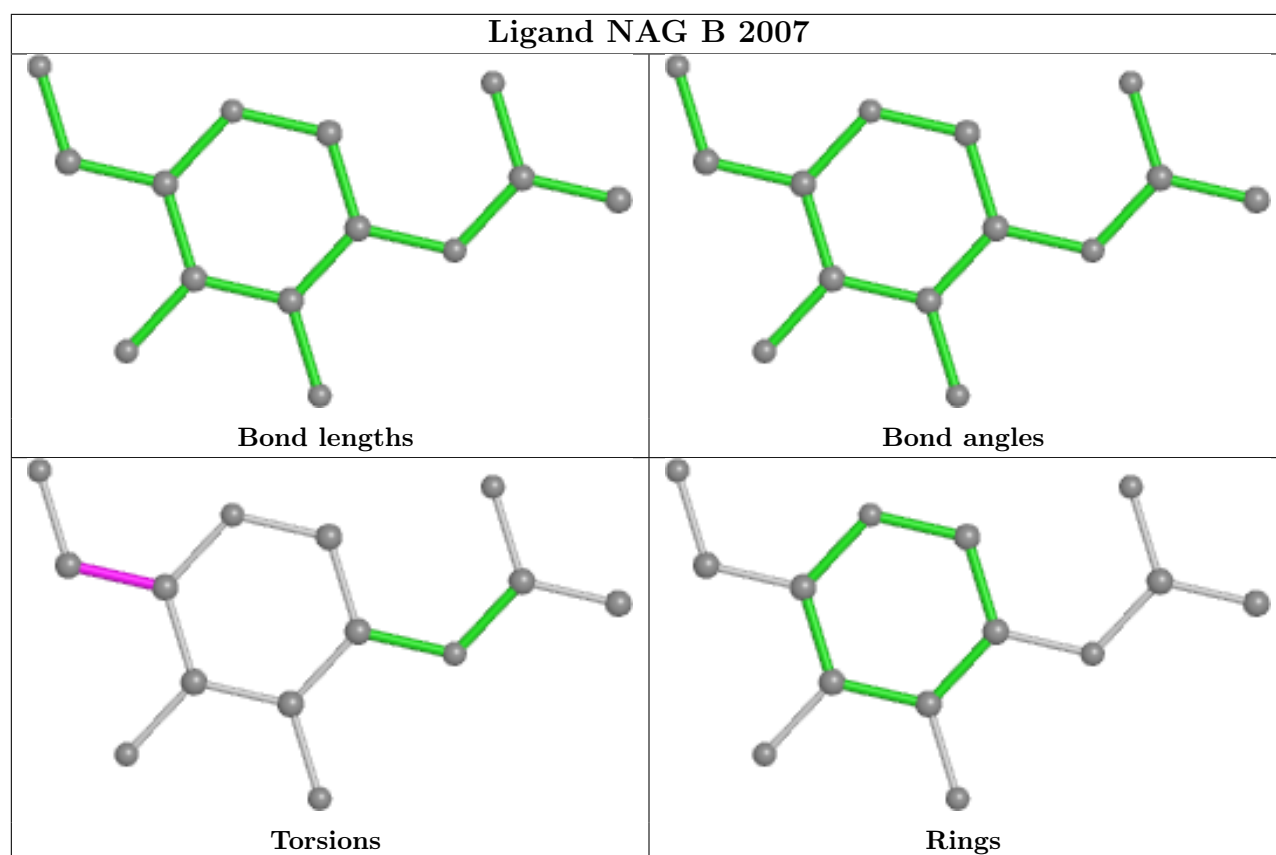


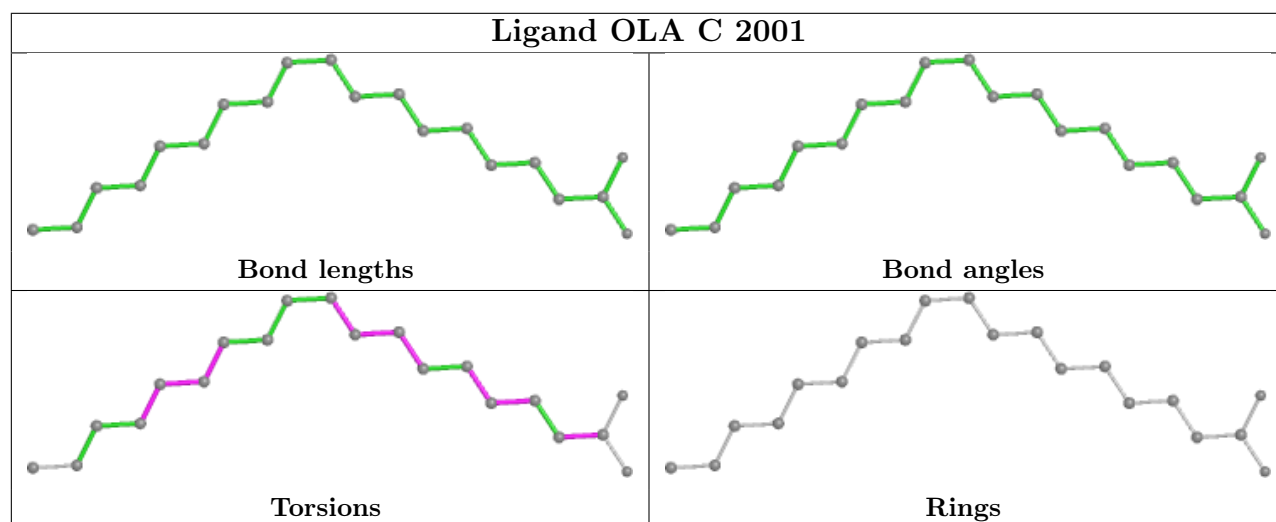
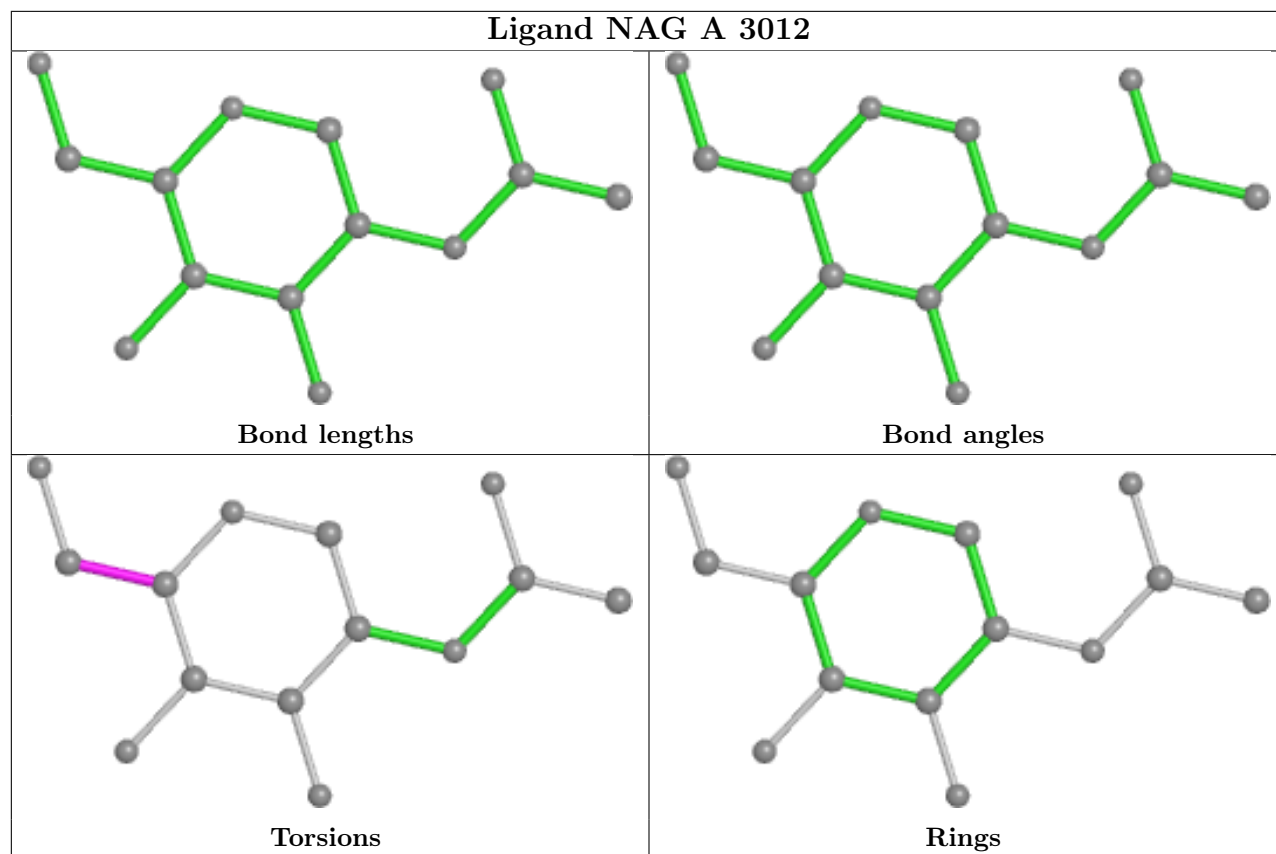


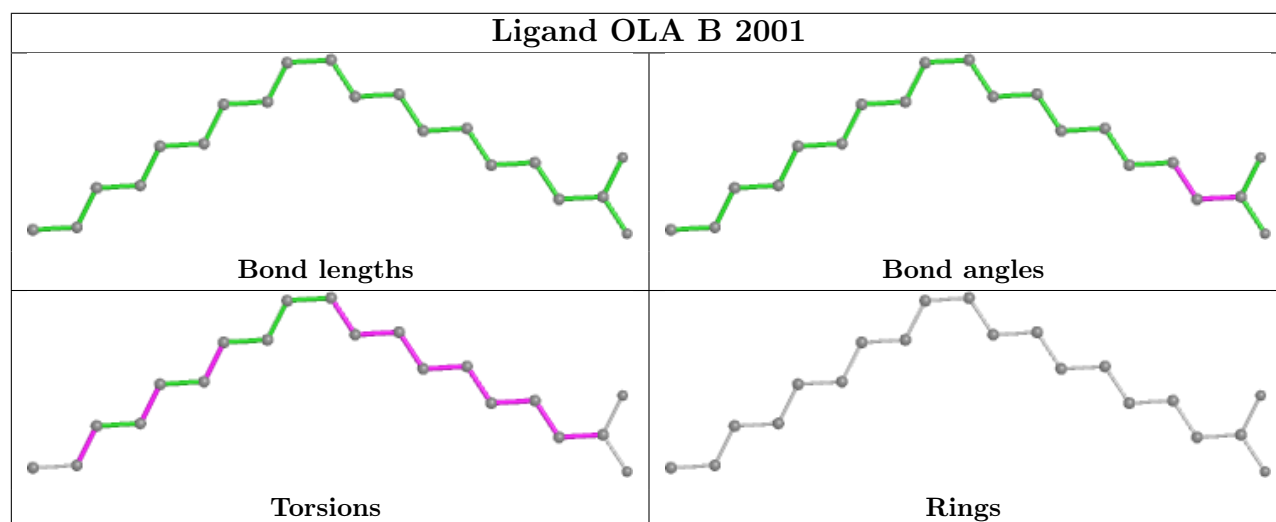
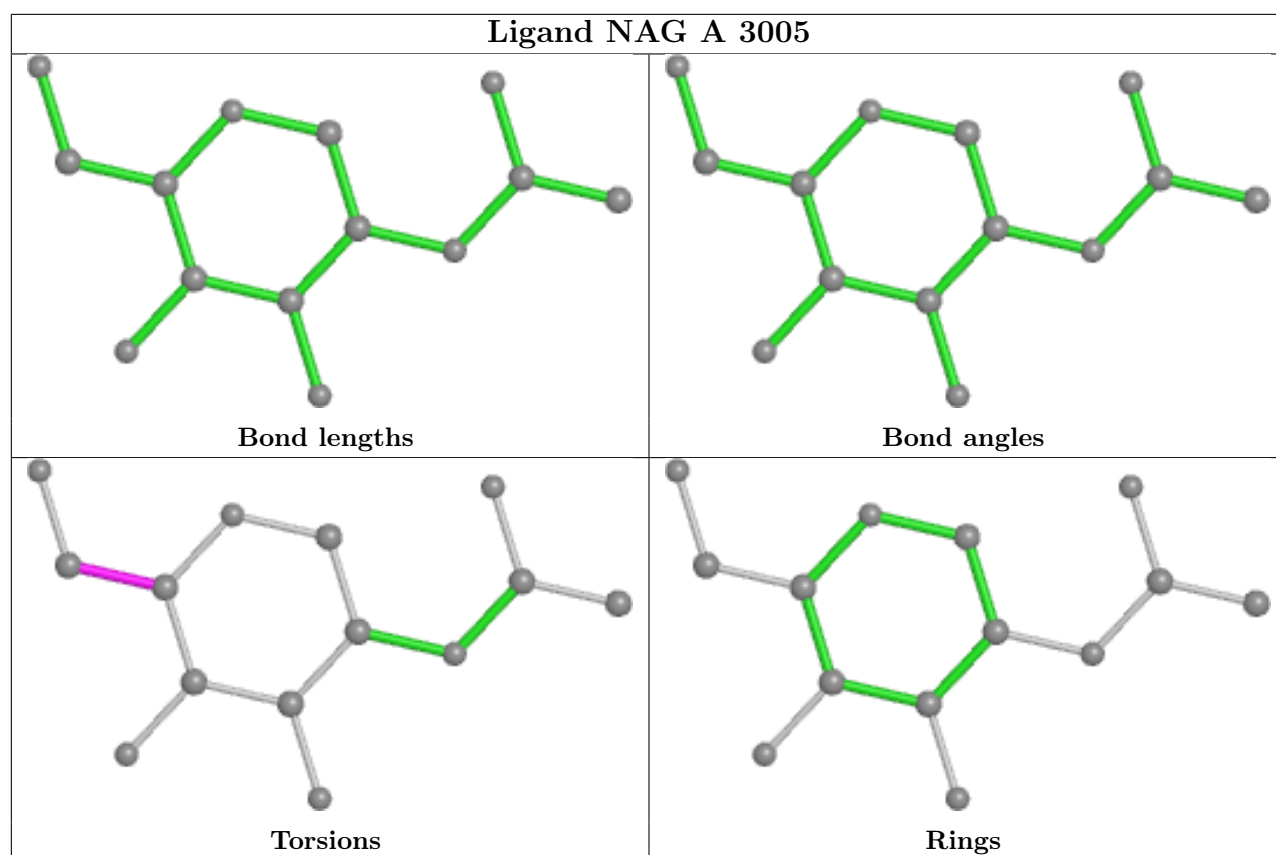


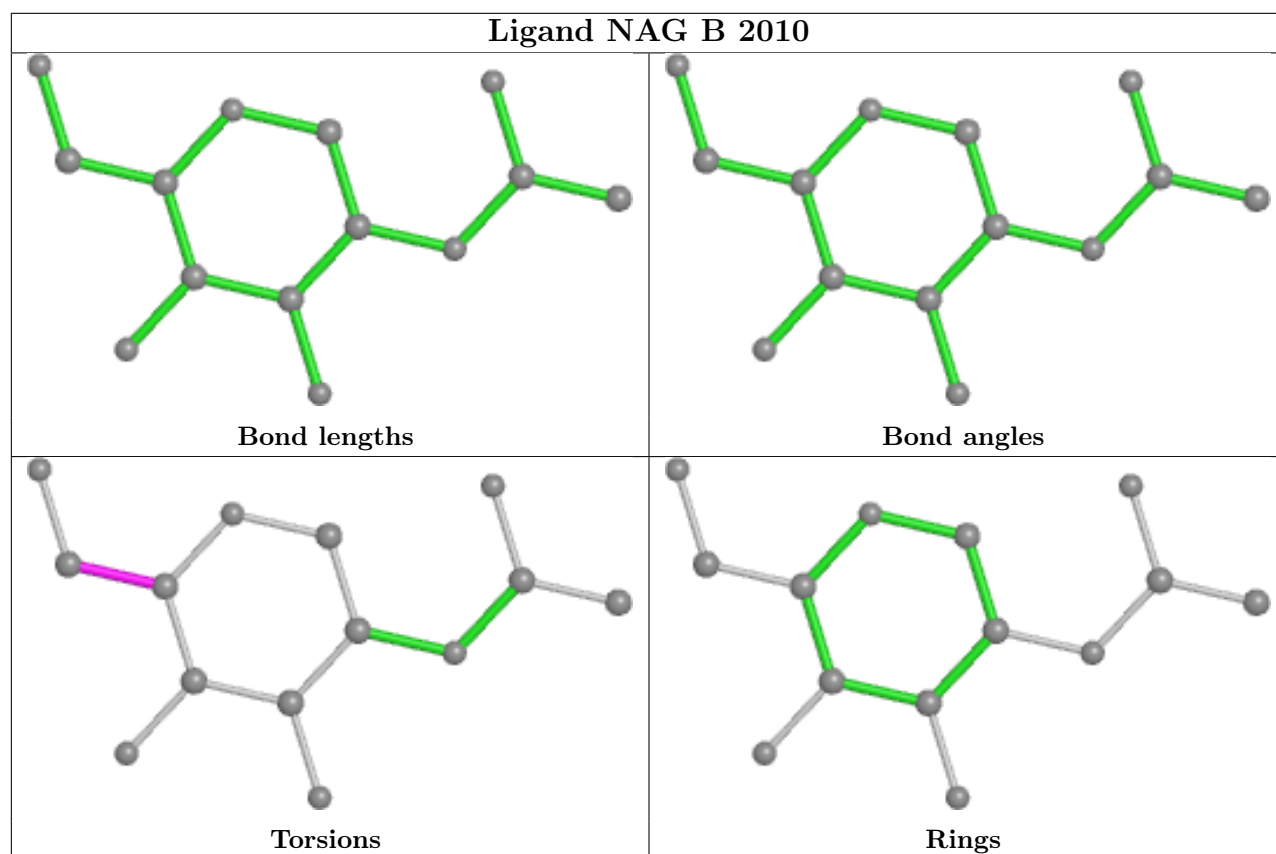
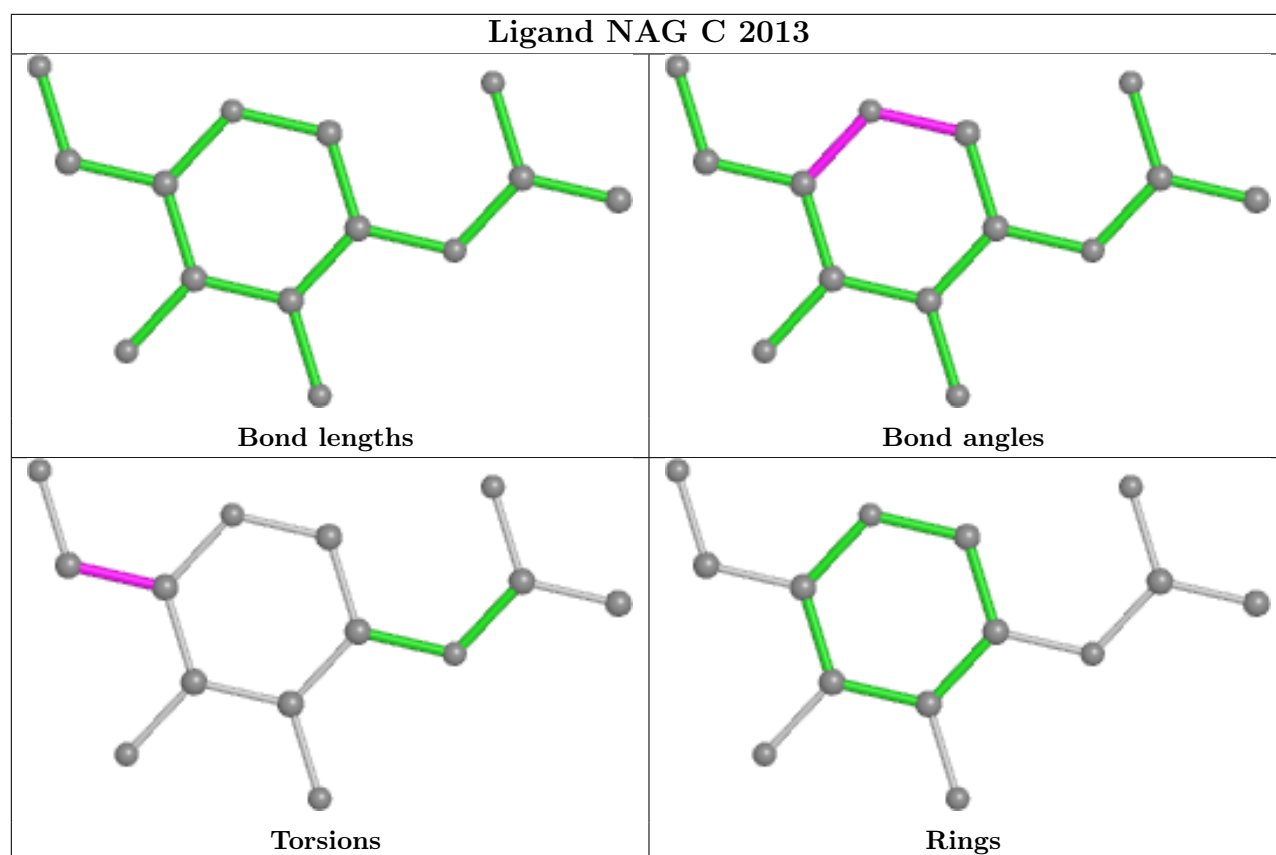


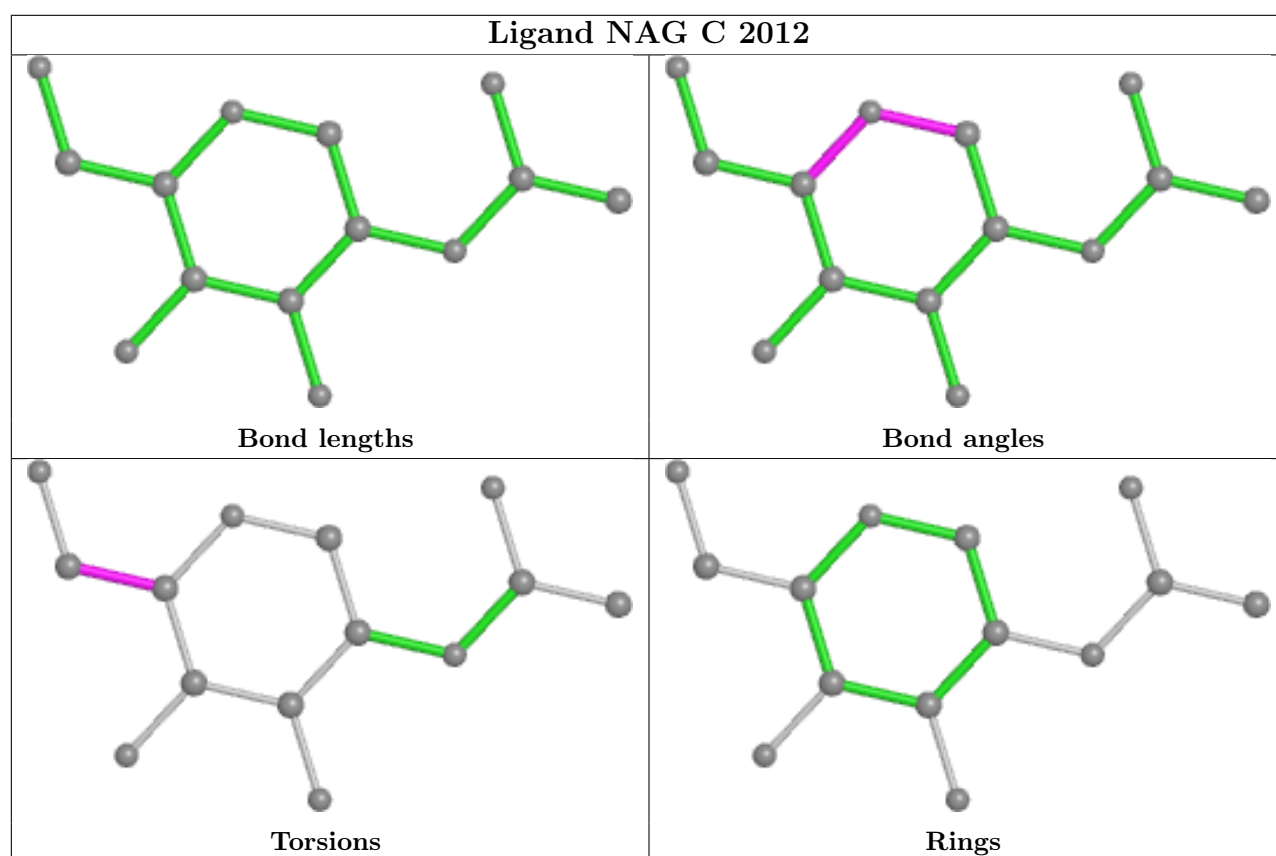
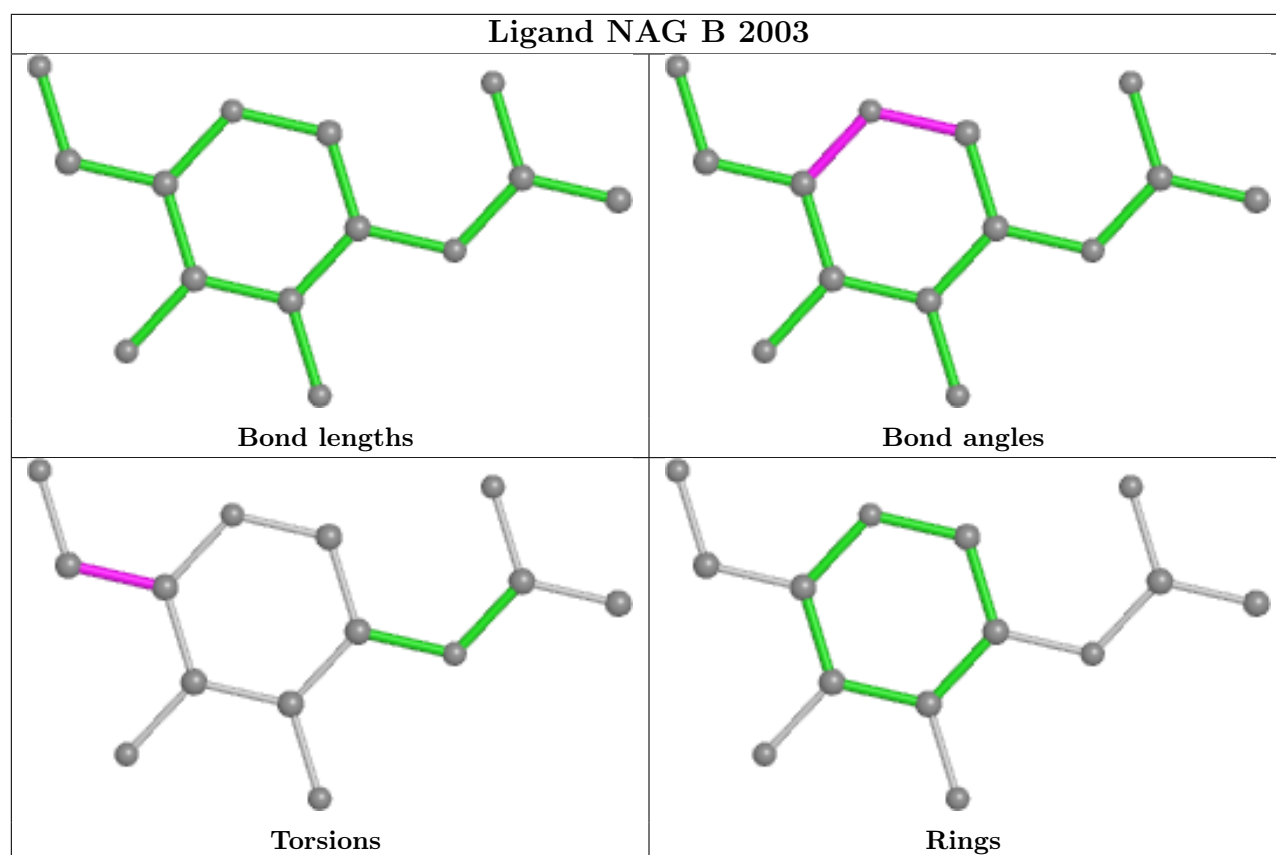


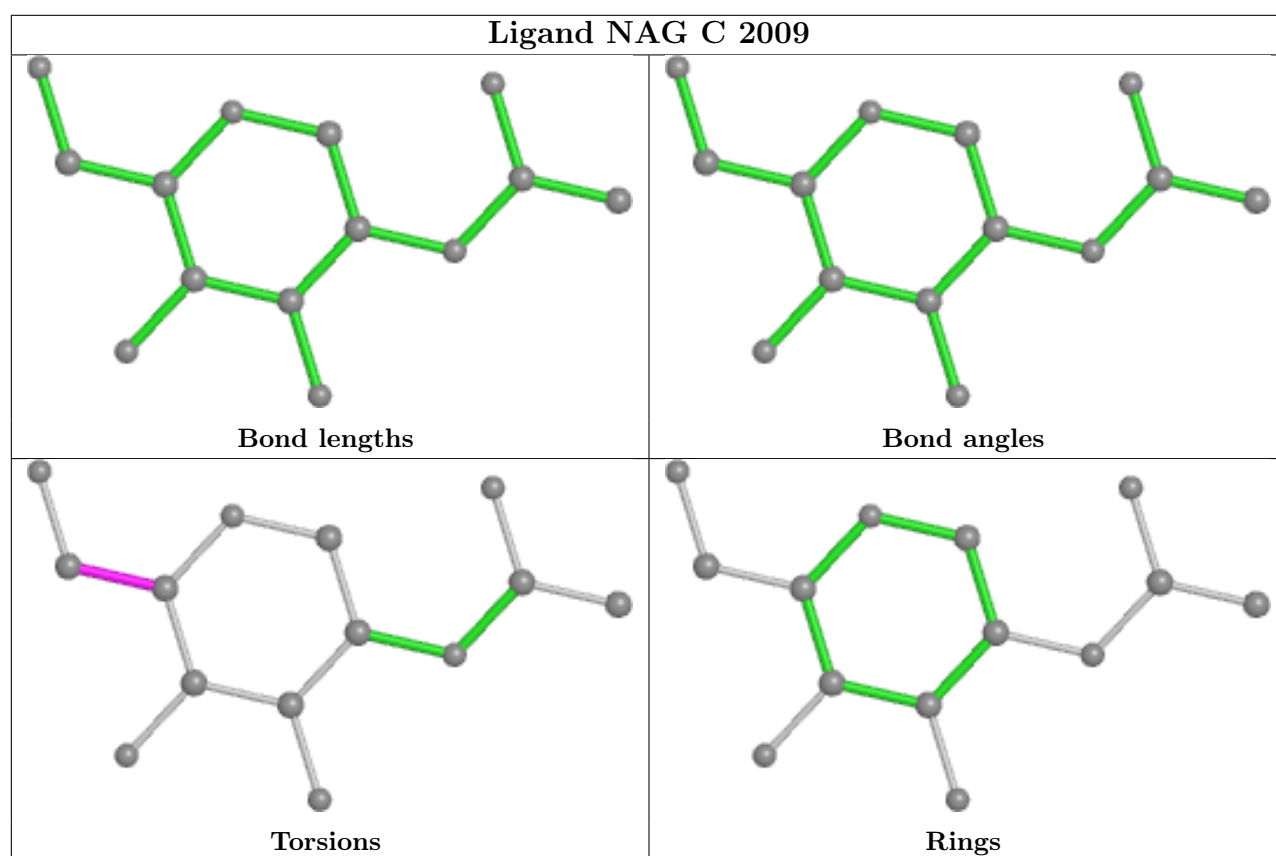
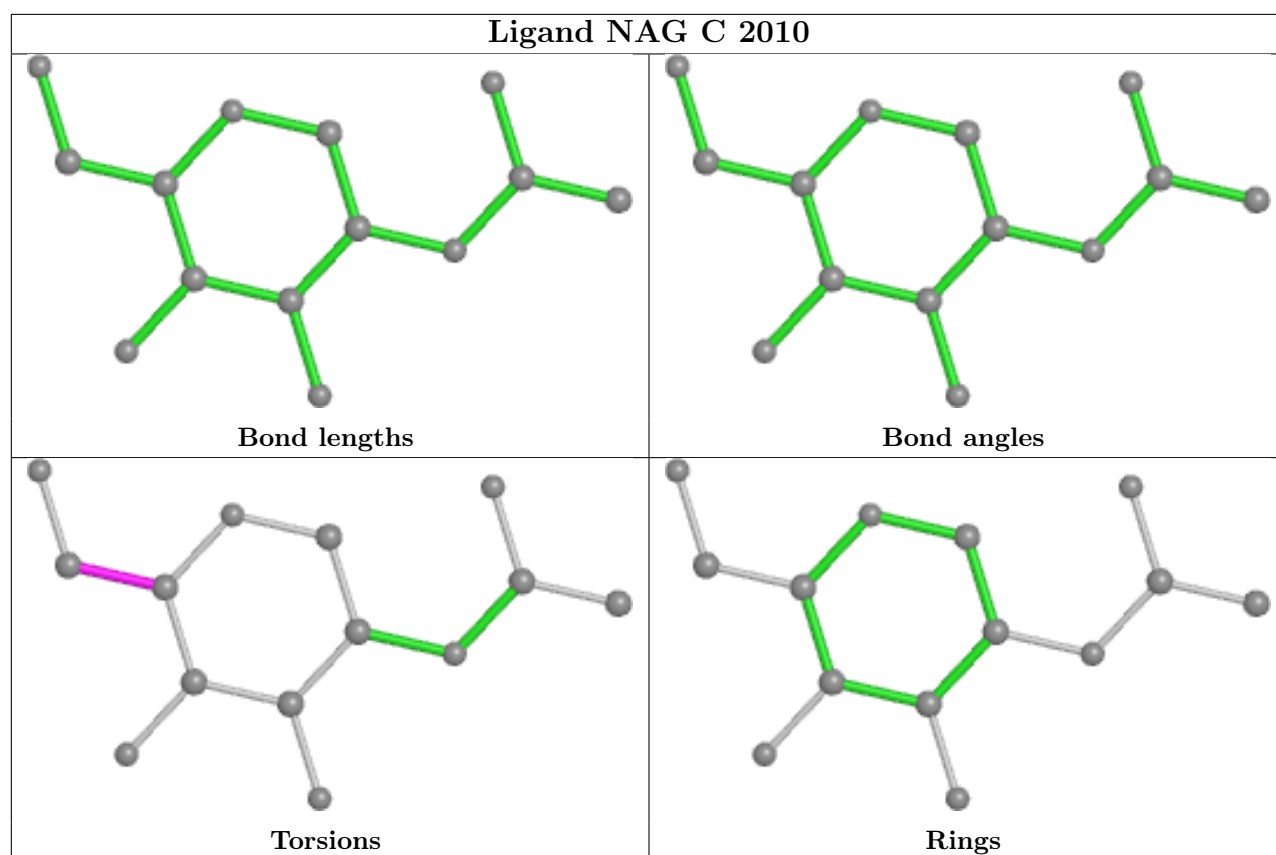


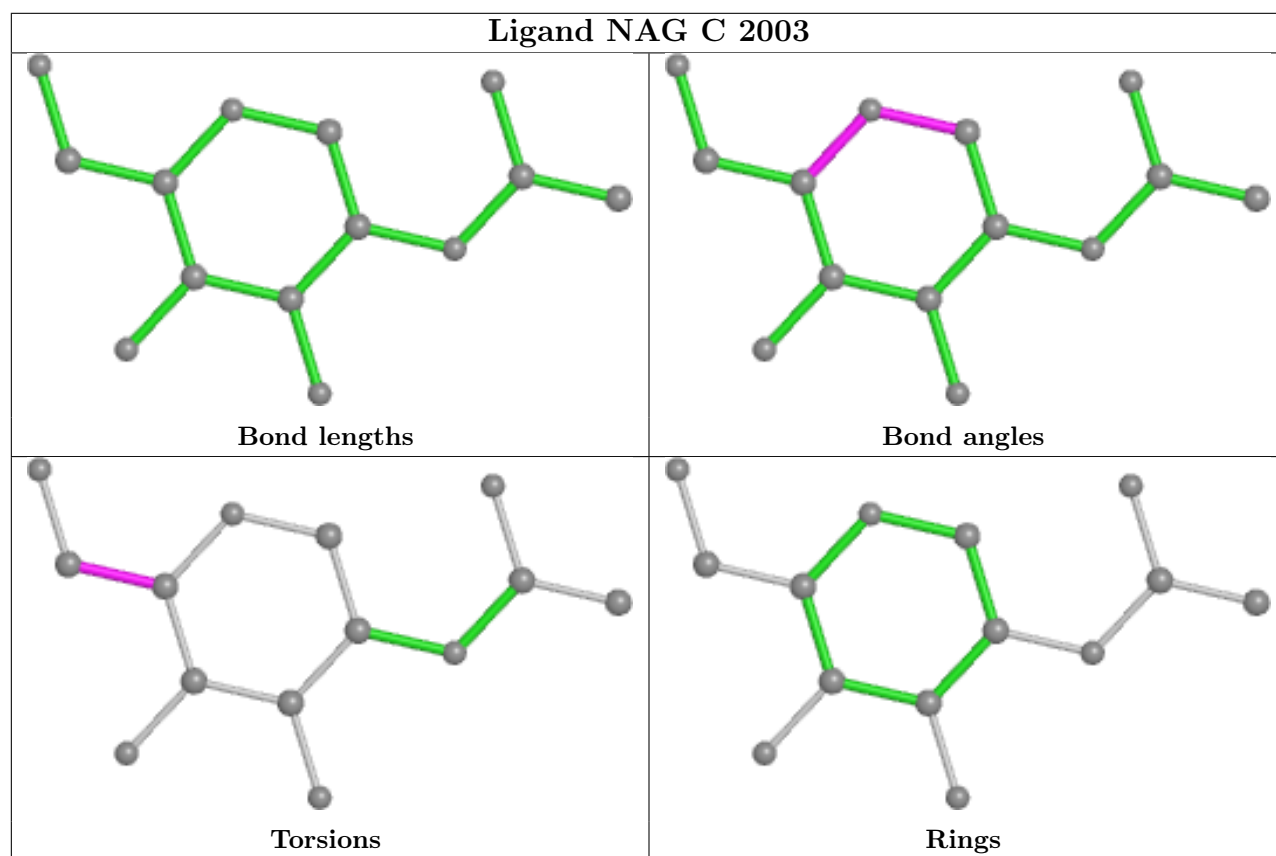
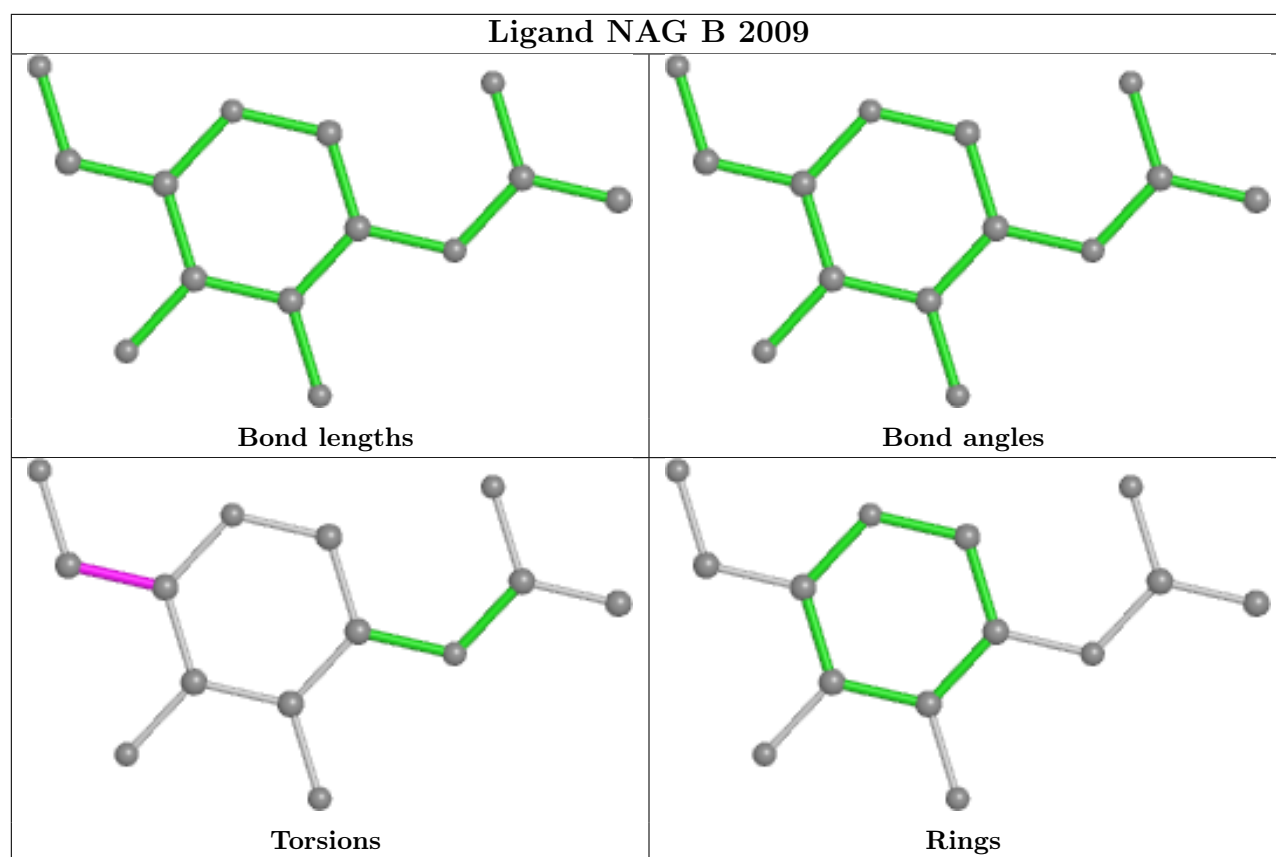












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

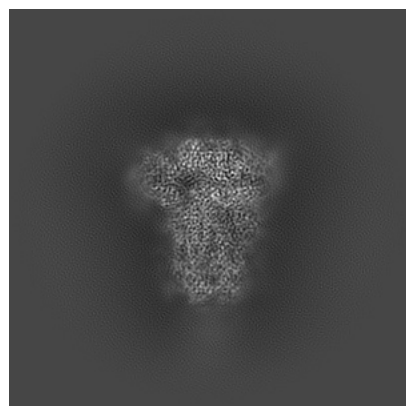
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62522. These allow visual inspection of the internal detail of the map and identification of artifacts.

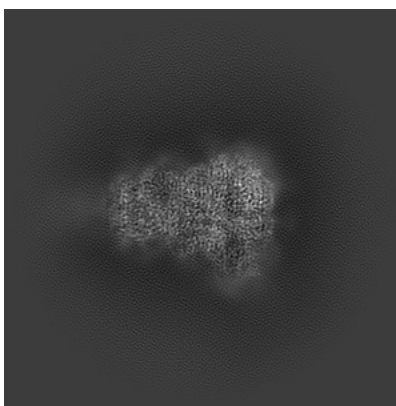
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

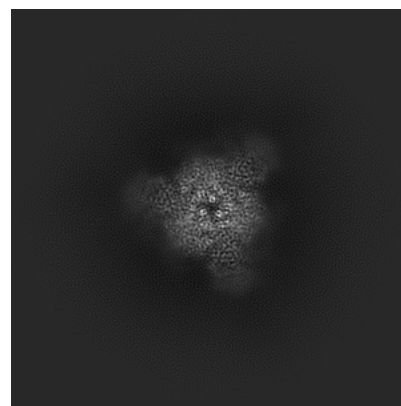
6.1.1 Primary map



X

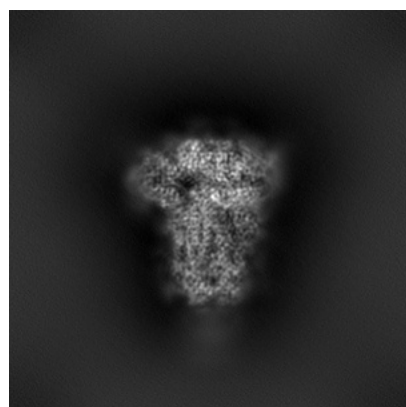


Y

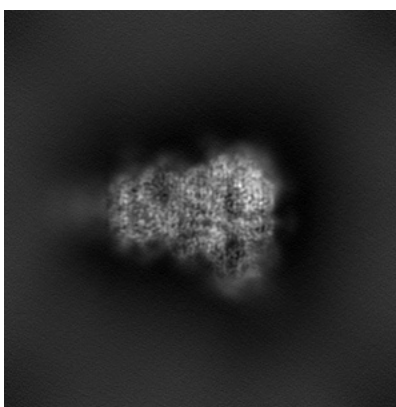


Z

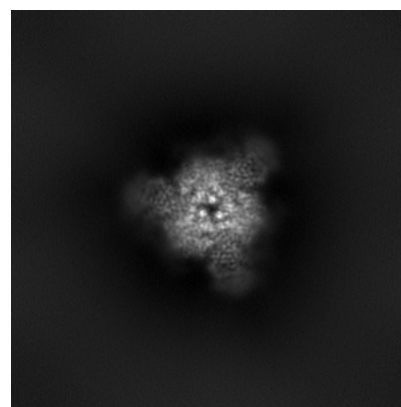
6.1.2 Raw map



X



Y

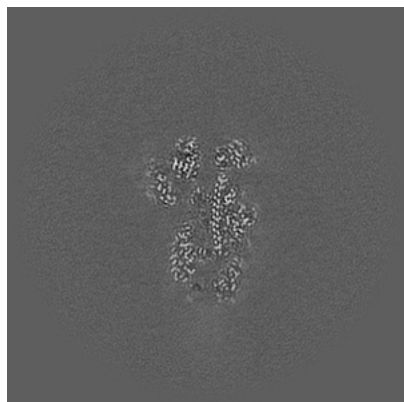


Z

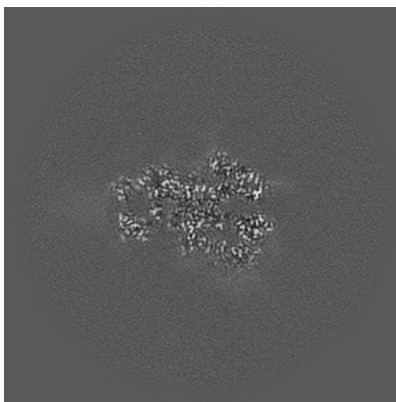
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

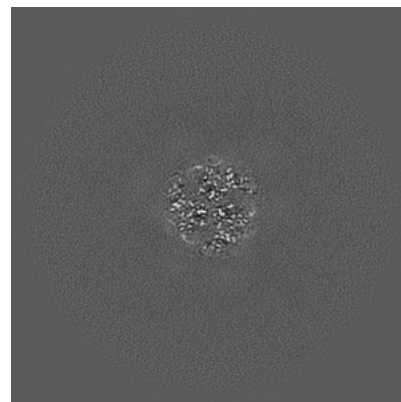
6.2.1 Primary map



X Index: 160

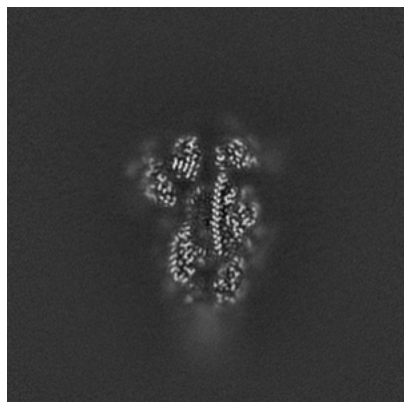


Y Index: 160

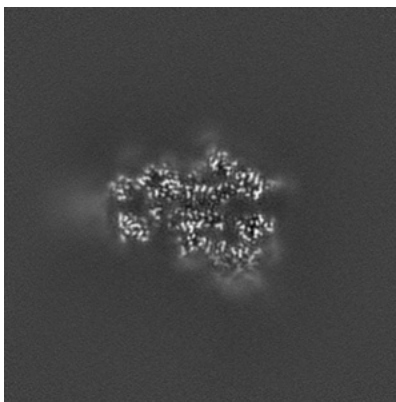


Z Index: 160

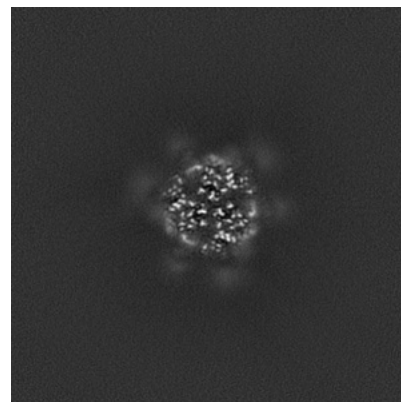
6.2.2 Raw map



X Index: 160



Y Index: 160

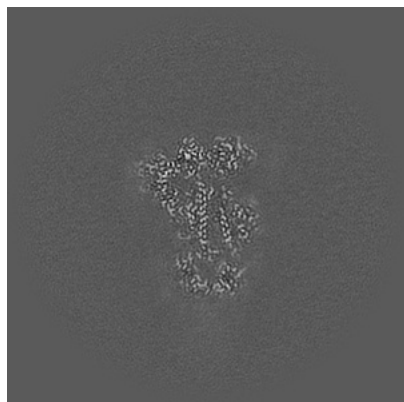


Z Index: 160

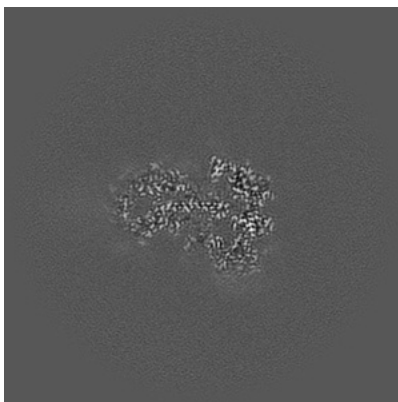
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

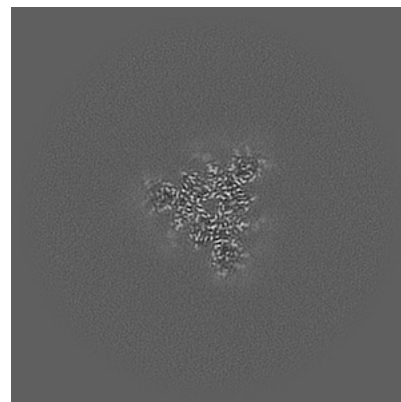
6.3.1 Primary map



X Index: 166

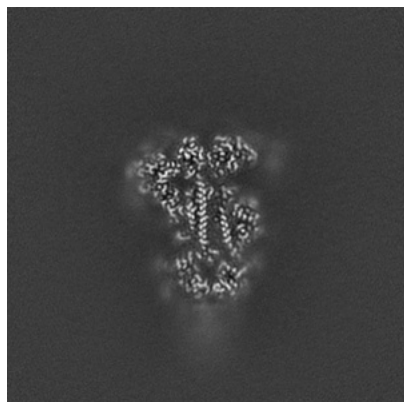


Y Index: 167

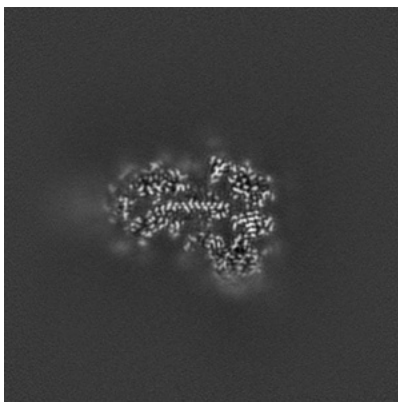


Z Index: 194

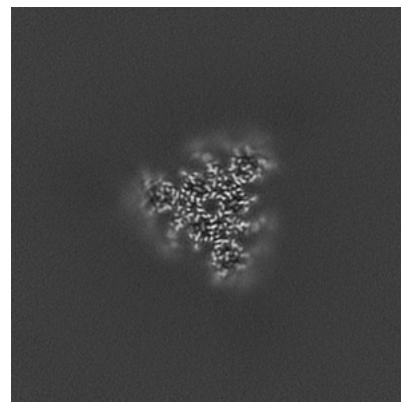
6.3.2 Raw map



X Index: 166



Y Index: 167

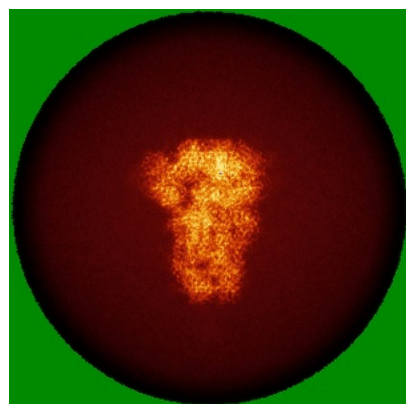


Z Index: 194

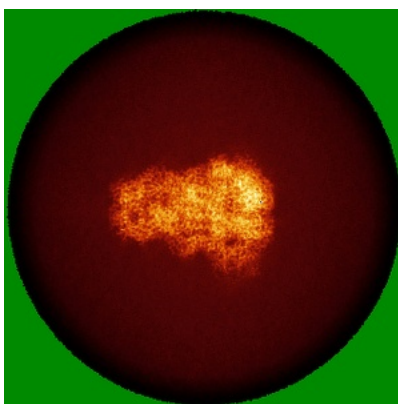
The images above show the largest variance slices of the map in three orthogonal directions.

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

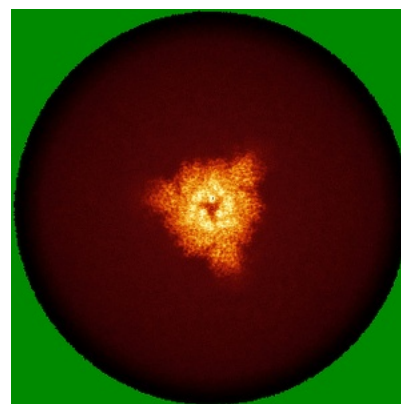
6.4.1 Primary map



X

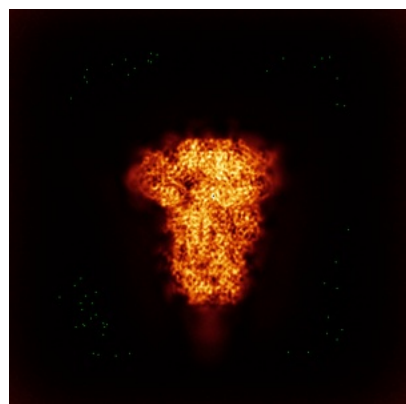


Y

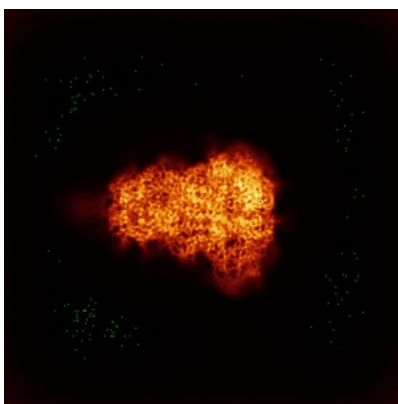


Z

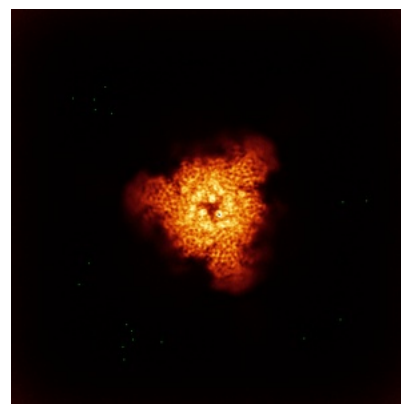
6.4.2 Raw map



X



Y

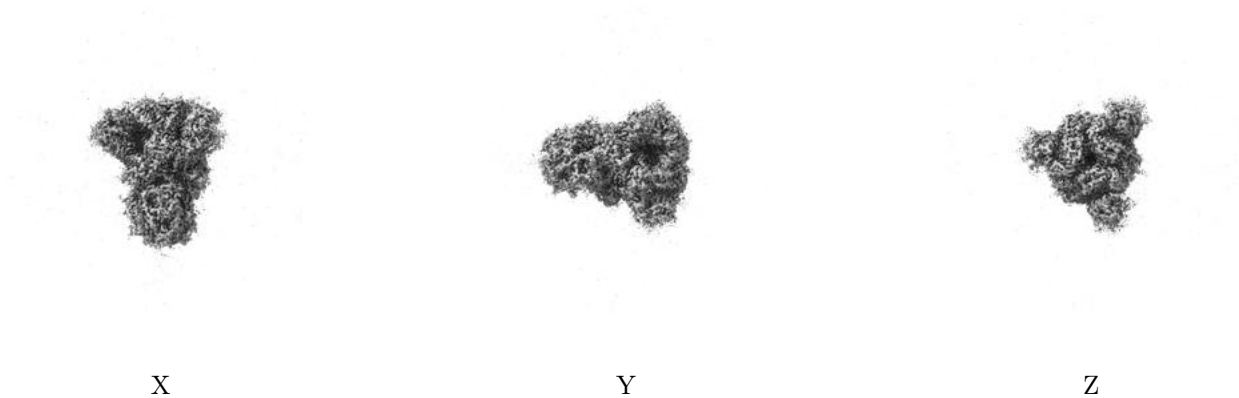


Z

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.

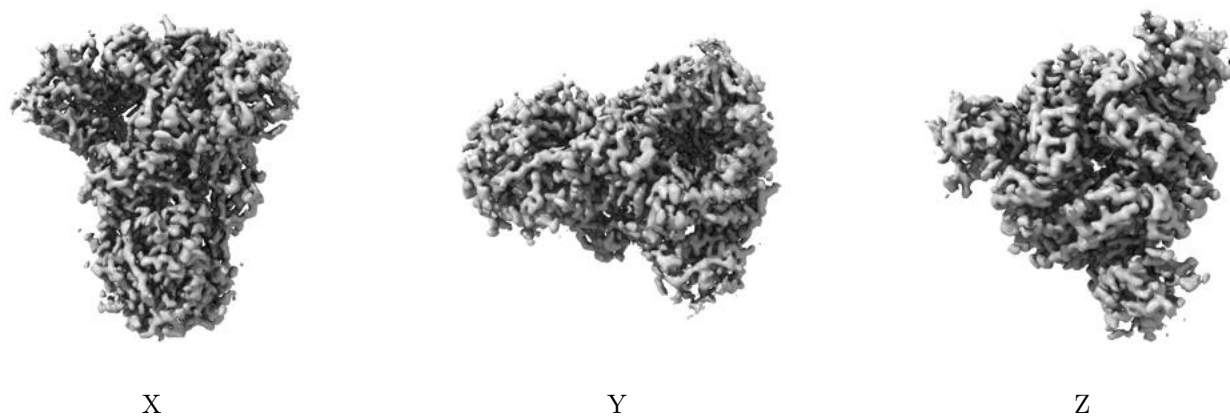
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.6. 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.

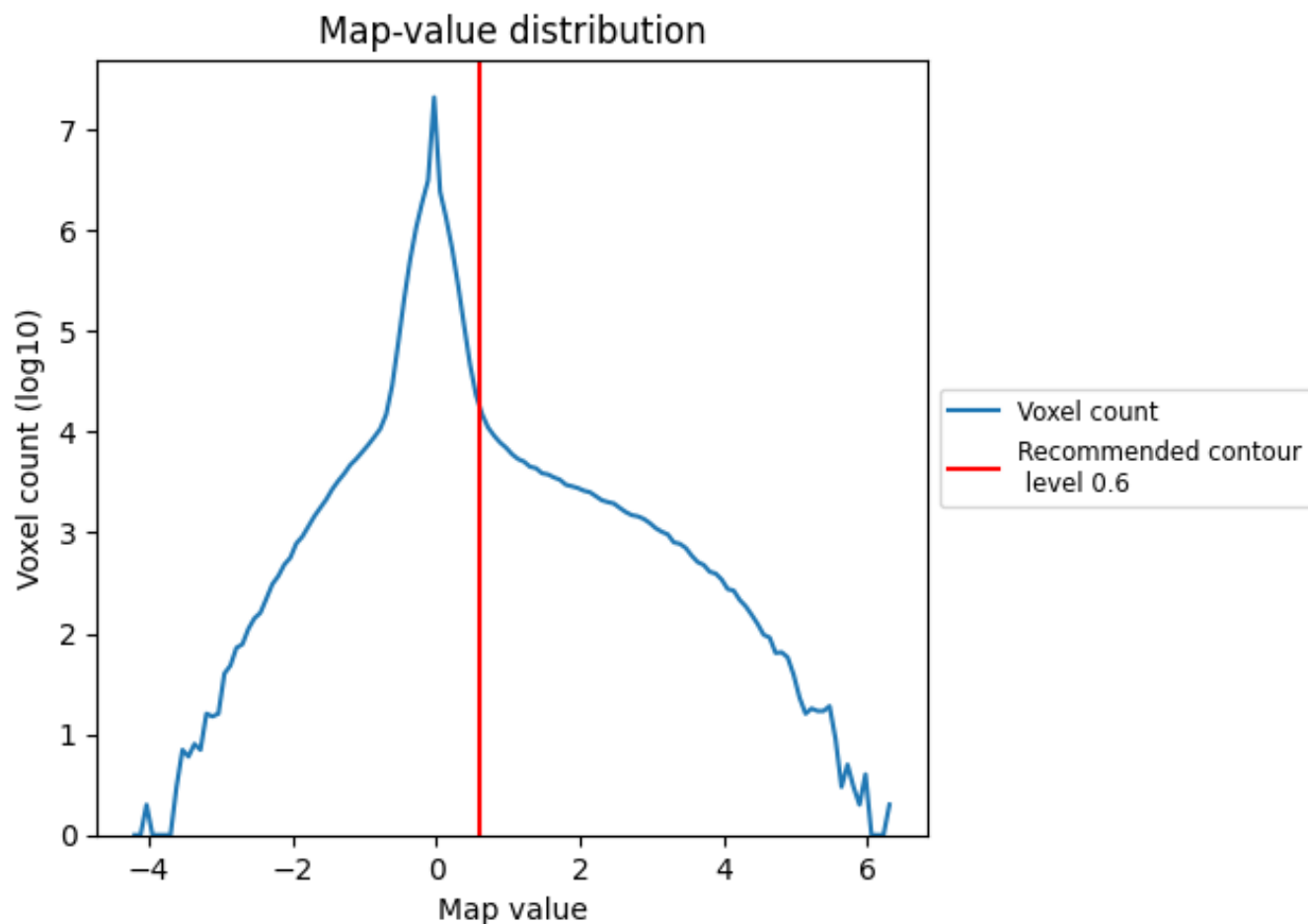
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

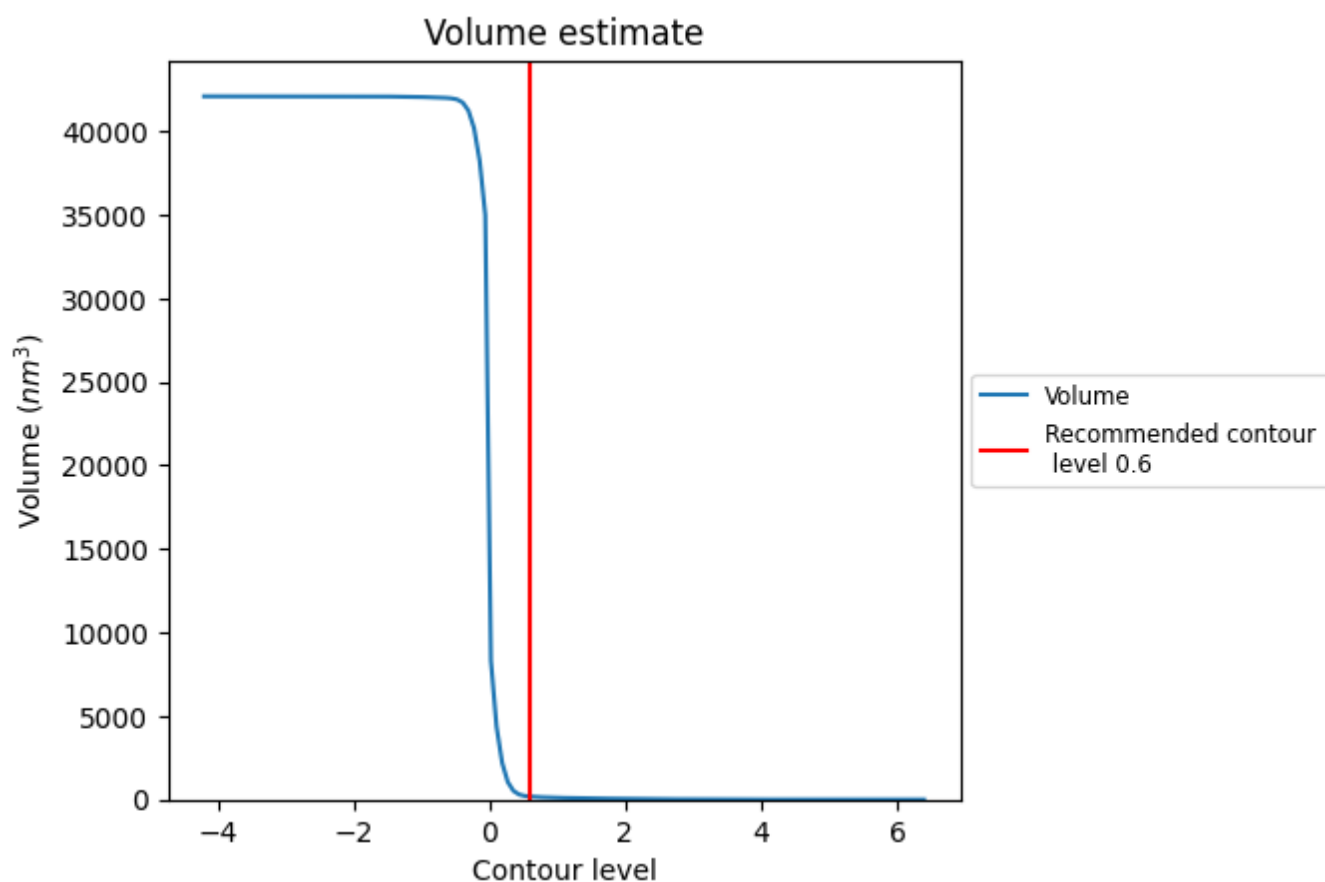
This section contains the results of statistical analysis of the map.

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.

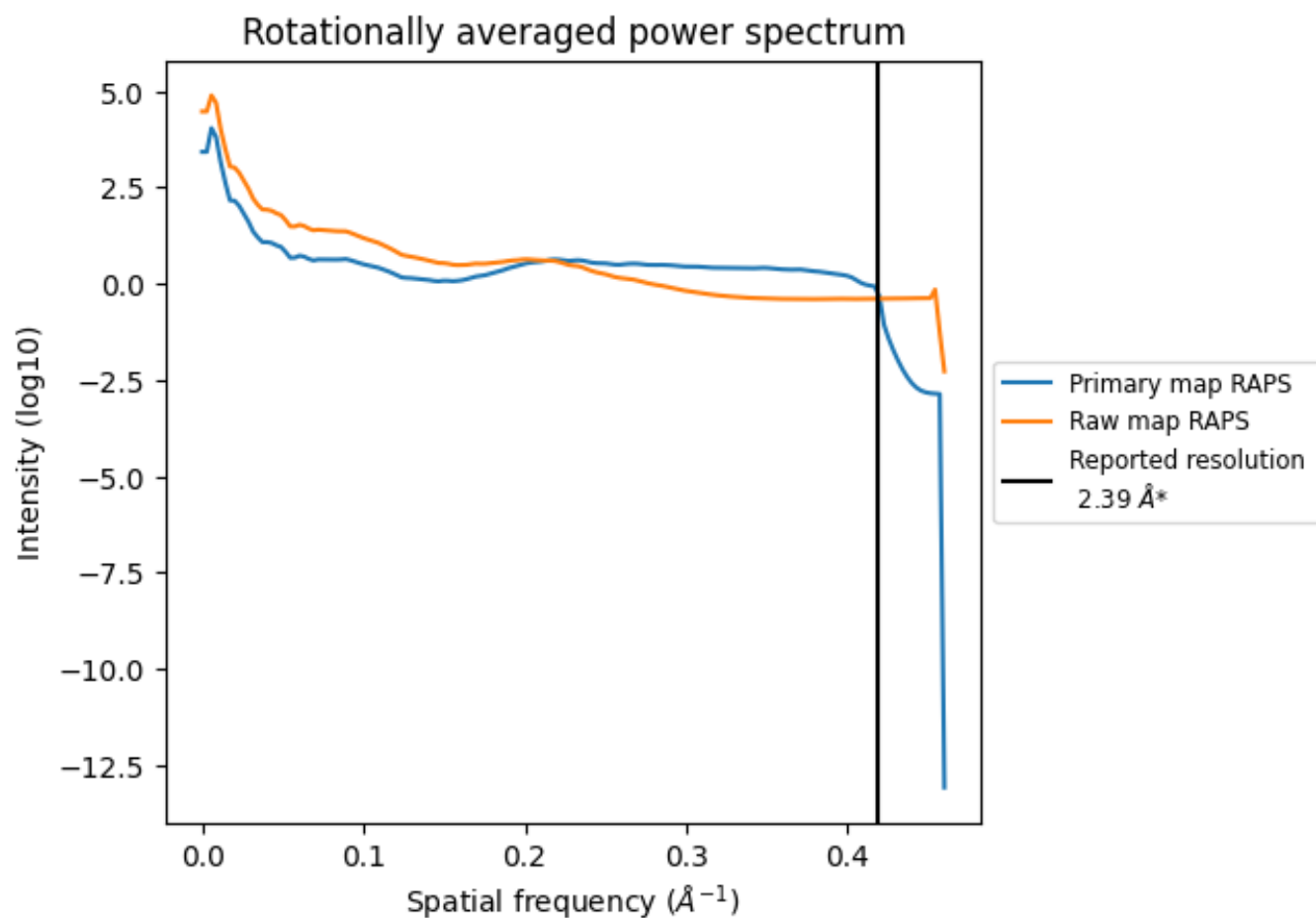
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 180 nm³; this corresponds to an approximate mass of 163 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 ⓘ

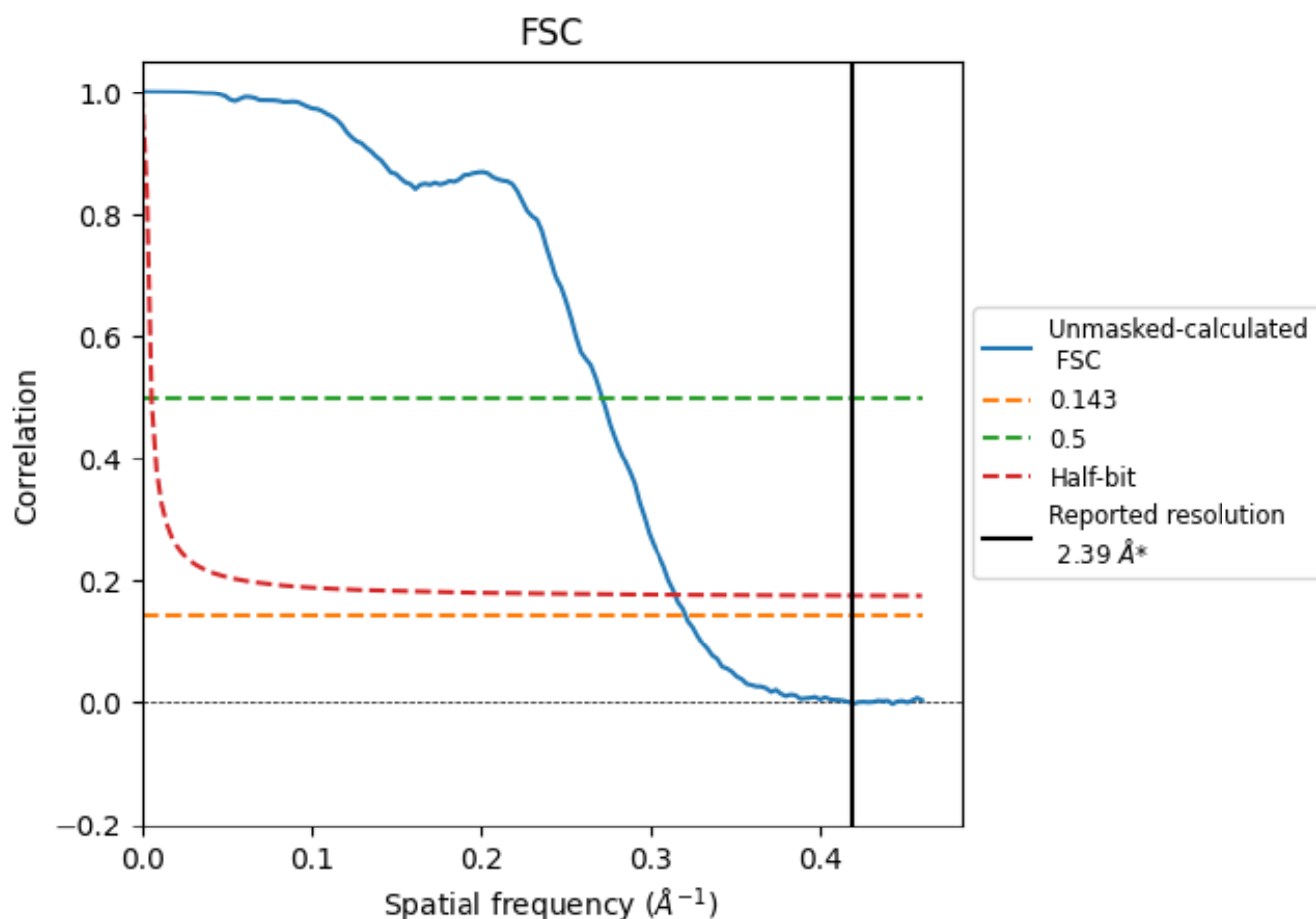


*Reported resolution corresponds to spatial frequency of 0.418 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.418 Å⁻¹

8.2 Resolution estimates [i](#)

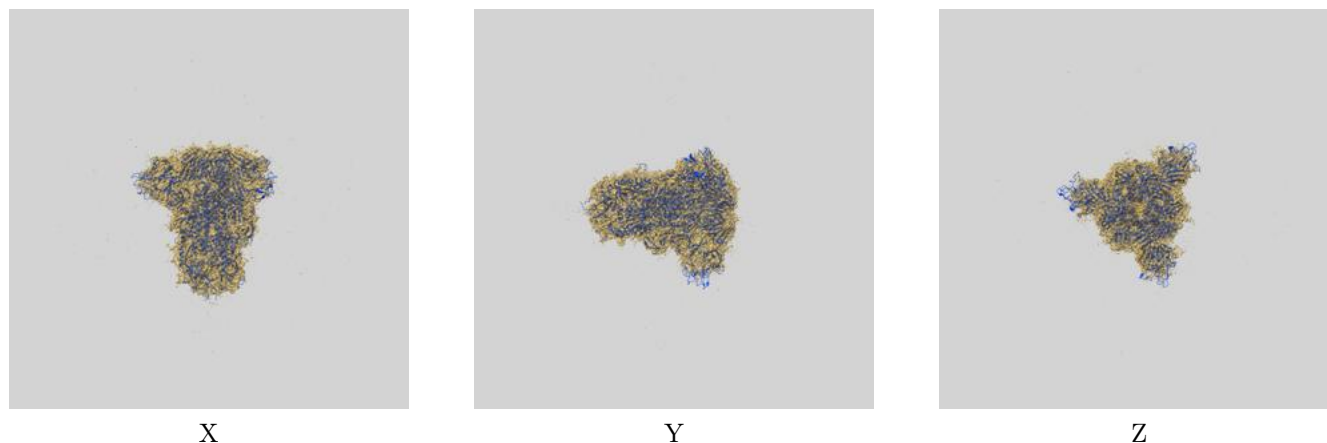
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.39	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.12	3.69	3.18

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.12 differs from the reported value 2.39 by more than 10 %

9 Map-model fit [i](#)

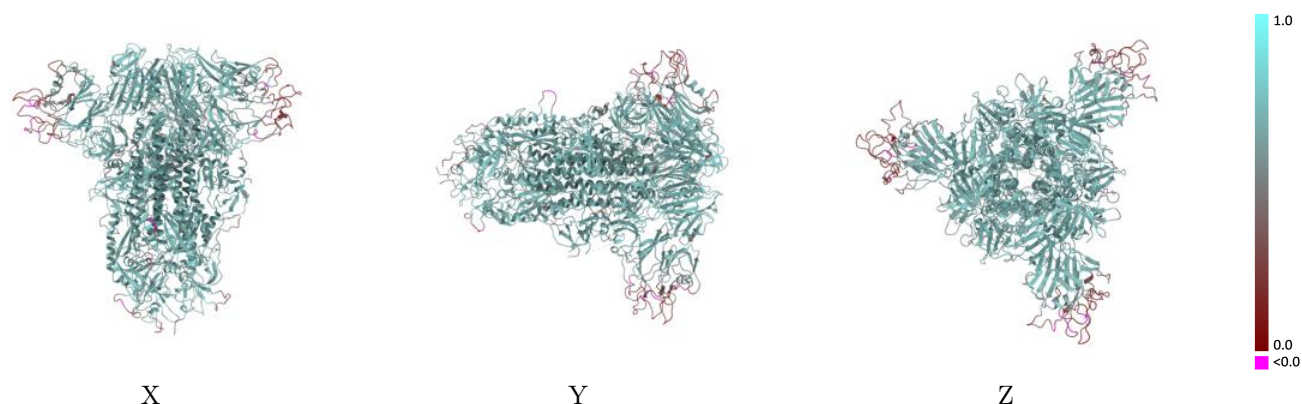
This section contains information regarding the fit between EMDB map EMD-62522 and PDB model 9KR8. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



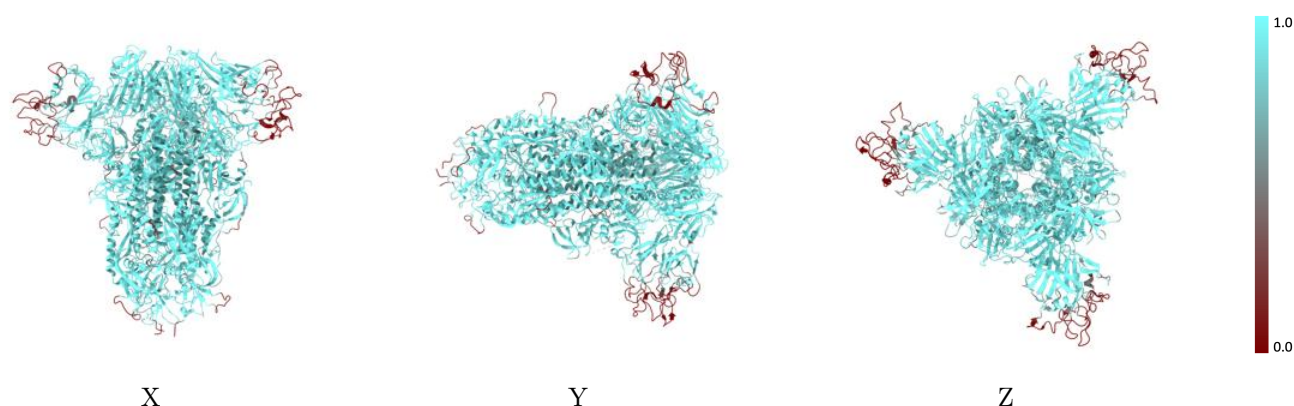
The images above show the 3D surface view of the map at the recommended contour level 0.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



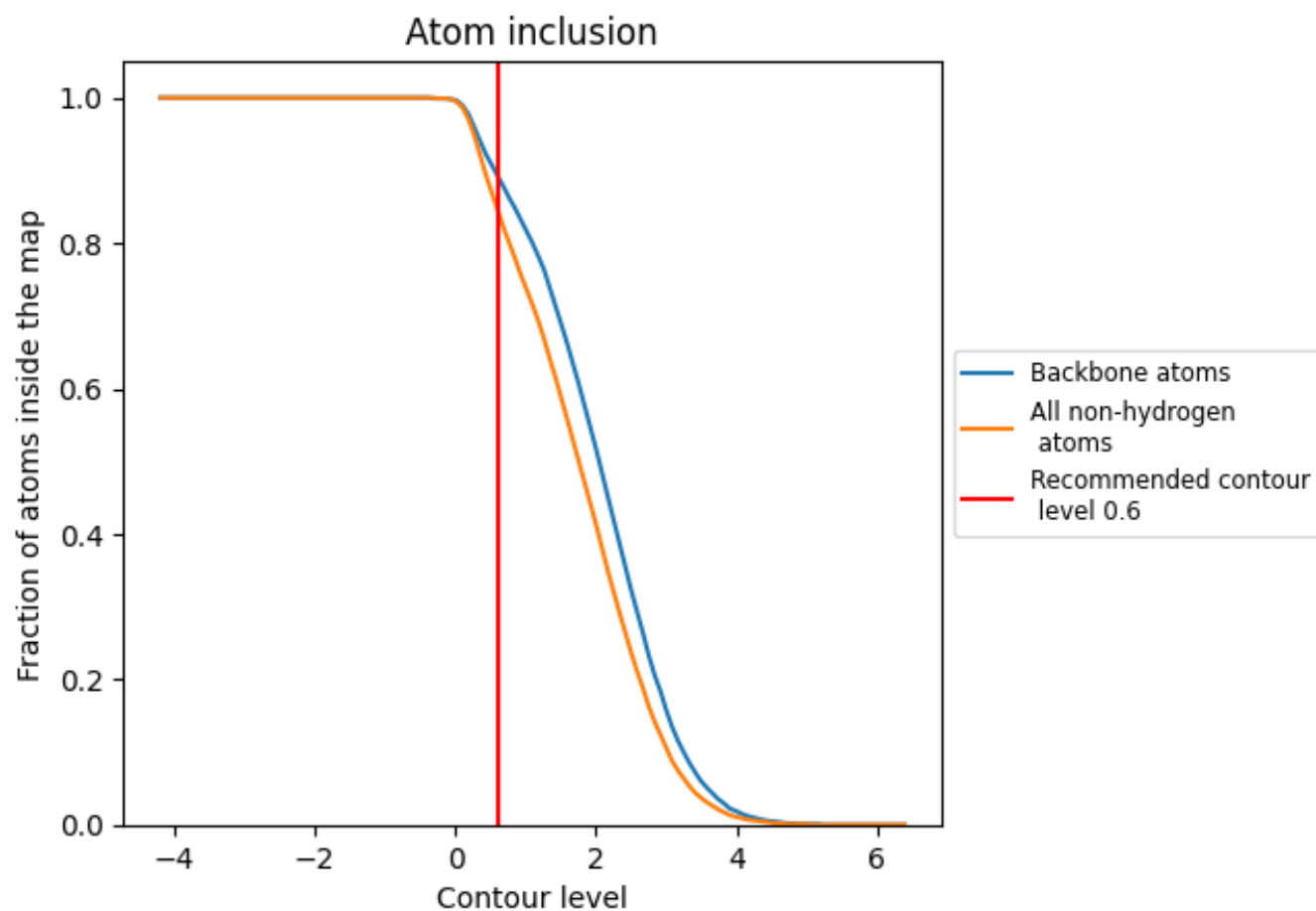
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.6).

























































9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 85% 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 (0.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8460	 0.6150
A	 0.8560	 0.6200
B	 0.8560	 0.6160
C	 0.8430	 0.6170
D	 0.7140	 0.5280
E	 0.6070	 0.4780
F	 0.7860	 0.4750
G	 0.4640	 0.4860
H	 0.7860	 0.5350
I	 0.4640	 0.4700
J	 0.5710	 0.5330
K	 0.7860	 0.5810
L	 0.6430	 0.4700
M	 0.6070	 0.4810
N	 0.7500	 0.5060
O	 0.5710	 0.5230
P	 0.7860	 0.5290
Q	 0.3570	 0.4510
R	 0.5000	 0.4890
S	 0.8570	 0.6020
T	 0.6790	 0.5600
U	 0.5000	 0.4090
V	 0.7860	 0.5000
W	 0.5360	 0.5560
X	 0.7500	 0.5530
Y	 0.3930	 0.4070
Z	 0.5360	 0.4470
a	 0.8570	 0.5790

