



Full wwPDB EM Validation Report ⓘ

Mar 24, 2026 – 07:02 AM UTC

PDB ID : 8FU8 / pdb_00008fu8
EMDB ID : EMD-29455
Title : Structure of Covid Spike variant deltaN135 with one erect RBD
Authors : Yu, X.; Juraszek, J.; Rutten, L.; Bakkers, M.J.G.; Blokland, S.; Van den Broek, N.J.F.; Verwilligen, A.Y.W.; Abeywickrema, P.; Vingerhoets, J.; Neefs, J.; Bakhsh, S.A.M.; Roychoudhury, P.; Greninger, A.; Sharma, S.; Langedijk, J.P.M.
Deposited on : 2023-01-16
Resolution : 3.08 Å(reported)

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

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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:

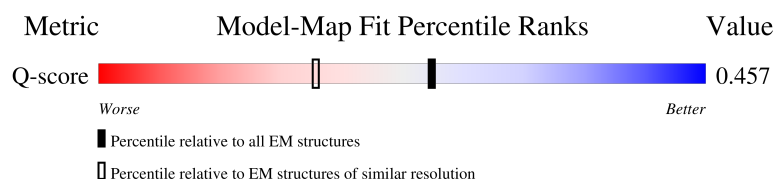
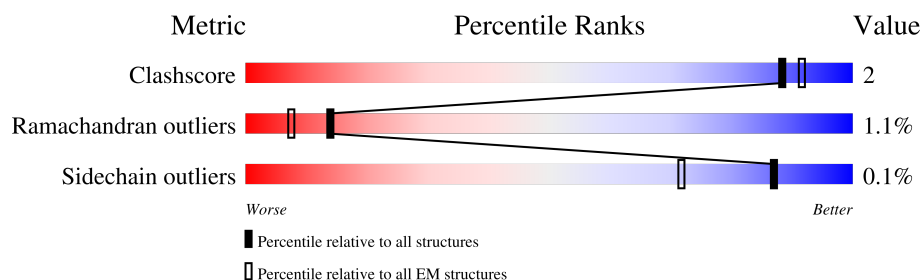
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.08 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	14000 (2.58 - 3.58)

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	1192	9% 79% 7% 12%
1	B	1192	15% 81% 7% 10%
1	C	1192	11% 81% 7% 12%

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
2	NAG	A	1206	X	-	-	-

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 25469 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	1046	Total	C	N	O	S	0	0
			8183	5229	1363	1555	36		
1	B	1069	Total	C	N	O	S	0	0
			8360	5335	1398	1591	36		
1	C	1050	Total	C	N	O	S	0	0
			8211	5244	1368	1562	37		

There are 78 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	9	LEU	PRO	conflict	UNP P0DTC2
A	?	-	CYS	deletion	UNP P0DTC2
A	?	-	ASN	deletion	UNP P0DTC2
A	?	-	ASP	deletion	UNP P0DTC2
A	?	-	PRO	deletion	UNP P0DTC2
A	?	-	PHE	deletion	UNP P0DTC2
A	?	-	LEU	deletion	UNP P0DTC2
A	?	-	GLY	deletion	UNP P0DTC2
A	?	-	VAL	deletion	UNP P0DTC2
A	?	-	TYR	deletion	UNP P0DTC2
A	?	-	TRP	deletion	UNP P0DTC2
A	?	-	THR	deletion	UNP P0DTC2
A	?	-	ALA	deletion	UNP P0DTC2
A	?	-	GLY	deletion	UNP P0DTC2
A	?	-	ALA	deletion	UNP P0DTC2
A	?	-	ALA	deletion	UNP P0DTC2
A	?	-	ALA	deletion	UNP P0DTC2
A	468	LYS	GLU	conflict	UNP P0DTC2
A	478	PRO	SER	conflict	UNP P0DTC2
A	598	GLY	ASP	conflict	UNP P0DTC2
A	666	SER	ARG	conflict	UNP P0DTC2
A	669	GLY	ARG	conflict	UNP P0DTC2
A	876	PRO	ALA	engineered mutation	UNP P0DTC2
A	926	PRO	ALA	engineered mutation	UNP P0DTC2

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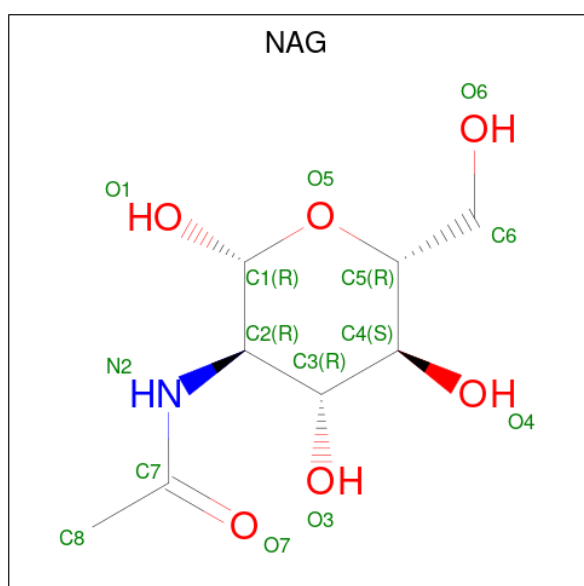
Chain	Residue	Modelled	Actual	Comment	Reference
A	971	PRO	VAL	engineered mutation	UNP P0DTC2
A	1160	PHE	VAL	conflict	UNP P0DTC2
B	9	LEU	PRO	conflict	UNP P0DTC2
B	?	-	CYS	deletion	UNP P0DTC2
B	?	-	ASN	deletion	UNP P0DTC2
B	?	-	ASP	deletion	UNP P0DTC2
B	?	-	PRO	deletion	UNP P0DTC2
B	?	-	PHE	deletion	UNP P0DTC2
B	?	-	LEU	deletion	UNP P0DTC2
B	?	-	GLY	deletion	UNP P0DTC2
B	?	-	VAL	deletion	UNP P0DTC2
B	?	-	TYR	deletion	UNP P0DTC2
B	?	-	TRP	deletion	UNP P0DTC2
B	?	-	THR	deletion	UNP P0DTC2
B	?	-	ALA	deletion	UNP P0DTC2
B	?	-	GLY	deletion	UNP P0DTC2
B	?	-	ALA	deletion	UNP P0DTC2
B	?	-	ALA	deletion	UNP P0DTC2
B	468	LYS	GLU	conflict	UNP P0DTC2
B	478	PRO	SER	conflict	UNP P0DTC2
B	598	GLY	ASP	conflict	UNP P0DTC2
B	666	SER	ARG	conflict	UNP P0DTC2
B	669	GLY	ARG	conflict	UNP P0DTC2
B	876	PRO	ALA	engineered mutation	UNP P0DTC2
B	926	PRO	ALA	engineered mutation	UNP P0DTC2
B	971	PRO	VAL	engineered mutation	UNP P0DTC2
B	1160	PHE	VAL	conflict	UNP P0DTC2
C	9	LEU	PRO	conflict	UNP P0DTC2
C	?	-	CYS	deletion	UNP P0DTC2
C	?	-	ASN	deletion	UNP P0DTC2
C	?	-	ASP	deletion	UNP P0DTC2
C	?	-	PRO	deletion	UNP P0DTC2
C	?	-	PHE	deletion	UNP P0DTC2
C	?	-	LEU	deletion	UNP P0DTC2
C	?	-	GLY	deletion	UNP P0DTC2
C	?	-	VAL	deletion	UNP P0DTC2
C	?	-	TYR	deletion	UNP P0DTC2
C	?	-	TRP	deletion	UNP P0DTC2
C	?	-	THR	deletion	UNP P0DTC2
C	?	-	ALA	deletion	UNP P0DTC2
C	?	-	GLY	deletion	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	ALA	deletion	UNP P0DTC2
C	?	-	ALA	deletion	UNP P0DTC2
C	?	-	ALA	deletion	UNP P0DTC2
C	468	LYS	GLU	conflict	UNP P0DTC2
C	478	PRO	SER	conflict	UNP P0DTC2
C	598	GLY	ASP	conflict	UNP P0DTC2
C	666	SER	ARG	conflict	UNP P0DTC2
C	669	GLY	ARG	conflict	UNP P0DTC2
C	876	PRO	ALA	engineered mutation	UNP P0DTC2
C	926	PRO	ALA	engineered mutation	UNP P0DTC2
C	971	PRO	VAL	engineered mutation	UNP P0DTC2
C	1160	PHE	VAL	conflict	UNP P0DTC2

- Molecule 2 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
2	A	1	Total	C	N	O	0
			15	8	1	6	
2	A	1	Total	C	N	O	0
			15	8	1	6	
2	A	1	Total	C	N	O	0
			15	8	1	6	
2	A	1	Total	C	N	O	0
			15	8	1	6	
2	A	1	Total	C	N	O	0
			15	8	1	6	

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Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	A	1	Total	C	N	O	0
			15	8	1	6	
2	A	1	Total	C	N	O	0
			15	8	1	6	
2	A	1	Total	C	N	O	0
			15	8	1	6	
2	A	1	Total	C	N	O	0
			15	8	1	6	
2	A	1	Total	C	N	O	0
			15	8	1	6	
2	A	1	Total	C	N	O	0
			15	8	1	6	
2	A	1	Total	C	N	O	0
			15	8	1	6	
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	A	1	Total	C	N	O	0
			15	8	1	6	
2	A	1	Total	C	N	O	0
			15	8	1	6	
2	B	1	Total	C	N	O	0
			15	8	1	6	
2	B	1	Total	C	N	O	0
			15	8	1	6	
2	B	1	Total	C	N	O	0
			15	8	1	6	
2	B	1	Total	C	N	O	0
			15	8	1	6	
2	B	1	Total	C	N	O	0
			15	8	1	6	
2	B	1	Total	C	N	O	0
			15	8	1	6	
2	B	1	Total	C	N	O	0
			15	8	1	6	
2	B	1	Total	C	N	O	0
			15	8	1	6	

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Mol	Chain	Residues	Atoms				AltConf
2	B	1	Total	C	N	O	0
			14	8	1	5	
2	B	1	Total	C	N	O	0
			15	8	1	6	
2	B	1	Total	C	N	O	0
			15	8	1	6	
2	B	1	Total	C	N	O	0
			15	8	1	6	
2	B	1	Total	C	N	O	0
			15	8	1	6	
2	C	1	Total	C	N	O	0
			15	8	1	6	
2	C	1	Total	C	N	O	0
			15	8	1	6	
2	C	1	Total	C	N	O	0
			15	8	1	6	
2	C	1	Total	C	N	O	0
			14	8	1	5	
2	C	1	Total	C	N	O	0
			15	8	1	6	
2	C	1	Total	C	N	O	0
			15	8	1	6	
2	C	1	Total	C	N	O	0
			15	8	1	6	
2	C	1	Total	C	N	O	0
			15	8	1	6	
2	C	1	Total	C	N	O	0
			15	8	1	6	
2	C	1	Total	C	N	O	0
			15	8	1	6	
2	C	1	Total	C	N	O	0
			14	8	1	5	
2	C	1	Total	C	N	O	0
			15	8	1	6	
2	C	1	Total	C	N	O	0
			15	8	1	6	
2	C	1	Total	C	N	O	0
			15	8	1	6	

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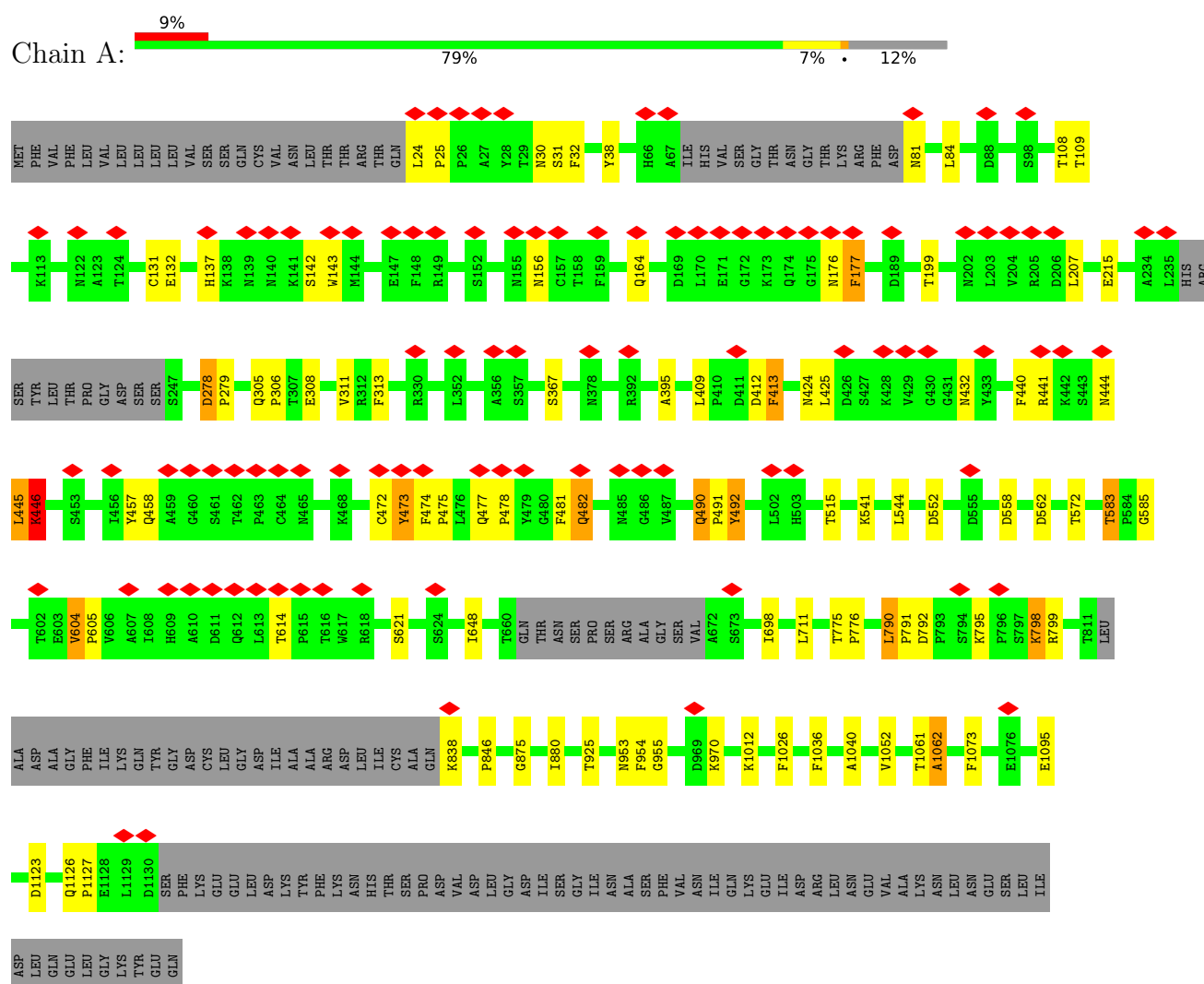
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Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
2	C	1	15	8	1	6	0

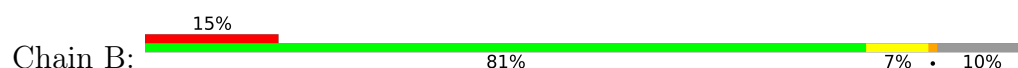
3 Residue-property plots

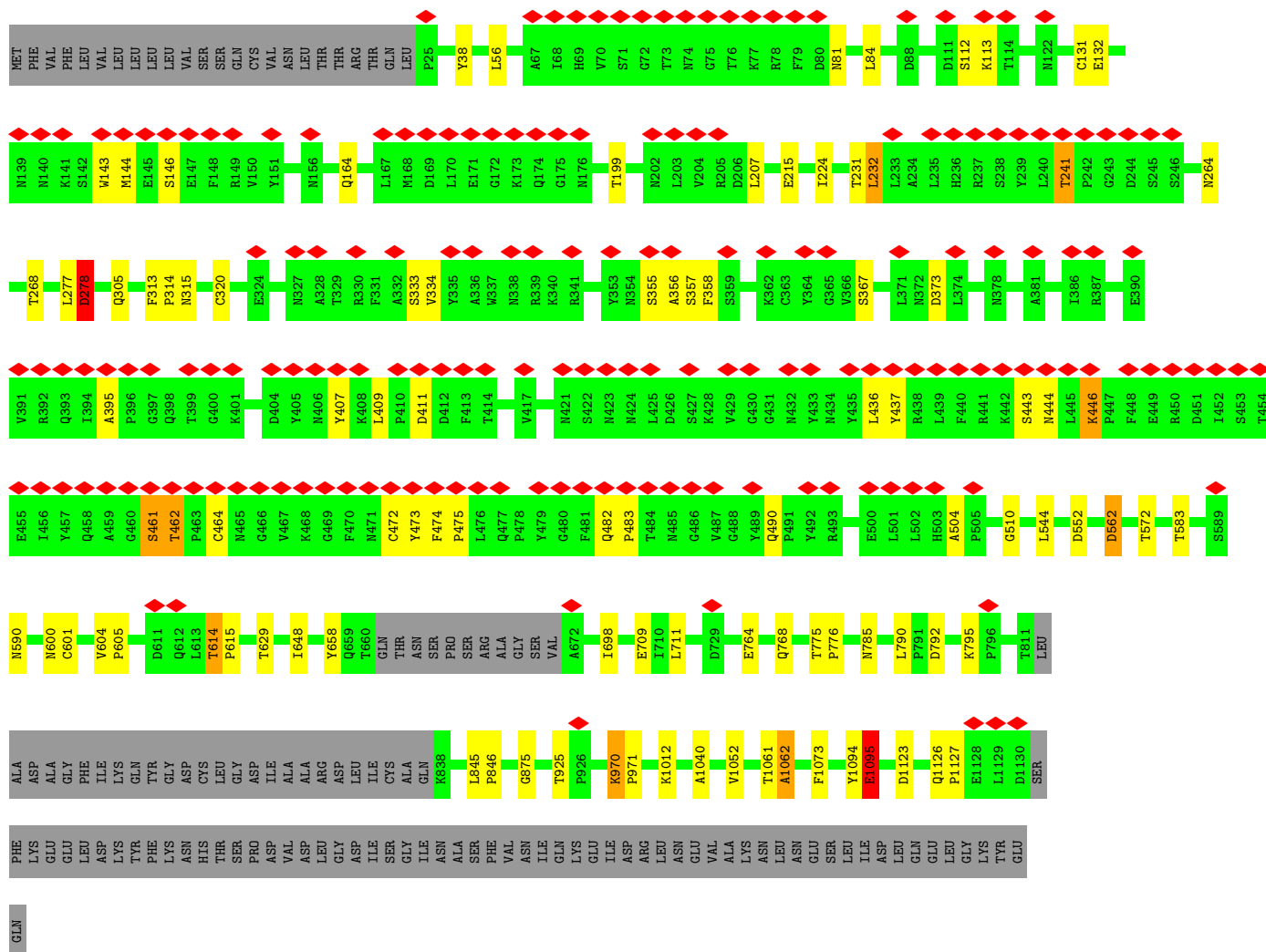
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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

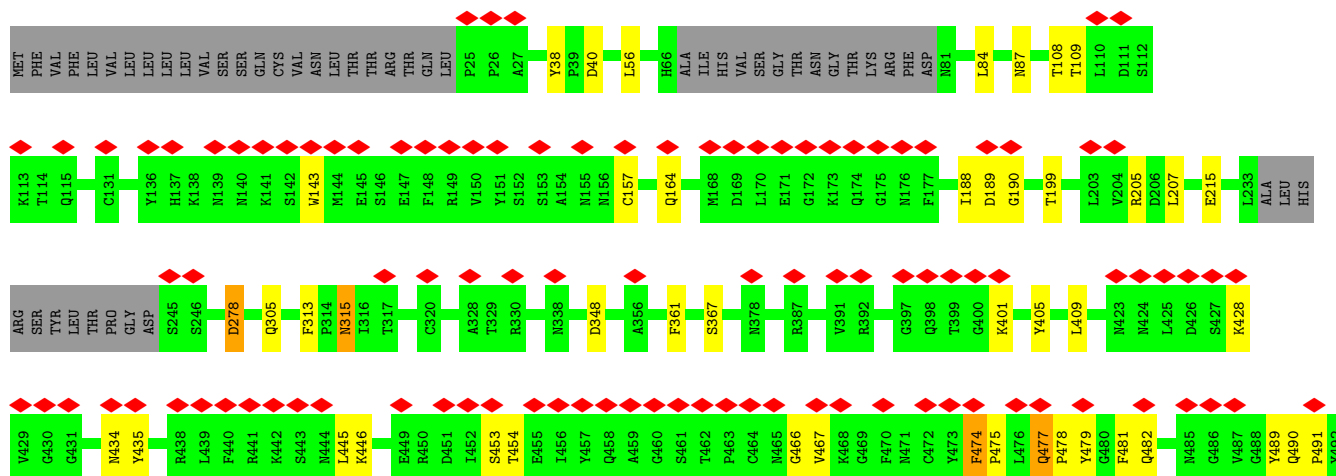
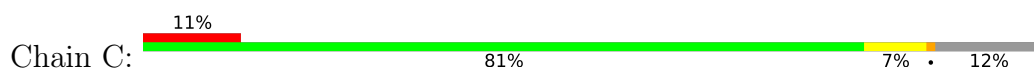


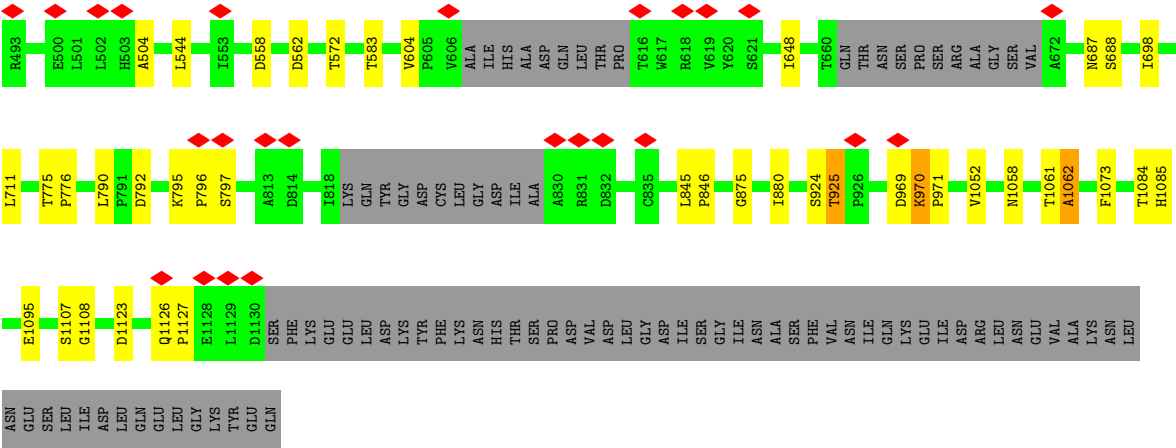
• Molecule 1: Spike glycoprotein





• Molecule 1: Spike glycoprotein





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	378064	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 ($e^-/\text{\AA}^2$)	52	Depositor
Minimum defocus (nm)	1400	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.073	Depositor
Minimum map value	-0.037	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0084	Depositor
Map size (Å)	366.168, 366.168, 366.168	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8322, 0.8322, 0.8322	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

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	0.63	0/8376	0.97	88/11402 (0.8%)
1	B	0.64	0/8560	0.96	90/11653 (0.8%)
1	C	0.65	0/8402	0.95	75/11431 (0.7%)
All	All	0.64	0/25338	0.96	253/34486 (0.7%)

There are no bond length outliers.

All (253) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	207	LEU	CA-C-N	8.56	128.29	119.56
1	C	207	LEU	C-N-CA	8.56	128.29	119.56
1	C	845	LEU	CA-C-N	8.39	125.70	119.66
1	C	845	LEU	C-N-CA	8.39	125.70	119.66
1	A	25	PRO	CA-C-N	8.27	128.42	120.31
1	A	25	PRO	C-N-CA	8.27	128.42	120.31
1	A	207	LEU	CA-C-N	8.18	128.06	120.21
1	A	207	LEU	C-N-CA	8.18	128.06	120.21
1	A	775	THR	CA-C-N	8.04	125.45	119.66
1	A	775	THR	C-N-CA	8.04	125.45	119.66
1	B	845	LEU	CA-C-N	8.00	125.42	119.66
1	B	845	LEU	C-N-CA	8.00	125.42	119.66
1	B	490	GLN	CA-C-N	7.83	127.89	119.90
1	B	490	GLN	C-N-CA	7.83	127.89	119.90
1	C	278	ASP	CA-C-N	7.52	127.23	119.56
1	C	278	ASP	C-N-CA	7.52	127.23	119.56
1	B	1062	ALA	CA-C-N	7.49	127.86	119.32
1	B	1062	ALA	C-N-CA	7.49	127.86	119.32
1	B	698	ILE	CA-C-N	7.47	127.52	119.90
1	B	698	ILE	C-N-CA	7.47	127.52	119.90
1	A	698	ILE	CA-C-N	7.46	127.50	119.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	698	ILE	C-N-CA	7.46	127.50	119.89
1	C	846	PRO	CA-C-N	7.43	127.36	119.85
1	C	846	PRO	C-N-CA	7.43	127.36	119.85
1	B	462	THR	CA-C-N	7.37	127.33	120.03
1	B	462	THR	C-N-CA	7.37	127.33	120.03
1	A	199	THR	CA-C-N	7.33	127.38	119.90
1	A	199	THR	C-N-CA	7.33	127.38	119.90
1	C	604	VAL	CA-C-N	7.29	127.27	119.76
1	C	604	VAL	C-N-CA	7.29	127.27	119.76
1	A	367	SER	CA-C-N	7.22	126.93	119.56
1	A	367	SER	C-N-CA	7.22	126.93	119.56
1	B	409	LEU	CA-C-N	7.12	126.82	119.56
1	B	409	LEU	C-N-CA	7.12	126.82	119.56
1	A	846	PRO	CA-C-N	7.09	127.05	120.03
1	A	846	PRO	C-N-CA	7.09	127.05	120.03
1	B	846	PRO	CA-C-N	6.99	126.91	119.85
1	B	846	PRO	C-N-CA	6.99	126.91	119.85
1	B	776	PRO	CA-C-N	6.97	126.60	119.56
1	B	776	PRO	C-N-CA	6.97	126.60	119.56
1	C	84	LEU	CA-C-N	6.94	126.97	119.89
1	C	84	LEU	C-N-CA	6.94	126.97	119.89
1	C	776	PRO	CA-C-N	6.89	126.52	119.56
1	C	776	PRO	C-N-CA	6.89	126.52	119.56
1	C	1062	ALA	CA-C-N	6.88	126.51	119.56
1	C	1062	ALA	C-N-CA	6.88	126.51	119.56
1	A	776	PRO	CA-C-N	6.85	126.55	119.56
1	A	776	PRO	C-N-CA	6.85	126.55	119.56
1	A	1062	ALA	CA-C-N	6.84	126.47	119.56
1	A	1062	ALA	C-N-CA	6.84	126.47	119.56
1	A	583	THR	CA-C-N	6.77	126.91	119.87
1	A	583	THR	C-N-CA	6.77	126.91	119.87
1	C	367	SER	CA-C-N	6.74	126.43	119.56
1	C	367	SER	C-N-CA	6.74	126.43	119.56
1	A	925	THR	CA-C-N	6.66	126.29	119.56
1	A	925	THR	C-N-CA	6.66	126.29	119.56
1	A	305	GLN	CA-C-N	6.66	126.61	119.28
1	A	305	GLN	C-N-CA	6.66	126.61	119.28
1	A	38	TYR	CA-C-N	6.56	126.18	119.56
1	A	38	TYR	C-N-CA	6.56	126.18	119.56
1	B	207	LEU	CA-C-N	6.56	126.47	119.85
1	B	207	LEU	C-N-CA	6.56	126.47	119.85
1	C	562	ASP	CA-C-N	6.54	126.23	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	562	ASP	C-N-CA	6.54	126.23	119.56
1	B	278	ASP	CA-C-N	6.50	127.01	119.47
1	B	278	ASP	C-N-CA	6.50	127.01	119.47
1	C	313	PHE	CA-C-N	6.48	126.51	119.90
1	C	313	PHE	C-N-CA	6.48	126.51	119.90
1	C	1052	VAL	CA-C-N	6.47	126.43	119.76
1	C	1052	VAL	C-N-CA	6.47	126.43	119.76
1	A	1052	VAL	CA-C-N	6.47	126.42	119.76
1	A	1052	VAL	C-N-CA	6.47	126.42	119.76
1	A	562	ASP	CA-C-N	6.46	126.15	119.56
1	A	562	ASP	C-N-CA	6.46	126.15	119.56
1	B	1095	GLU	CA-C-N	6.44	126.36	119.85
1	B	1095	GLU	C-N-CA	6.44	126.36	119.85
1	C	38	TYR	CA-C-N	6.44	126.07	119.56
1	C	38	TYR	C-N-CA	6.44	126.07	119.56
1	B	1052	VAL	CA-C-N	6.39	126.37	119.78
1	B	1052	VAL	C-N-CA	6.39	126.37	119.78
1	A	792	ASP	CA-C-N	6.37	126.50	119.87
1	A	792	ASP	C-N-CA	6.37	126.50	119.87
1	B	510	GLY	CA-C-N	6.37	126.32	119.76
1	B	510	GLY	C-N-CA	6.37	126.32	119.76
1	B	1123	ASP	CA-C-N	6.36	126.48	119.87
1	B	1123	ASP	C-N-CA	6.36	126.48	119.87
1	B	792	ASP	CA-C-N	6.34	126.47	119.87
1	B	792	ASP	C-N-CA	6.34	126.47	119.87
1	A	409	LEU	CA-C-N	6.31	126.28	120.03
1	A	409	LEU	C-N-CA	6.31	126.28	120.03
1	C	305	GLN	CA-C-N	6.30	126.06	119.76
1	C	305	GLN	C-N-CA	6.30	126.06	119.76
1	B	305	GLN	CA-C-N	6.29	126.20	119.85
1	B	305	GLN	C-N-CA	6.29	126.20	119.85
1	B	38	TYR	CA-C-N	6.28	126.40	119.87
1	B	38	TYR	C-N-CA	6.28	126.40	119.87
1	A	1123	ASP	CA-C-N	6.28	126.40	119.87
1	A	1123	ASP	C-N-CA	6.28	126.40	119.87
1	B	395	ALA	CA-C-N	6.28	125.96	119.56
1	B	395	ALA	C-N-CA	6.28	125.96	119.56
1	B	795	LYS	CA-C-N	6.26	126.46	119.32
1	B	795	LYS	C-N-CA	6.26	126.46	119.32
1	C	698	ILE	CA-C-N	6.26	126.21	119.76
1	C	698	ILE	C-N-CA	6.26	126.21	119.76
1	C	409	LEU	CA-C-N	6.21	126.17	119.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	409	LEU	C-N-CA	6.21	126.17	119.78
1	C	1095	GLU	CA-C-N	6.19	126.40	119.90
1	C	1095	GLU	C-N-CA	6.19	126.40	119.90
1	A	24	LEU	CA-C-N	6.18	126.75	120.38
1	A	24	LEU	C-N-CA	6.18	126.75	120.38
1	B	562	ASP	CA-C-N	6.17	125.79	119.56
1	B	562	ASP	C-N-CA	6.17	125.79	119.56
1	B	446	LYS	CA-C-N	6.16	126.19	119.90
1	B	446	LYS	C-N-CA	6.16	126.19	119.90
1	C	792	ASP	CA-C-N	6.14	126.26	119.87
1	C	792	ASP	C-N-CA	6.14	126.26	119.87
1	B	711	LEU	CA-C-N	6.14	126.09	119.76
1	B	711	LEU	C-N-CA	6.14	126.09	119.76
1	A	614	THR	CA-C-N	6.14	126.59	119.47
1	A	614	THR	C-N-CA	6.14	126.59	119.47
1	A	711	LEU	CA-C-N	6.13	126.08	119.76
1	A	711	LEU	C-N-CA	6.13	126.08	119.76
1	C	925	THR	CA-C-N	6.12	126.56	119.47
1	C	925	THR	C-N-CA	6.12	126.56	119.47
1	A	164	GLN	CA-C-N	6.10	126.01	119.85
1	A	164	GLN	C-N-CA	6.10	126.01	119.85
1	B	925	THR	CA-C-N	6.09	126.62	120.04
1	B	925	THR	C-N-CA	6.09	126.62	120.04
1	B	583	THR	CA-C-N	6.08	126.43	119.92
1	B	583	THR	C-N-CA	6.08	126.43	119.92
1	A	790	LEU	CA-C-N	6.07	126.01	119.76
1	A	790	LEU	C-N-CA	6.07	126.01	119.76
1	A	81	ASN	CA-C-N	6.04	126.00	119.78
1	A	81	ASN	C-N-CA	6.04	126.00	119.78
1	A	278	ASP	CA-C-N	5.99	126.42	119.47
1	A	278	ASP	C-N-CA	5.99	126.42	119.47
1	C	875	GLY	CA-C-N	5.98	126.17	120.31
1	C	875	GLY	C-N-CA	5.98	126.17	120.31
1	B	504	ALA	CA-C-N	5.96	125.98	119.90
1	B	504	ALA	C-N-CA	5.96	125.98	119.90
1	A	313	PHE	CA-C-N	5.95	125.91	119.78
1	A	313	PHE	C-N-CA	5.95	125.91	119.78
1	B	367	SER	CA-C-N	5.93	126.35	119.47
1	B	367	SER	C-N-CA	5.93	126.35	119.47
1	C	583	THR	CA-C-N	5.93	126.39	120.52
1	C	583	THR	C-N-CA	5.93	126.39	120.52
1	A	1095	GLU	CA-C-N	5.91	126.11	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1095	GLU	C-N-CA	5.91	126.11	119.90
1	B	241	THR	CA-C-N	5.90	125.52	119.56
1	B	241	THR	C-N-CA	5.90	125.52	119.56
1	A	875	GLY	CA-C-N	5.90	125.81	119.85
1	A	875	GLY	C-N-CA	5.90	125.81	119.85
1	A	215	GLU	CA-C-N	5.82	127.11	119.84
1	A	215	GLU	C-N-CA	5.82	127.11	119.84
1	B	215	GLU	CA-C-N	5.78	127.07	119.84
1	B	215	GLU	C-N-CA	5.78	127.07	119.84
1	B	790	LEU	CA-C-N	5.77	125.70	119.76
1	B	790	LEU	C-N-CA	5.77	125.70	119.76
1	B	875	GLY	CA-C-N	5.74	125.93	120.31
1	B	875	GLY	C-N-CA	5.74	125.93	120.31
1	B	614	THR	CA-C-N	5.69	126.95	119.84
1	B	614	THR	C-N-CA	5.69	126.95	119.84
1	B	648	ILE	CA-C-N	5.65	125.41	119.76
1	B	648	ILE	C-N-CA	5.65	125.41	119.76
1	B	775	THR	CA-C-N	5.64	126.19	120.38
1	B	775	THR	C-N-CA	5.64	126.19	120.38
1	C	880	ILE	CA-C-N	5.63	125.64	119.90
1	C	880	ILE	C-N-CA	5.63	125.64	119.90
1	C	1123	ASP	CA-C-N	5.62	126.86	119.84
1	C	1123	ASP	C-N-CA	5.62	126.86	119.84
1	A	395	ALA	CA-C-N	5.58	126.82	119.84
1	A	395	ALA	C-N-CA	5.58	126.82	119.84
1	A	798	LYS	CA-C-N	5.57	131.72	121.70
1	A	798	LYS	C-N-CA	5.57	131.72	121.70
1	C	215	GLU	CA-C-N	5.56	125.57	119.90
1	C	215	GLU	C-N-CA	5.56	125.57	119.90
1	A	482	GLN	CA-C-N	5.53	125.85	119.93
1	A	482	GLN	C-N-CA	5.53	125.85	119.93
1	A	544	LEU	CA-C-N	5.53	126.75	119.84
1	A	544	LEU	C-N-CA	5.53	126.75	119.84
1	A	795	LYS	CA-C-N	5.51	126.73	119.84
1	A	795	LYS	C-N-CA	5.51	126.73	119.84
1	C	790	LEU	CA-C-N	5.49	125.81	119.93
1	C	790	LEU	C-N-CA	5.49	125.81	119.93
1	C	775	THR	CA-C-N	5.48	126.02	120.38
1	C	775	THR	C-N-CA	5.48	126.02	120.38
1	C	572	THR	CA-C-N	5.47	125.44	120.03
1	C	572	THR	C-N-CA	5.47	125.44	120.03
1	C	711	LEU	CA-C-N	5.46	125.36	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	711	LEU	C-N-CA	5.46	125.36	119.85
1	B	84	LEU	CA-C-N	5.43	125.33	119.85
1	B	84	LEU	C-N-CA	5.43	125.33	119.85
1	B	199	THR	CA-C-N	5.43	125.60	119.90
1	B	199	THR	C-N-CA	5.43	125.60	119.90
1	B	544	LEU	CA-C-N	5.39	126.58	119.84
1	B	544	LEU	C-N-CA	5.39	126.58	119.84
1	A	648	ILE	CA-C-N	5.38	125.14	119.76
1	A	648	ILE	C-N-CA	5.38	125.14	119.76
1	C	544	LEU	CA-C-N	5.38	126.57	119.84
1	C	544	LEU	C-N-CA	5.38	126.57	119.84
1	C	164	GLN	CA-C-N	5.37	125.29	119.76
1	C	164	GLN	C-N-CA	5.37	125.29	119.76
1	C	504	ALA	CA-C-N	5.37	125.38	119.90
1	C	504	ALA	C-N-CA	5.37	125.38	119.90
1	C	474	PHE	CA-CB-CG	5.36	119.16	113.80
1	B	1040	ALA	CA-C-N	5.34	126.52	119.84
1	B	1040	ALA	C-N-CA	5.34	126.52	119.84
1	C	199	THR	CA-C-N	5.32	125.48	119.90
1	C	199	THR	C-N-CA	5.32	125.48	119.90
1	C	482	GLN	CA-C-N	5.29	125.20	119.85
1	C	482	GLN	C-N-CA	5.29	125.20	119.85
1	B	164	GLN	CA-C-N	5.29	125.23	119.78
1	B	164	GLN	C-N-CA	5.29	125.23	119.78
1	B	320	CYS	CA-C-N	5.26	126.41	119.84
1	B	320	CYS	C-N-CA	5.26	126.41	119.84
1	C	56	LEU	CA-C-N	5.26	125.26	119.90
1	C	56	LEU	C-N-CA	5.26	125.26	119.90
1	C	648	ILE	CA-C-N	5.24	125.00	119.76
1	C	648	ILE	C-N-CA	5.24	125.00	119.76
1	A	1036	PHE	CA-C-N	5.21	125.12	119.85
1	A	1036	PHE	C-N-CA	5.21	125.12	119.85
1	A	1073	PHE	CA-C-N	5.21	125.11	119.85
1	A	1073	PHE	C-N-CA	5.21	125.11	119.85
1	B	313	PHE	CA-C-N	5.18	126.32	119.84
1	B	313	PHE	C-N-CA	5.18	126.32	119.84
1	B	970	LYS	CA-C-N	5.14	124.76	119.56
1	B	970	LYS	C-N-CA	5.14	124.76	119.56
1	A	84	LEU	CA-C-N	5.14	125.04	119.85
1	A	84	LEU	C-N-CA	5.14	125.04	119.85
1	A	604	VAL	CA-C-N	5.11	124.78	119.56
1	A	604	VAL	C-N-CA	5.11	124.78	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	970	LYS	CA-C-N	5.10	124.76	119.56
1	A	970	LYS	C-N-CA	5.10	124.76	119.56
1	B	1073	PHE	CA-C-N	5.10	124.86	119.76
1	B	1073	PHE	C-N-CA	5.10	124.86	119.76
1	C	1073	PHE	CA-C-N	5.09	125.00	119.85
1	C	1073	PHE	C-N-CA	5.09	125.00	119.85
1	A	572	THR	CA-C-N	5.08	125.08	119.90
1	A	572	THR	C-N-CA	5.08	125.08	119.90
1	B	56	LEU	CA-C-N	5.08	125.01	119.78
1	B	56	LEU	C-N-CA	5.08	125.01	119.78
1	A	1040	ALA	CA-C-N	5.04	126.14	119.84
1	A	1040	ALA	C-N-CA	5.04	126.14	119.84
1	B	572	THR	CA-C-N	5.03	124.93	119.85
1	B	572	THR	C-N-CA	5.03	124.93	119.85
1	A	446	LYS	CA-C-N	5.03	125.31	119.93
1	A	446	LYS	C-N-CA	5.03	125.31	119.93
1	C	477	GLN	CA-C-N	5.02	125.46	120.14
1	C	477	GLN	C-N-CA	5.02	125.46	120.14
1	A	880	ILE	CA-C-N	5.01	125.01	119.90
1	A	880	ILE	C-N-CA	5.01	125.01	119.90
1	B	81	ASN	CA-C-N	5.00	124.90	119.85
1	B	81	ASN	C-N-CA	5.00	124.90	119.85

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	8183	0	8028	34	0
1	B	8360	0	8194	33	0
1	C	8211	0	8051	30	0
2	A	253	0	251	0	0
2	B	224	0	223	2	0
2	C	238	0	236	1	0
All	All	25469	0	24983	96	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 2.

All (96) 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:481:PHE:O	1:A:482:GLN:C	2.41	0.63
1:B:709:GLU:OE2	1:B:1012:LYS:NZ	2.34	0.60
1:A:541:LYS:NZ	1:A:558:ASP:OD2	2.34	0.60
1:B:590:ASN:ND2	1:B:658:TYR:OH	2.34	0.59
1:A:490:GLN:N	1:A:491:PRO:CD	2.66	0.59
1:C:490:GLN:N	1:C:491:PRO:HD3	2.18	0.57
1:B:1094:TYR:O	1:B:1095:GLU:C	2.46	0.57
1:A:838:LYS:NZ	1:C:558:ASP:OD1	2.38	0.56
1:A:108:THR:O	1:A:109:THR:C	2.49	0.55
1:C:428:LYS:NZ	1:C:489:TYR:O	2.39	0.55
1:B:436:LEU:O	1:B:437:TYR:C	2.50	0.55
1:A:798:LYS:HA	1:A:799:ARG:HB3	1.90	0.54
1:A:477:GLN:N	1:A:478:PRO:CD	2.70	0.54
1:B:264:ASN:ND2	1:B:268:THR:OG1	2.42	0.51
1:A:444:ASN:O	1:A:445:LEU:C	2.53	0.51
1:B:1126:GLN:N	1:B:1127:PRO:HD2	2.25	0.51
1:A:1012:LYS:NZ	1:A:1026:PHE:O	2.43	0.50
1:B:131:CYS:SG	1:B:132:GLU:N	2.85	0.50
1:B:461:SER:OG	1:B:462:THR:N	2.45	0.50
1:A:412:ASP:O	1:A:413:PHE:C	2.55	0.50
1:C:970:LYS:HB3	1:C:971:PRO:HD3	1.94	0.49
1:C:1107:SER:OG	1:C:1108:GLY:N	2.45	0.49
1:B:355:SER:OG	1:B:356:ALA:N	2.46	0.49
1:C:108:THR:O	1:C:109:THR:C	2.56	0.49
1:C:428:LYS:NZ	1:C:481:PHE:O	2.36	0.48
1:B:600:ASN:OD1	1:B:601:CYS:N	2.46	0.48
1:A:604:VAL:N	1:A:605:PRO:HD2	2.29	0.48
1:B:357:SER:OG	1:B:358:PHE:N	2.46	0.48
1:A:142:SER:OG	1:A:143:TRP:N	2.44	0.48
1:C:1126:GLN:N	1:C:1127:PRO:HD2	2.29	0.48
1:B:604:VAL:N	1:B:605:PRO:CD	2.77	0.47
1:B:474:PHE:N	1:B:475:PRO:CD	2.77	0.47
1:B:764:GLU:O	1:B:768:GLN:NE2	2.48	0.47
1:A:953:ASN:O	1:A:955:GLY:N	2.47	0.47
1:A:491:PRO:O	1:A:492:TYR:HB2	2.14	0.47
1:B:443:SER:O	1:B:444:ASN:C	2.58	0.47
1:C:490:GLN:N	1:C:491:PRO:CD	2.78	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1126:GLN:N	1:A:1127:PRO:HD2	2.29	0.46
1:C:924:SER:O	1:C:925:THR:C	2.59	0.46
1:A:440:PHE:O	1:A:441:ARG:HB2	2.16	0.46
1:A:472:CYS:O	1:A:473:TYR:CB	2.64	0.46
1:B:482:GLN:HB2	1:B:483:PRO:CD	2.45	0.46
1:C:969:ASP:O	1:C:970:LYS:CB	2.65	0.45
1:C:315:ASN:OD1	1:C:315:ASN:N	2.45	0.45
1:C:479:TYR:CG	1:C:479:TYR:O	2.70	0.45
1:C:1058:ASN:HD21	2:C:1210:NAG:H82	1.82	0.45
1:B:970:LYS:HB3	1:B:971:PRO:HD3	1.99	0.45
1:A:306:PRO:O	1:A:308:GLU:N	2.50	0.44
1:B:112:SER:OG	1:B:113:LYS:N	2.49	0.44
1:B:333:SER:OG	1:B:334:VAL:N	2.48	0.44
1:A:583:THR:HG22	1:A:585:GLY:H	1.83	0.44
1:A:176:ASN:O	1:A:177:PHE:HB2	2.18	0.44
1:A:474:PHE:N	1:A:475:PRO:HD2	2.34	0.43
1:A:445:LEU:O	1:A:446:LYS:HB2	2.18	0.43
1:B:562:ASP:OD1	1:B:562:ASP:C	2.61	0.43
1:C:453:SER:OG	1:C:454:THR:N	2.45	0.43
1:A:311:VAL:H	1:A:515:THR:HG22	1.82	0.43
1:B:143:TRP:N	1:B:146:SER:OG	2.52	0.43
1:A:457:TYR:O	1:A:458:GLN:C	2.61	0.43
1:B:315:ASN:ND2	2:B:1211:NAG:O1	2.51	0.43
1:B:472:CYS:O	1:B:473:TYR:HB3	2.18	0.43
1:C:474:PHE:N	1:C:475:PRO:HD2	2.33	0.43
1:C:477:GLN:HB2	1:C:478:PRO:HD3	2.01	0.43
1:B:231:THR:O	1:B:232:LEU:C	2.61	0.43
1:C:795:LYS:O	1:C:797:SER:N	2.52	0.42
1:B:474:PHE:N	1:B:475:PRO:HD3	2.34	0.42
1:C:445:LEU:O	1:C:446:LYS:HB2	2.20	0.42
1:A:131:CYS:SG	1:A:132:GLU:N	2.92	0.42
1:A:31:SER:OG	1:A:32:PHE:N	2.52	0.42
1:A:1061:THR:OG1	1:A:1062:ALA:N	2.52	0.42
1:C:477:GLN:CB	1:C:478:PRO:CD	2.97	0.42
1:B:143:TRP:CG	1:B:144:MET:N	2.88	0.42
1:B:277:LEU:O	1:B:278:ASP:HB3	2.20	0.42
1:C:348:ASP:OD1	1:C:348:ASP:N	2.48	0.42
1:C:40:ASP:OD1	1:C:40:ASP:C	2.62	0.41
1:C:687:ASN:OD1	1:C:688:SER:N	2.53	0.41
1:B:357:SER:O	1:B:358:PHE:C	2.64	0.41
1:A:30:ASN:HB3	1:A:32:PHE:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:278:ASP:HB2	1:A:279:PRO:HD2	2.03	0.41
1:B:1061:THR:OG1	1:B:1062:ALA:N	2.53	0.41
1:A:424:ASN:O	1:A:425:LEU:HB2	2.21	0.41
1:A:798:LYS:HA	1:A:799:ARG:CB	2.49	0.41
1:C:434:ASN:O	1:C:435:TYR:HB2	2.20	0.41
1:A:490:GLN:N	1:A:491:PRO:HD2	2.34	0.41
1:A:552:ASP:OD1	1:A:552:ASP:C	2.64	0.41
1:B:552:ASP:OD1	1:B:552:ASP:C	2.62	0.41
1:C:1061:THR:OG1	1:C:1062:ALA:N	2.54	0.41
1:A:790:LEU:HA	1:A:791:PRO:HD3	1.94	0.41
1:C:188:ILE:O	1:C:190:GLY:N	2.54	0.41
1:C:969:ASP:OD1	1:C:969:ASP:N	2.46	0.41
1:C:1084:THR:OG1	1:C:1085:HIS:N	2.52	0.40
1:B:143:TRP:CG	1:B:144:MET:H	2.40	0.40
1:C:401:LYS:O	1:C:405:TYR:CD2	2.74	0.40
1:B:614:THR:HA	1:B:615:PRO:HD3	1.96	0.40
1:B:785:ASN:ND2	2:B:1208:NAG:O5	2.54	0.40
1:C:477:GLN:HB2	1:C:478:PRO:CD	2.50	0.40

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	1036/1192 (87%)	964 (93%)	61 (6%)	11 (1%)	11	36
1	B	1063/1192 (89%)	999 (94%)	52 (5%)	12 (1%)	11	36
1	C	1038/1192 (87%)	973 (94%)	55 (5%)	10 (1%)	12	39
All	All	3137/3576 (88%)	2936 (94%)	168 (5%)	33 (1%)	14	36

All (33) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	156	ASN
1	A	954	PHE
1	C	970	LYS
1	A	413	PHE
1	A	445	LEU
1	A	492	TYR
1	B	224	ILE
1	B	232	LEU
1	B	411	ASP
1	B	464	CYS
1	C	87	ASN
1	A	473	TYR
1	C	189	ASP
1	C	205	ARG
1	B	407	TYR
1	B	446	LYS
1	B	461	SER
1	C	361	PHE
1	C	796	PRO
1	A	177	PHE
1	A	432	ASN
1	C	157	CYS
1	A	621	SER
1	B	373	ASP
1	C	143	TRP
1	C	466	GLY
1	A	490	GLN
1	B	278	ASP
1	B	241	THR
1	A	446	LYS
1	B	314	PRO
1	B	1095	GLU
1	C	278	ASP

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	916/1044 (88%)	915 (100%)	1 (0%)	88	89
1	B	936/1044 (90%)	935 (100%)	1 (0%)	88	89
1	C	919/1044 (88%)	917 (100%)	2 (0%)	87	87
All	All	2771/3132 (88%)	2767 (100%)	4 (0%)	87	89

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	137	HIS
1	B	629	THR
1	C	315	ASN
1	C	467	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	209	GLN
1	A	305	GLN
1	A	612	GLN
1	B	266	ASN
1	B	444	ASN
1	B	520	ASN
1	B	548	GLN
1	B	693	ASN
1	B	994	GLN
1	B	1042	HIS
1	B	1058	ASN
1	C	81	ASN
1	C	134	GLN
1	C	202	ASN
1	C	301	ASN
1	C	398	GLN
1	C	490	GLN
1	C	597	GLN
1	C	639	HIS
1	C	659	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

48 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$
2	NAG	C	1208	-	15,15,15	1.21	2 (13%)	21,21,21	0.98	1 (4%)
2	NAG	C	1214	-	15,15,15	1.28	2 (13%)	21,21,21	0.98	2 (9%)
2	NAG	A	1214	-	15,15,15	1.31	2 (13%)	21,21,21	0.93	1 (4%)
2	NAG	B	1201	-	15,15,15	1.32	2 (13%)	21,21,21	0.98	1 (4%)
2	NAG	B	1210	1	14,14,15	1.22	2 (14%)	17,19,21	1.08	1 (5%)
2	NAG	C	1204	1	14,14,15	1.52	2 (14%)	17,19,21	1.31	2 (11%)
2	NAG	A	1209	-	15,15,15	1.31	2 (13%)	21,21,21	0.96	1 (4%)
2	NAG	C	1210	-	15,15,15	1.30	2 (13%)	21,21,21	0.99	1 (4%)
2	NAG	A	1212	-	15,15,15	1.26	2 (13%)	21,21,21	0.98	1 (4%)
2	NAG	B	1214	-	15,15,15	1.30	2 (13%)	21,21,21	0.98	1 (4%)
2	NAG	C	1206	-	15,15,15	1.36	2 (13%)	21,21,21	0.94	1 (4%)
2	NAG	B	1208	-	15,15,15	1.28	2 (13%)	21,21,21	0.93	1 (4%)
2	NAG	C	1211	-	15,15,15	1.31	2 (13%)	21,21,21	1.01	2 (9%)
2	NAG	A	1213	-	15,15,15	1.34	2 (13%)	21,21,21	0.92	1 (4%)
2	NAG	B	1206	-	15,15,15	1.30	2 (13%)	21,21,21	1.02	2 (9%)
2	NAG	B	1203	-	15,15,15	1.41	2 (13%)	21,21,21	0.99	1 (4%)
2	NAG	C	1205	-	15,15,15	1.29	2 (13%)	21,21,21	0.97	1 (4%)
2	NAG	A	1207	-	15,15,15	1.30	2 (13%)	21,21,21	0.95	1 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	A	1204	-	15,15,15	1.31	2 (13%)	21,21,21	1.03	2 (9%)
2	NAG	B	1211	-	15,15,15	1.30	2 (13%)	21,21,21	0.92	1 (4%)
2	NAG	C	1207	-	15,15,15	1.31	2 (13%)	21,21,21	1.00	1 (4%)
2	NAG	A	1217	-	15,15,15	1.32	2 (13%)	21,21,21	1.08	1 (4%)
2	NAG	A	1210	-	15,15,15	1.24	2 (13%)	21,21,21	0.99	1 (4%)
2	NAG	A	1208	-	15,15,15	1.32	2 (13%)	21,21,21	0.93	1 (4%)
2	NAG	B	1202	-	15,15,15	1.31	2 (13%)	21,21,21	0.94	1 (4%)
2	NAG	A	1202	-	15,15,15	1.33	2 (13%)	21,21,21	0.95	1 (4%)
2	NAG	C	1202	-	15,15,15	1.35	2 (13%)	21,21,21	0.95	1 (4%)
2	NAG	A	1211	-	15,15,15	1.36	2 (13%)	21,21,21	0.98	1 (4%)
2	NAG	C	1213	-	15,15,15	1.30	2 (13%)	21,21,21	0.98	2 (9%)
2	NAG	A	1203	-	15,15,15	1.33	2 (13%)	21,21,21	0.97	1 (4%)
2	NAG	C	1216	-	15,15,15	1.28	2 (13%)	21,21,21	0.99	2 (9%)
2	NAG	C	1203	-	15,15,15	1.30	2 (13%)	21,21,21	0.97	1 (4%)
2	NAG	A	1216	-	15,15,15	1.32	2 (13%)	21,21,21	0.93	1 (4%)
2	NAG	B	1205	-	15,15,15	1.33	2 (13%)	21,21,21	0.97	1 (4%)
2	NAG	A	1205	-	15,15,15	1.31	2 (13%)	21,21,21	0.95	1 (4%)
2	NAG	A	1206	1	14,14,15	1.37	2 (14%)	17,19,21	1.13	2 (11%)
2	NAG	B	1212	-	15,15,15	1.31	2 (13%)	21,21,21	0.99	1 (4%)
2	NAG	C	1209	-	15,15,15	1.27	2 (13%)	21,21,21	1.02	1 (4%)
2	NAG	A	1201	-	15,15,15	1.33	2 (13%)	21,21,21	1.03	2 (9%)
2	NAG	B	1207	-	15,15,15	1.27	2 (13%)	21,21,21	0.94	1 (4%)
2	NAG	C	1201	-	15,15,15	1.37	2 (13%)	21,21,21	1.09	2 (9%)
2	NAG	B	1215	-	15,15,15	1.32	2 (13%)	21,21,21	1.04	2 (9%)
2	NAG	C	1212	1	14,14,15	1.43	2 (14%)	17,19,21	1.15	1 (5%)
2	NAG	C	1215	-	15,15,15	1.33	2 (13%)	21,21,21	0.98	1 (4%)
2	NAG	B	1209	-	15,15,15	1.27	2 (13%)	21,21,21	0.99	1 (4%)
2	NAG	B	1204	-	15,15,15	1.29	2 (13%)	21,21,21	1.03	2 (9%)
2	NAG	A	1215	1	14,14,15	1.33	2 (14%)	17,19,21	1.05	1 (5%)
2	NAG	B	1213	-	15,15,15	1.36	2 (13%)	21,21,21	0.97	1 (4%)

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	C	1208	-	-	0/6/26/26	0/1/1/1
2	NAG	C	1214	-	-	0/6/26/26	0/1/1/1
2	NAG	A	1214	-	-	1/6/26/26	0/1/1/1
2	NAG	B	1201	-	-	1/6/26/26	0/1/1/1
2	NAG	B	1210	1	-	0/6/23/26	0/1/1/1
2	NAG	C	1204	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1209	-	-	1/6/26/26	0/1/1/1
2	NAG	C	1210	-	-	2/6/26/26	0/1/1/1
2	NAG	A	1212	-	-	0/6/26/26	0/1/1/1
2	NAG	B	1214	-	-	1/6/26/26	0/1/1/1
2	NAG	C	1206	-	-	0/6/26/26	0/1/1/1
2	NAG	B	1208	-	-	0/6/26/26	0/1/1/1
2	NAG	C	1211	-	-	2/6/26/26	0/1/1/1
2	NAG	A	1213	-	-	1/6/26/26	0/1/1/1
2	NAG	B	1206	-	-	1/6/26/26	0/1/1/1
2	NAG	B	1203	-	-	1/6/26/26	0/1/1/1
2	NAG	C	1205	-	-	1/6/26/26	0/1/1/1
2	NAG	A	1207	-	-	1/6/26/26	0/1/1/1
2	NAG	A	1204	-	-	1/6/26/26	0/1/1/1
2	NAG	B	1211	-	-	1/6/26/26	0/1/1/1
2	NAG	C	1207	-	-	1/6/26/26	0/1/1/1
2	NAG	A	1217	-	-	1/6/26/26	0/1/1/1
2	NAG	A	1210	-	-	1/6/26/26	0/1/1/1
2	NAG	A	1208	-	-	1/6/26/26	0/1/1/1
2	NAG	B	1202	-	-	1/6/26/26	0/1/1/1
2	NAG	A	1202	-	-	0/6/26/26	0/1/1/1
2	NAG	C	1202	-	-	0/6/26/26	0/1/1/1
2	NAG	A	1211	-	-	0/6/26/26	0/1/1/1
2	NAG	C	1213	-	-	1/6/26/26	0/1/1/1
2	NAG	A	1203	-	-	1/6/26/26	0/1/1/1
2	NAG	C	1216	-	-	0/6/26/26	0/1/1/1
2	NAG	C	1203	-	-	0/6/26/26	0/1/1/1
2	NAG	A	1216	-	-	1/6/26/26	0/1/1/1
2	NAG	B	1205	-	-	1/6/26/26	0/1/1/1
2	NAG	A	1205	-	-	1/6/26/26	0/1/1/1
2	NAG	A	1206	1	1/1/5/7	0/6/23/26	0/1/1/1
2	NAG	B	1212	-	-	1/6/26/26	0/1/1/1
2	NAG	C	1209	-	-	0/6/26/26	0/1/1/1
2	NAG	A	1201	-	-	2/6/26/26	0/1/1/1
2	NAG	B	1207	-	-	0/6/26/26	0/1/1/1
2	NAG	C	1201	-	-	1/6/26/26	0/1/1/1
2	NAG	B	1215	-	-	2/6/26/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	C	1212	1	-	0/6/23/26	0/1/1/1
2	NAG	C	1215	-	-	0/6/26/26	0/1/1/1
2	NAG	B	1209	-	-	2/6/26/26	0/1/1/1
2	NAG	B	1204	-	-	1/6/26/26	0/1/1/1
2	NAG	A	1215	1	-	1/6/23/26	0/1/1/1
2	NAG	B	1213	-	-	1/6/26/26	0/1/1/1

All (96) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1204	NAG	C1-C2	4.29	1.58	1.52
2	C	1212	NAG	C1-C2	4.16	1.58	1.52
2	A	1206	NAG	C1-C2	4.11	1.57	1.52
2	A	1215	NAG	C1-C2	3.89	1.57	1.52
2	B	1203	NAG	C1-C2	3.64	1.57	1.52
2	A	1211	NAG	C1-C2	3.58	1.57	1.52
2	B	1213	NAG	C1-C2	3.58	1.57	1.52
2	C	1206	NAG	C1-C2	3.56	1.57	1.52
2	A	1213	NAG	C1-C2	3.54	1.57	1.52
2	C	1201	NAG	C1-C2	3.50	1.57	1.52
2	A	1202	NAG	C1-C2	3.47	1.57	1.52
2	A	1208	NAG	C1-C2	3.45	1.57	1.52
2	C	1215	NAG	C1-C2	3.43	1.57	1.52
2	A	1209	NAG	C1-C2	3.43	1.57	1.52
2	B	1201	NAG	C1-C2	3.42	1.57	1.52
2	A	1201	NAG	C1-C2	3.41	1.57	1.52
2	C	1202	NAG	C1-C2	3.40	1.57	1.52
2	C	1207	NAG	C1-C2	3.38	1.57	1.52
2	B	1210	NAG	C1-C2	3.37	1.56	1.52
2	B	1205	NAG	C1-C2	3.35	1.56	1.52
2	A	1216	NAG	C1-C2	3.34	1.56	1.52
2	B	1215	NAG	C1-C2	3.33	1.56	1.52
2	C	1210	NAG	C1-C2	3.33	1.56	1.52
2	A	1214	NAG	C1-C2	3.32	1.56	1.52
2	C	1211	NAG	C1-C2	3.32	1.56	1.52
2	A	1203	NAG	C1-C2	3.32	1.56	1.52
2	B	1214	NAG	C1-C2	3.31	1.56	1.52
2	C	1205	NAG	C1-C2	3.31	1.56	1.52
2	B	1212	NAG	C1-C2	3.31	1.56	1.52
2	B	1211	NAG	C1-C2	3.31	1.56	1.52
2	C	1203	NAG	C1-C2	3.31	1.56	1.52
2	A	1205	NAG	C1-C2	3.31	1.56	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1202	NAG	C1-C2	3.29	1.56	1.52
2	A	1204	NAG	C1-C2	3.28	1.56	1.52
2	B	1206	NAG	C1-C2	3.28	1.56	1.52
2	B	1207	NAG	C1-C2	3.27	1.56	1.52
2	A	1207	NAG	C1-C2	3.27	1.56	1.52
2	A	1217	NAG	C1-C2	3.26	1.56	1.52
2	B	1208	NAG	C1-C2	3.26	1.56	1.52
2	C	1209	NAG	C1-C2	3.24	1.56	1.52
2	B	1209	NAG	C1-C2	3.23	1.56	1.52
2	C	1213	NAG	C1-C2	3.21	1.56	1.52
2	A	1212	NAG	C1-C2	3.19	1.56	1.52
2	B	1204	NAG	C1-C2	3.13	1.56	1.52
2	C	1214	NAG	C1-C2	3.13	1.56	1.52
2	C	1216	NAG	C1-C2	3.12	1.56	1.52
2	A	1210	NAG	C1-C2	3.08	1.56	1.52
2	C	1208	NAG	C1-C2	2.97	1.56	1.52
2	B	1203	NAG	O1-C1	2.90	1.48	1.39
2	B	1204	NAG	O1-C1	2.87	1.48	1.39
2	C	1215	NAG	O1-C1	2.87	1.48	1.39
2	A	1211	NAG	O1-C1	2.86	1.48	1.39
2	C	1213	NAG	O1-C1	2.85	1.48	1.39
2	B	1212	NAG	O1-C1	2.85	1.48	1.39
2	C	1202	NAG	O1-C1	2.84	1.48	1.39
2	C	1206	NAG	O1-C1	2.84	1.48	1.39
2	A	1204	NAG	O1-C1	2.83	1.48	1.39
2	A	1205	NAG	O1-C1	2.82	1.48	1.39
2	A	1213	NAG	O1-C1	2.82	1.48	1.39
2	C	1203	NAG	O1-C1	2.82	1.48	1.39
2	C	1211	NAG	O1-C1	2.82	1.48	1.39
2	B	1201	NAG	O1-C1	2.81	1.48	1.39
2	B	1205	NAG	O1-C1	2.81	1.48	1.39
2	A	1216	NAG	O1-C1	2.81	1.48	1.39
2	A	1209	NAG	O1-C1	2.81	1.48	1.39
2	B	1208	NAG	O1-C1	2.81	1.48	1.39
2	B	1214	NAG	O1-C1	2.80	1.48	1.39
2	C	1214	NAG	O1-C1	2.80	1.48	1.39
2	C	1209	NAG	O1-C1	2.80	1.48	1.39
2	A	1203	NAG	O1-C1	2.80	1.48	1.39
2	B	1202	NAG	O1-C1	2.79	1.48	1.39
2	C	1216	NAG	O1-C1	2.79	1.48	1.39
2	A	1214	NAG	O1-C1	2.79	1.48	1.39
2	A	1201	NAG	O1-C1	2.78	1.48	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1207	NAG	O1-C1	2.78	1.48	1.39
2	A	1217	NAG	O1-C1	2.78	1.48	1.39
2	B	1211	NAG	O1-C1	2.77	1.48	1.39
2	B	1213	NAG	O1-C1	2.77	1.48	1.39
2	A	1210	NAG	O1-C1	2.77	1.48	1.39
2	A	1208	NAG	O1-C1	2.77	1.48	1.39
2	C	1208	NAG	O1-C1	2.76	1.48	1.39
2	B	1207	NAG	O1-C1	2.76	1.48	1.39
2	A	1202	NAG	O1-C1	2.76	1.48	1.39
2	C	1207	NAG	O1-C1	2.75	1.48	1.39
2	B	1206	NAG	O1-C1	2.75	1.48	1.39
2	C	1210	NAG	O1-C1	2.74	1.48	1.39
2	B	1215	NAG	O1-C1	2.74	1.48	1.39
2	C	1201	NAG	O1-C1	2.71	1.48	1.39
2	C	1205	NAG	O1-C1	2.70	1.48	1.39
2	B	1209	NAG	O1-C1	2.69	1.48	1.39
2	A	1212	NAG	O1-C1	2.68	1.48	1.39
2	C	1212	NAG	O5-C5	2.46	1.48	1.43
2	C	1204	NAG	O5-C5	2.40	1.48	1.43
2	B	1210	NAG	O5-C5	2.12	1.47	1.43
2	A	1206	NAG	O5-C5	2.11	1.47	1.43
2	A	1215	NAG	O5-C5	2.10	1.47	1.43

All (60) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1204	NAG	C8-C7-N2	3.22	121.46	116.12
2	C	1212	NAG	C8-C7-N2	2.80	120.76	116.12
2	A	1217	NAG	C8-C7-N2	2.79	120.75	116.12
2	C	1209	NAG	C8-C7-N2	2.70	120.60	116.12
2	A	1211	NAG	C8-C7-N2	2.70	120.59	116.12
2	B	1210	NAG	C8-C7-N2	2.68	120.56	116.12
2	C	1210	NAG	C8-C7-N2	2.65	120.51	116.12
2	C	1207	NAG	C8-C7-N2	2.64	120.49	116.12
2	A	1201	NAG	C8-C7-N2	2.62	120.47	116.12
2	C	1205	NAG	C8-C7-N2	2.61	120.45	116.12
2	C	1208	NAG	C8-C7-N2	2.59	120.42	116.12
2	A	1207	NAG	C8-C7-N2	2.59	120.41	116.12
2	B	1209	NAG	C8-C7-N2	2.57	120.38	116.12
2	B	1214	NAG	C8-C7-N2	2.57	120.38	116.12
2	A	1210	NAG	C8-C7-N2	2.57	120.38	116.12
2	B	1206	NAG	C8-C7-N2	2.55	120.35	116.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1212	NAG	C8-C7-N2	2.55	120.34	116.12
2	B	1215	NAG	C8-C7-N2	2.54	120.34	116.12
2	A	1209	NAG	C8-C7-N2	2.53	120.31	116.12
2	A	1212	NAG	C8-C7-N2	2.52	120.29	116.12
2	C	1215	NAG	C8-C7-N2	2.51	120.28	116.12
2	A	1204	NAG	C8-C7-N2	2.50	120.27	116.12
2	B	1202	NAG	C8-C7-N2	2.49	120.25	116.12
2	B	1201	NAG	C8-C7-N2	2.49	120.25	116.12
2	A	1215	NAG	C8-C7-N2	2.49	120.25	116.12
2	A	1205	NAG	C8-C7-N2	2.49	120.25	116.12
2	B	1207	NAG	C8-C7-N2	2.48	120.24	116.12
2	B	1204	NAG	C8-C7-N2	2.48	120.23	116.12
2	A	1202	NAG	C8-C7-N2	2.47	120.22	116.12
2	A	1206	NAG	C8-C7-N2	2.47	120.21	116.12
2	A	1208	NAG	C8-C7-N2	2.47	120.21	116.12
2	B	1205	NAG	C8-C7-N2	2.47	120.21	116.12
2	C	1213	NAG	C8-C7-N2	2.45	120.19	116.12
2	C	1202	NAG	C8-C7-N2	2.45	120.18	116.12
2	C	1201	NAG	C1-C2-N2	-2.43	107.91	110.73
2	C	1216	NAG	C8-C7-N2	2.43	120.15	116.12
2	A	1214	NAG	C8-C7-N2	2.43	120.14	116.12
2	C	1206	NAG	C8-C7-N2	2.42	120.12	116.12
2	B	1203	NAG	C8-C7-N2	2.39	120.08	116.12
2	C	1211	NAG	C8-C7-N2	2.38	120.07	116.12
2	B	1213	NAG	C8-C7-N2	2.38	120.07	116.12
2	A	1203	NAG	C8-C7-N2	2.38	120.06	116.12
2	C	1203	NAG	C8-C7-N2	2.38	120.06	116.12
2	A	1213	NAG	C8-C7-N2	2.37	120.05	116.12
2	C	1201	NAG	C8-C7-N2	2.33	119.98	116.12
2	A	1216	NAG	C8-C7-N2	2.31	119.95	116.12
2	B	1204	NAG	C1-C2-N2	-2.29	108.08	110.73
2	B	1208	NAG	C8-C7-N2	2.28	119.91	116.12
2	C	1214	NAG	C8-C7-N2	2.24	119.83	116.12
2	B	1215	NAG	C1-C2-N2	-2.24	108.14	110.73
2	C	1204	NAG	O7-C7-C8	-2.18	118.17	122.05
2	C	1216	NAG	C1-C2-N2	-2.18	108.20	110.73
2	B	1211	NAG	C8-C7-N2	2.18	119.73	116.12
2	C	1214	NAG	C1-C2-N2	-2.18	108.20	110.73
2	C	1211	NAG	C1-C2-N2	-2.13	108.26	110.73
2	B	1206	NAG	C1-C2-N2	-2.10	108.30	110.73
2	A	1204	NAG	C1-C2-N2	-2.07	108.33	110.73
2	A	1206	NAG	C2-N2-C7	-2.05	120.15	122.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1201	NAG	C1-C2-N2	-2.04	108.36	110.73
2	C	1213	NAG	C1-C2-N2	-2.00	108.41	110.73

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	1206	NAG	C1

All (38) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	1204	NAG	O5-C5-C6-O6
2	C	1204	NAG	C4-C5-C6-O6
2	A	1201	NAG	C1-C2-N2-C7
2	A	1207	NAG	O5-C5-C6-O6
2	A	1209	NAG	O5-C5-C6-O6
2	A	1213	NAG	O5-C5-C6-O6
2	A	1203	NAG	O5-C5-C6-O6
2	B	1204	NAG	O5-C5-C6-O6
2	A	1217	NAG	O5-C5-C6-O6
2	B	1205	NAG	O5-C5-C6-O6
2	A	1208	NAG	O5-C5-C6-O6
2	A	1214	NAG	O5-C5-C6-O6
2	A	1201	NAG	O5-C5-C6-O6
2	A	1205	NAG	O5-C5-C6-O6
2	B	1202	NAG	O5-C5-C6-O6
2	B	1211	NAG	O5-C5-C6-O6
2	C	1207	NAG	O5-C5-C6-O6
2	B	1214	NAG	O5-C5-C6-O6
2	B	1215	NAG	O5-C5-C6-O6
2	A	1210	NAG	O5-C5-C6-O6
2	A	1215	NAG	O5-C5-C6-O6
2	A	1216	NAG	O5-C5-C6-O6
2	B	1201	NAG	O5-C5-C6-O6
2	B	1212	NAG	O5-C5-C6-O6
2	C	1201	NAG	O5-C5-C6-O6
2	A	1204	NAG	O5-C5-C6-O6
2	B	1213	NAG	O5-C5-C6-O6
2	C	1205	NAG	O5-C5-C6-O6
2	C	1211	NAG	O5-C5-C6-O6
2	C	1213	NAG	O5-C5-C6-O6
2	B	1203	NAG	O5-C5-C6-O6

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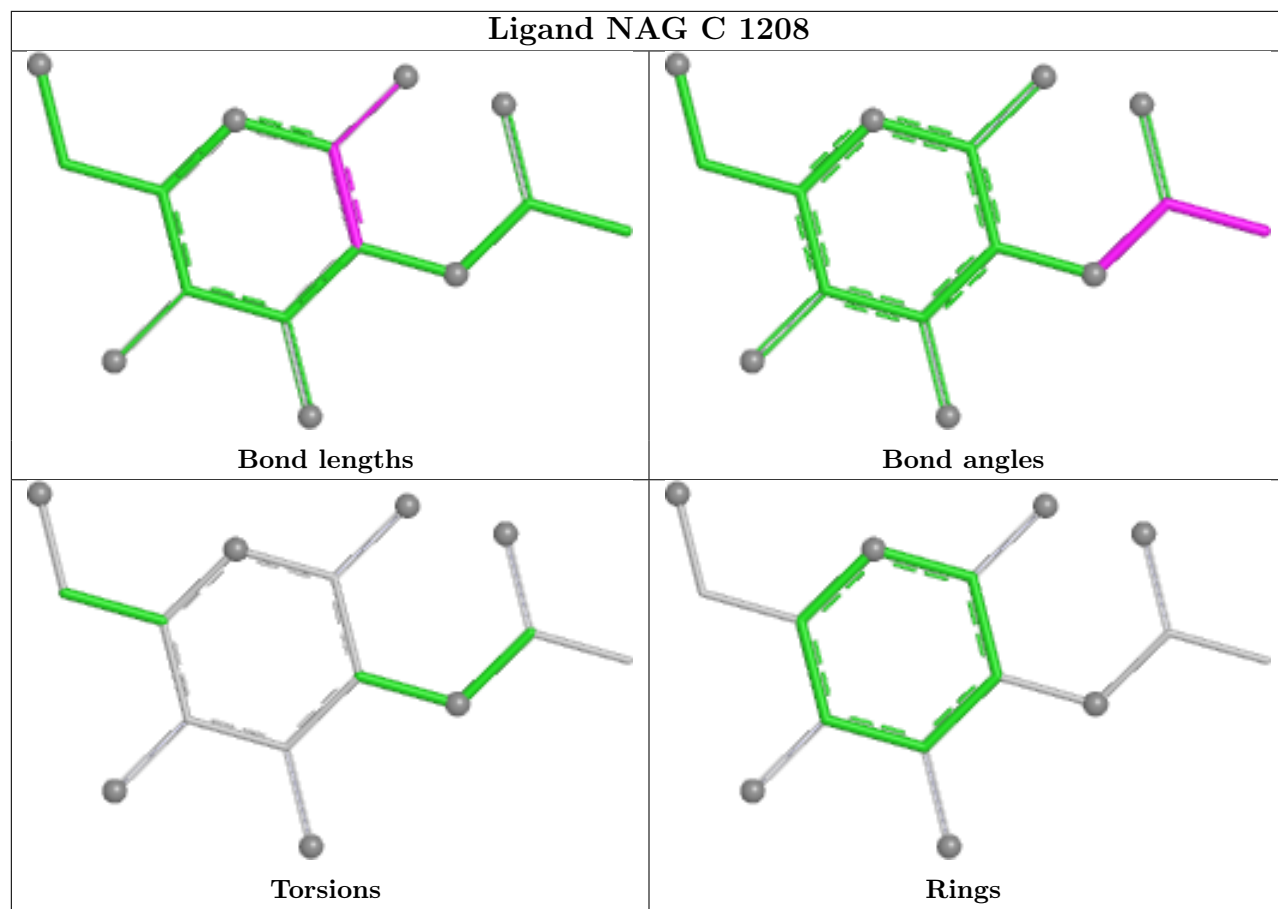
Mol	Chain	Res	Type	Atoms
2	B	1209	NAG	C4-C5-C6-O6
2	B	1209	NAG	O5-C5-C6-O6
2	B	1206	NAG	C1-C2-N2-C7
2	B	1215	NAG	C1-C2-N2-C7
2	C	1211	NAG	C1-C2-N2-C7
2	C	1210	NAG	C4-C5-C6-O6
2	C	1210	NAG	O5-C5-C6-O6

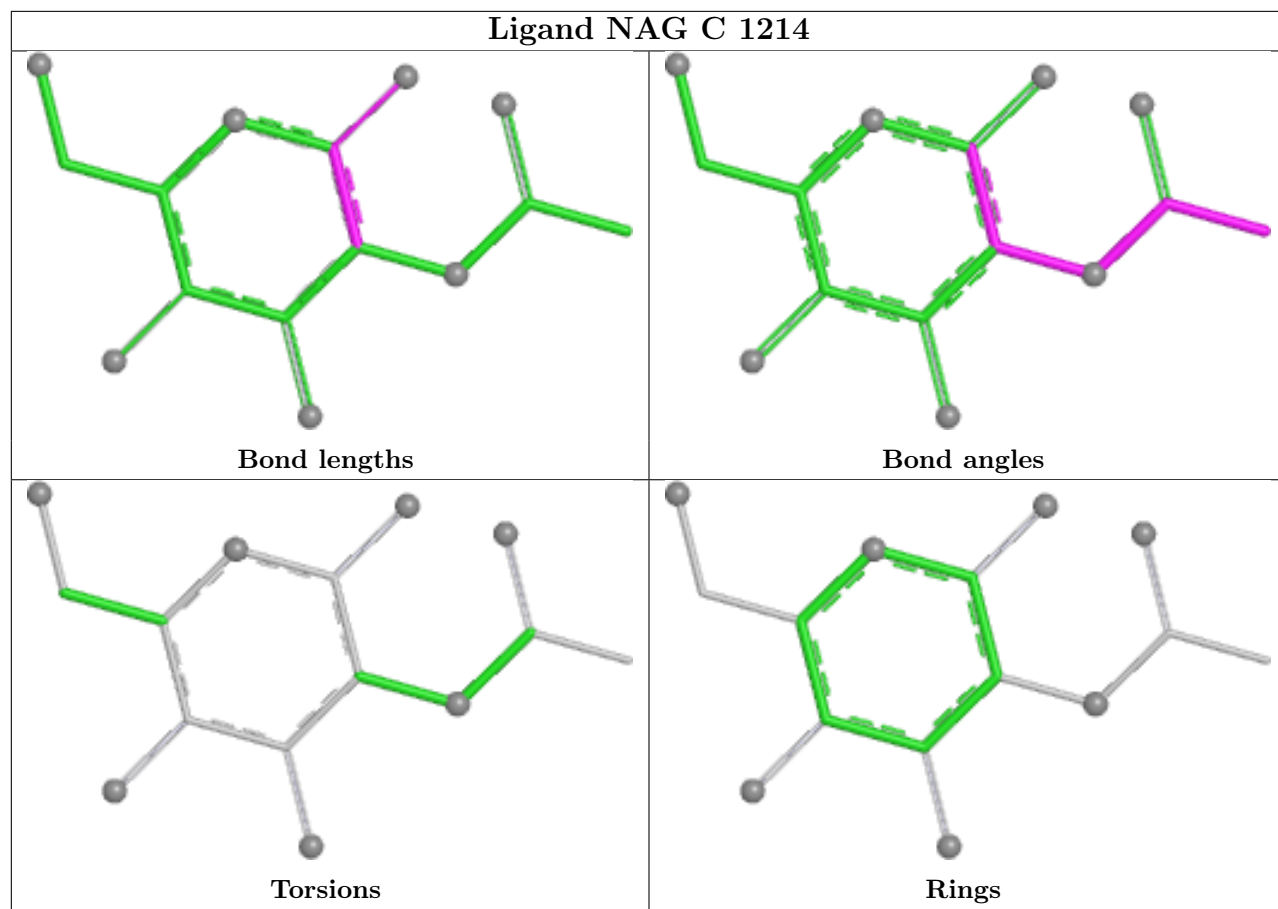
There are no ring outliers.

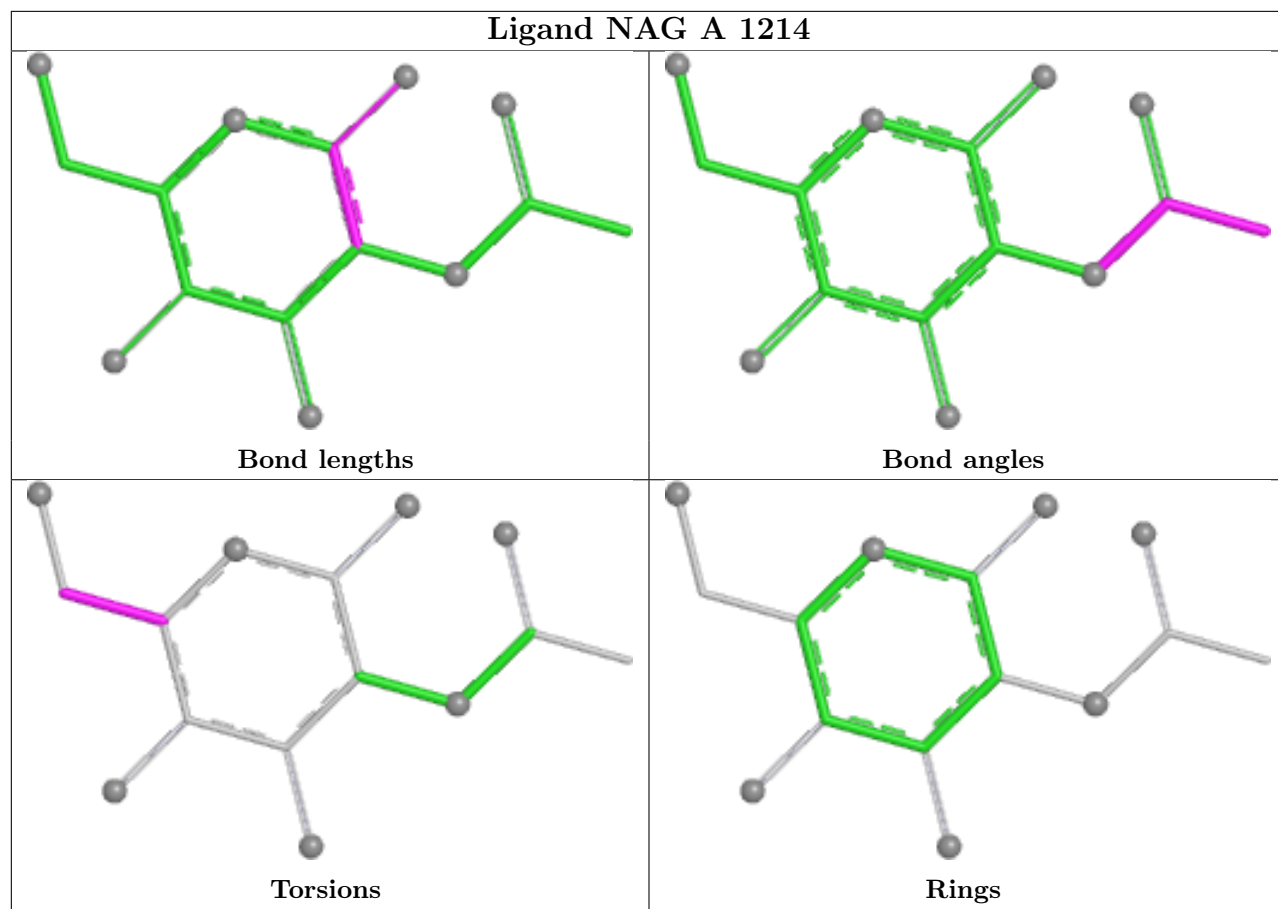
3 monomers are involved in 3 short contacts:

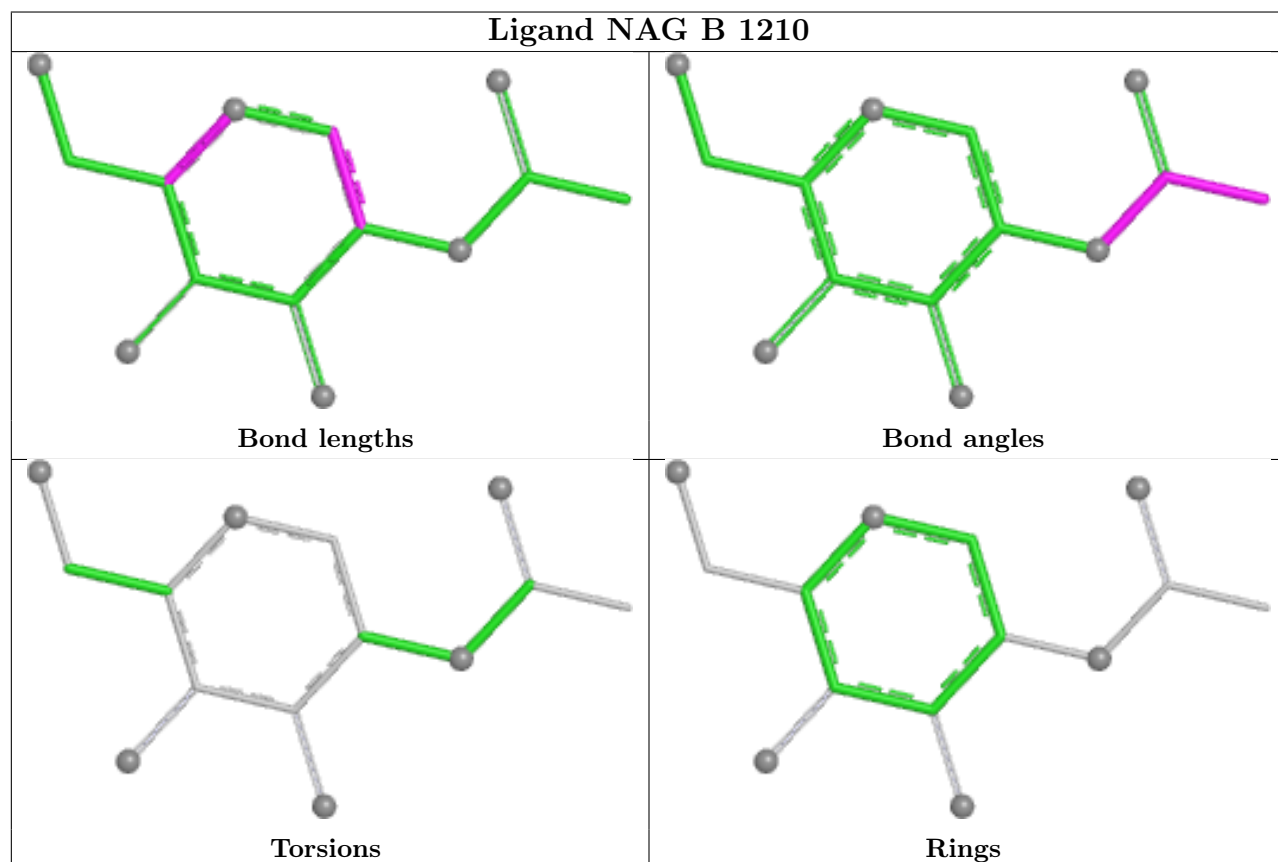
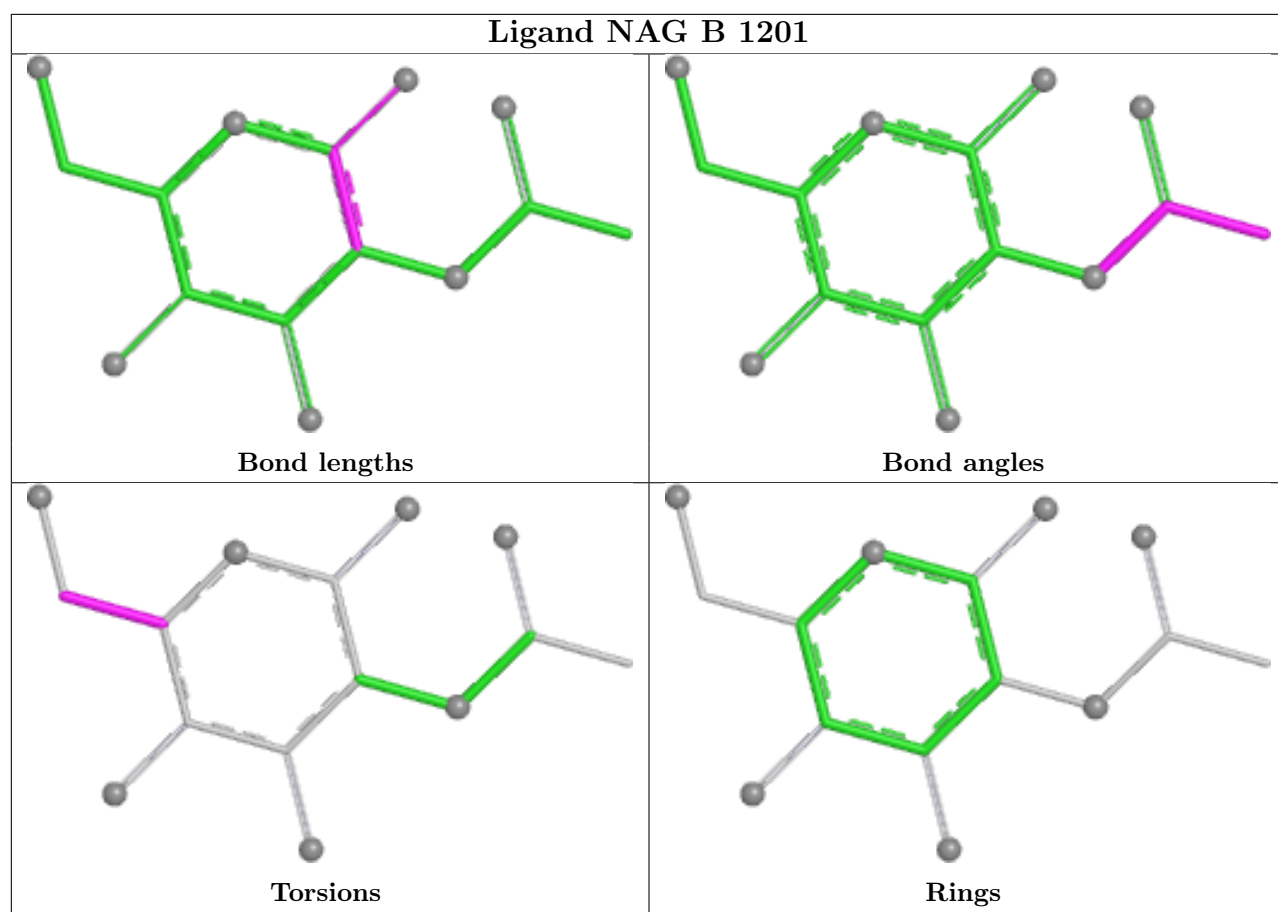
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1210	NAG	1	0
2	B	1208	NAG	1	0
2	B	1211	NAG	1	0

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.

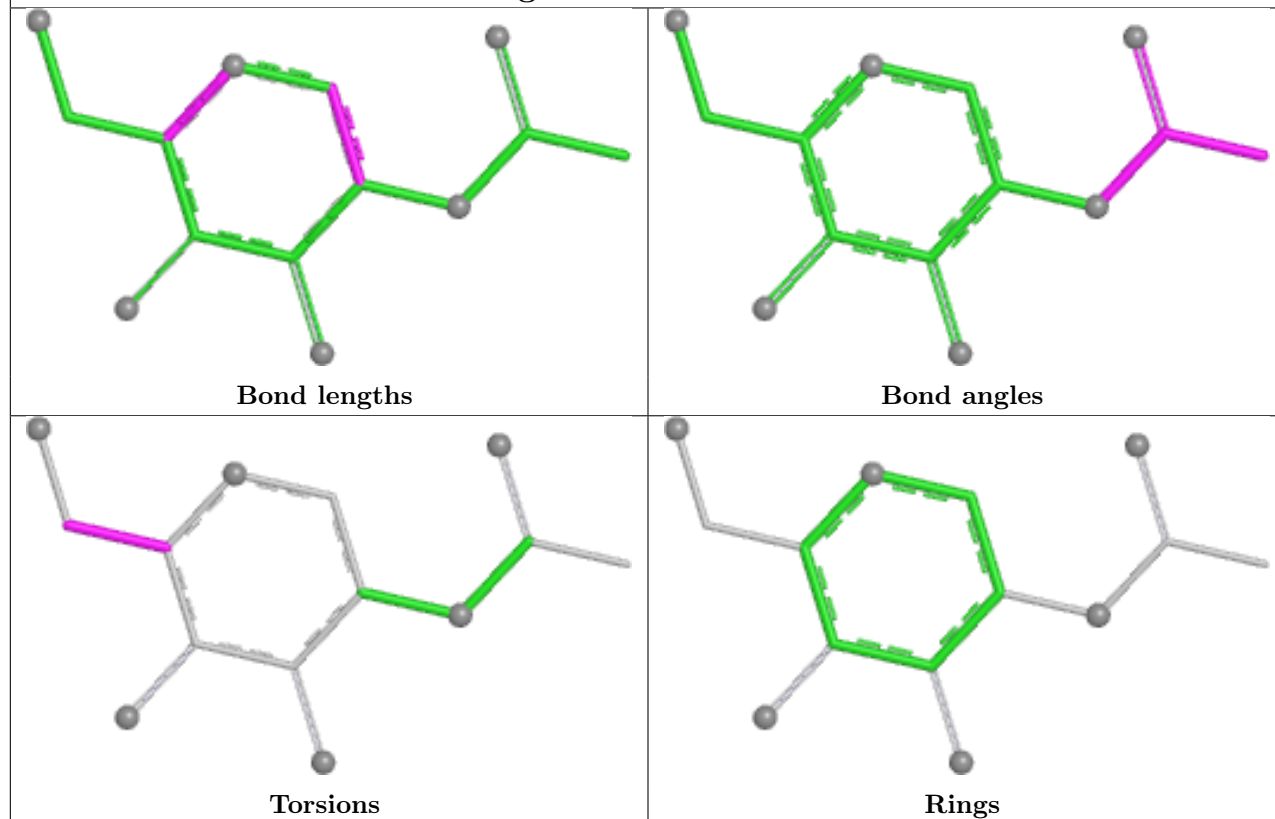




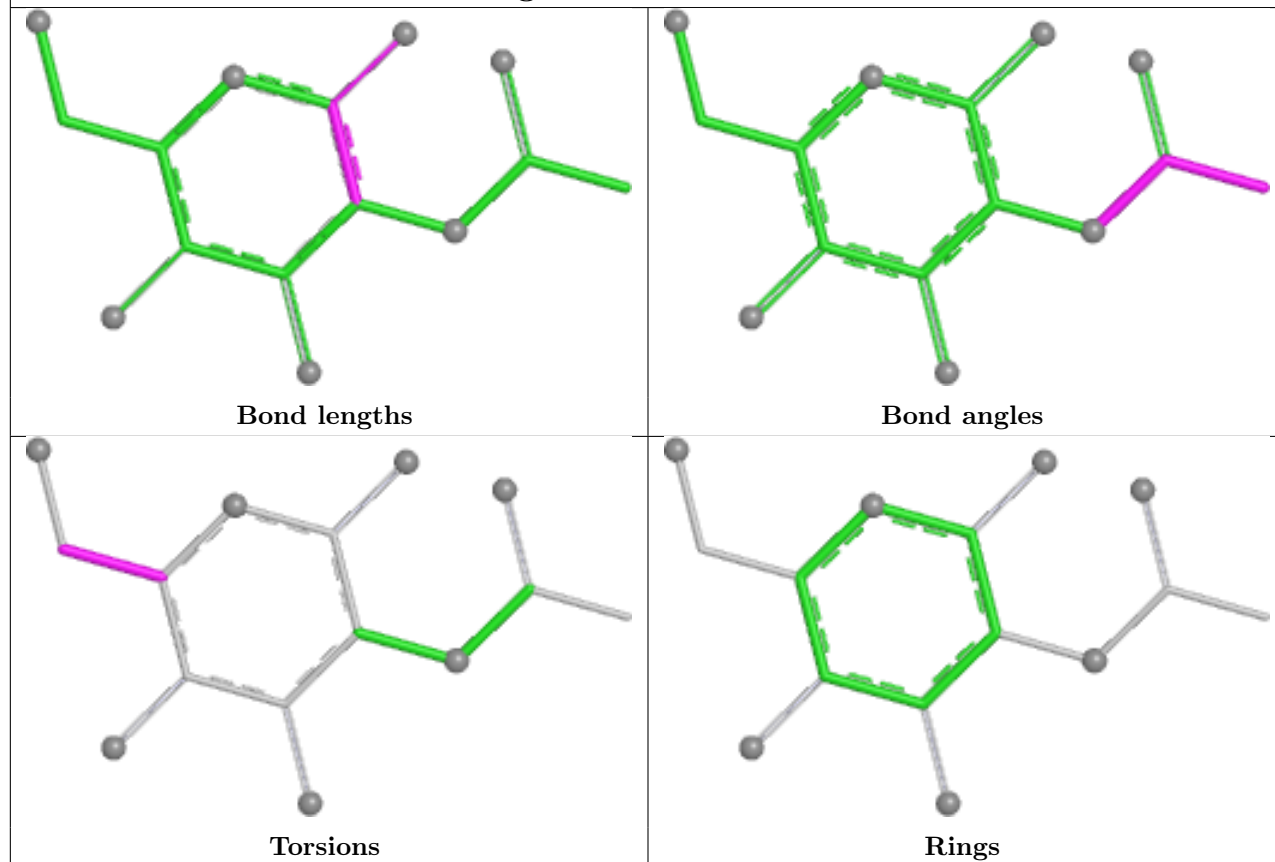


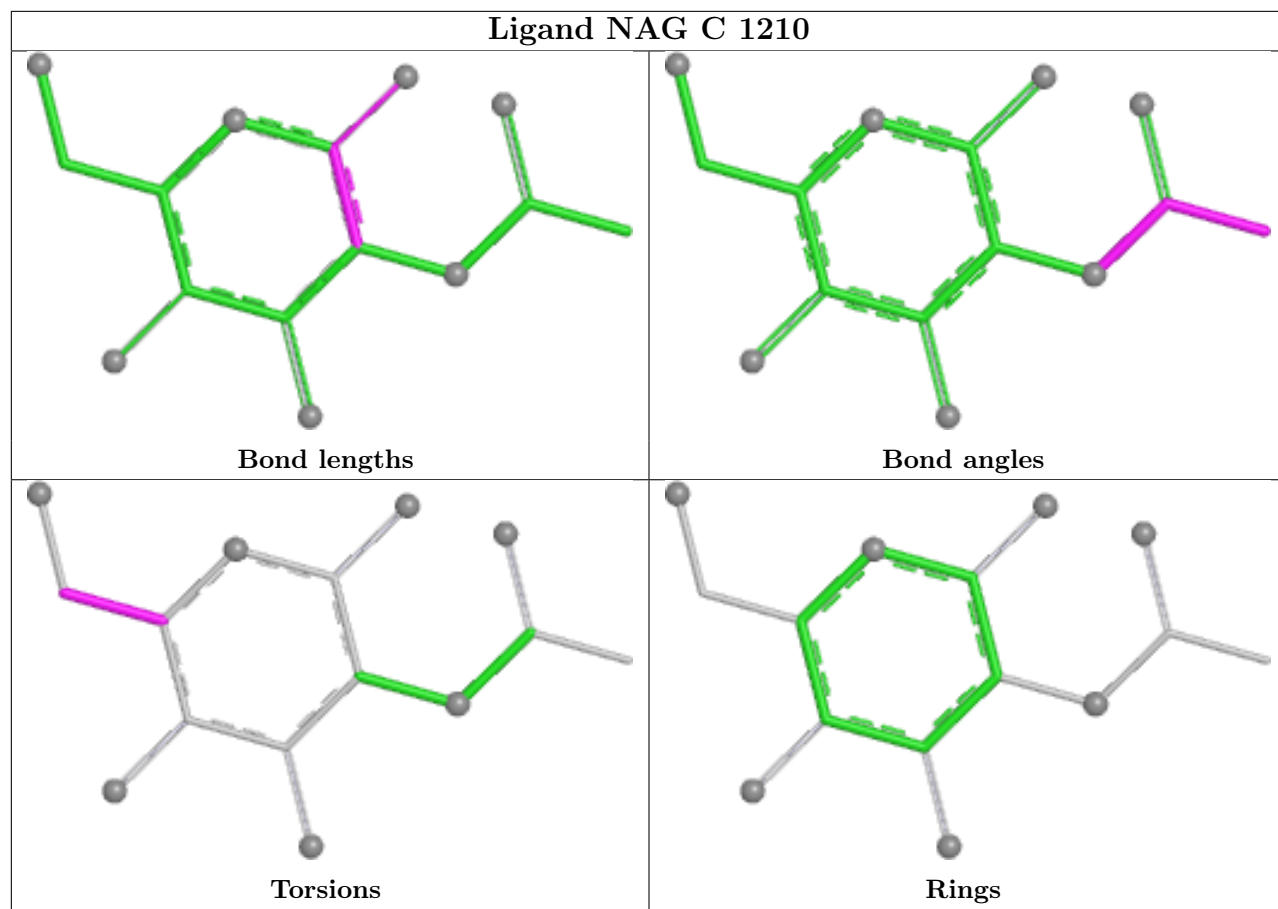


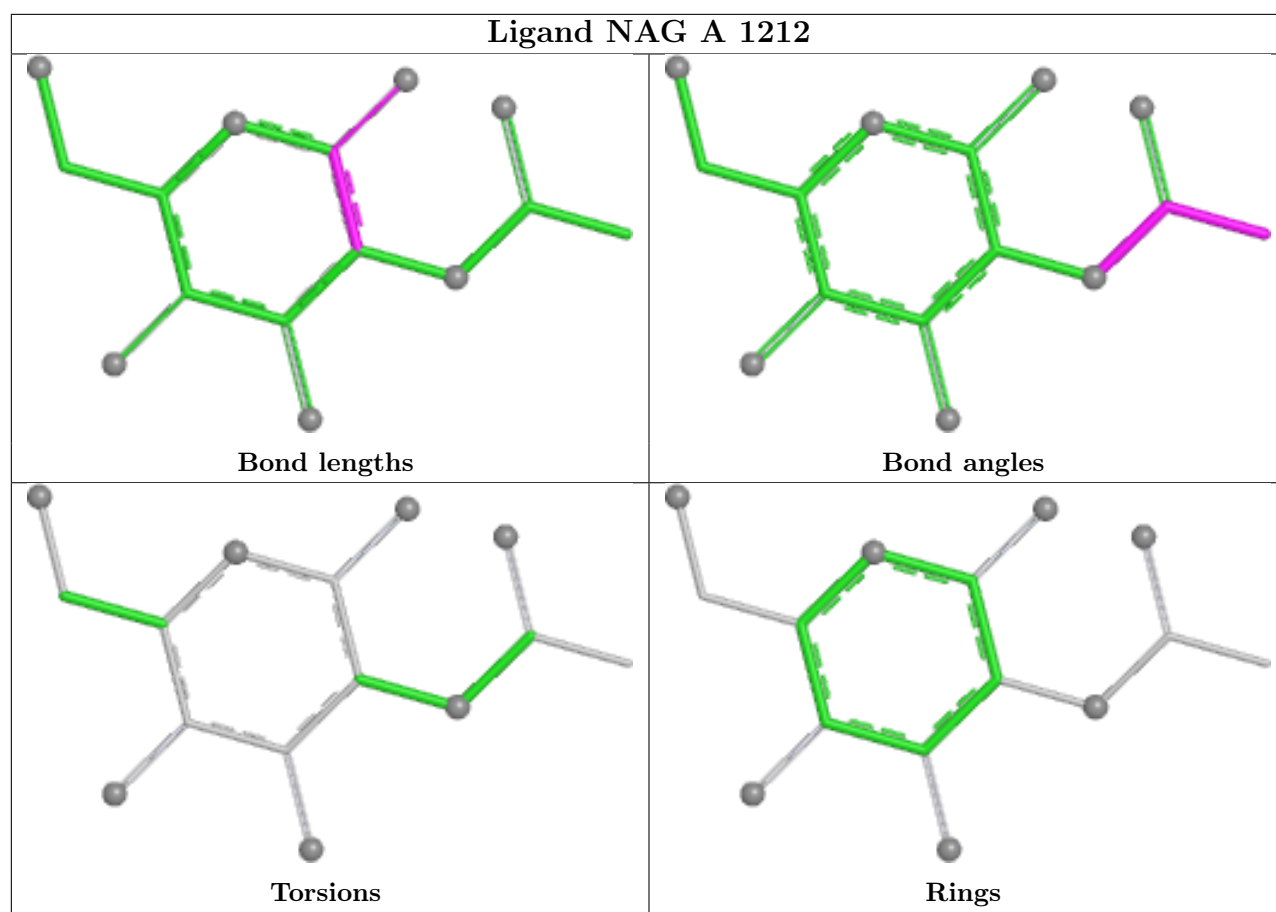
Ligand NAG C 1204

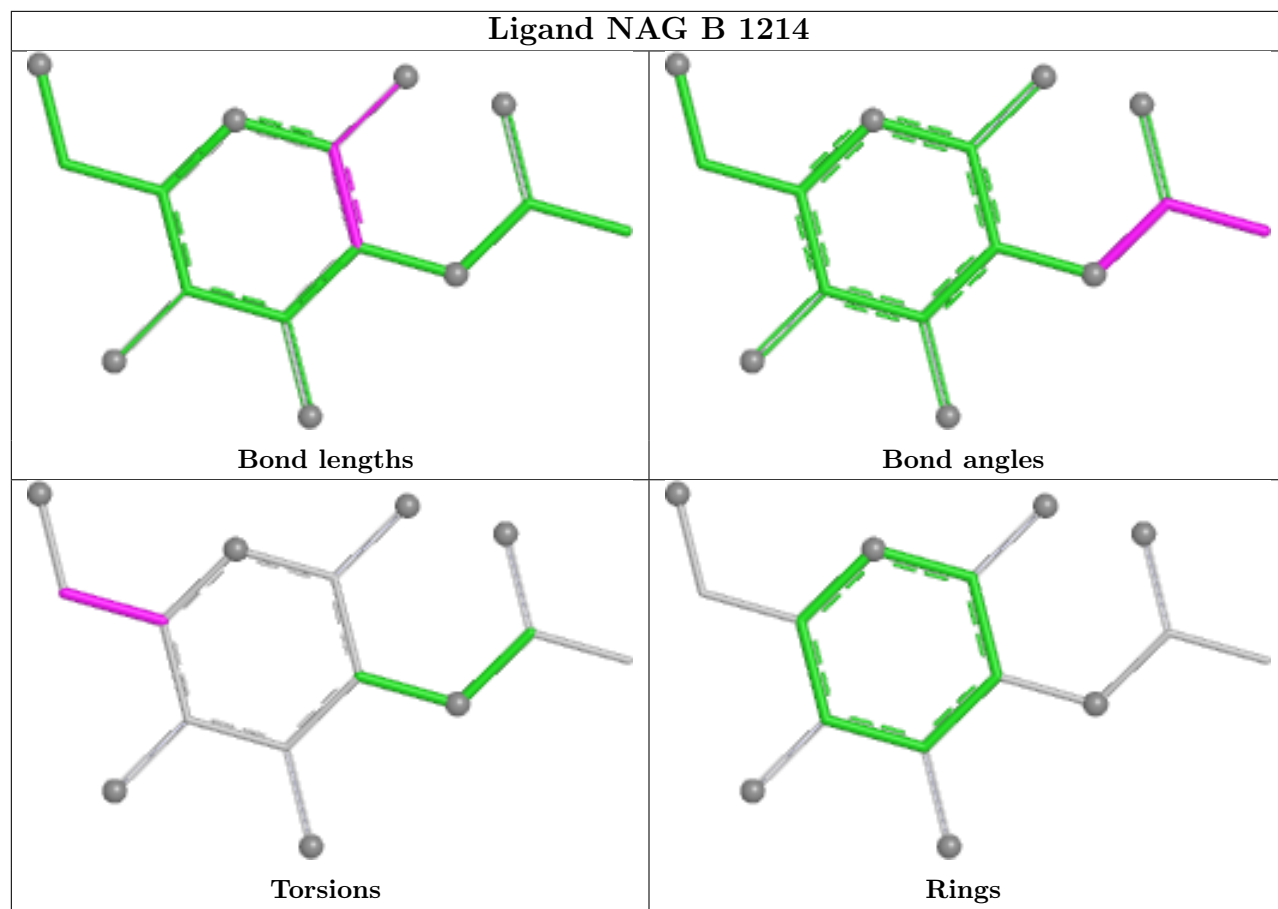


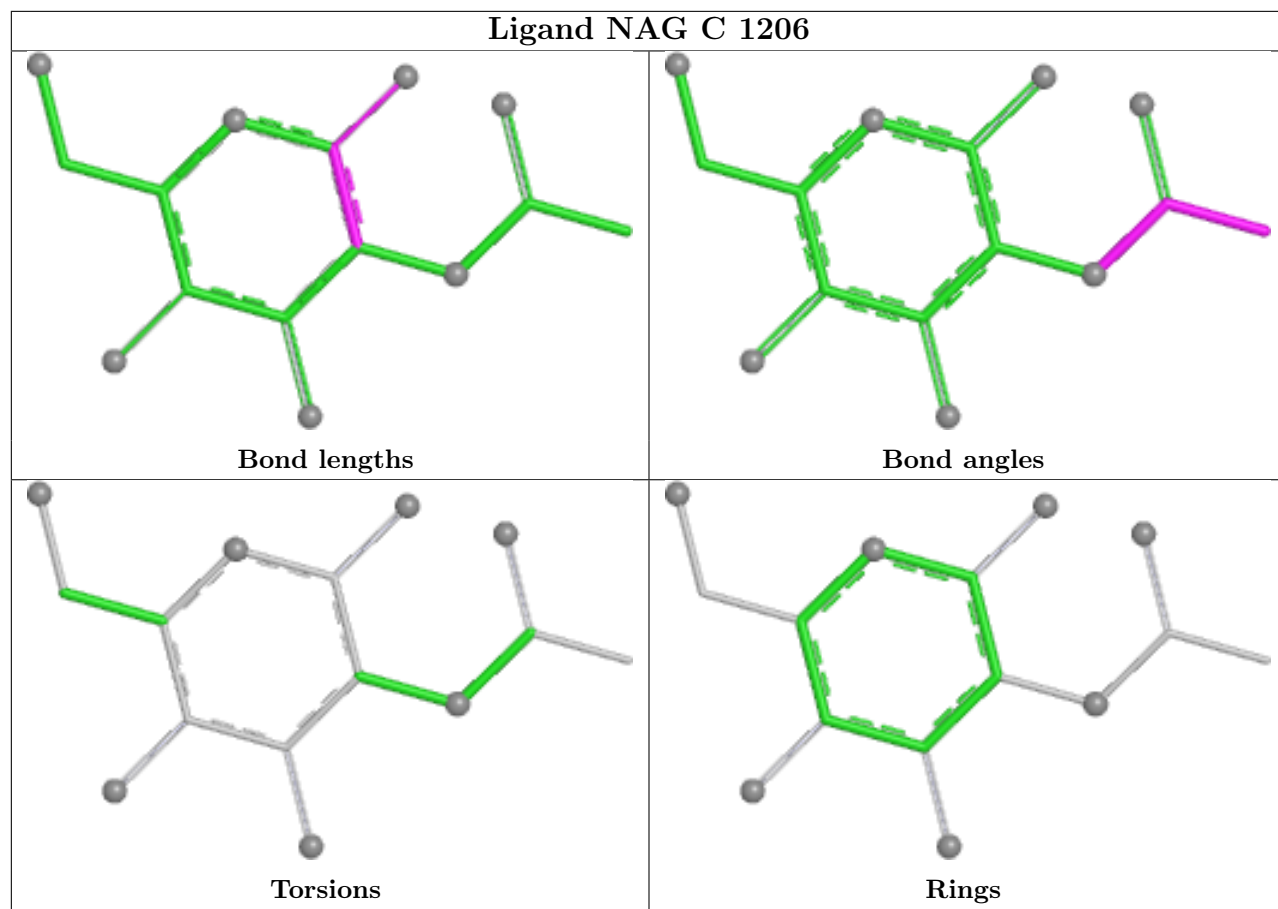
Ligand NAG A 1209

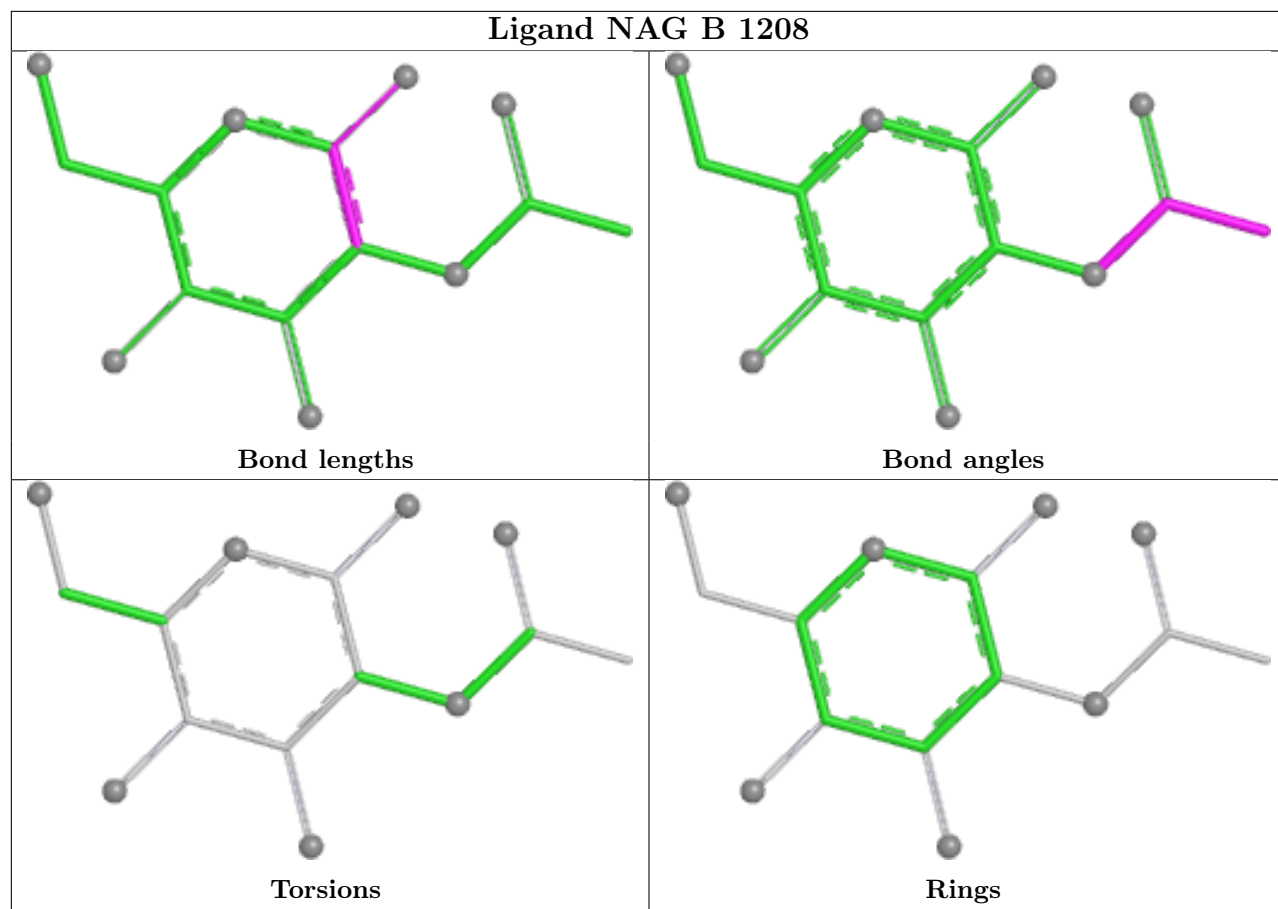


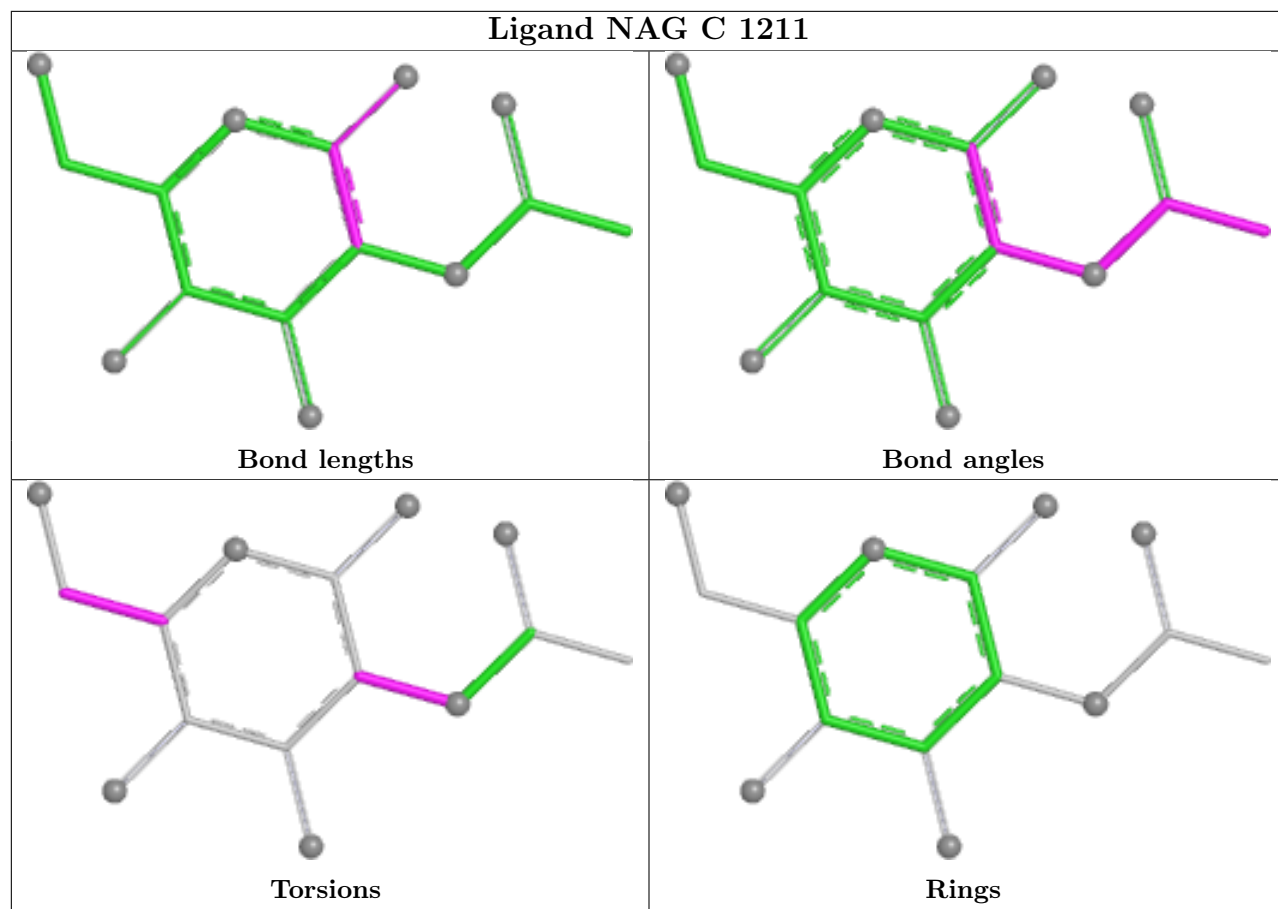


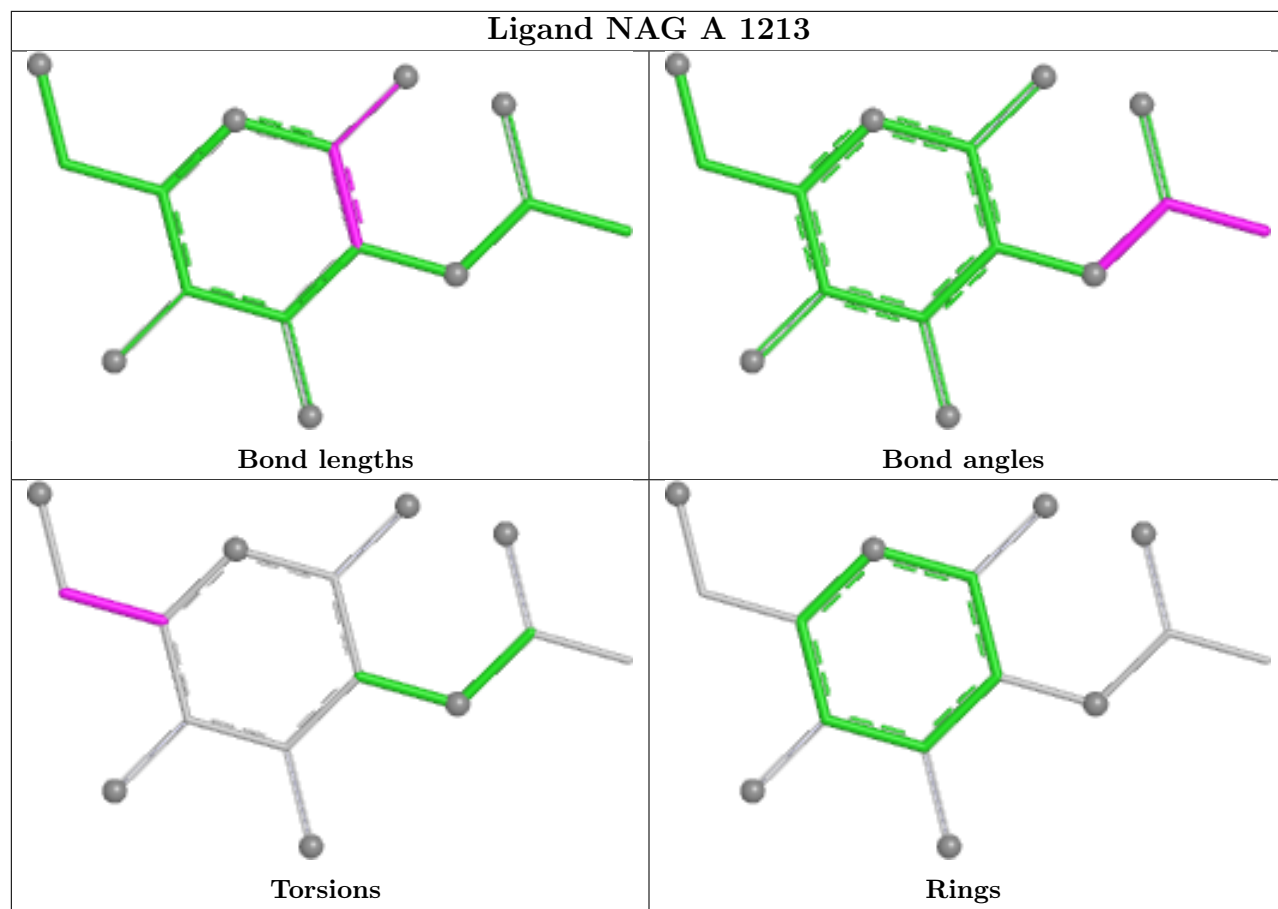


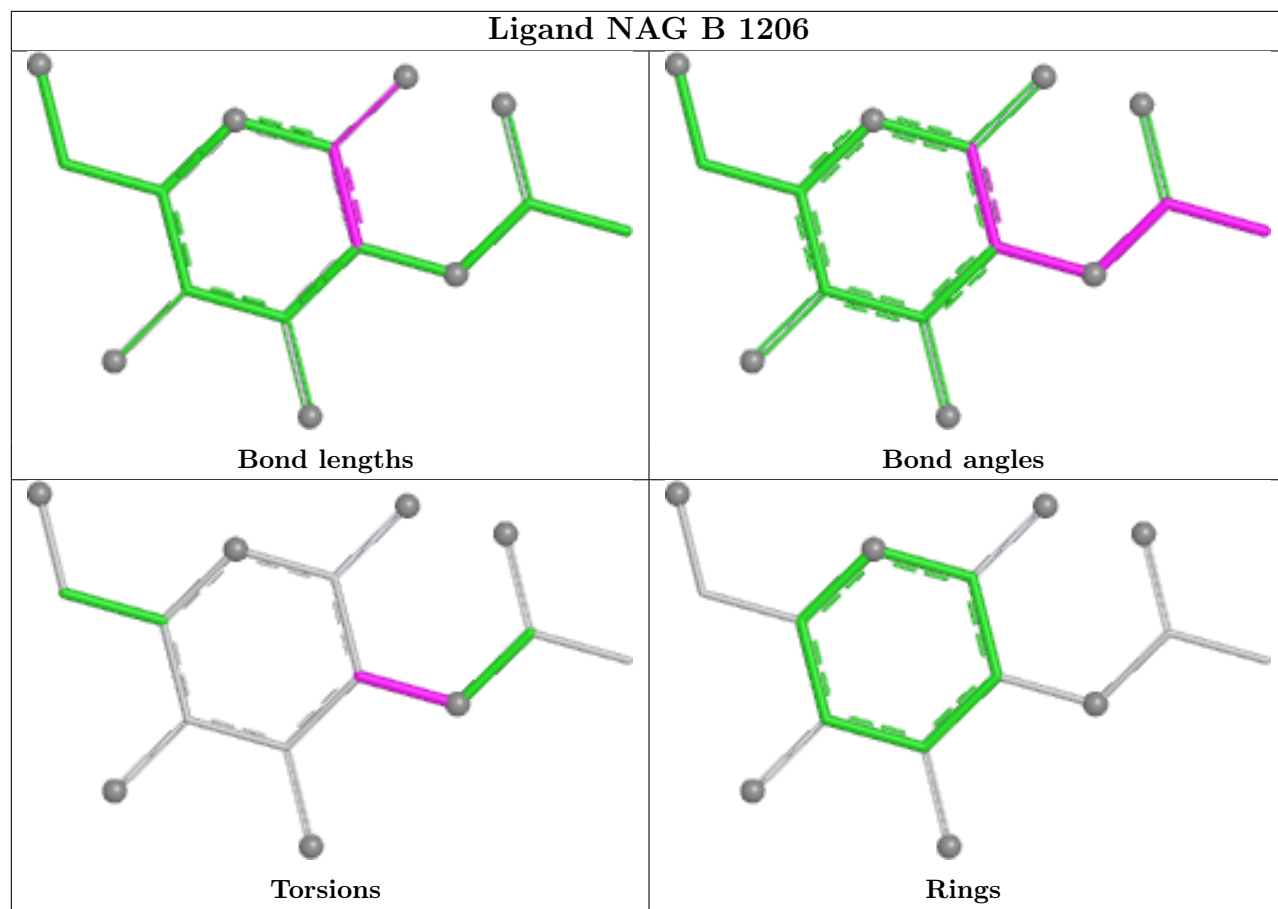


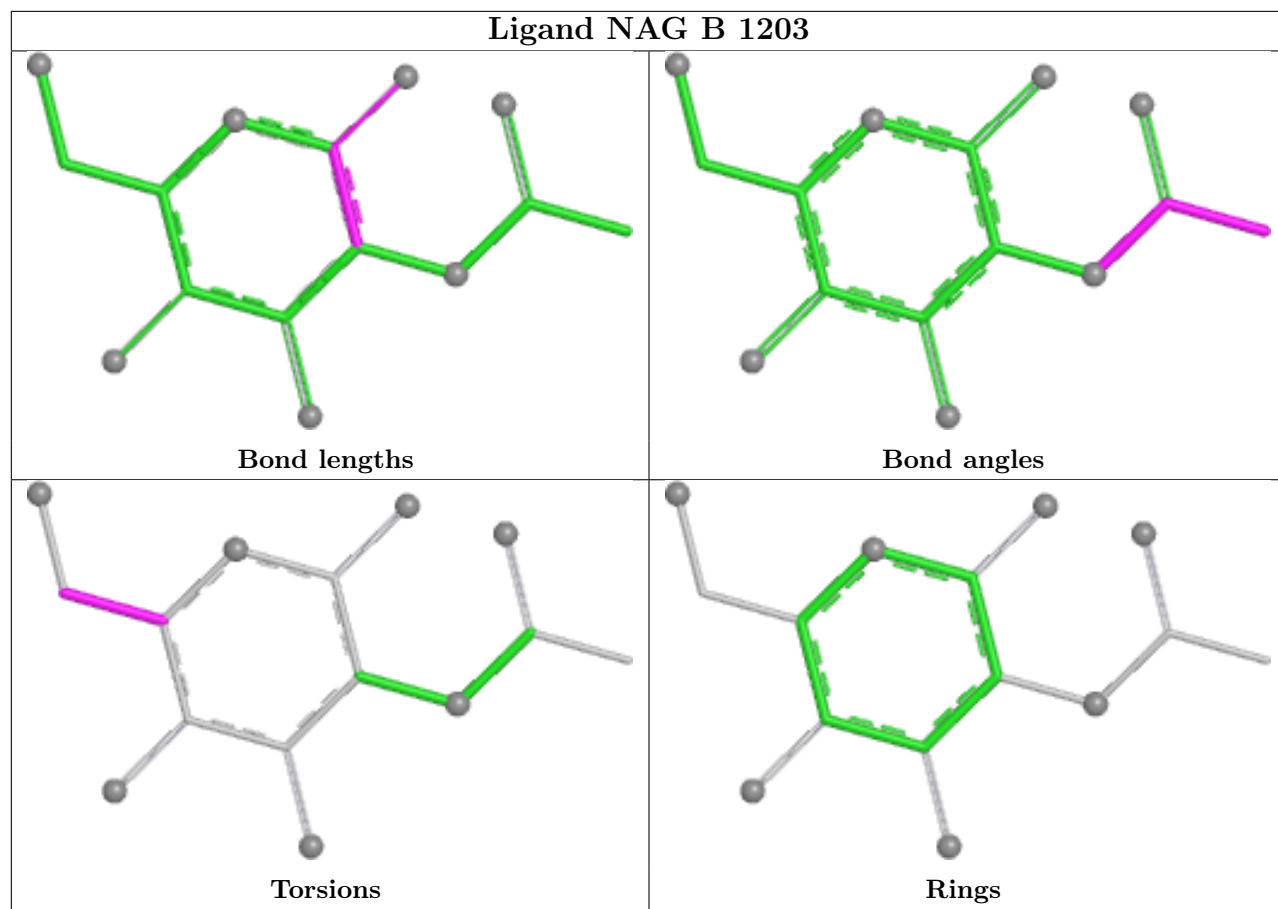


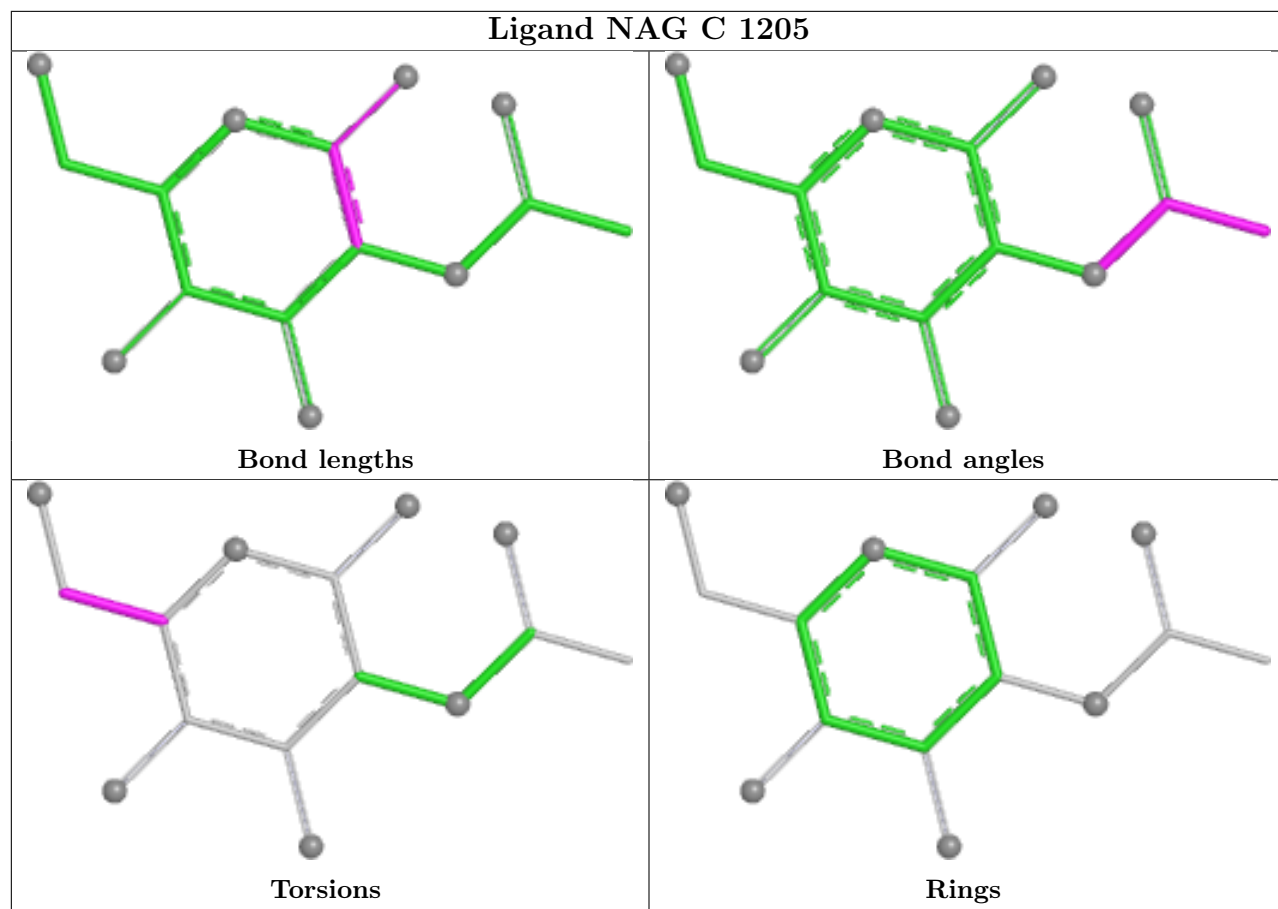


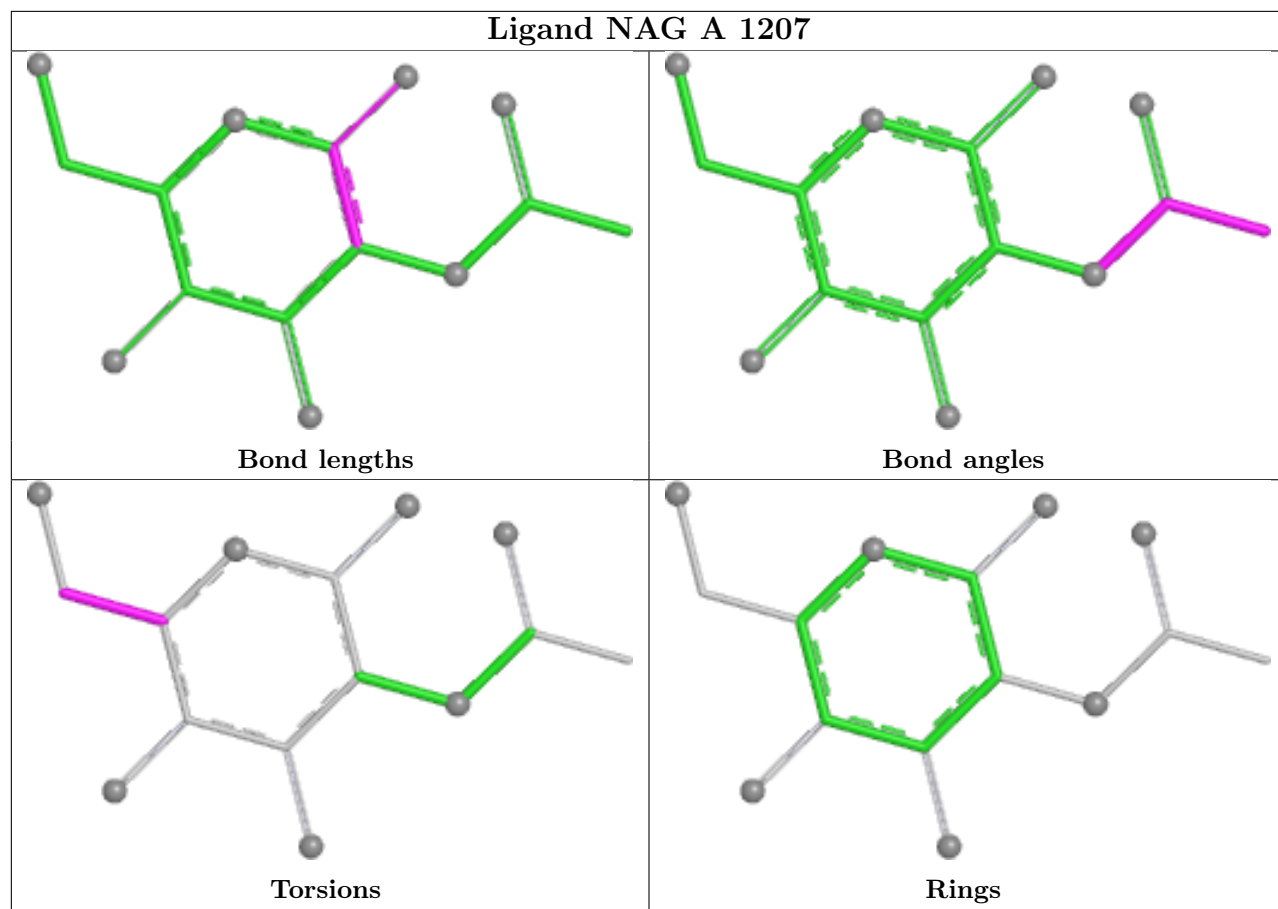


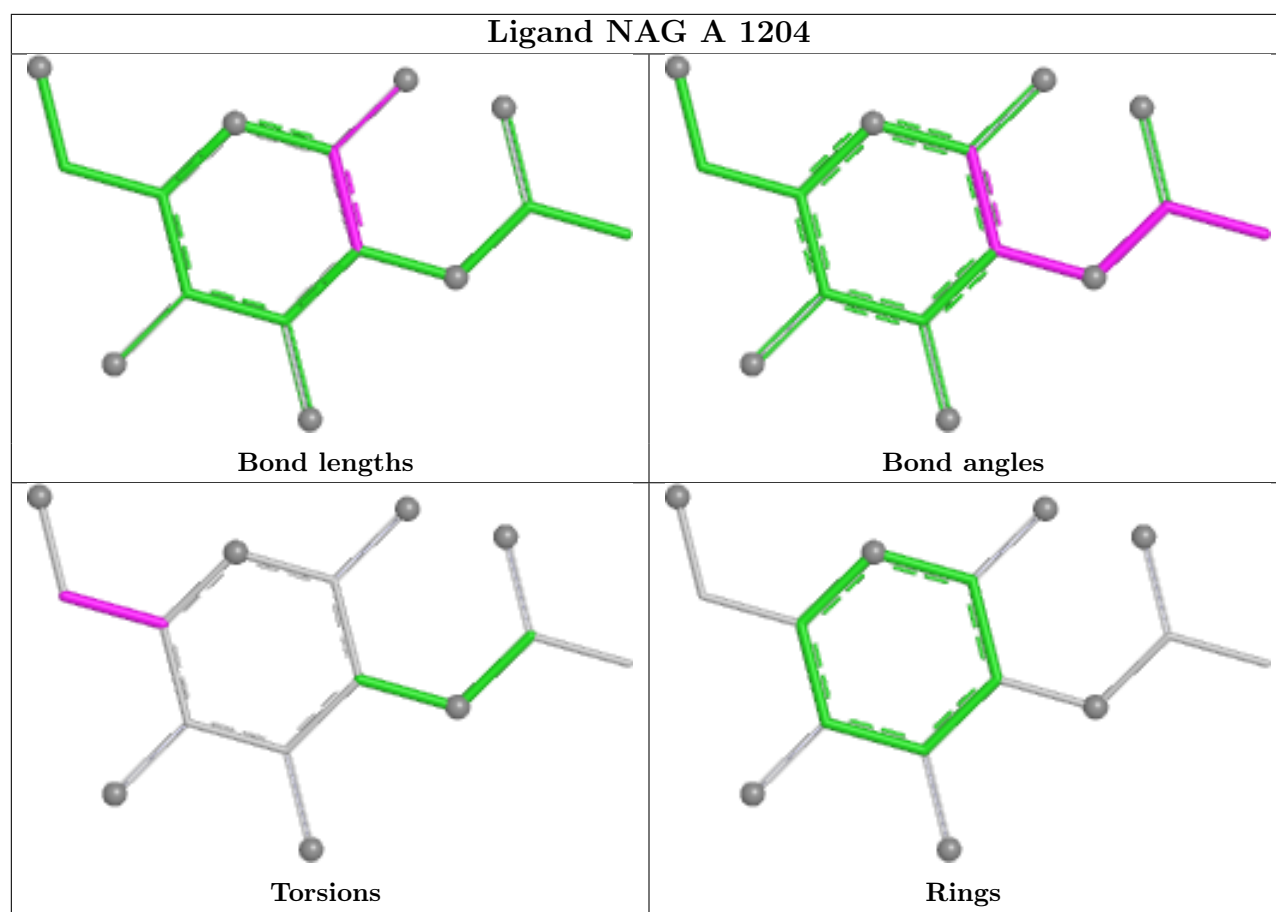


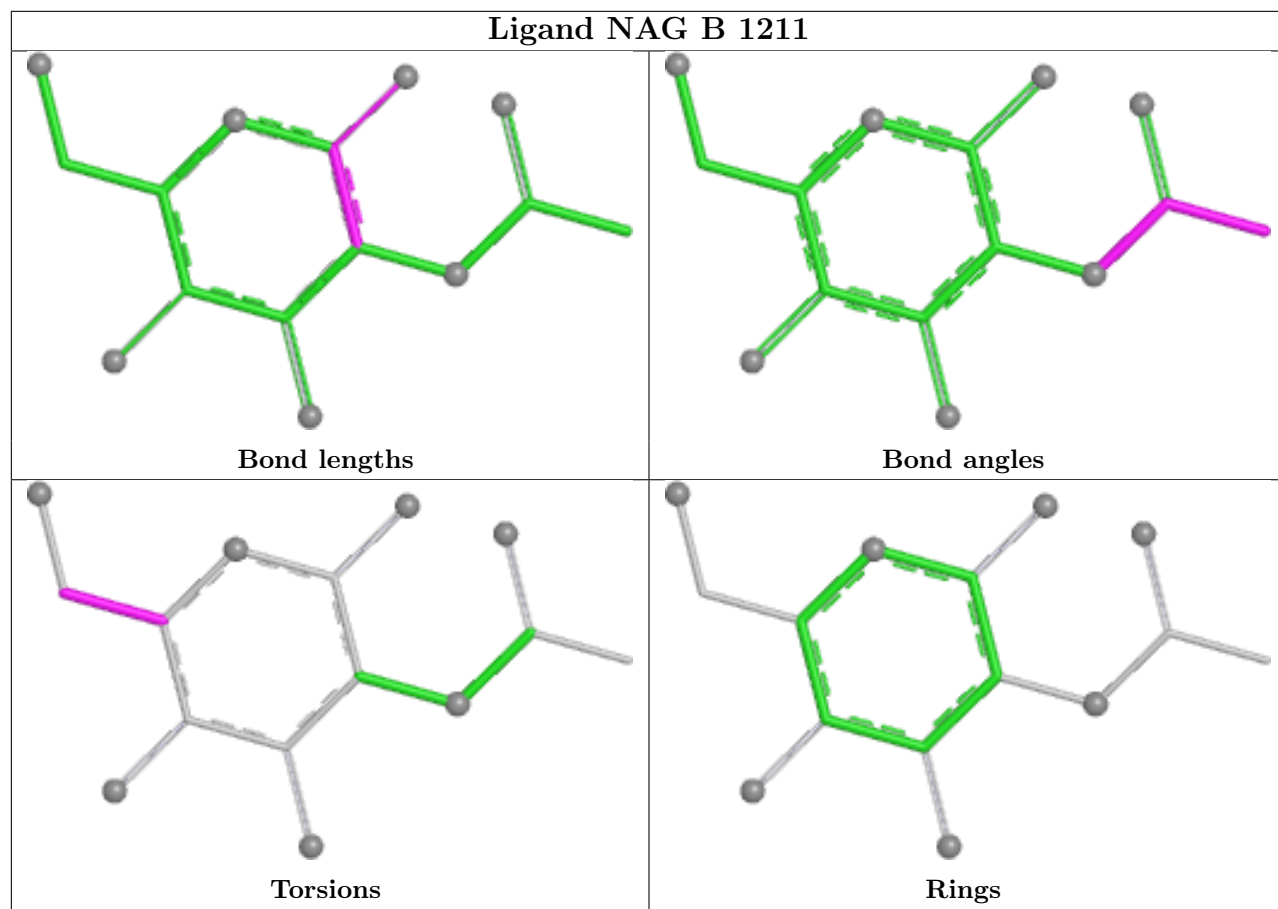


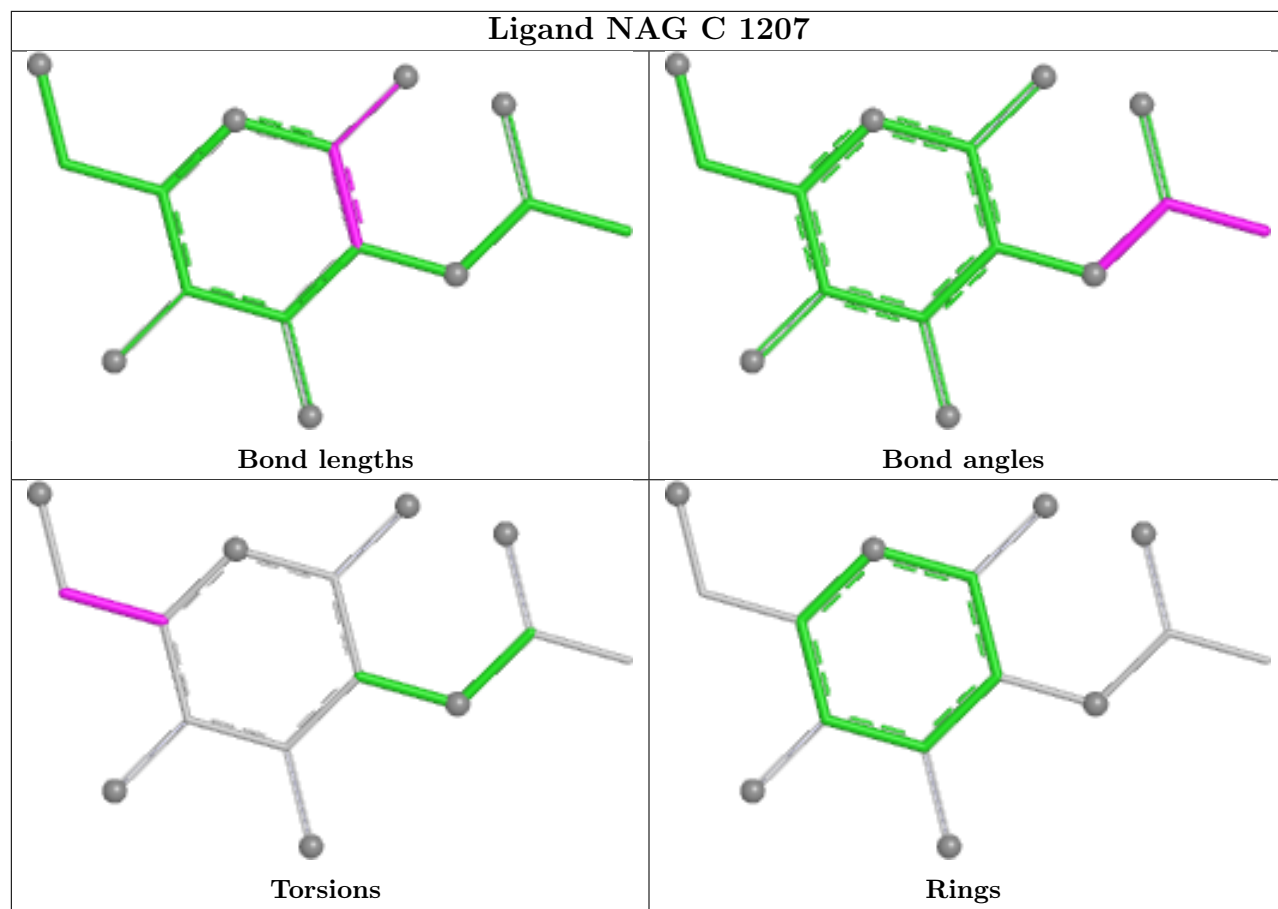


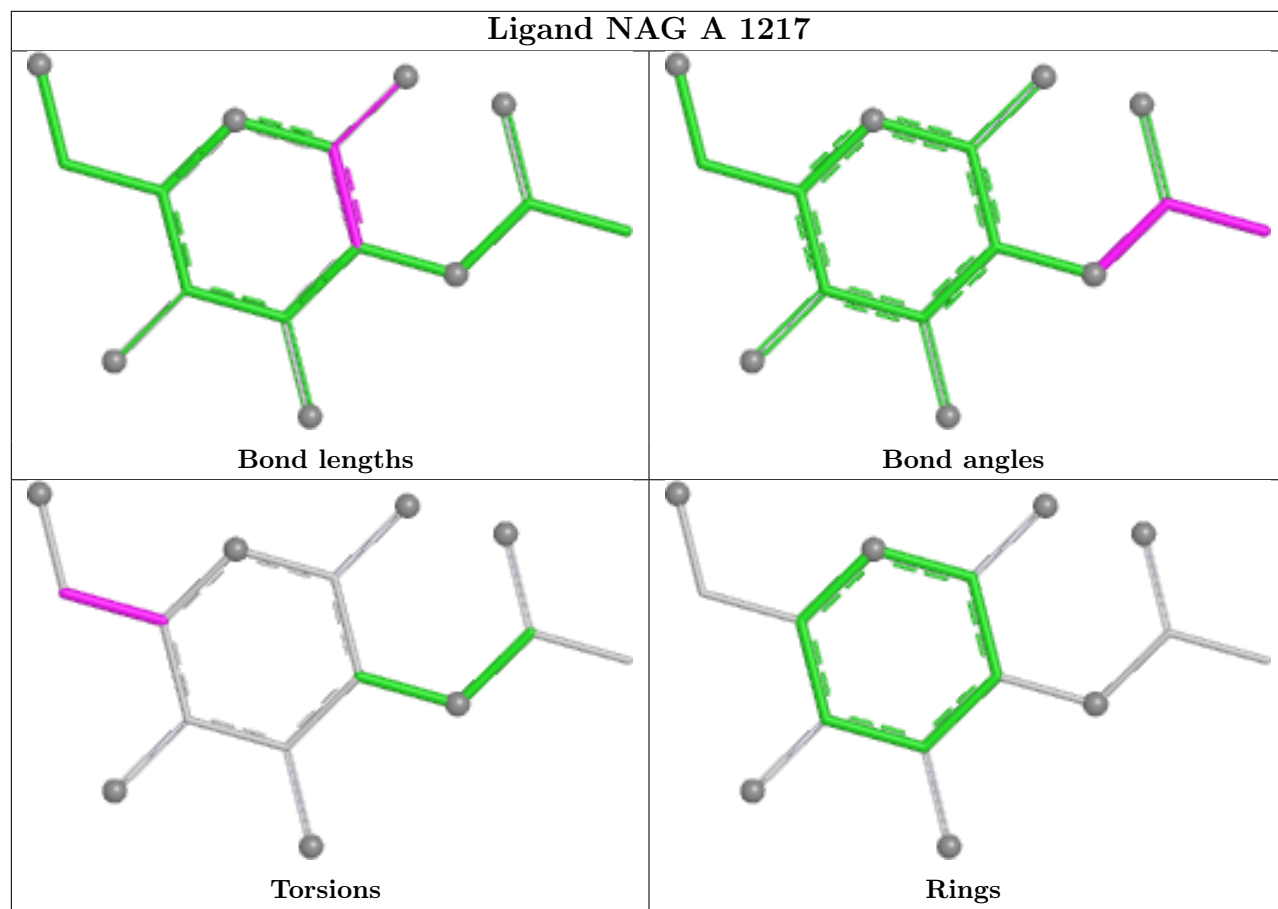


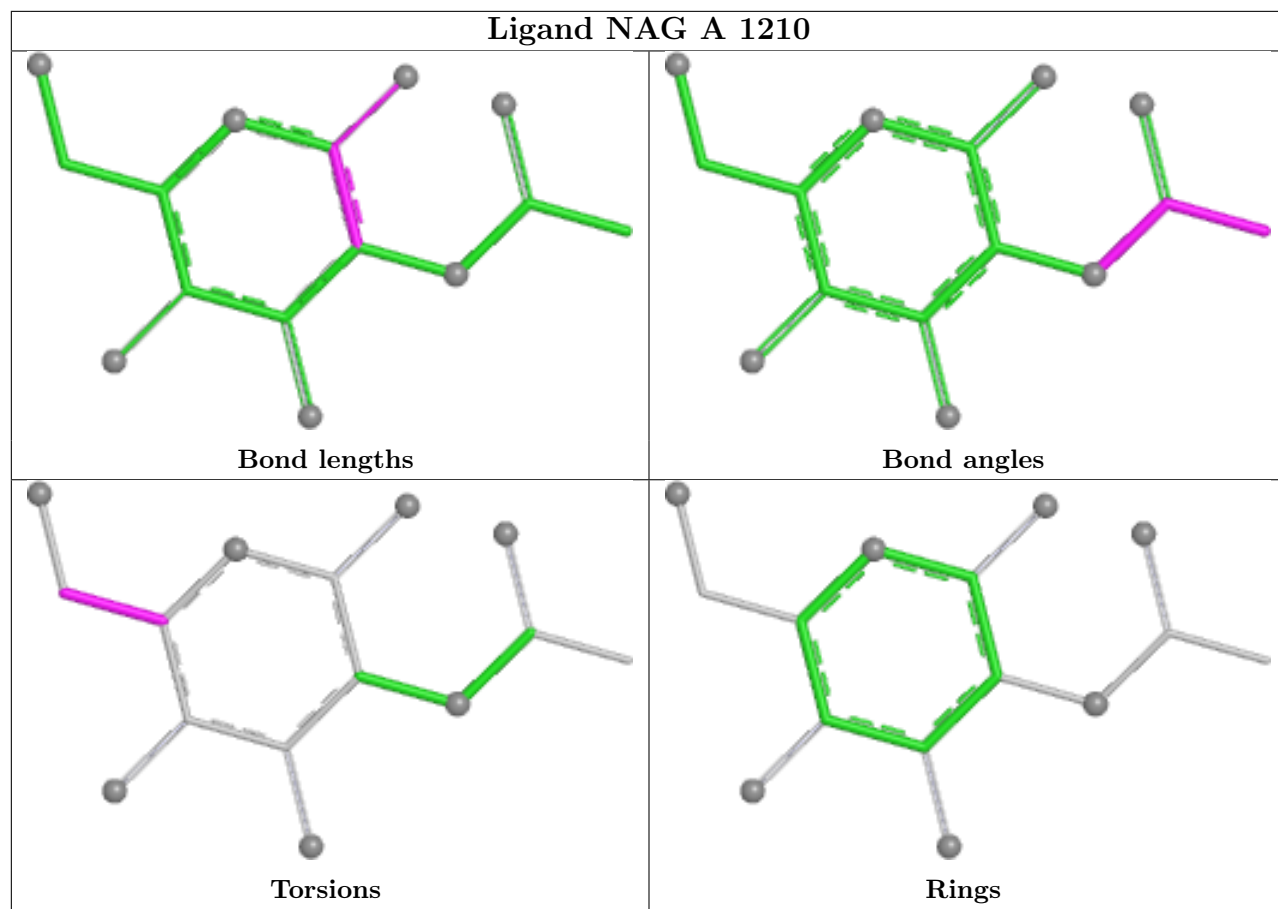


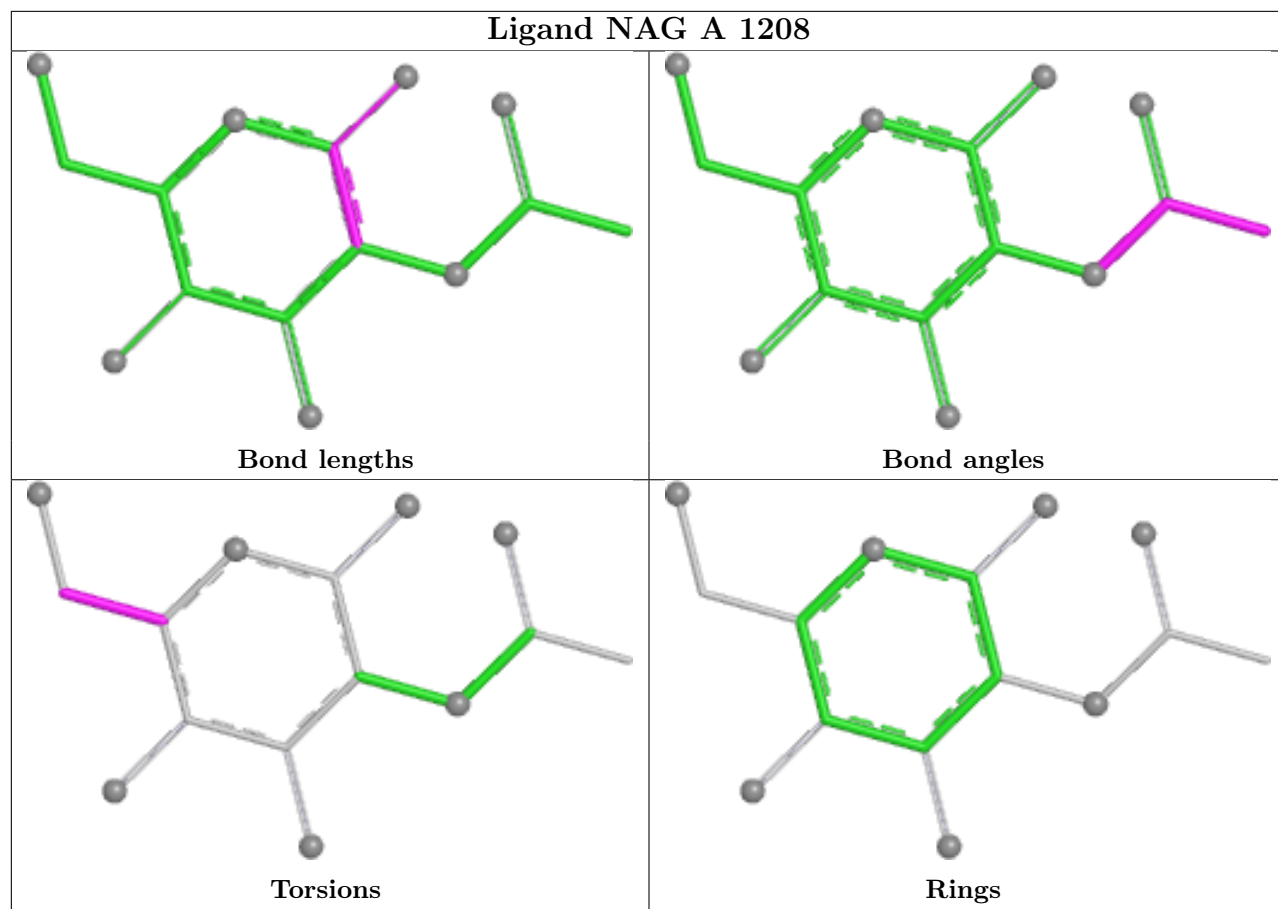


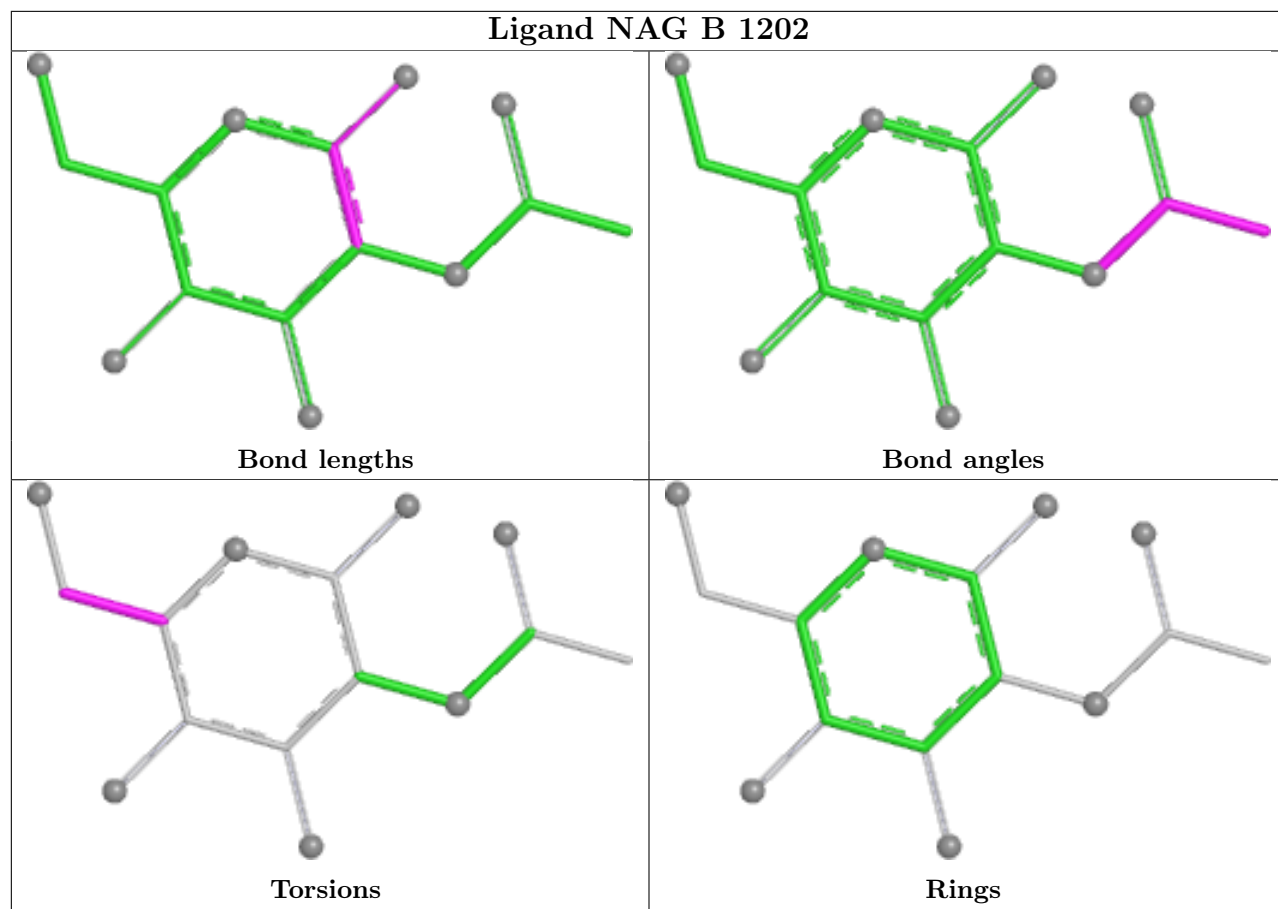


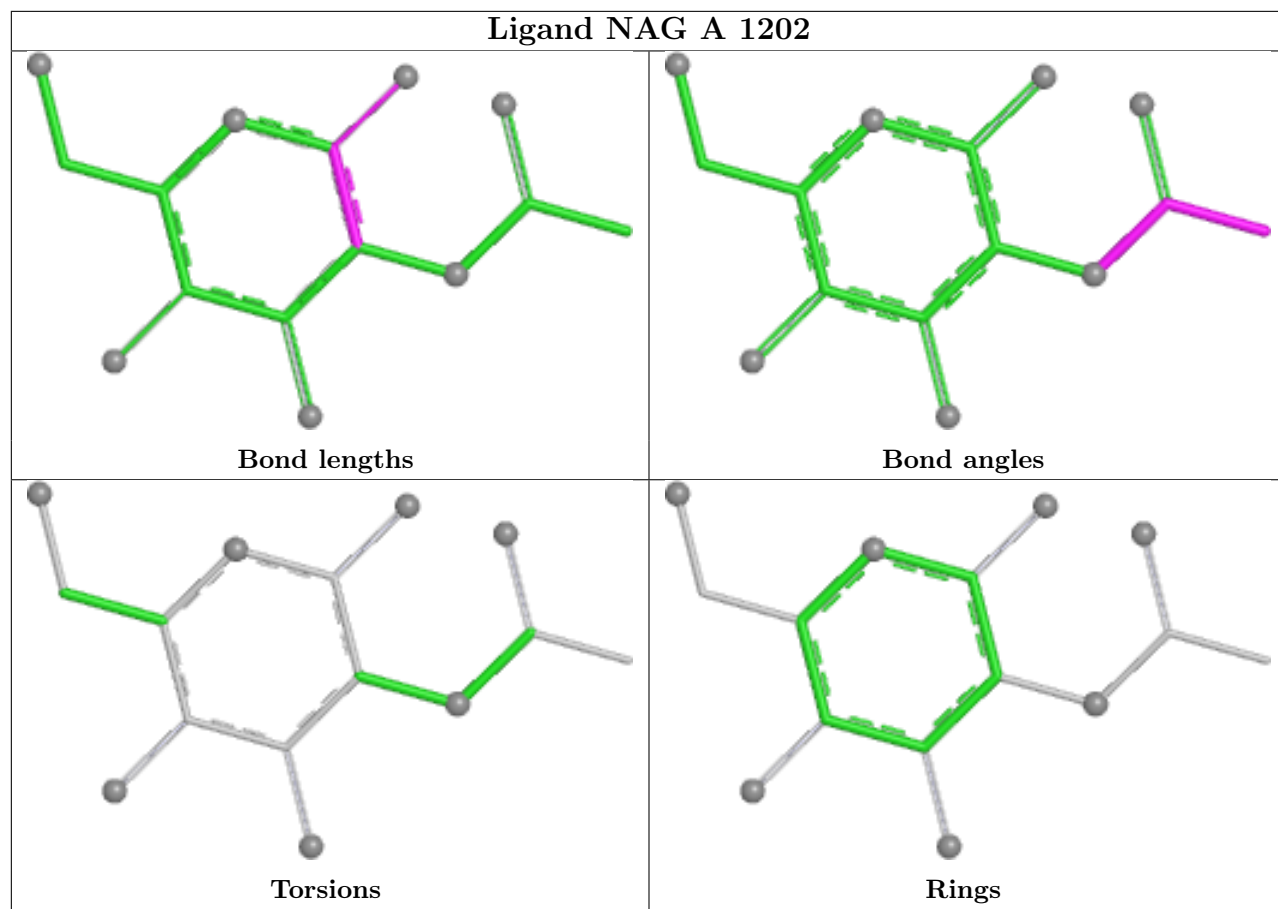


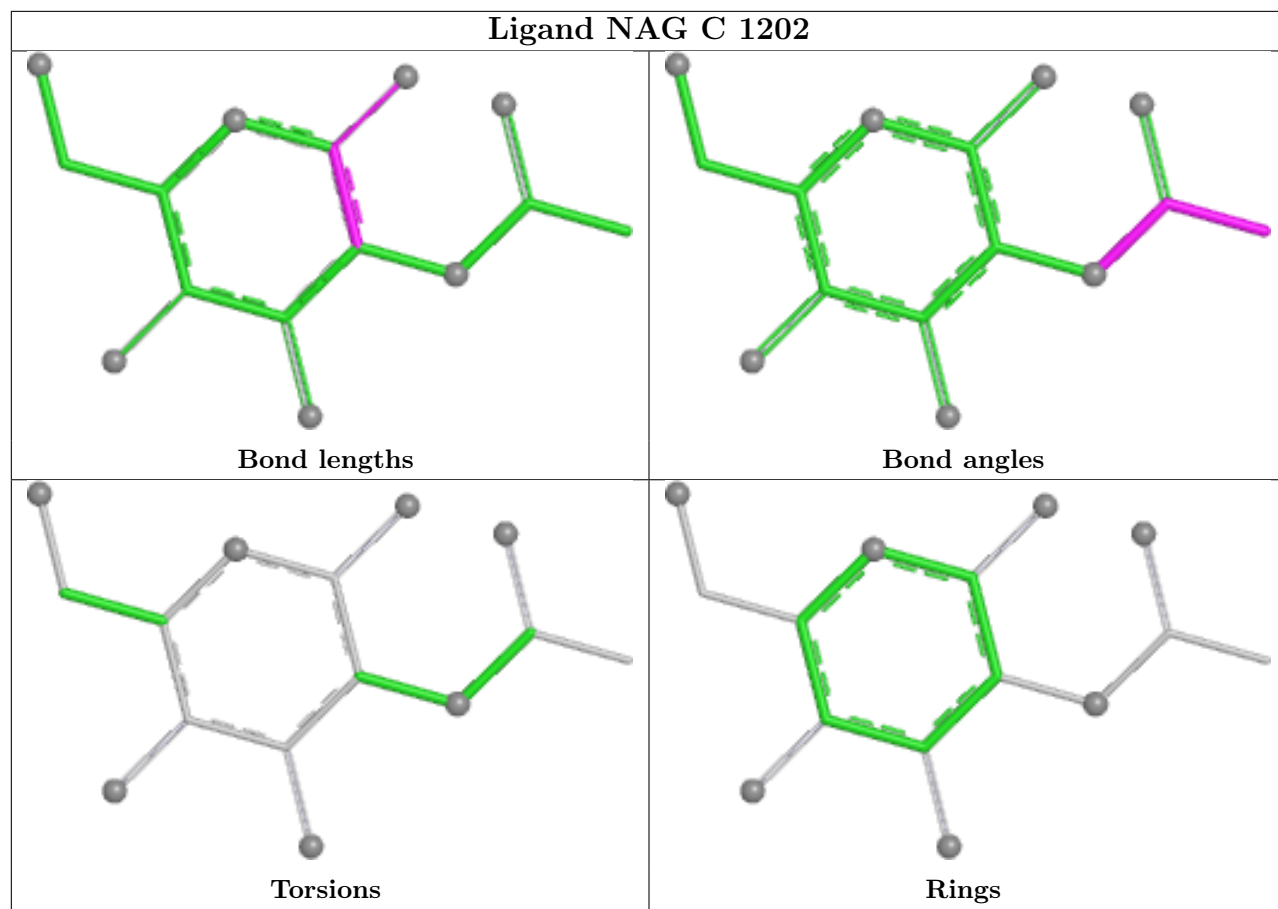


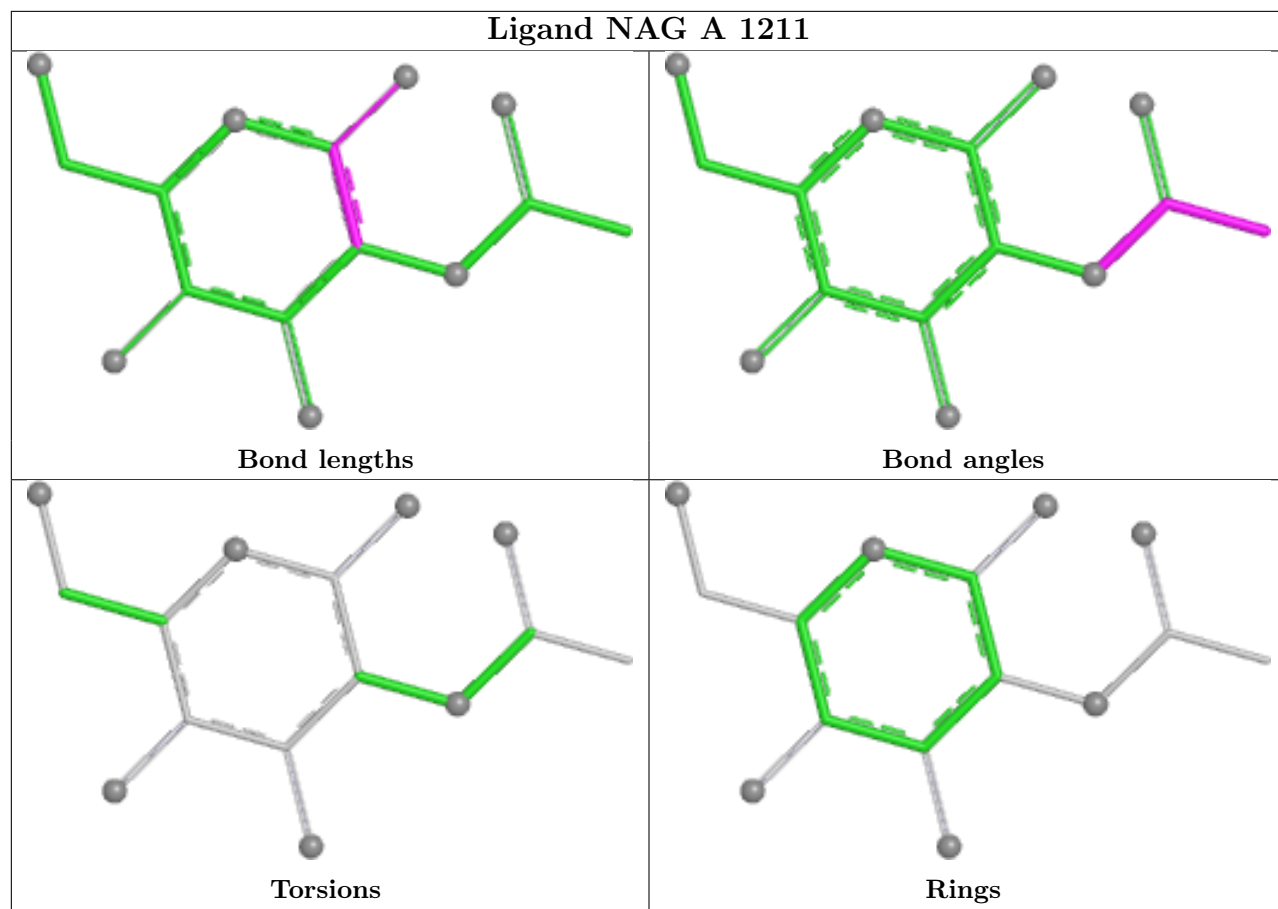


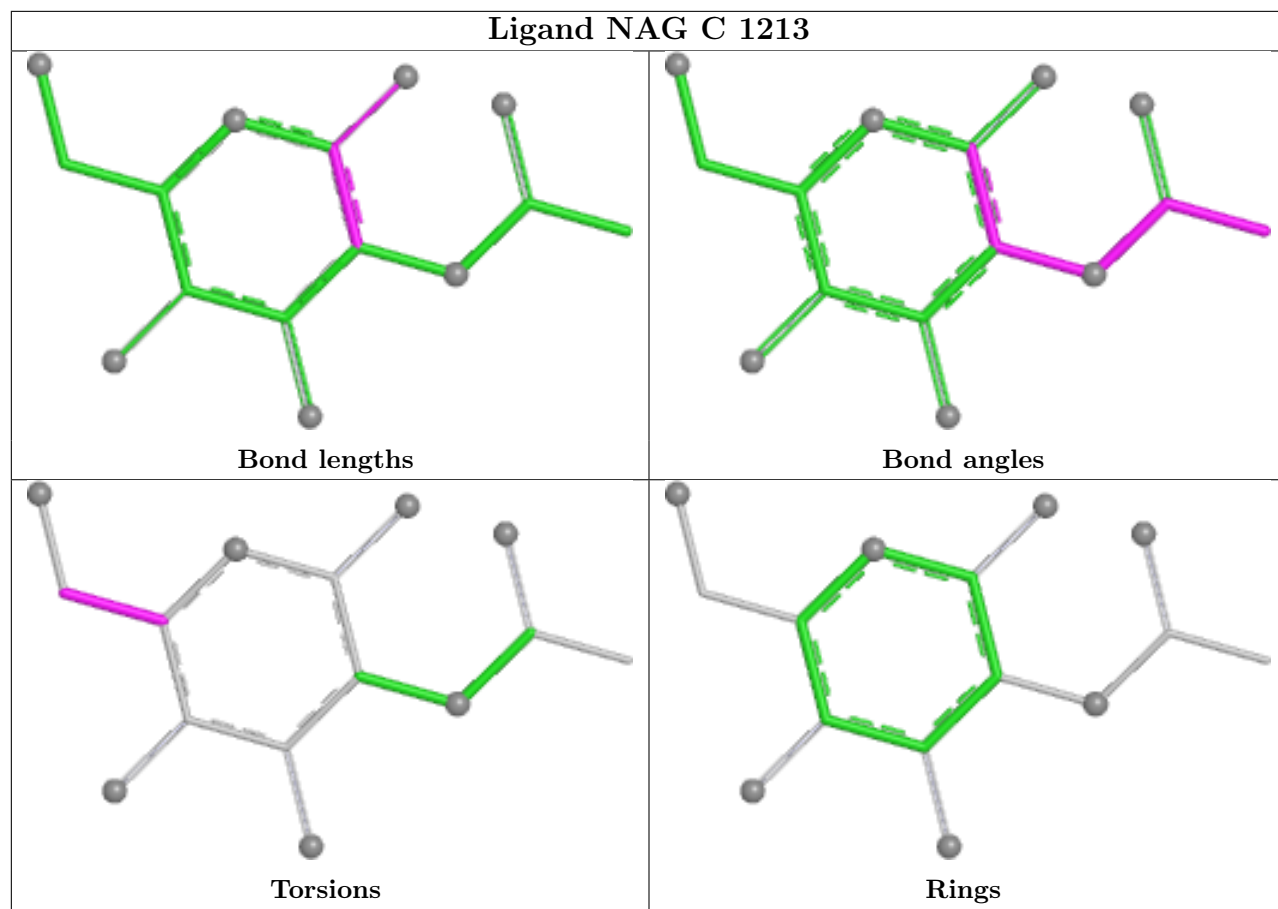


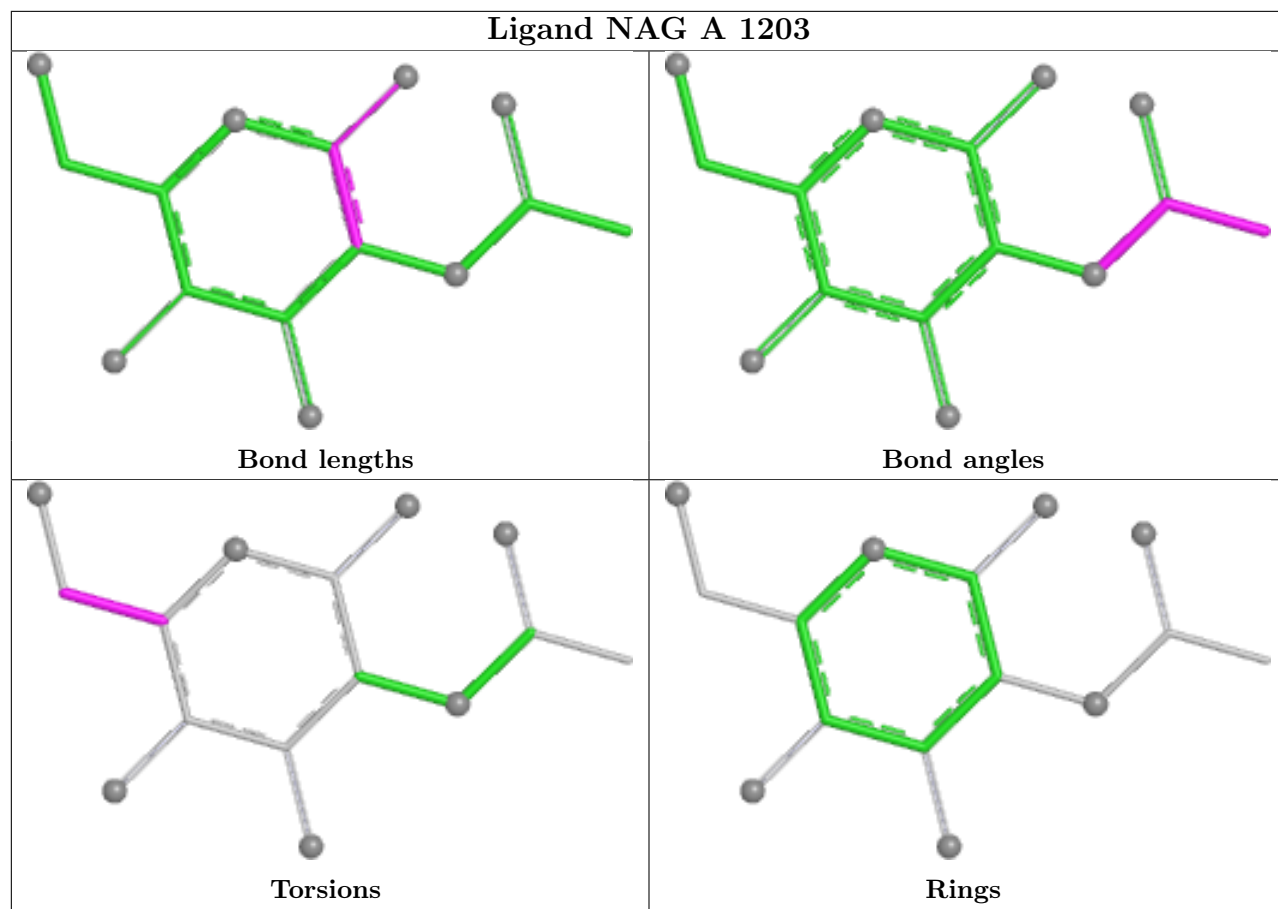


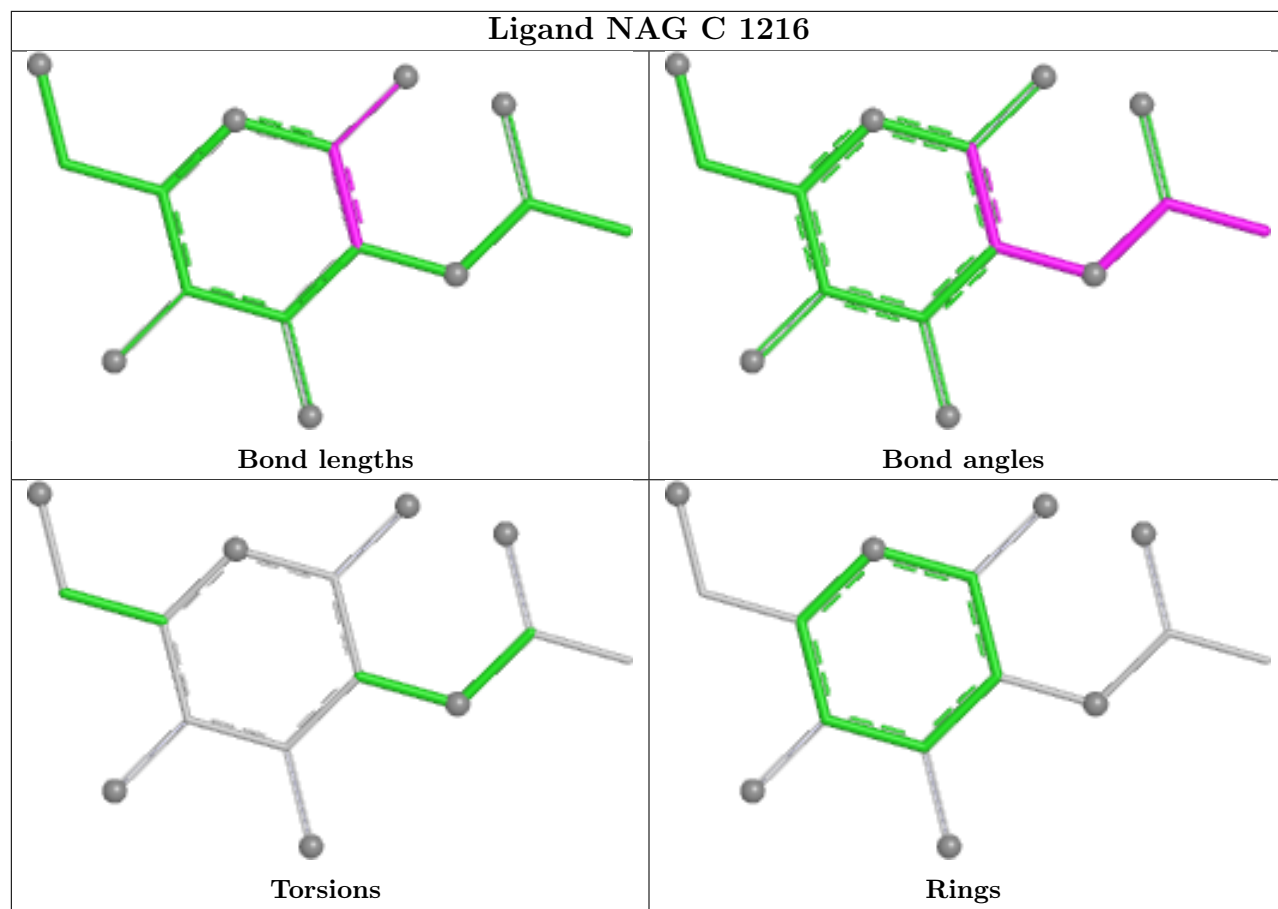


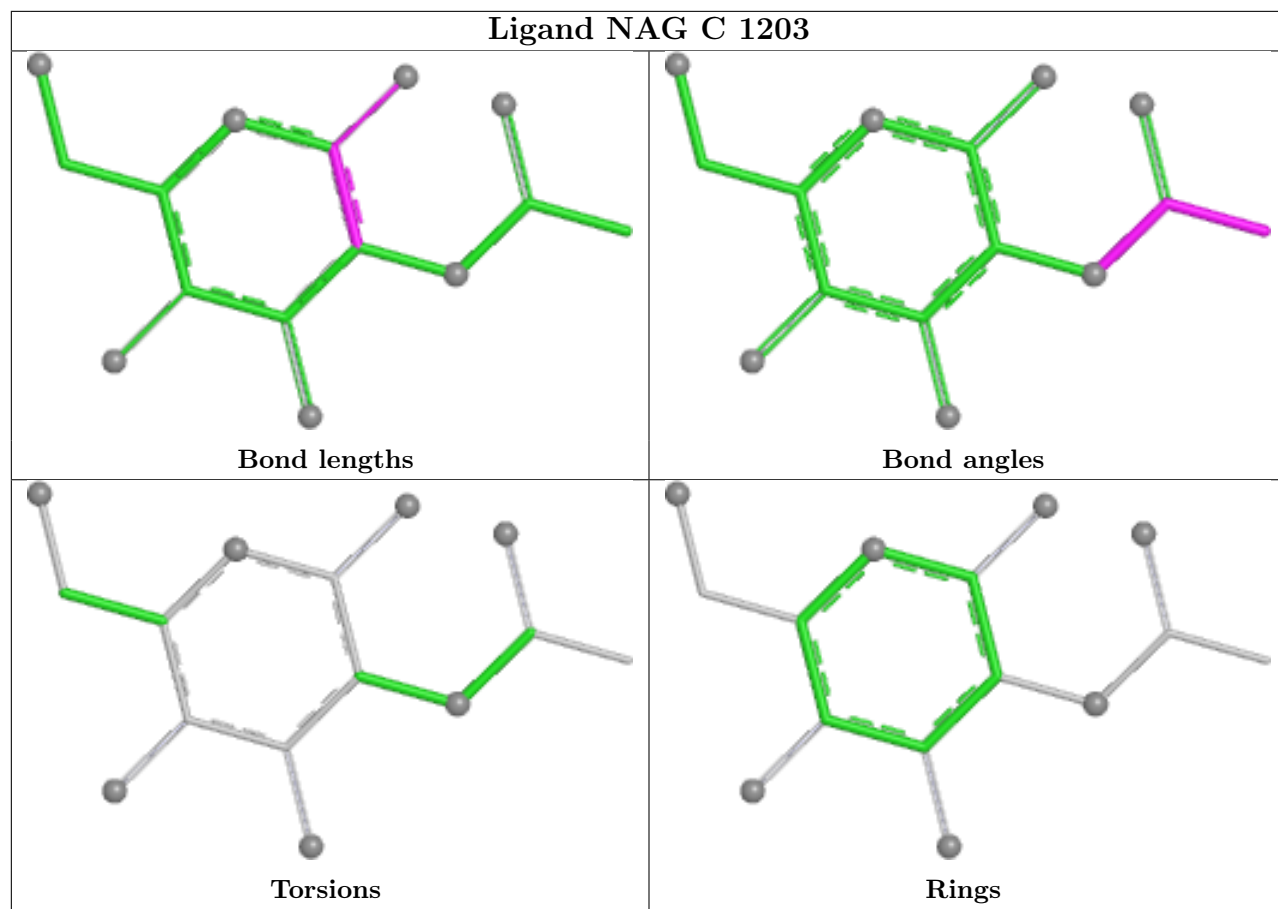


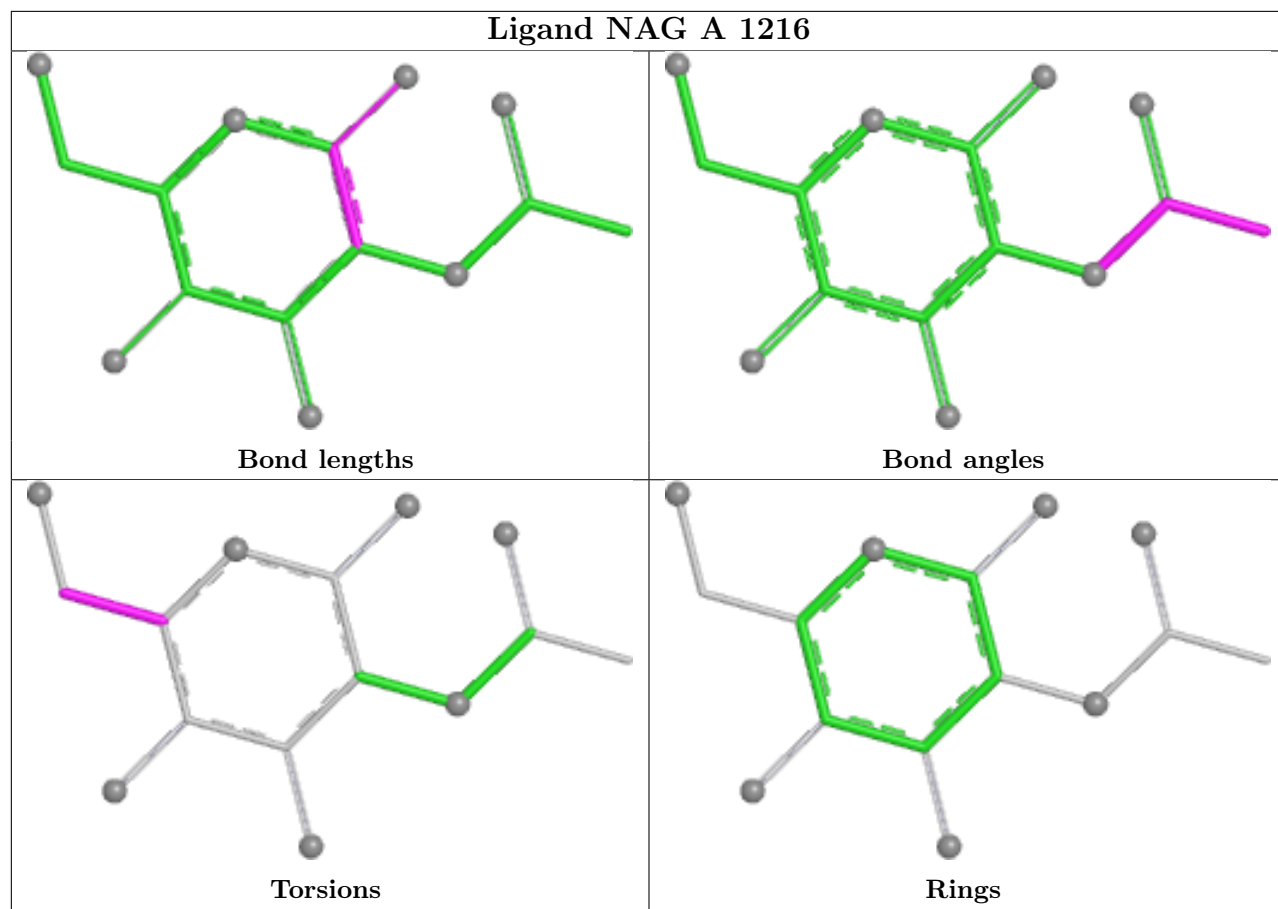


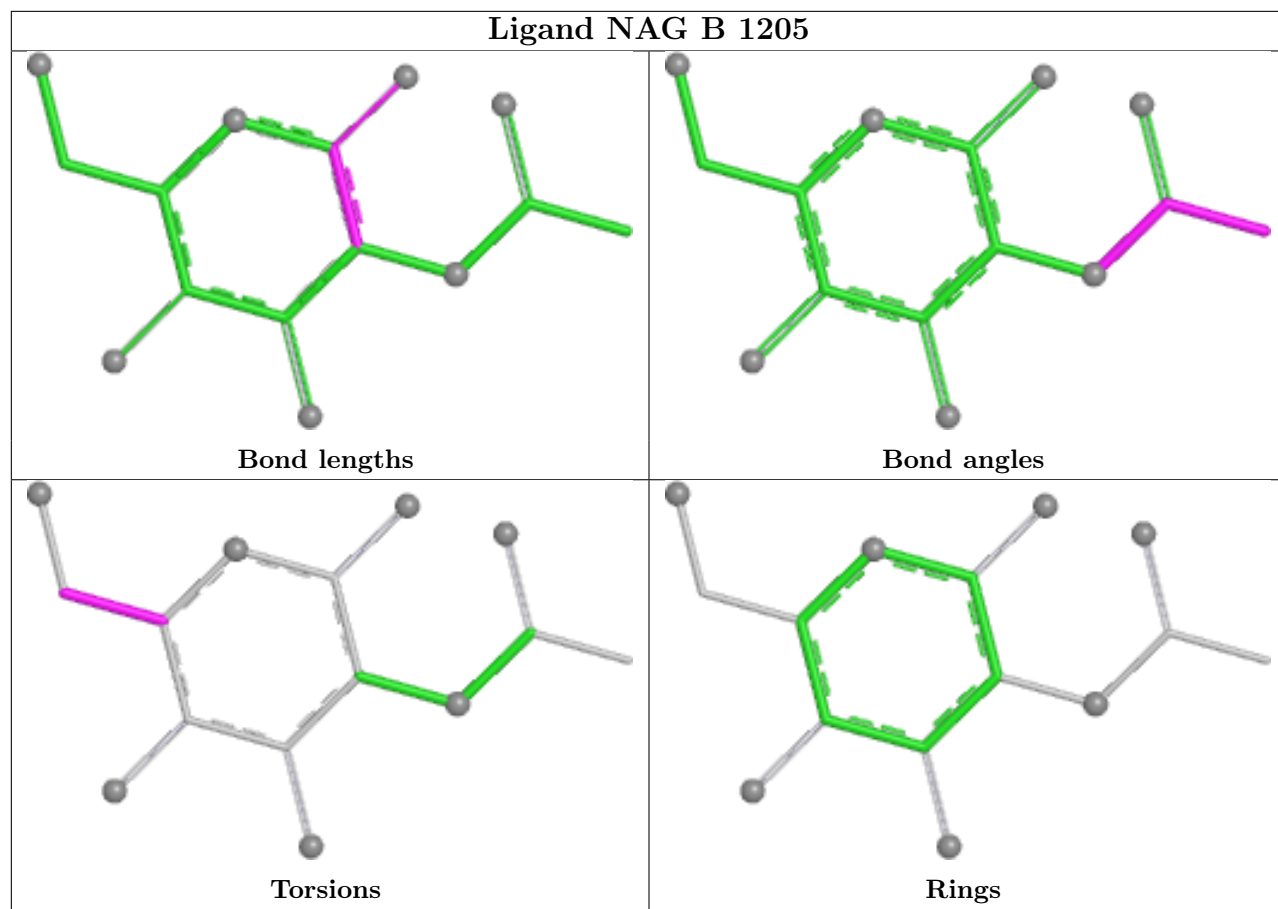




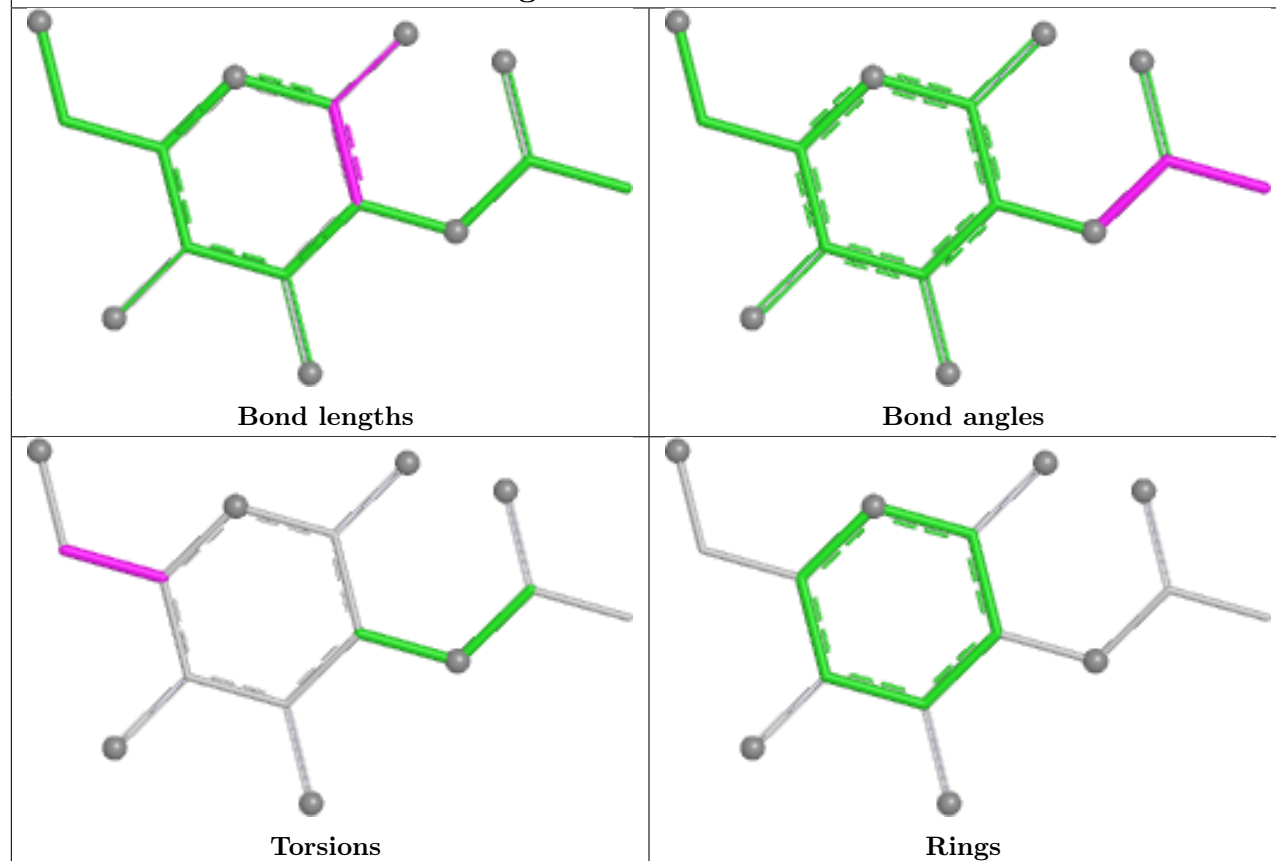




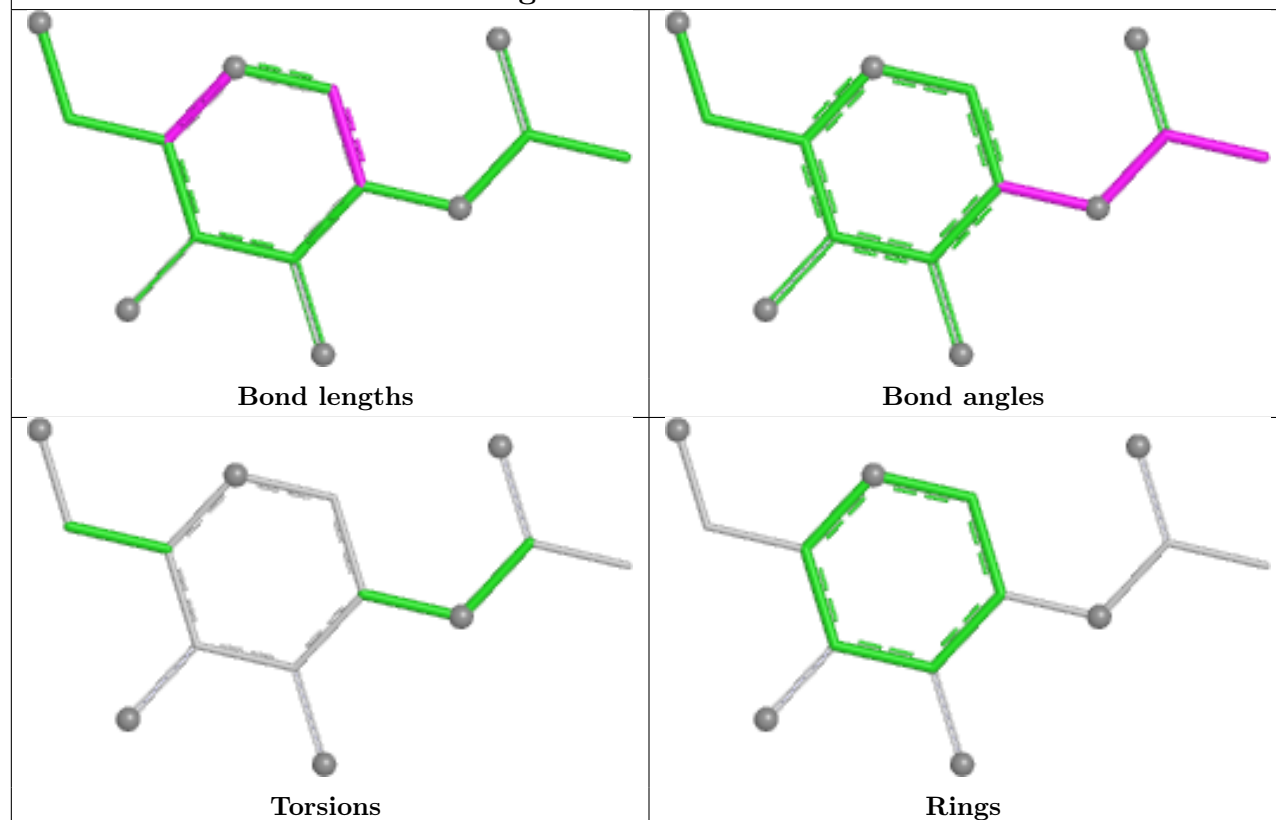


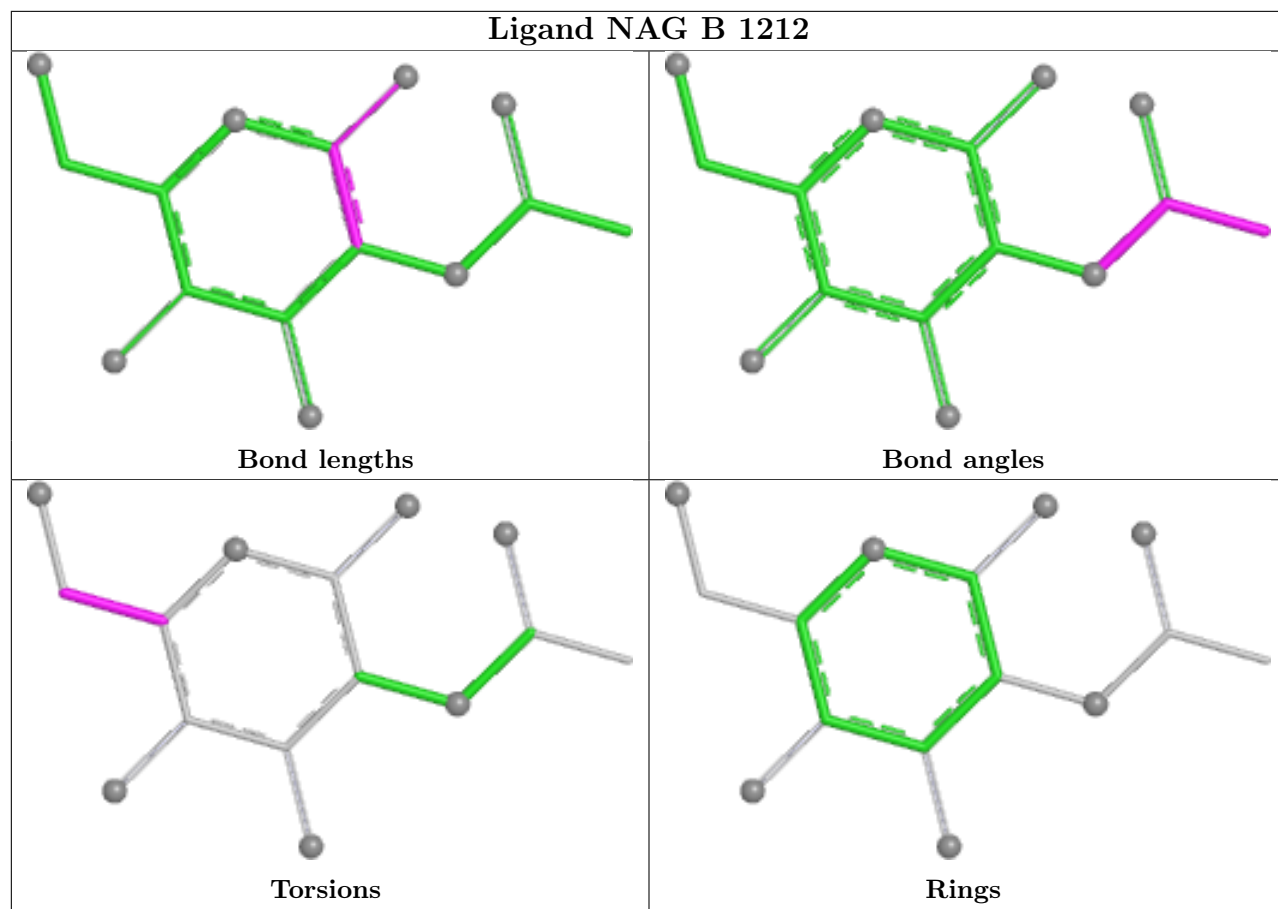


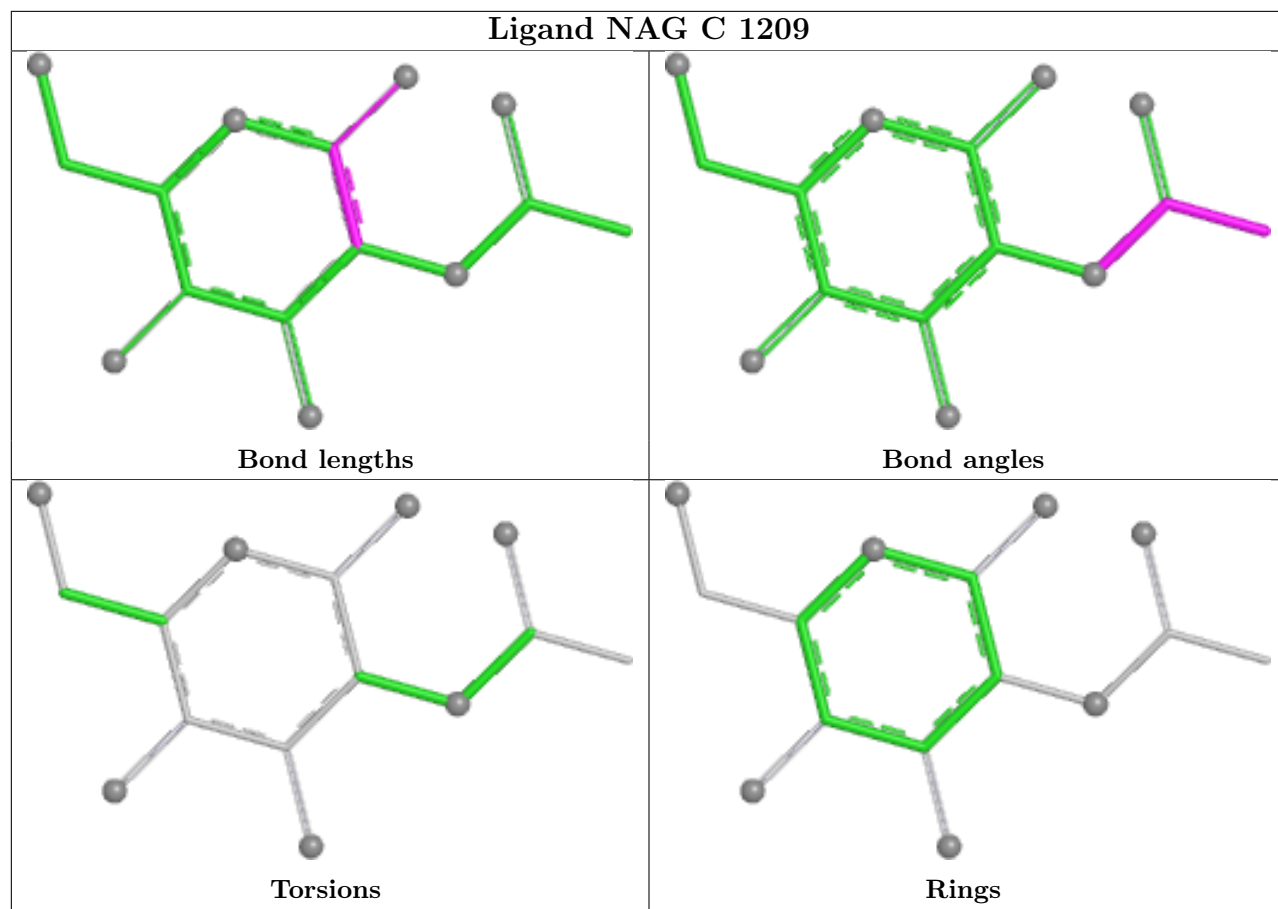
Ligand NAG A 1205

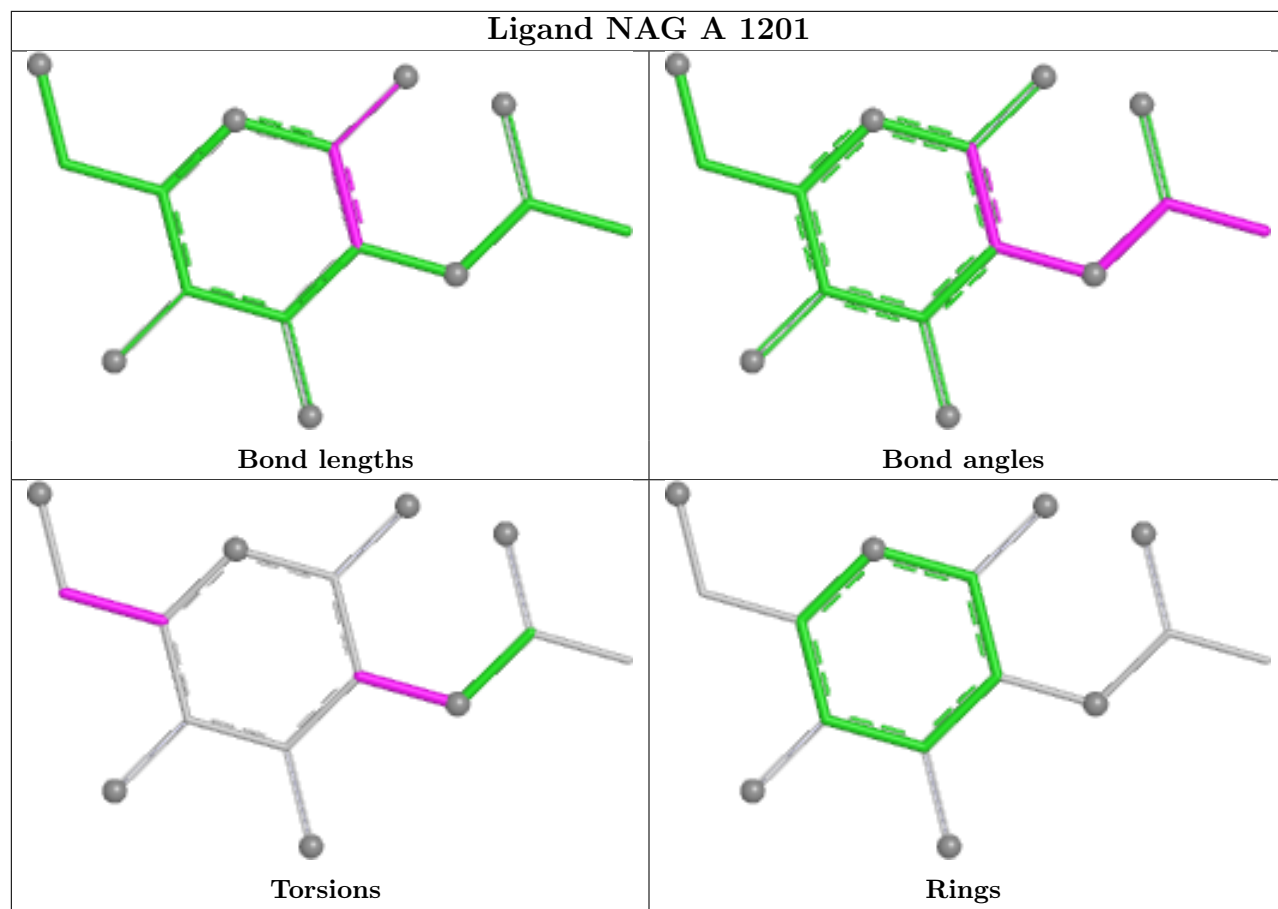


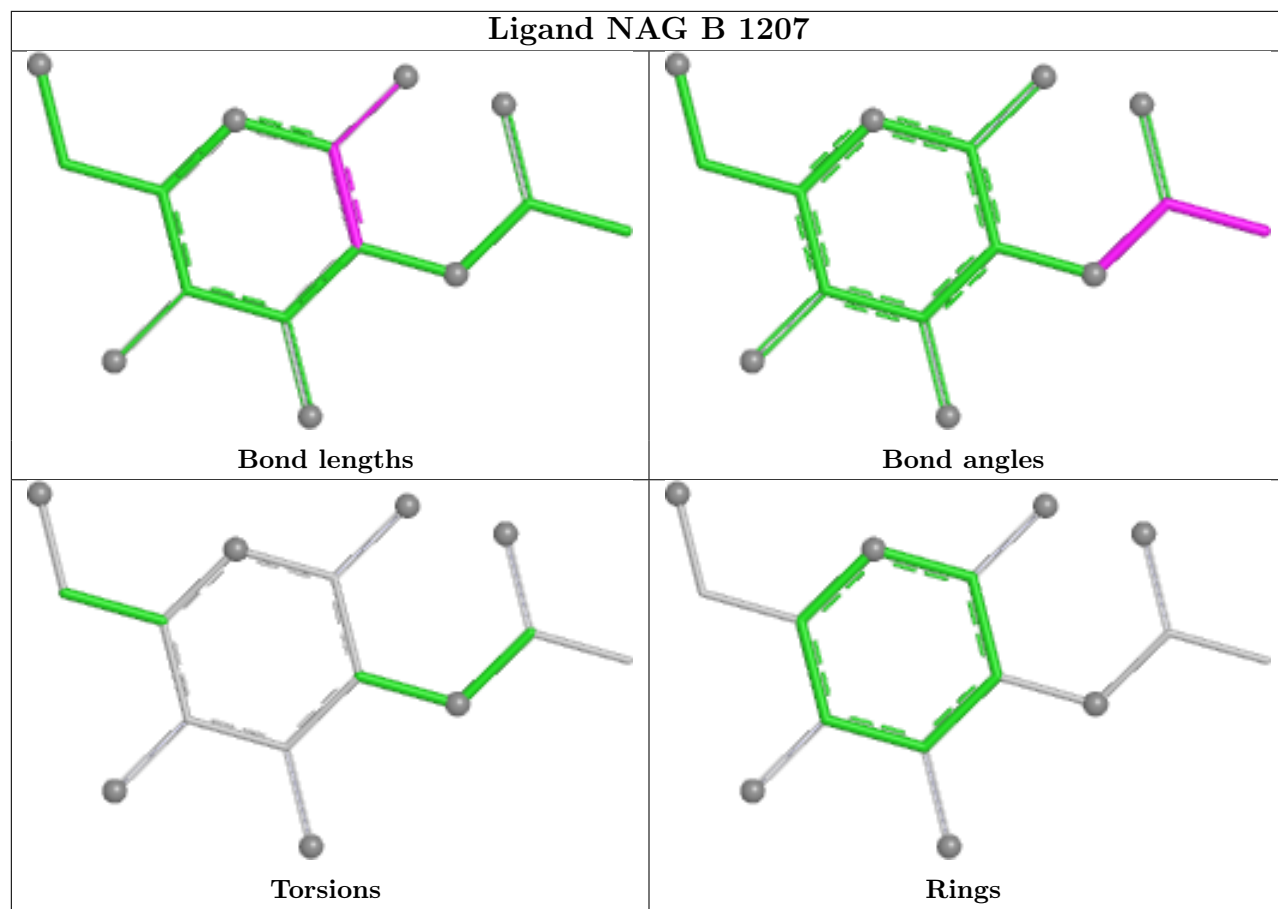
Ligand NAG A 1206

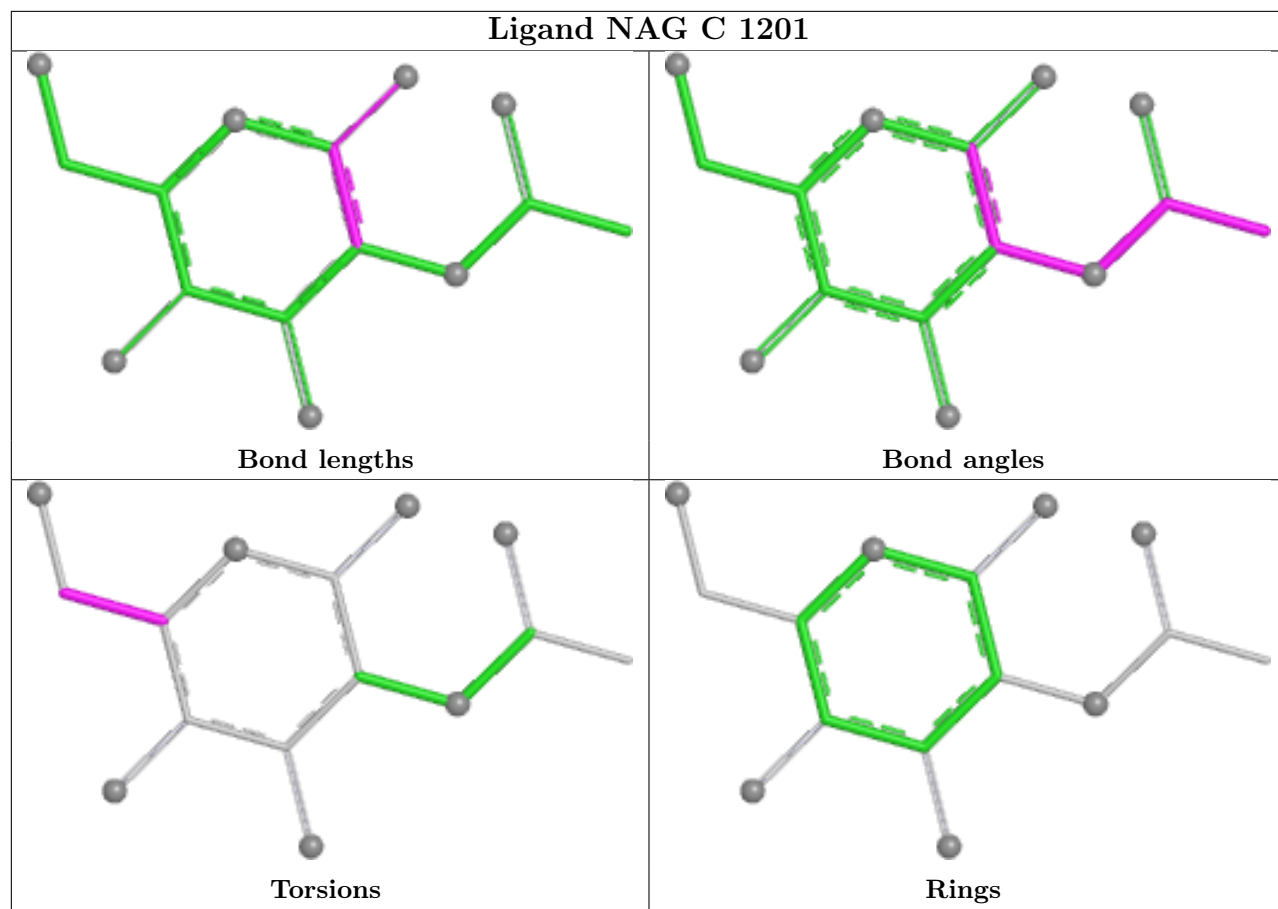


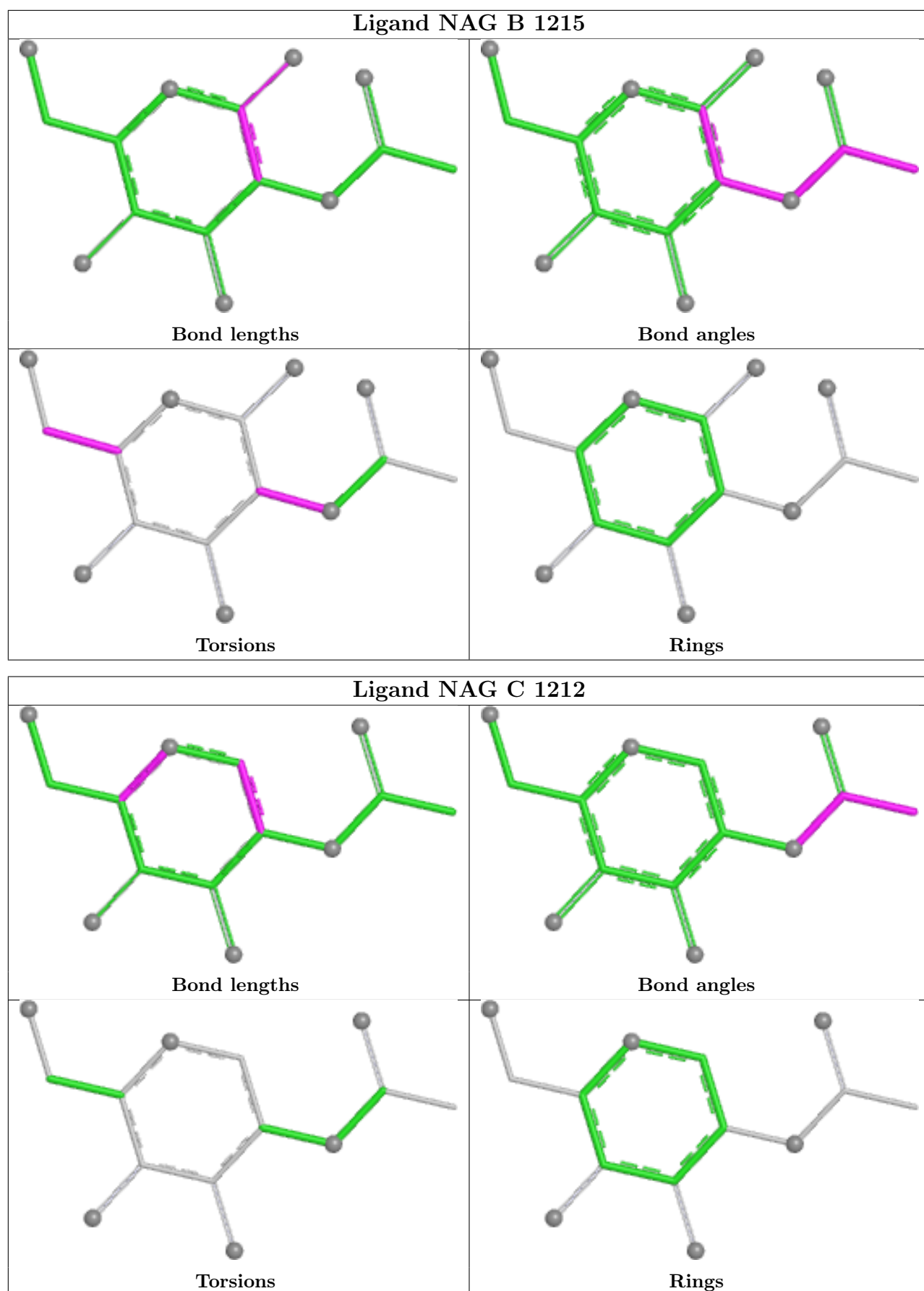


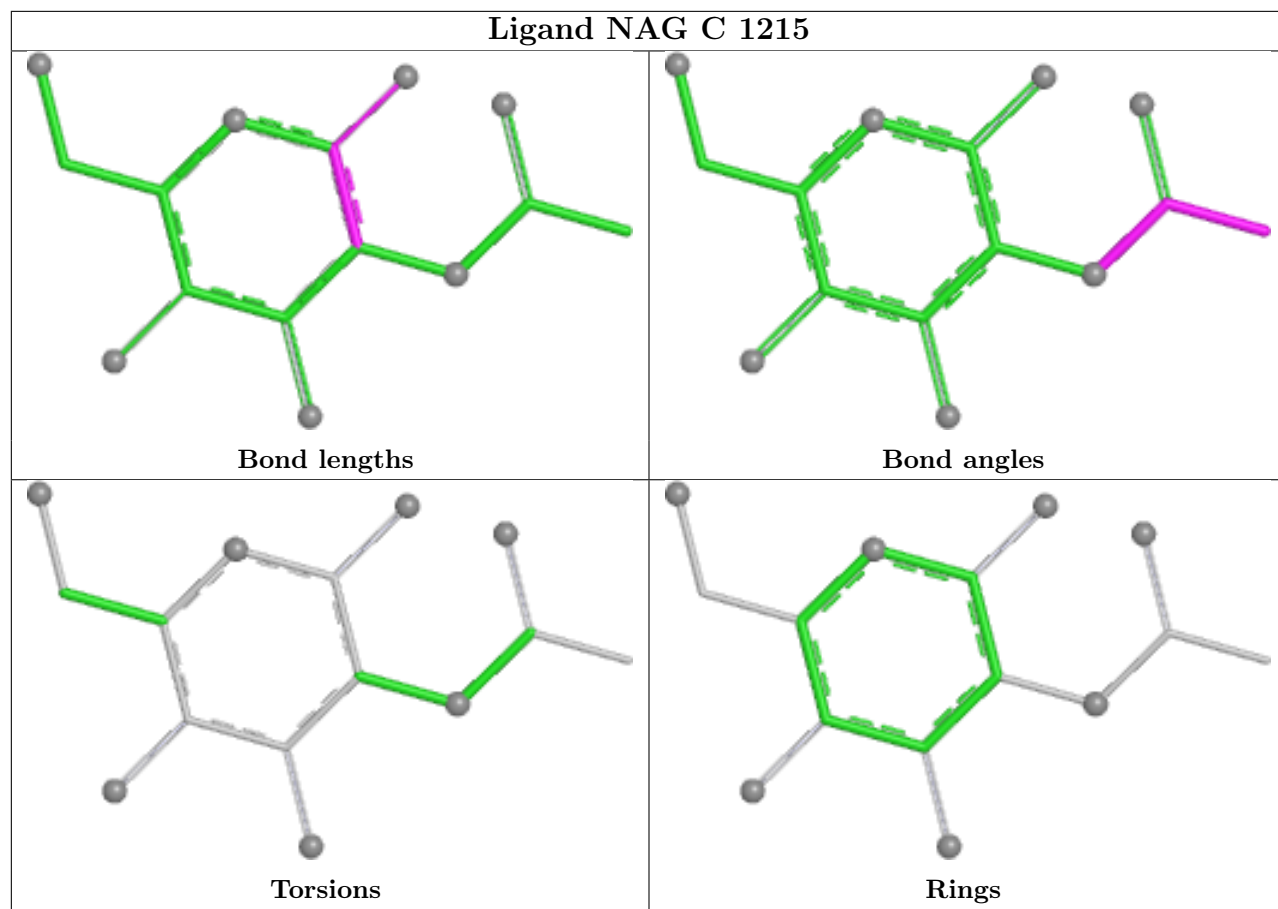


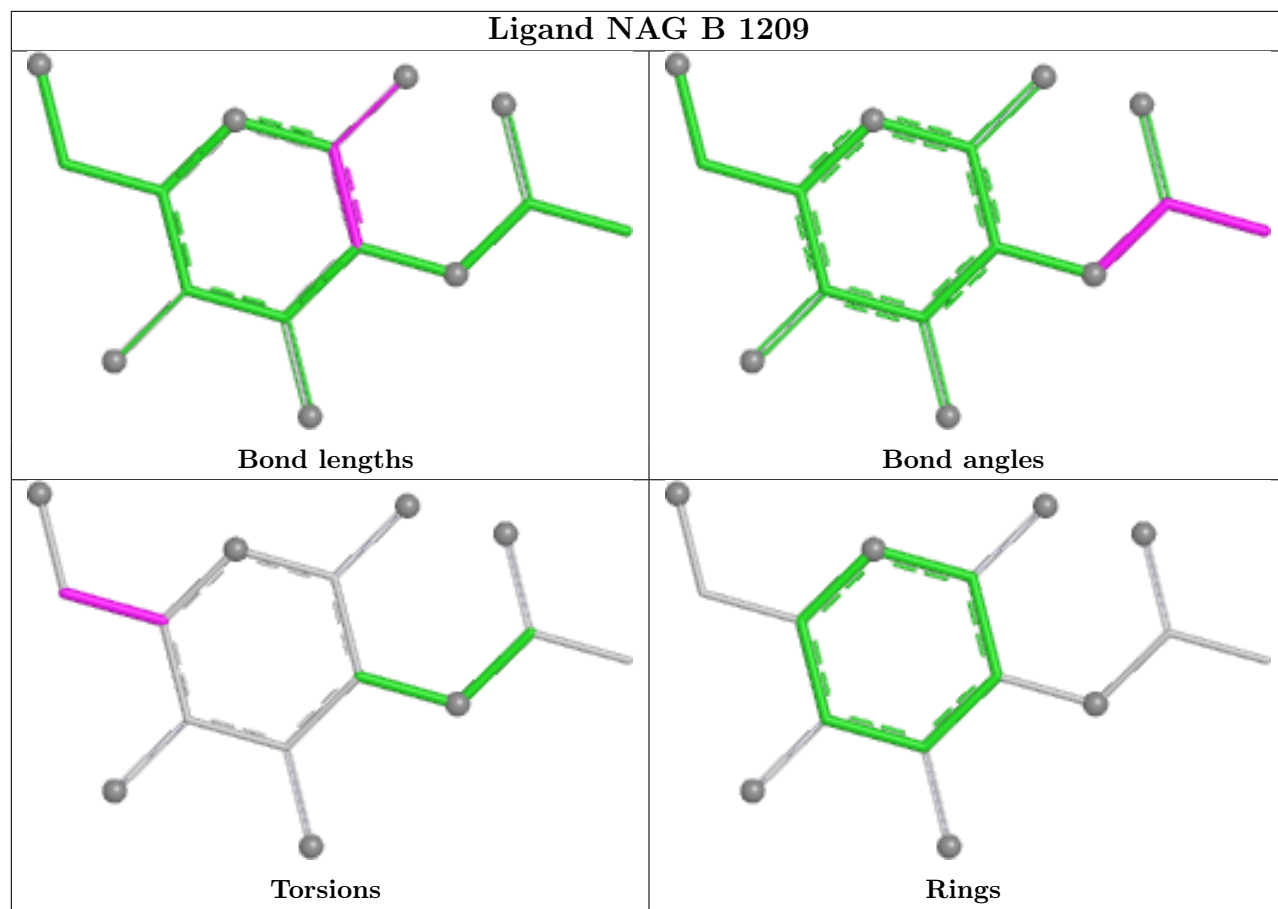


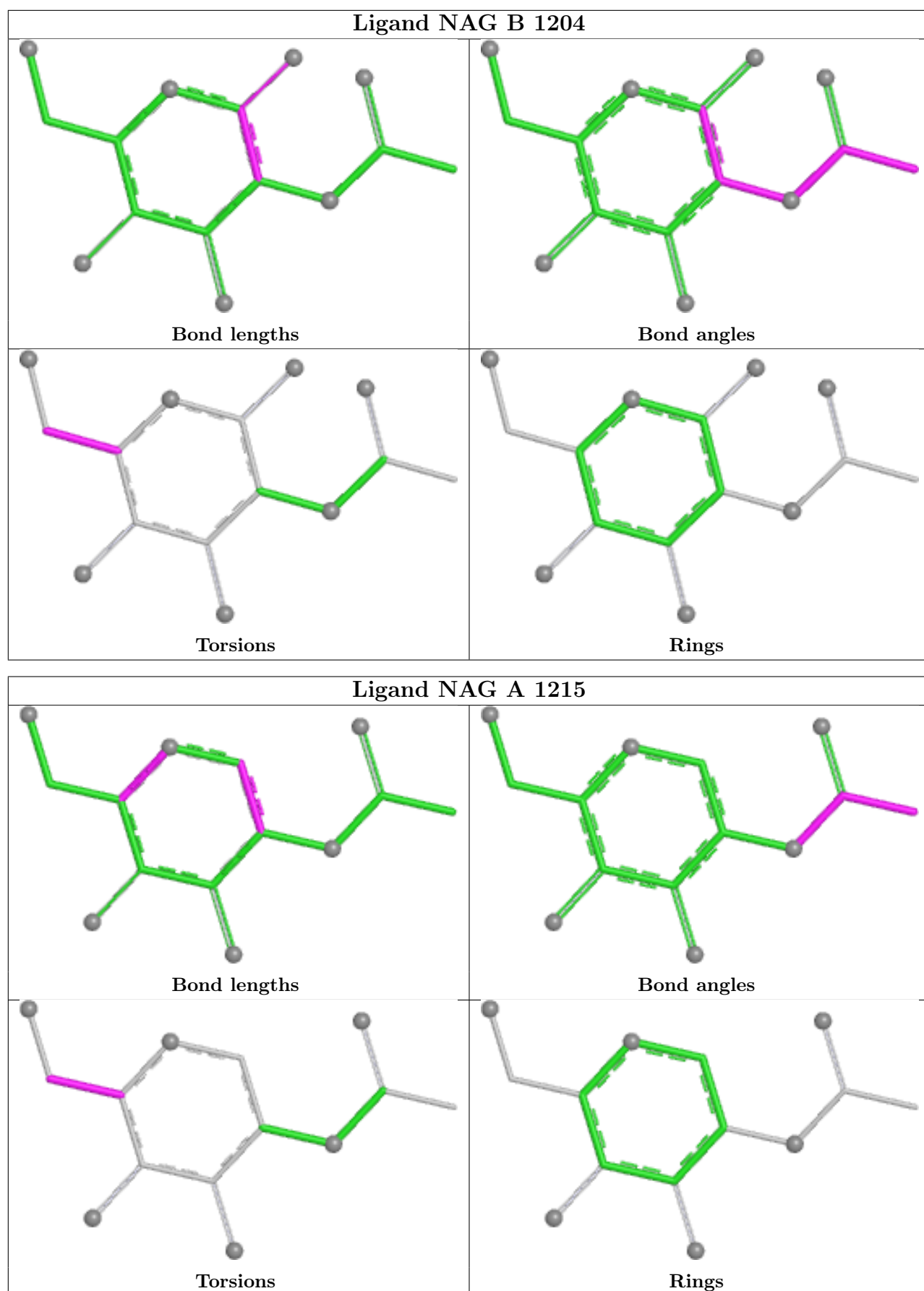


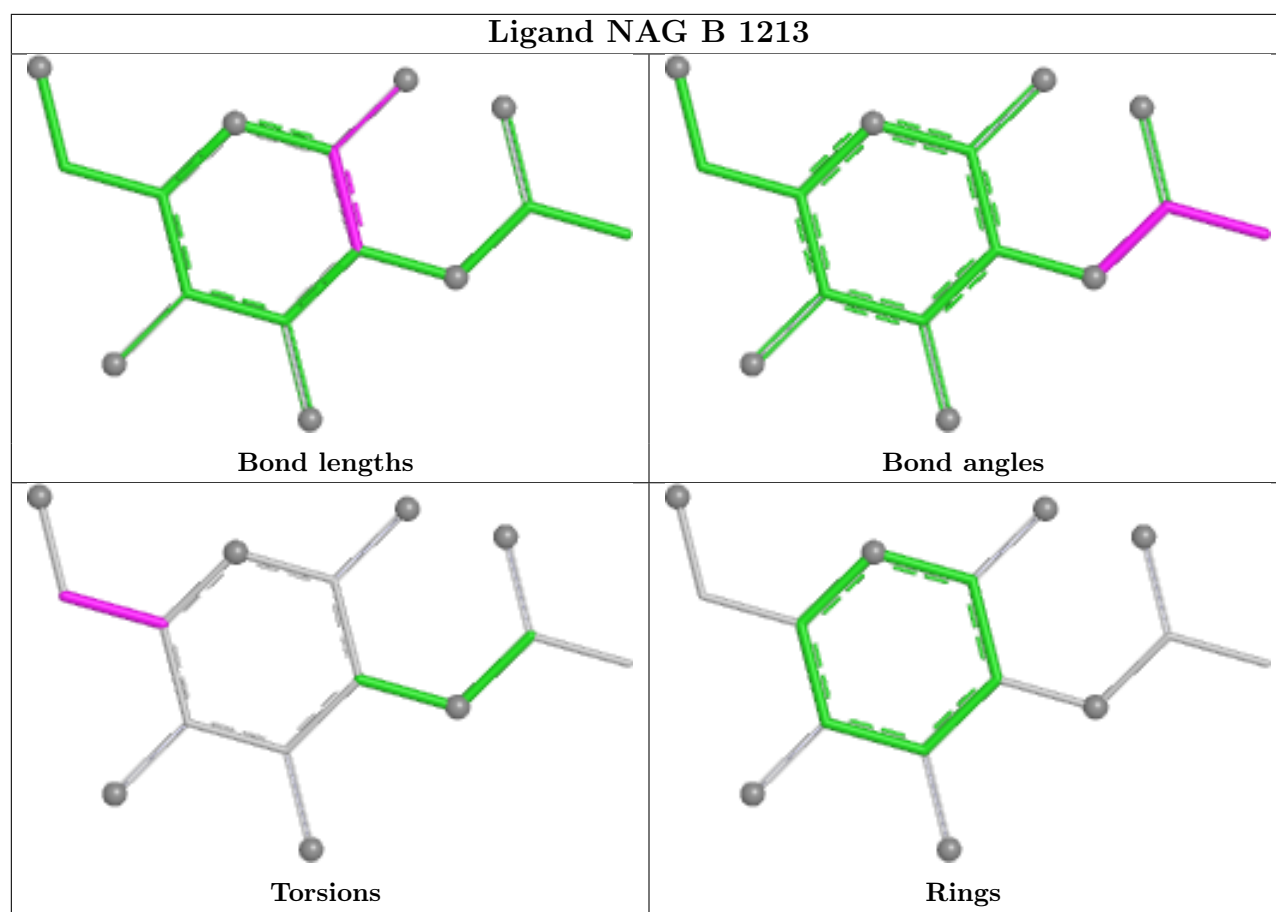












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

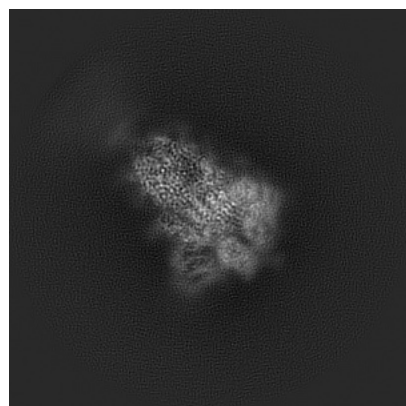
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29455. These allow visual inspection of the internal detail of the map and identification of artifacts.

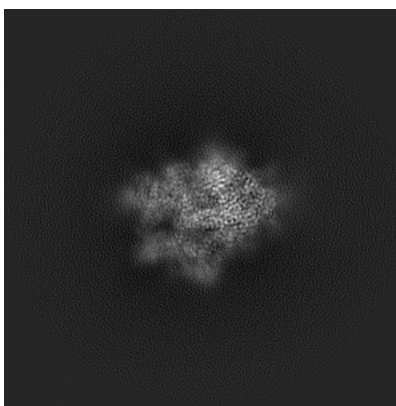
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

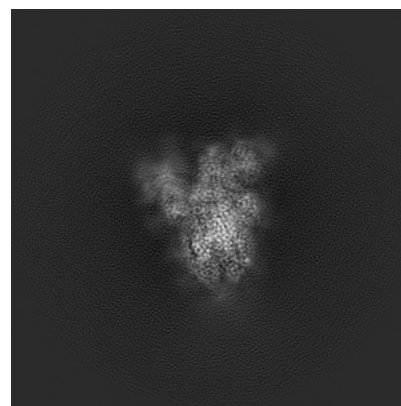
6.1.1 Primary map



X

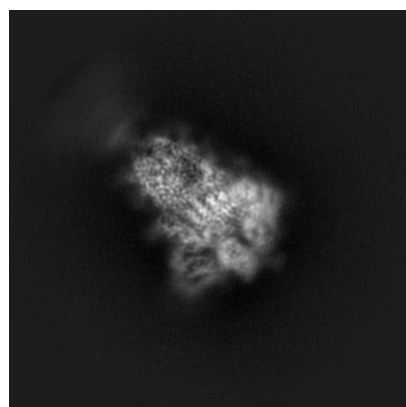


Y

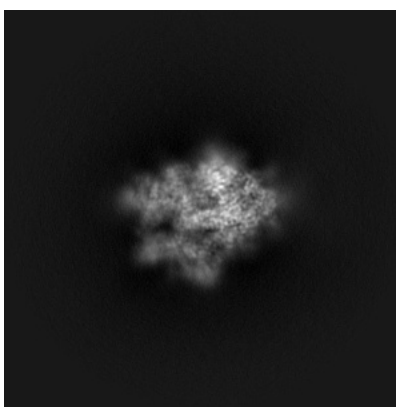


Z

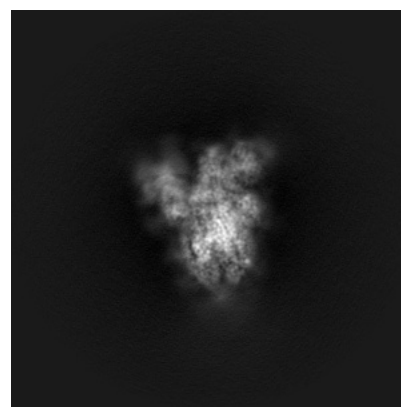
6.1.2 Raw map



X



Y

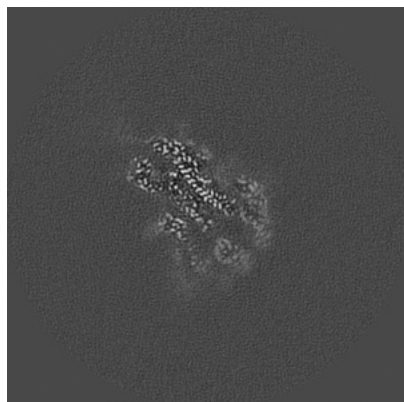


Z

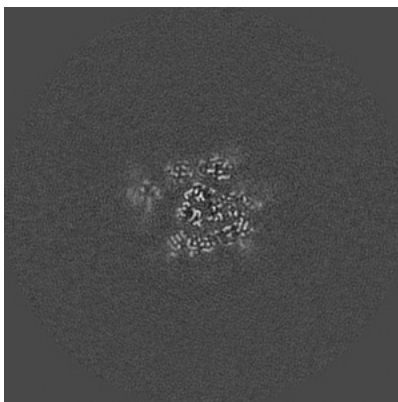
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

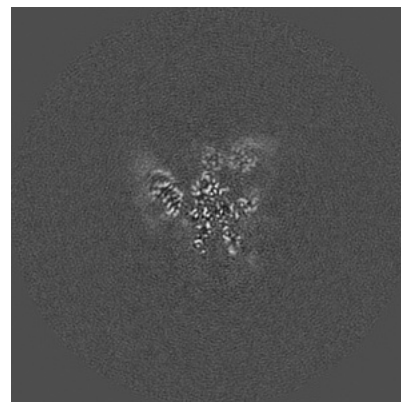
6.2.1 Primary map



X Index: 220

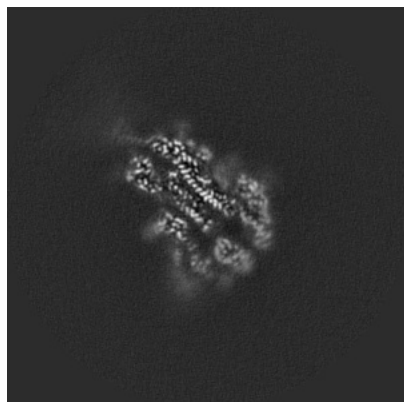


Y Index: 220

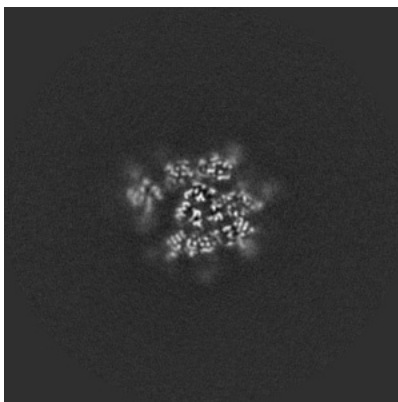


Z Index: 220

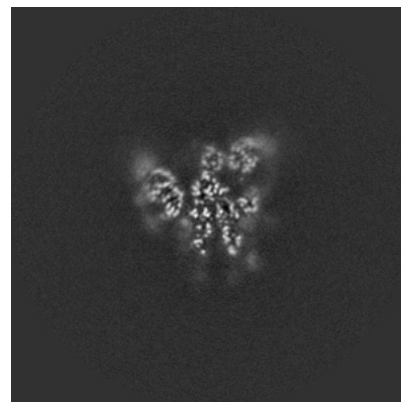
6.2.2 Raw map



X Index: 220



Y Index: 220

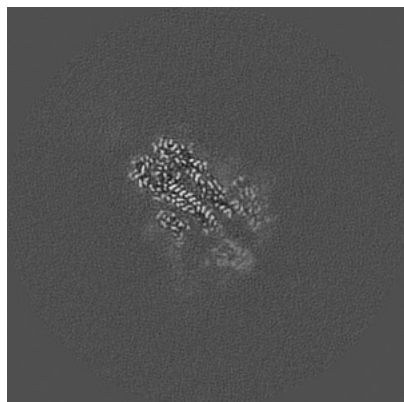


Z Index: 220

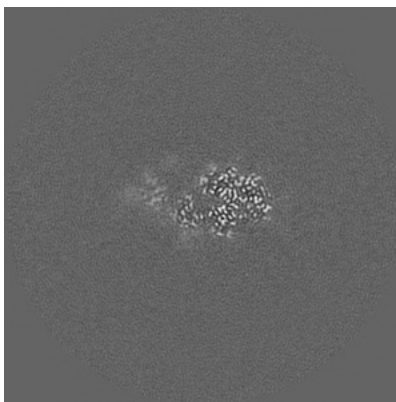
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

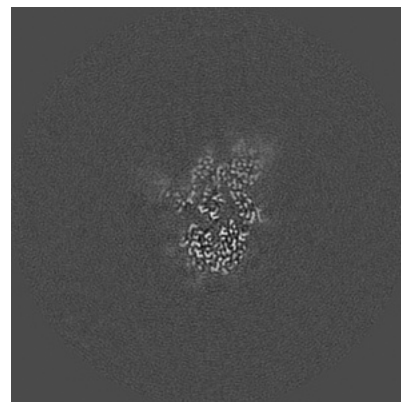
6.3.1 Primary map



X Index: 215

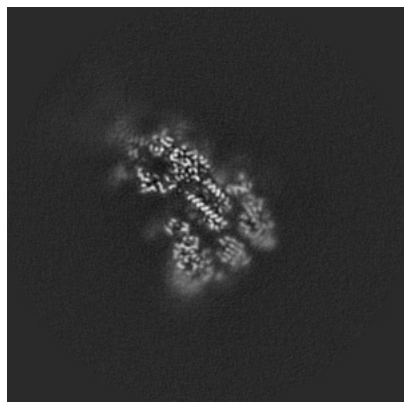


Y Index: 185

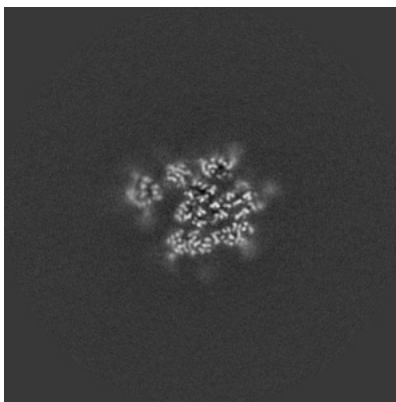


Z Index: 239

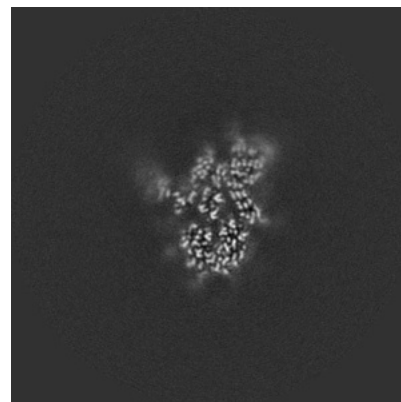
6.3.2 Raw map



X Index: 228



Y Index: 217

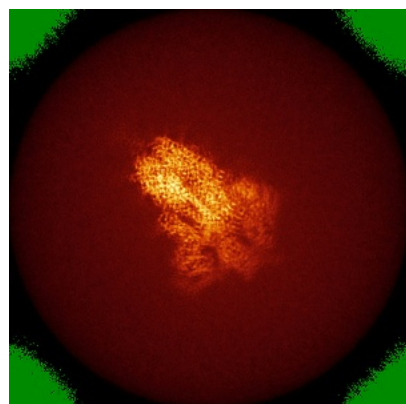


Z Index: 238

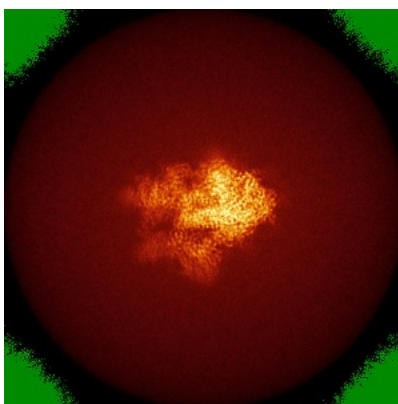
The images above show the largest variance slices of the map in three orthogonal directions.

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

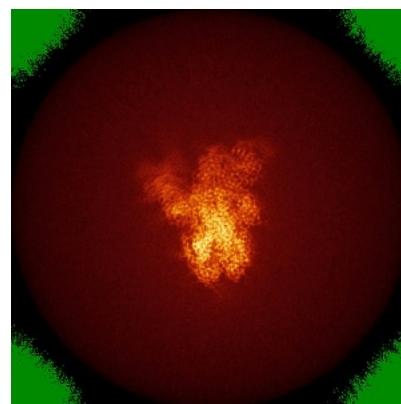
6.4.1 Primary map



X

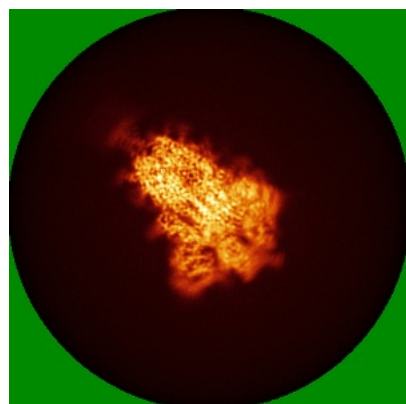


Y

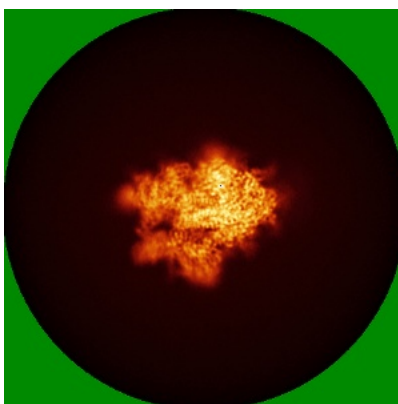


Z

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



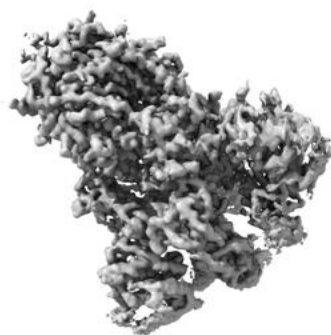
Y



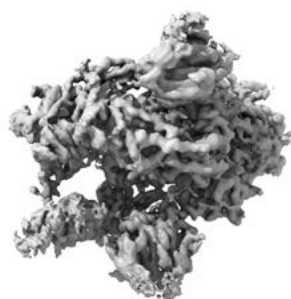
Z

The images above show the 3D surface view of the map at the recommended contour level 0.0084. 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.

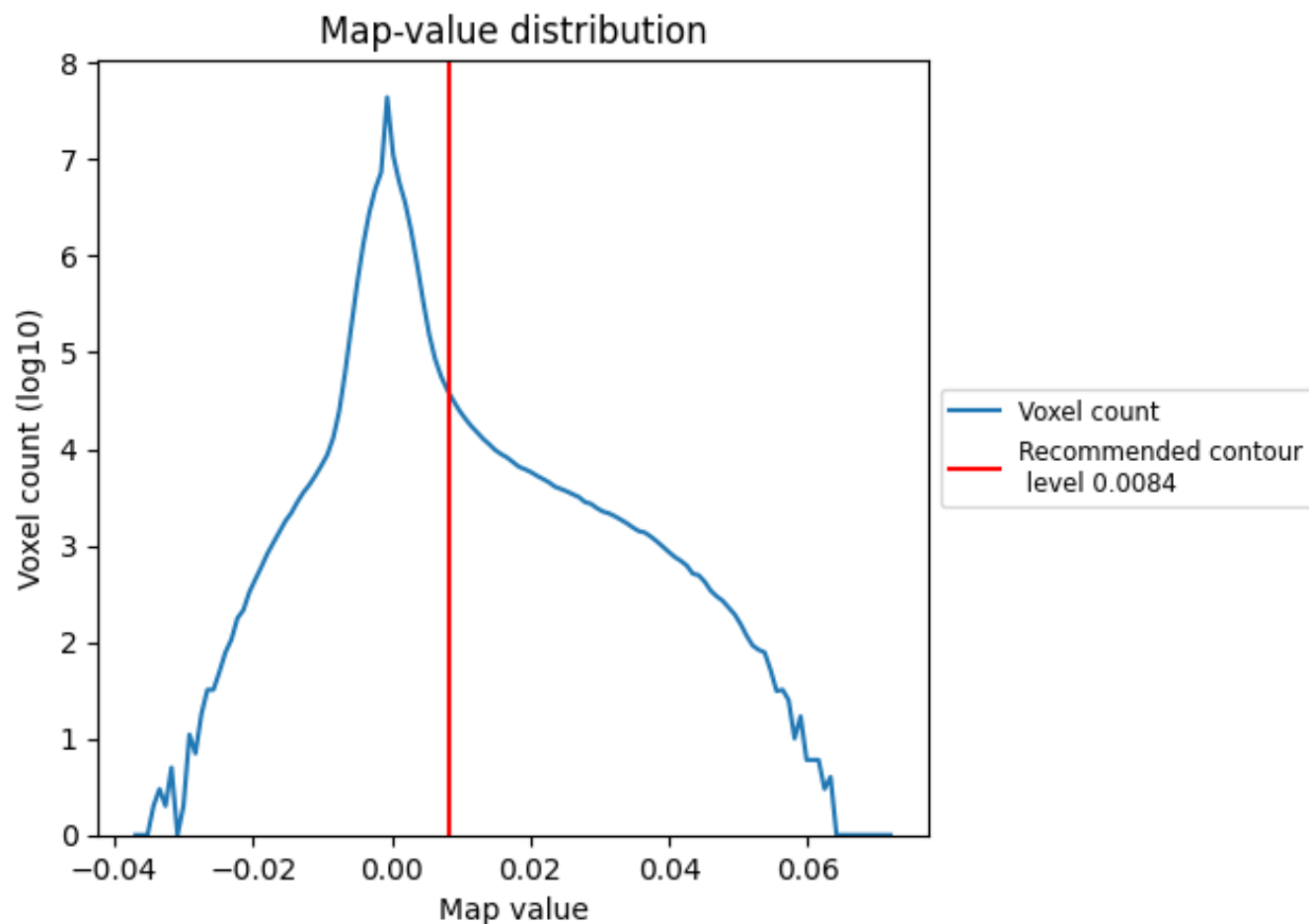
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

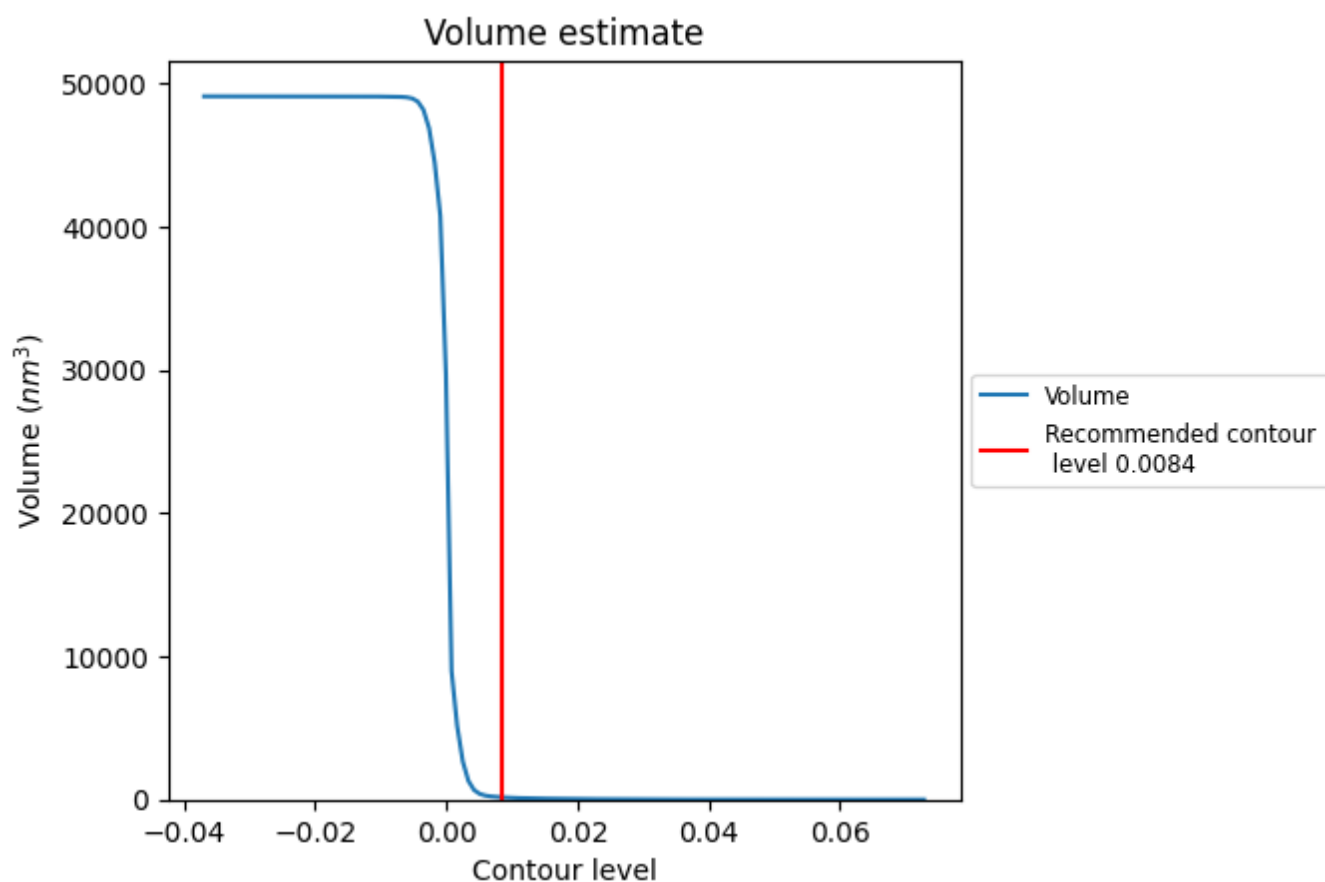
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

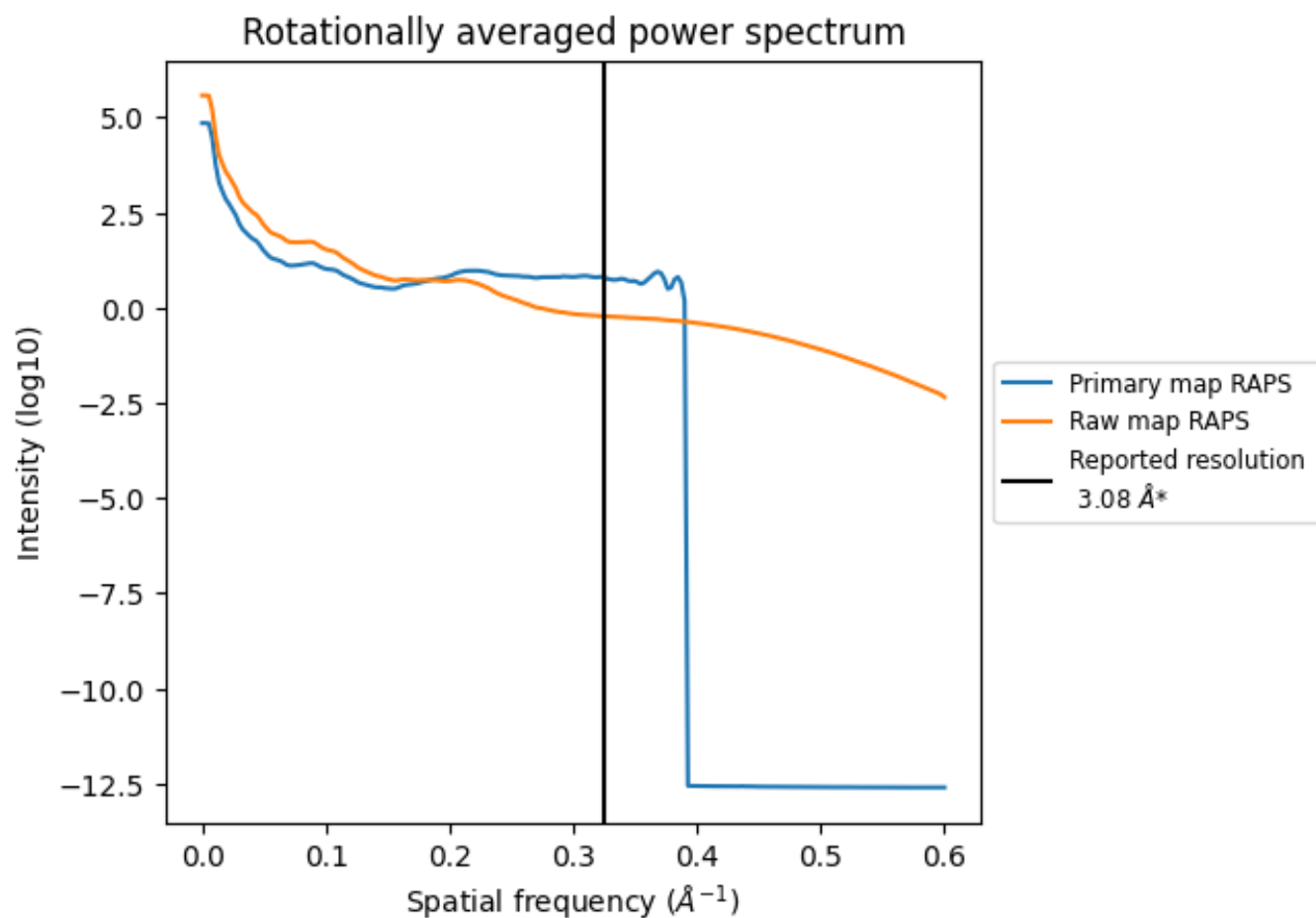
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 157 nm³; this corresponds to an approximate mass of 142 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

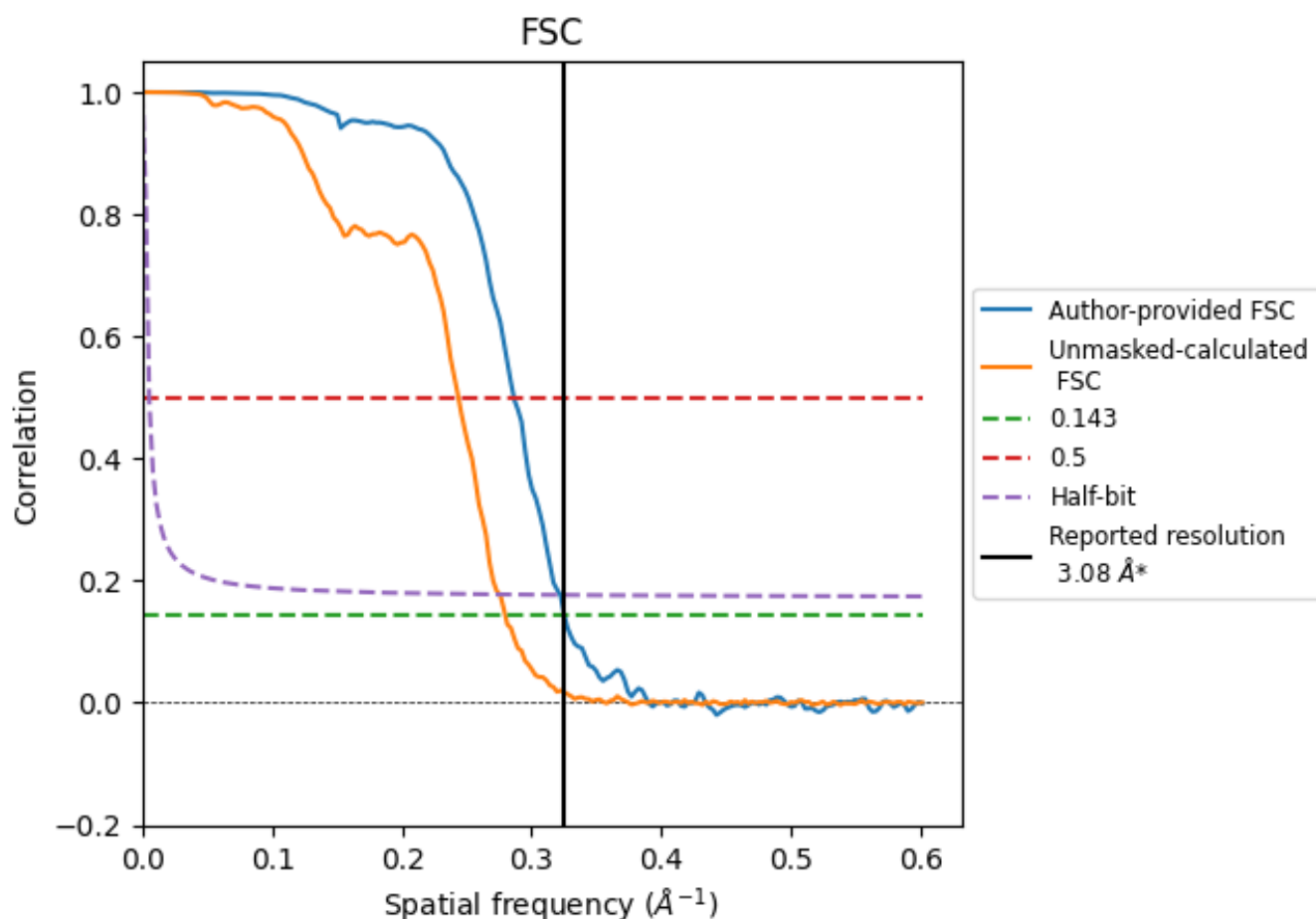


*Reported resolution corresponds to spatial frequency of 0.325 $\text{\AA}^{-1}$

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 $0.325 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

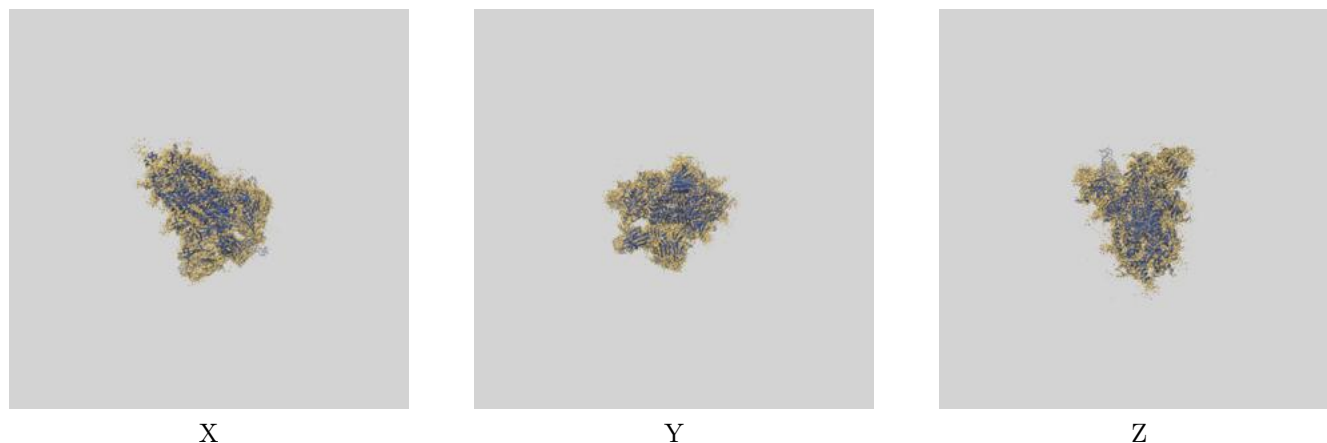
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.08	-	-
Author-provided FSC curve	3.08	3.49	3.11
Unmasked-calculated*	3.58	4.11	3.63

*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 3.58 differs from the reported value 3.08 by more than 10 %

9 Map-model fit [i](#)

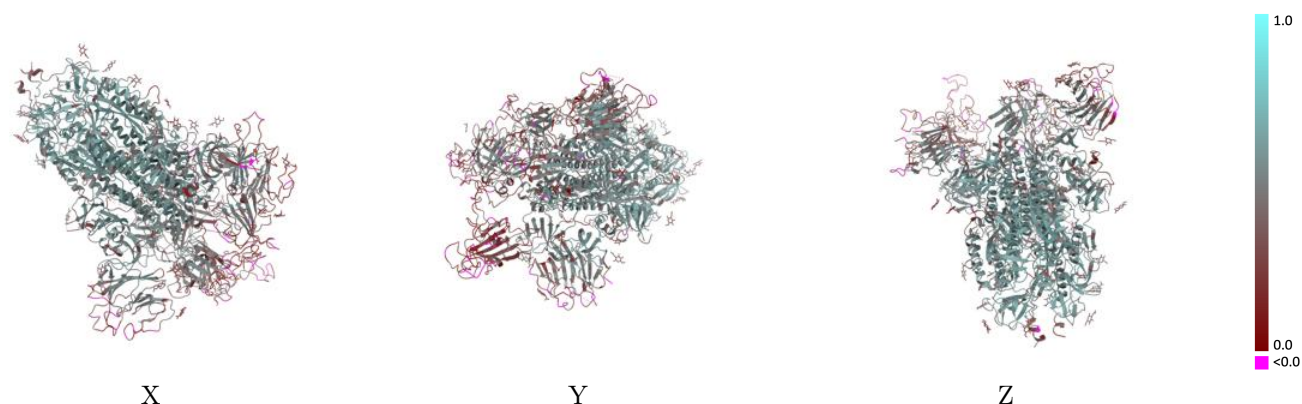
This section contains information regarding the fit between EMDB map EMD-29455 and PDB model 8FU8. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



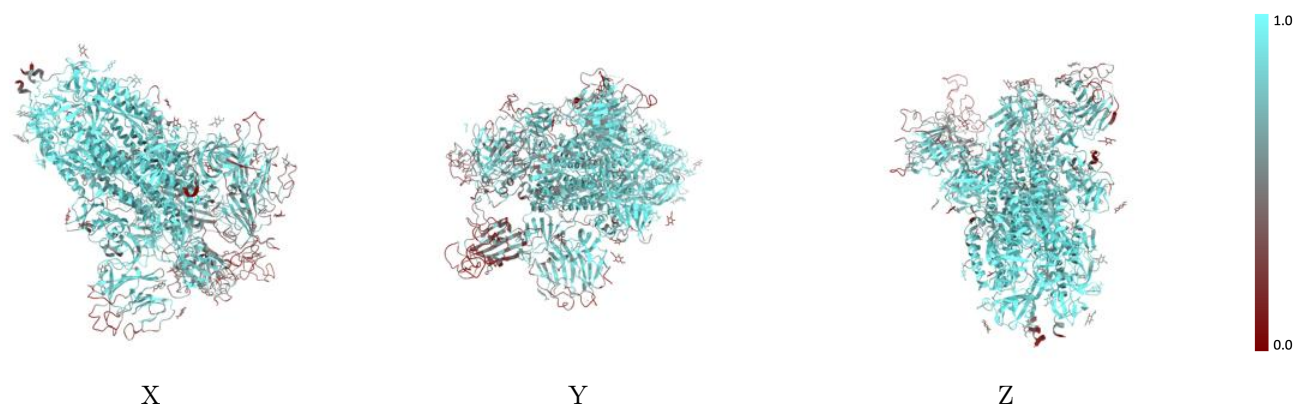
The images above show the 3D surface view of the map at the recommended contour level 0.0084 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



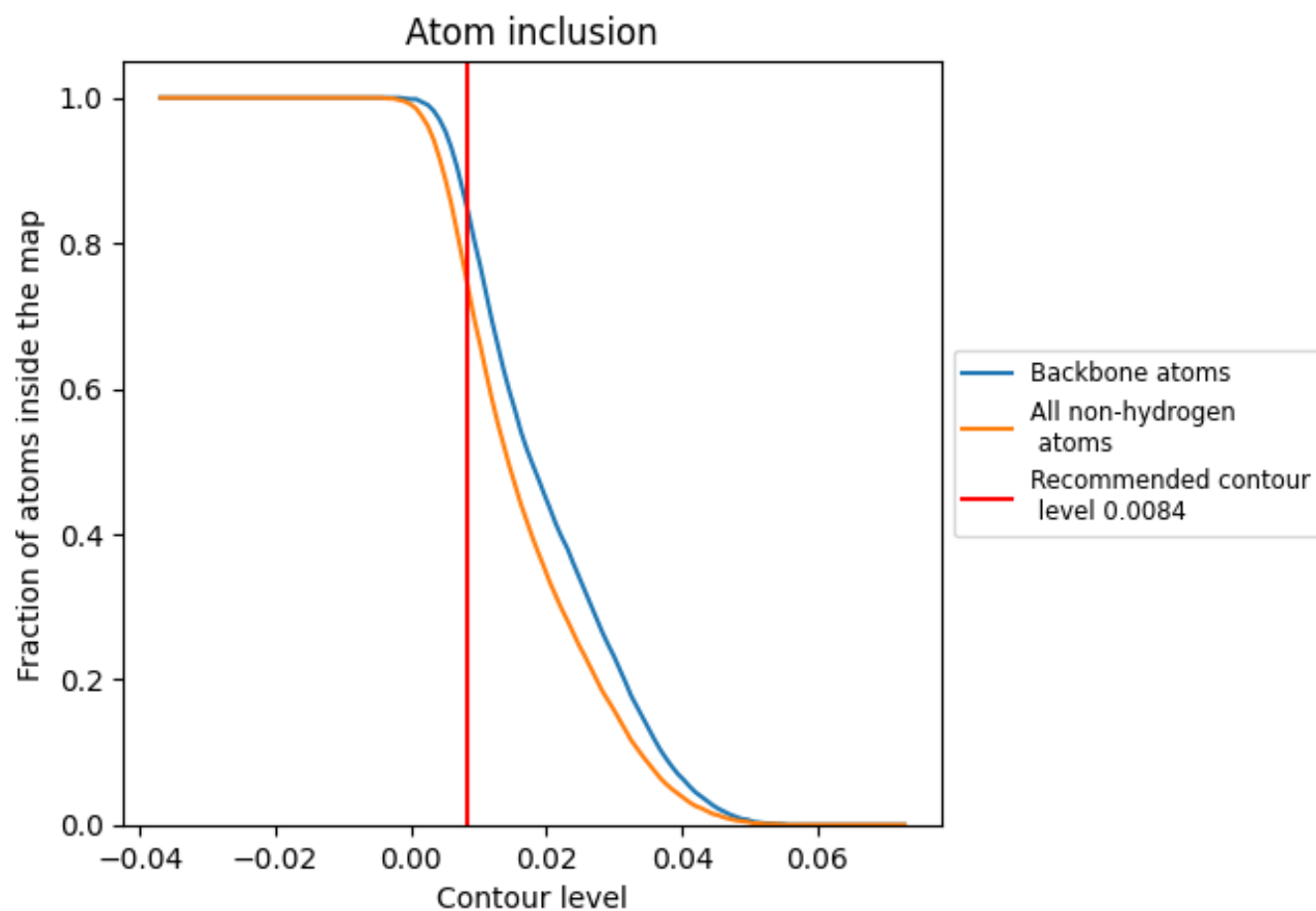
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0084).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 74% 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 (0.0084) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7400	0.4570
A	0.7570	0.4600
B	0.7180	0.4500
C	0.7460	0.4600

