



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 12:35 PM UTC

PDB ID : 9J6G / pdb_00009j6g
EMDB ID : EMD-61170
Title : Cryo-EM structure of Bat SARS-like coronavirus Khosta-1 spike protein
Authors : Pan, X.Q.; Li, L.J.; Liu, K.F.; Qi, J.X.; Gao, G.F.
Deposited on : 2024-08-15
Resolution : 2.80 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

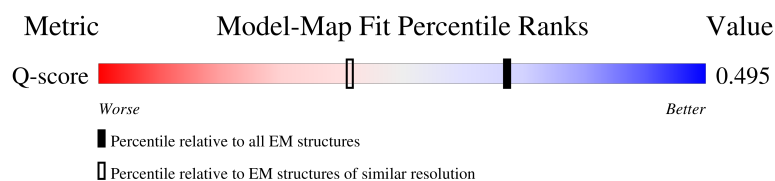
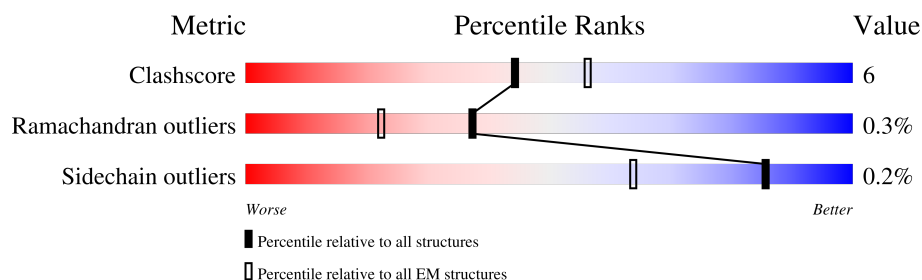
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11806 (2.30 - 3.30)

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	1167	
1	B	1167	
1	C	1167	
2	D	4	

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Mol	Chain	Length	Quality of chain
2	P	4	
3	E	2	
3	F	2	
3	G	2	
3	H	2	
3	I	2	
3	J	2	
3	L	2	
3	M	2	
3	N	2	
3	O	2	
3	Q	2	
3	R	2	
3	S	2	
3	T	2	
4	K	4	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 26136 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	B	1065	Total	C	N	O	S	0	0
			8299	5273	1384	1599	43		
1	A	1084	Total	C	N	O	S	0	0
			8433	5356	1407	1626	44		
1	C	1082	Total	C	N	O	S	0	0
			8414	5344	1402	1624	44		

There are 162 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	798	PRO	PHE	conflict	UNP A0A8E6M825
B	873	PRO	ALA	conflict	UNP A0A8E6M825
B	880	PRO	ALA	conflict	UNP A0A8E6M825
B	923	PRO	THR	conflict	UNP A0A8E6M825
B	967	PRO	LYS	conflict	UNP A0A8E6M825
B	968	PRO	VAL	conflict	UNP A0A8E6M825
B	1120	GLY	-	expression tag	UNP A0A8E6M825
B	1121	GLY	-	expression tag	UNP A0A8E6M825
B	1122	GLY	-	expression tag	UNP A0A8E6M825
B	1123	SER	-	expression tag	UNP A0A8E6M825
B	1124	GLY	-	expression tag	UNP A0A8E6M825
B	1125	GLY	-	expression tag	UNP A0A8E6M825
B	1126	GLY	-	expression tag	UNP A0A8E6M825
B	1127	SER	-	expression tag	UNP A0A8E6M825
B	1128	GLY	-	expression tag	UNP A0A8E6M825
B	1129	TYR	-	expression tag	UNP A0A8E6M825
B	1130	ILE	-	expression tag	UNP A0A8E6M825
B	1131	PRO	-	expression tag	UNP A0A8E6M825
B	1132	GLU	-	expression tag	UNP A0A8E6M825
B	1133	ALA	-	expression tag	UNP A0A8E6M825
B	1134	PRO	-	expression tag	UNP A0A8E6M825
B	1135	ARG	-	expression tag	UNP A0A8E6M825
B	1136	ASP	-	expression tag	UNP A0A8E6M825
B	1137	GLY	-	expression tag	UNP A0A8E6M825

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1138	GLN	-	expression tag	UNP A0A8E6M825
B	1139	ALA	-	expression tag	UNP A0A8E6M825
B	1140	TYR	-	expression tag	UNP A0A8E6M825
B	1141	VAL	-	expression tag	UNP A0A8E6M825
B	1142	ARG	-	expression tag	UNP A0A8E6M825
B	1143	LYS	-	expression tag	UNP A0A8E6M825
B	1144	ASP	-	expression tag	UNP A0A8E6M825
B	1145	GLY	-	expression tag	UNP A0A8E6M825
B	1146	GLU	-	expression tag	UNP A0A8E6M825
B	1147	TRP	-	expression tag	UNP A0A8E6M825
B	1148	VAL	-	expression tag	UNP A0A8E6M825
B	1149	LEU	-	expression tag	UNP A0A8E6M825
B	1150	LEU	-	expression tag	UNP A0A8E6M825
B	1151	SER	-	expression tag	UNP A0A8E6M825
B	1152	THR	-	expression tag	UNP A0A8E6M825
B	1153	PHE	-	expression tag	UNP A0A8E6M825
B	1154	LEU	-	expression tag	UNP A0A8E6M825
B	1155	GLY	-	expression tag	UNP A0A8E6M825
B	1156	GLY	-	expression tag	UNP A0A8E6M825
B	1157	GLY	-	expression tag	UNP A0A8E6M825
B	1158	SER	-	expression tag	UNP A0A8E6M825
B	1159	ALA	-	expression tag	UNP A0A8E6M825
B	1160	TRP	-	expression tag	UNP A0A8E6M825
B	1161	SER	-	expression tag	UNP A0A8E6M825
B	1162	HIS	-	expression tag	UNP A0A8E6M825
B	1163	PRO	-	expression tag	UNP A0A8E6M825
B	1164	GLN	-	expression tag	UNP A0A8E6M825
B	1165	PHE	-	expression tag	UNP A0A8E6M825
B	1166	GLU	-	expression tag	UNP A0A8E6M825
B	1167	LYS	-	expression tag	UNP A0A8E6M825
A	798	PRO	PHE	conflict	UNP A0A8E6M825
A	873	PRO	ALA	conflict	UNP A0A8E6M825
A	880	PRO	ALA	conflict	UNP A0A8E6M825
A	923	PRO	THR	conflict	UNP A0A8E6M825
A	967	PRO	LYS	conflict	UNP A0A8E6M825
A	968	PRO	VAL	conflict	UNP A0A8E6M825
A	1120	GLY	-	expression tag	UNP A0A8E6M825
A	1121	GLY	-	expression tag	UNP A0A8E6M825
A	1122	GLY	-	expression tag	UNP A0A8E6M825
A	1123	SER	-	expression tag	UNP A0A8E6M825
A	1124	GLY	-	expression tag	UNP A0A8E6M825
A	1125	GLY	-	expression tag	UNP A0A8E6M825

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1126	GLY	-	expression tag	UNP A0A8E6M825
A	1127	SER	-	expression tag	UNP A0A8E6M825
A	1128	GLY	-	expression tag	UNP A0A8E6M825
A	1129	TYR	-	expression tag	UNP A0A8E6M825
A	1130	ILE	-	expression tag	UNP A0A8E6M825
A	1131	PRO	-	expression tag	UNP A0A8E6M825
A	1132	GLU	-	expression tag	UNP A0A8E6M825
A	1133	ALA	-	expression tag	UNP A0A8E6M825
A	1134	PRO	-	expression tag	UNP A0A8E6M825
A	1135	ARG	-	expression tag	UNP A0A8E6M825
A	1136	ASP	-	expression tag	UNP A0A8E6M825
A	1137	GLY	-	expression tag	UNP A0A8E6M825
A	1138	GLN	-	expression tag	UNP A0A8E6M825
A	1139	ALA	-	expression tag	UNP A0A8E6M825
A	1140	TYR	-	expression tag	UNP A0A8E6M825
A	1141	VAL	-	expression tag	UNP A0A8E6M825
A	1142	ARG	-	expression tag	UNP A0A8E6M825
A	1143	LYS	-	expression tag	UNP A0A8E6M825
A	1144	ASP	-	expression tag	UNP A0A8E6M825
A	1145	GLY	-	expression tag	UNP A0A8E6M825
A	1146	GLU	-	expression tag	UNP A0A8E6M825
A	1147	TRP	-	expression tag	UNP A0A8E6M825
A	1148	VAL	-	expression tag	UNP A0A8E6M825
A	1149	LEU	-	expression tag	UNP A0A8E6M825
A	1150	LEU	-	expression tag	UNP A0A8E6M825
A	1151	SER	-	expression tag	UNP A0A8E6M825
A	1152	THR	-	expression tag	UNP A0A8E6M825
A	1153	PHE	-	expression tag	UNP A0A8E6M825
A	1154	LEU	-	expression tag	UNP A0A8E6M825
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A	1156	GLY	-	expression tag	UNP A0A8E6M825
A	1157	GLY	-	expression tag	UNP A0A8E6M825
A	1158	SER	-	expression tag	UNP A0A8E6M825
A	1159	ALA	-	expression tag	UNP A0A8E6M825
A	1160	TRP	-	expression tag	UNP A0A8E6M825
A	1161	SER	-	expression tag	UNP A0A8E6M825
A	1162	HIS	-	expression tag	UNP A0A8E6M825
A	1163	PRO	-	expression tag	UNP A0A8E6M825
A	1164	GLN	-	expression tag	UNP A0A8E6M825
A	1165	PHE	-	expression tag	UNP A0A8E6M825
A	1166	GLU	-	expression tag	UNP A0A8E6M825
A	1167	LYS	-	expression tag	UNP A0A8E6M825

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Chain	Residue	Modelled	Actual	Comment	Reference
C	798	PRO	PHE	conflict	UNP A0A8E6M825
C	873	PRO	ALA	conflict	UNP A0A8E6M825
C	880	PRO	ALA	conflict	UNP A0A8E6M825
C	923	PRO	THR	conflict	UNP A0A8E6M825
C	967	PRO	LYS	conflict	UNP A0A8E6M825
C	968	PRO	VAL	conflict	UNP A0A8E6M825
C	1120	GLY	-	expression tag	UNP A0A8E6M825
C	1121	GLY	-	expression tag	UNP A0A8E6M825
C	1122	GLY	-	expression tag	UNP A0A8E6M825
C	1123	SER	-	expression tag	UNP A0A8E6M825
C	1124	GLY	-	expression tag	UNP A0A8E6M825
C	1125	GLY	-	expression tag	UNP A0A8E6M825
C	1126	GLY	-	expression tag	UNP A0A8E6M825
C	1127	SER	-	expression tag	UNP A0A8E6M825
C	1128	GLY	-	expression tag	UNP A0A8E6M825
C	1129	TYR	-	expression tag	UNP A0A8E6M825
C	1130	ILE	-	expression tag	UNP A0A8E6M825
C	1131	PRO	-	expression tag	UNP A0A8E6M825
C	1132	GLU	-	expression tag	UNP A0A8E6M825
C	1133	ALA	-	expression tag	UNP A0A8E6M825
C	1134	PRO	-	expression tag	UNP A0A8E6M825
C	1135	ARG	-	expression tag	UNP A0A8E6M825
C	1136	ASP	-	expression tag	UNP A0A8E6M825
C	1137	GLY	-	expression tag	UNP A0A8E6M825
C	1138	GLN	-	expression tag	UNP A0A8E6M825
C	1139	ALA	-	expression tag	UNP A0A8E6M825
C	1140	TYR	-	expression tag	UNP A0A8E6M825
C	1141	VAL	-	expression tag	UNP A0A8E6M825
C	1142	ARG	-	expression tag	UNP A0A8E6M825
C	1143	LYS	-	expression tag	UNP A0A8E6M825
C	1144	ASP	-	expression tag	UNP A0A8E6M825
C	1145	GLY	-	expression tag	UNP A0A8E6M825
C	1146	GLU	-	expression tag	UNP A0A8E6M825
C	1147	TRP	-	expression tag	UNP A0A8E6M825
C	1148	VAL	-	expression tag	UNP A0A8E6M825
C	1149	LEU	-	expression tag	UNP A0A8E6M825
C	1150	LEU	-	expression tag	UNP A0A8E6M825
C	1151	SER	-	expression tag	UNP A0A8E6M825
C	1152	THR	-	expression tag	UNP A0A8E6M825
C	1153	PHE	-	expression tag	UNP A0A8E6M825
C	1154	LEU	-	expression tag	UNP A0A8E6M825
C	1155	GLY	-	expression tag	UNP A0A8E6M825

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1156	GLY	-	expression tag	UNP A0A8E6M825
C	1157	GLY	-	expression tag	UNP A0A8E6M825
C	1158	SER	-	expression tag	UNP A0A8E6M825
C	1159	ALA	-	expression tag	UNP A0A8E6M825
C	1160	TRP	-	expression tag	UNP A0A8E6M825
C	1161	SER	-	expression tag	UNP A0A8E6M825
C	1162	HIS	-	expression tag	UNP A0A8E6M825
C	1163	PRO	-	expression tag	UNP A0A8E6M825
C	1164	GLN	-	expression tag	UNP A0A8E6M825
C	1165	PHE	-	expression tag	UNP A0A8E6M825
C	1166	GLU	-	expression tag	UNP A0A8E6M825
C	1167	LYS	-	expression tag	UNP A0A8E6M825

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



Mol	Chain	Residues	Atoms				AltConf	Trace
2	D	4	Total	C	N	O	0	0
			50	28	2	20		
2	P	4	Total	C	N	O	0	0
			50	28	2	20		

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



Mol	Chain	Residues	Atoms				AltConf	Trace
3	E	2	Total	C	N	O	0	0
			28	16	2	10		
3	F	2	Total	C	N	O	0	0
			28	16	2	10		
3	G	2	Total	C	N	O	0	0
			28	16	2	10		

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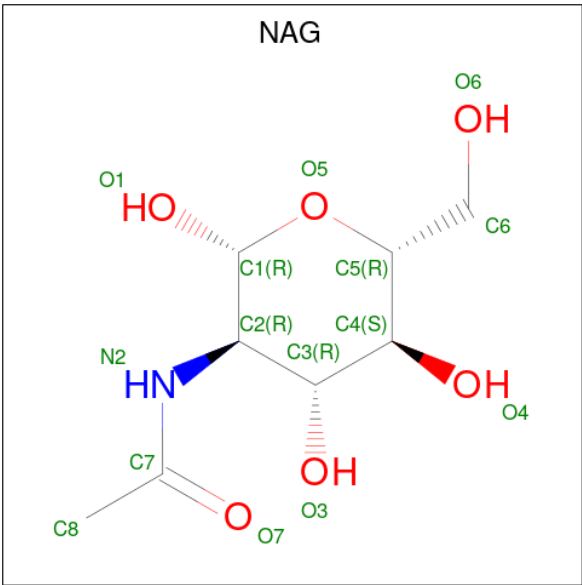
Mol	Chain	Residues	Atoms				AltConf	Trace
3	H	2	Total	C	N	O	0	0
			28	16	2	10		
3	I	2	Total	C	N	O	0	0
			28	16	2	10		
3	J	2	Total	C	N	O	0	0
			28	16	2	10		
3	L	2	Total	C	N	O	0	0
			28	16	2	10		
3	M	2	Total	C	N	O	0	0
			28	16	2	10		
3	N	2	Total	C	N	O	0	0
			28	16	2	10		
3	O	2	Total	C	N	O	0	0
			28	16	2	10		
3	Q	2	Total	C	N	O	0	0
			28	16	2	10		
3	R	2	Total	C	N	O	0	0
			28	16	2	10		
3	S	2	Total	C	N	O	0	0
			28	16	2	10		
3	T	2	Total	C	N	O	0	0
			28	16	2	10		

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



Mol	Chain	Residues	Atoms				AltConf	Trace
4	K	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆) (labeled as "Ligand of Interest" by depositor).



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

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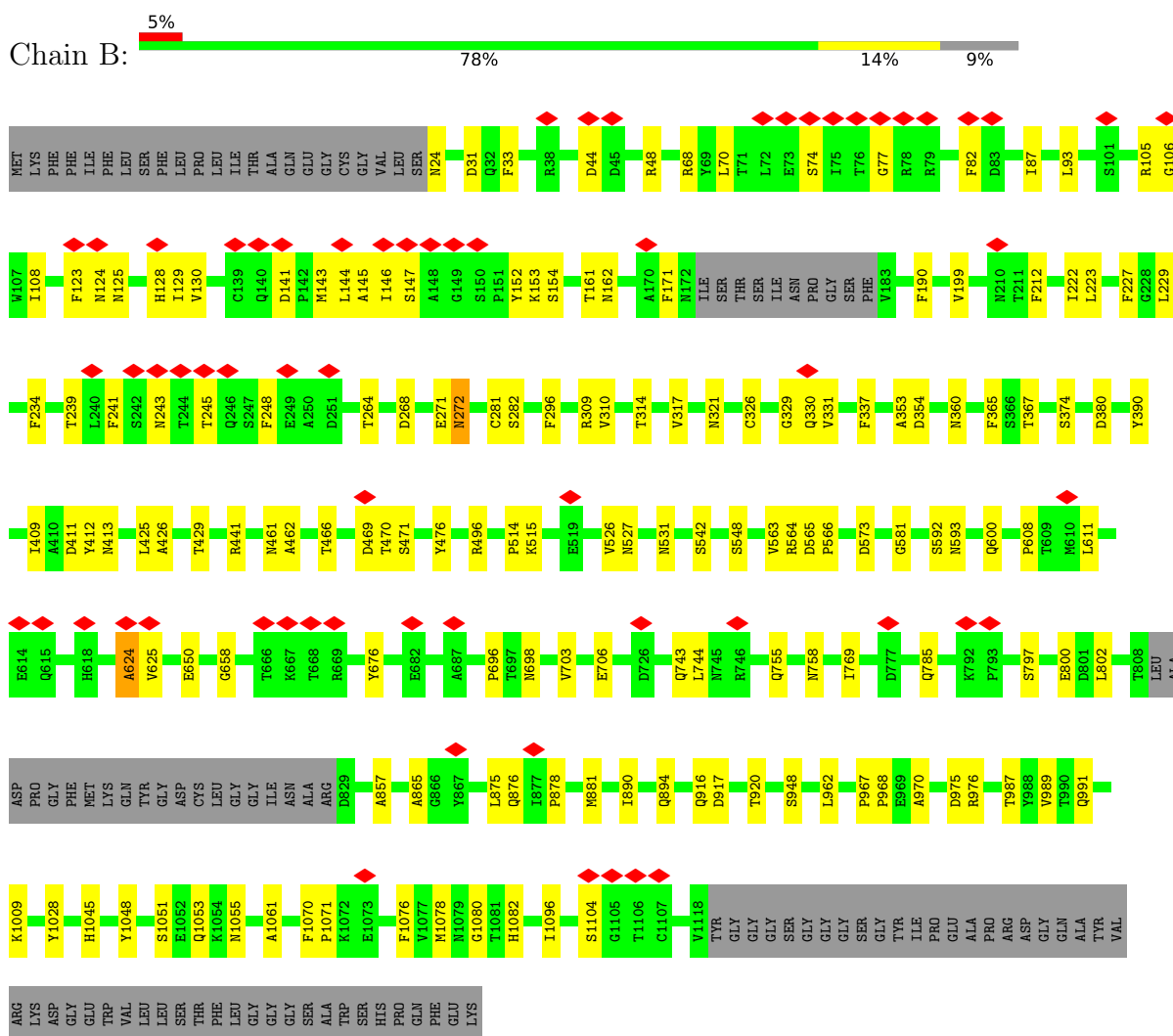
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Mol	Chain	Residues	Atoms				AltConf
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	A	1	Total	C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

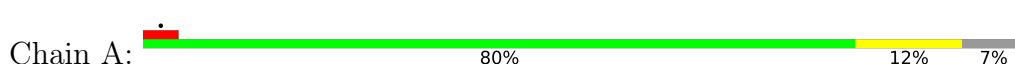
3 Residue-property plots

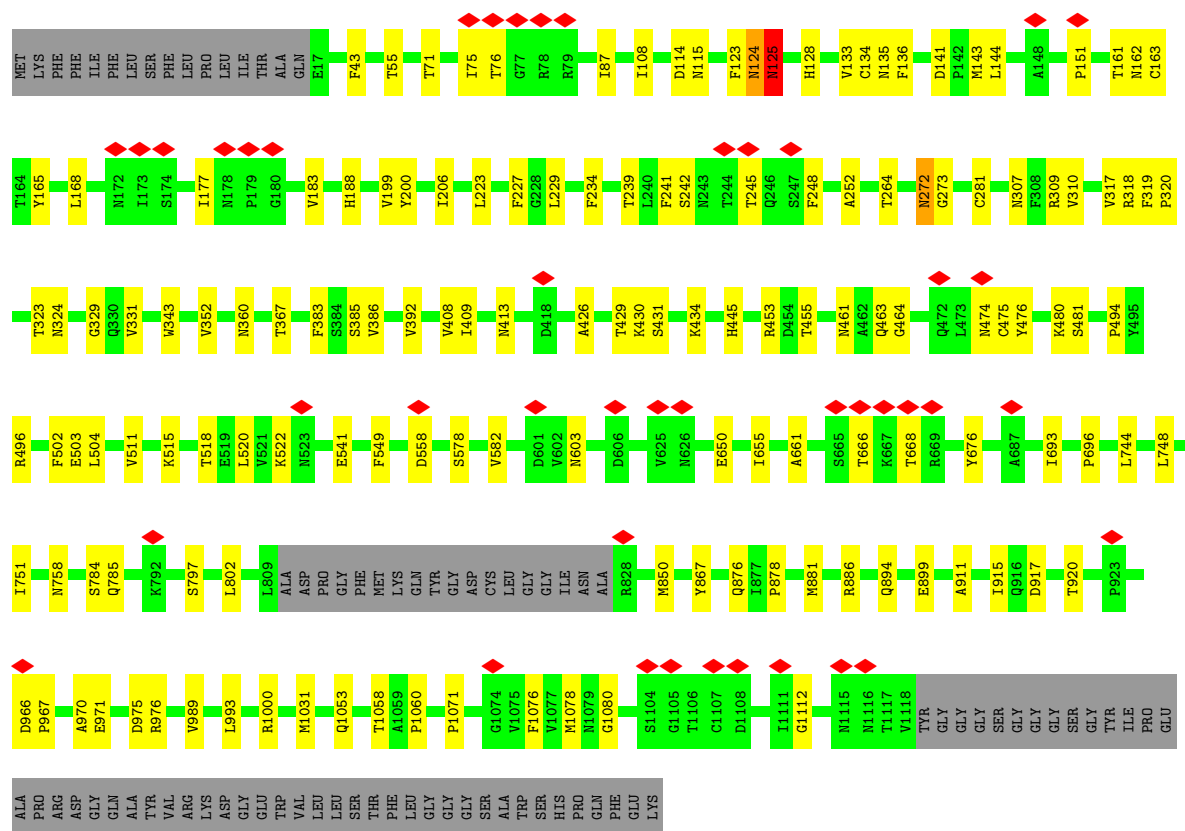
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: Spike glycoprotein

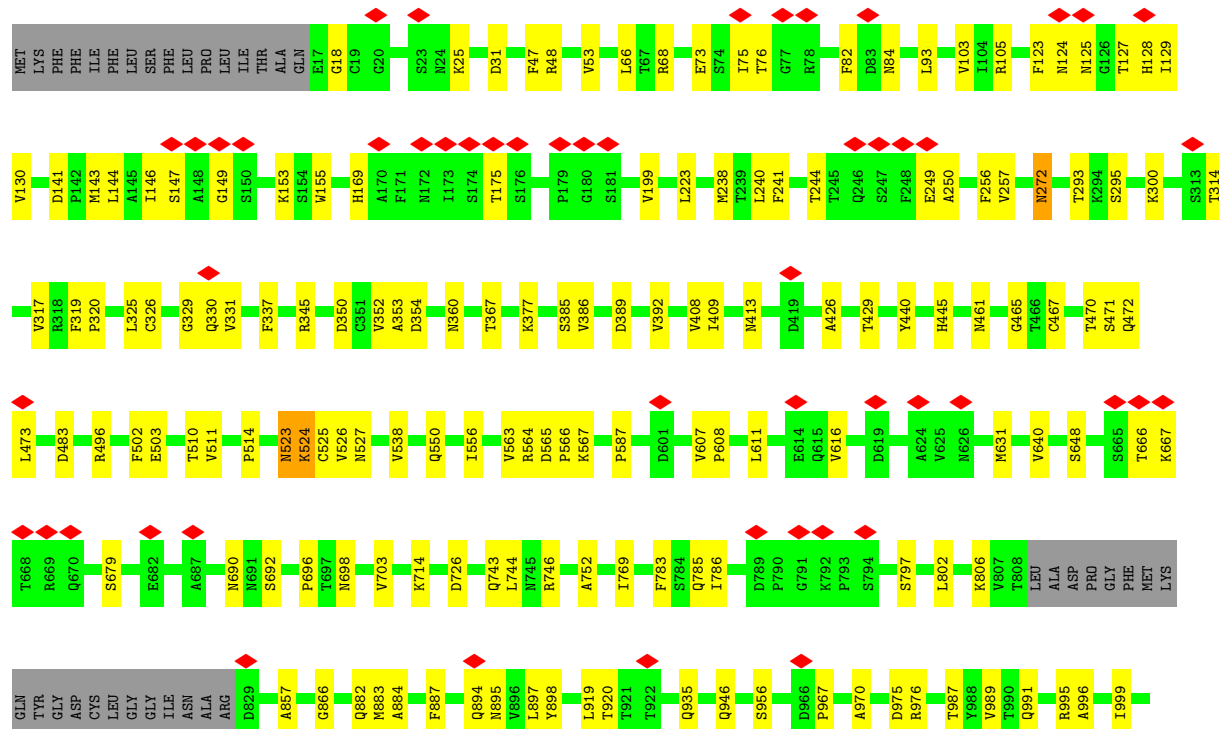
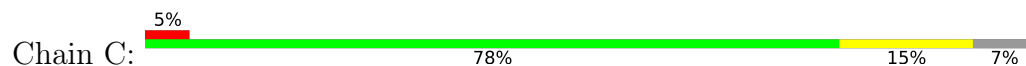


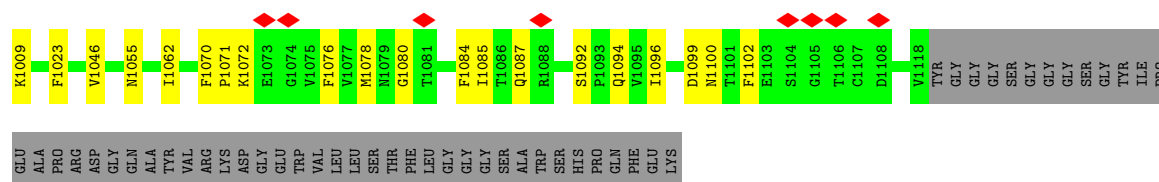
• Molecule 1: Spike glycoprotein





• Molecule 1: Spike glycoprotein





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

Chain D: 25% 75%



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

Chain P: 25% 75% 25%



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

Chain E: 50% 50% 50%



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

Chain F: 50% 50% 50%



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

Chain G: 50% 50% 50%



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



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



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



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



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



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





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



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



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



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



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



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



HA01	HA02	HA03	HA04
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	312075	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)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.872	Depositor
Minimum map value	-0.416	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.026	Depositor
Recommended contour level	0.2	Depositor
Map size ($\text{\AA}$)	331.2, 331.2, 331.2	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.69, 0.69, 0.69	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.22	0/8628	0.44	2/11750 (0.0%)
1	B	0.19	0/8491	0.41	1/11563 (0.0%)
1	C	0.24	0/8609	0.44	1/11725 (0.0%)
All	All	0.22	0/25728	0.43	4/35038 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	624	ALA	CB-CA-C	-5.38	109.91	117.23
1	A	603	ASN	CB-CA-C	-5.29	102.64	110.67
1	A	125	ASN	CA-CB-CG	5.07	117.67	112.60
1	C	690	ASN	CA-CB-CG	5.07	117.67	112.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	8433	0	8180	98	0
1	B	8299	0	8041	114	0
1	C	8414	0	8156	121	0
2	D	50	0	43	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	P	50	0	43	2	0
3	E	28	0	25	2	0
3	F	28	0	25	1	0
3	G	28	0	25	1	0
3	H	28	0	25	1	0
3	I	28	0	25	1	0
3	J	28	0	25	1	0
3	L	28	0	25	0	0
3	M	28	0	25	4	0
3	N	28	0	25	1	0
3	O	28	0	25	0	0
3	Q	28	0	25	0	0
3	R	28	0	25	3	0
3	S	28	0	25	3	0
3	T	28	0	25	0	0
4	K	50	0	43	1	0
5	A	154	0	143	7	0
5	B	154	0	143	8	0
5	C	140	0	130	2	0
All	All	26136	0	25272	329	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 6.

The worst 5 of 329 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:784:SER:HB3	5:A:1211:NAG:C1	1.82	1.09
1:A:151:PRO:HB3	5:A:1202:NAG:H81	1.47	0.96
5:B:1210:NAG:H4	1:A:876:GLN:OE1	1.68	0.92
4:K:1:NAG:H62	4:K:2:NAG:HN2	1.36	0.91
1:B:82:PHE:CD2	5:B:1201:NAG:H81	2.08	0.88

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	1080/1167 (92%)	996 (92%)	80 (7%)	4 (0%)	30	60
1	B	1059/1167 (91%)	988 (93%)	69 (6%)	2 (0%)	43	72
1	C	1078/1167 (92%)	999 (93%)	76 (7%)	3 (0%)	36	66
All	All	3217/3501 (92%)	2983 (93%)	225 (7%)	9 (0%)	37	66

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	471	SER
1	C	244	THR
1	C	523	ASN
1	A	125	ASN
1	A	323	THR

5.3.2 Protein sidechains [i](#)

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	947/1008 (94%)	945 (100%)	2 (0%)	87	96
1	B	931/1008 (92%)	929 (100%)	2 (0%)	87	96
1	C	945/1008 (94%)	943 (100%)	2 (0%)	87	96
All	All	2823/3024 (93%)	2817 (100%)	6 (0%)	85	96

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

Mol	Chain	Res	Type
1	A	272	ASN
1	C	272	ASN
1	C	524	LYS
1	B	272	ASN
1	B	24	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1064	HIS
1	C	743	GLN
1	C	32	GLN
1	C	445	HIS
1	C	903	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 ⓘ

40 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	2,1	14,14,15	0.32	0	17,19,21	0.98	1 (5%)
2	NAG	D	2	2	14,14,15	0.39	0	17,19,21	1.24	2 (11%)
2	BMA	D	3	2	11,11,12	0.32	0	15,15,17	1.53	2 (13%)
2	BMA	D	4	2	11,11,12	0.25	0	15,15,17	0.66	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	E	1	1,3	14,14,15	0.50	0	17,19,21	0.73	0
3	NAG	E	2	3	14,14,15	0.32	0	17,19,21	0.58	0
3	NAG	F	1	1,3	14,14,15	0.34	0	17,19,21	1.15	2 (11%)
3	NAG	F	2	3	14,14,15	0.31	0	17,19,21	0.78	0
3	NAG	G	1	1,3	14,14,15	0.56	0	17,19,21	0.93	1 (5%)
3	NAG	G	2	3	14,14,15	0.31	0	17,19,21	0.83	1 (5%)
3	NAG	H	1	1,3	14,14,15	0.66	0	17,19,21	0.87	1 (5%)
3	NAG	H	2	3	14,14,15	0.35	0	17,19,21	0.75	1 (5%)
3	NAG	I	1	1,3	14,14,15	0.39	0	17,19,21	0.69	0
3	NAG	I	2	3	14,14,15	0.35	0	17,19,21	0.73	0
3	NAG	J	1	1,3	14,14,15	0.47	0	17,19,21	0.86	0
3	NAG	J	2	3	14,14,15	0.36	0	17,19,21	0.68	0
4	NAG	K	1	4,1	14,14,15	0.36	0	17,19,21	0.91	1 (5%)
4	NAG	K	2	4	14,14,15	0.32	0	17,19,21	0.91	1 (5%)
4	BMA	K	3	4	11,11,12	0.28	0	15,15,17	0.69	0
4	MAN	K	4	4	11,11,12	0.24	0	15,15,17	0.56	0
3	NAG	L	1	1,3	14,14,15	0.49	0	17,19,21	0.86	1 (5%)
3	NAG	L	2	3	14,14,15	0.32	0	17,19,21	0.72	0
3	NAG	M	1	1,3	14,14,15	0.56	0	17,19,21	0.90	1 (5%)
3	NAG	M	2	3	14,14,15	0.34	0	17,19,21	0.64	0
3	NAG	N	1	1,3	14,14,15	0.36	0	17,19,21	0.82	1 (5%)
3	NAG	N	2	3	14,14,15	0.34	0	17,19,21	0.82	0
3	NAG	O	1	1,3	14,14,15	0.56	0	17,19,21	0.86	1 (5%)
3	NAG	O	2	3	14,14,15	0.33	0	17,19,21	0.65	0
2	NAG	P	1	2,1	14,14,15	0.57	0	17,19,21	1.15	2 (11%)
2	NAG	P	2	2	14,14,15	0.45	0	17,19,21	1.44	2 (11%)
2	BMA	P	3	2	11,11,12	0.47	0	15,15,17	1.05	1 (6%)
2	BMA	P	4	2	11,11,12	0.33	0	15,15,17	0.84	0
3	NAG	Q	1	1,3	14,14,15	0.69	0	17,19,21	0.92	1 (5%)
3	NAG	Q	2	3	14,14,15	0.39	0	17,19,21	0.65	0
3	NAG	R	1	1,3	14,14,15	0.59	0	17,19,21	1.16	1 (5%)
3	NAG	R	2	3	14,14,15	0.32	0	17,19,21	0.59	0
3	NAG	S	1	1,3	14,14,15	0.30	0	17,19,21	1.30	2 (11%)
3	NAG	S	2	3	14,14,15	0.29	0	17,19,21	0.80	0
3	NAG	T	1	1,3	14,14,15	0.42	0	17,19,21	0.87	0
3	NAG	T	2	3	14,14,15	0.26	0	17,19,21	0.63	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.
'-' means no outliers of that kind were identified.

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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	S	2	3	-	3/6/23/26	0/1/1/1
3	NAG	T	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	T	2	3	-	3/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	3	BMA	C1-O5-C5	4.34	118.01	112.19
2	P	2	NAG	C1-O5-C5	3.41	116.76	112.19
2	P	1	NAG	C1-O5-C5	3.33	116.65	112.19
2	P	2	NAG	O4-C4-C3	-3.18	102.88	110.38
2	P	3	BMA	O4-C4-C5	-3.17	101.52	109.32

There are no chirality outliers.

5 of 54 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	P	2	NAG	C8-C7-N2-C2
2	P	2	NAG	O7-C7-N2-C2
3	F	1	NAG	O7-C7-N2-C2
3	G	1	NAG	C8-C7-N2-C2
3	G	1	NAG	O7-C7-N2-C2

There are no ring outliers.

24 monomers are involved in 26 short contacts:

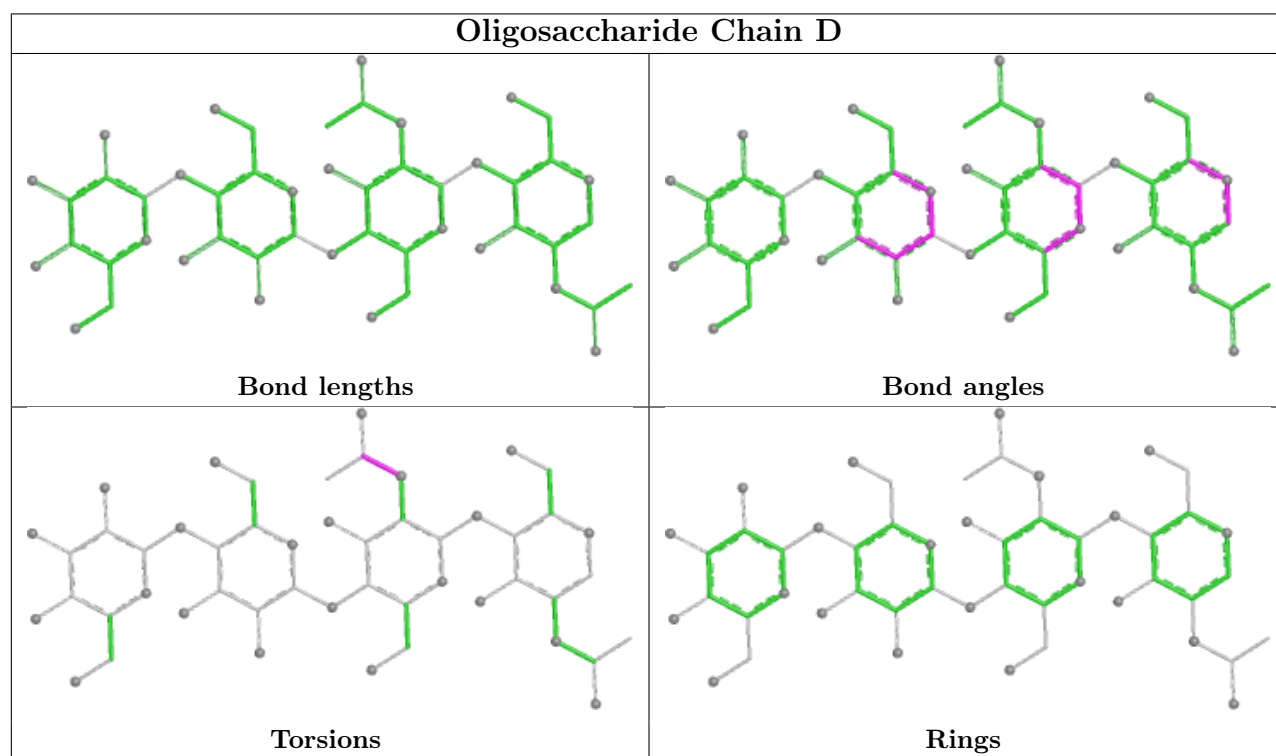
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	4	BMA	2	0
4	K	2	NAG	1	0
3	H	2	NAG	1	0
3	I	2	NAG	1	0
3	M	2	NAG	3	0
3	M	1	NAG	1	0
3	J	1	NAG	1	0
3	N	1	NAG	1	0
3	G	1	NAG	1	0
3	R	1	NAG	3	0
3	E	1	NAG	2	0
2	D	2	NAG	1	0

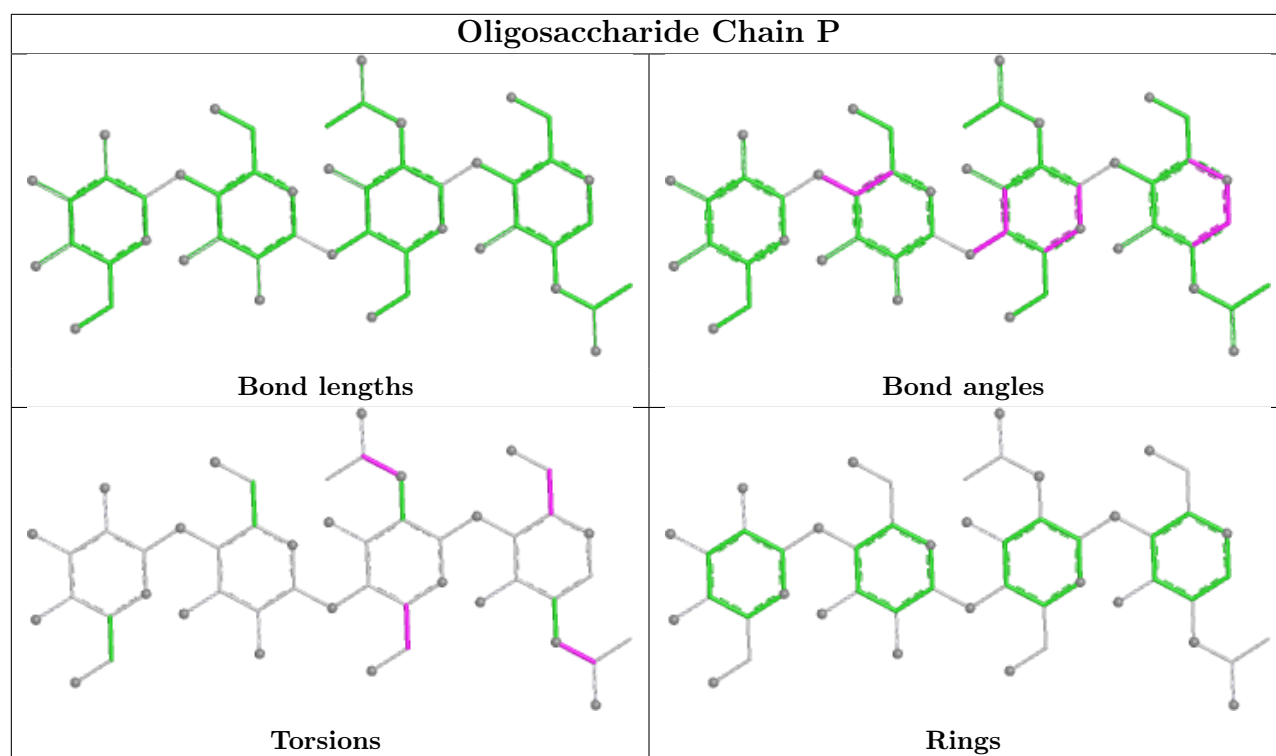
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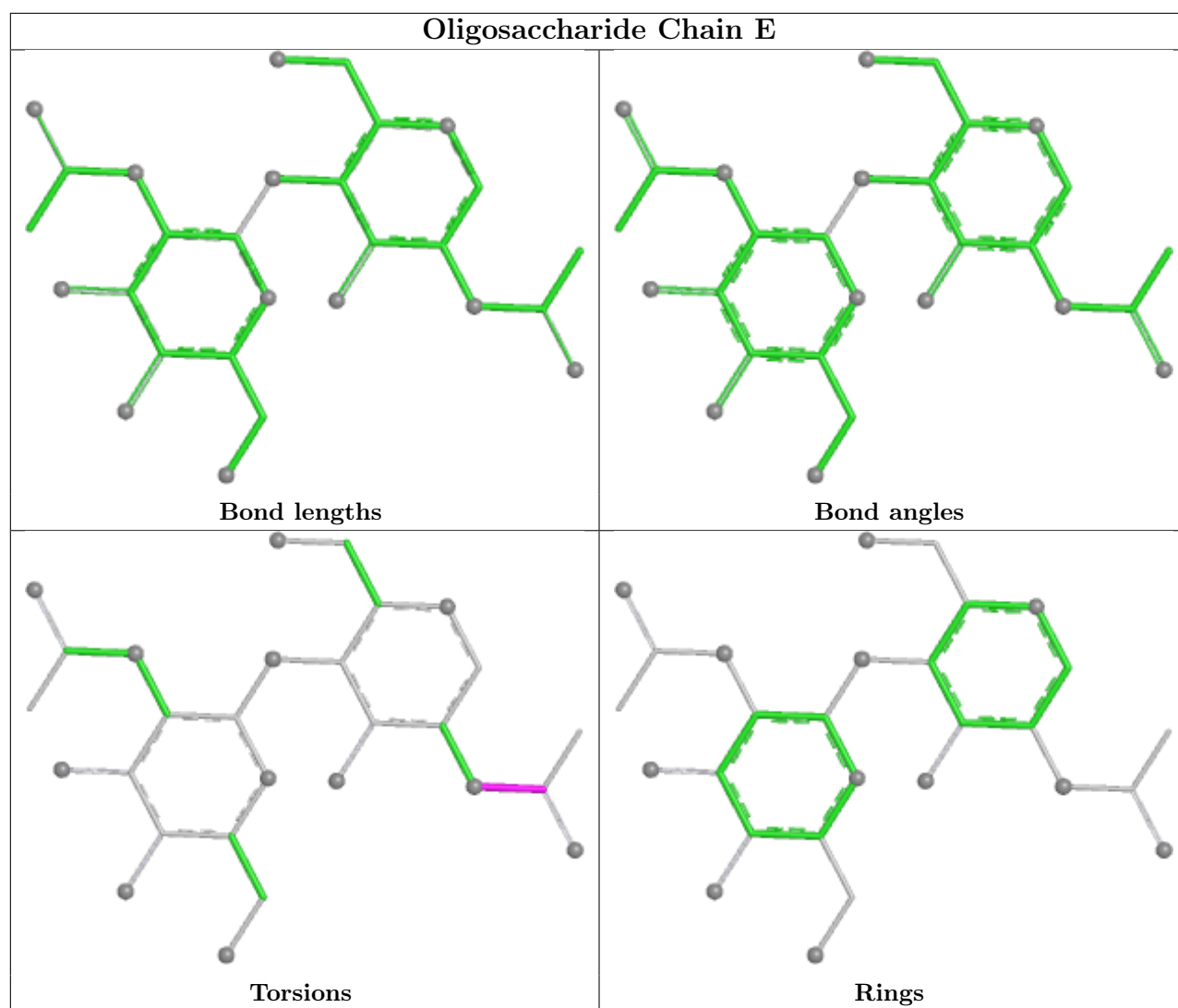
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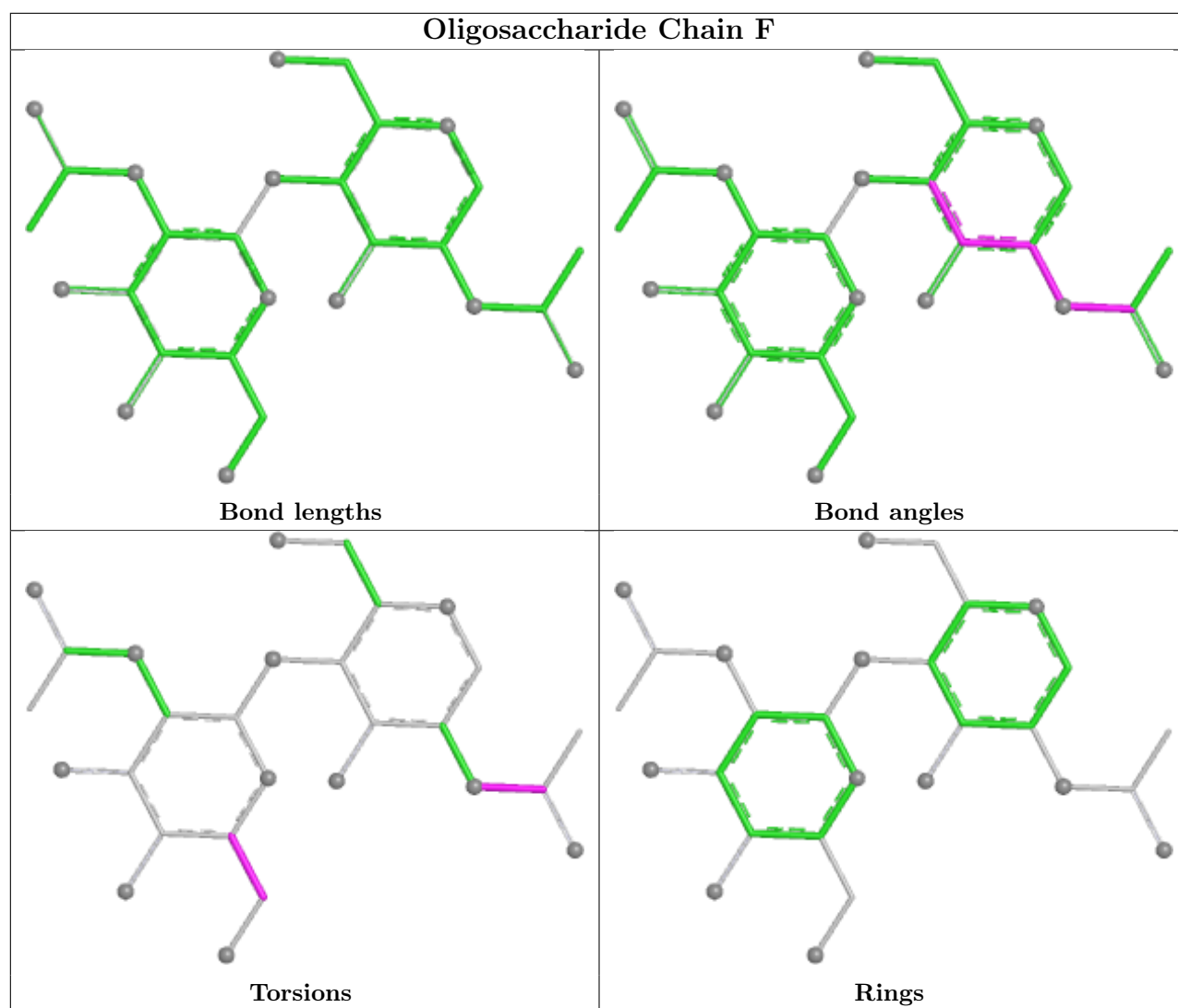
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	S	2	NAG	2	0
3	F	1	NAG	1	0
3	N	2	NAG	1	0
3	J	2	NAG	1	0
3	S	1	NAG	3	0
2	P	4	BMA	1	0
2	P	3	BMA	1	0
3	I	1	NAG	1	0
4	K	1	NAG	1	0
2	D	3	BMA	2	0
2	D	1	NAG	1	0
3	H	1	NAG	1	0

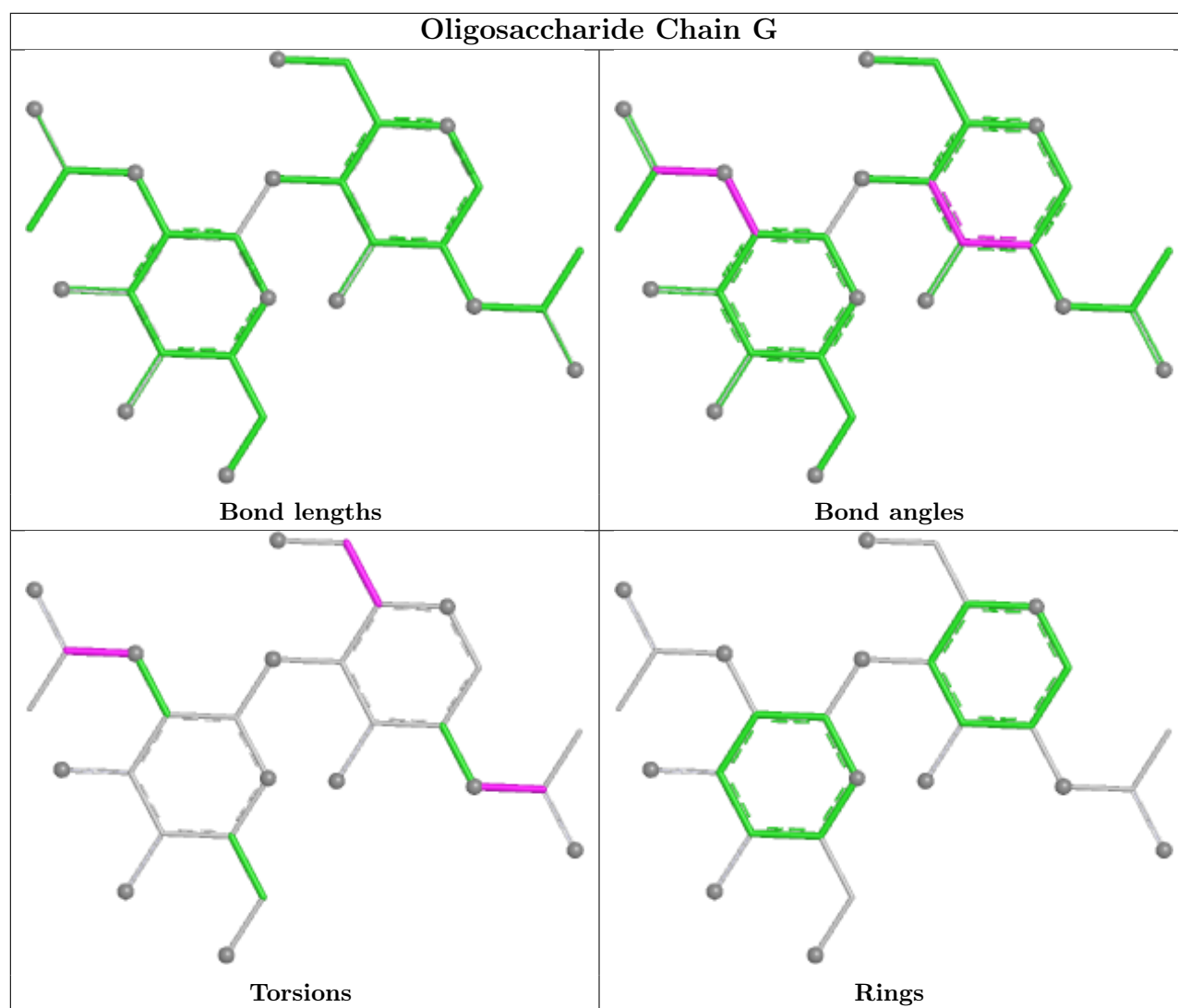
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

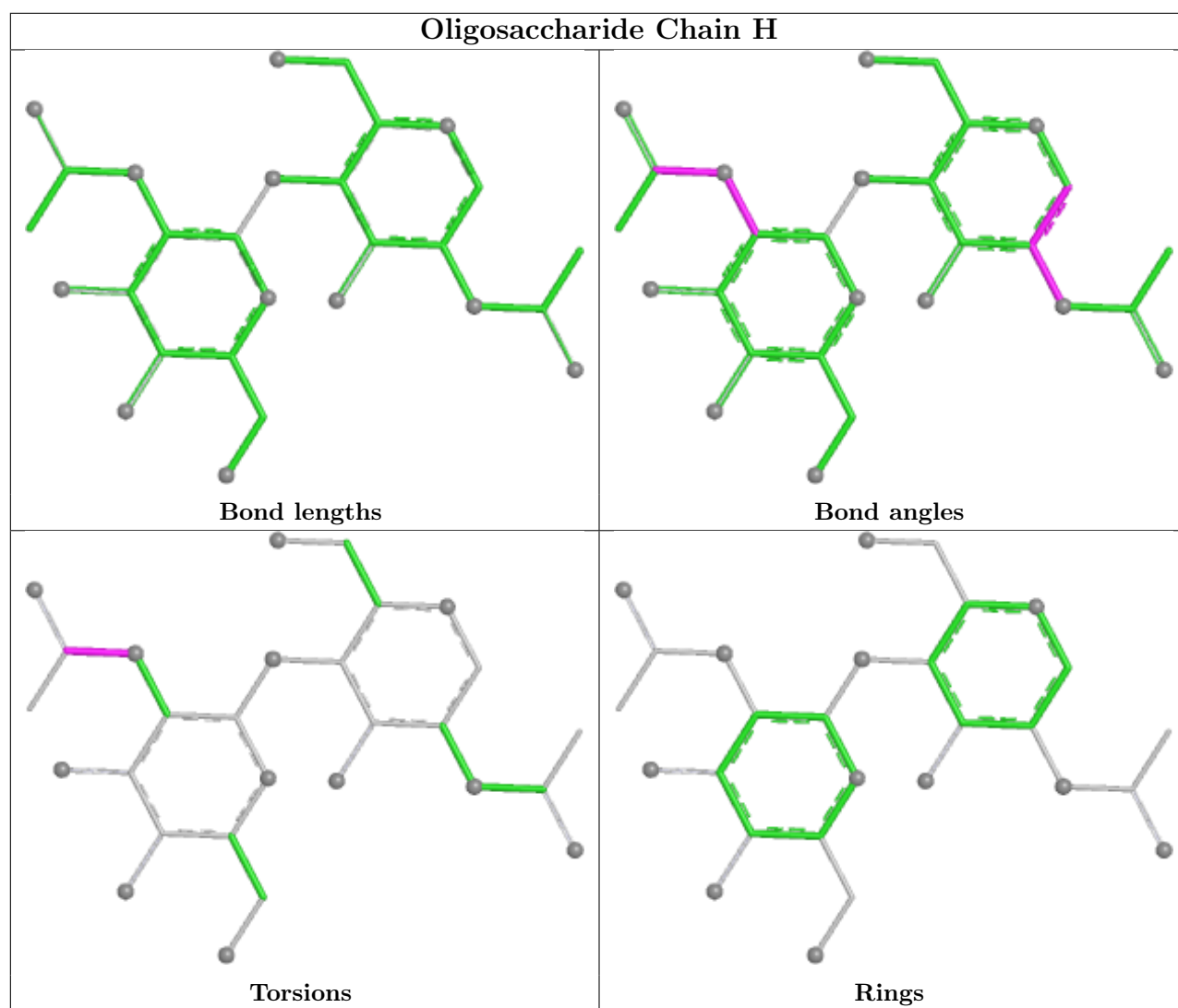


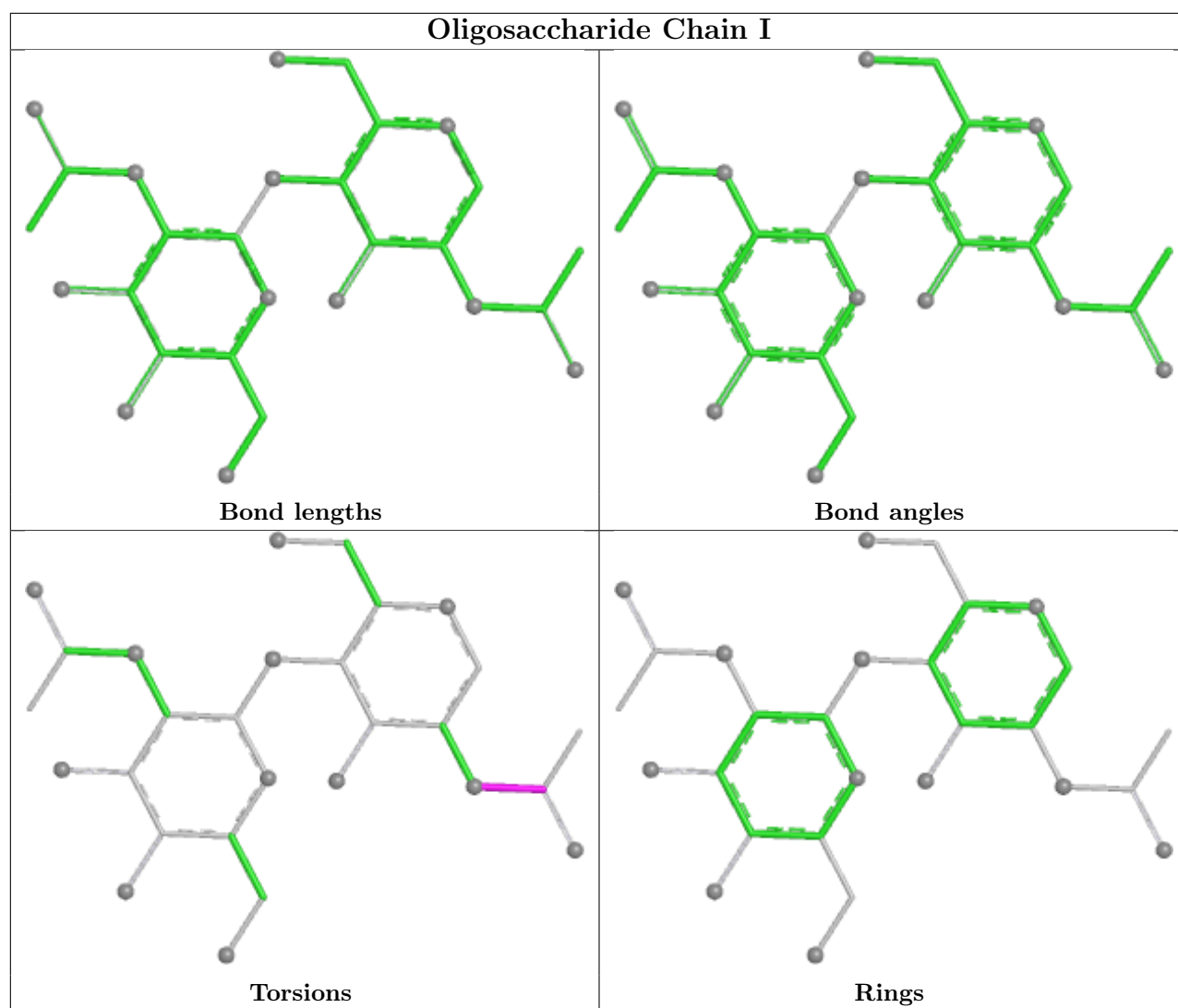


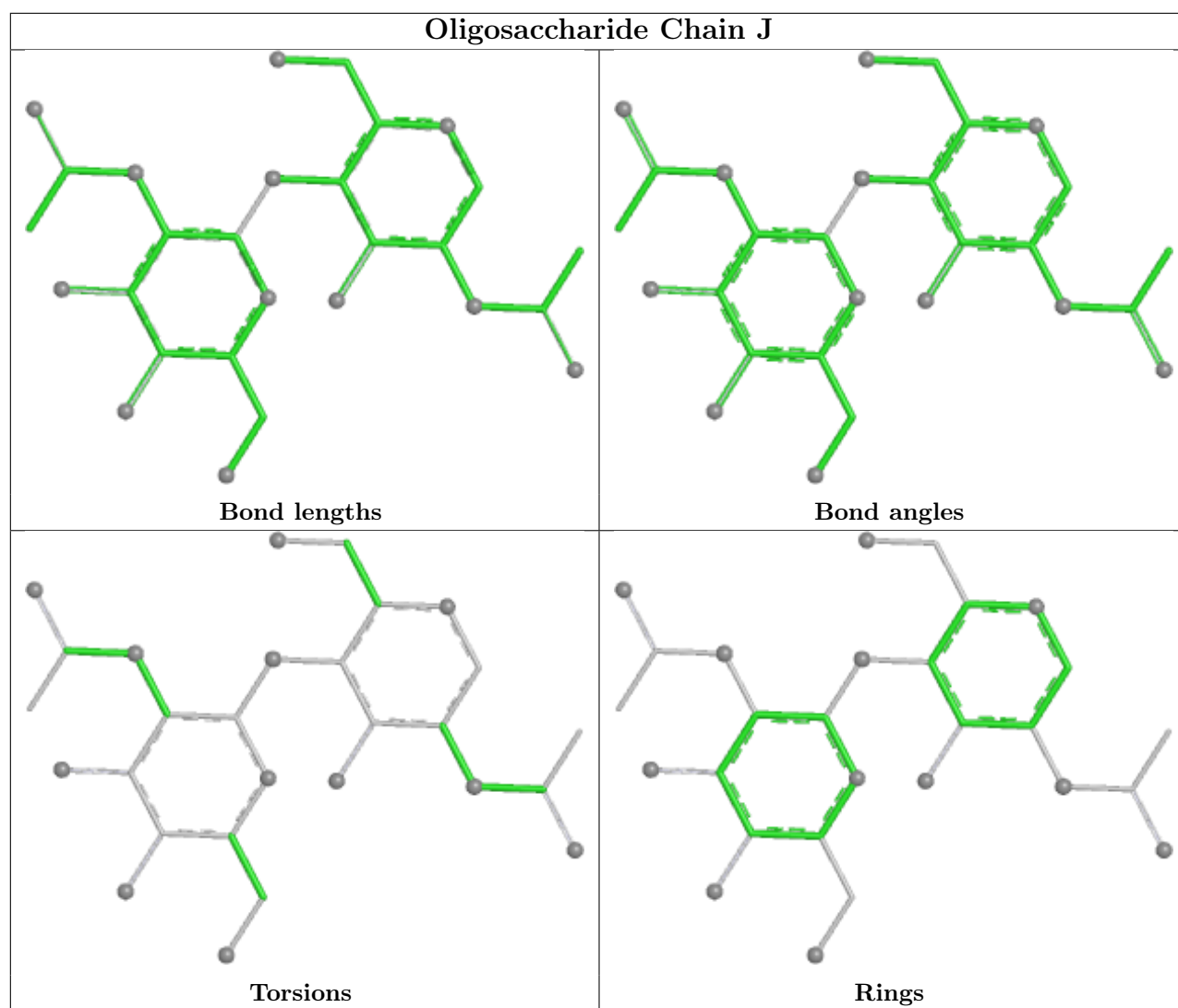


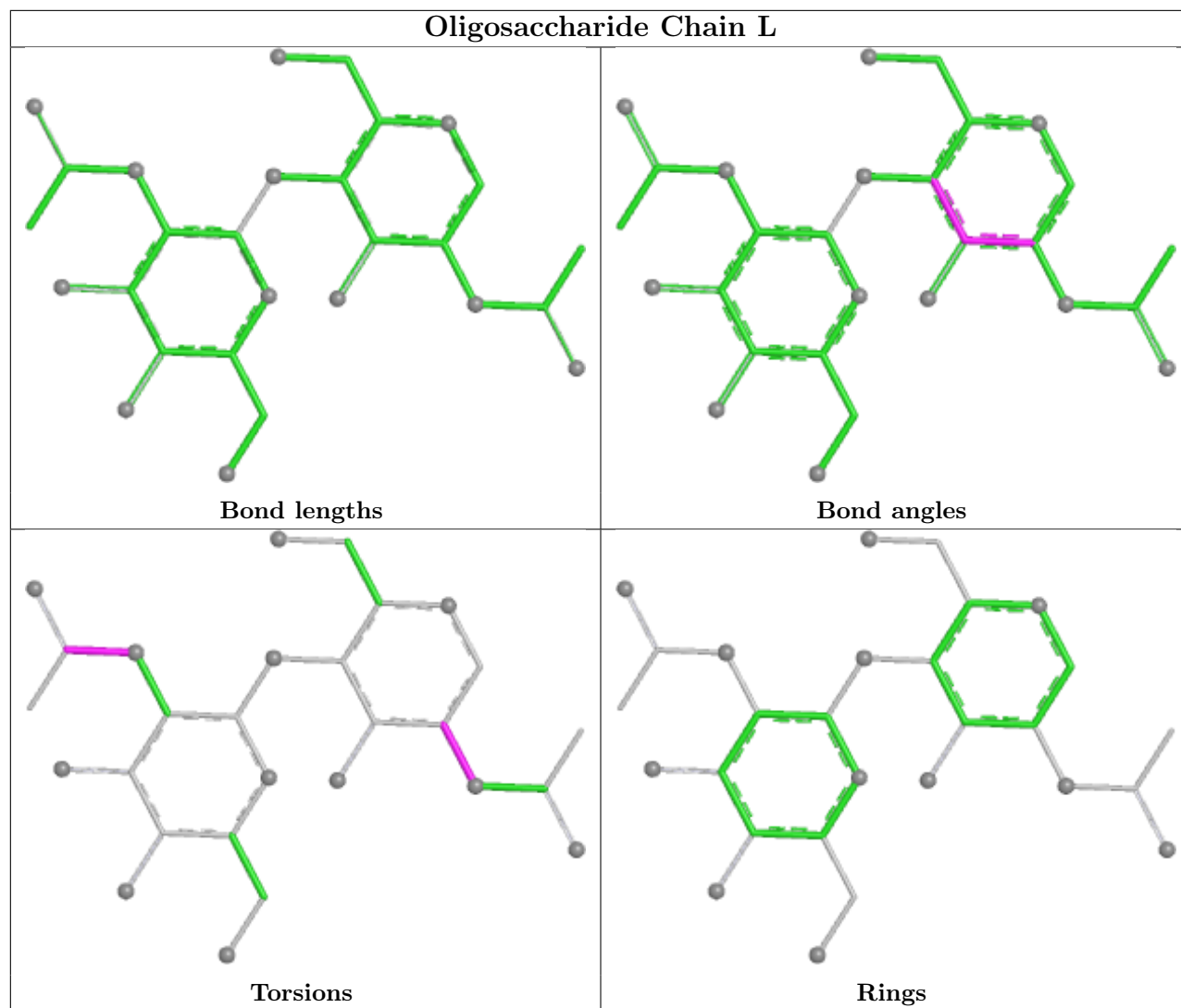


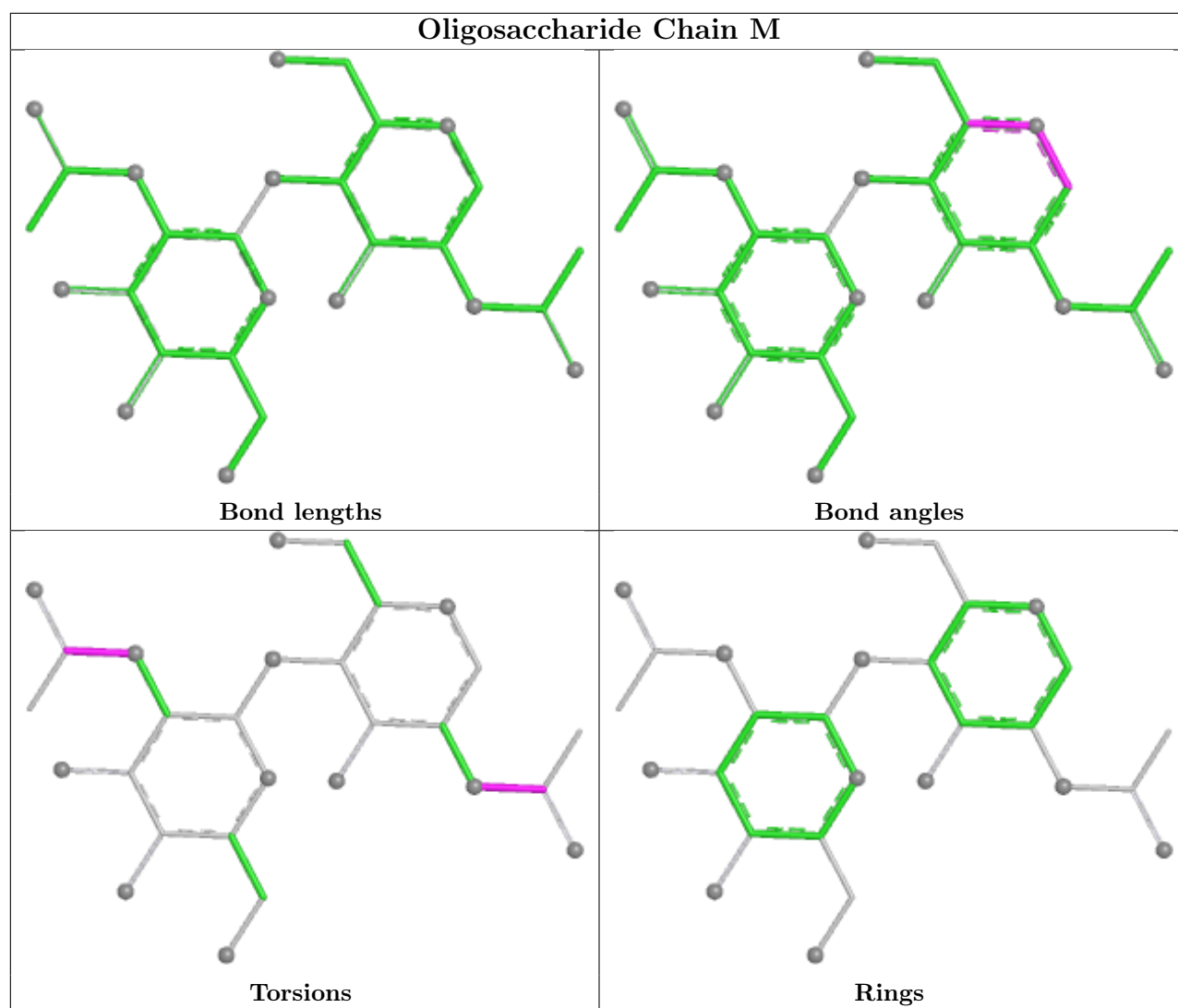


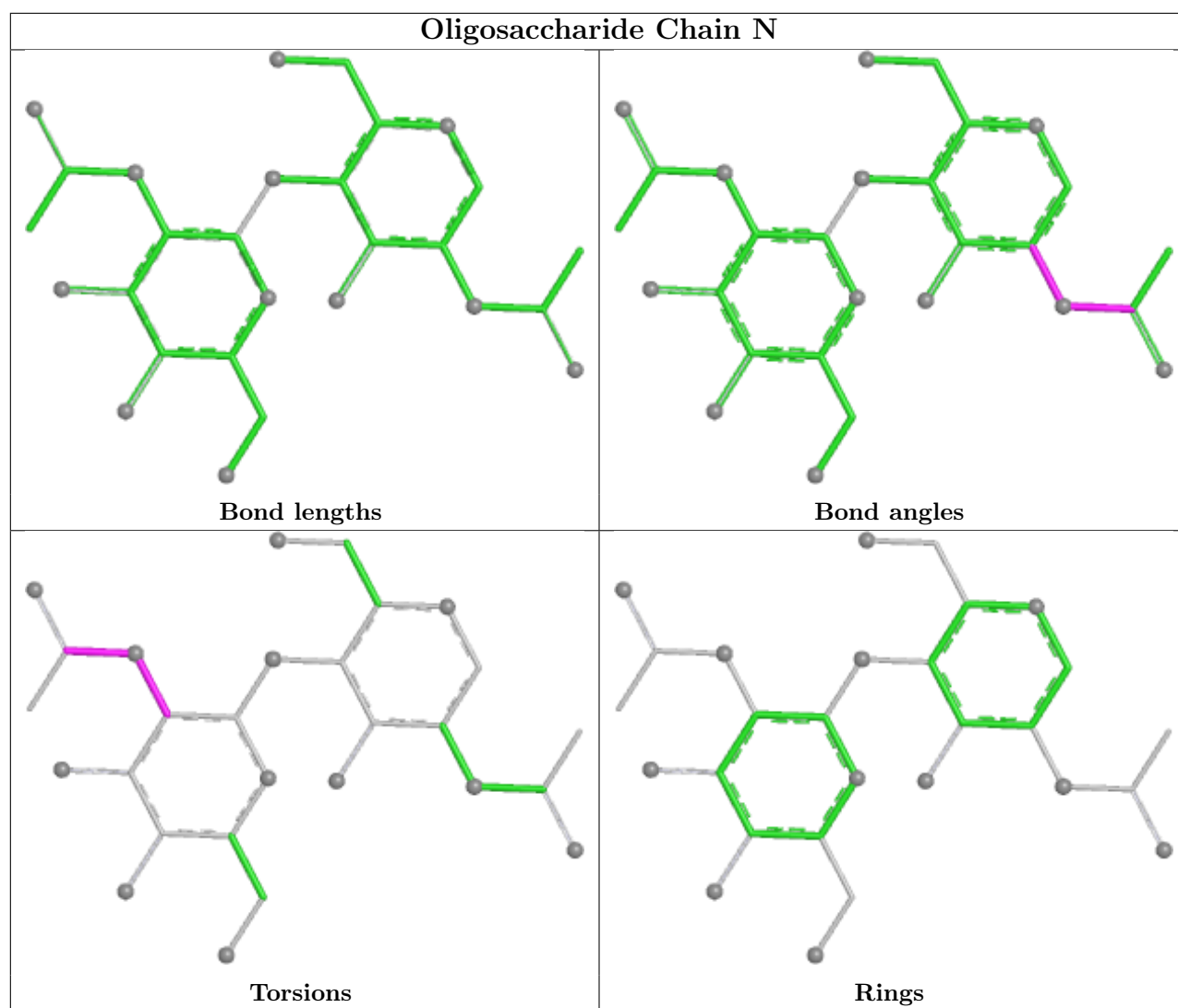


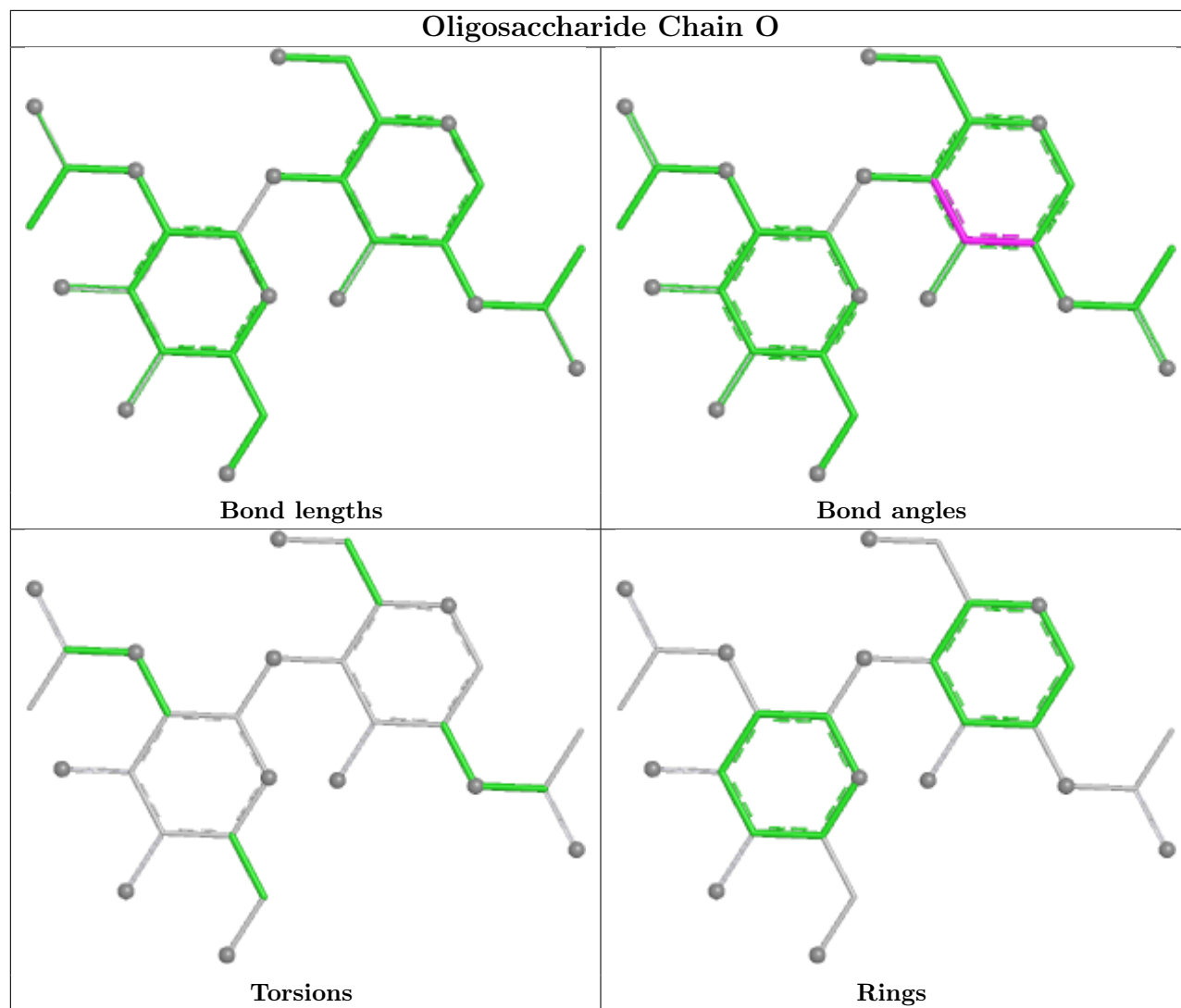


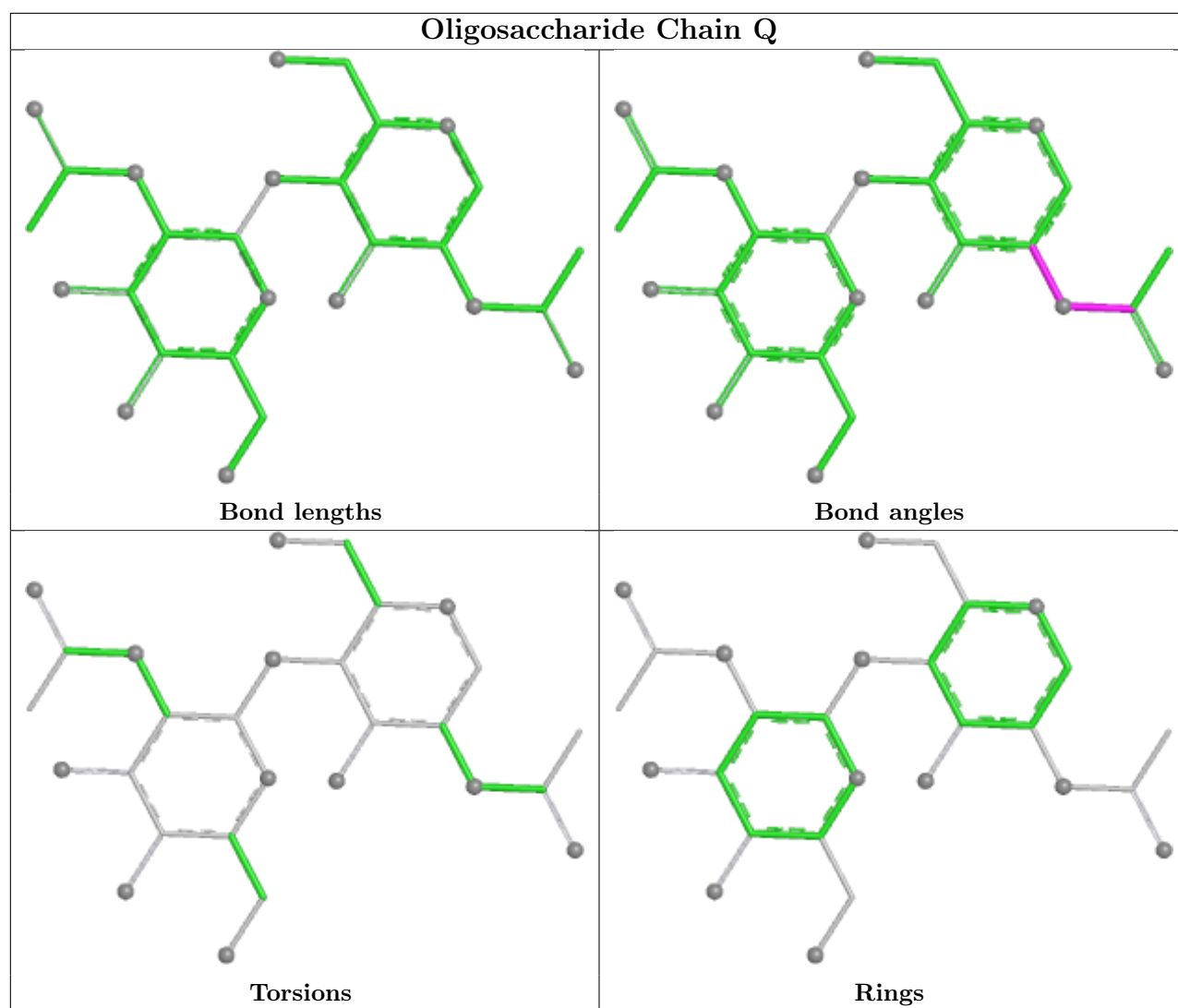


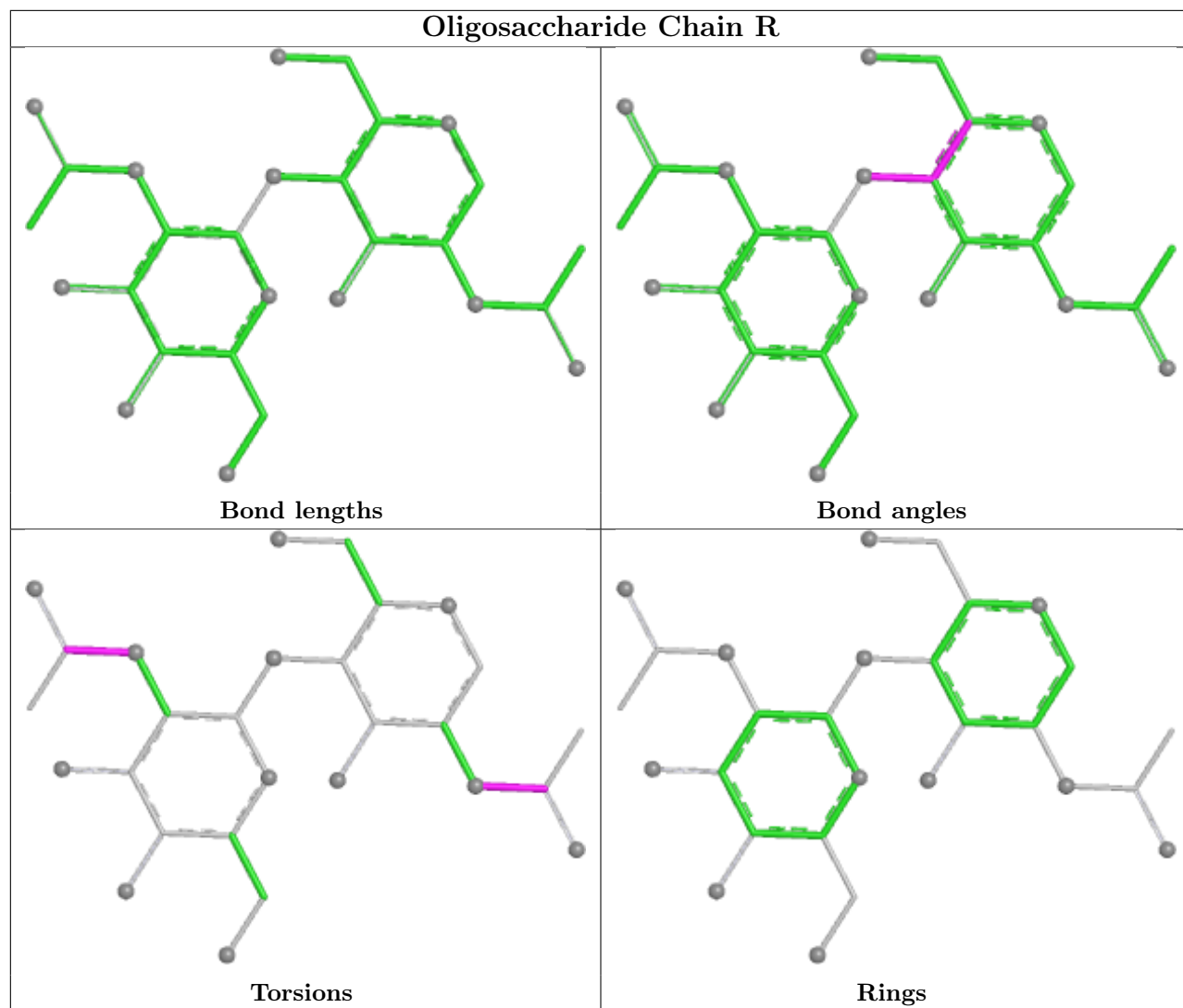


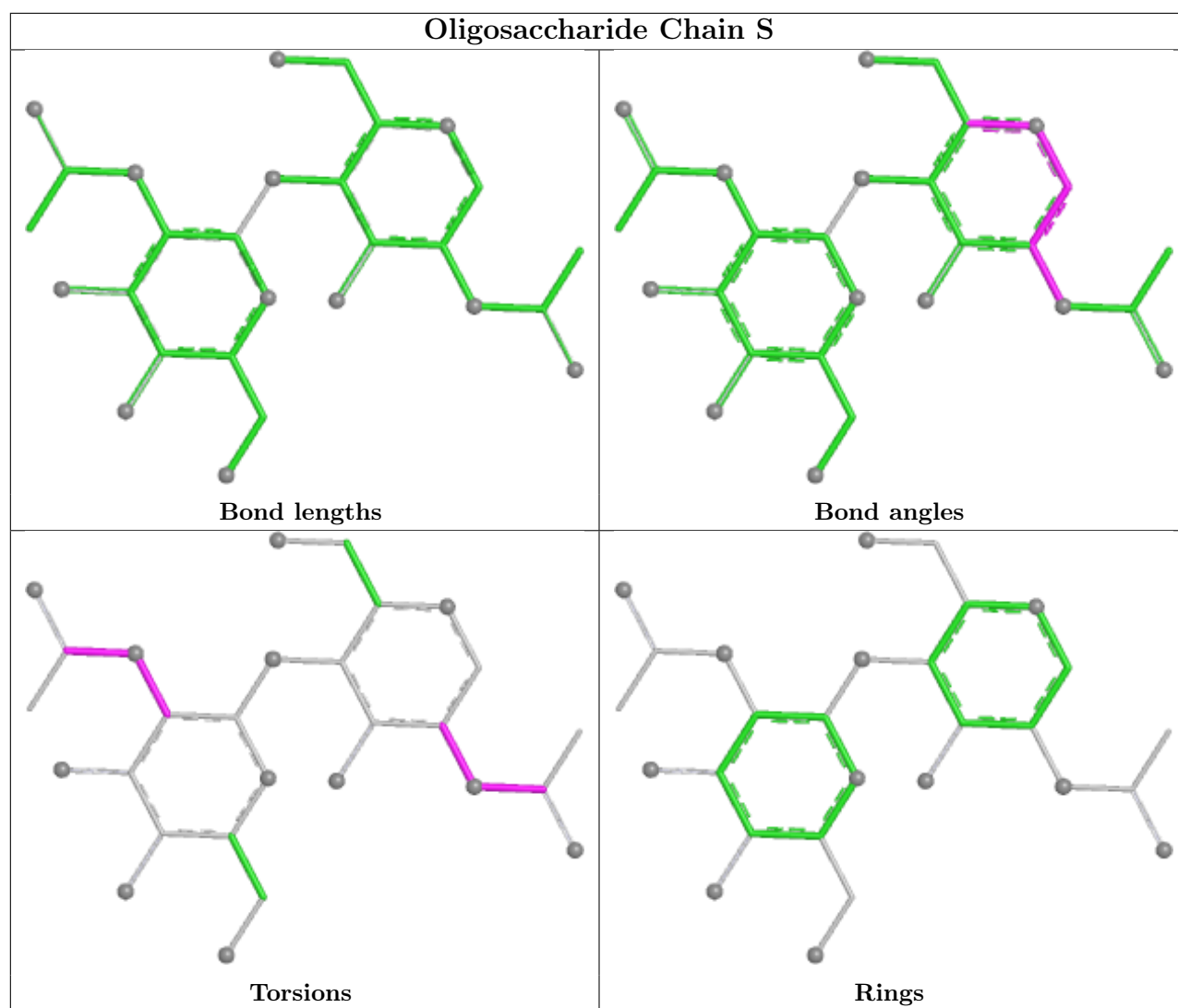


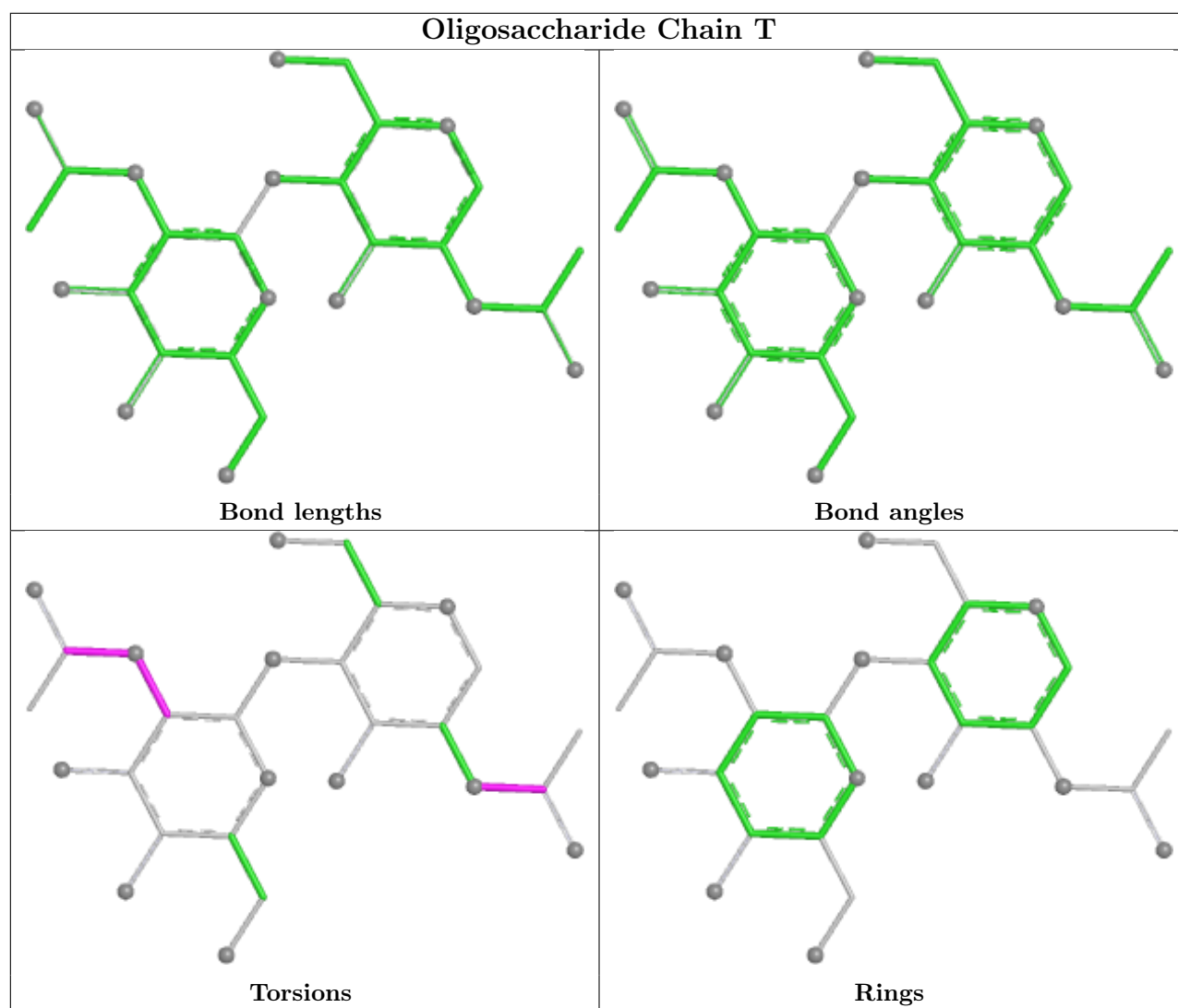


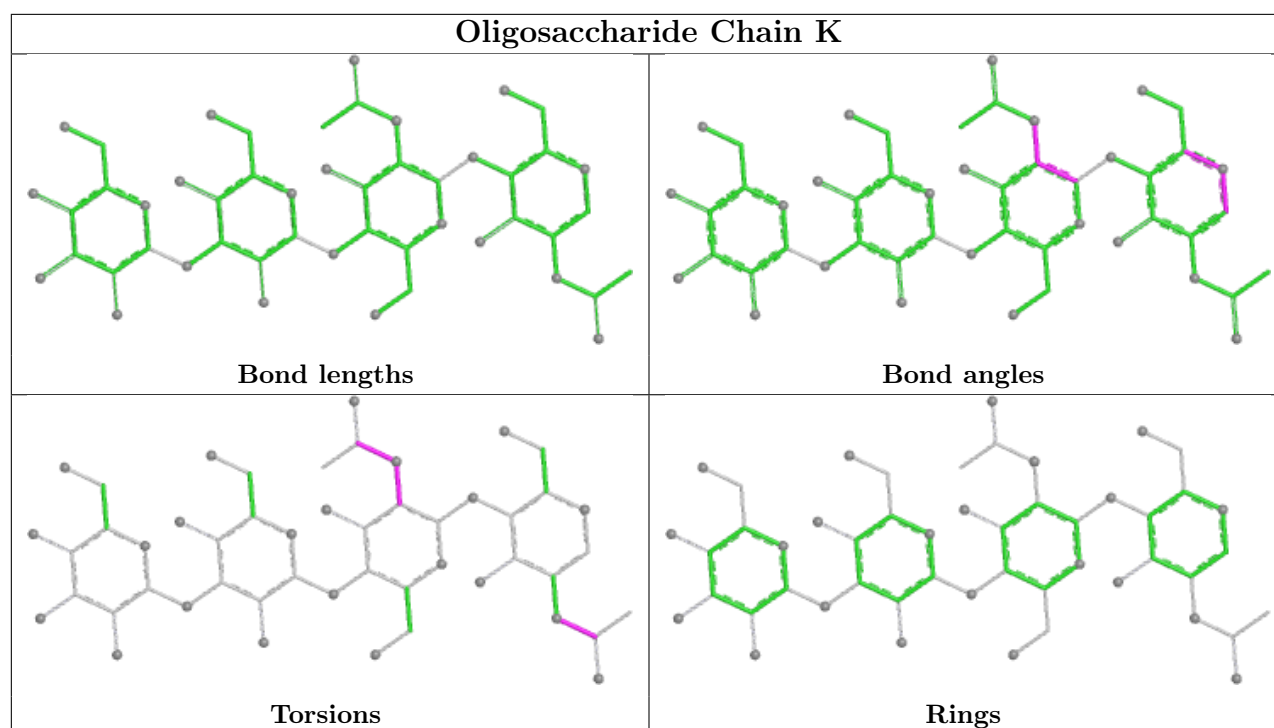












5.6 Ligand geometry [i](#)

32 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	NAG	B	1201	1	14,14,15	0.30	0	17,19,21	0.94	0
5	NAG	C	1201	1	14,14,15	0.31	0	17,19,21	0.74	0
5	NAG	C	1209	1	14,14,15	0.35	0	17,19,21	0.64	0
5	NAG	B	1206	1	14,14,15	0.30	0	17,19,21	0.66	0
5	NAG	A	1211	1	14,14,15	0.68	1 (7%)	17,19,21	1.91	3 (17%)
5	NAG	A	1204	1	14,14,15	0.38	0	17,19,21	0.69	0
5	NAG	B	1205	1	14,14,15	0.28	0	17,19,21	0.91	1 (5%)
5	NAG	B	1209	1	14,14,15	0.46	0	17,19,21	0.98	2 (11%)
5	NAG	A	1203	1	14,14,15	0.40	0	17,19,21	0.82	1 (5%)
5	NAG	C	1202	1	14,14,15	0.37	0	17,19,21	0.66	0
5	NAG	C	1208	1	14,14,15	0.31	0	17,19,21	0.63	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	B	1208	1	14,14,15	0.29	0	17,19,21	0.70	0
5	NAG	C	1207	1	14,14,15	0.38	0	17,19,21	0.69	0
5	NAG	A	1202	1	14,14,15	0.49	0	17,19,21	1.31	1 (5%)
5	NAG	B	1202	1	14,14,15	0.32	0	17,19,21	0.69	0
5	NAG	B	1211	1	14,14,15	0.41	0	17,19,21	1.27	4 (23%)
5	NAG	B	1207	1	14,14,15	0.36	0	17,19,21	0.84	1 (5%)
5	NAG	A	1209	1	14,14,15	0.29	0	17,19,21	0.68	0
5	NAG	B	1210	1	14,14,15	0.33	0	17,19,21	0.74	1 (5%)
5	NAG	A	1210	1	14,14,15	0.32	0	17,19,21	0.74	1 (5%)
5	NAG	A	1207	1	14,14,15	0.31	0	17,19,21	0.68	0
5	NAG	B	1203	1	14,14,15	0.45	0	17,19,21	0.71	1 (5%)
5	NAG	A	1206	1	14,14,15	0.31	0	17,19,21	0.74	0
5	NAG	C	1204	1	14,14,15	0.29	0	17,19,21	0.62	0
5	NAG	C	1205	1	14,14,15	0.25	0	17,19,21	0.62	0
5	NAG	A	1201	1	14,14,15	0.49	0	17,19,21	0.86	1 (5%)
5	NAG	C	1210	1	14,14,15	0.40	0	17,19,21	0.99	1 (5%)
5	NAG	C	1206	1	14,14,15	0.28	0	17,19,21	0.71	0
5	NAG	C	1203	1	14,14,15	0.45	0	17,19,21	0.88	2 (11%)
5	NAG	A	1205	1	14,14,15	0.30	0	17,19,21	1.05	1 (5%)
5	NAG	A	1208	1	14,14,15	0.46	0	17,19,21	0.82	0
5	NAG	B	1204	1	14,14,15	0.39	0	17,19,21	0.60	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	B	1201	1	-	4/6/23/26	0/1/1/1
5	NAG	C	1201	1	-	3/6/23/26	0/1/1/1
5	NAG	C	1209	1	-	3/6/23/26	0/1/1/1
5	NAG	B	1206	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1211	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1204	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1205	1	-	3/6/23/26	0/1/1/1
5	NAG	B	1209	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1203	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1202	1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	C	1208	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1208	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1207	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1202	1	-	1/6/23/26	0/1/1/1
5	NAG	B	1202	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1211	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1207	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1209	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1210	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1210	1	-	4/6/23/26	0/1/1/1
5	NAG	A	1207	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1203	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1206	1	-	1/6/23/26	0/1/1/1
5	NAG	C	1204	1	-	4/6/23/26	0/1/1/1
5	NAG	C	1205	1	-	3/6/23/26	0/1/1/1
5	NAG	A	1201	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1210	1	-	0/6/23/26	0/1/1/1
5	NAG	C	1206	1	-	3/6/23/26	0/1/1/1
5	NAG	C	1203	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1205	1	-	3/6/23/26	0/1/1/1
5	NAG	A	1208	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1204	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)
5	A	1211	NAG	C1-C2	2.02	1.55	1.52

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1211	NAG	O5-C1-C2	-5.23	103.20	111.29
5	A	1211	NAG	C1-O5-C5	4.45	118.14	112.19
5	A	1202	NAG	C2-N2-C7	-3.86	117.73	122.90
5	C	1210	NAG	C4-C3-C2	-3.06	106.53	111.02
5	B	1211	NAG	C2-N2-C7	-2.79	119.16	122.90

There are no chirality outliers.

5 of 66 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	1202	NAG	C8-C7-N2-C2
5	B	1202	NAG	O7-C7-N2-C2
5	B	1205	NAG	C3-C2-N2-C7
5	B	1205	NAG	C8-C7-N2-C2
5	B	1205	NAG	O7-C7-N2-C2

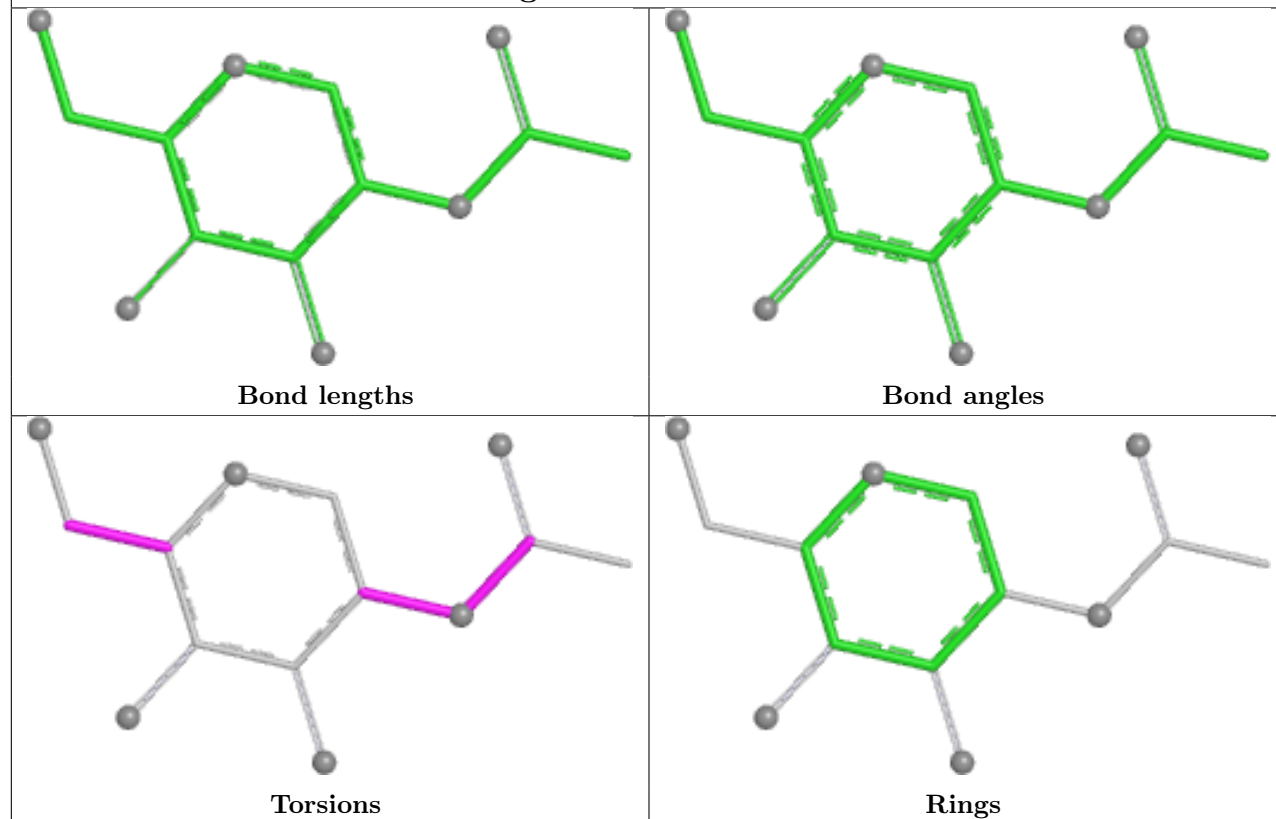
There are no ring outliers.

8 monomers are involved in 17 short contacts:

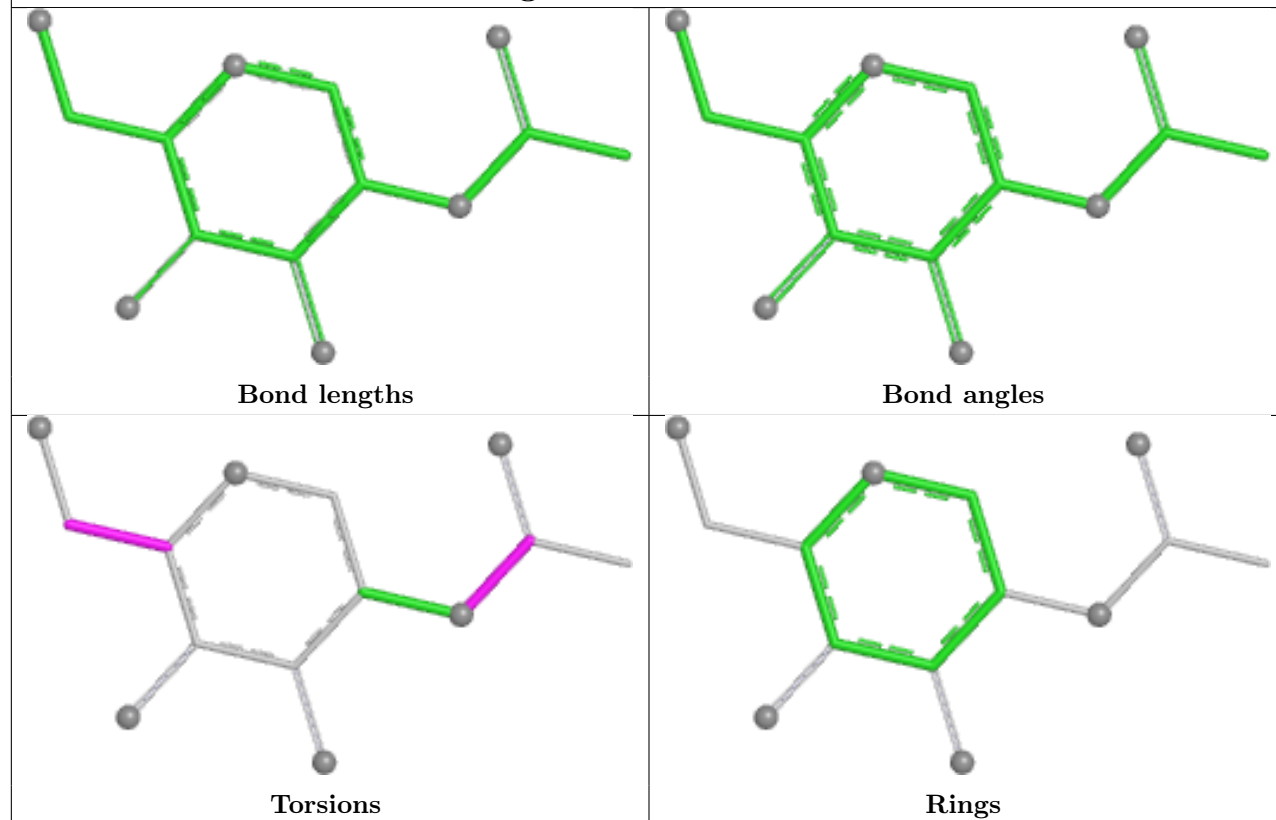
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	1201	NAG	3	0
5	A	1211	NAG	2	0
5	A	1202	NAG	5	0
5	B	1211	NAG	2	0
5	B	1207	NAG	1	0
5	B	1210	NAG	2	0
5	C	1205	NAG	1	0
5	C	1210	NAG	1	0

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.

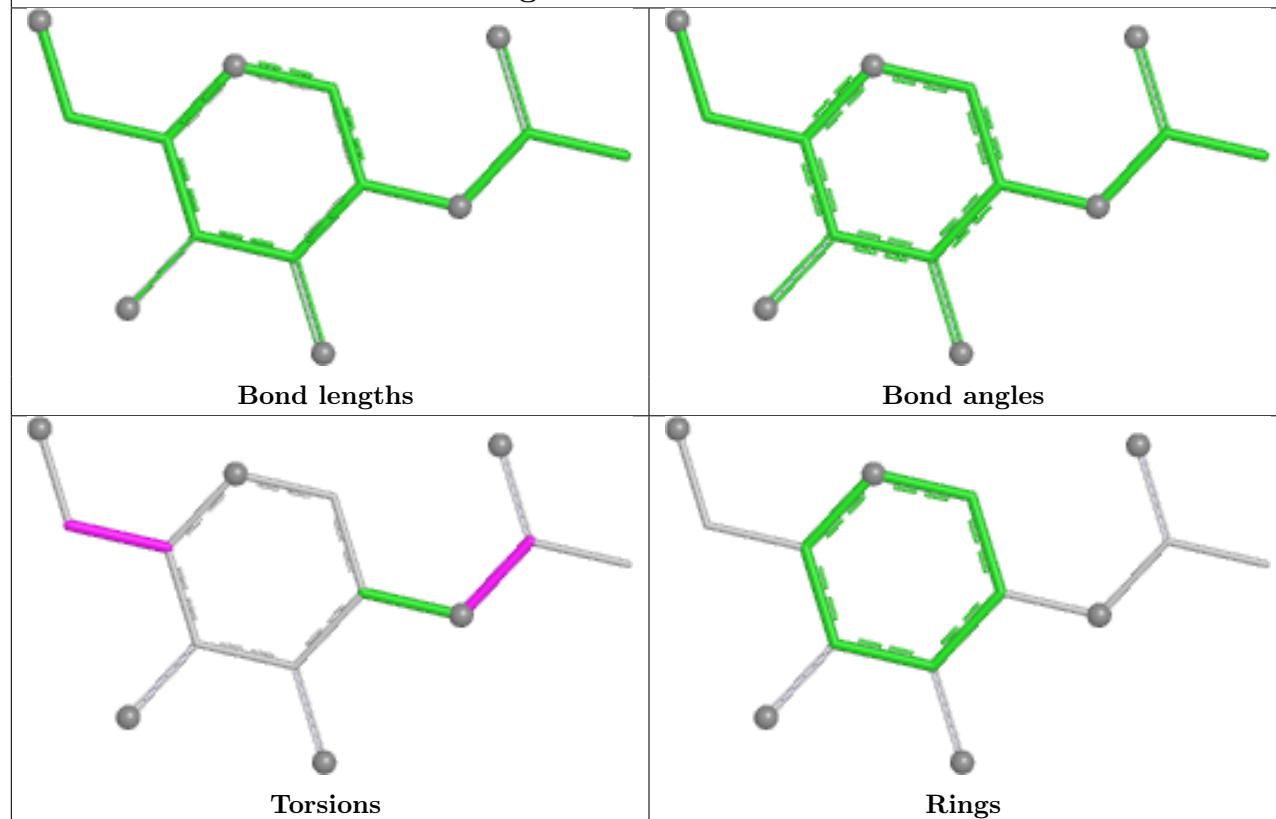
Ligand NAG B 1201



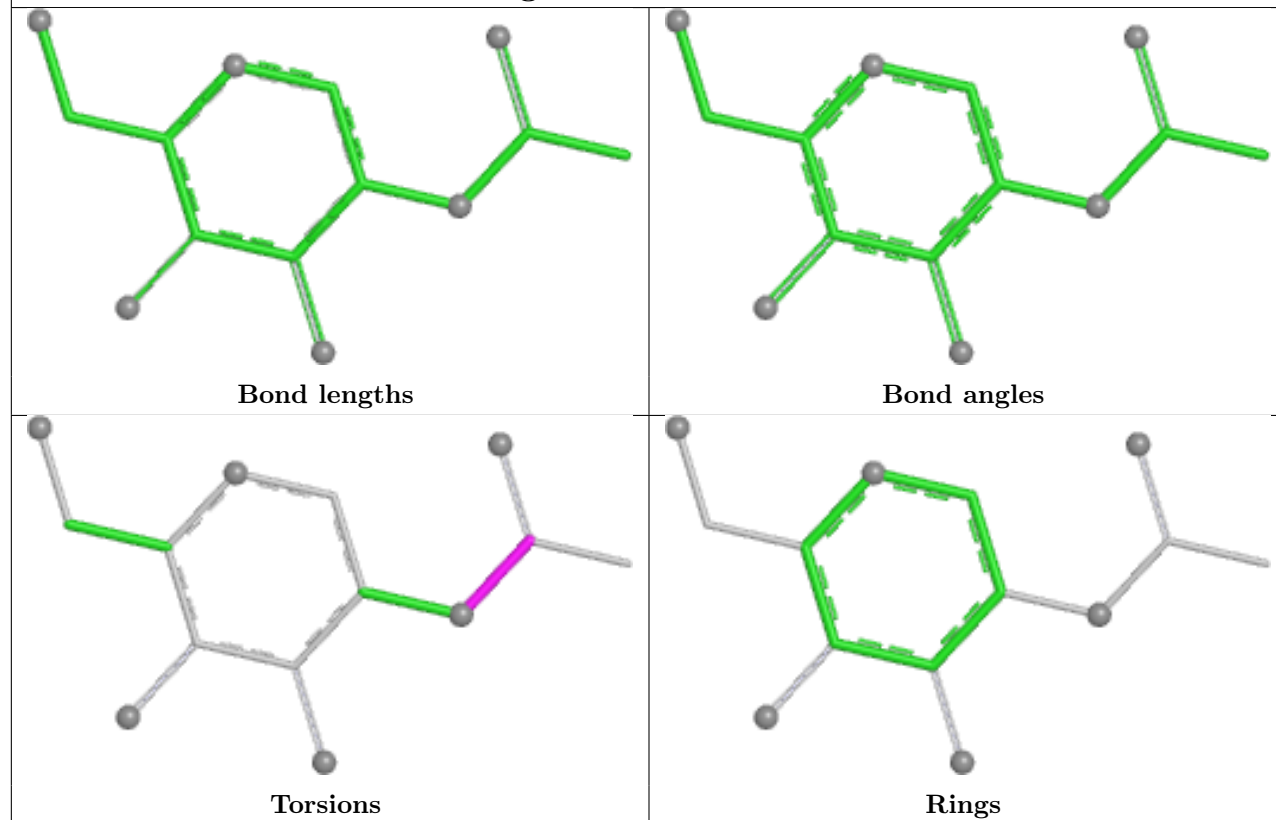
Ligand NAG C 1201



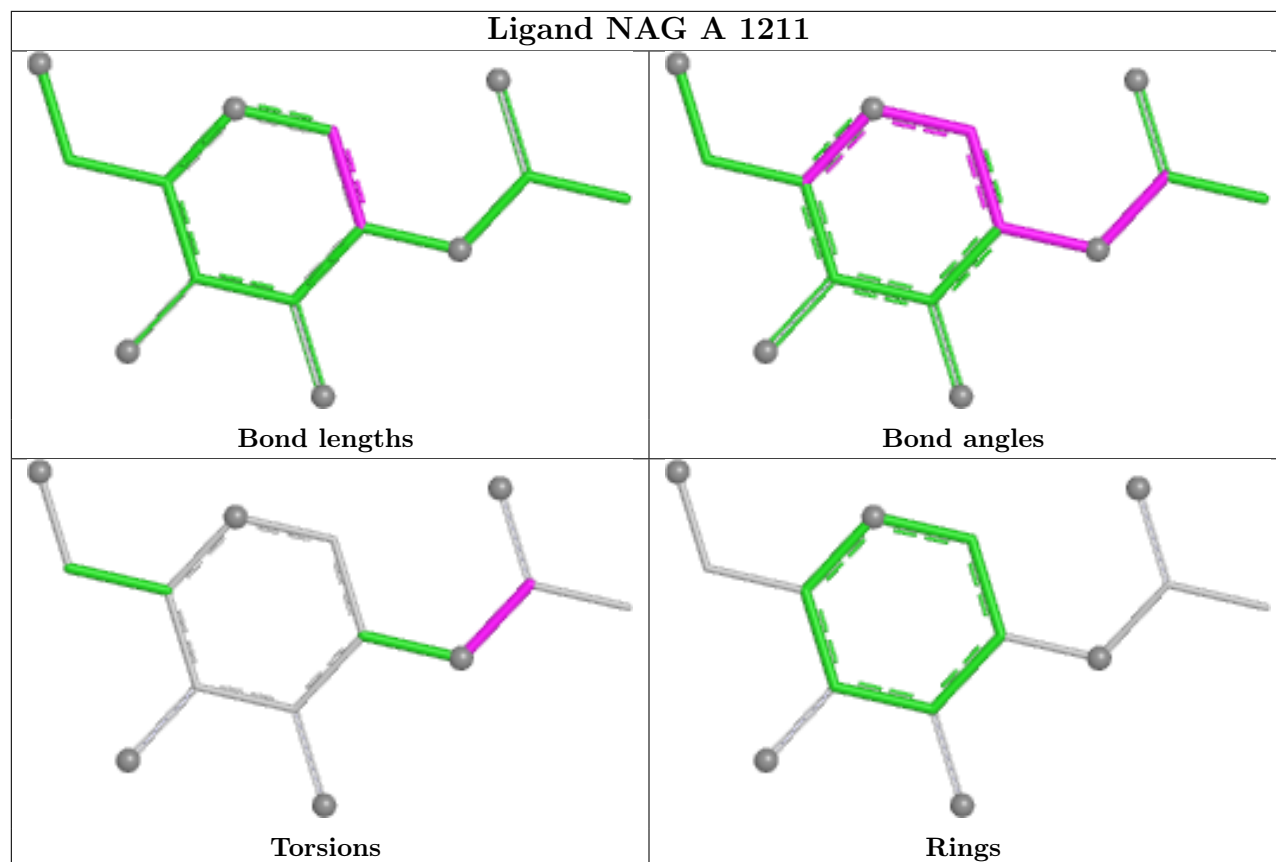
Ligand NAG C 1209



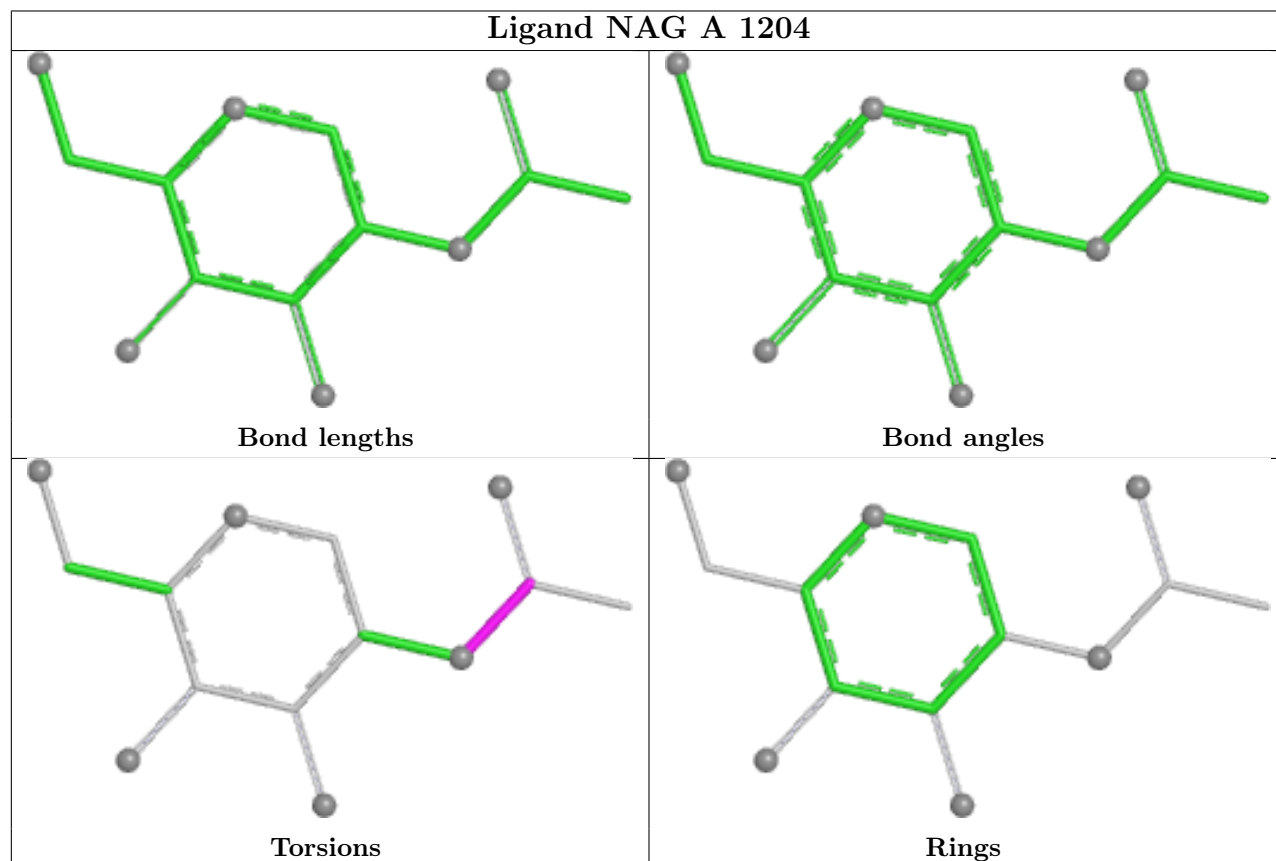
Ligand NAG B 1206



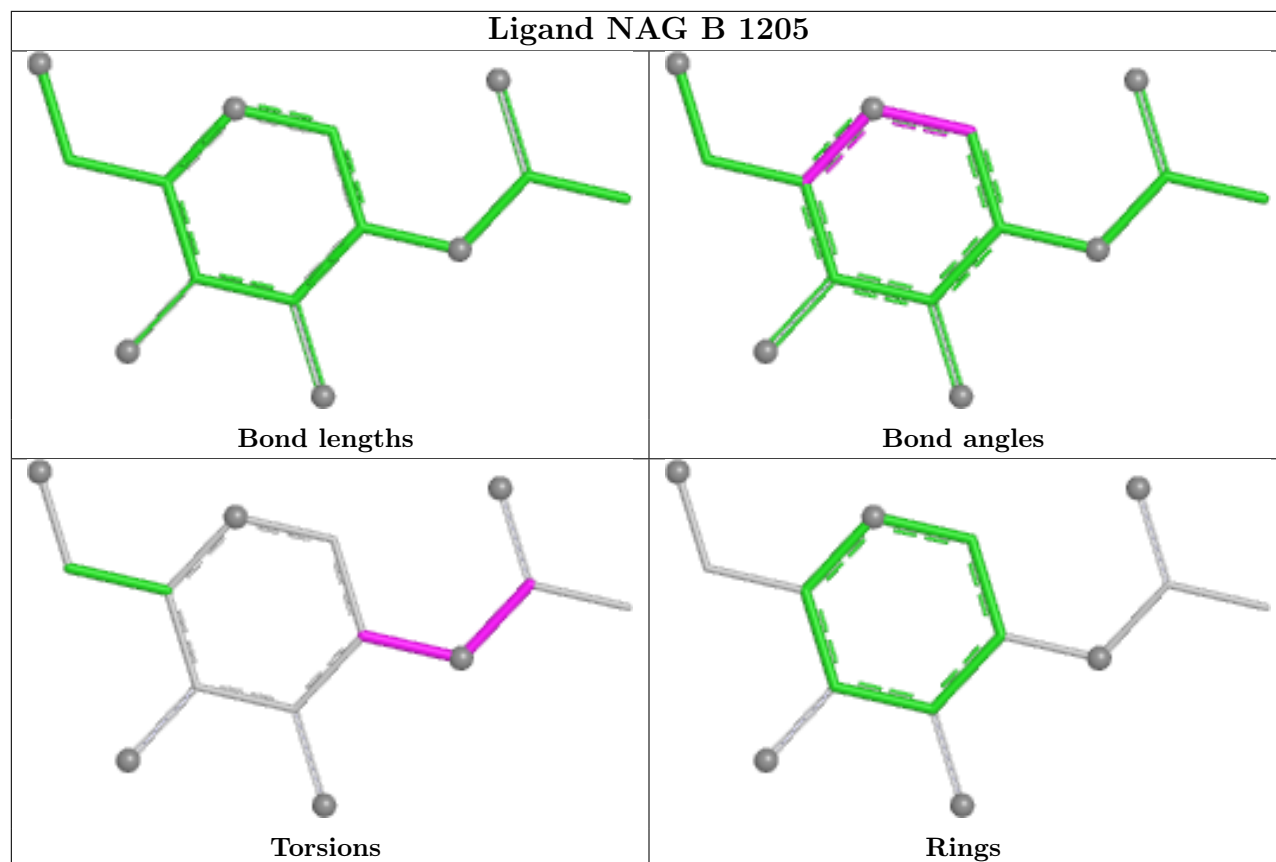
Ligand NAG A 1211



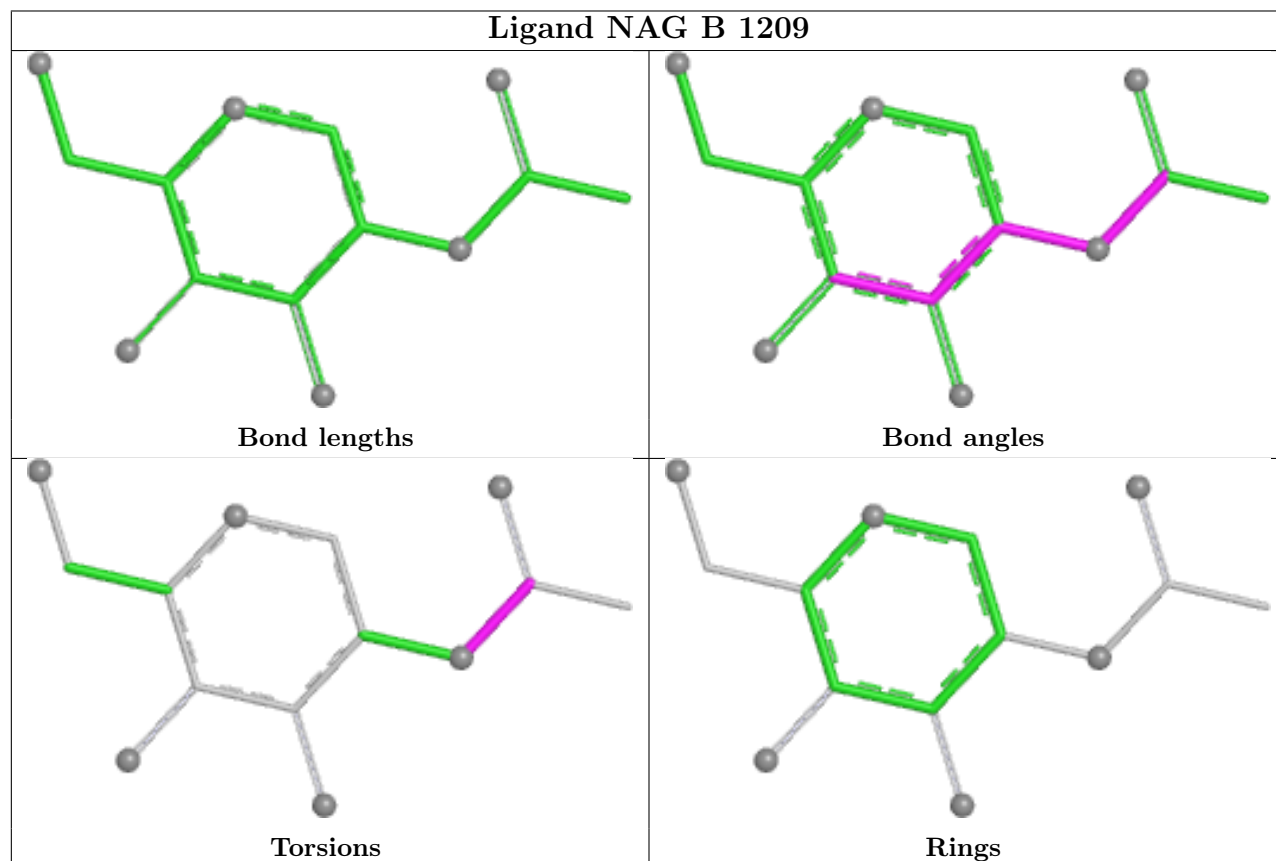
Ligand NAG A 1204



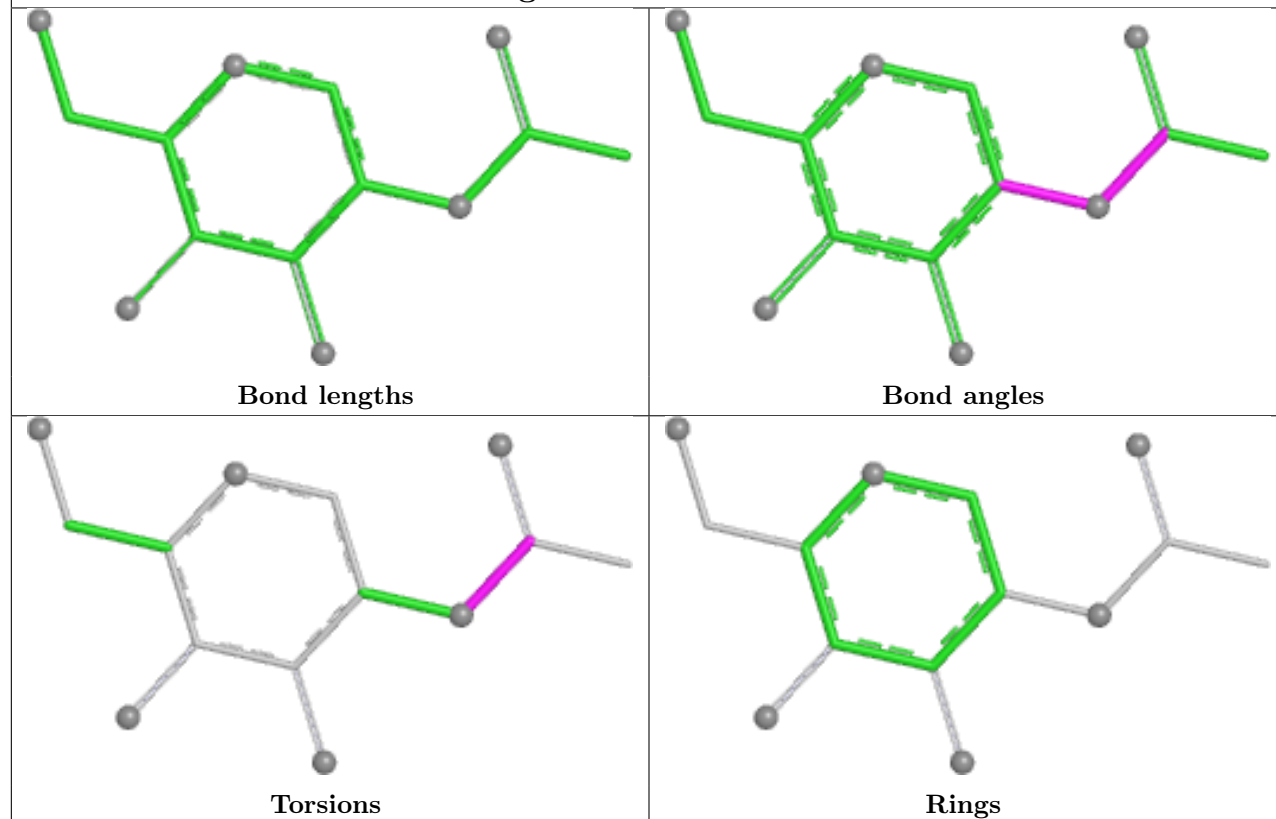
Ligand NAG B 1205



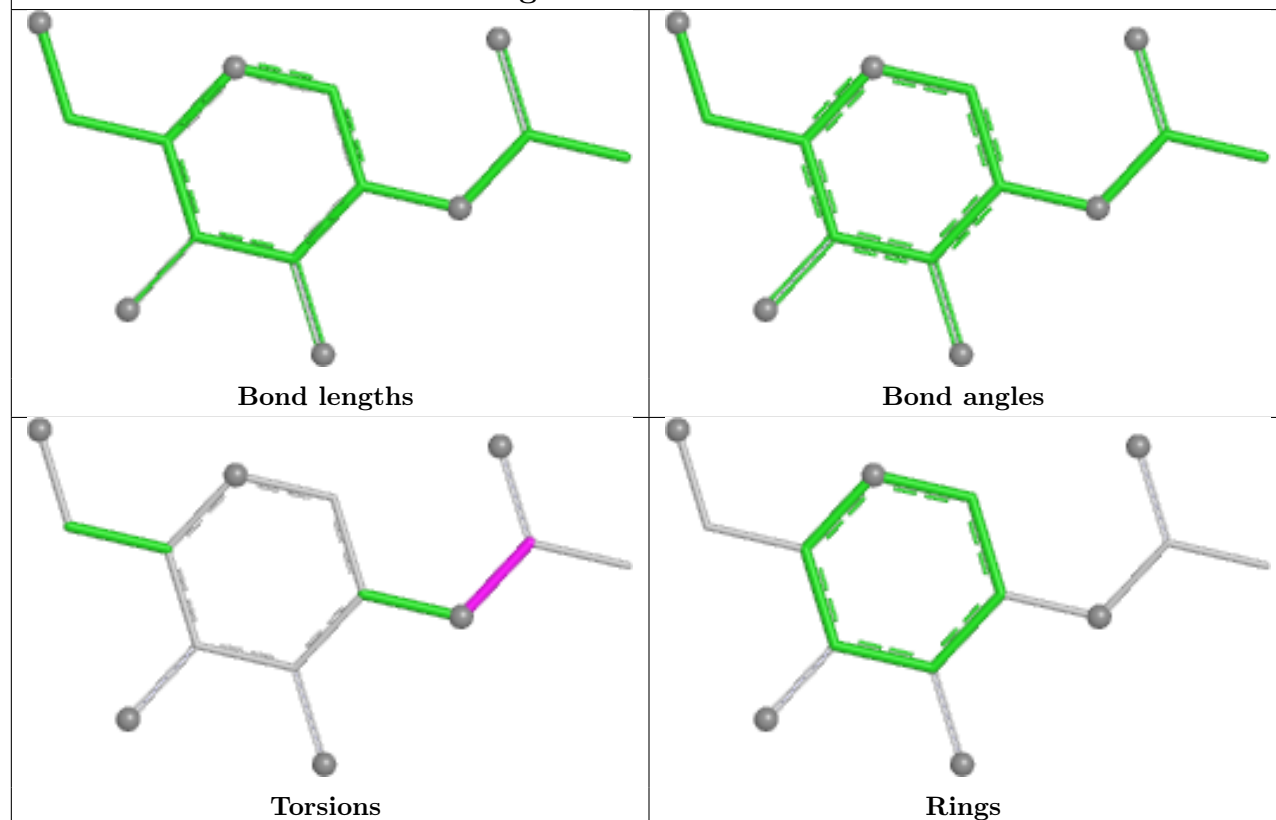
Ligand NAG B 1209



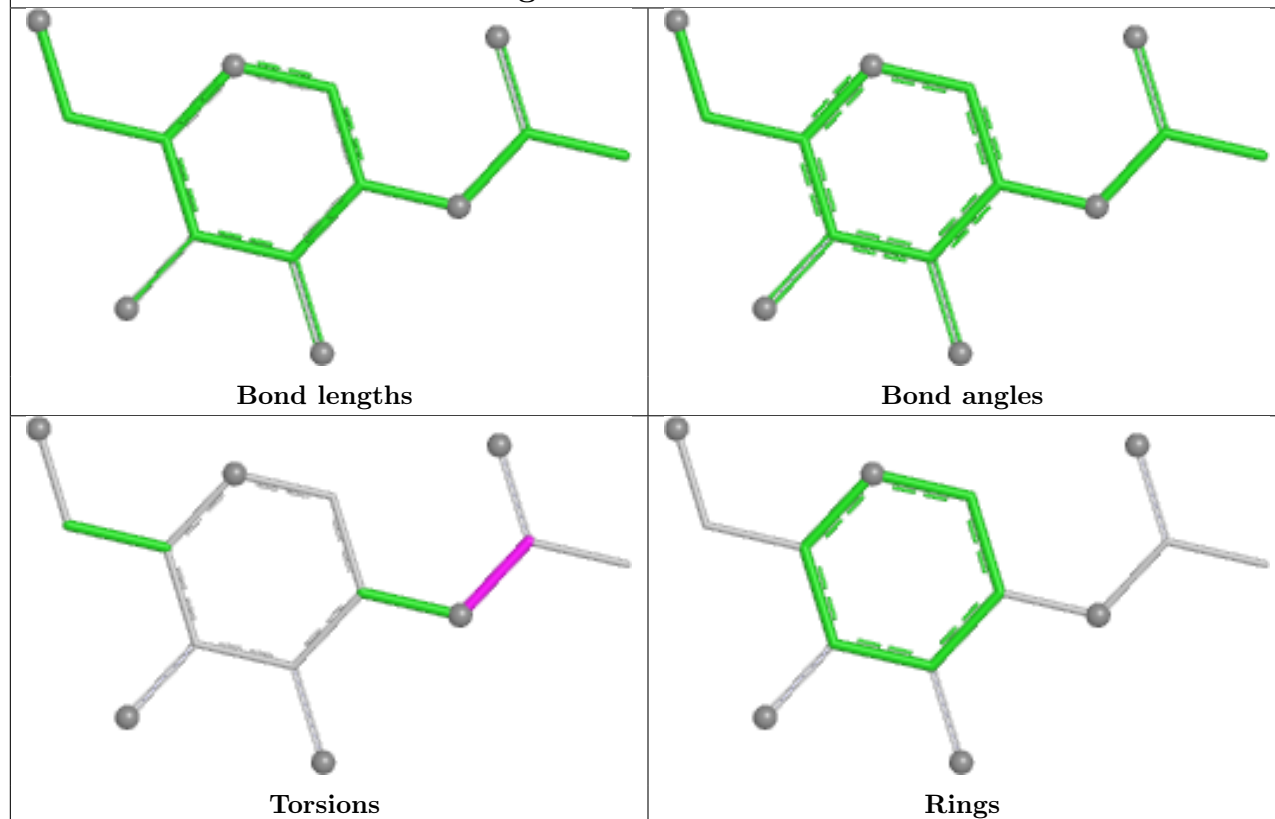
Ligand NAG A 1203



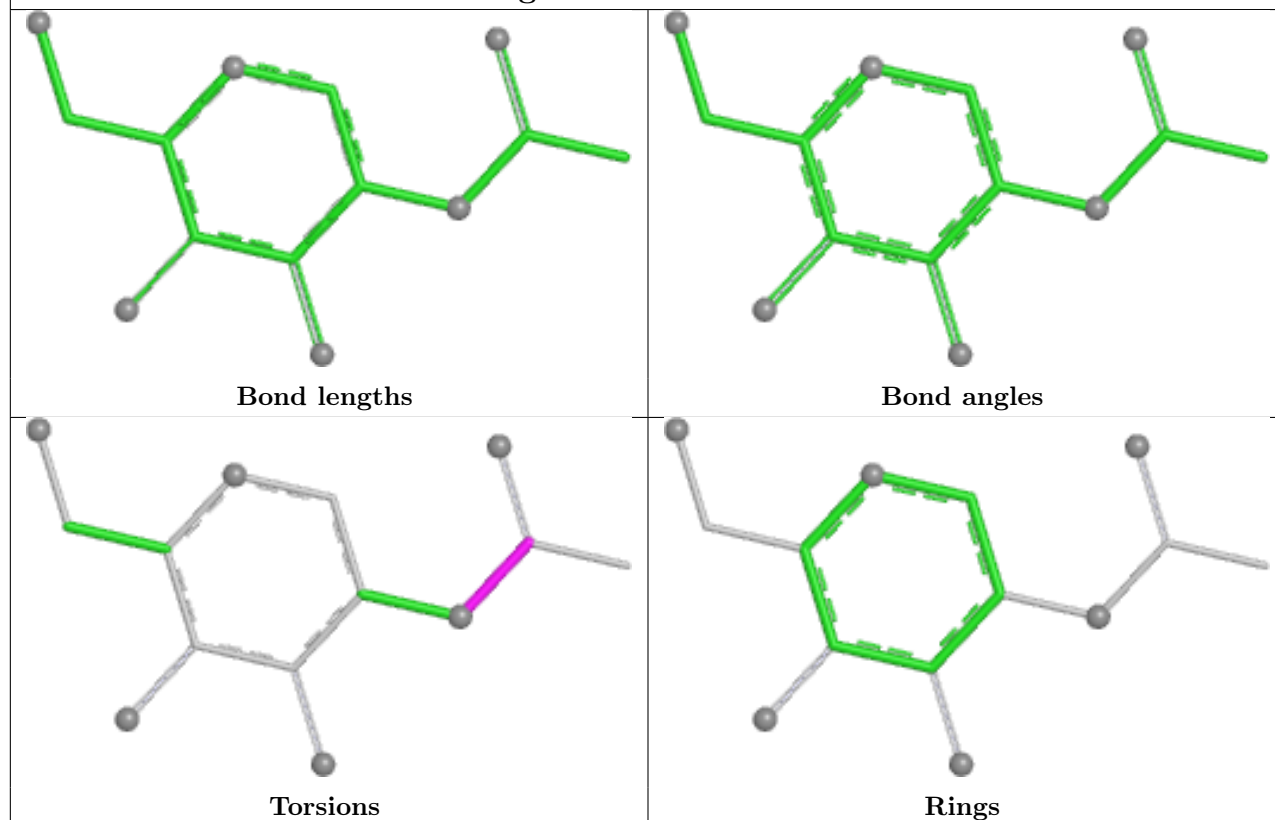
Ligand NAG C 1202



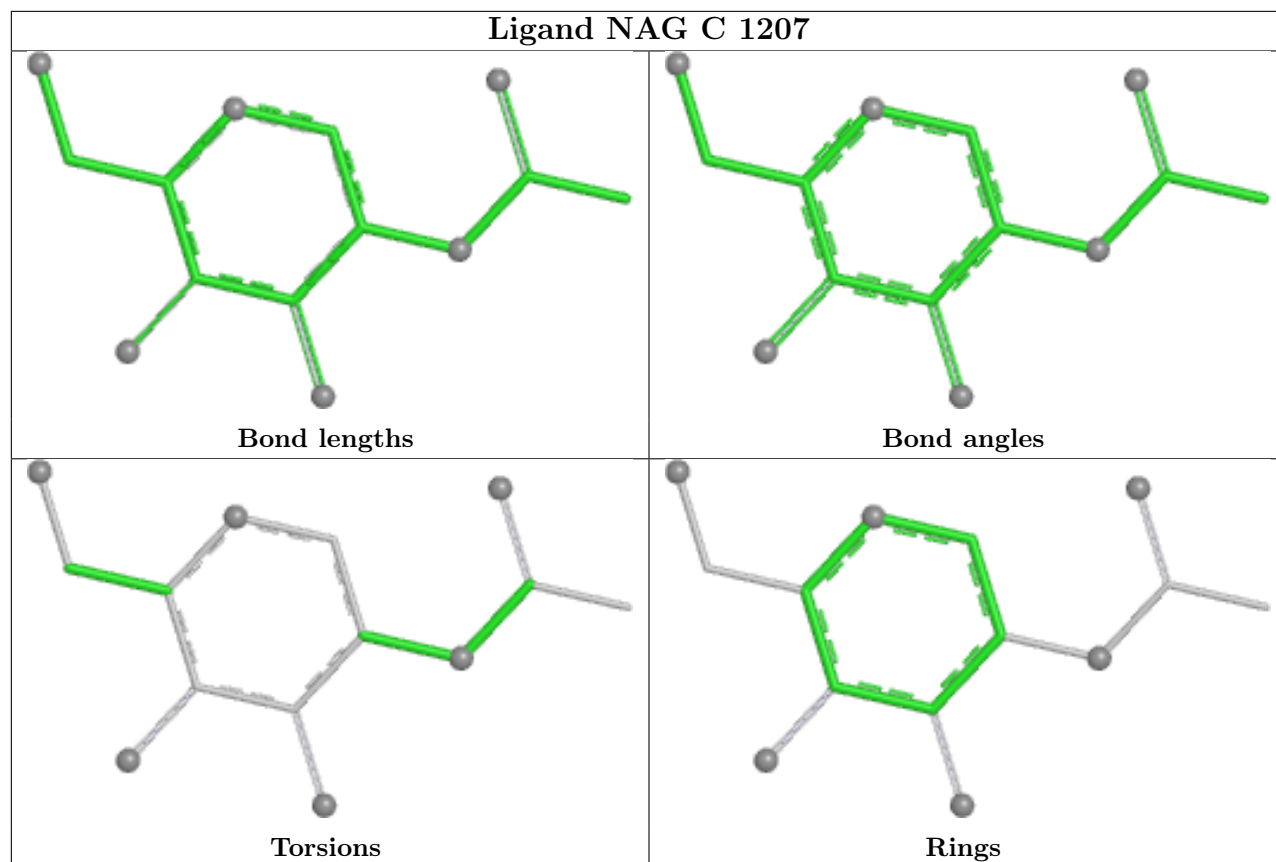
Ligand NAG C 1208



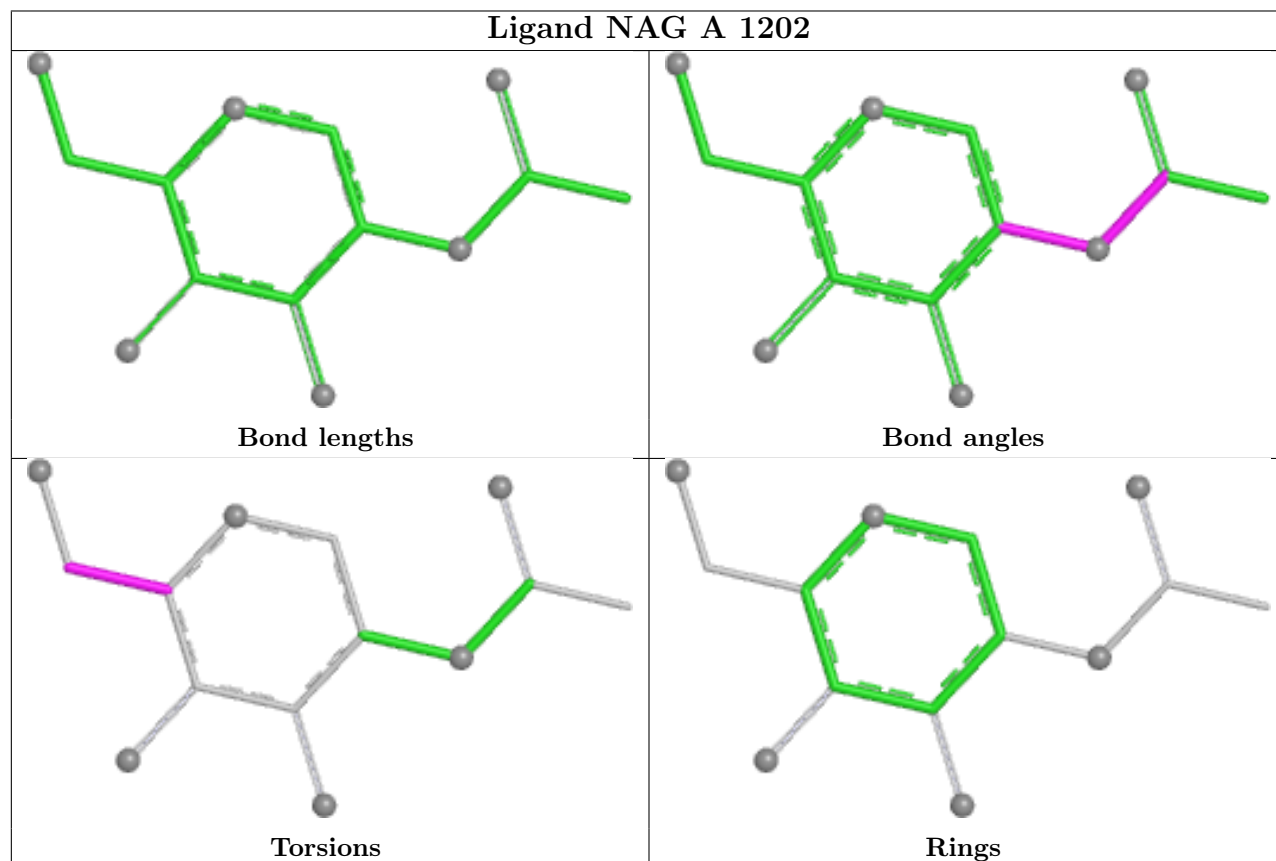
Ligand NAG B 1208



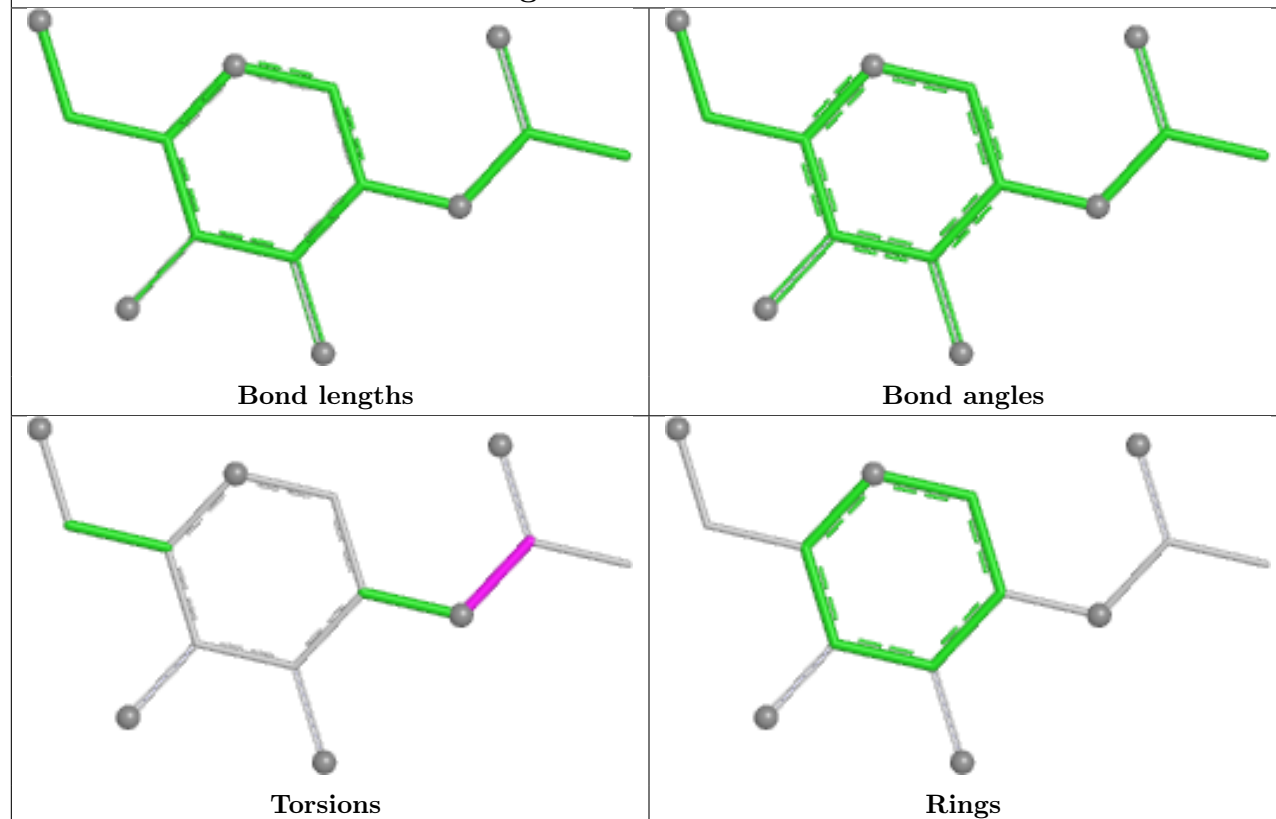
Ligand NAG C 1207



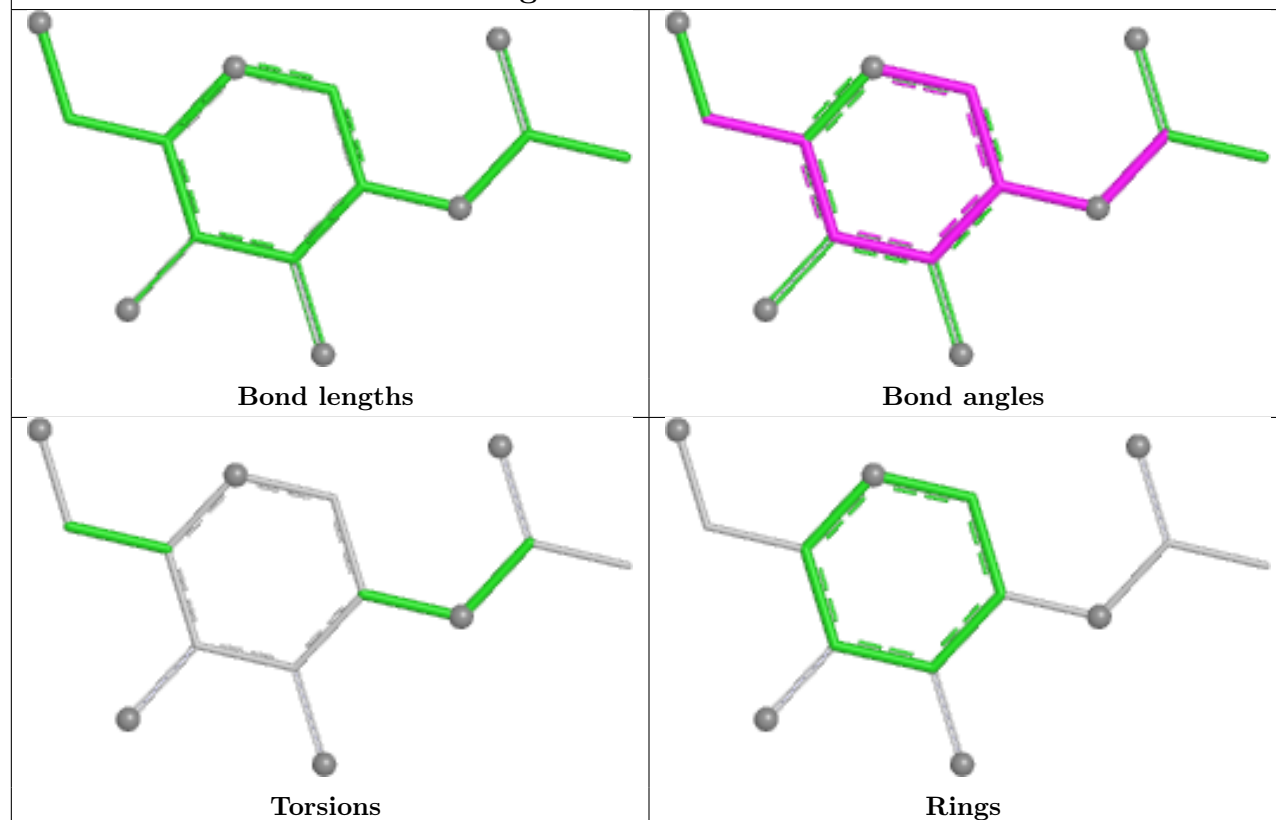
Ligand NAG A 1202



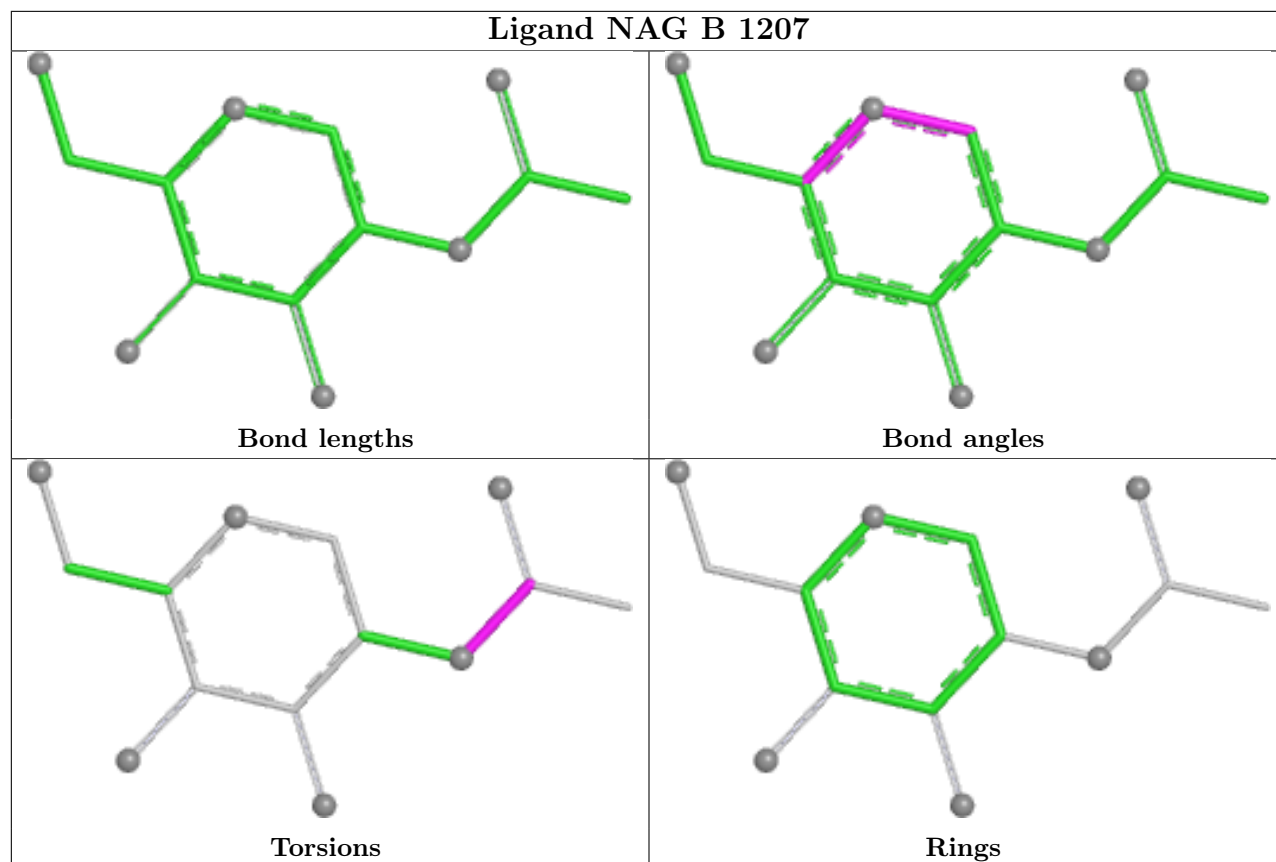
Ligand NAG B 1202



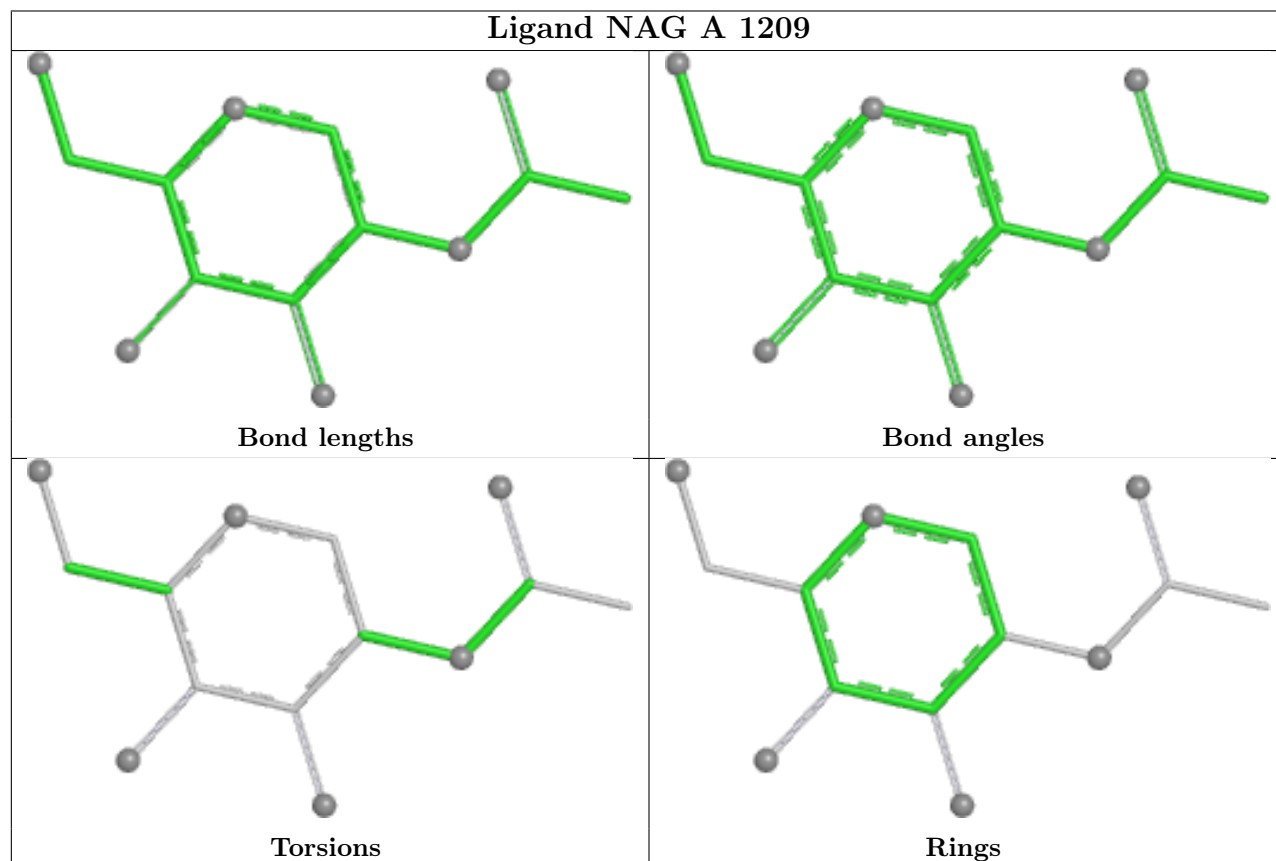
Ligand NAG B 1211



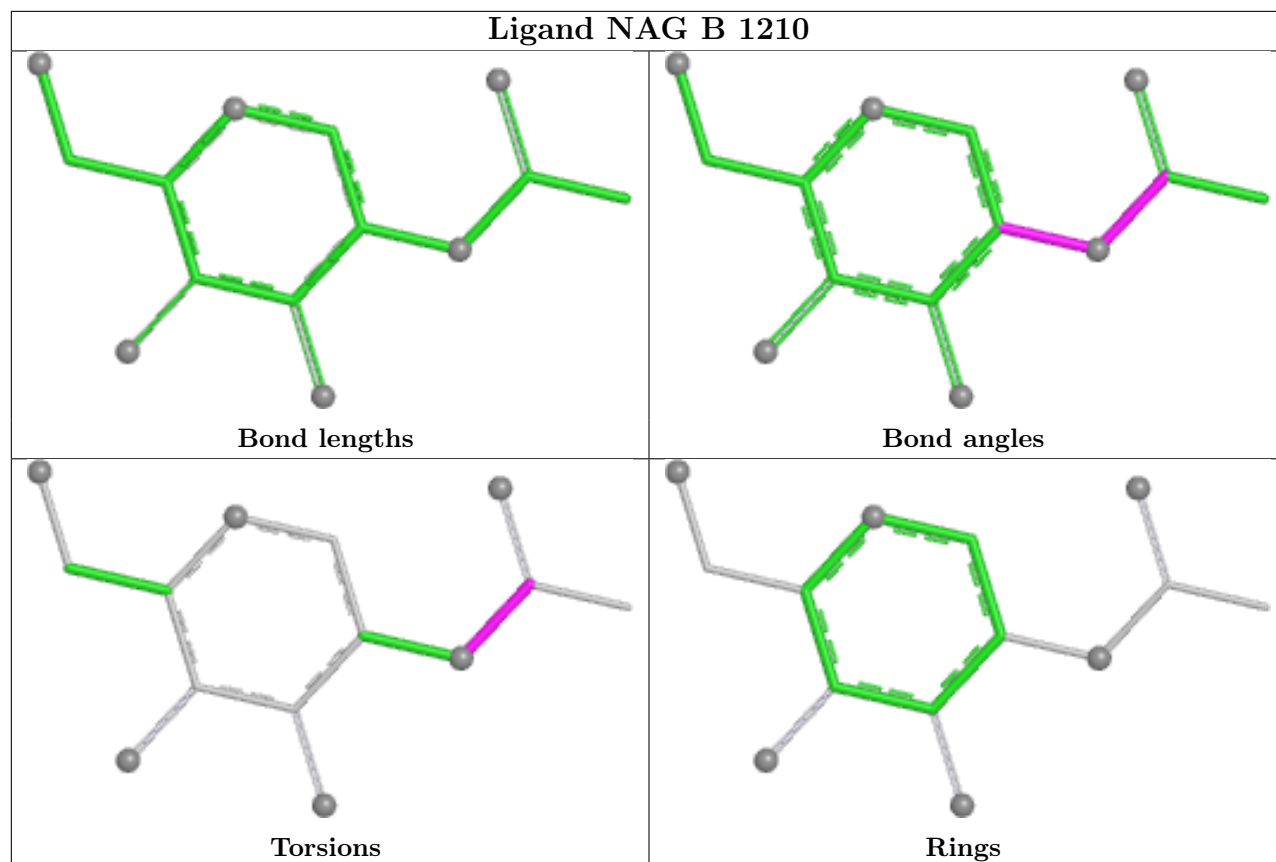
Ligand NAG B 1207



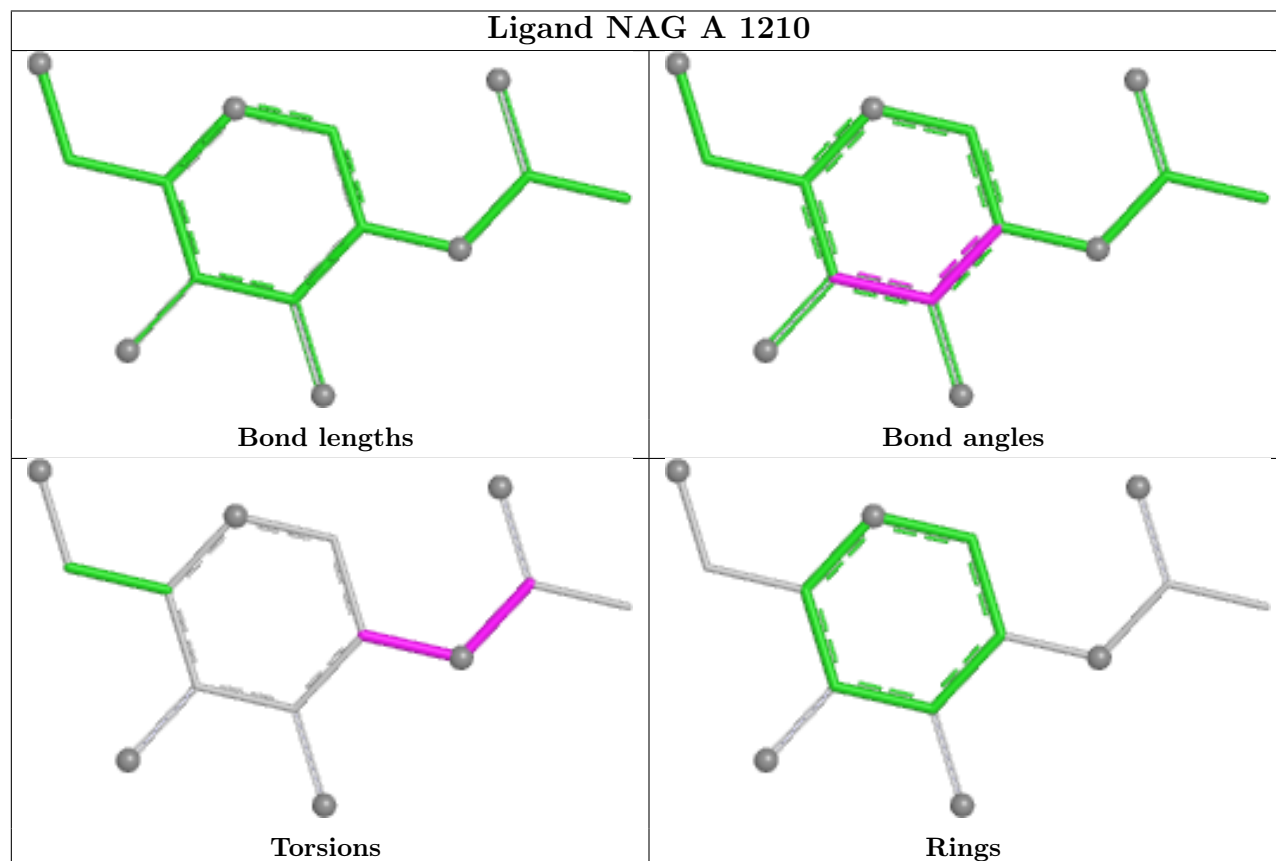
Ligand NAG A 1209



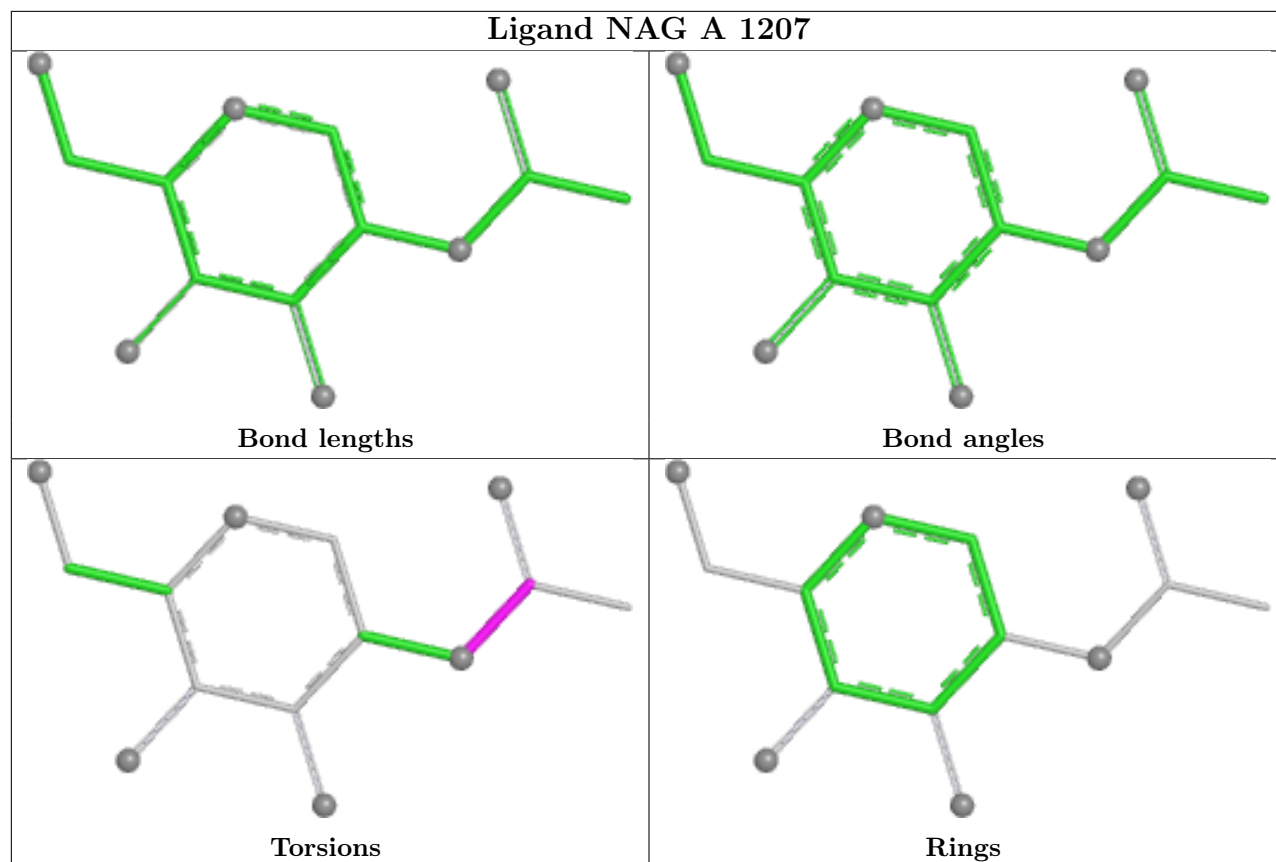
Ligand NAG B 1210



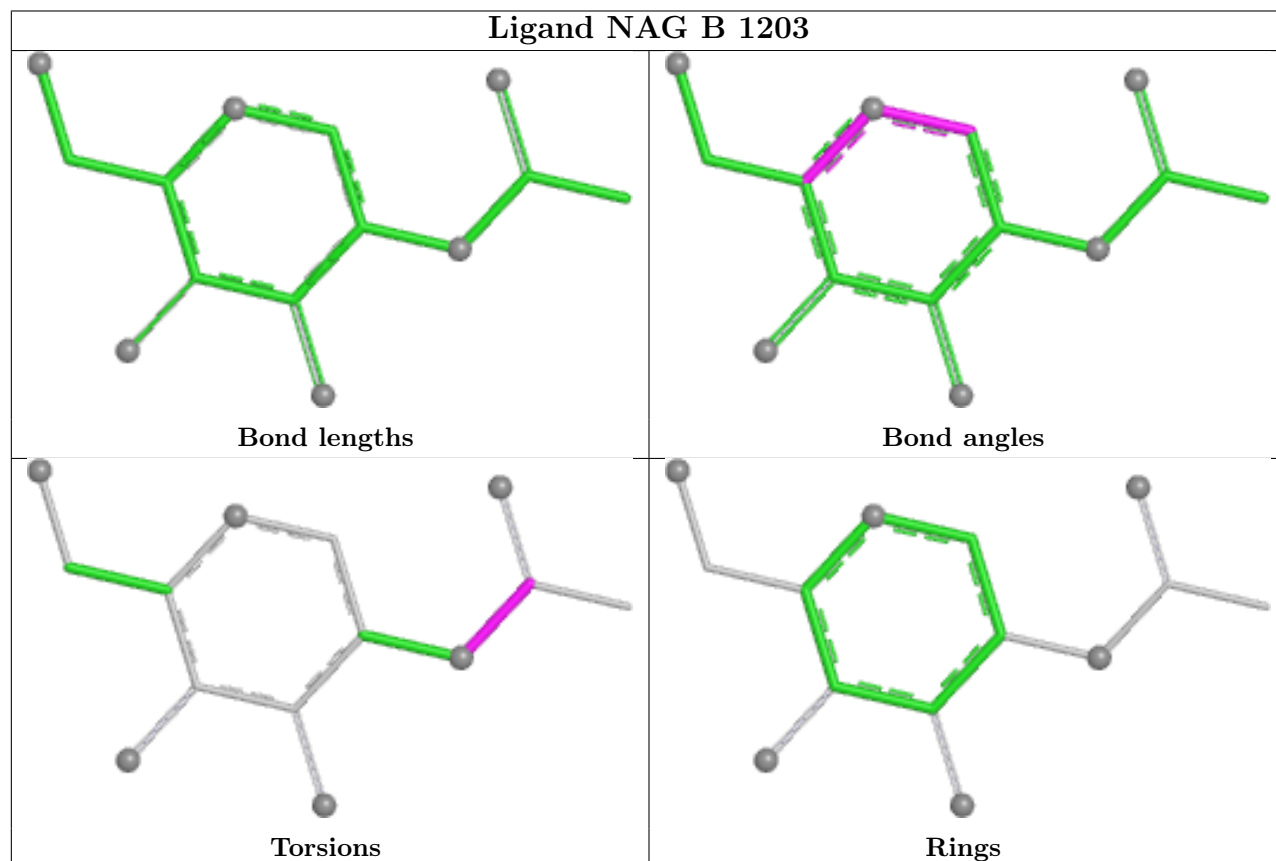
Ligand NAG A 1210



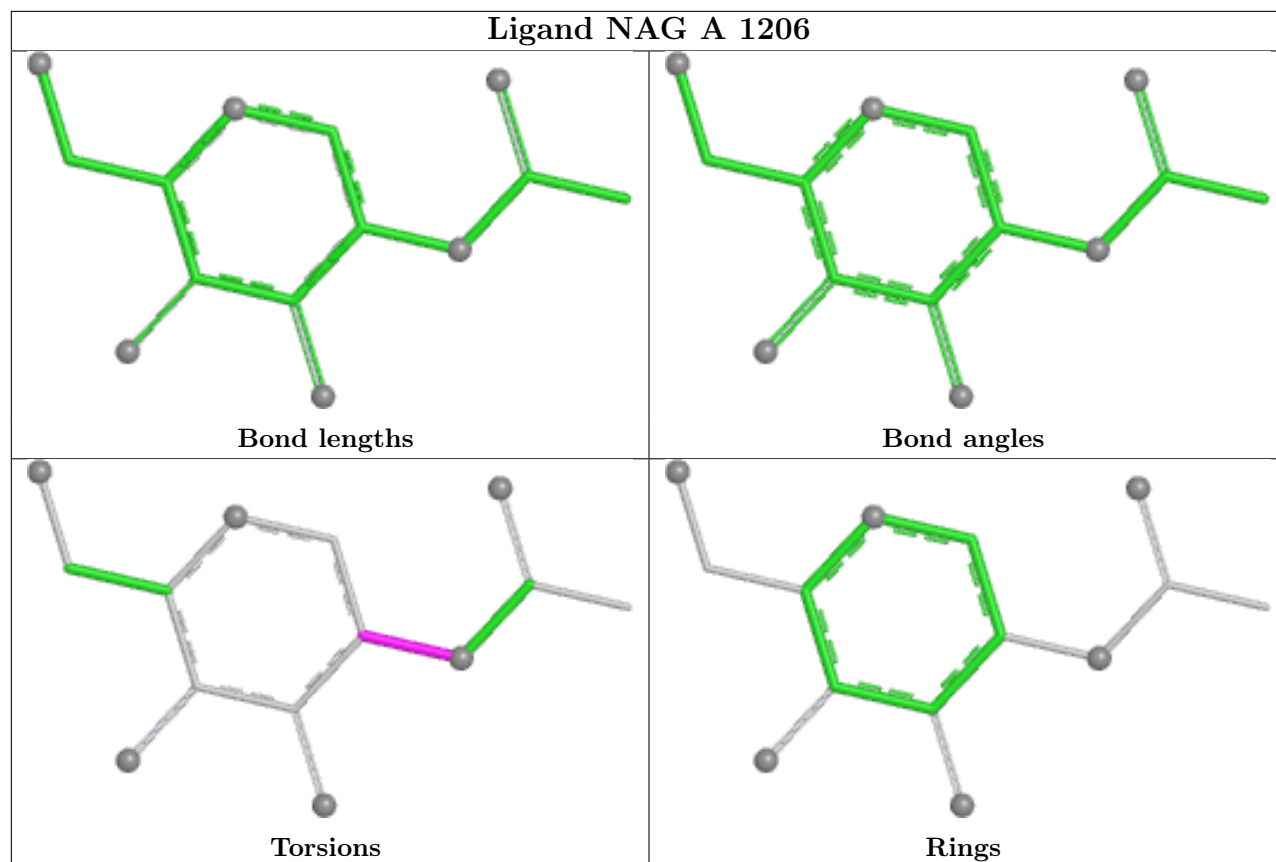
Ligand NAG A 1207



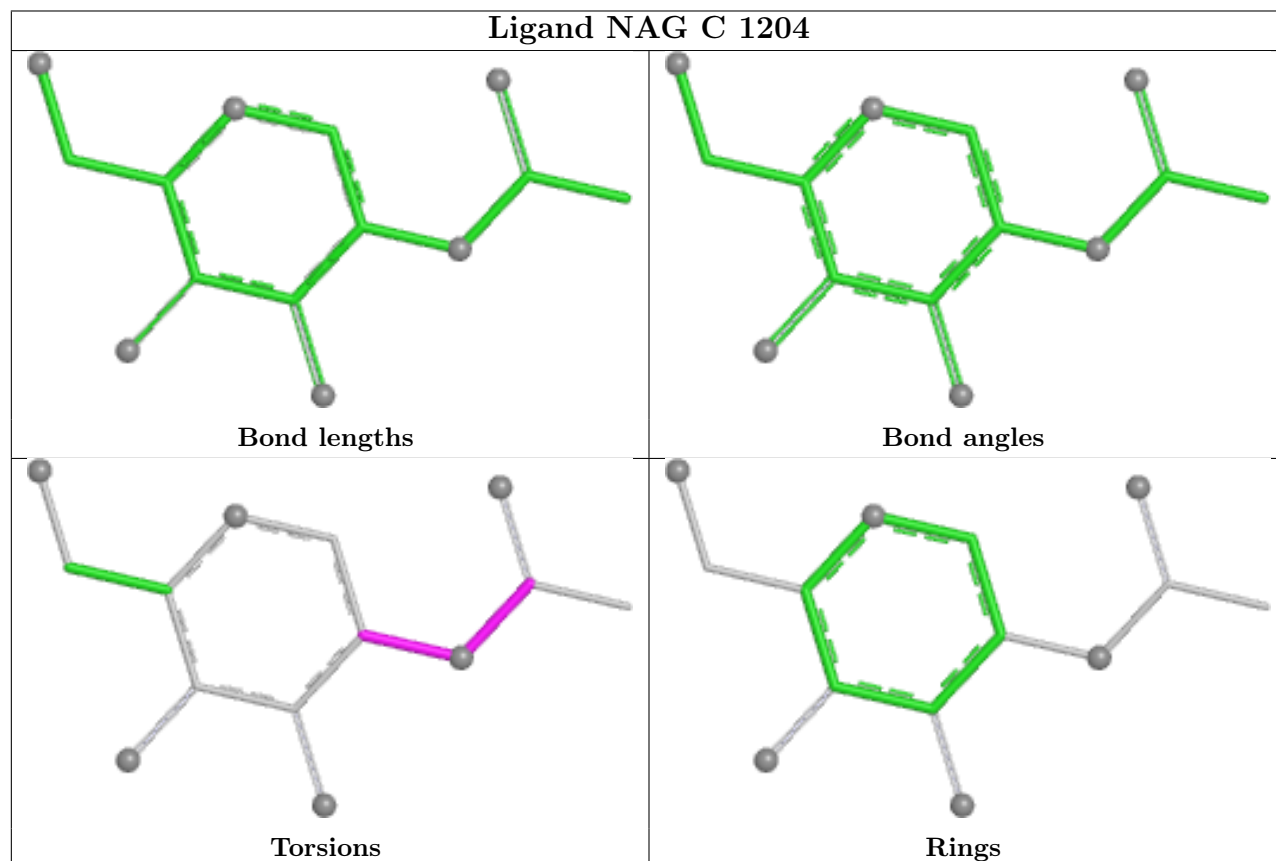
Ligand NAG B 1203



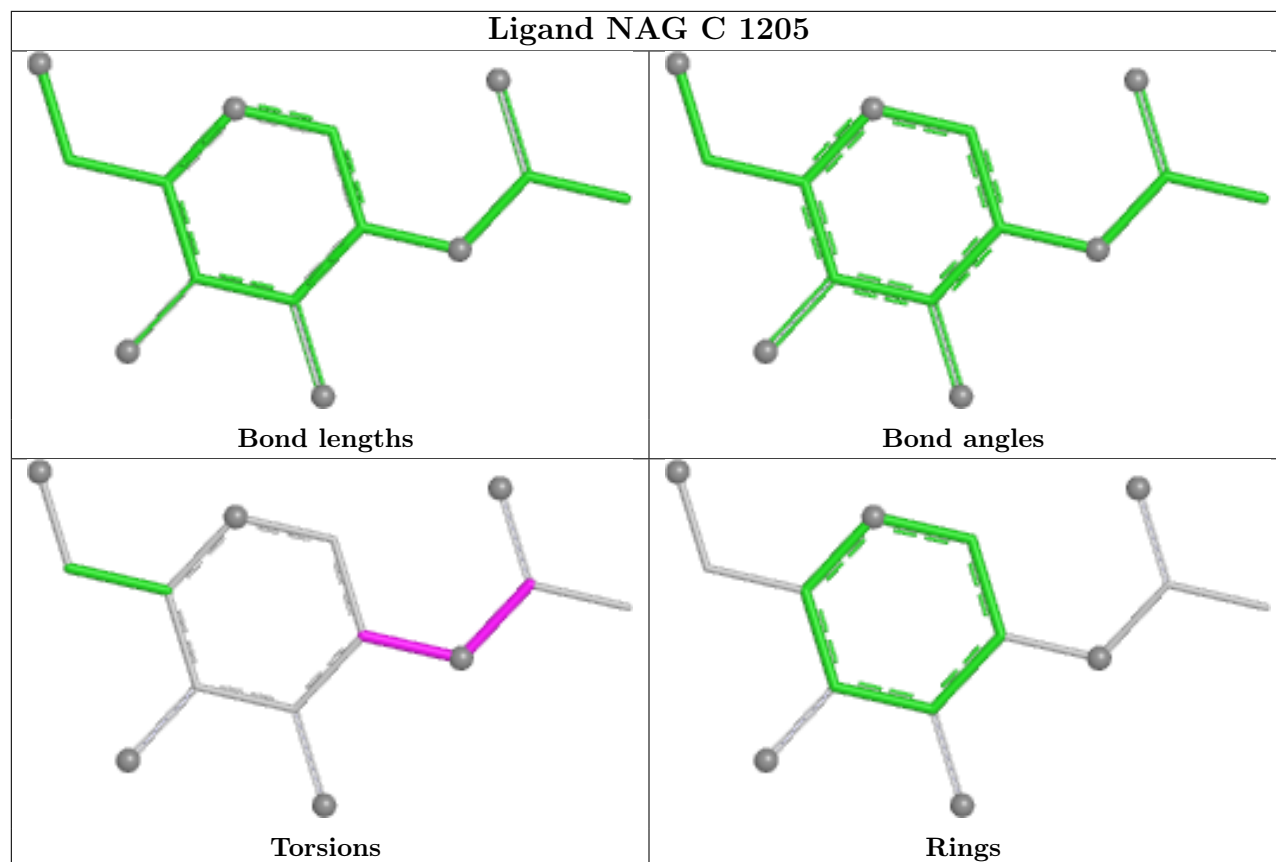
Ligand NAG A 1206



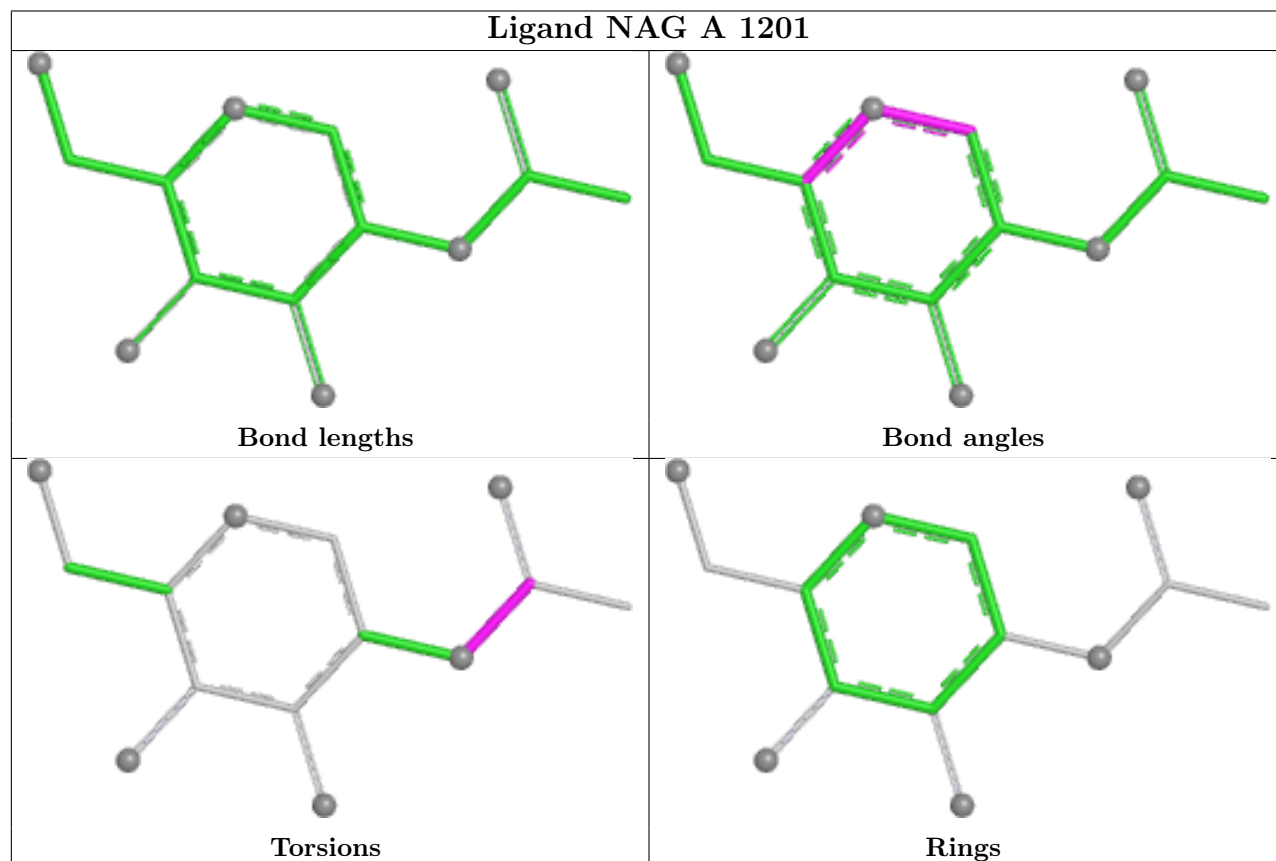
Ligand NAG C 1204

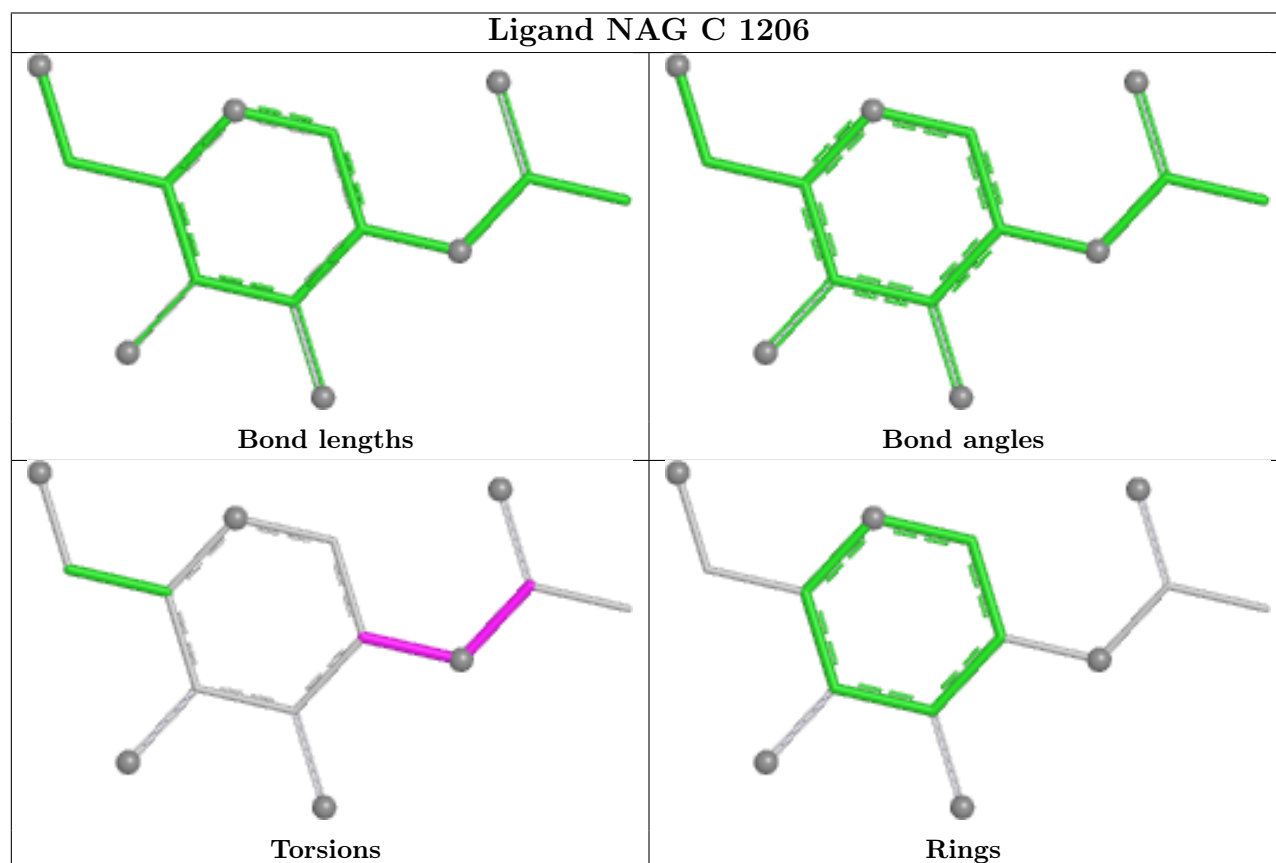
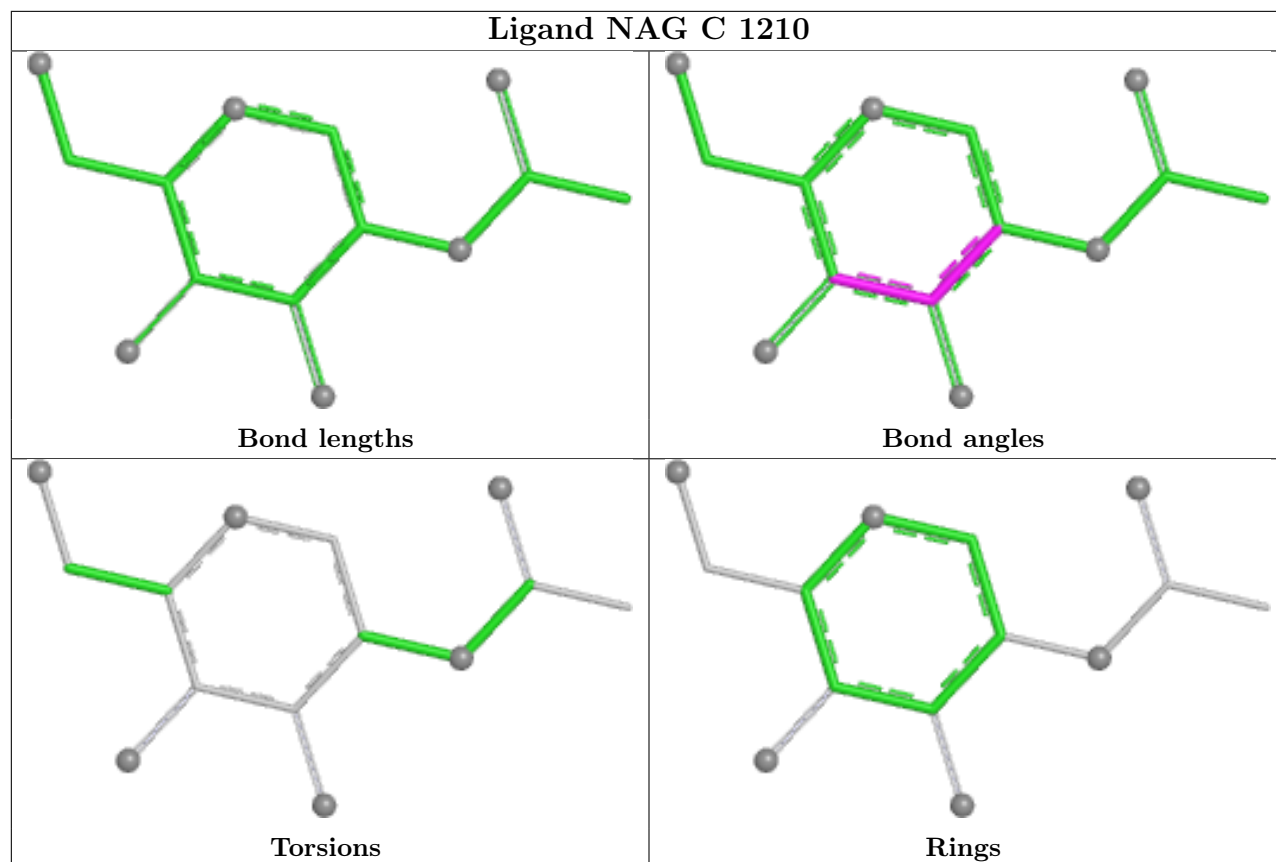


Ligand NAG C 1205

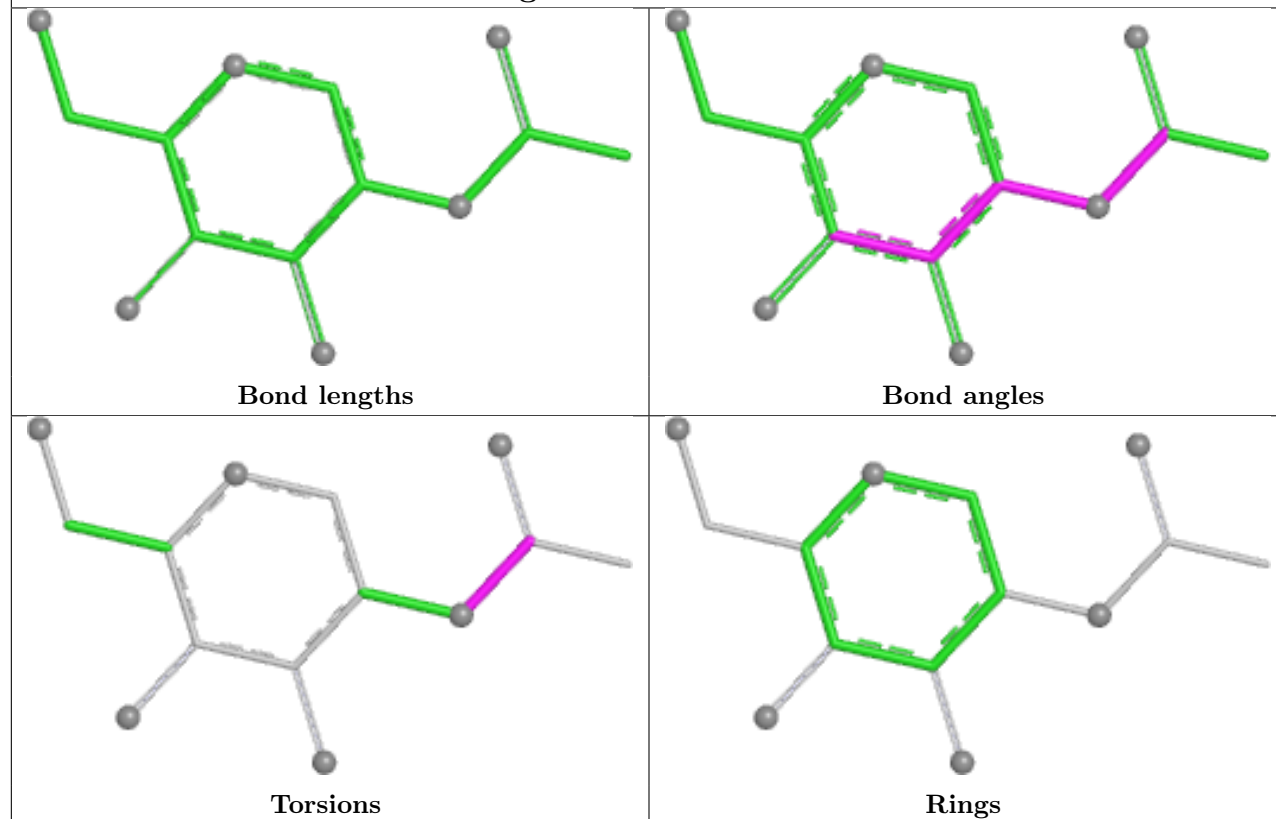


Ligand NAG A 1201

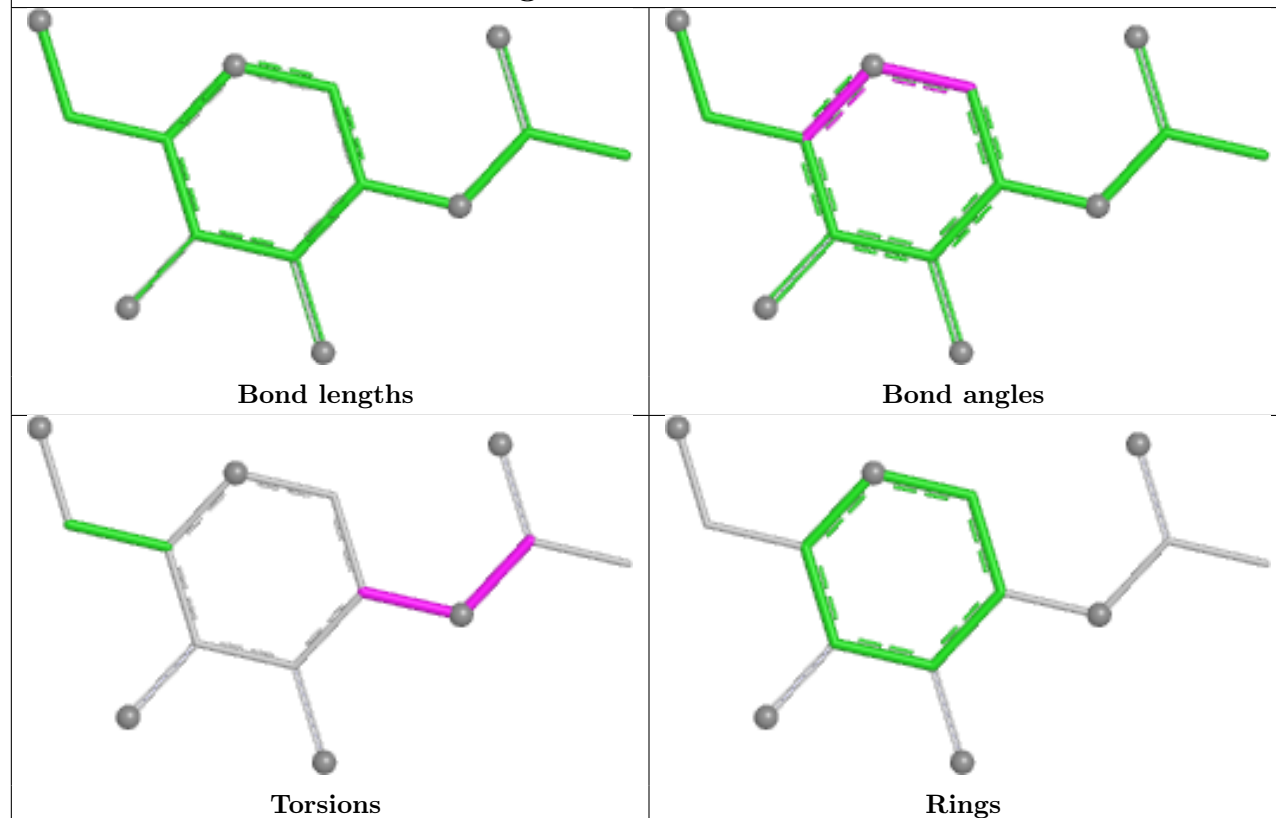




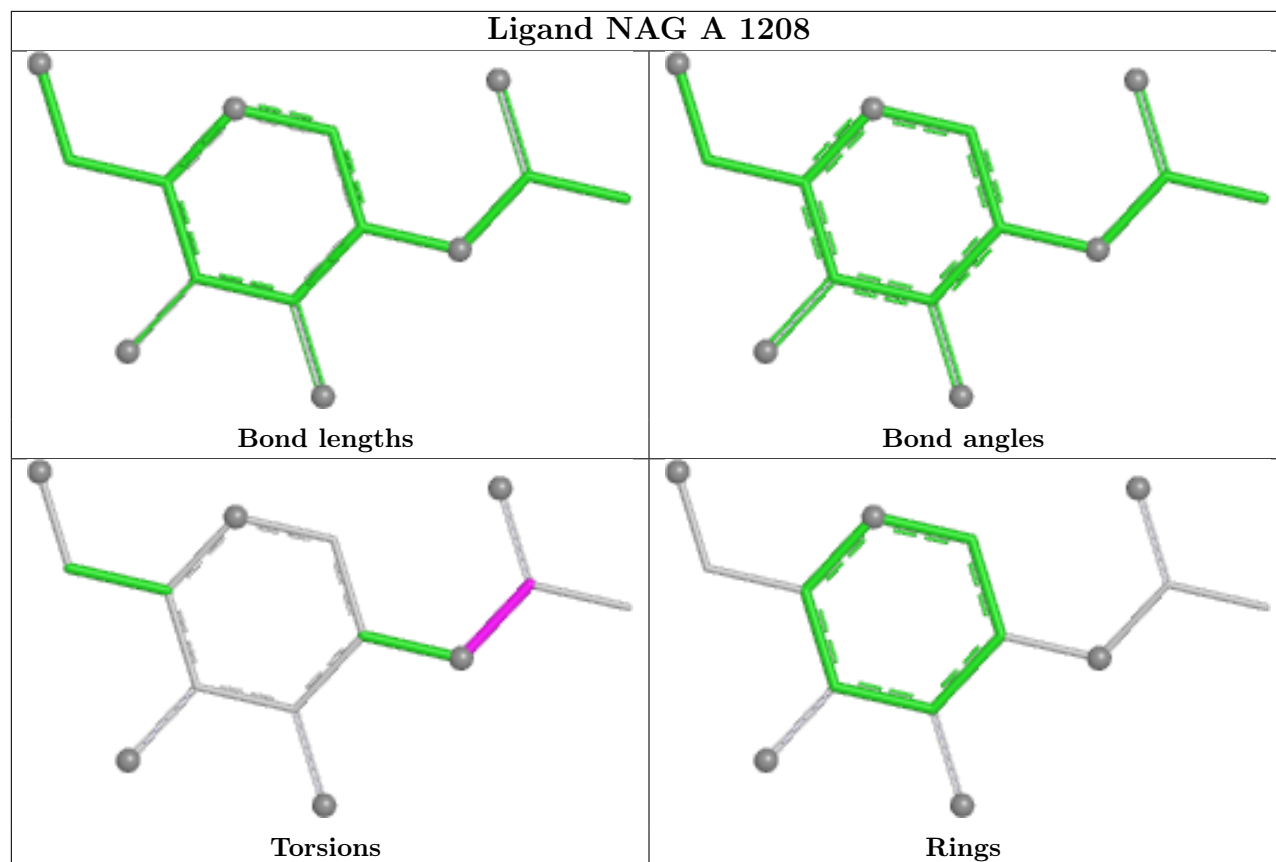
Ligand NAG C 1203



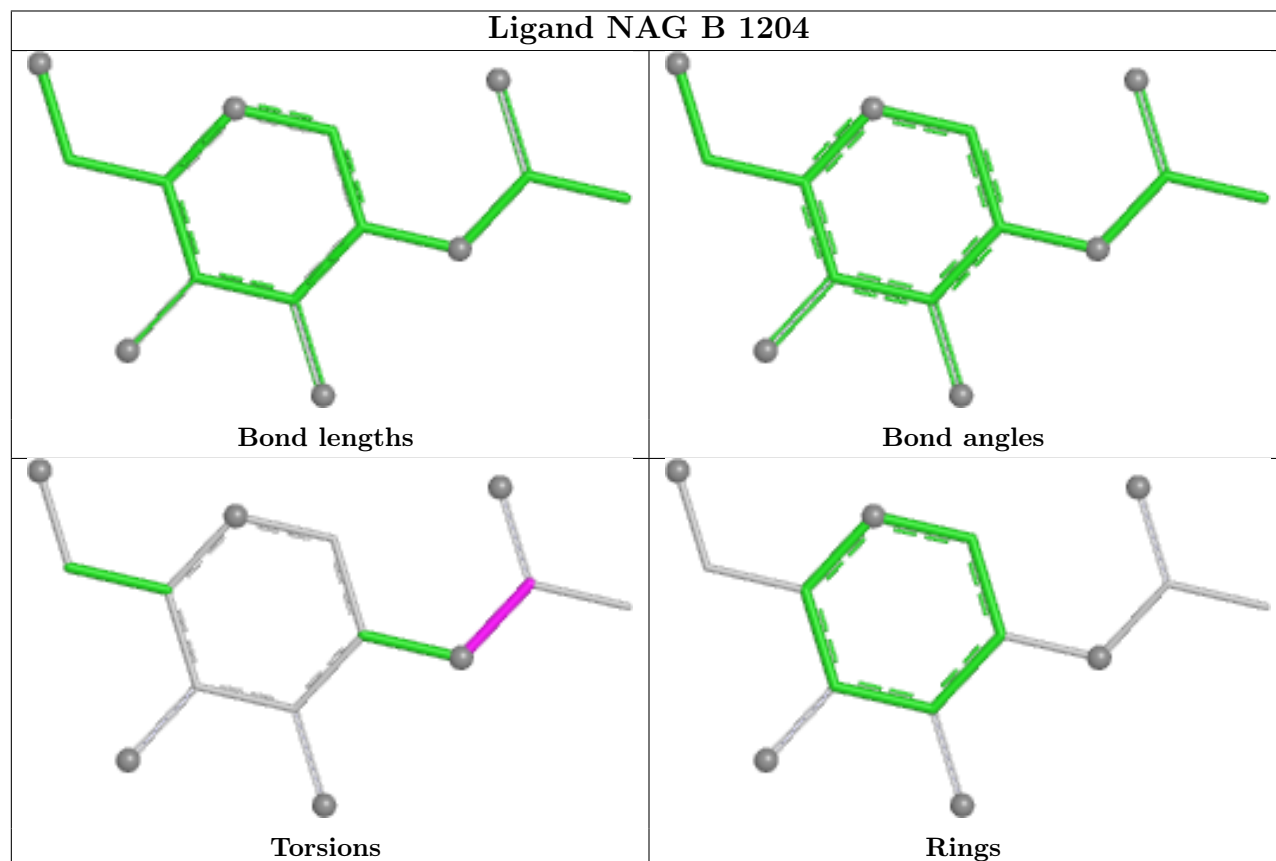
Ligand NAG A 1205



Ligand NAG A 1208



Ligand NAG B 1204



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.

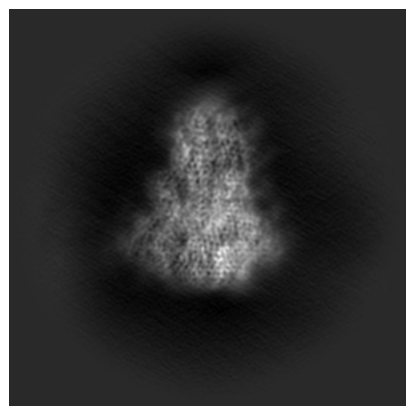
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-61170. These allow visual inspection of the internal detail of the map and identification of artifacts.

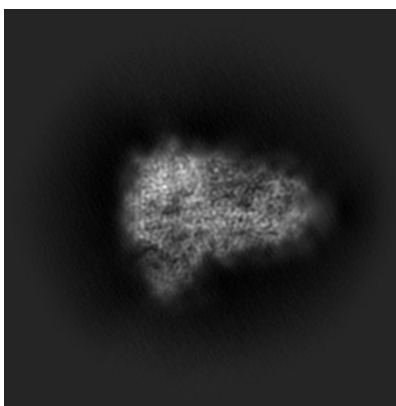
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

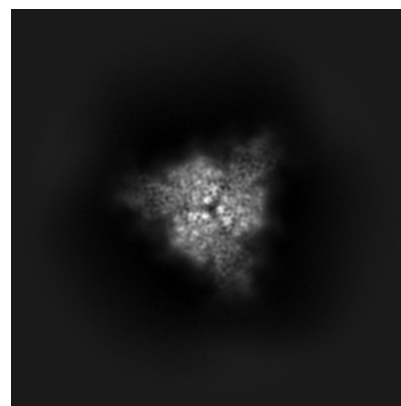
6.1.1 Primary map



X

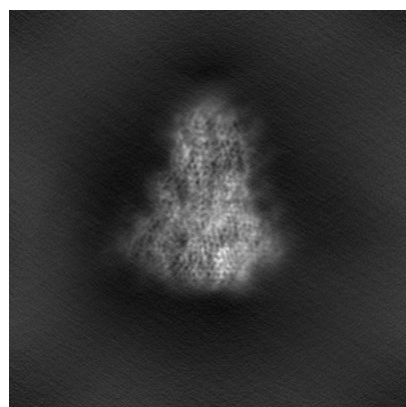


Y

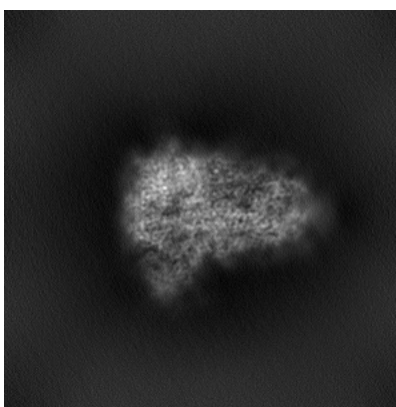


Z

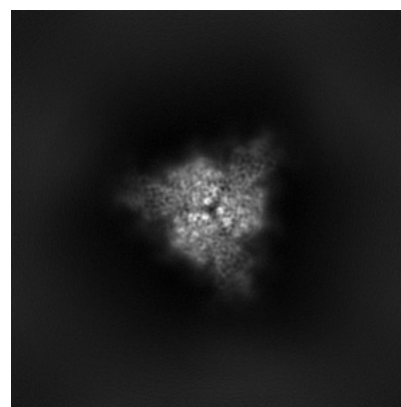
6.1.2 Raw map



X



Y

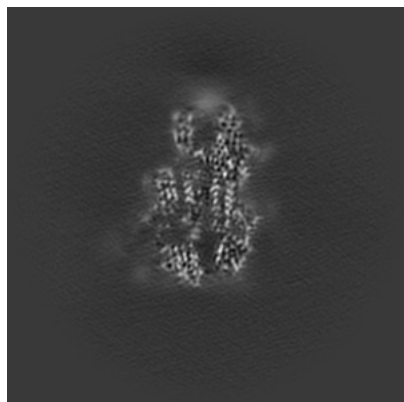


Z

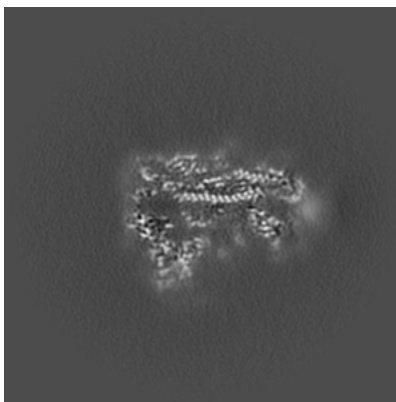
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

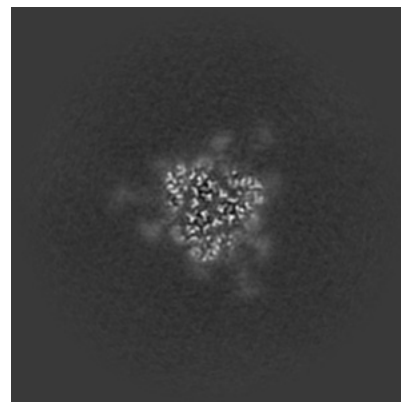
6.2.1 Primary map



X Index: 240

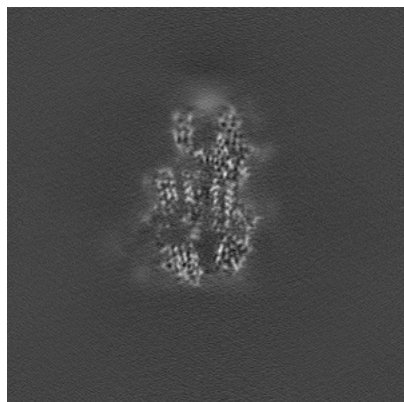


Y Index: 240

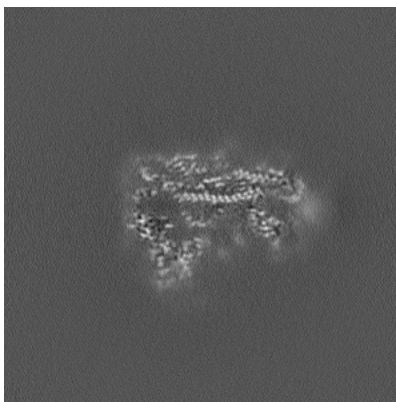


Z Index: 240

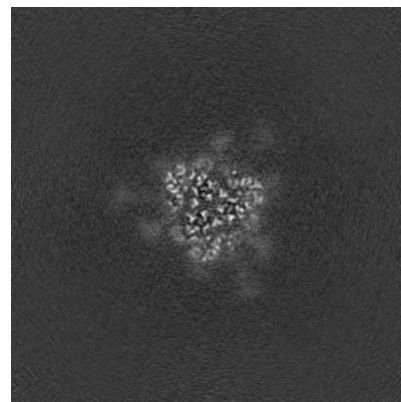
6.2.2 Raw map



X Index: 240



Y Index: 240

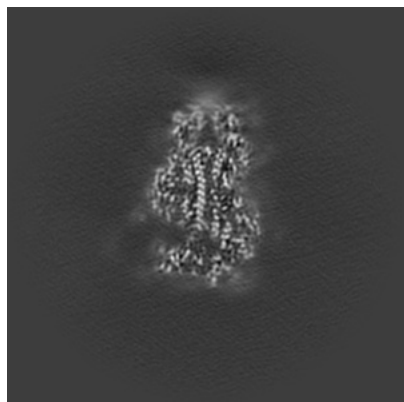


Z Index: 240

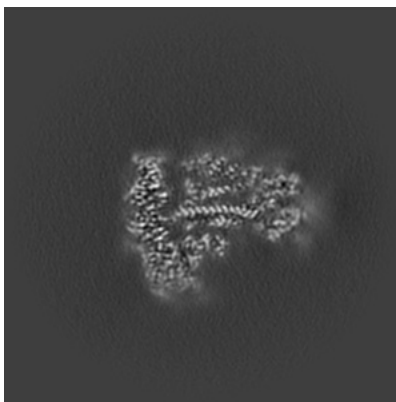
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

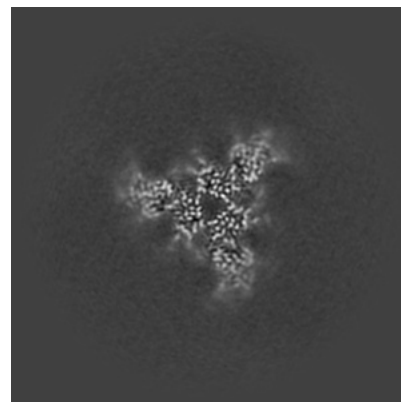
6.3.1 Primary map



X Index: 232

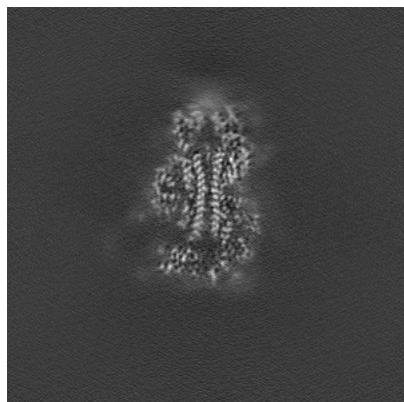


Y Index: 252

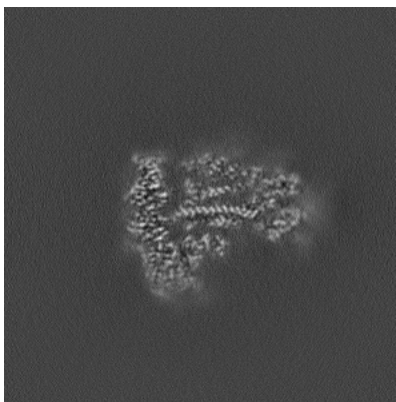


Z Index: 193

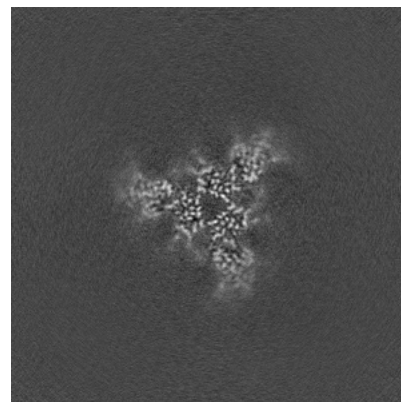
6.3.2 Raw map



X Index: 234



Y Index: 252

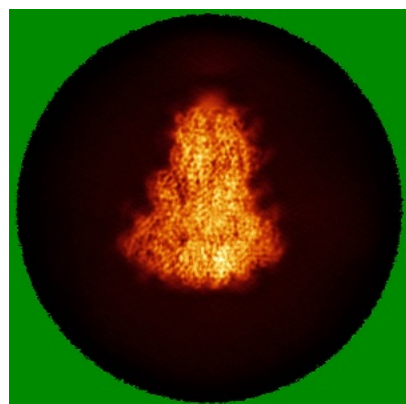


Z Index: 193

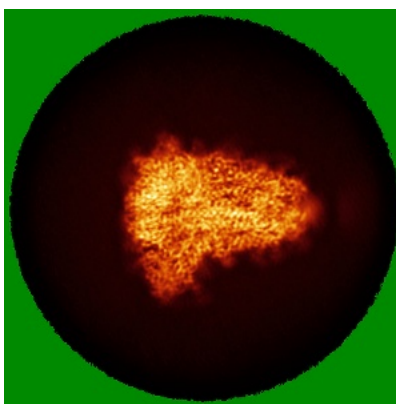
The images above show the largest variance slices of the map in three orthogonal directions.

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

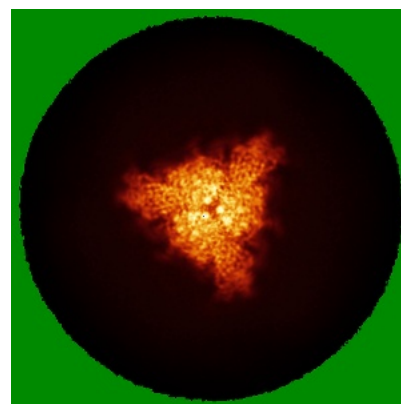
6.4.1 Primary map



X

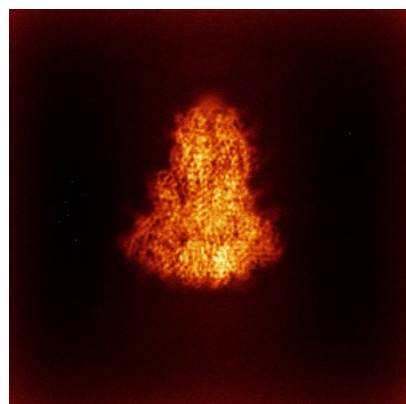


Y

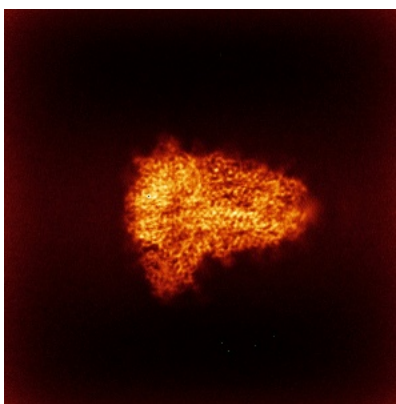


Z

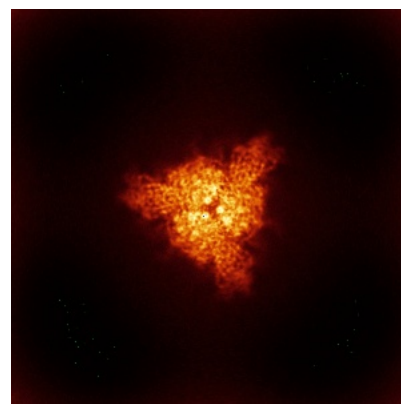
6.4.2 Raw map



X



Y

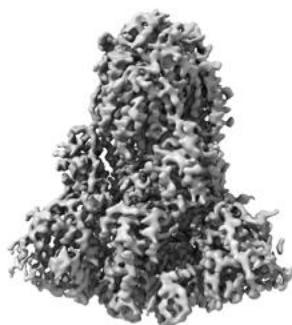


Z

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

6.5 Orthogonal surface views [i](#)

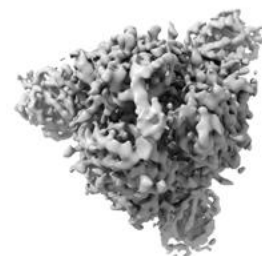
6.5.1 Primary map



X



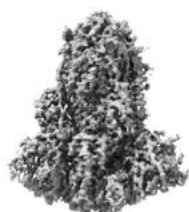
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.2. 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



X



Y



Z

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.

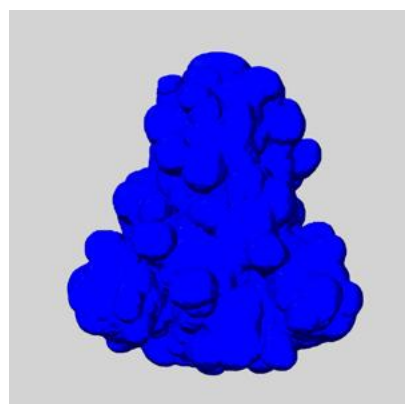
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

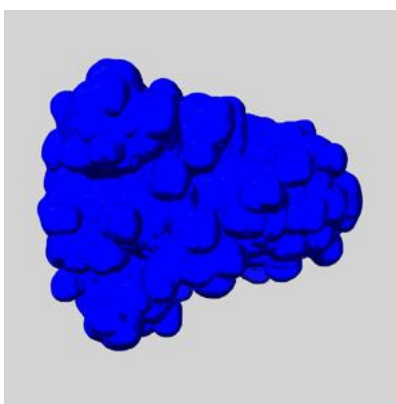
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

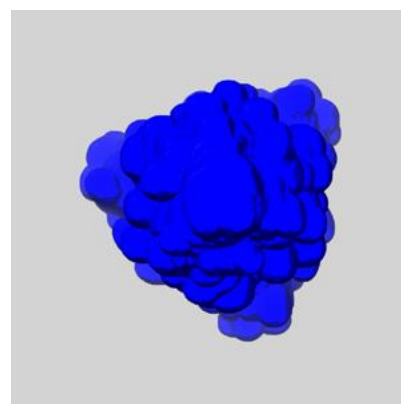
6.6.1 emd_61170_msk_1.map [i](#)



X



Y

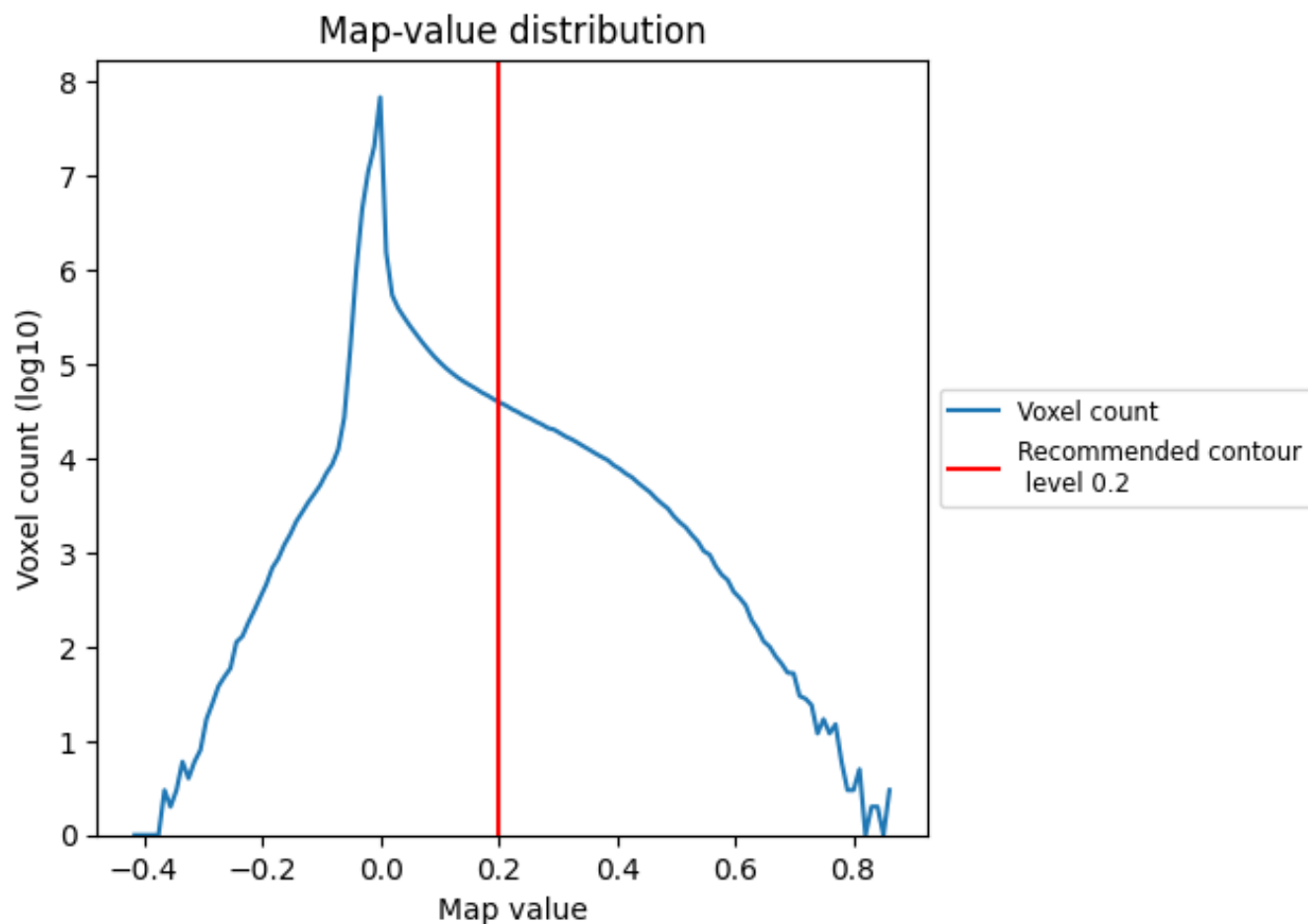


Z

7 Map analysis [i](#)

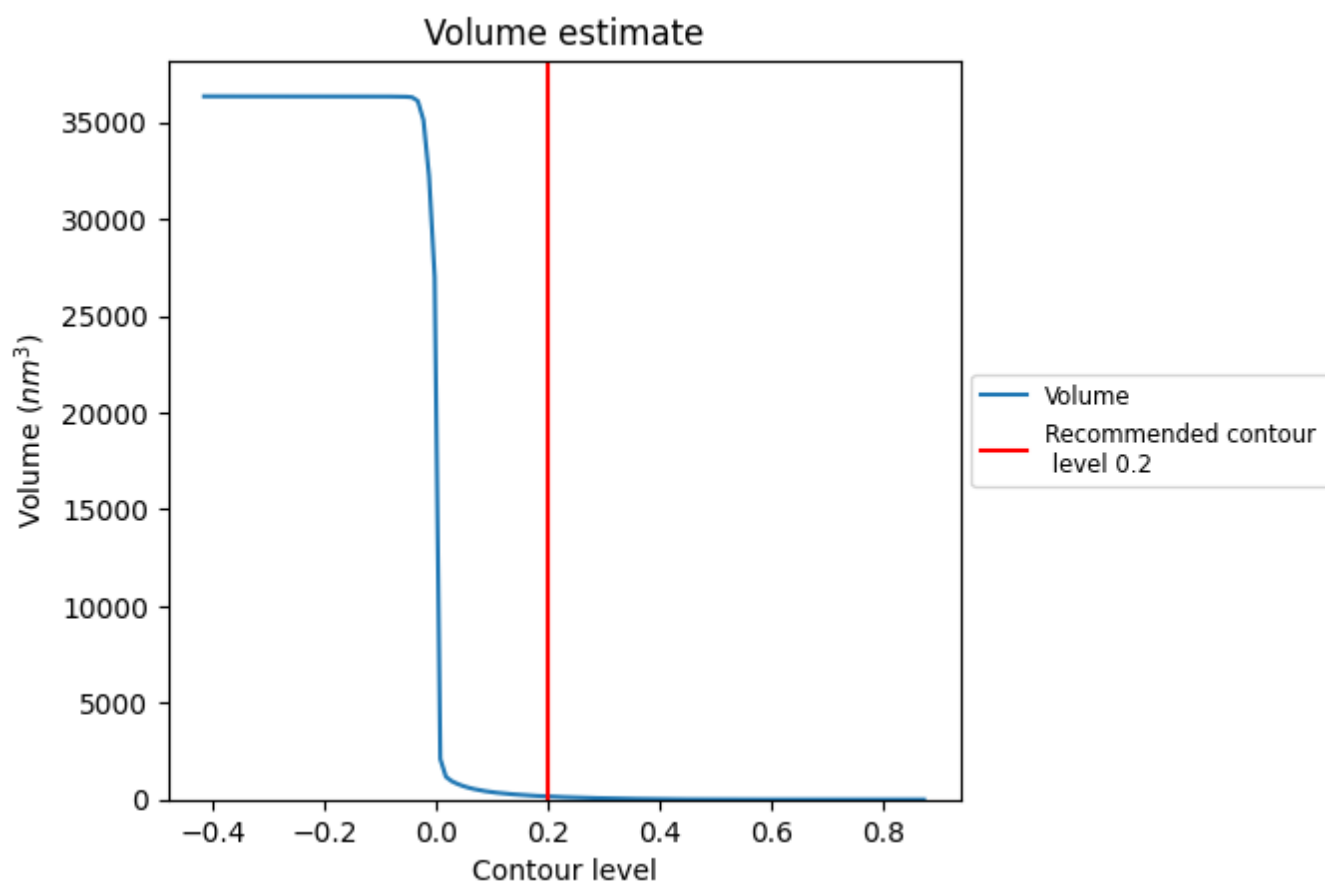
This section contains the results of statistical analysis of the map.

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.

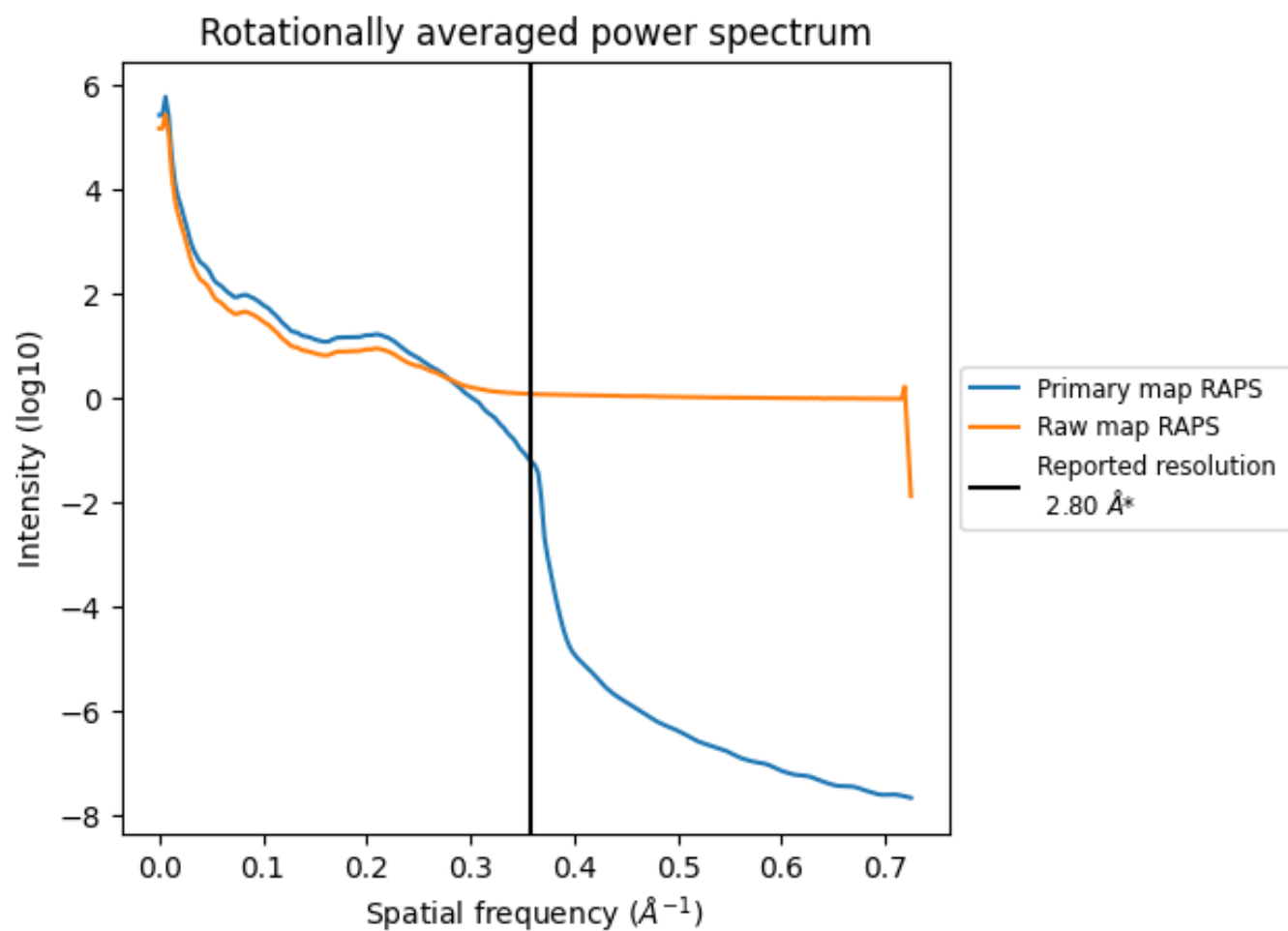
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 160 nm³; this corresponds to an approximate mass of 144 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 ⓘ

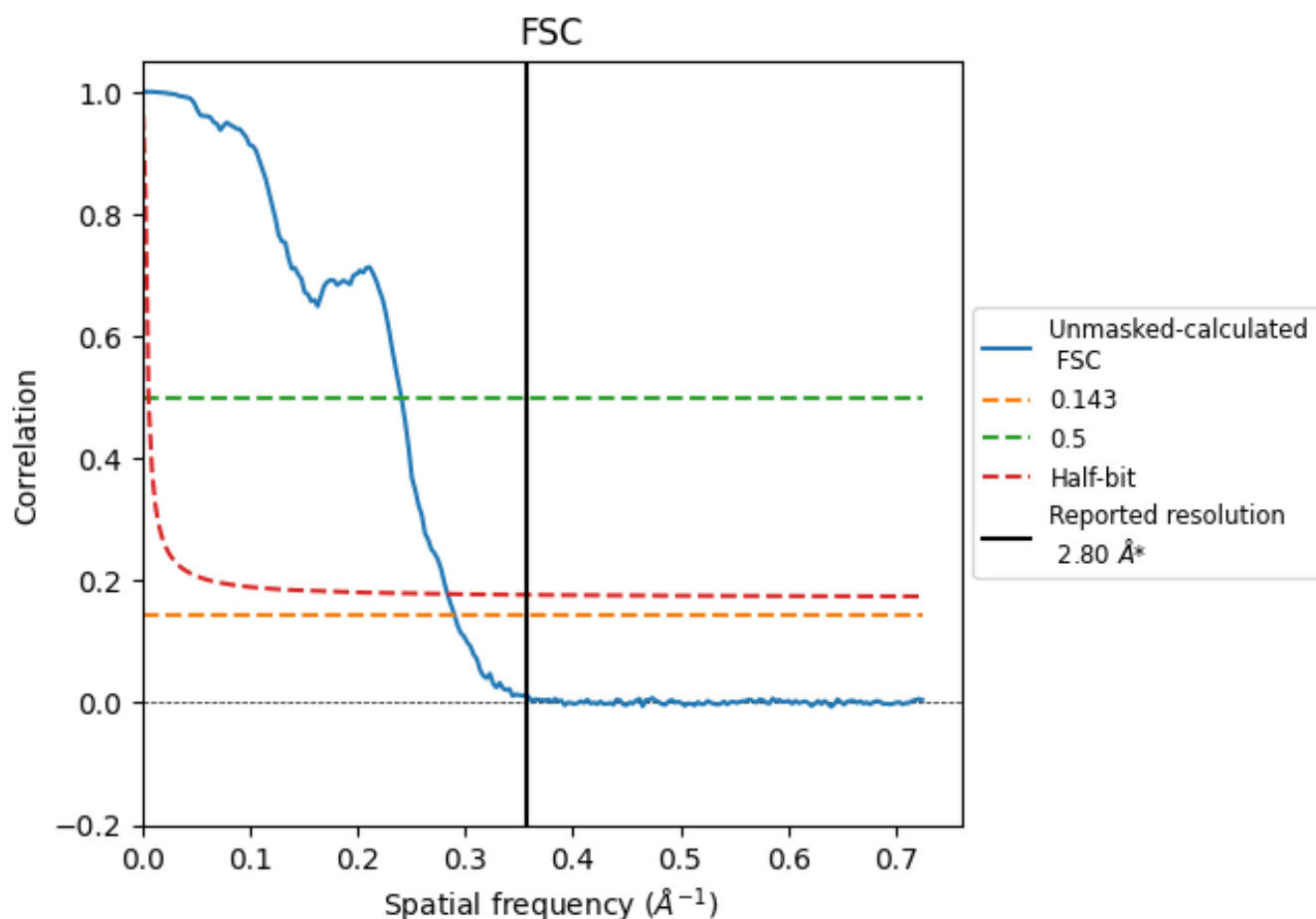


*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

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 0.357 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.45	4.15	3.53

*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 3.45 differs from the reported value 2.8 by more than 10 %

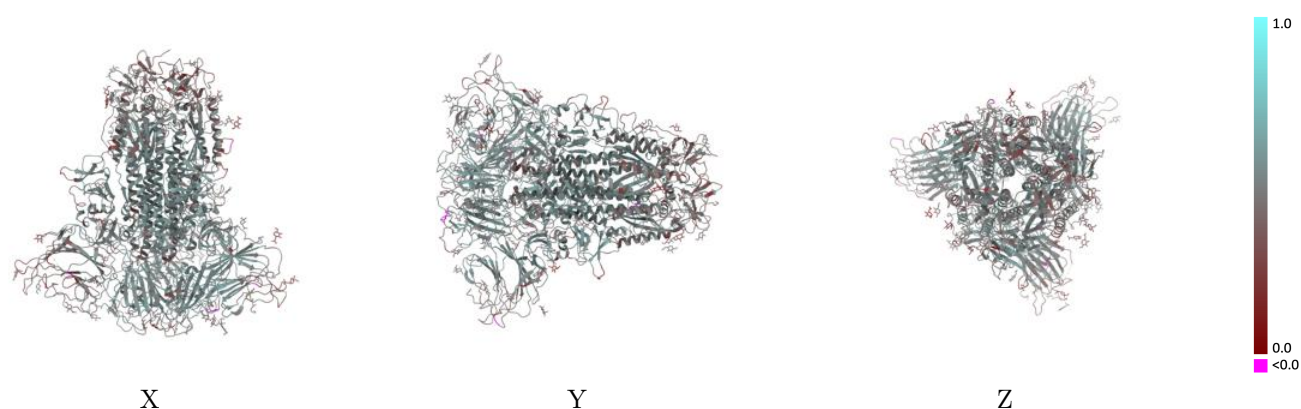
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-61170 and PDB model 9J6G. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)

This section was not generated.

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

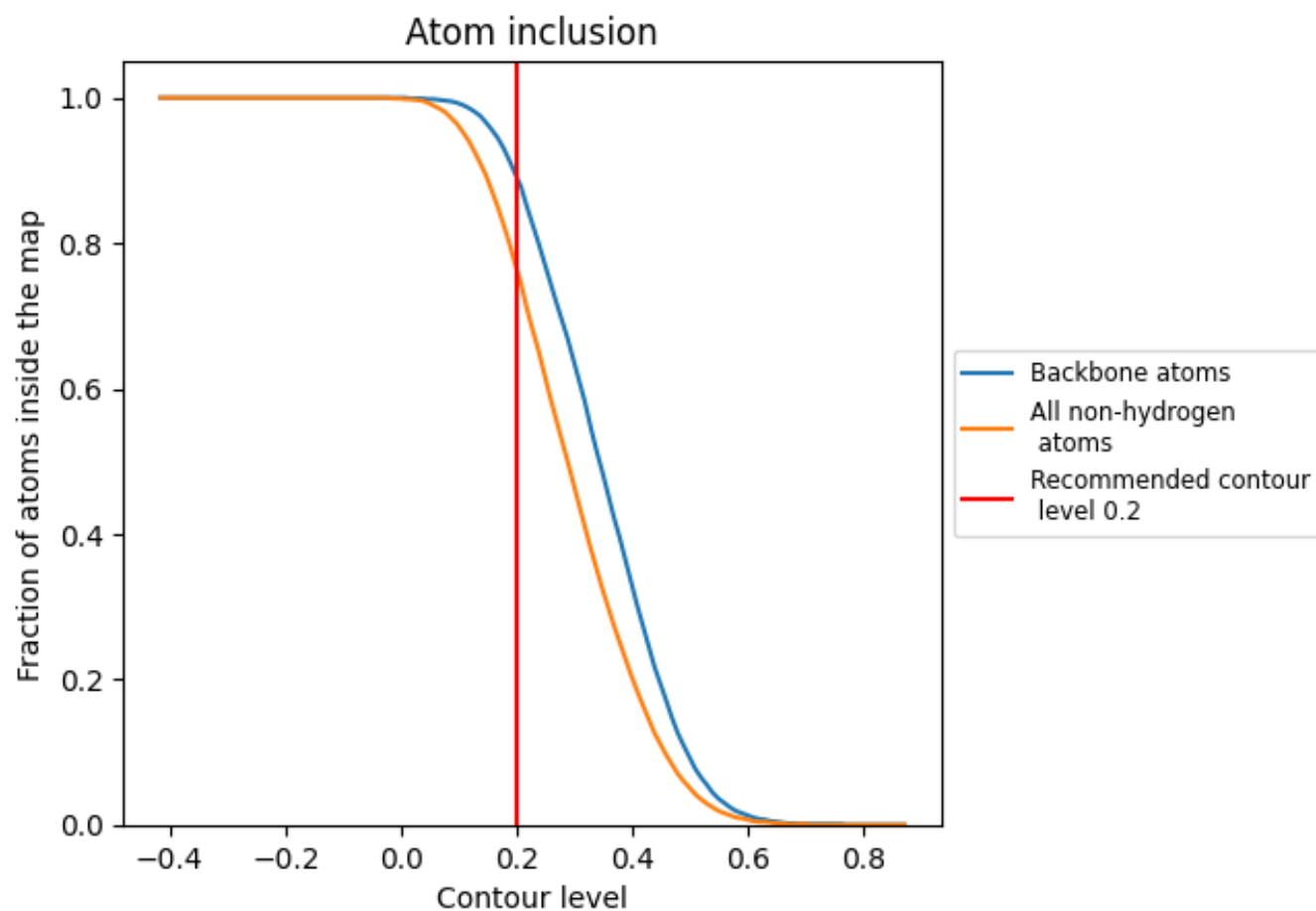


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 76% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7650	 0.4950
A	 0.7890	 0.5040
B	 0.7580	 0.4900
C	 0.7690	 0.4980
D	 0.5600	 0.4020
E	 0.2860	 0.3160
F	 0.2500	 0.2820
G	 0.4290	 0.3790
H	 0.3570	 0.4080
I	 0.3570	 0.3760
J	 0.3570	 0.3830
K	 0.7200	 0.4500
L	 0.2500	 0.2100
M	 0.3930	 0.2390
N	 0.4640	 0.4130
O	 0.3210	 0.4610
P	 0.6800	 0.4050
Q	 0.5360	 0.5120
R	 0.3570	 0.3170
S	 0.4290	 0.4070
T	 0.2500	 0.2510

