



Full wwPDB EM Validation Report ⓘ

Nov 11, 2024 – 10:24 PM JST

PDB ID : 7WPR
EMDB ID : EMD-32689
Title : VWF D'D3 dimer complexed with D1D2 at 4.39 angstrom resolution(VWF tube)
Authors : Zeng, J.W.; Shu, Z.M.; Zhou, A.W.
Deposited on : 2022-01-24
Resolution : 4.39 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev113
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

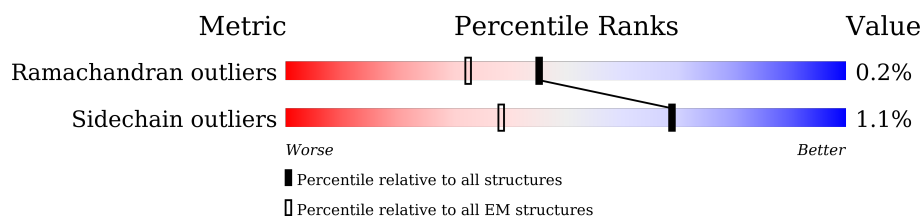
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.39 Å.

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



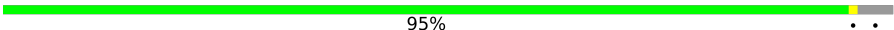

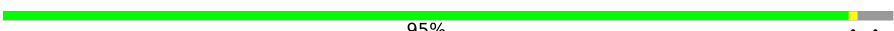
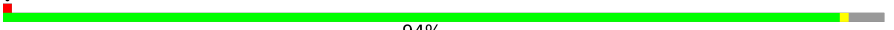
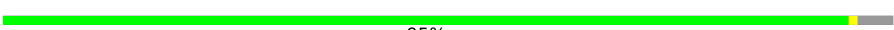





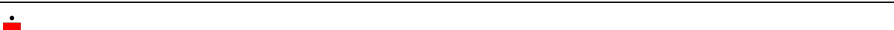

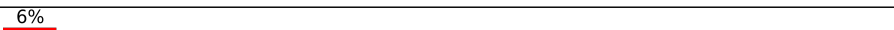
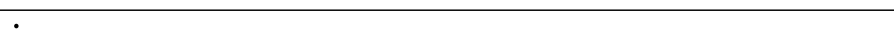
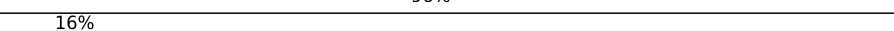
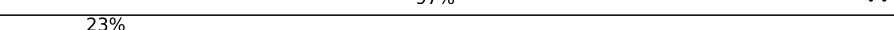
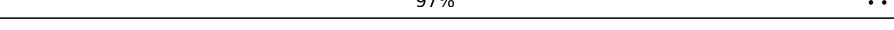
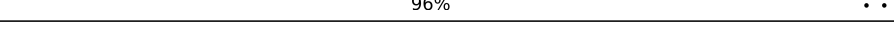
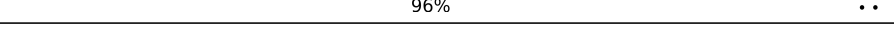
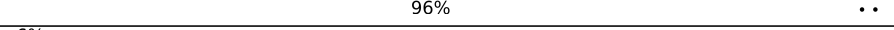
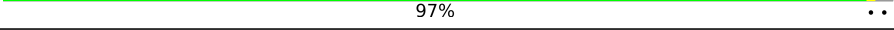
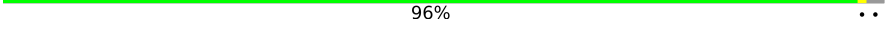
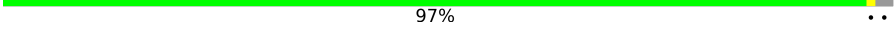
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	741	95%
1	B	741	94%
1	E	741	94%
1	F	741	95%
1	G	741	94%
1	H	741	95%
1	I	741	94%
1	J	741	9% 95%
1	K	741	16% 95%

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Mol	Chain	Length	Quality of chain
1	L	741	 95% ..
1	M	741	 94% ..
1	N	741	 95% ..
1	O	741	 94% ..
1	P	741	 95% ..
1	Q	741	 95% ..
1	R	741	 95% ..
2	C	490	 97% ..
2	D	490	 96% ..
2	S	490	 96% ..
2	T	490	 96% ..
2	U	490	 94% ..
2	V	490	 97% ..
2	W	490	 96% ..
2	X	490	 97% ..
2	Y	490	 97% ..
2	Z	490	 96% ..
2	a	490	 96% ..
2	b	490	 96% ..
2	c	490	 97% ..
2	d	490	 96% ..
2	e	490	 97% ..
2	f	490	 97% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 145764 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 von Willebrand antigen 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	711	Total	C	N	O	S	0	0
			5421	3353	929	1061	78		
1	B	711	Total	C	N	O	S	0	0
			5421	3353	929	1061	78		
1	E	711	Total	C	N	O	S	0	0
			5421	3353	929	1061	78		
1	F	711	Total	C	N	O	S	0	0
			5421	3353	929	1061	78		
1	G	711	Total	C	N	O	S	0	0
			5421	3353	929	1061	78		
1	H	711	Total	C	N	O	S	0	0
			5421	3353	929	1061	78		
1	I	711	Total	C	N	O	S	0	0
			5421	3353	929	1061	78		
1	J	711	Total	C	N	O	S	0	0
			5421	3353	929	1061	78		
1	K	711	Total	C	N	O	S	0	0
			5421	3353	929	1061	78		
1	L	711	Total	C	N	O	S	0	0
			5421	3353	929	1061	78		
1	M	711	Total	C	N	O	S	0	0
			5421	3353	929	1061	78		
1	N	711	Total	C	N	O	S	0	0
			5421	3353	929	1061	78		
1	O	711	Total	C	N	O	S	0	0
			5421	3353	929	1061	78		
1	P	711	Total	C	N	O	S	0	0
			5421	3353	929	1061	78		
1	Q	711	Total	C	N	O	S	0	0
			5421	3353	929	1061	78		
1	R	711	Total	C	N	O	S	0	0
			5421	3353	929	1061	78		

- Molecule 2 is a protein called von Willebrand factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	a	478	Total	C	N	O	S	1	0
			3649	2247	631	711	60		
2	b	478	Total	C	N	O	S	1	0
			3649	2247	631	711	60		
2	C	478	Total	C	N	O	S	1	0
			3649	2247	631	711	60		
2	c	478	Total	C	N	O	S	1	0
			3649	2247	631	711	60		
2	D	478	Total	C	N	O	S	1	0
			3649	2247	631	711	60		
2	d	478	Total	C	N	O	S	1	0
			3649	2247	631	711	60		
2	e	478	Total	C	N	O	S	1	0
			3649	2247	631	711	60		
2	f	478	Total	C	N	O	S	1	0
			3649	2247	631	711	60		
2	S	478	Total	C	N	O	S	1	0
			3649	2247	631	711	60		
2	T	478	Total	C	N	O	S	1	0
			3649	2247	631	711	60		
2	U	478	Total	C	N	O	S	1	0
			3649	2247	631	711	60		
2	V	478	Total	C	N	O	S	1	0
			3649	2247	631	711	60		
2	W	478	Total	C	N	O	S	1	0
			3649	2247	631	711	60		
2	X	478	Total	C	N	O	S	1	0
			3649	2247	631	711	60		
2	Y	478	Total	C	N	O	S	1	0
			3649	2247	631	711	60		
2	Z	478	Total	C	N	O	S	1	0
			3649	2247	631	711	60		

There are 192 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	1242	GLY	-	expression tag	UNP P04275
a	1243	LEU	-	expression tag	UNP P04275
a	1244	VAL	-	expression tag	UNP P04275
a	1245	VAL	-	expression tag	UNP P04275
a	1246	PRO	-	expression tag	UNP P04275
a	1247	PRO	-	expression tag	UNP P04275
a	1248	HIS	-	expression tag	UNP P04275
a	1249	HIS	-	expression tag	UNP P04275

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Chain	Residue	Modelled	Actual	Comment	Reference
a	1250	HIS	-	expression tag	UNP P04275
a	1251	HIS	-	expression tag	UNP P04275
a	1252	HIS	-	expression tag	UNP P04275
a	1253	HIS	-	expression tag	UNP P04275
b	1242	GLY	-	expression tag	UNP P04275
b	1243	LEU	-	expression tag	UNP P04275
b	1244	VAL	-	expression tag	UNP P04275
b	1245	VAL	-	expression tag	UNP P04275
b	1246	PRO	-	expression tag	UNP P04275
b	1247	PRO	-	expression tag	UNP P04275
b	1248	HIS	-	expression tag	UNP P04275
b	1249	HIS	-	expression tag	UNP P04275
b	1250	HIS	-	expression tag	UNP P04275
b	1251	HIS	-	expression tag	UNP P04275
b	1252	HIS	-	expression tag	UNP P04275
b	1253	HIS	-	expression tag	UNP P04275
C	1242	GLY	-	expression tag	UNP P04275
C	1243	LEU	-	expression tag	UNP P04275
C	1244	VAL	-	expression tag	UNP P04275
C	1245	VAL	-	expression tag	UNP P04275
C	1246	PRO	-	expression tag	UNP P04275
C	1247	PRO	-	expression tag	UNP P04275
C	1248	HIS	-	expression tag	UNP P04275
C	1249	HIS	-	expression tag	UNP P04275
C	1250	HIS	-	expression tag	UNP P04275
C	1251	HIS	-	expression tag	UNP P04275
C	1252	HIS	-	expression tag	UNP P04275
C	1253	HIS	-	expression tag	UNP P04275
c	1242	GLY	-	expression tag	UNP P04275
c	1243	LEU	-	expression tag	UNP P04275
c	1244	VAL	-	expression tag	UNP P04275
c	1245	VAL	-	expression tag	UNP P04275
c	1246	PRO	-	expression tag	UNP P04275
c	1247	PRO	-	expression tag	UNP P04275
c	1248	HIS	-	expression tag	UNP P04275
c	1249	HIS	-	expression tag	UNP P04275
c	1250	HIS	-	expression tag	UNP P04275
c	1251	HIS	-	expression tag	UNP P04275
c	1252	HIS	-	expression tag	UNP P04275
c	1253	HIS	-	expression tag	UNP P04275
D	1242	GLY	-	expression tag	UNP P04275
D	1243	LEU	-	expression tag	UNP P04275

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Chain	Residue	Modelled	Actual	Comment	Reference
D	1244	VAL	-	expression tag	UNP P04275
D	1245	VAL	-	expression tag	UNP P04275
D	1246	PRO	-	expression tag	UNP P04275
D	1247	PRO	-	expression tag	UNP P04275
D	1248	HIS	-	expression tag	UNP P04275
D	1249	HIS	-	expression tag	UNP P04275
D	1250	HIS	-	expression tag	UNP P04275
D	1251	HIS	-	expression tag	UNP P04275
D	1252	HIS	-	expression tag	UNP P04275
D	1253	HIS	-	expression tag	UNP P04275
d	1242	GLY	-	expression tag	UNP P04275
d	1243	LEU	-	expression tag	UNP P04275
d	1244	VAL	-	expression tag	UNP P04275
d	1245	VAL	-	expression tag	UNP P04275
d	1246	PRO	-	expression tag	UNP P04275
d	1247	PRO	-	expression tag	UNP P04275
d	1248	HIS	-	expression tag	UNP P04275
d	1249	HIS	-	expression tag	UNP P04275
d	1250	HIS	-	expression tag	UNP P04275
d	1251	HIS	-	expression tag	UNP P04275
d	1252	HIS	-	expression tag	UNP P04275
d	1253	HIS	-	expression tag	UNP P04275
e	1242	GLY	-	expression tag	UNP P04275
e	1243	LEU	-	expression tag	UNP P04275
e	1244	VAL	-	expression tag	UNP P04275
e	1245	VAL	-	expression tag	UNP P04275
e	1246	PRO	-	expression tag	UNP P04275
e	1247	PRO	-	expression tag	UNP P04275
e	1248	HIS	-	expression tag	UNP P04275
e	1249	HIS	-	expression tag	UNP P04275
e	1250	HIS	-	expression tag	UNP P04275
e	1251	HIS	-	expression tag	UNP P04275
e	1252	HIS	-	expression tag	UNP P04275
e	1253	HIS	-	expression tag	UNP P04275
f	1242	GLY	-	expression tag	UNP P04275
f	1243	LEU	-	expression tag	UNP P04275
f	1244	VAL	-	expression tag	UNP P04275
f	1245	VAL	-	expression tag	UNP P04275
f	1246	PRO	-	expression tag	UNP P04275
f	1247	PRO	-	expression tag	UNP P04275
f	1248	HIS	-	expression tag	UNP P04275
f	1249	HIS	-	expression tag	UNP P04275

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Chain	Residue	Modelled	Actual	Comment	Reference
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f	1251	HIS	-	expression tag	UNP P04275
f	1252	HIS	-	expression tag	UNP P04275
f	1253	HIS	-	expression tag	UNP P04275
S	1242	GLY	-	expression tag	UNP P04275
S	1243	LEU	-	expression tag	UNP P04275
S	1244	VAL	-	expression tag	UNP P04275
S	1245	VAL	-	expression tag	UNP P04275
S	1246	PRO	-	expression tag	UNP P04275
S	1247	PRO	-	expression tag	UNP P04275
S	1248	HIS	-	expression tag	UNP P04275
S	1249	HIS	-	expression tag	UNP P04275
S	1250	HIS	-	expression tag	UNP P04275
S	1251	HIS	-	expression tag	UNP P04275
S	1252	HIS	-	expression tag	UNP P04275
S	1253	HIS	-	expression tag	UNP P04275
T	1242	GLY	-	expression tag	UNP P04275
T	1243	LEU	-	expression tag	UNP P04275
T	1244	VAL	-	expression tag	UNP P04275
T	1245	VAL	-	expression tag	UNP P04275
T	1246	PRO	-	expression tag	UNP P04275
T	1247	PRO	-	expression tag	UNP P04275
T	1248	HIS	-	expression tag	UNP P04275
T	1249	HIS	-	expression tag	UNP P04275
T	1250	HIS	-	expression tag	UNP P04275
T	1251	HIS	-	expression tag	UNP P04275
T	1252	HIS	-	expression tag	UNP P04275
T	1253	HIS	-	expression tag	UNP P04275
U	1242	GLY	-	expression tag	UNP P04275
U	1243	LEU	-	expression tag	UNP P04275
U	1244	VAL	-	expression tag	UNP P04275
U	1245	VAL	-	expression tag	UNP P04275
U	1246	PRO	-	expression tag	UNP P04275
U	1247	PRO	-	expression tag	UNP P04275
U	1248	HIS	-	expression tag	UNP P04275
U	1249	HIS	-	expression tag	UNP P04275
U	1250	HIS	-	expression tag	UNP P04275
U	1251	HIS	-	expression tag	UNP P04275
U	1252	HIS	-	expression tag	UNP P04275
U	1253	HIS	-	expression tag	UNP P04275
V	1242	GLY	-	expression tag	UNP P04275
V	1243	LEU	-	expression tag	UNP P04275

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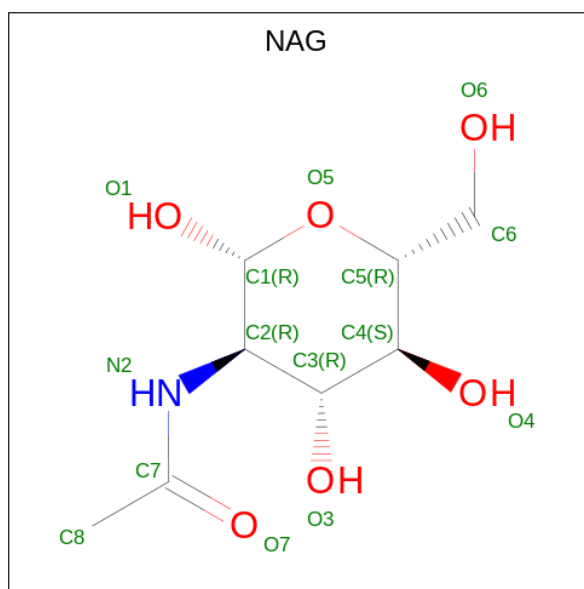
Chain	Residue	Modelled	Actual	Comment	Reference
V	1244	VAL	-	expression tag	UNP P04275
V	1245	VAL	-	expression tag	UNP P04275
V	1246	PRO	-	expression tag	UNP P04275
V	1247	PRO	-	expression tag	UNP P04275
V	1248	HIS	-	expression tag	UNP P04275
V	1249	HIS	-	expression tag	UNP P04275
V	1250	HIS	-	expression tag	UNP P04275
V	1251	HIS	-	expression tag	UNP P04275
V	1252	HIS	-	expression tag	UNP P04275
V	1253	HIS	-	expression tag	UNP P04275
W	1242	GLY	-	expression tag	UNP P04275
W	1243	LEU	-	expression tag	UNP P04275
W	1244	VAL	-	expression tag	UNP P04275
W	1245	VAL	-	expression tag	UNP P04275
W	1246	PRO	-	expression tag	UNP P04275
W	1247	PRO	-	expression tag	UNP P04275
W	1248	HIS	-	expression tag	UNP P04275
W	1249	HIS	-	expression tag	UNP P04275
W	1250	HIS	-	expression tag	UNP P04275
W	1251	HIS	-	expression tag	UNP P04275
W	1252	HIS	-	expression tag	UNP P04275
W	1253	HIS	-	expression tag	UNP P04275
X	1242	GLY	-	expression tag	UNP P04275
X	1243	LEU	-	expression tag	UNP P04275
X	1244	VAL	-	expression tag	UNP P04275
X	1245	VAL	-	expression tag	UNP P04275
X	1246	PRO	-	expression tag	UNP P04275
X	1247	PRO	-	expression tag	UNP P04275
X	1248	HIS	-	expression tag	UNP P04275
X	1249	HIS	-	expression tag	UNP P04275
X	1250	HIS	-	expression tag	UNP P04275
X	1251	HIS	-	expression tag	UNP P04275
X	1252	HIS	-	expression tag	UNP P04275
X	1253	HIS	-	expression tag	UNP P04275
Y	1242	GLY	-	expression tag	UNP P04275
Y	1243	LEU	-	expression tag	UNP P04275
Y	1244	VAL	-	expression tag	UNP P04275
Y	1245	VAL	-	expression tag	UNP P04275
Y	1246	PRO	-	expression tag	UNP P04275
Y	1247	PRO	-	expression tag	UNP P04275
Y	1248	HIS	-	expression tag	UNP P04275
Y	1249	HIS	-	expression tag	UNP P04275

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Chain	Residue	Modelled	Actual	Comment	Reference
Y	1250	HIS	-	expression tag	UNP P04275
Y	1251	HIS	-	expression tag	UNP P04275
Y	1252	HIS	-	expression tag	UNP P04275
Y	1253	HIS	-	expression tag	UNP P04275
Z	1242	GLY	-	expression tag	UNP P04275
Z	1243	LEU	-	expression tag	UNP P04275
Z	1244	VAL	-	expression tag	UNP P04275
Z	1245	VAL	-	expression tag	UNP P04275
Z	1246	PRO	-	expression tag	UNP P04275
Z	1247	PRO	-	expression tag	UNP P04275
Z	1248	HIS	-	expression tag	UNP P04275
Z	1249	HIS	-	expression tag	UNP P04275
Z	1250	HIS	-	expression tag	UNP P04275
Z	1251	HIS	-	expression tag	UNP P04275
Z	1252	HIS	-	expression tag	UNP P04275
Z	1253	HIS	-	expression tag	UNP P04275

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$) (labeled as "Ligand of Interest" by depositor).



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

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Mol	Chain	Residues	Atoms				AltConf
3	a	1	Total	C	N	O	0
			14	8	1	5	
3	B	1	Total	C	N	O	0
			14	8	1	5	
3	B	1	Total	C	N	O	0
			14	8	1	5	
3	b	1	Total	C	N	O	0
			14	8	1	5	
3	b	1	Total	C	N	O	0
			14	8	1	5	
3	C	1	Total	C	N	O	0
			14	8	1	5	
3	C	1	Total	C	N	O	0
			14	8	1	5	
3	D	1	Total	C	N	O	0
			14	8	1	5	
3	D	1	Total	C	N	O	0
			14	8	1	5	
3	d	1	Total	C	N	O	0
			14	8	1	5	
3	E	1	Total	C	N	O	0
			14	8	1	5	
3	E	1	Total	C	N	O	0
			14	8	1	5	
3	F	1	Total	C	N	O	0
			14	8	1	5	
3	F	1	Total	C	N	O	0
			14	8	1	5	
3	G	1	Total	C	N	O	0
			14	8	1	5	
3	G	1	Total	C	N	O	0
			14	8	1	5	
3	I	1	Total	C	N	O	0
			14	8	1	5	
3	I	1	Total	C	N	O	0
			14	8	1	5	
3	L	1	Total	C	N	O	0
			14	8	1	5	
3	L	1	Total	C	N	O	0
			14	8	1	5	
3	M	1	Total	C	N	O	0
			14	8	1	5	

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Mol	Chain	Residues	Atoms				AltConf
3	M	1	Total	C	N	O	0
			14	8	1	5	
3	N	1	Total	C	N	O	0
			14	8	1	5	
3	N	1	Total	C	N	O	0
			14	8	1	5	
3	O	1	Total	C	N	O	0
			14	8	1	5	
3	O	1	Total	C	N	O	0
			14	8	1	5	
3	P	1	Total	C	N	O	0
			14	8	1	5	
3	P	1	Total	C	N	O	0
			14	8	1	5	
3	S	1	Total	C	N	O	0
			14	8	1	5	
3	S	1	Total	C	N	O	0
			14	8	1	5	
3	T	1	Total	C	N	O	0
			14	8	1	5	
3	T	1	Total	C	N	O	0
			14	8	1	5	
3	U	1	Total	C	N	O	0
			14	8	1	5	
3	U	1	Total	C	N	O	0
			14	8	1	5	
3	V	1	Total	C	N	O	0
			14	8	1	5	
3	W	1	Total	C	N	O	0
			14	8	1	5	
3	W	1	Total	C	N	O	0
			14	8	1	5	
3	Z	1	Total	C	N	O	0
			14	8	1	5	
3	Z	1	Total	C	N	O	0
			14	8	1	5	

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
4	A	2	Total	Ca	0
			2	2	

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Mol	Chain	Residues	Atoms		AltConf
4	a	1	Total 1	Ca 1	0
4	B	2	Total 2	Ca 2	0
4	b	1	Total 1	Ca 1	0
4	C	2	Total 2	Ca 2	0
4	c	1	Total 1	Ca 1	0
4	D	1	Total 1	Ca 1	0
4	d	1	Total 1	Ca 1	0
4	E	2	Total 2	Ca 2	0
4	e	1	Total 1	Ca 1	0
4	F	2	Total 2	Ca 2	0
4	f	1	Total 1	Ca 1	0
4	G	2	Total 2	Ca 2	0
4	H	2	Total 2	Ca 2	0
4	I	2	Total 2	Ca 2	0
4	J	2	Total 2	Ca 2	0
4	K	2	Total 2	Ca 2	0
4	L	2	Total 2	Ca 2	0
4	M	2	Total 2	Ca 2	0
4	N	2	Total 2	Ca 2	0
4	O	2	Total 2	Ca 2	0
4	P	2	Total 2	Ca 2	0

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Mol	Chain	Residues	Atoms		AltConf
4	Q	2	Total 2	Ca 2	0
4	R	2	Total 2	Ca 2	0
4	S	2	Total 2	Ca 2	0
4	T	2	Total 2	Ca 2	0
4	U	2	Total 2	Ca 2	0
4	V	2	Total 2	Ca 2	0
4	W	2	Total 2	Ca 2	0
4	X	2	Total 2	Ca 2	0
4	Y	2	Total 2	Ca 2	0
4	Z	1	Total 1	Ca 1	0

3 Residue-property plots [i](#)

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

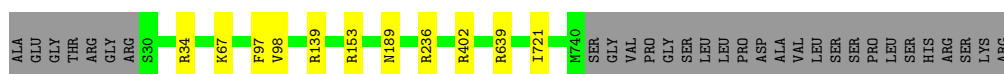
- Molecule 1: von Willebrand antigen 2

Chain A:  95%



- Molecule 1: von Willebrand antigen 2

Chain B:  94%



- Molecule 1: von Willebrand antigen 2

Chain E:  94%



- Molecule 1: von Willebrand antigen 2

Chain F:  95%



- Molecule 1: von Willebrand antigen 2

Chain G:  94%



- Molecule 1: von Willebrand antigen 2

ALA	GLU	THR	ARG	GLY	ARG	R34	K67	R139	R153	N189	T212	R236	R402	R639	I721	M740	SER	GLY	VAL	PRO	GLY	SER	LEU	LEU	PRO	ASP	ALA	VAL	LEU	SER	SER	PRO	PRO	LEU	SER	HIS	ARG	SER	LYS	ARG
-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Chain I:  94% ..

ALA	GLU	GLY	THR	ARG	GLY	ARG	S30	R34	K67	V98	R139	R153	N156	N189	I212	R236	R402	R639	I721	M740	SER	GLY	VAL	PRO	GLY	SER	SER	LEU	LEU	PRO	ASP	ALA	VAL	LEU	SER	SER	PRO	LEU	SER	HIS	ARG	SER	LYS	ARG
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Chain J:  9% 95%

Protein	Residue	Score	Rank	Category
Protein A	PRO ASP	C295	1	High
	ALA ALA	P296	2	High
	VAL THR	A297	3	High
	LEU THR	C298	4	High
	SER SER	P332	5	High
	PRO LEU	E333	6	High
	SER HIS	G340	7	High
	ARG ARG	L341	8	High
	LYS ARG	R402	9	High
	ARG ARG	R639	10	High
Protein B	PRO ASP	E644	11	High
	ALA ALA	P645	12	High
	VAL THR	G646	13	High
	LEU THR	E649	14	High
	SER SER	L650	15	High
	PRO LEU	N651	16	High
	SER HIS	C652	17	High
	ARG ARG	P653	18	High
	LYS ARG	K654	19	High
	ARG ARG	G655	20	High
Protein C	PRO ASP	Q656	21	High
	ALA ALA	P657	22	High
	VAL THR	Y658	23	High
	LEU THR	L659	24	High
	SER SER	Q660	25	High
	PRO LEU	C661	26	High
	SER HIS	G662	27	High
	ARG ARG	T663	28	High
	LYS ARG	C679	29	High
	ARG ARG	N680	30	High
Protein D	PRO ASP	E681	31	High
	ALA ALA	A682	32	High
	VAL THR	C683	33	High
	LEU THR	L684	34	High
	SER SER	P690	35	High
	PRO LEU	P691	36	High
	SER HIS	G692	37	High
	ARG ARG	L693	38	High
	LYS ARG	F703	39	High
	ARG ARG	I721	40	High
Protein E	PRO ASP	M740	41	High
	ALA ALA	SER	42	High
	VAL THR	GLY	43	High
	LEU THR	VAL	44	High
	SER SER	PRO	45	High
	PRO LEU	GLY	46	High
	SER SER	SER	47	High
	PRO LEU	LEU	48	High
	SER SER	LEU	49	High
	PRO LEU	LEU	50	High
Protein F	PRO ASP	ALA	51	High
	ALA ALA	GLU	52	High
	VAL THR	GLY	53	High
	LEU THR	THR	54	High
	SER SER	ARG	55	High
	PRO LEU	GLY	56	High
	SER SER	ARG	57	High
	PRO LEU	S30	58	High
	SER SER	R34	59	High
	PRO LEU	K67	60	High
Protein G	PRO ASP	R108	61	High
	ALA ALA	V109	62	High
	VAL THR	S110	63	High
	LEU THR	R139	64	High
	SER SER	R153	65	High
	PRO LEU	N189	66	High
	SER SER	S207	67	High
	PRO LEU	S208	68	High
	SER SER	C210	69	High
	PRO LEU	N211	70	High
Protein H	PRO ASP	T212	71	High
	ALA ALA	S213	72	High
	VAL THR	S214	73	High
	LEU THR	G215	74	High
	SER SER	E216	75	High
	PRO LEU	N217	76	High
	SER SER	Q218	77	High
	PRO LEU	K219	78	High
	SER SER	C220	79	High
	PRO LEU	L221	80	High
Protein I	PRO ASP	W222	81	High
	ALA ALA	S230	82	High
	VAL THR	T231	83	High
	LEU THR	S232	84	High
	SER SER	R236	85	High
	PRO LEU	C255	86	High
	SER SER	E256	87	High
	PRO LEU	C257	88	High
	SER SER	A258	89	High
	PRO LEU	G259	90	High
Protein J	PRO ASP	G260	91	High
	ALA ALA	L261	92	High
	VAL THR	E262	93	High
	LEU THR	D287	94	High
	SER SER	A290	95	High
	PRO LEU	GLY	96	High
	SER SER	SER	97	High
	PRO LEU	LEU	98	High
	SER SER	LEU	99	High
	PRO LEU	LEU	100	High

- Chain K:  16% 95% ...

LEU	SER	SER	PRO	LEU	SER	SER	HIS	ARG	ARG	SER	SER	LYS	ARG	ALA	GLU	GLY	THR	ARG	GLY	ARG	S30	S30	R34	K67	Q77	N99	D106	Q107	R108	R139	R153	I167	F168	N189	E197	S207	S208	S209	C210	N211	I212	S213	S214	G215	E216	M217	Q218	K219	G220	L221	W222	E223	Q224	C225	Q226	L227	L228	K229	S230	T231	S232	V233	F234
A235	R236	C237	H238	P239	L240	V241	D242	P243	E244	F245	V247	A248	L249	C250	E251	K252	T253	L254	C255	E256	C257	A258	G259	G260	L261	E262	C263	C265	L268	Y271	A272	C275	A276	Q277	E278	G279	M280	V281	L282	Y283	G284	W285	L286	D287	H288	S289	A290	C291	S292	P293	A297	Q298	W299										
E300	Y301	R302	Q303	C304	V305	C331	P332	E333	G334	Q335	L336	L341	C342	V343	E344	S345	T346	E347	G360	R373	M374	R402	R639	V640	A641	E644	P645	G646	R647	C648	E649	L650	M651	C652	P653	K654	I721	M740	SER	GLY	VAL	PRO	GLY	SER	LEU	LEU	PRO	ASP	ALA	VAL													

- Chain L:  95% ...



• Molecule 1: von Willebrand antigen 2

Chain M: 94%



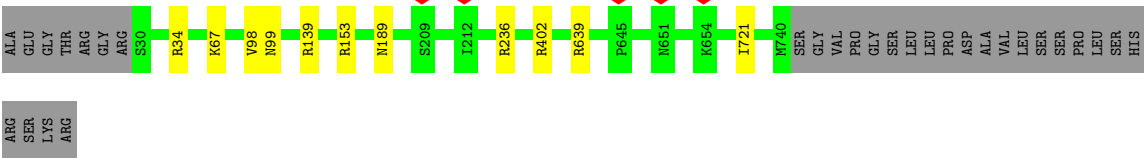
• Molecule 1: von Willebrand antigen 2

Chain N: 95%



• Molecule 1: von Willebrand antigen 2

Chain O: 94%



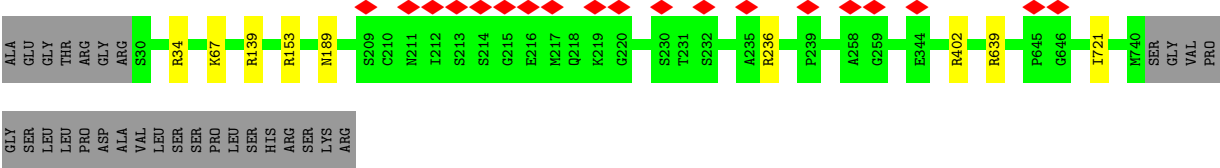
• Molecule 1: von Willebrand antigen 2

Chain P: 95%



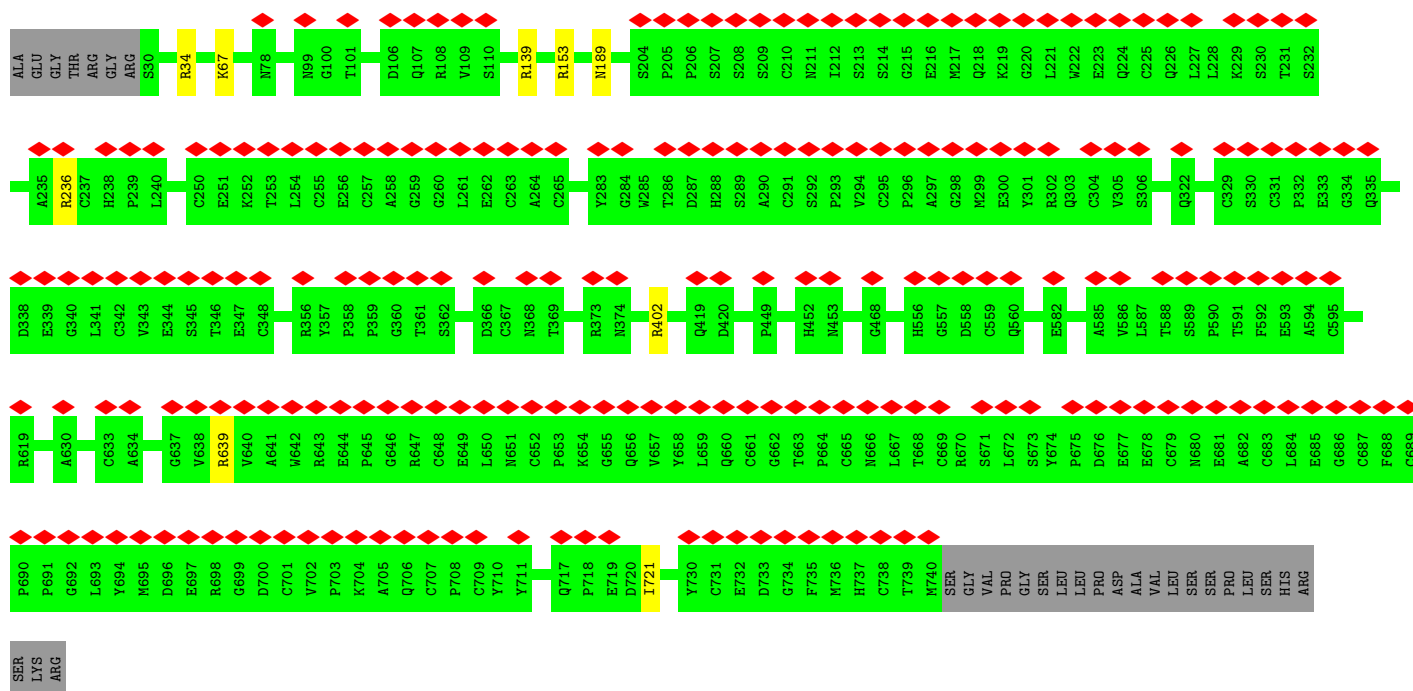
• Molecule 1: von Willebrand antigen 2

Chain Q: 95%



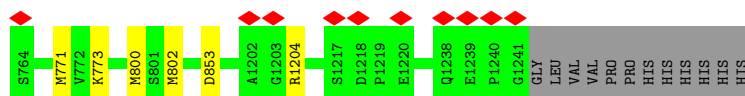
• Molecule 1: von Willebrand antigen 2

Chain R: 30% 95%



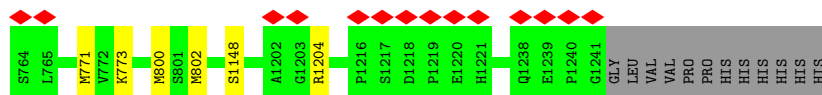
- Molecule 2: von Willebrand factor

Chain a: 96%



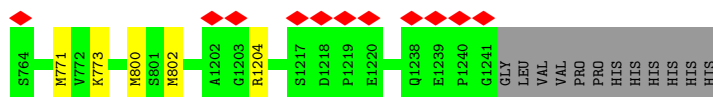
- Molecule 2: von Willebrand factor

Chain b: 96%



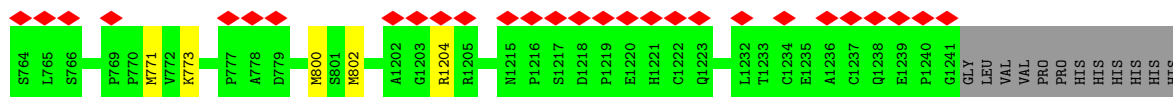
- Molecule 2: von Willebrand factor

Chain C: 97%



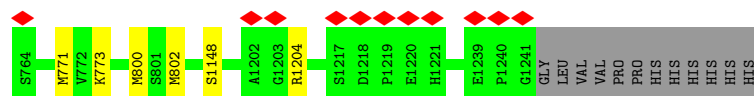
- Molecule 2: von Willebrand factor

Chain c: 6%



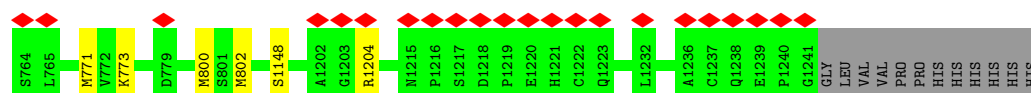
- Molecule 2: von Willebrand factor

Chain D:  96%



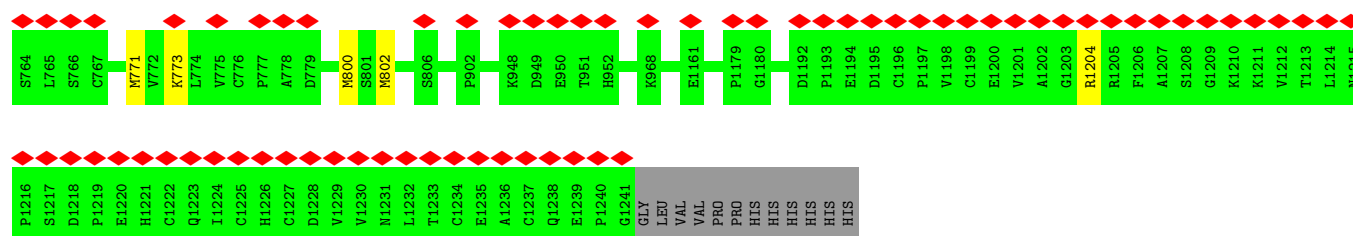
- Molecule 2: von Willebrand factor

Chain d:  96%



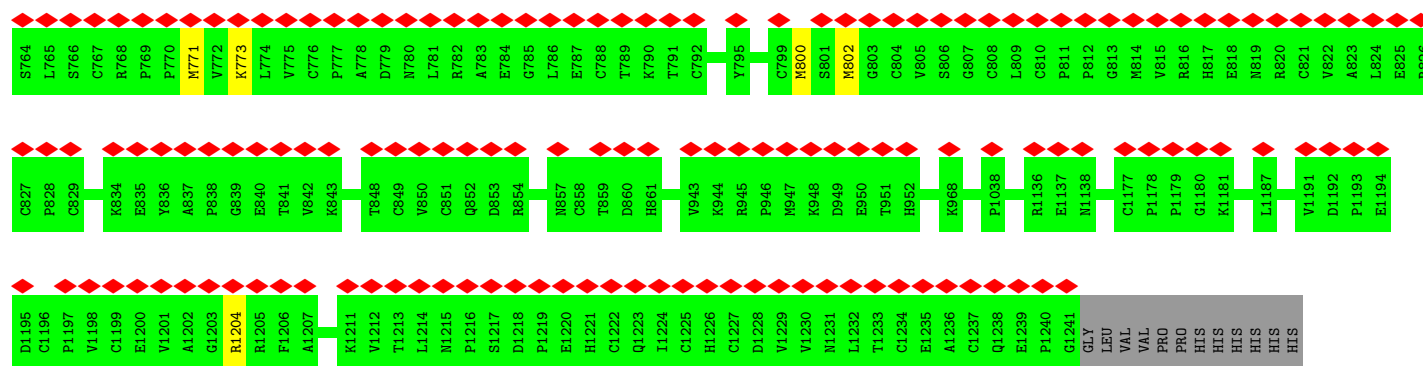
- Molecule 2: von Willebrand factor

Chain e:  14% 97%



- Molecule 2: von Willebrand factor

Chain f:  30% 97%



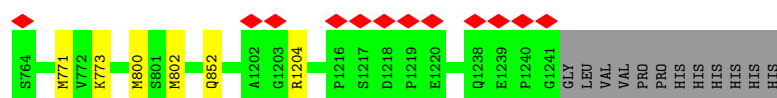
- Molecule 2: von Willebrand factor

Chain S:  96%



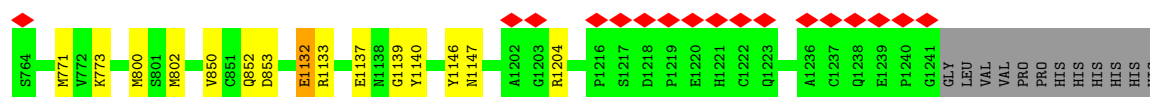
- Molecule 2: von Willebrand factor

Chain T:  96%



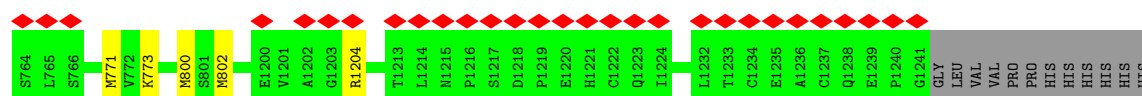
- Molecule 2: von Willebrand factor

Chain U:  94%



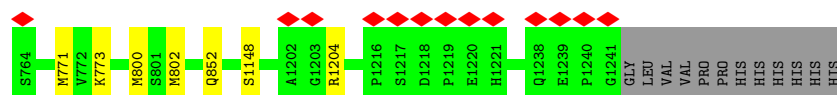
- Molecule 2: von Willebrand factor

Chain V:  97%



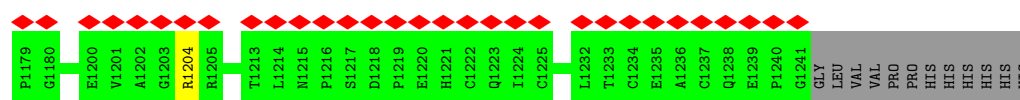
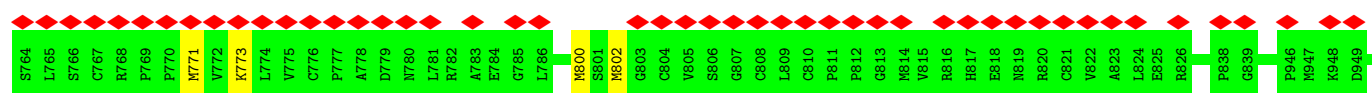
- Molecule 2: von Willebrand factor

Chain W:  96%



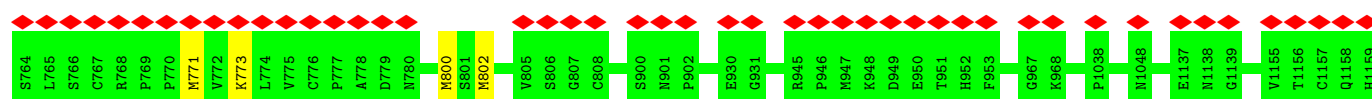
- Molecule 2: von Willebrand factor

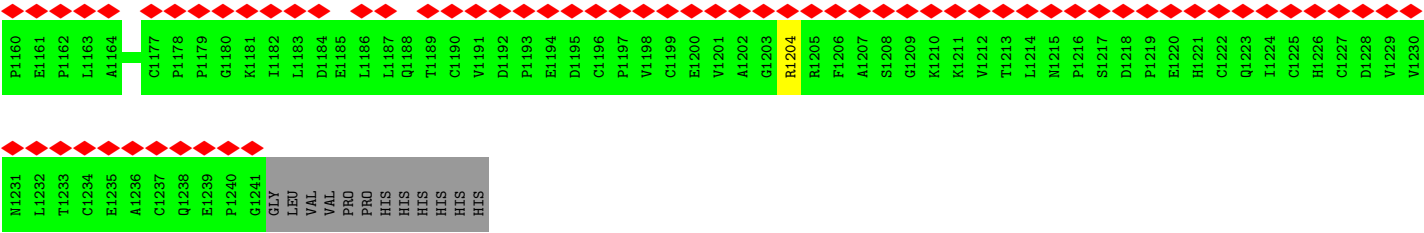
Chain X:  97%



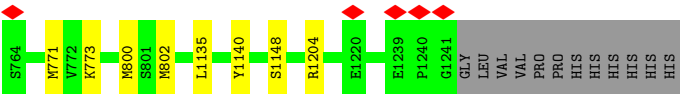
- Molecule 2: von Willebrand factor

Chain Y:  97%





• Molecule 2: von Willebrand factor



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	323041	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 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.114	Depositor
Minimum map value	-0.030	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	562.1248, 562.1248, 562.1248	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.1958, 2.1958, 2.1958	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, 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	0.44	0/5547	0.66	2/7520 (0.0%)
1	B	0.44	0/5547	0.66	2/7520 (0.0%)
1	E	0.44	0/5547	0.66	2/7520 (0.0%)
1	F	0.44	0/5547	0.66	2/7520 (0.0%)
1	G	0.44	0/5547	0.66	2/7520 (0.0%)
1	H	0.44	0/5547	0.66	2/7520 (0.0%)
1	I	0.44	0/5547	0.66	2/7520 (0.0%)
1	J	0.44	0/5547	0.66	2/7520 (0.0%)
1	K	0.44	0/5547	0.66	2/7520 (0.0%)
1	L	0.44	0/5547	0.66	2/7520 (0.0%)
1	M	0.44	0/5547	0.66	2/7520 (0.0%)
1	N	0.44	0/5547	0.66	2/7520 (0.0%)
1	O	0.44	0/5547	0.66	2/7520 (0.0%)
1	P	0.44	0/5547	0.66	2/7520 (0.0%)
1	Q	0.44	0/5547	0.66	2/7520 (0.0%)
1	R	0.44	0/5547	0.66	2/7520 (0.0%)
2	C	0.38	0/3728	0.59	0/5066
2	D	0.39	0/3728	0.59	0/5066
2	S	0.38	0/3728	0.59	0/5066
2	T	0.38	0/3728	0.59	0/5066
2	U	0.39	0/3728	0.59	0/5066
2	V	0.38	0/3728	0.59	0/5066
2	W	0.38	0/3728	0.59	0/5066
2	X	0.38	0/3728	0.59	0/5066
2	Y	0.38	0/3728	0.59	0/5066
2	Z	0.39	0/3728	0.59	0/5066
2	a	0.38	0/3728	0.59	0/5066
2	b	0.38	0/3728	0.59	0/5066
2	c	0.38	0/3728	0.59	0/5066
2	d	0.38	0/3728	0.59	0/5066
2	e	0.38	0/3728	0.59	0/5066
2	f	0.38	0/3728	0.59	0/5066

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
All	All	0.42	0/148400	0.63	32/201376 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	E	0	1
1	F	0	1
1	G	0	1
1	H	0	1
1	I	0	1
1	J	0	1
1	K	0	1
1	L	0	1
1	M	0	1
1	N	0	1
1	O	0	1
1	P	0	1
1	Q	0	1
1	R	0	1
All	All	0	16

There are no bond length outliers.

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	153	ARG	NE-CZ-NH1	5.50	123.05	120.30
1	H	153	ARG	NE-CZ-NH1	5.47	123.04	120.30
1	P	153	ARG	NE-CZ-NH1	5.46	123.03	120.30
1	Q	153	ARG	NE-CZ-NH1	5.45	123.03	120.30
1	A	153	ARG	NE-CZ-NH1	5.43	123.02	120.30
1	A	402	ARG	NE-CZ-NH2	-5.41	117.60	120.30
1	Q	402	ARG	NE-CZ-NH2	-5.38	117.61	120.30
1	O	153	ARG	NE-CZ-NH1	5.33	122.96	120.30
1	G	153	ARG	NE-CZ-NH1	5.32	122.96	120.30
1	K	402	ARG	NE-CZ-NH2	-5.32	117.64	120.30
1	I	402	ARG	NE-CZ-NH2	-5.29	117.66	120.30
1	G	402	ARG	NE-CZ-NH2	-5.27	117.67	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	402	ARG	NE-CZ-NH2	-5.27	117.67	120.30
1	L	153	ARG	NE-CZ-NH1	5.26	122.93	120.30
1	J	153	ARG	NE-CZ-NH1	5.25	122.92	120.30
1	N	402	ARG	NE-CZ-NH2	-5.25	117.68	120.30
1	J	402	ARG	NE-CZ-NH2	-5.25	117.68	120.30
1	E	153	ARG	NE-CZ-NH1	5.24	122.92	120.30
1	B	153	ARG	NE-CZ-NH1	5.24	122.92	120.30
1	E	402	ARG	NE-CZ-NH2	-5.24	117.68	120.30
1	P	402	ARG	NE-CZ-NH2	-5.23	117.68	120.30
1	K	153	ARG	NE-CZ-NH1	5.22	122.91	120.30
1	F	153	ARG	NE-CZ-NH1	5.21	122.91	120.30
1	M	153	ARG	NE-CZ-NH1	5.21	122.91	120.30
1	B	402	ARG	NE-CZ-NH2	-5.19	117.70	120.30
1	L	402	ARG	NE-CZ-NH2	-5.18	117.71	120.30
1	F	402	ARG	NE-CZ-NH2	-5.16	117.72	120.30
1	I	153	ARG	NE-CZ-NH1	5.16	122.88	120.30
1	R	153	ARG	NE-CZ-NH1	5.16	122.88	120.30
1	R	402	ARG	NE-CZ-NH2	-5.12	117.74	120.30
1	H	402	ARG	NE-CZ-NH2	-5.11	117.75	120.30
1	O	402	ARG	NE-CZ-NH2	-5.02	117.79	120.30

There are no chirality outliers.

All (16) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	721	ILE	Peptide
1	B	721	ILE	Peptide
1	E	721	ILE	Peptide
1	F	721	ILE	Peptide
1	G	721	ILE	Peptide
1	H	721	ILE	Peptide
1	I	721	ILE	Peptide
1	J	721	ILE	Peptide
1	K	721	ILE	Peptide
1	L	721	ILE	Peptide
1	M	721	ILE	Peptide
1	N	721	ILE	Peptide
1	O	721	ILE	Peptide
1	P	721	ILE	Peptide
1	Q	721	ILE	Peptide
1	R	721	ILE	Peptide

5.2 Too-close contacts ⓘ

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

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	709/741 (96%)	646 (91%)	62 (9%)	1 (0%)	48	83
1	B	709/741 (96%)	648 (91%)	60 (8%)	1 (0%)	48	83
1	E	709/741 (96%)	644 (91%)	62 (9%)	3 (0%)	30	67
1	F	709/741 (96%)	646 (91%)	63 (9%)	0	100	100
1	G	709/741 (96%)	638 (90%)	68 (10%)	3 (0%)	30	67
1	H	709/741 (96%)	646 (91%)	63 (9%)	0	100	100
1	I	709/741 (96%)	643 (91%)	64 (9%)	2 (0%)	37	72
1	J	709/741 (96%)	647 (91%)	62 (9%)	0	100	100
1	K	709/741 (96%)	647 (91%)	62 (9%)	0	100	100
1	L	709/741 (96%)	648 (91%)	61 (9%)	0	100	100
1	M	709/741 (96%)	646 (91%)	61 (9%)	2 (0%)	37	72
1	N	709/741 (96%)	643 (91%)	65 (9%)	1 (0%)	48	83
1	O	709/741 (96%)	644 (91%)	63 (9%)	2 (0%)	37	72
1	P	709/741 (96%)	647 (91%)	62 (9%)	0	100	100
1	Q	709/741 (96%)	648 (91%)	61 (9%)	0	100	100
1	R	709/741 (96%)	649 (92%)	60 (8%)	0	100	100
2	C	477/490 (97%)	424 (89%)	53 (11%)	0	100	100
2	D	477/490 (97%)	426 (89%)	50 (10%)	1 (0%)	44	78
2	S	477/490 (97%)	425 (89%)	51 (11%)	1 (0%)	44	78
2	T	477/490 (97%)	425 (89%)	52 (11%)	0	100	100
2	U	477/490 (97%)	415 (87%)	55 (12%)	7 (2%)	8	39

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	V	477/490 (97%)	427 (90%)	50 (10%)	0	100	100
2	W	477/490 (97%)	426 (89%)	50 (10%)	1 (0%)	44	78
2	X	477/490 (97%)	425 (89%)	52 (11%)	0	100	100
2	Y	477/490 (97%)	425 (89%)	52 (11%)	0	100	100
2	Z	477/490 (97%)	420 (88%)	55 (12%)	2 (0%)	30	67
2	a	477/490 (97%)	427 (90%)	49 (10%)	1 (0%)	44	78
2	b	477/490 (97%)	425 (89%)	51 (11%)	1 (0%)	44	78
2	c	477/490 (97%)	425 (89%)	52 (11%)	0	100	100
2	d	477/490 (97%)	424 (89%)	52 (11%)	1 (0%)	44	78
2	e	477/490 (97%)	425 (89%)	52 (11%)	0	100	100
2	f	477/490 (97%)	425 (89%)	52 (11%)	0	100	100
All	All	18976/19696 (96%)	17119 (90%)	1827 (10%)	30 (0%)	45	78

All (30) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	M	98	VAL
1	M	99	ASN
1	O	98	VAL
1	O	99	ASN
2	W	1148	SER
1	B	98	VAL
2	b	1148	SER
2	D	1148	SER
2	d	1148	SER
1	E	98	VAL
1	E	99	ASN
1	E	100	GLY
1	G	98	VAL
1	I	98	VAL
2	U	1132	GLU
2	U	1139	GLY
2	U	1146	TYR
2	Z	1140	TYR
1	G	172	ASP
1	I	156	ASN
1	N	98	VAL
2	S	1148	SER

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Mol	Chain	Res	Type
2	U	1137	GLU
2	Z	1148	SER
2	a	853	ASP
2	U	853	ASP
2	U	1133	ARG
1	G	170	GLU
2	U	852	GLN
1	A	100	GLY

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	599/628 (95%)	593 (99%)	6 (1%)	73	82
1	B	599/628 (95%)	592 (99%)	7 (1%)	67	79
1	E	599/628 (95%)	593 (99%)	6 (1%)	73	82
1	F	599/628 (95%)	593 (99%)	6 (1%)	73	82
1	G	599/628 (95%)	592 (99%)	7 (1%)	67	79
1	H	599/628 (95%)	593 (99%)	6 (1%)	73	82
1	I	599/628 (95%)	593 (99%)	6 (1%)	73	82
1	J	599/628 (95%)	593 (99%)	6 (1%)	73	82
1	K	599/628 (95%)	593 (99%)	6 (1%)	73	82
1	L	599/628 (95%)	593 (99%)	6 (1%)	73	82
1	M	599/628 (95%)	593 (99%)	6 (1%)	73	82
1	N	599/628 (95%)	593 (99%)	6 (1%)	73	82
1	O	599/628 (95%)	593 (99%)	6 (1%)	73	82
1	P	599/628 (95%)	592 (99%)	7 (1%)	67	79
1	Q	599/628 (95%)	593 (99%)	6 (1%)	73	82
1	R	599/628 (95%)	593 (99%)	6 (1%)	73	82
2	C	423/436 (97%)	418 (99%)	5 (1%)	67	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D	423/436 (97%)	418 (99%)	5 (1%)	67	79
2	S	423/436 (97%)	417 (99%)	6 (1%)	62	76
2	T	423/436 (97%)	417 (99%)	6 (1%)	62	76
2	U	423/436 (97%)	414 (98%)	9 (2%)	48	67
2	V	423/436 (97%)	418 (99%)	5 (1%)	67	79
2	W	423/436 (97%)	417 (99%)	6 (1%)	62	76
2	X	423/436 (97%)	418 (99%)	5 (1%)	67	79
2	Y	423/436 (97%)	418 (99%)	5 (1%)	67	79
2	Z	423/436 (97%)	417 (99%)	6 (1%)	62	76
2	a	423/436 (97%)	418 (99%)	5 (1%)	67	79
2	b	423/436 (97%)	418 (99%)	5 (1%)	67	79
2	c	423/436 (97%)	418 (99%)	5 (1%)	67	79
2	d	423/436 (97%)	418 (99%)	5 (1%)	67	79
2	e	423/436 (97%)	418 (99%)	5 (1%)	67	79
2	f	423/436 (97%)	418 (99%)	5 (1%)	67	79
All	All	16352/17024 (96%)	16165 (99%)	187 (1%)	69	80

All (187) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	ARG
1	A	67	LYS
1	A	139	ARG
1	A	189	ASN
1	A	236	ARG
1	A	639	ARG
2	a	771	MET
2	a	773	LYS
2	a	800	MET
2	a	802	MET
2	a	1204	ARG
1	B	34	ARG
1	B	67	LYS
1	B	97	PHE
1	B	139	ARG
1	B	189	ASN
1	B	236	ARG

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Mol	Chain	Res	Type
1	B	639	ARG
2	b	771	MET
2	b	773	LYS
2	b	800	MET
2	b	802	MET
2	b	1204	ARG
2	C	771	MET
2	C	773	LYS
2	C	800	MET
2	C	802	MET
2	C	1204	ARG
2	c	771	MET
2	c	773	LYS
2	c	800	MET
2	c	802	MET
2	c	1204	ARG
2	D	771	MET
2	D	773	LYS
2	D	800	MET
2	D	802	MET
2	D	1204	ARG
2	d	771	MET
2	d	773	LYS
2	d	800	MET
2	d	802	MET
2	d	1204	ARG
1	E	34	ARG
1	E	67	LYS
1	E	139	ARG
1	E	189	ASN
1	E	236	ARG
1	E	639	ARG
2	e	771	MET
2	e	773	LYS
2	e	800	MET
2	e	802	MET
2	e	1204	ARG
1	F	34	ARG
1	F	67	LYS
1	F	139	ARG
1	F	189	ASN
1	F	236	ARG

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Mol	Chain	Res	Type
1	F	639	ARG
2	f	771	MET
2	f	773	LYS
2	f	800	MET
2	f	802	MET
2	f	1204	ARG
1	G	34	ARG
1	G	67	LYS
1	G	139	ARG
1	G	157	LYS
1	G	189	ASN
1	G	236	ARG
1	G	639	ARG
1	H	34	ARG
1	H	67	LYS
1	H	139	ARG
1	H	189	ASN
1	H	236	ARG
1	H	639	ARG
1	I	34	ARG
1	I	67	LYS
1	I	139	ARG
1	I	189	ASN
1	I	236	ARG
1	I	639	ARG
1	J	34	ARG
1	J	67	LYS
1	J	139	ARG
1	J	189	ASN
1	J	236	ARG
1	J	639	ARG
1	K	34	ARG
1	K	67	LYS
1	K	139	ARG
1	K	189	ASN
1	K	236	ARG
1	K	639	ARG
1	L	34	ARG
1	L	67	LYS
1	L	139	ARG
1	L	189	ASN
1	L	236	ARG

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Mol	Chain	Res	Type
1	L	639	ARG
1	M	34	ARG
1	M	67	LYS
1	M	139	ARG
1	M	189	ASN
1	M	236	ARG
1	M	639	ARG
1	N	34	ARG
1	N	67	LYS
1	N	139	ARG
1	N	189	ASN
1	N	236	ARG
1	N	639	ARG
1	O	34	ARG
1	O	67	LYS
1	O	139	ARG
1	O	189	ASN
1	O	236	ARG
1	O	639	ARG
1	P	34	ARG
1	P	67	LYS
1	P	97	PHE
1	P	139	ARG
1	P	189	ASN
1	P	236	ARG
1	P	639	ARG
1	Q	34	ARG
1	Q	67	LYS
1	Q	139	ARG
1	Q	189	ASN
1	Q	236	ARG
1	Q	639	ARG
1	R	34	ARG
1	R	67	LYS
1	R	139	ARG
1	R	189	ASN
1	R	236	ARG
1	R	639	ARG
2	S	771	MET
2	S	773	LYS
2	S	800	MET
2	S	802	MET

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Mol	Chain	Res	Type
2	S	852	GLN
2	S	1204	ARG
2	T	771	MET
2	T	773	LYS
2	T	800	MET
2	T	802	MET
2	T	852	GLN
2	T	1204	ARG
2	U	771	MET
2	U	773	LYS
2	U	800	MET
2	U	802	MET
2	U	850	VAL
2	U	1132	GLU
2	U	1140	TYR
2	U	1147	ASN
2	U	1204	ARG
2	V	771	MET
2	V	773	LYS
2	V	800	MET
2	V	802	MET
2	V	1204	ARG
2	W	771	MET
2	W	773	LYS
2	W	800	MET
2	W	802	MET
2	W	852	GLN
2	W	1204	ARG
2	X	771	MET
2	X	773	LYS
2	X	800	MET
2	X	802	MET
2	X	1204	ARG
2	Y	771	MET
2	Y	773	LYS
2	Y	800	MET
2	Y	802	MET
2	Y	1204	ARG
2	Z	771	MET
2	Z	773	LYS
2	Z	800	MET
2	Z	802	MET

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Mol	Chain	Res	Type
2	Z	1135	LEU
2	Z	1204	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (52) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	368	ASN
2	a	852	GLN
1	B	368	ASN
1	B	563	GLN
2	C	1013	GLN
2	c	857	ASN
2	D	852	GLN
2	D	1174	HIS
2	d	857	ASN
1	E	166	ASN
1	E	368	ASN
1	E	563	GLN
2	e	857	ASN
1	F	368	ASN
1	F	563	GLN
2	f	857	ASN
1	G	368	ASN
1	H	368	ASN
1	H	469	GLN
1	H	563	GLN
1	I	368	ASN
1	J	368	ASN
1	J	563	GLN
1	K	368	ASN
1	K	469	GLN
1	K	563	GLN
1	L	368	ASN
1	M	368	ASN
1	N	368	ASN
1	O	368	ASN
1	O	469	GLN
1	O	472	GLN
1	O	563	GLN
1	P	368	ASN
1	Q	368	ASN
1	Q	469	GLN

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Mol	Chain	Res	Type
2	S	1013	GLN
2	T	852	GLN
2	T	1013	GLN
2	U	1013	GLN
2	U	1138	ASN
2	V	1013	GLN
2	W	852	GLN
2	W	1013	GLN
2	W	1176	HIS
2	X	857	ASN
2	X	1013	GLN
2	Y	857	ASN
2	Y	1013	GLN
2	Z	1138	ASN
2	Z	1174	HIS
2	Z	1188	GLN

5.3.3 RNA [i](#)

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](#)

Of 98 ligands modelled in this entry, 56 are monoatomic - leaving 42 for Mogul analysis.

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
3	NAG	S	1301	2	14,14,15	0.40	0	17,19,21	0.82	0
3	NAG	S	1302	2	14,14,15	0.39	0	17,19,21	0.82	0
3	NAG	B	802	1	14,14,15	0.29	0	17,19,21	0.67	0
3	NAG	W	1302	2	14,14,15	0.40	0	17,19,21	0.81	0
3	NAG	I	802	1	14,14,15	0.39	0	17,19,21	0.81	0
3	NAG	N	804	1	14,14,15	0.40	0	17,19,21	0.81	0
3	NAG	F	801	1	14,14,15	0.39	0	17,19,21	0.82	0
3	NAG	E	801	1	14,14,15	0.30	0	17,19,21	0.66	0
3	NAG	b	1302	2	14,14,15	0.40	0	17,19,21	0.81	0
3	NAG	P	801	1	14,14,15	0.39	0	17,19,21	0.81	0
3	NAG	Z	1302	2	14,14,15	0.40	0	17,19,21	0.81	0
3	NAG	L	801	1	14,14,15	0.42	0	17,19,21	0.81	0
3	NAG	Z	1301	2	14,14,15	0.28	0	17,19,21	0.65	0
3	NAG	L	802	1	14,14,15	0.42	0	17,19,21	0.82	0
3	NAG	C	1302	2	14,14,15	0.39	0	17,19,21	0.82	0
3	NAG	d	1301	2	14,14,15	0.40	0	17,19,21	0.82	0
3	NAG	D	1302	2	14,14,15	0.39	0	17,19,21	0.82	0
3	NAG	V	1301	2	14,14,15	0.42	0	17,19,21	0.82	0
3	NAG	A	802	1	14,14,15	0.28	0	17,19,21	0.66	0
3	NAG	G	802	1	14,14,15	0.40	0	17,19,21	0.81	0
3	NAG	M	801	1	14,14,15	0.40	0	17,19,21	0.82	0
3	NAG	a	1301	2	14,14,15	0.27	0	17,19,21	0.71	0
3	NAG	W	1301	2	14,14,15	0.41	0	17,19,21	0.81	0
3	NAG	F	802	1	14,14,15	0.38	0	17,19,21	0.81	0
3	NAG	B	801	1	14,14,15	0.40	0	17,19,21	0.81	0
3	NAG	I	801	1	14,14,15	0.37	0	17,19,21	0.81	0
3	NAG	A	801	1	14,14,15	0.40	0	17,19,21	0.81	0
3	NAG	M	802	1	14,14,15	0.40	0	17,19,21	0.82	0
3	NAG	N	801	1	14,14,15	0.39	0	17,19,21	0.80	0
3	NAG	T	1301	2	14,14,15	0.29	0	17,19,21	0.59	0
3	NAG	b	1301	2	14,14,15	0.39	0	17,19,21	0.81	0
3	NAG	T	1302	2	14,14,15	0.40	0	17,19,21	0.81	0
3	NAG	P	802	1	14,14,15	0.39	0	17,19,21	0.81	0
3	NAG	E	802	1	14,14,15	0.39	0	17,19,21	0.81	0
3	NAG	O	802	1	14,14,15	0.41	0	17,19,21	0.82	0
3	NAG	U	1303	2	14,14,15	0.42	0	17,19,21	0.81	0
3	NAG	C	1301	2	14,14,15	0.40	0	17,19,21	0.81	0
3	NAG	U	1302	2	14,14,15	0.40	0	17,19,21	0.82	0
3	NAG	a	1302	2	14,14,15	0.41	0	17,19,21	0.81	0
3	NAG	D	1301	2	14,14,15	0.40	0	17,19,21	0.82	0
3	NAG	G	801	1	14,14,15	0.41	0	17,19,21	0.81	0
3	NAG	O	801	1	14,14,15	0.39	0	17,19,21	0.82	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
3	NAG	S	1301	2	-	0/6/23/26	0/1/1/1
3	NAG	S	1302	2	-	0/6/23/26	0/1/1/1
3	NAG	B	802	1	-	2/6/23/26	0/1/1/1
3	NAG	W	1302	2	-	0/6/23/26	0/1/1/1
3	NAG	I	802	1	-	0/6/23/26	0/1/1/1
3	NAG	N	804	1	-	0/6/23/26	0/1/1/1
3	NAG	F	801	1	-	0/6/23/26	0/1/1/1
3	NAG	E	801	1	-	2/6/23/26	0/1/1/1
3	NAG	b	1302	2	-	0/6/23/26	0/1/1/1
3	NAG	P	801	1	-	0/6/23/26	0/1/1/1
3	NAG	Z	1302	2	-	0/6/23/26	0/1/1/1
3	NAG	L	801	1	-	0/6/23/26	0/1/1/1
3	NAG	Z	1301	2	-	0/6/23/26	0/1/1/1
3	NAG	L	802	1	-	0/6/23/26	0/1/1/1
3	NAG	C	1302	2	-	0/6/23/26	0/1/1/1
3	NAG	d	1301	2	-	0/6/23/26	0/1/1/1
3	NAG	D	1302	2	-	0/6/23/26	0/1/1/1
3	NAG	V	1301	2	-	0/6/23/26	0/1/1/1
3	NAG	A	802	1	-	2/6/23/26	0/1/1/1
3	NAG	G	802	1	-	0/6/23/26	0/1/1/1
3	NAG	M	801	1	-	0/6/23/26	0/1/1/1
3	NAG	a	1301	2	-	4/6/23/26	0/1/1/1
3	NAG	W	1301	2	-	0/6/23/26	0/1/1/1
3	NAG	F	802	1	-	0/6/23/26	0/1/1/1
3	NAG	B	801	1	-	0/6/23/26	0/1/1/1
3	NAG	I	801	1	-	0/6/23/26	0/1/1/1
3	NAG	A	801	1	-	0/6/23/26	0/1/1/1
3	NAG	M	802	1	-	0/6/23/26	0/1/1/1
3	NAG	N	801	1	-	0/6/23/26	0/1/1/1
3	NAG	T	1301	2	-	1/6/23/26	0/1/1/1
3	NAG	b	1301	2	-	0/6/23/26	0/1/1/1
3	NAG	T	1302	2	-	0/6/23/26	0/1/1/1
3	NAG	P	802	1	-	0/6/23/26	0/1/1/1
3	NAG	E	802	1	-	0/6/23/26	0/1/1/1
3	NAG	O	802	1	-	0/6/23/26	0/1/1/1
3	NAG	U	1303	2	-	0/6/23/26	0/1/1/1
3	NAG	C	1301	2	-	0/6/23/26	0/1/1/1
3	NAG	U	1302	2	-	0/6/23/26	0/1/1/1

Continued on next page...

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	a	1302	2	-	0/6/23/26	0/1/1/1
3	NAG	D	1301	2	-	0/6/23/26	0/1/1/1
3	NAG	G	801	1	-	0/6/23/26	0/1/1/1
3	NAG	O	801	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

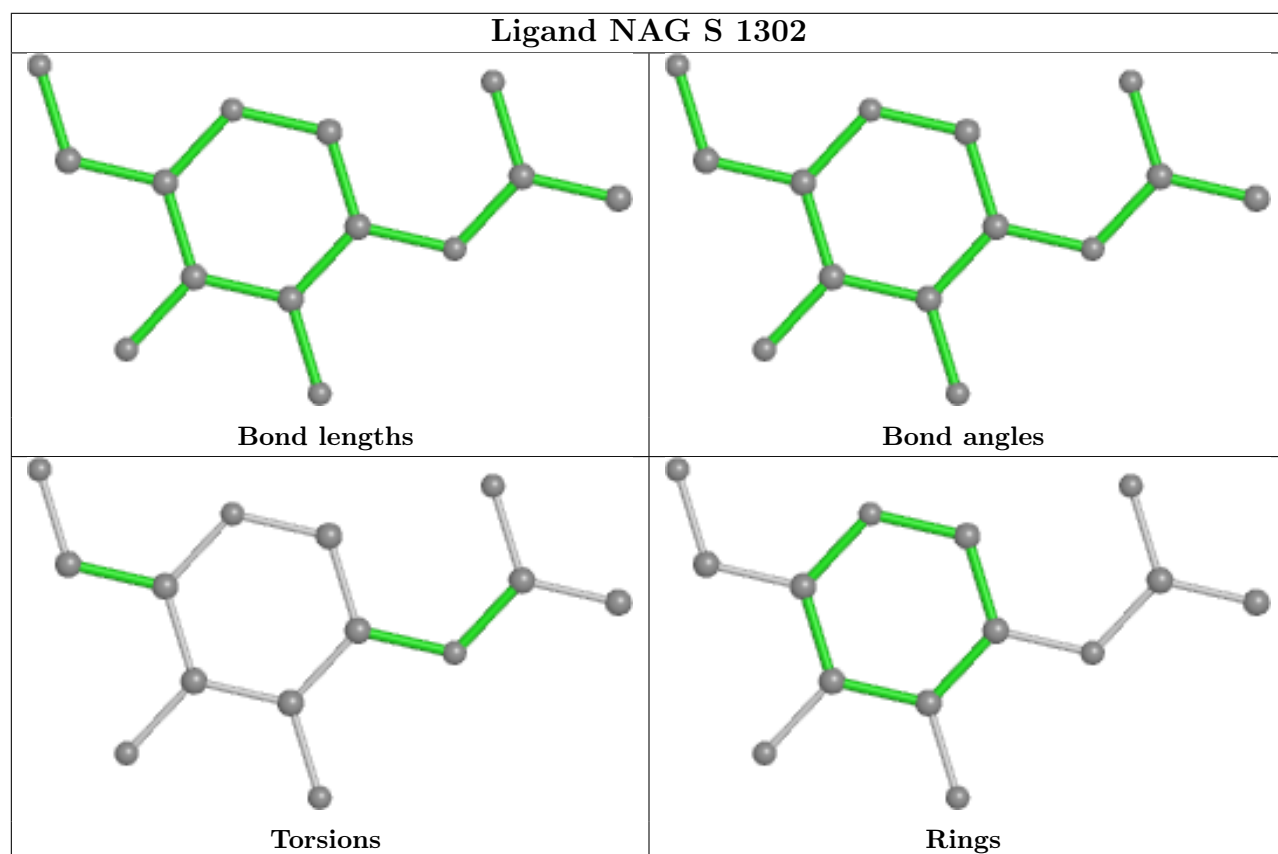
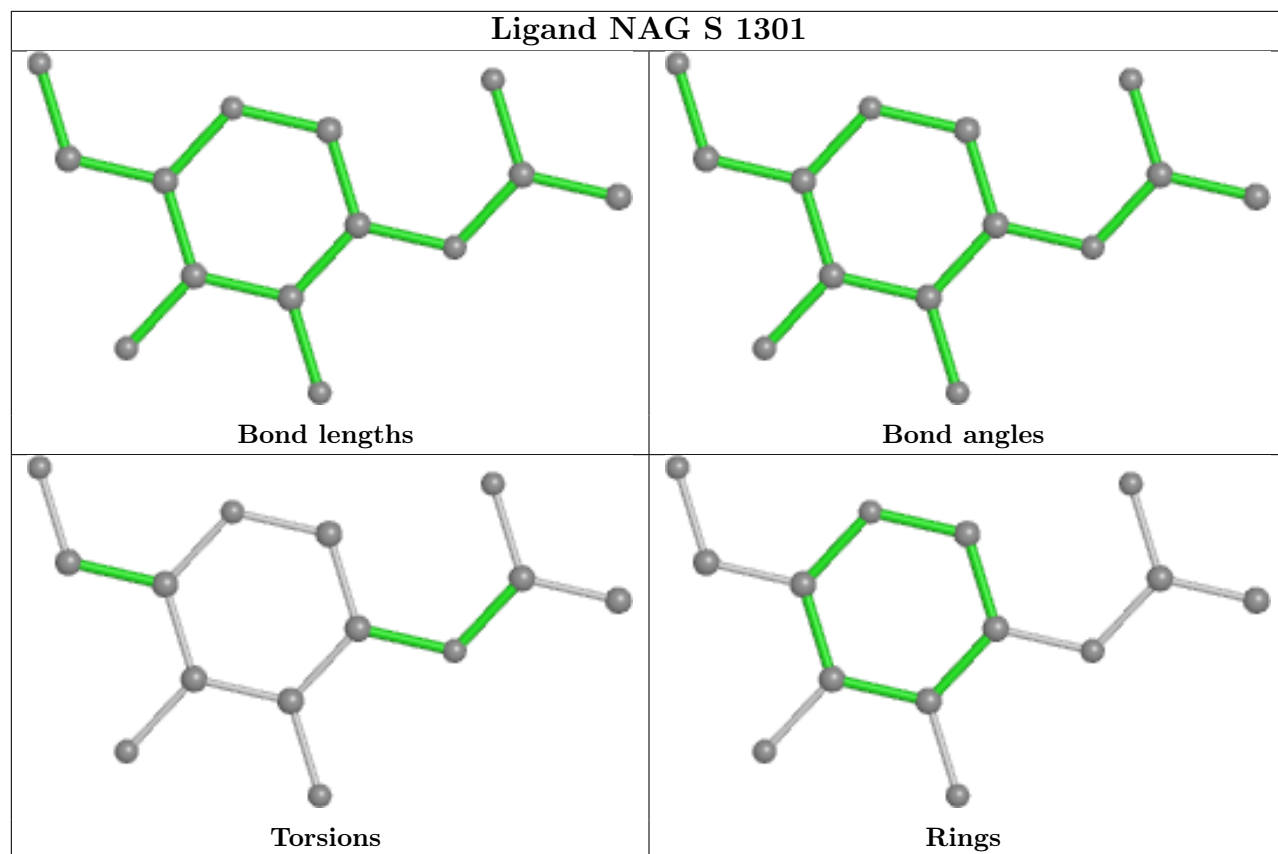
All (11) torsion outliers are listed below:

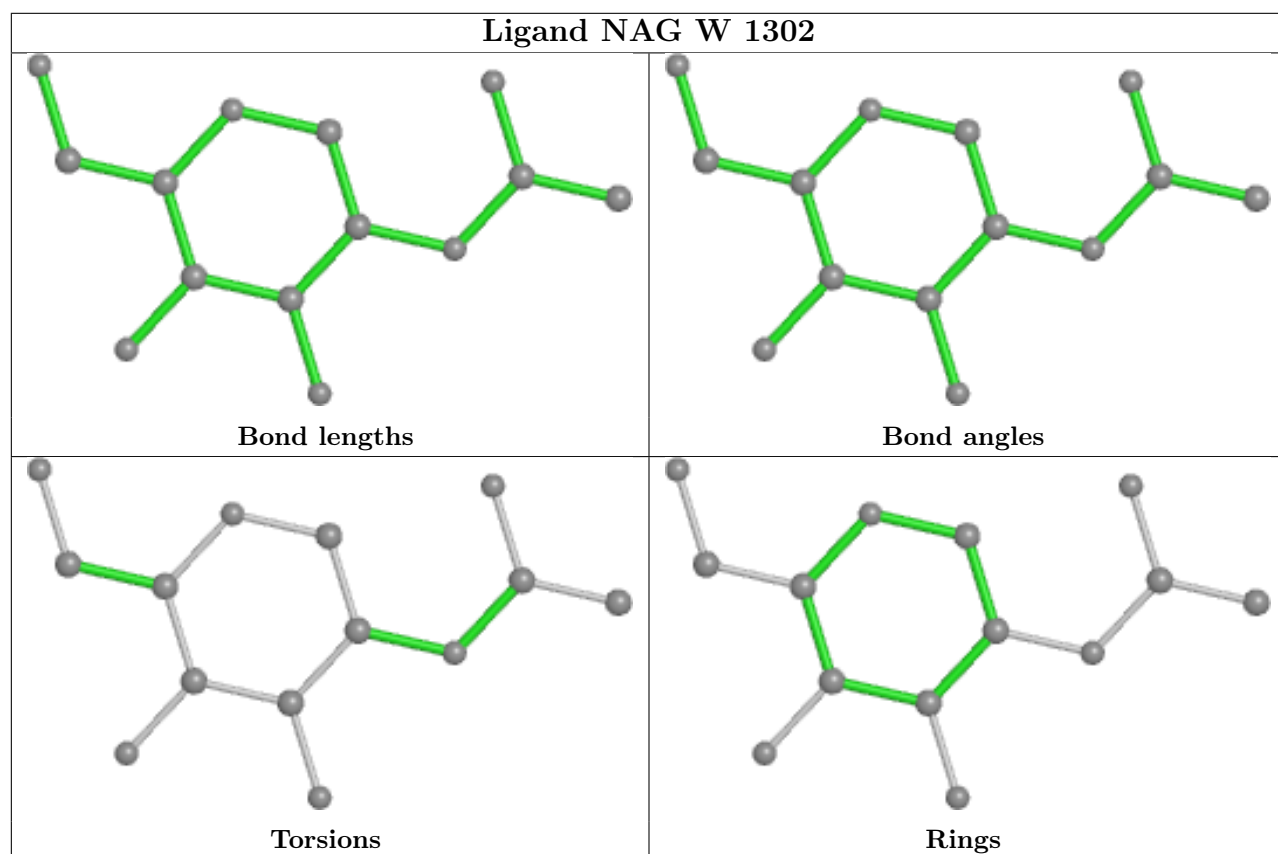
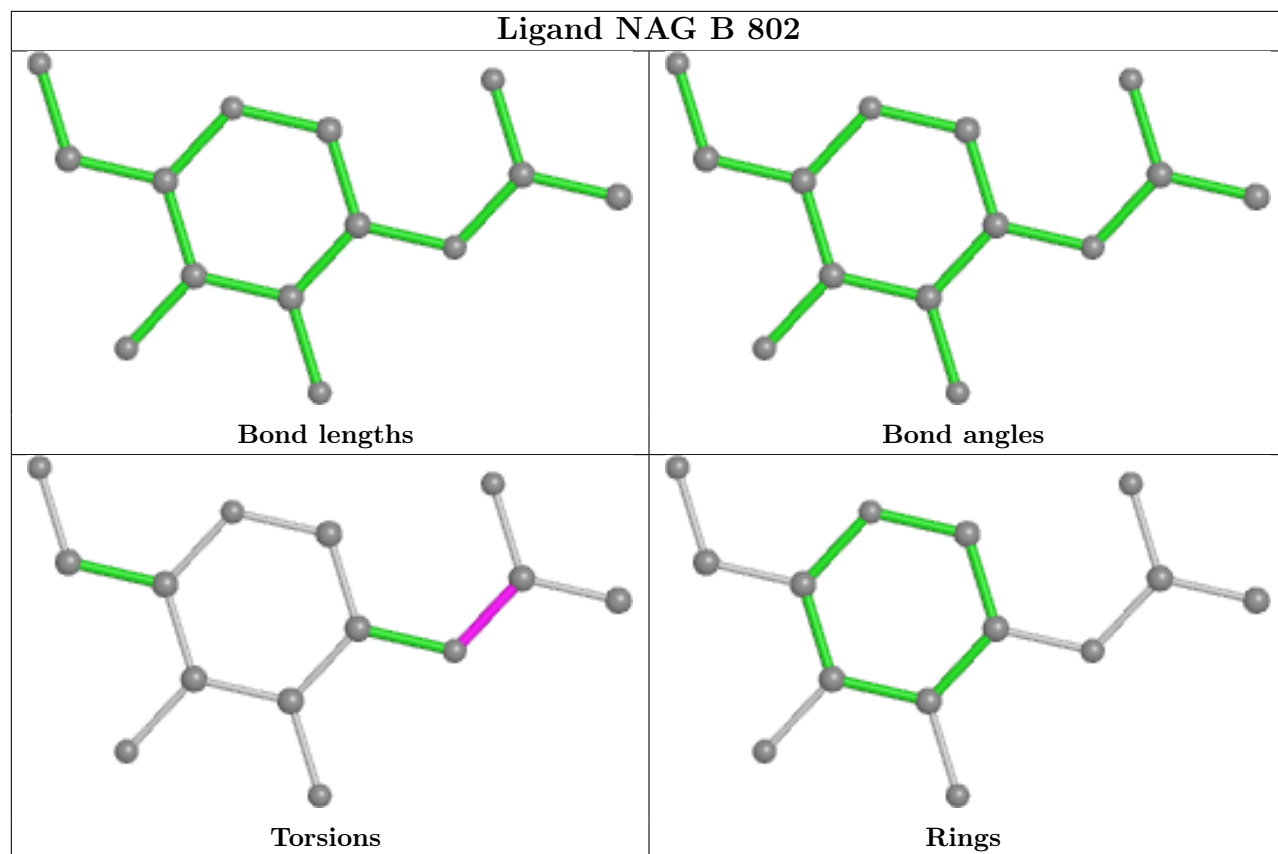
Mol	Chain	Res	Type	Atoms
3	a	1301	NAG	C3-C2-N2-C7
3	a	1301	NAG	C8-C7-N2-C2
3	a	1301	NAG	O7-C7-N2-C2
3	E	801	NAG	C8-C7-N2-C2
3	E	801	NAG	O7-C7-N2-C2
3	T	1301	NAG	O5-C5-C6-O6
3	A	802	NAG	C8-C7-N2-C2
3	a	1301	NAG	C1-C2-N2-C7
3	A	802	NAG	O7-C7-N2-C2
3	B	802	NAG	C8-C7-N2-C2
3	B	802	NAG	O7-C7-N2-C2

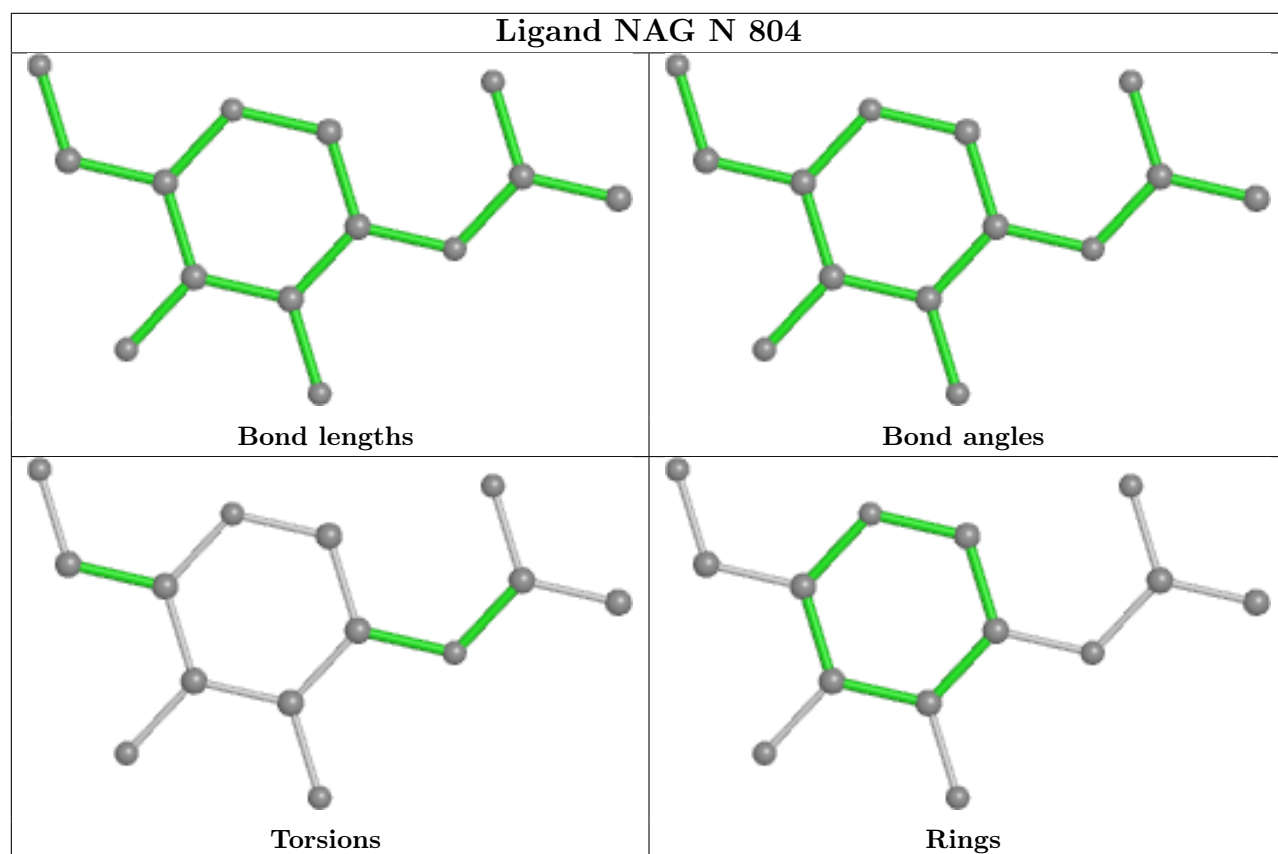
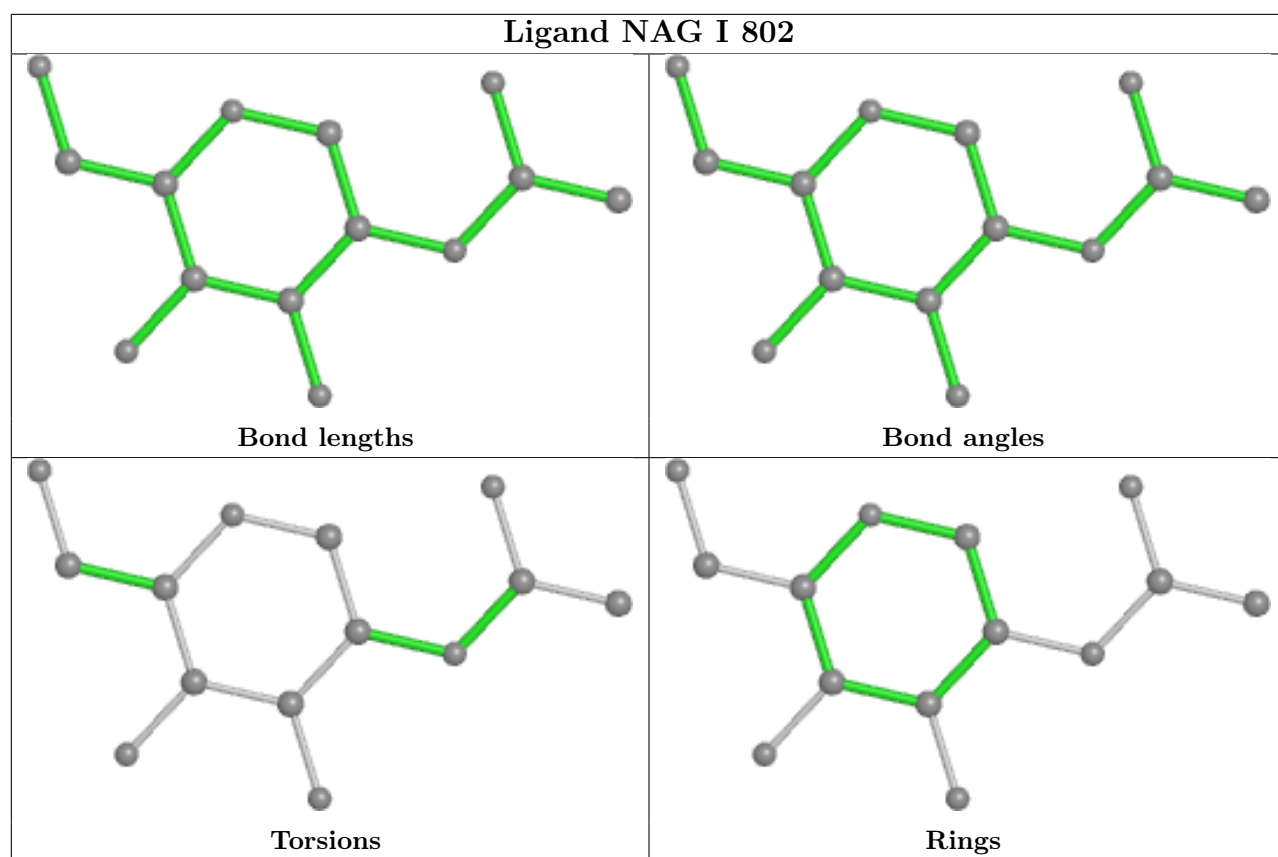
There are no ring outliers.

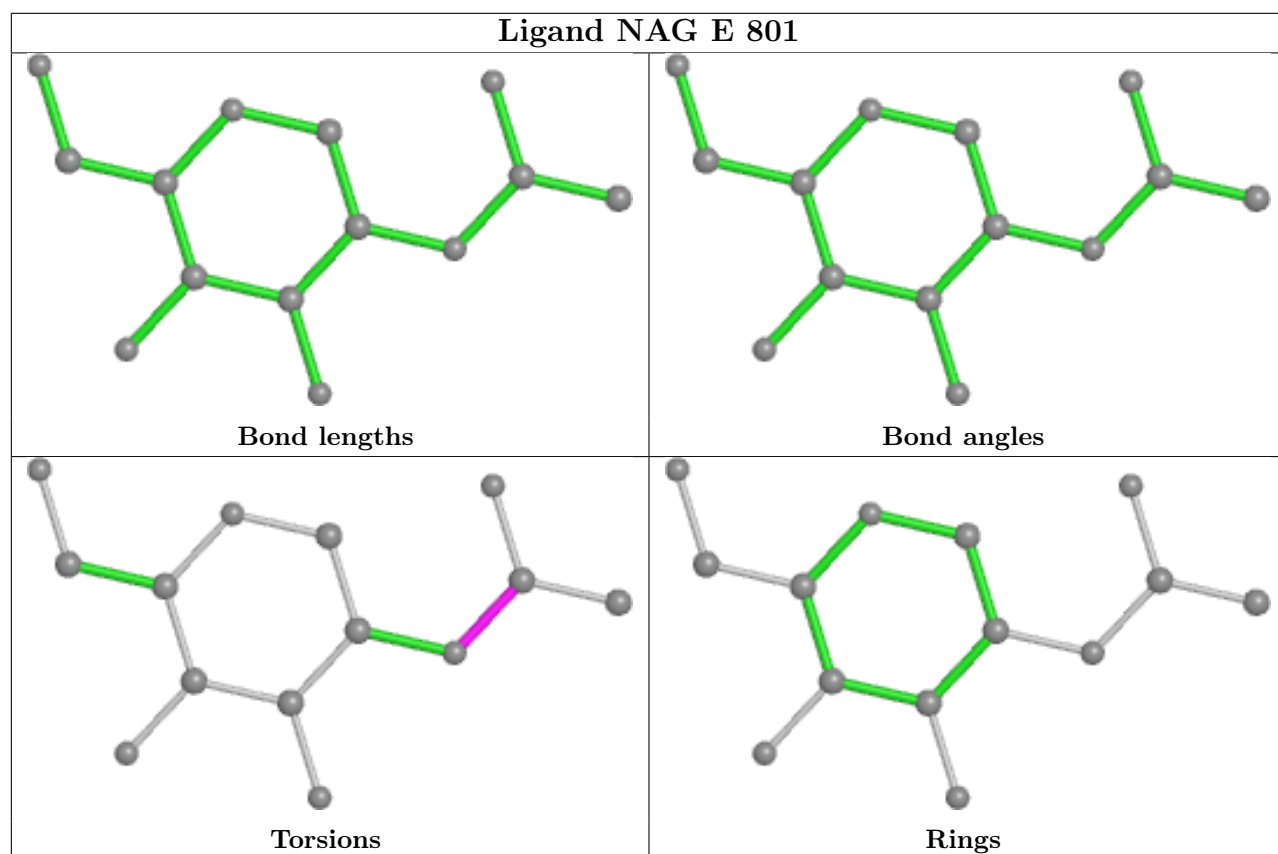
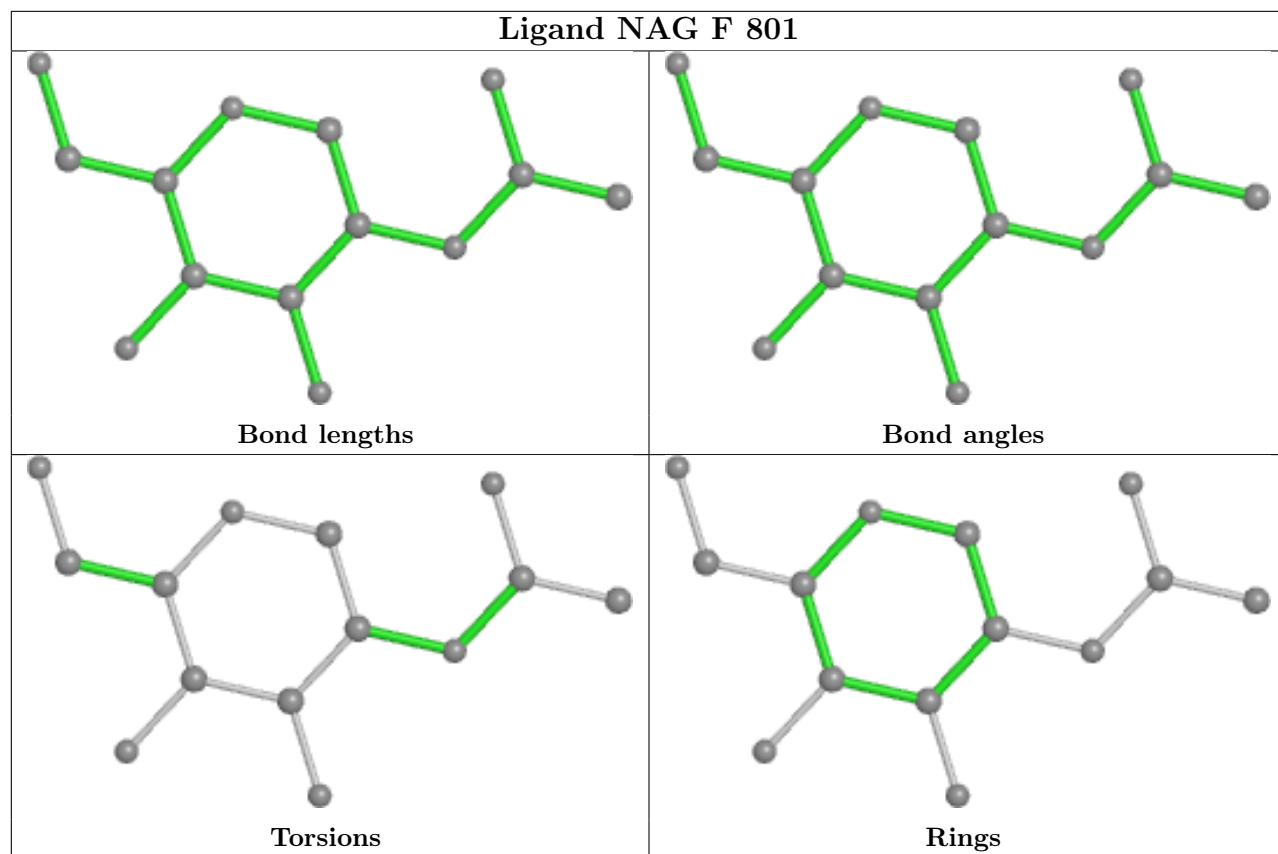
No monomer is involved in short contacts.

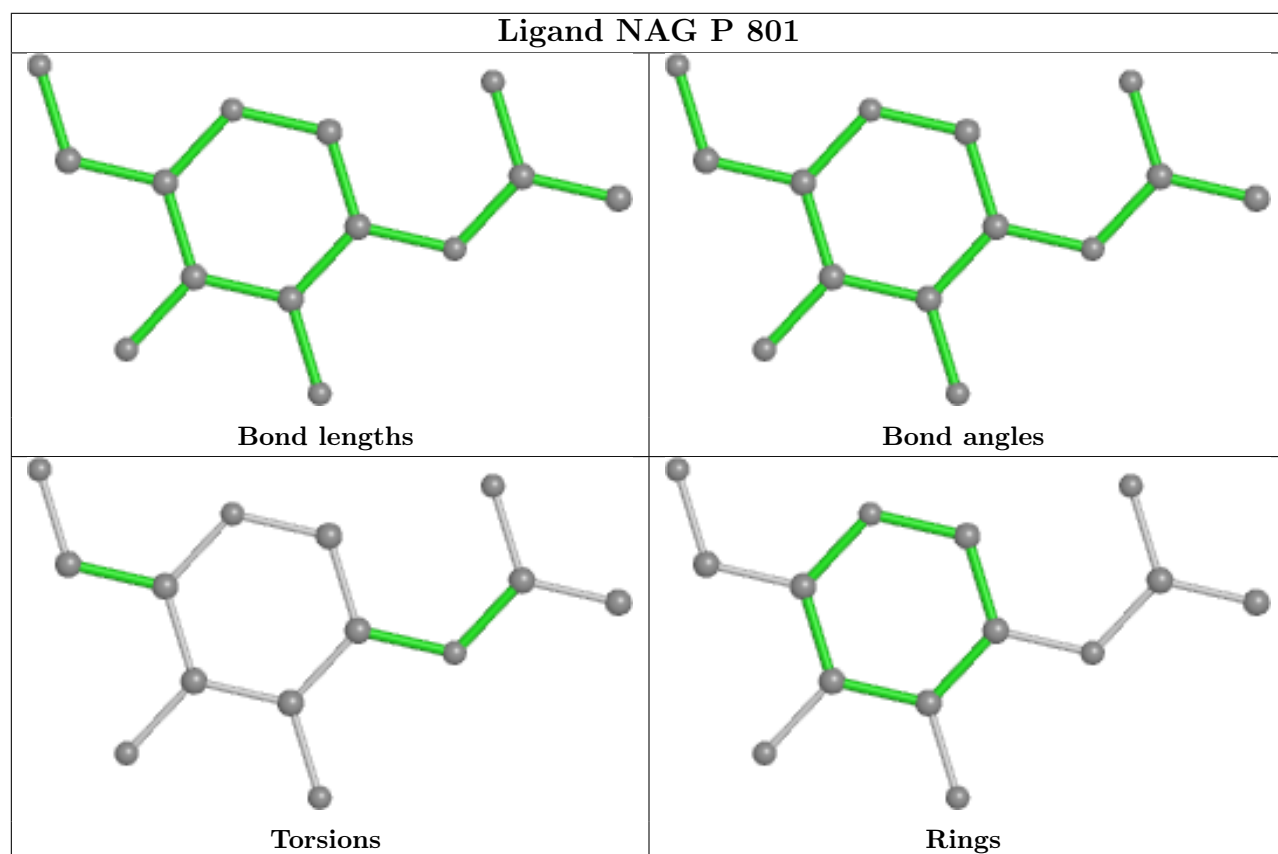
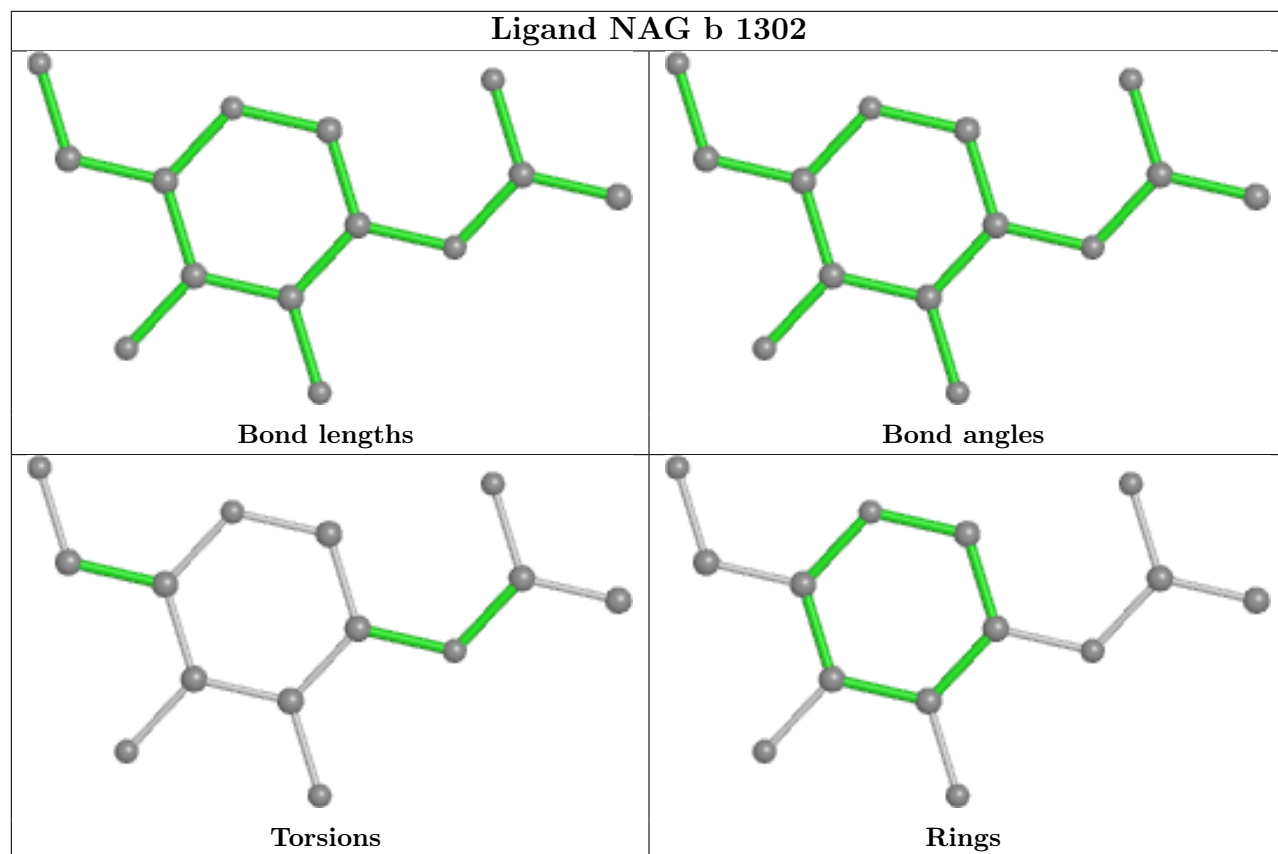
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

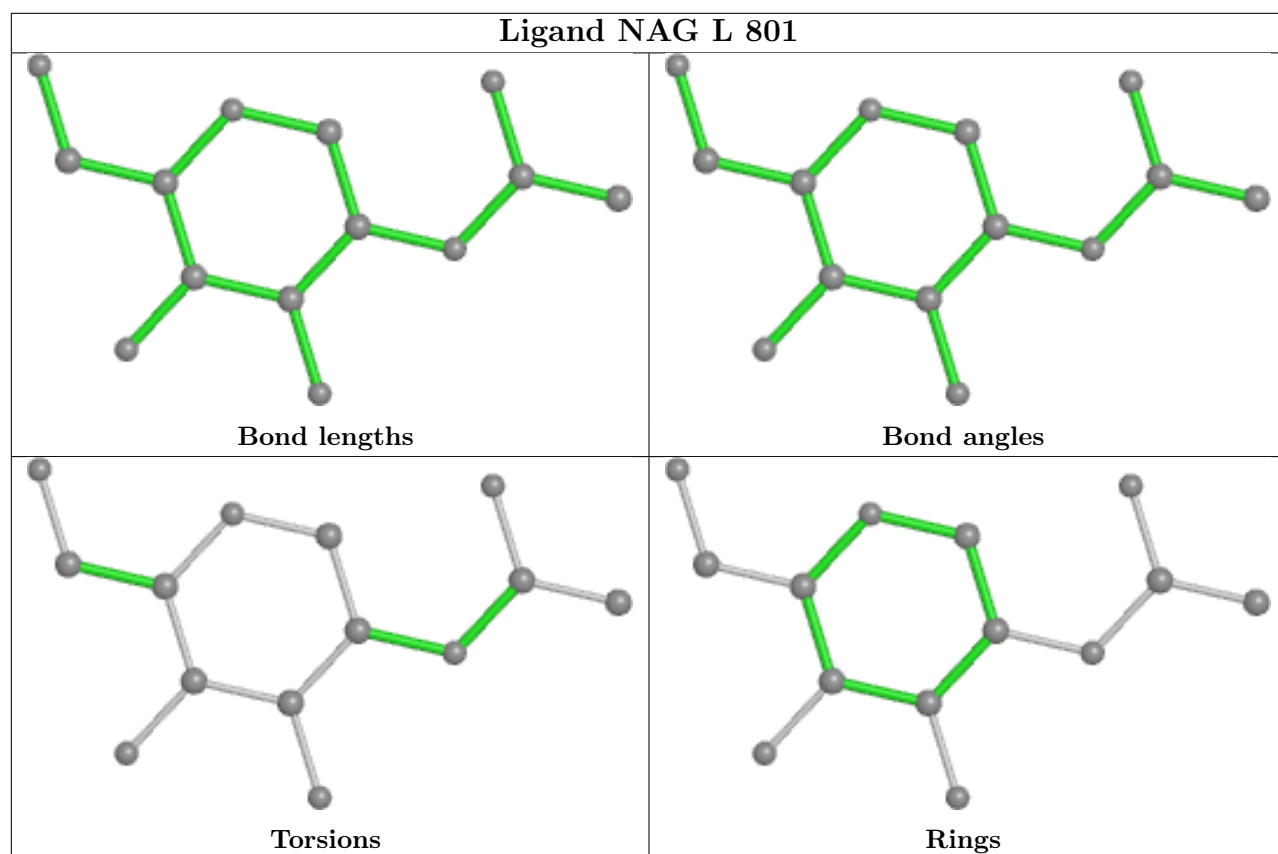
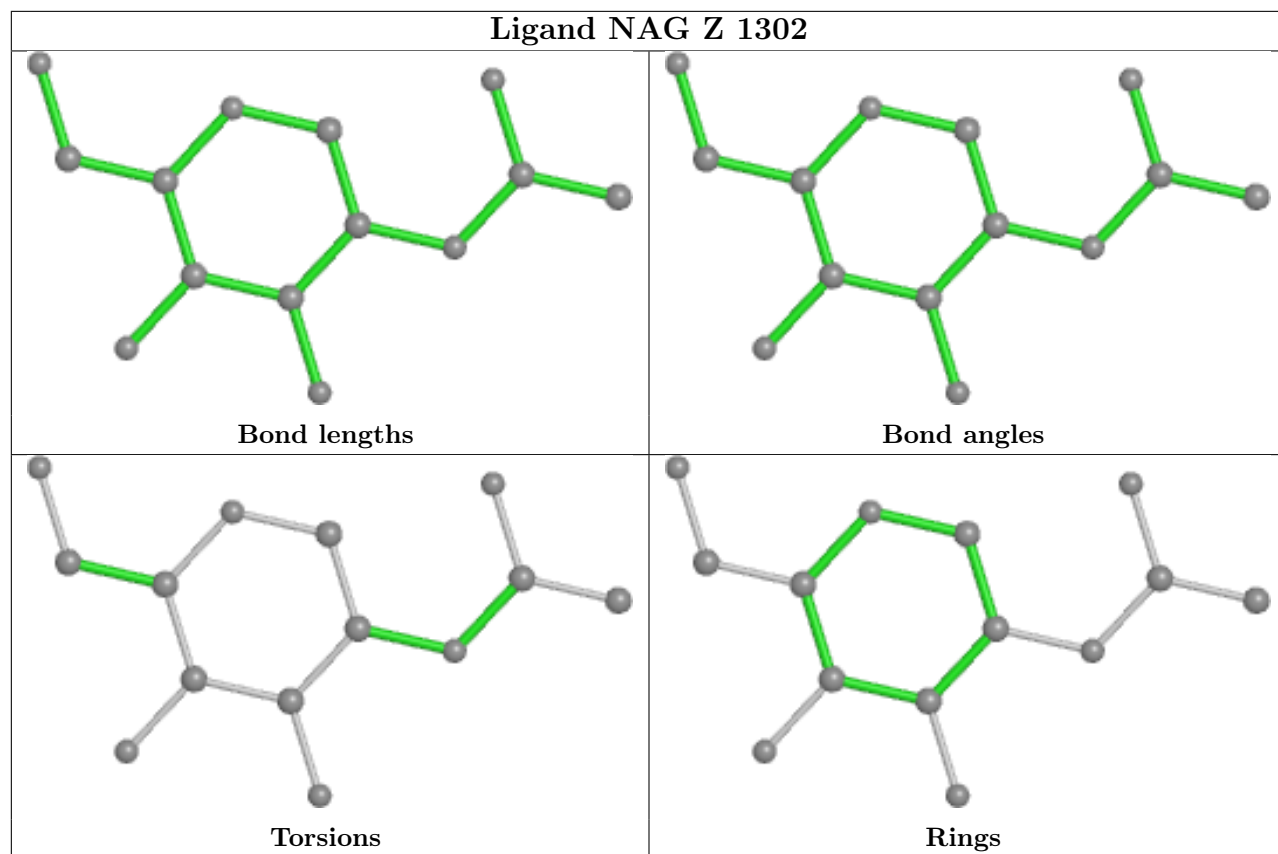


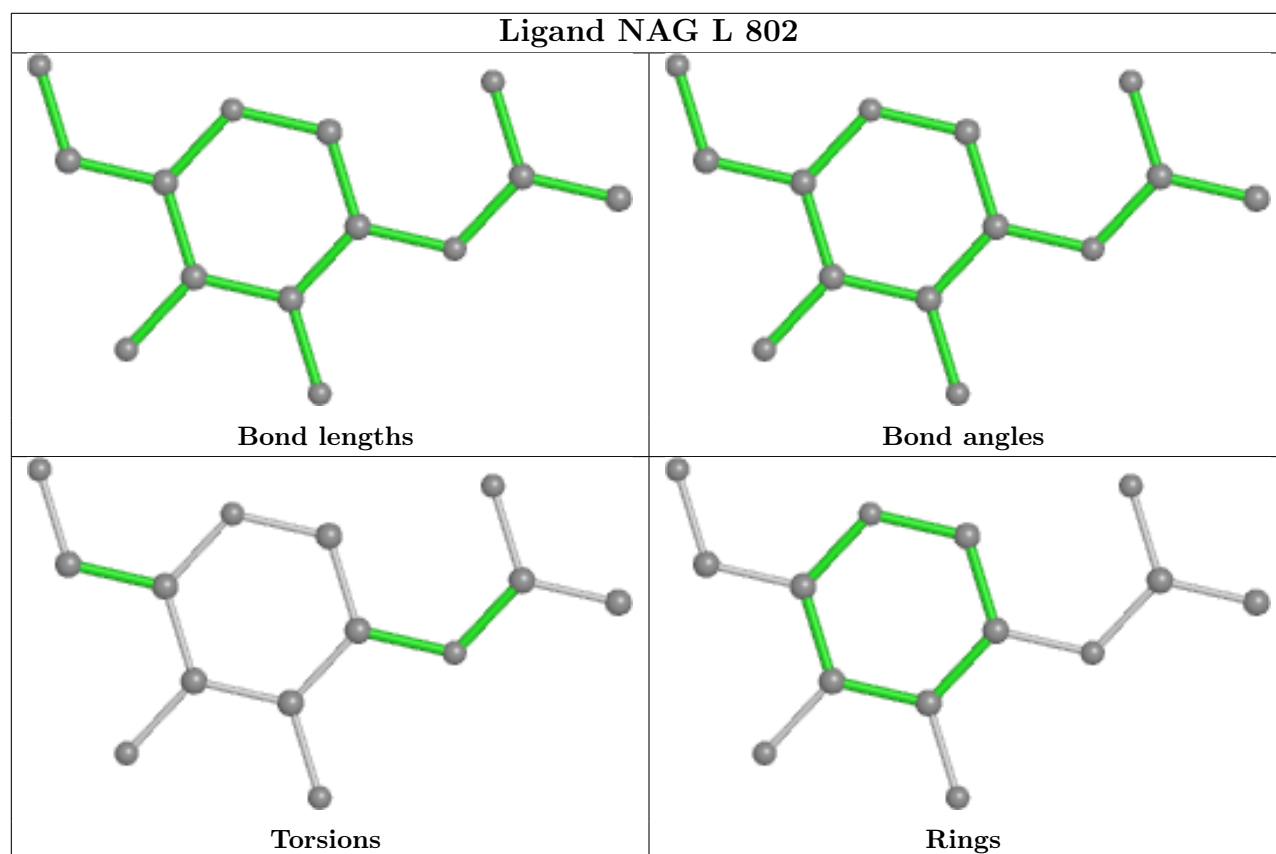
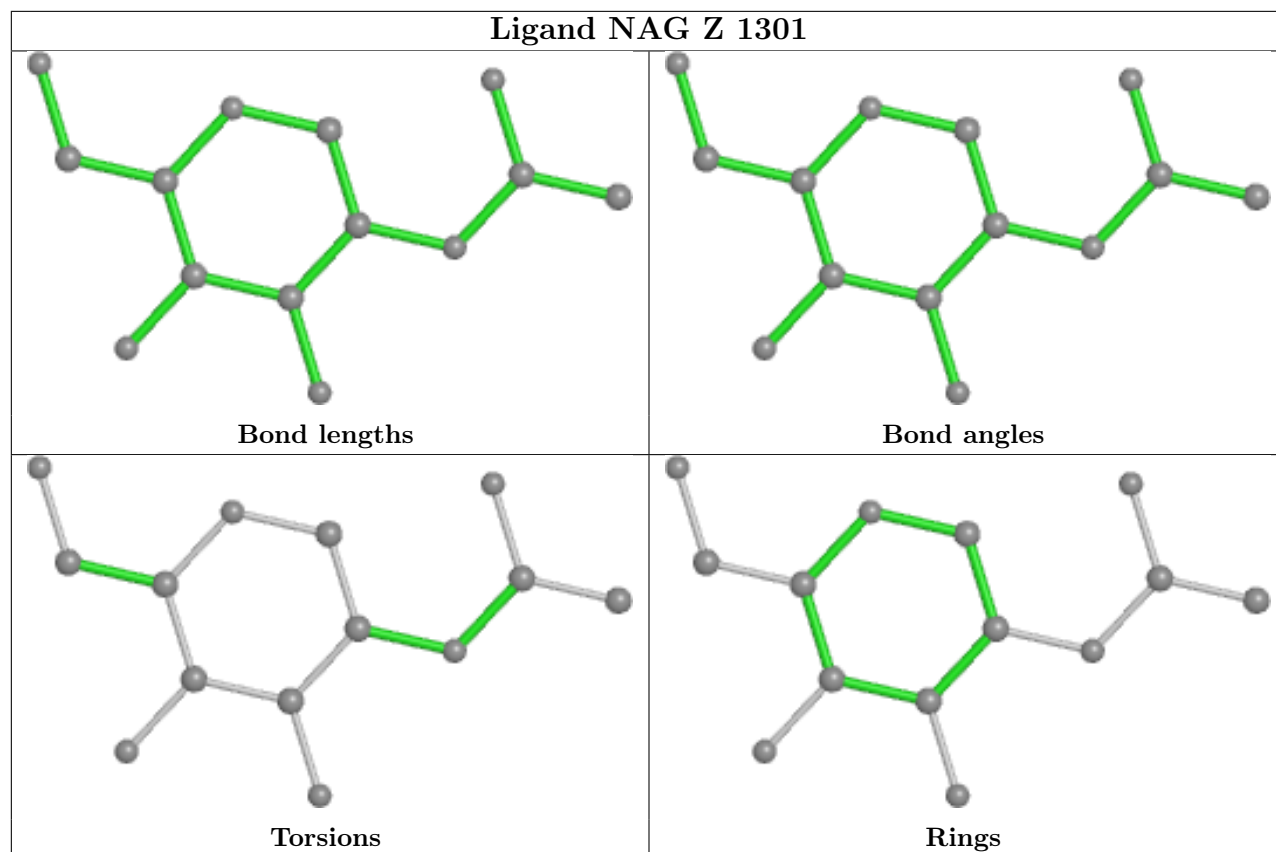


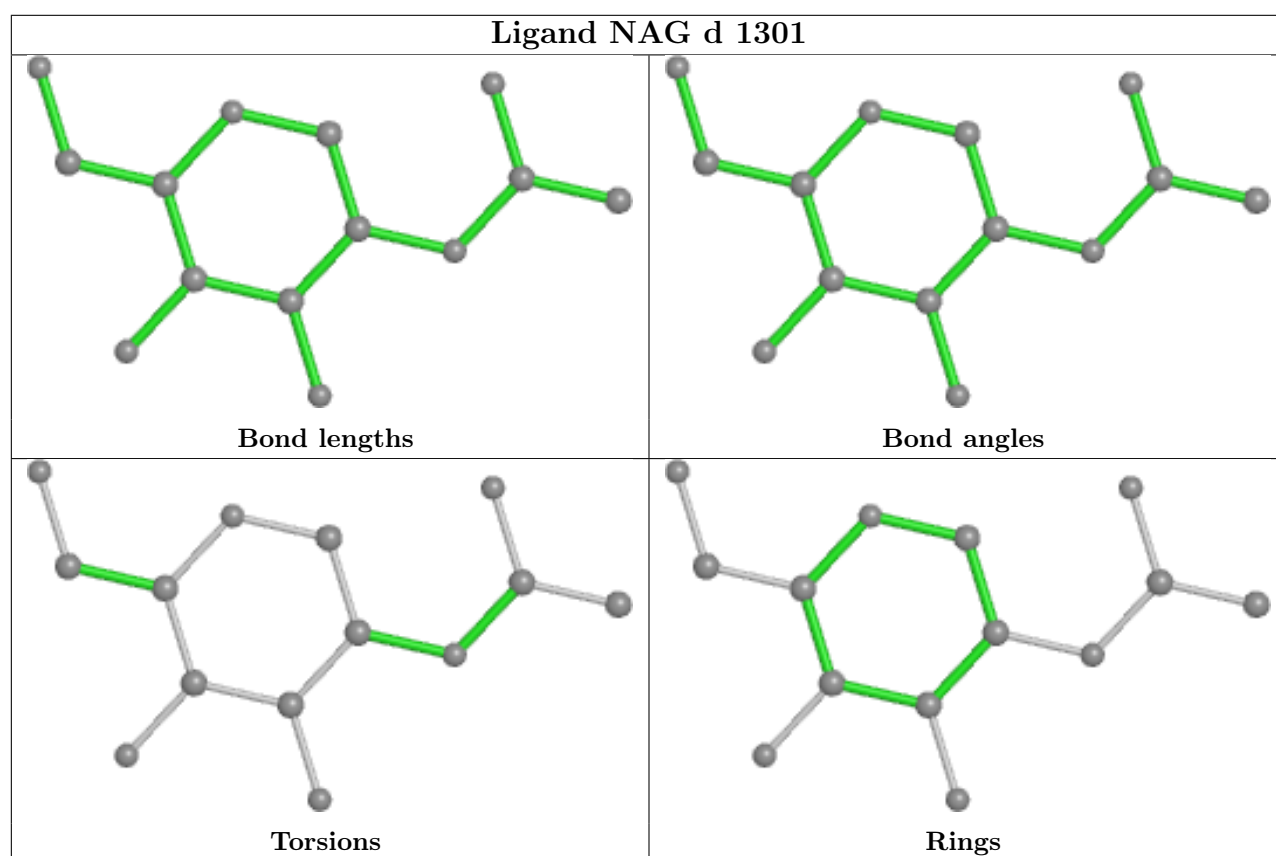
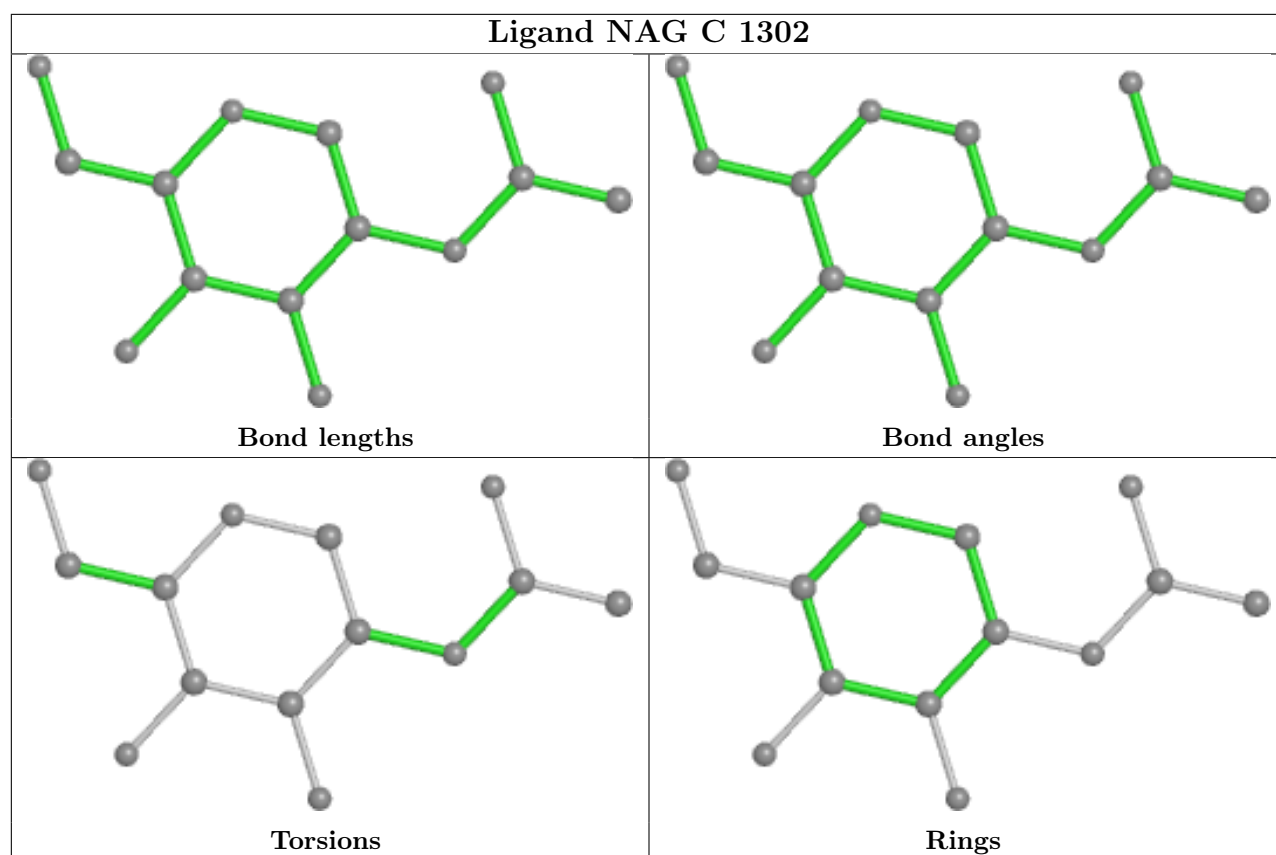




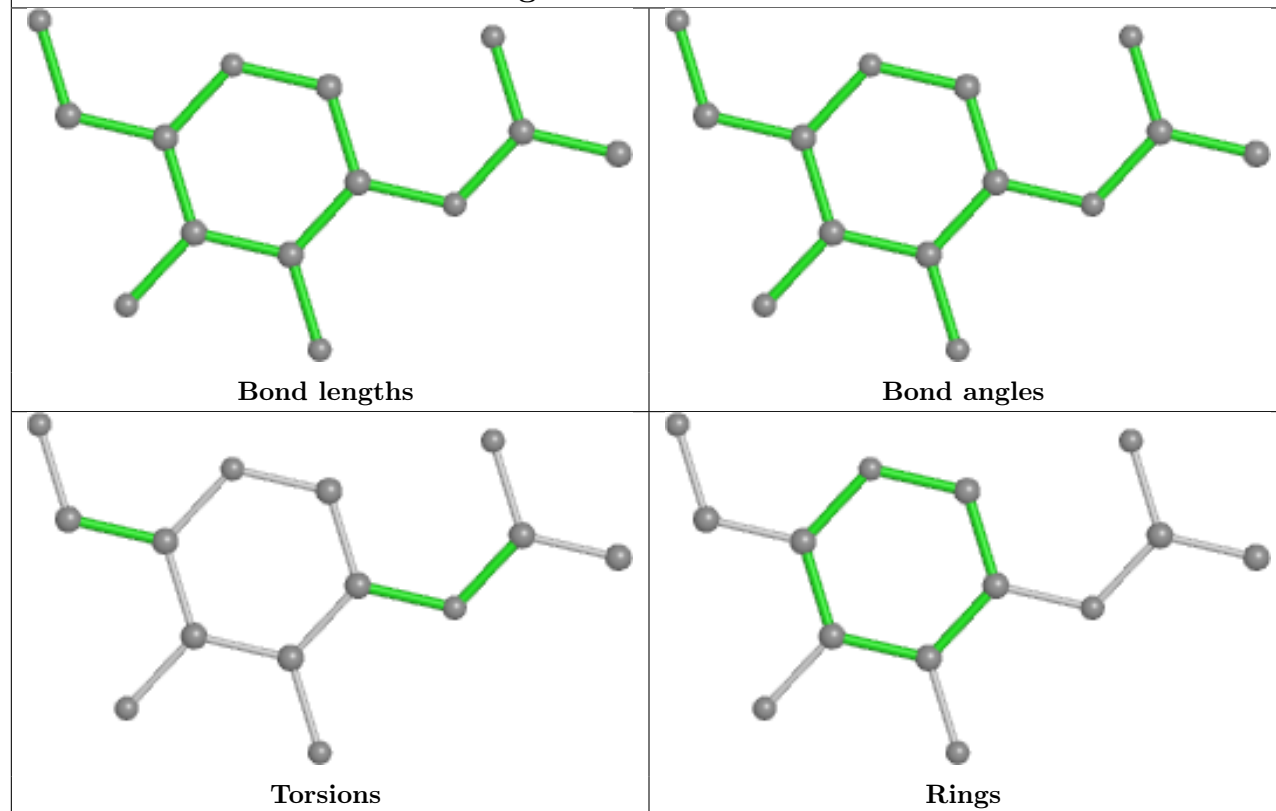




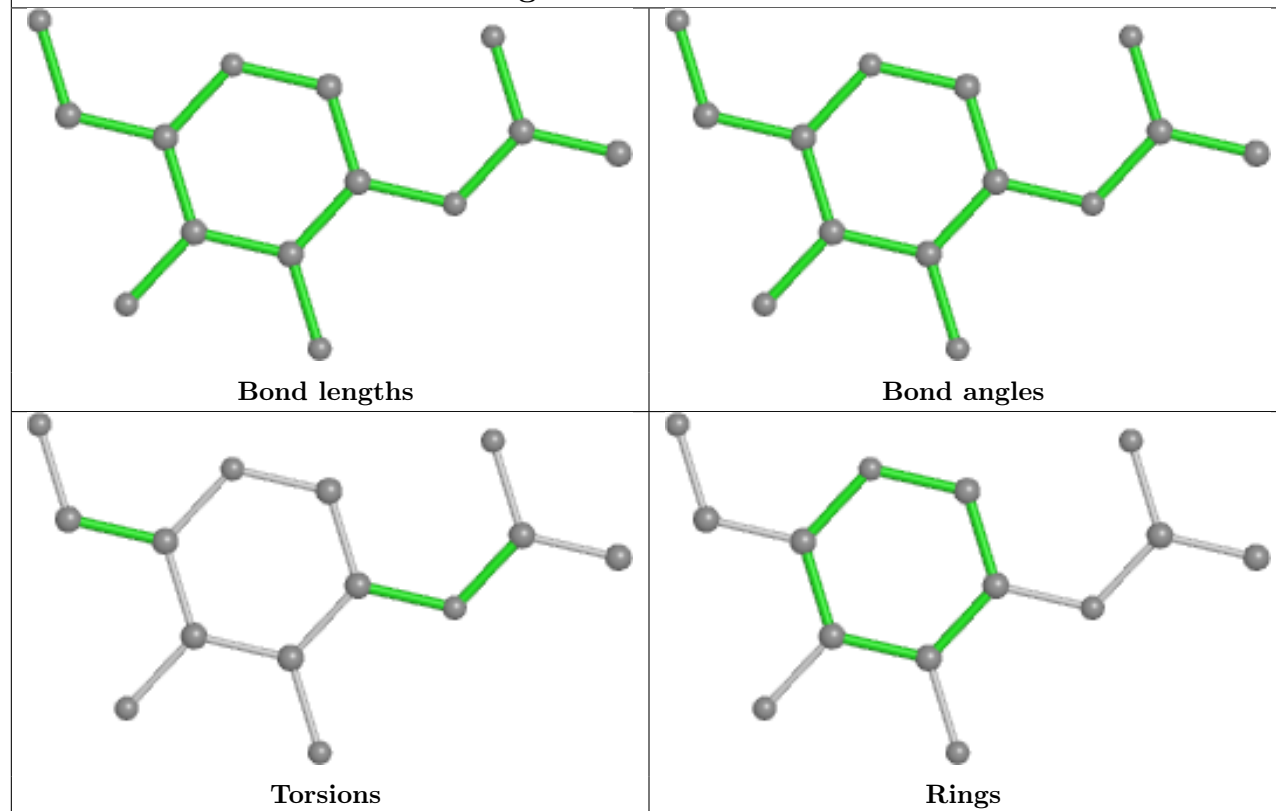


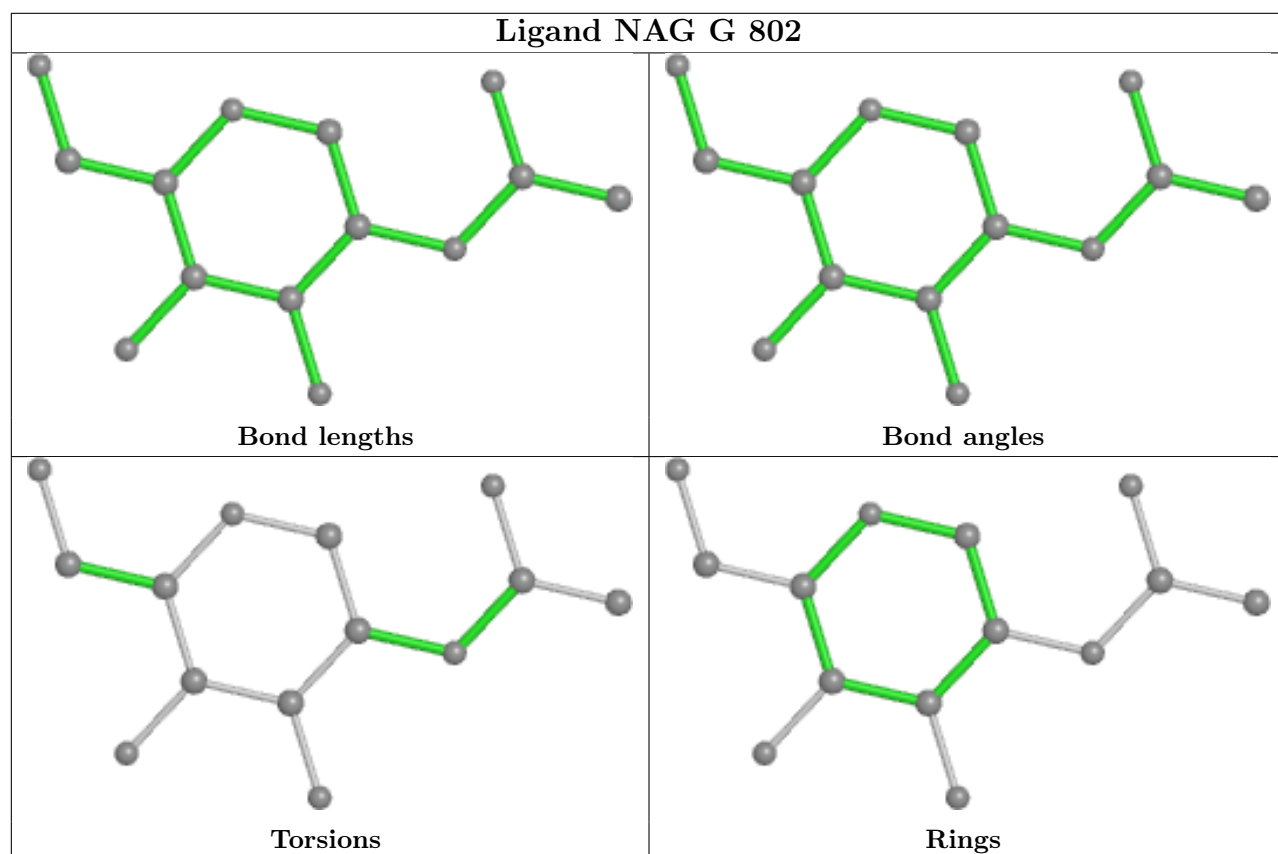
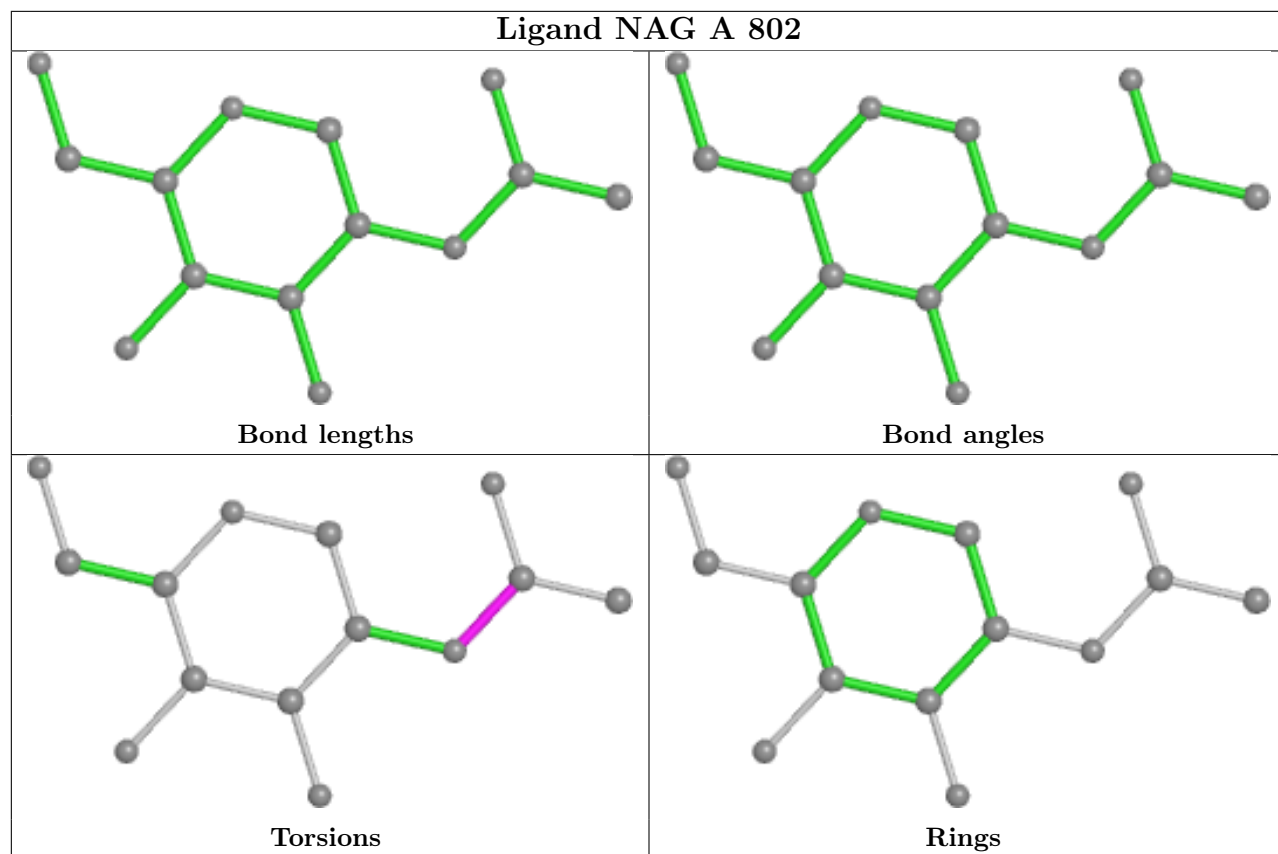


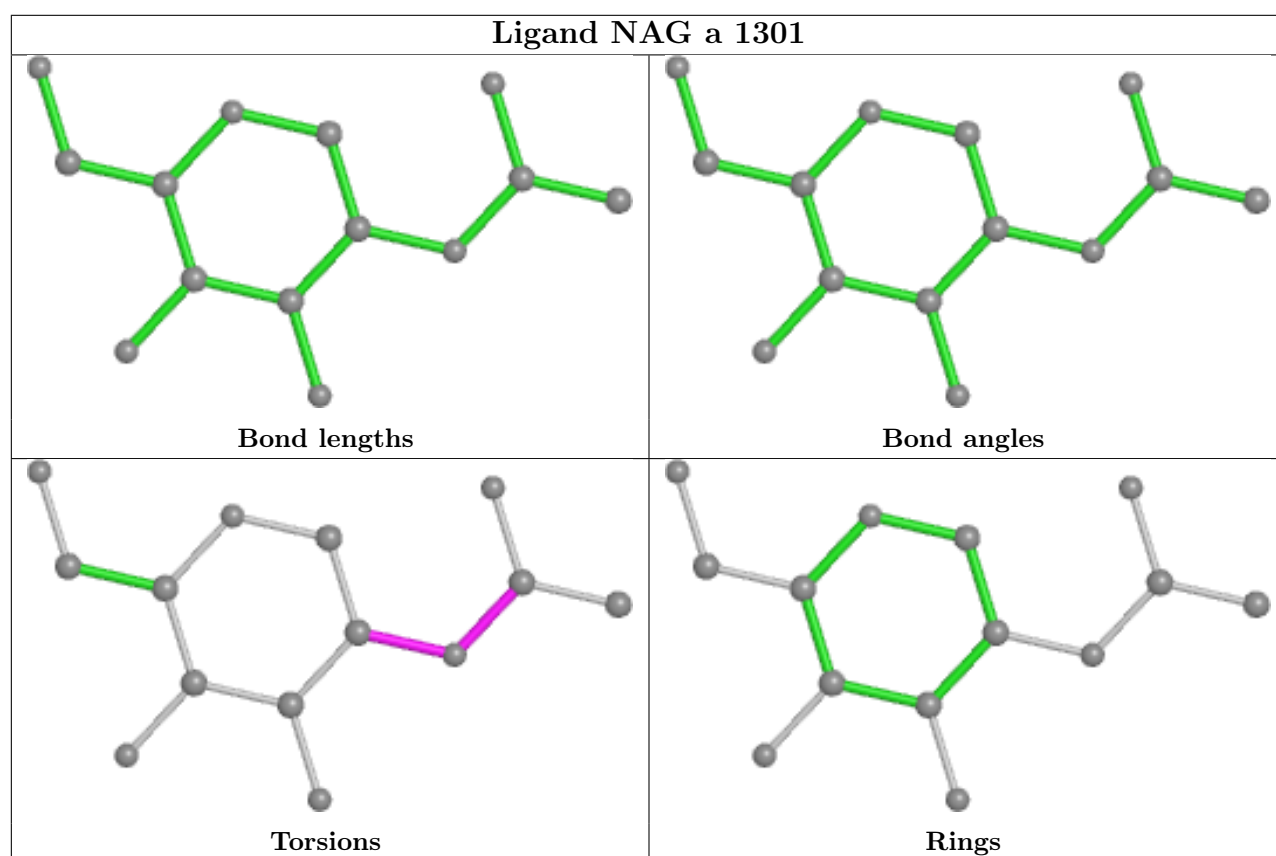
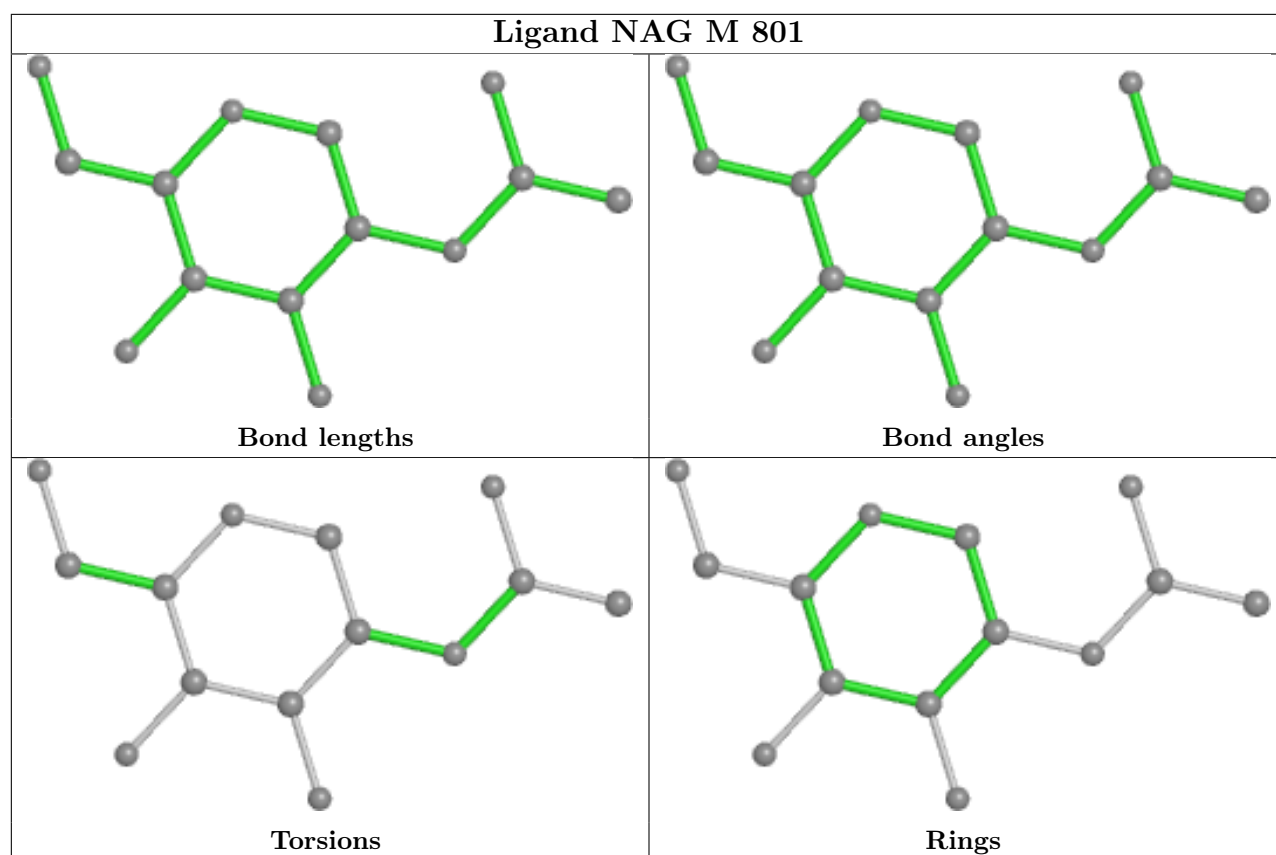
Ligand NAG D 1302



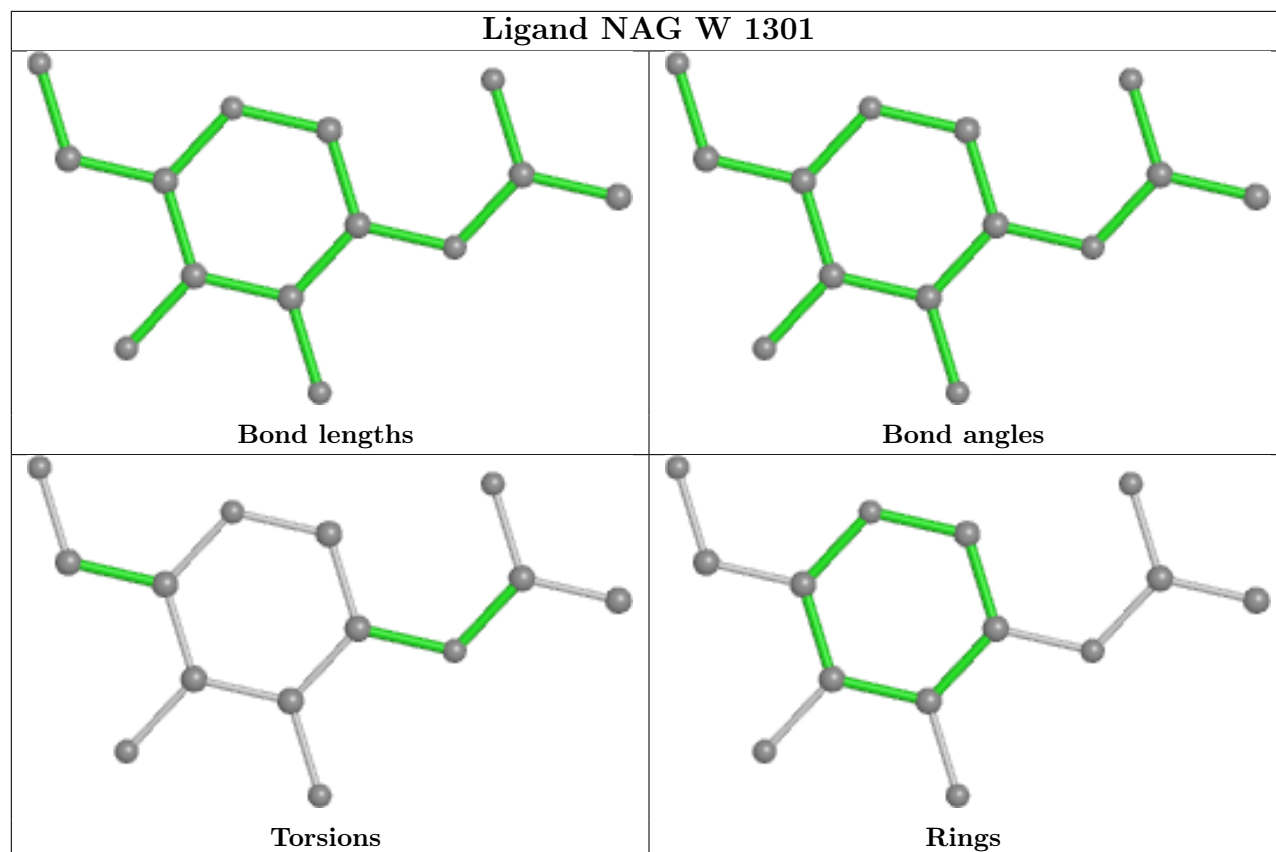
Ligand NAG V 1301



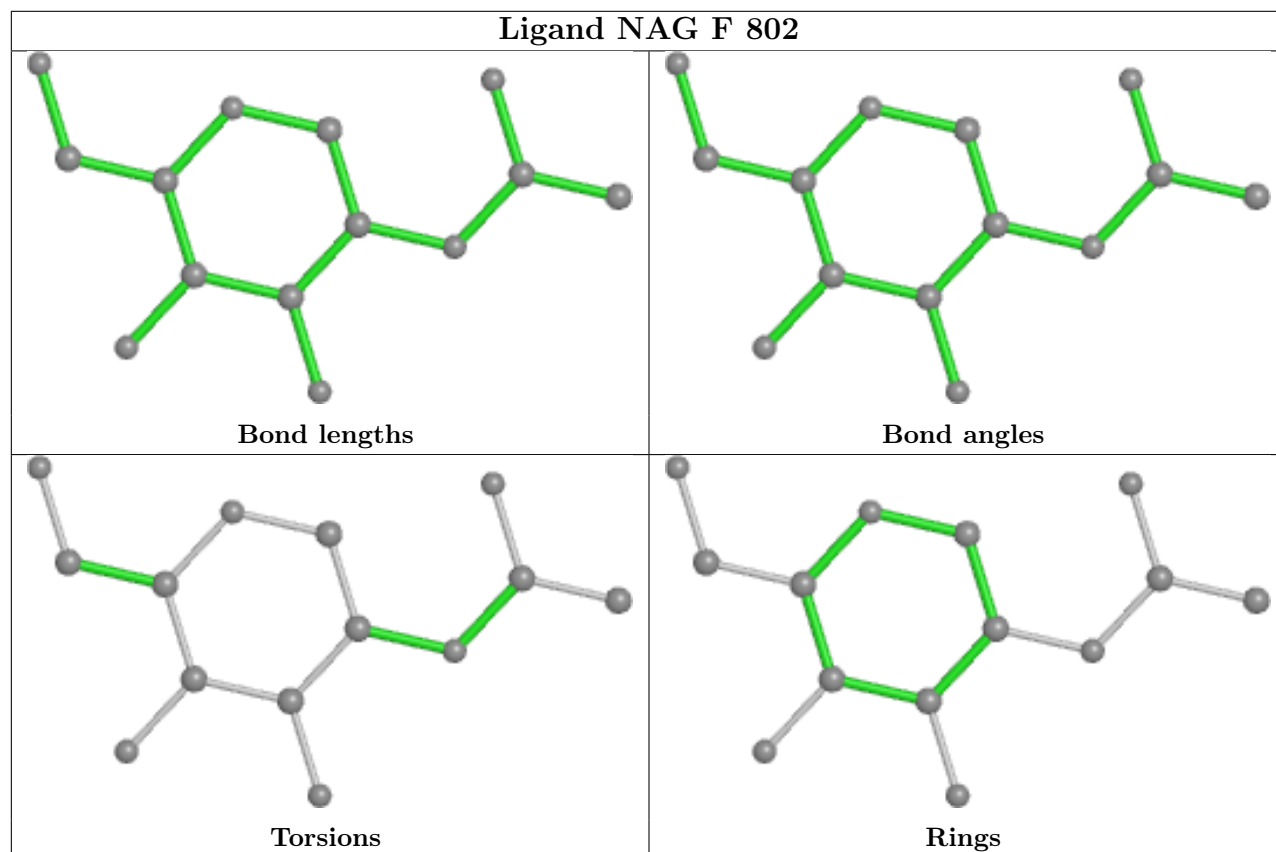


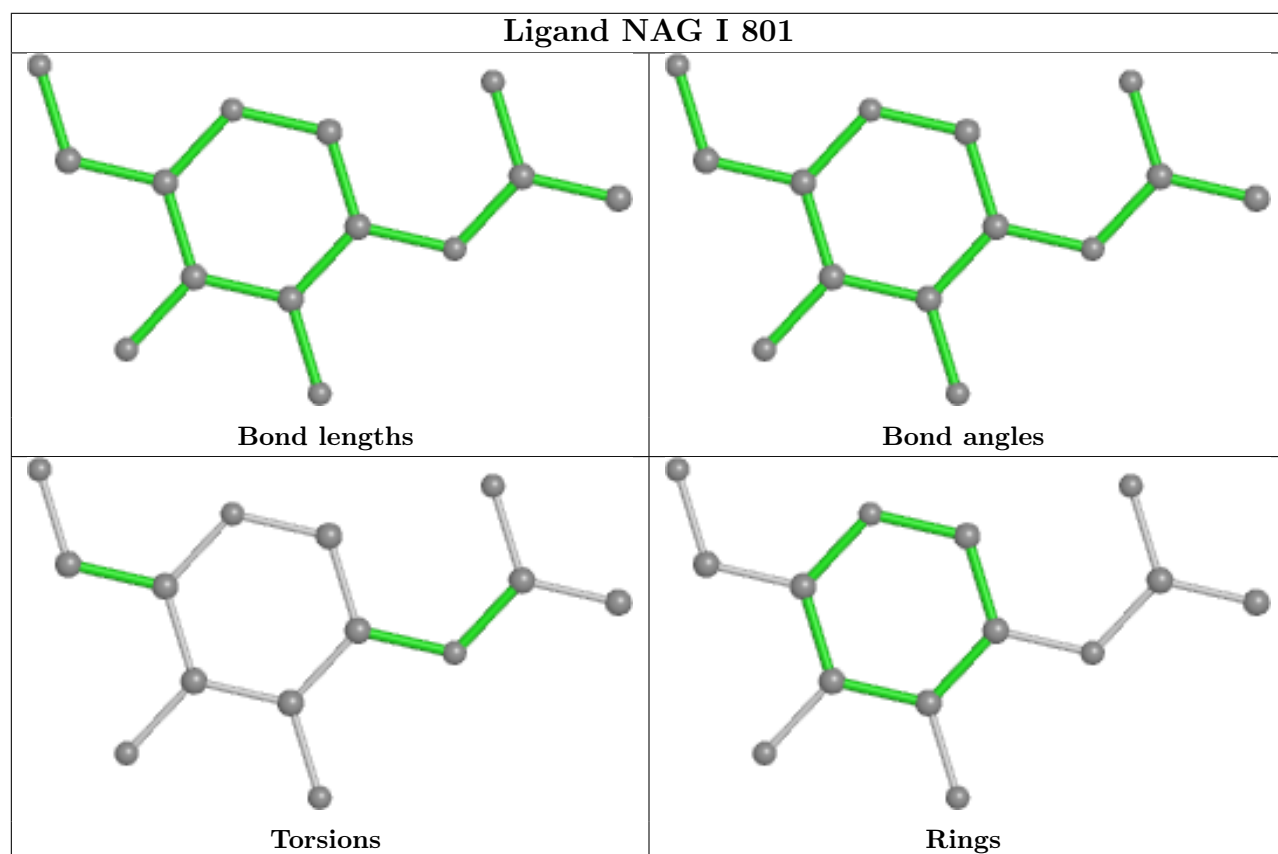
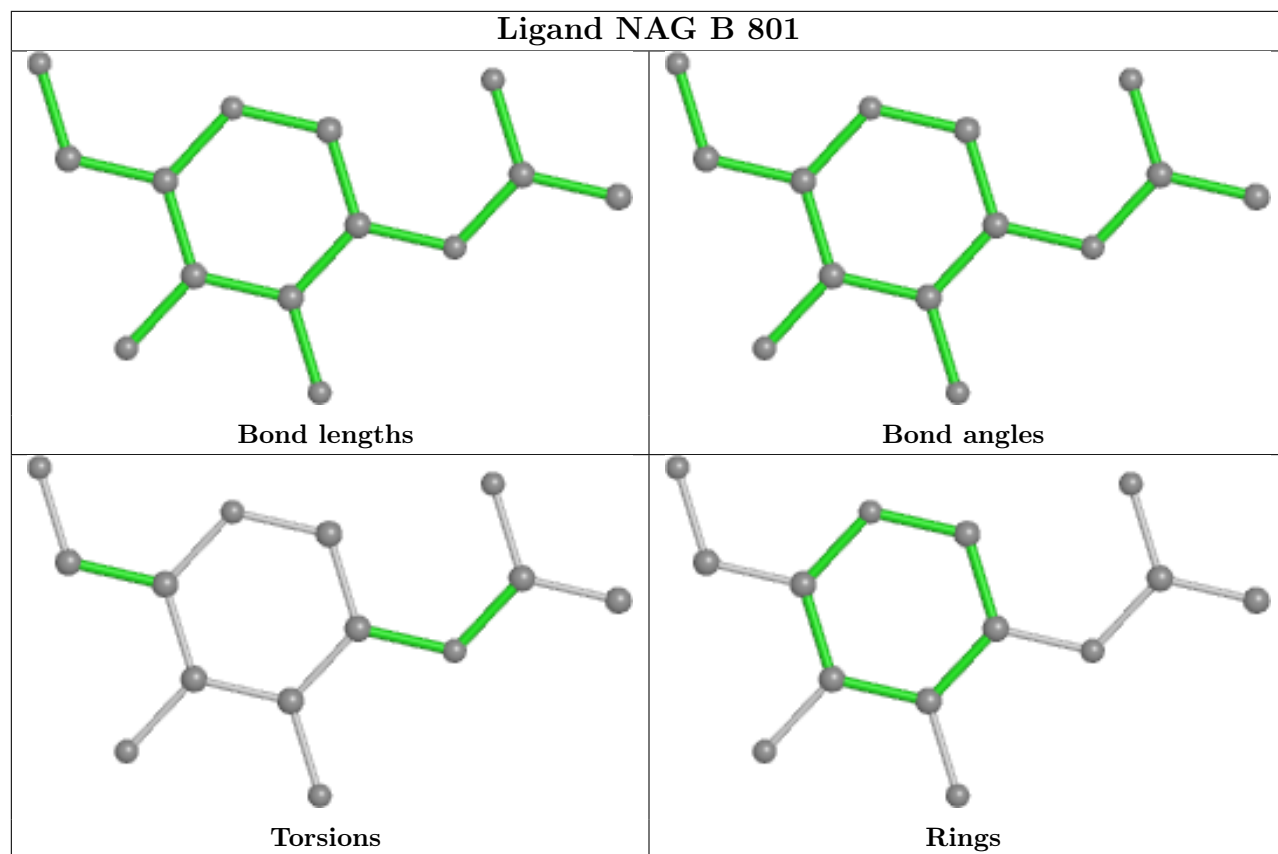


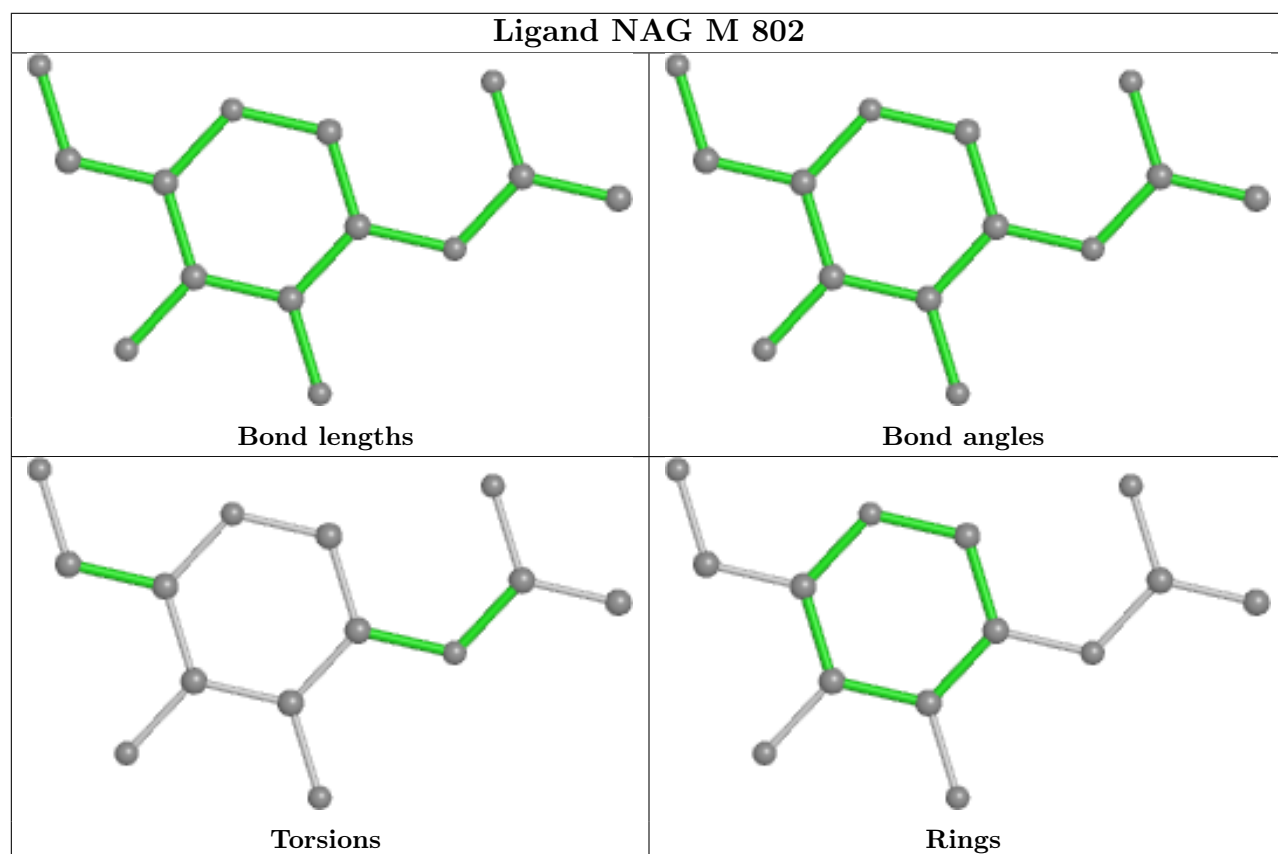
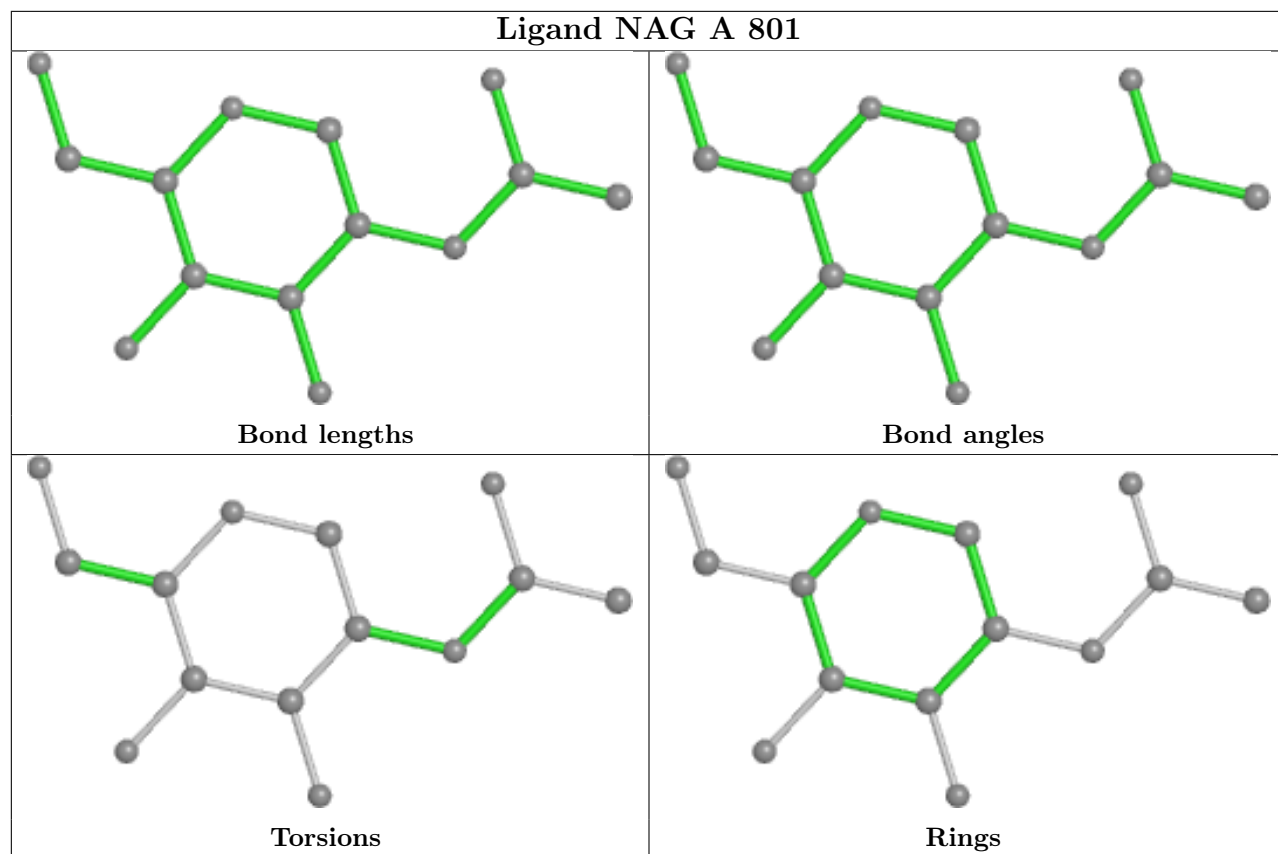
Ligand NAG W 1301

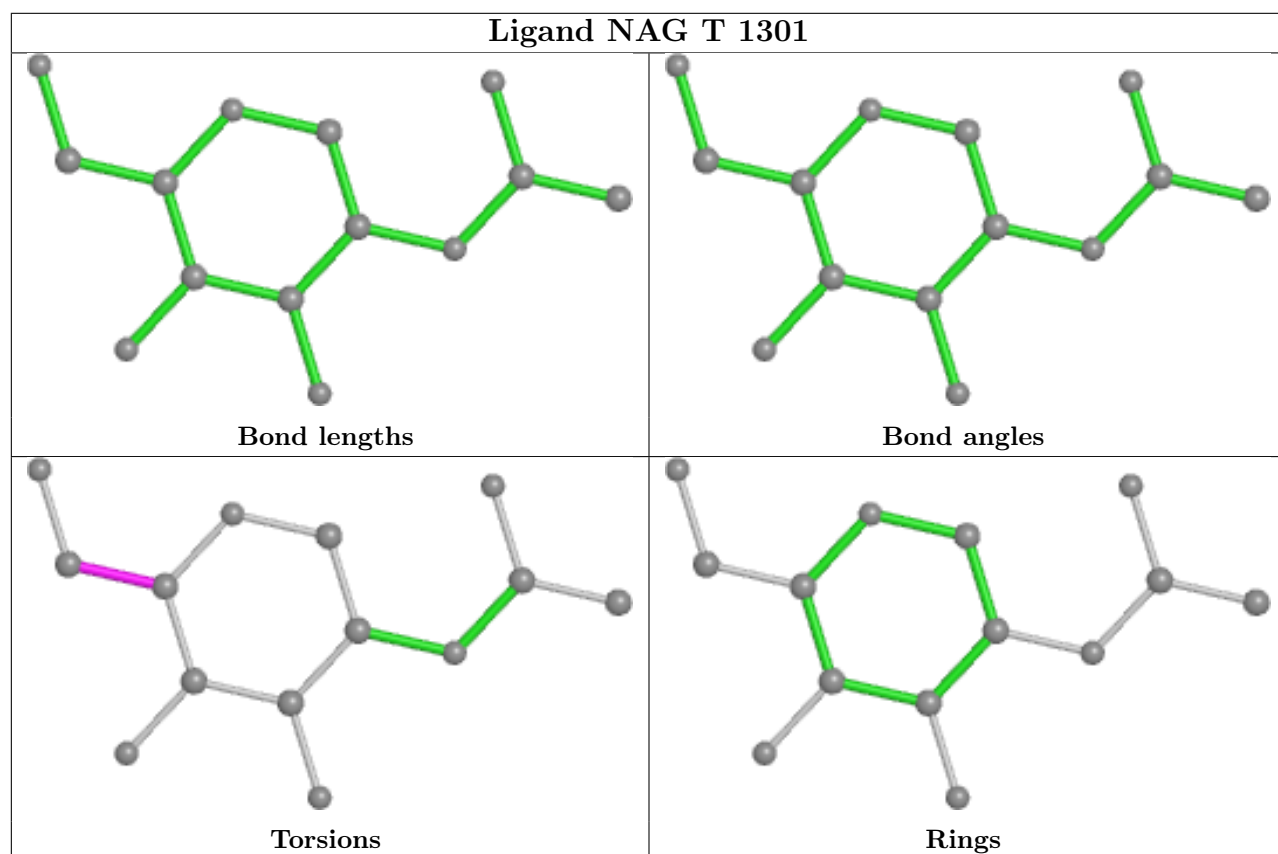
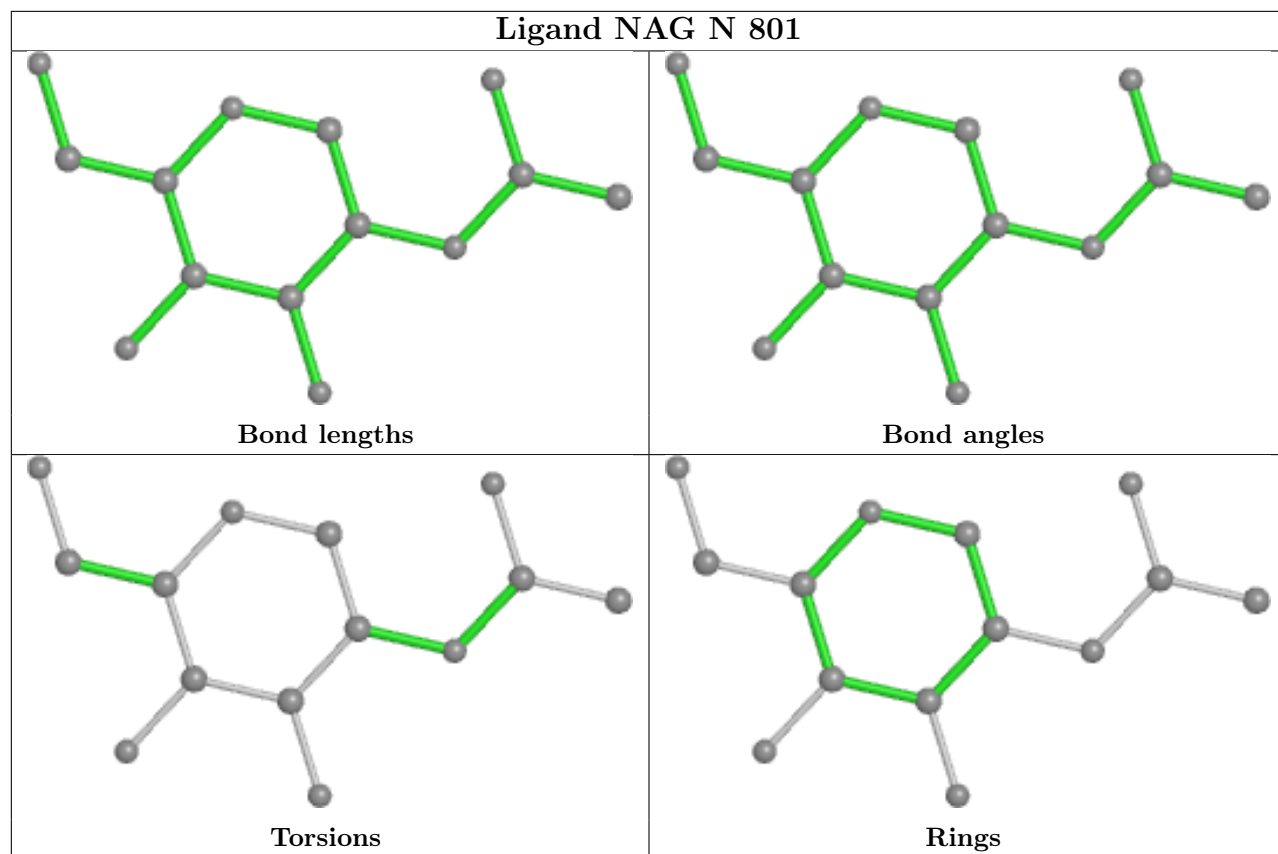


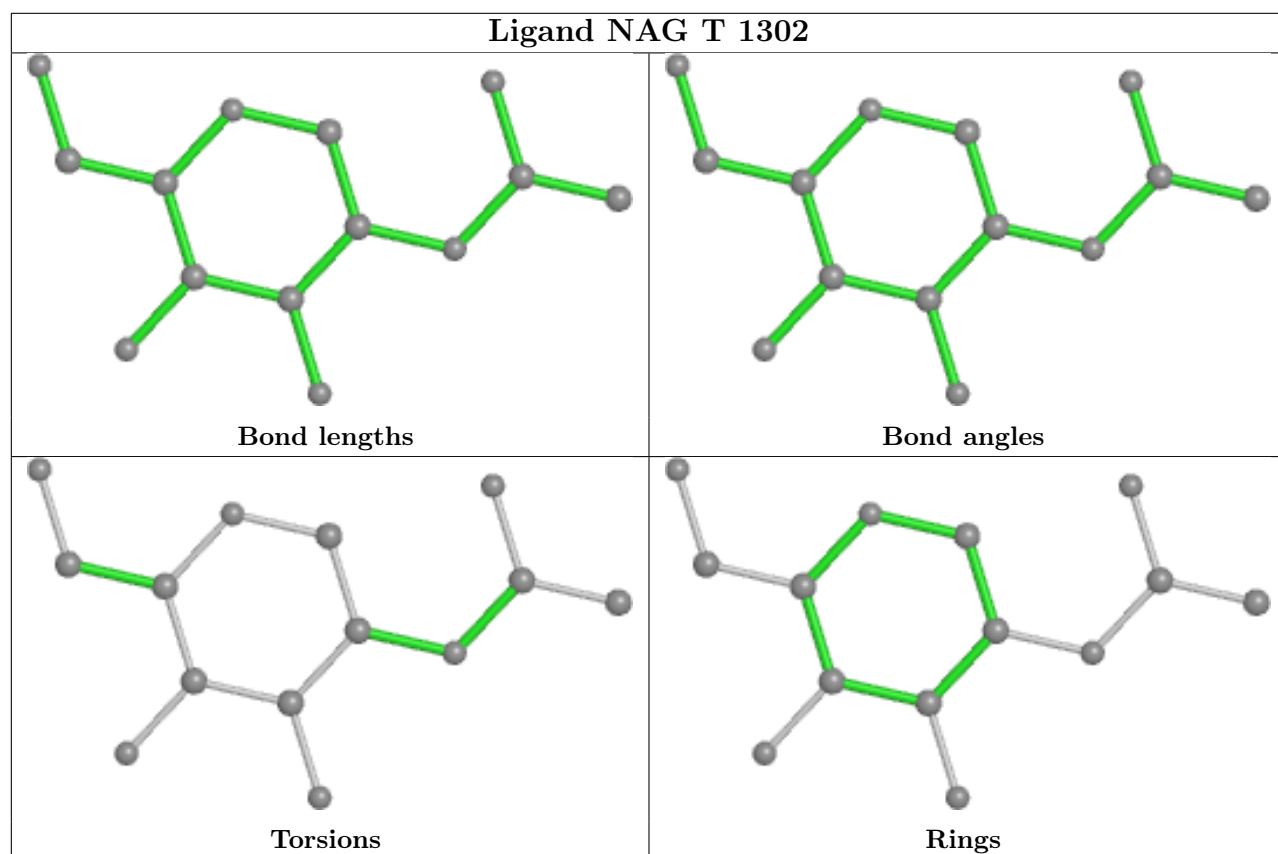
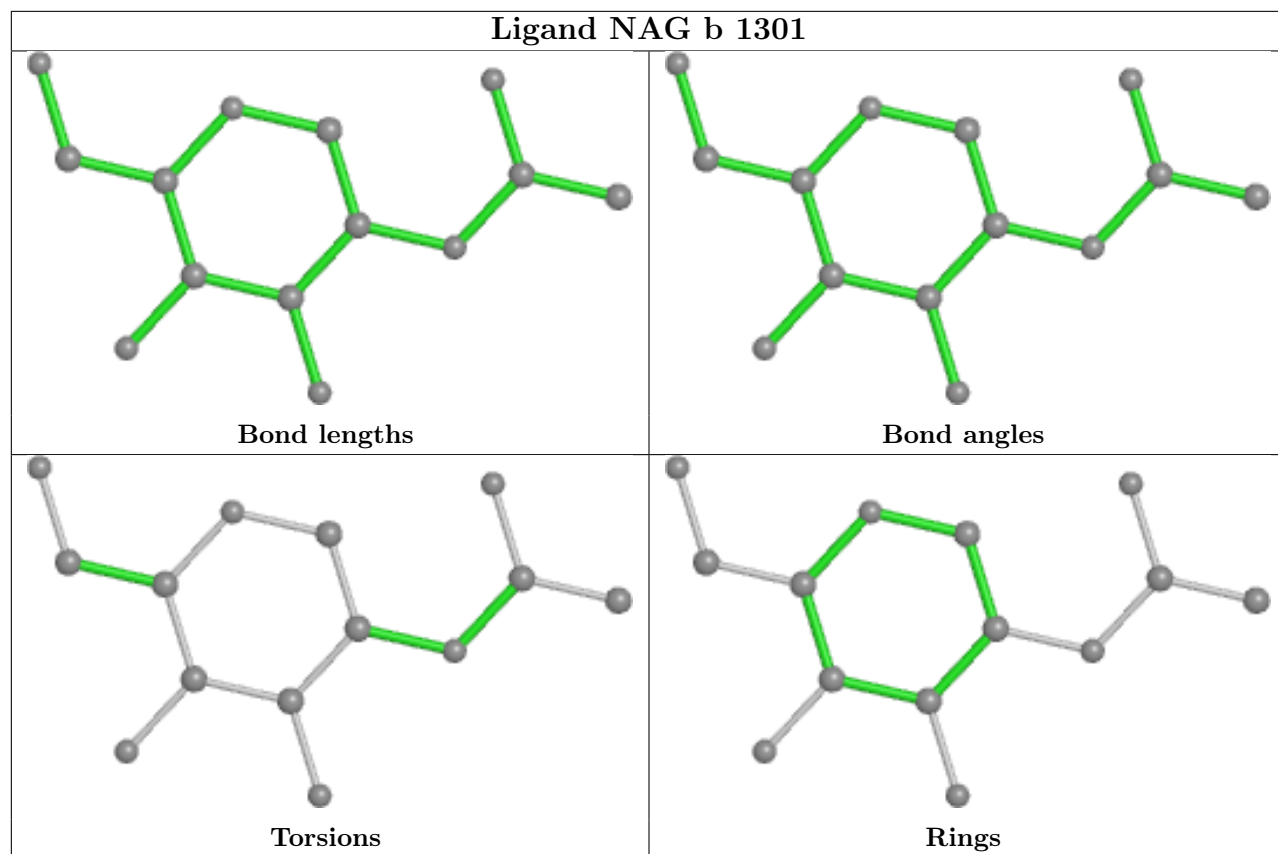
Ligand NAG F 802

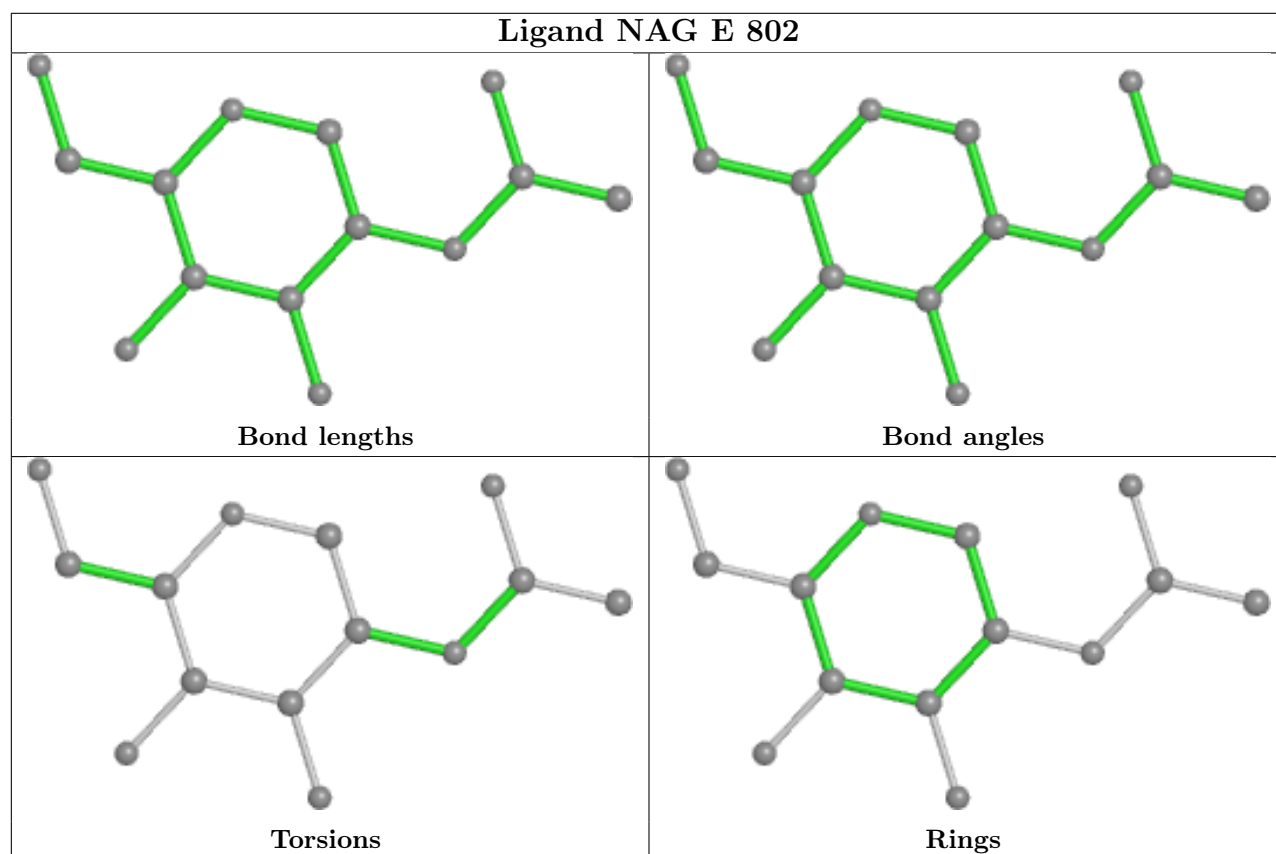
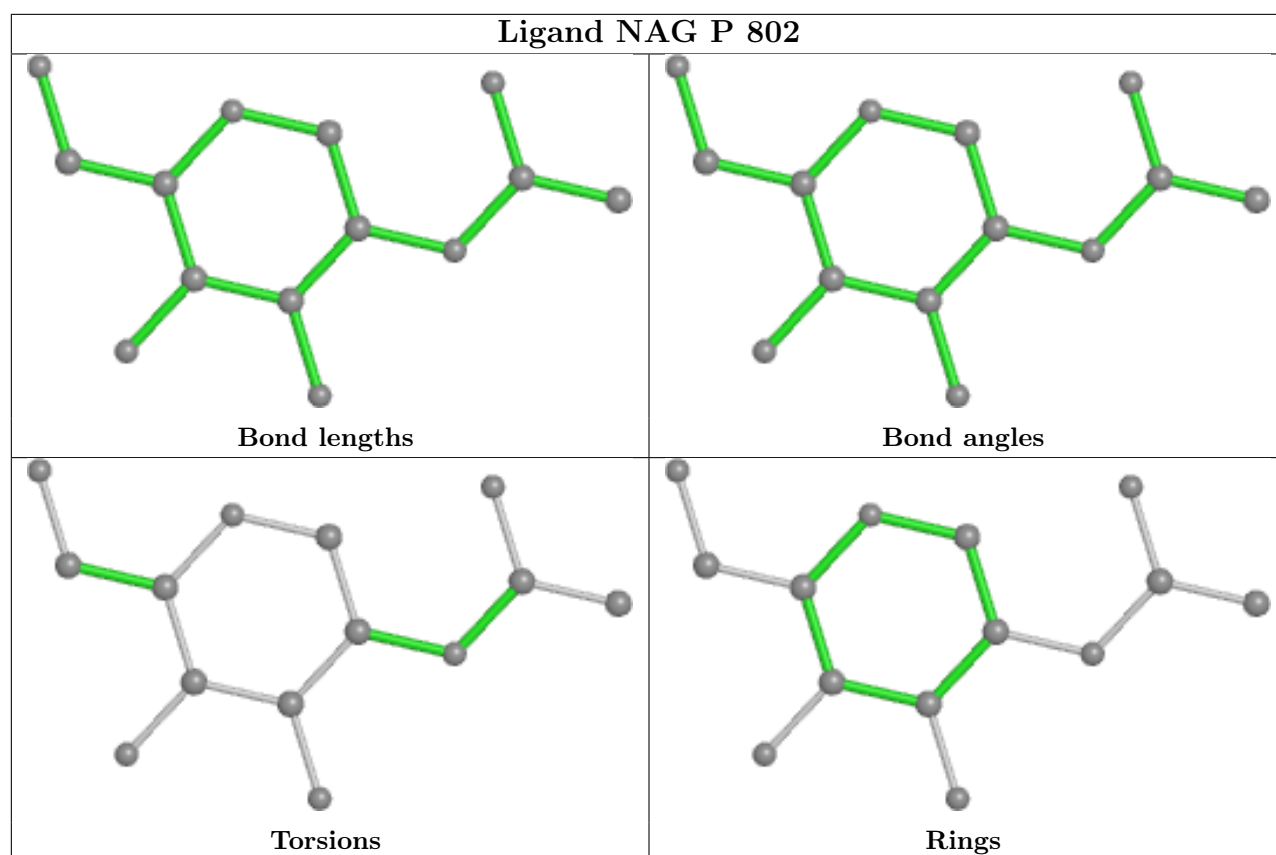


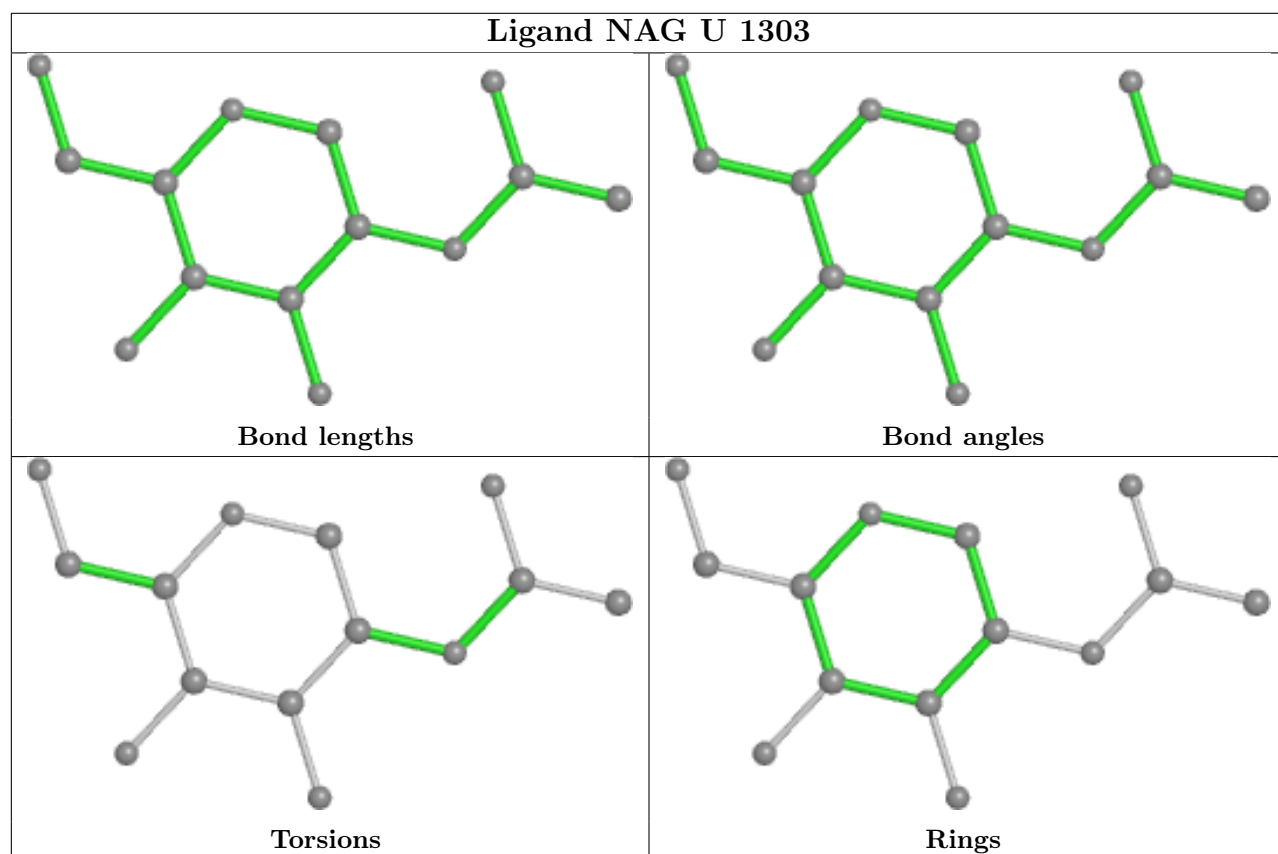
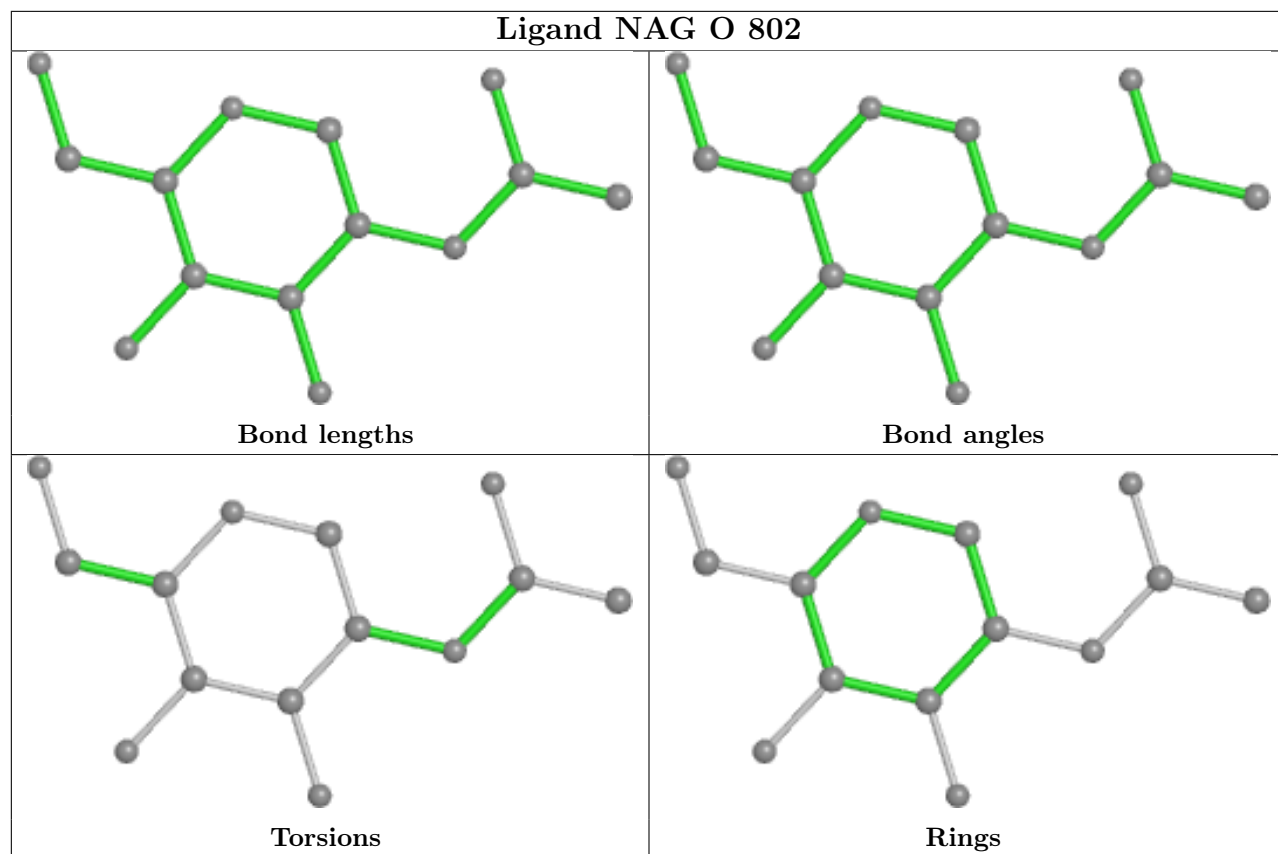


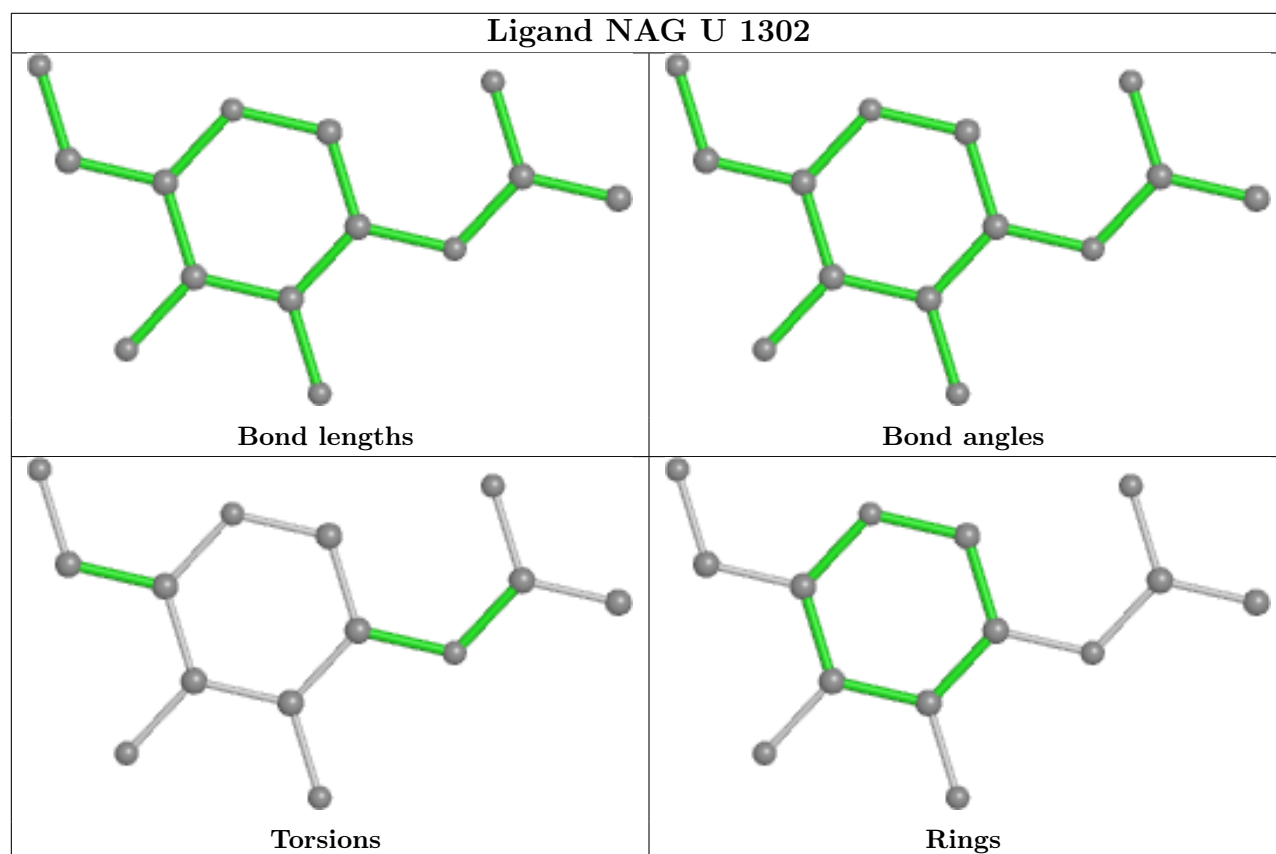
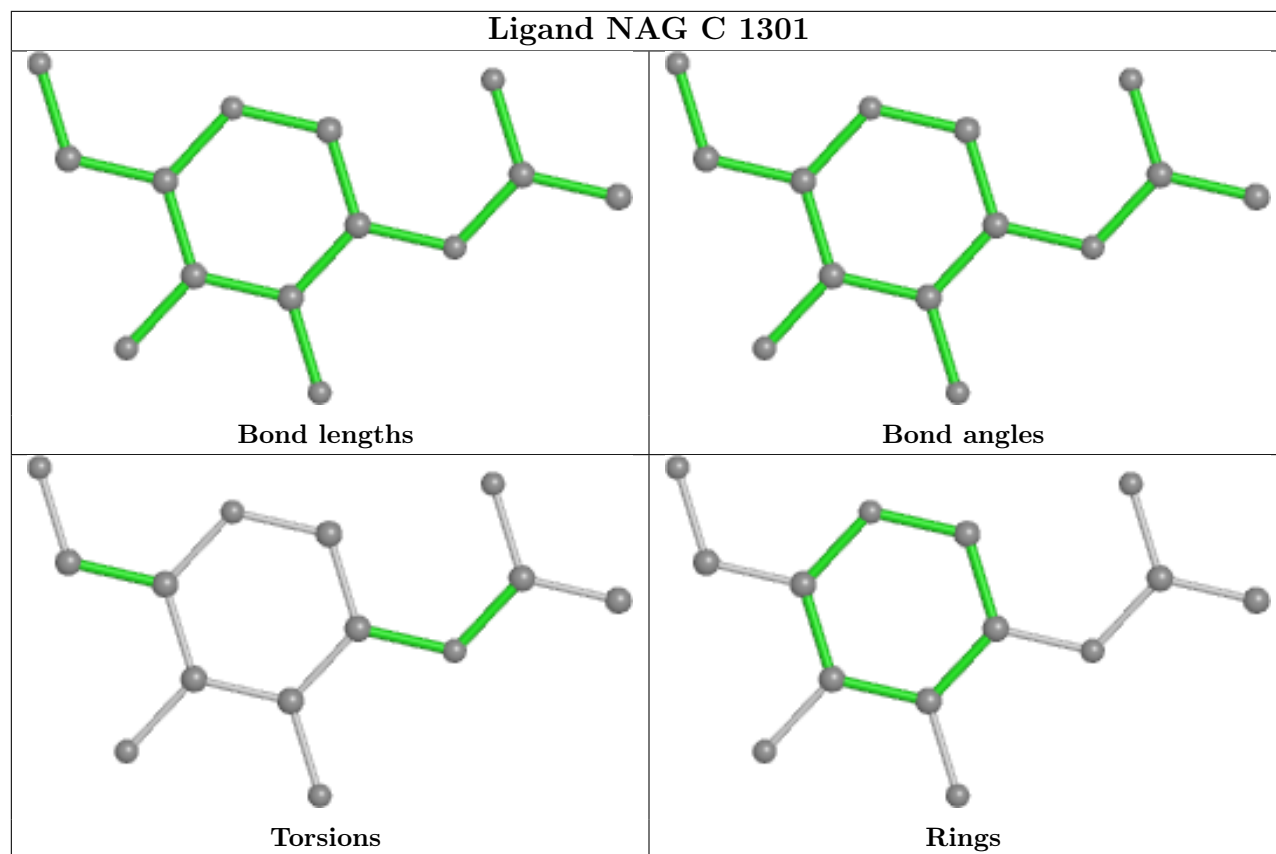


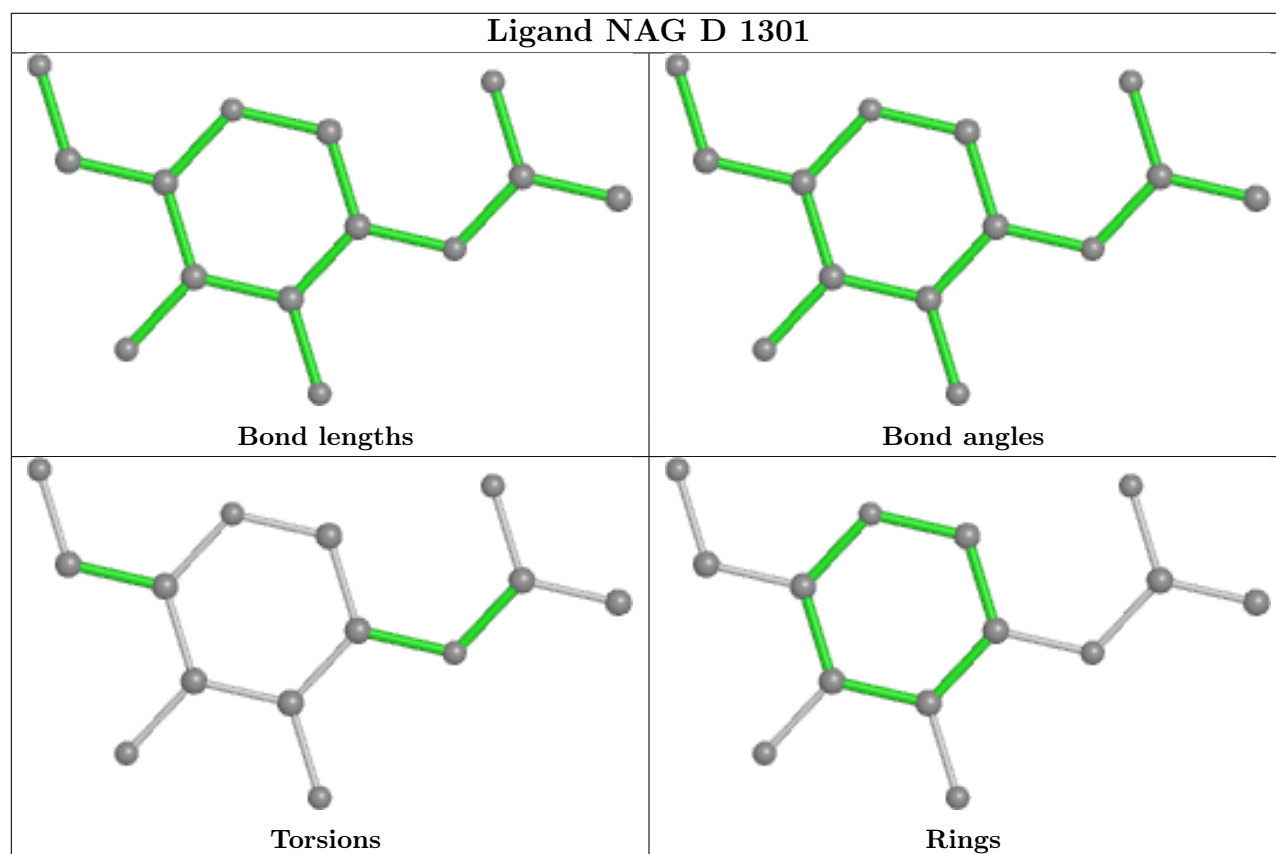
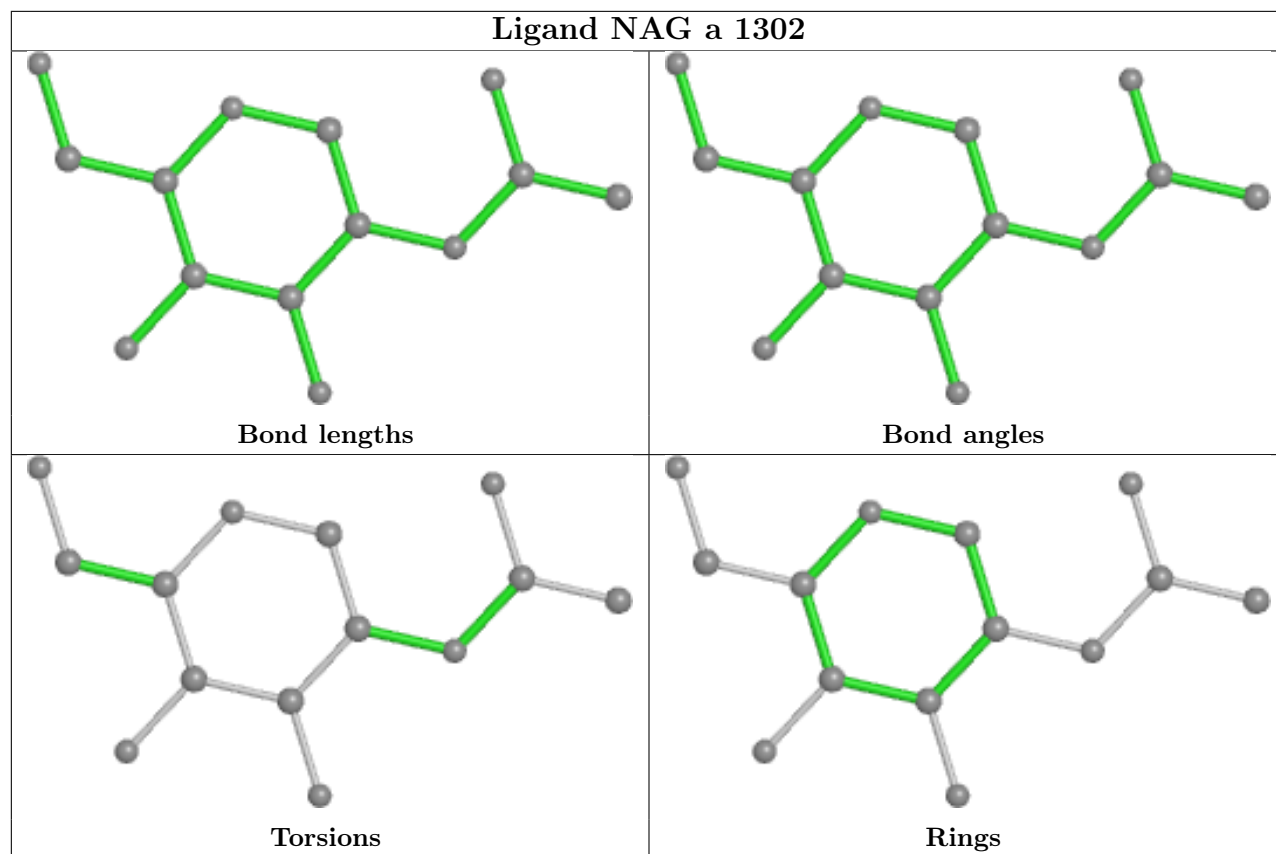


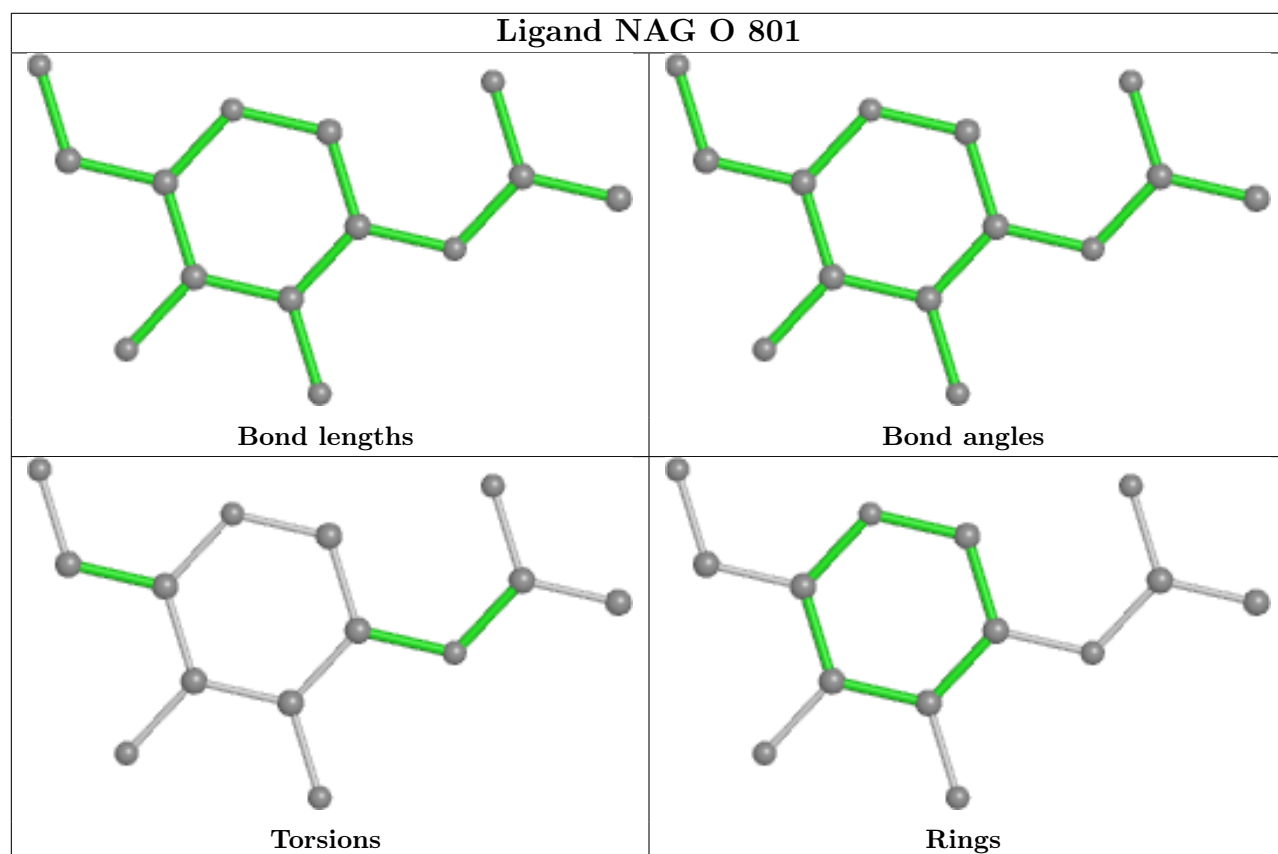
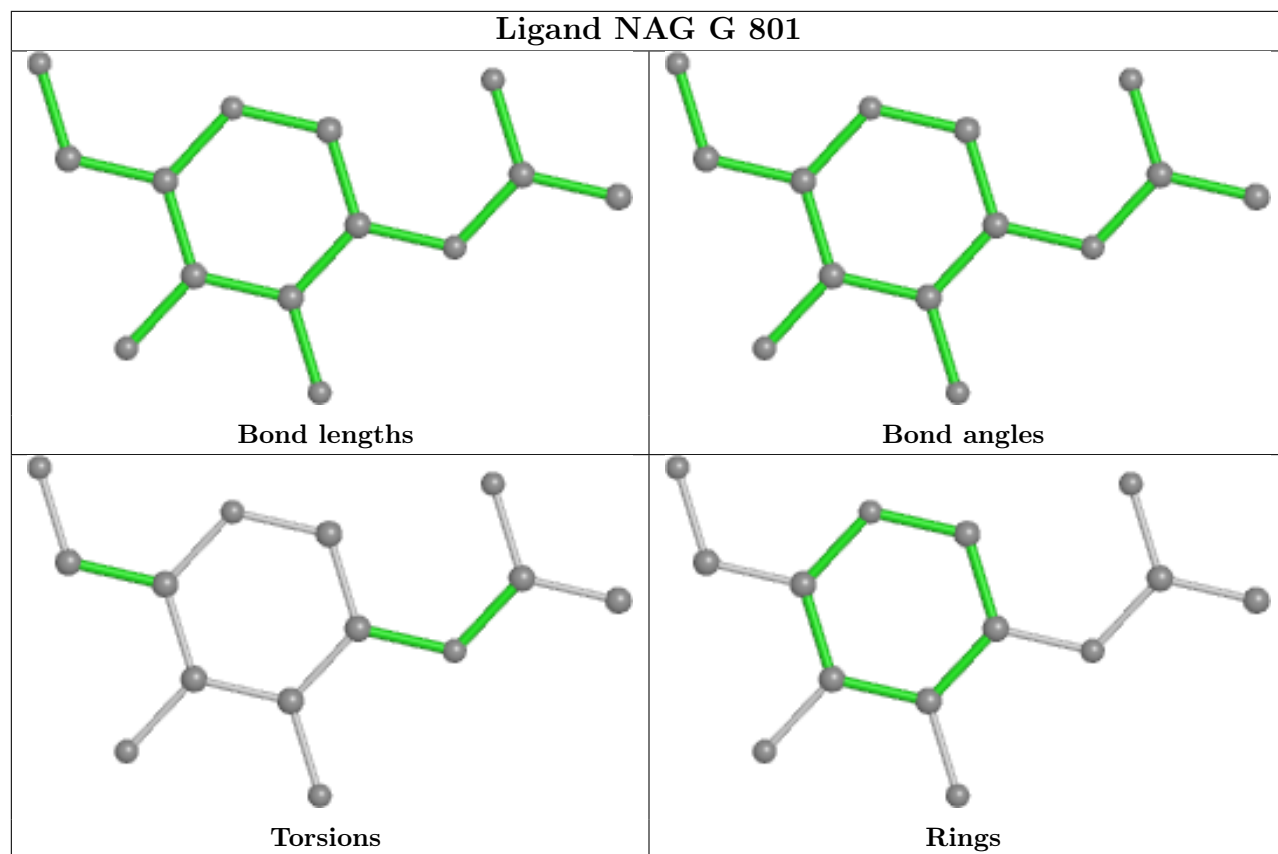












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

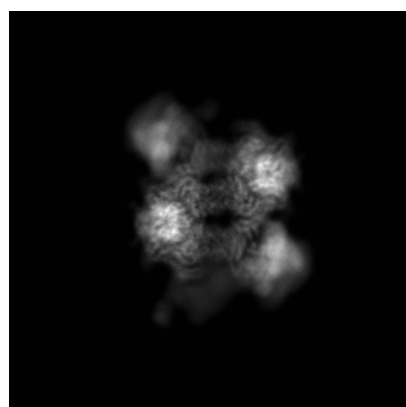
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32689. These allow visual inspection of the internal detail of the map and identification of artifacts.

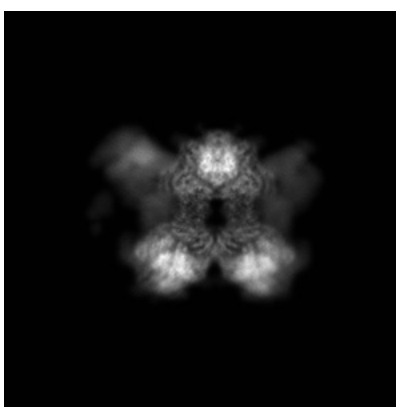
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

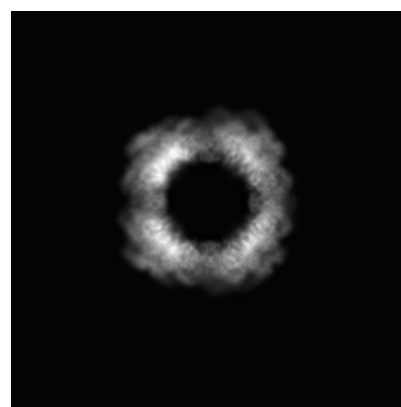
6.1.1 Primary map



X



Y

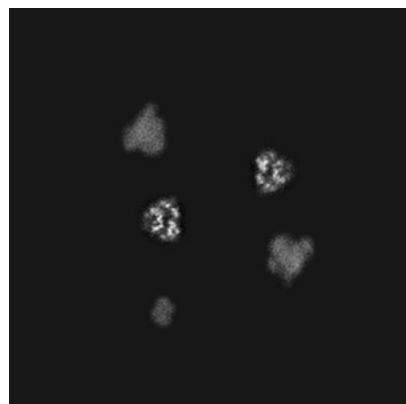


Z

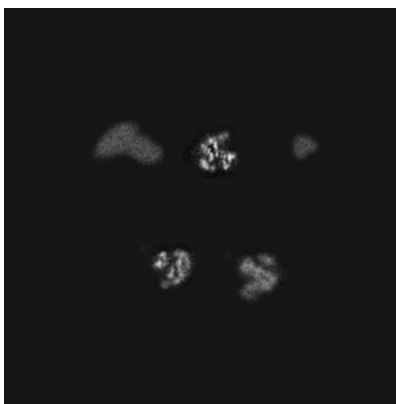
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

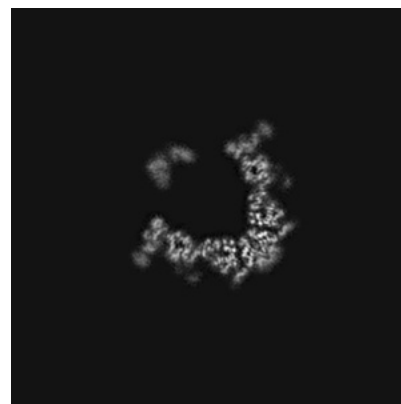
6.2.1 Primary map



X Index: 128



Y Index: 128

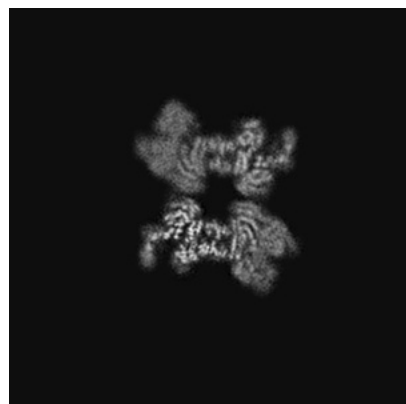


Z Index: 128

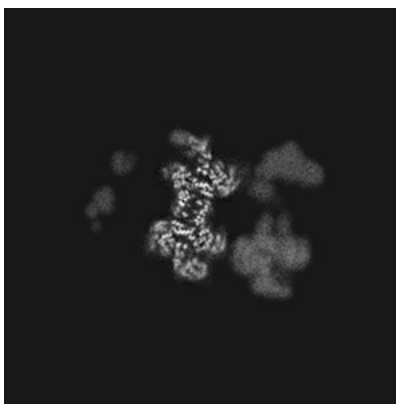
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

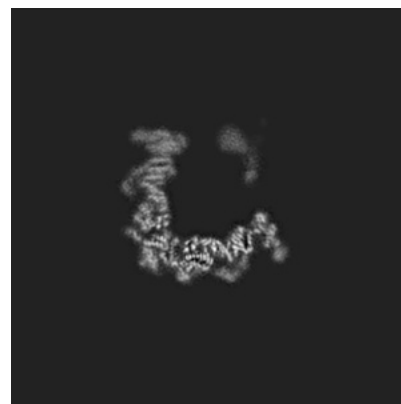
6.3.1 Primary map



X Index: 94



Y Index: 101

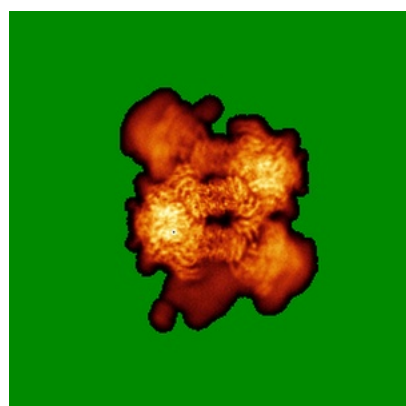


Z Index: 114

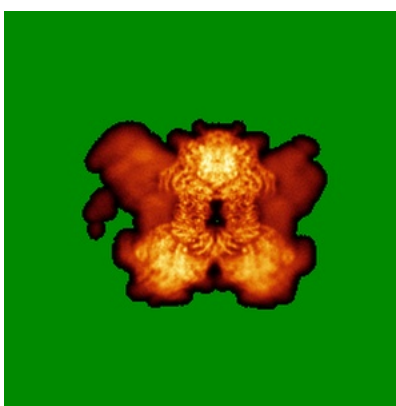
The images above show the largest variance slices of the map in three orthogonal directions.

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

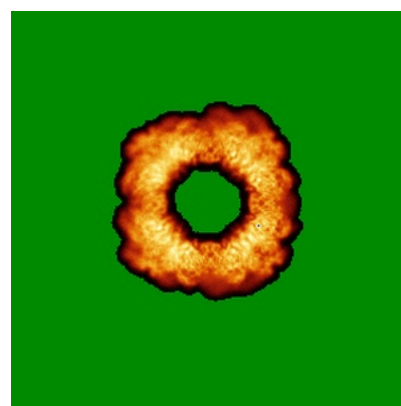
6.4.1 Primary map



X



Y

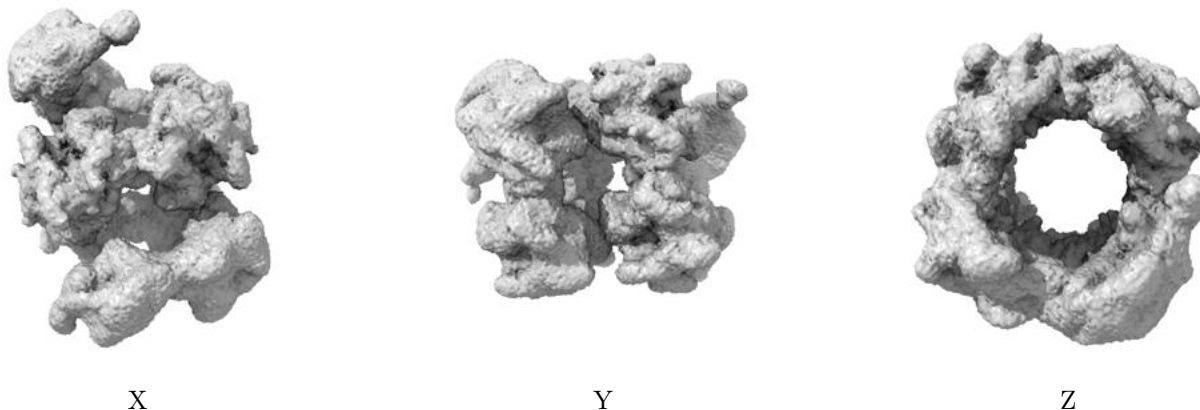


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

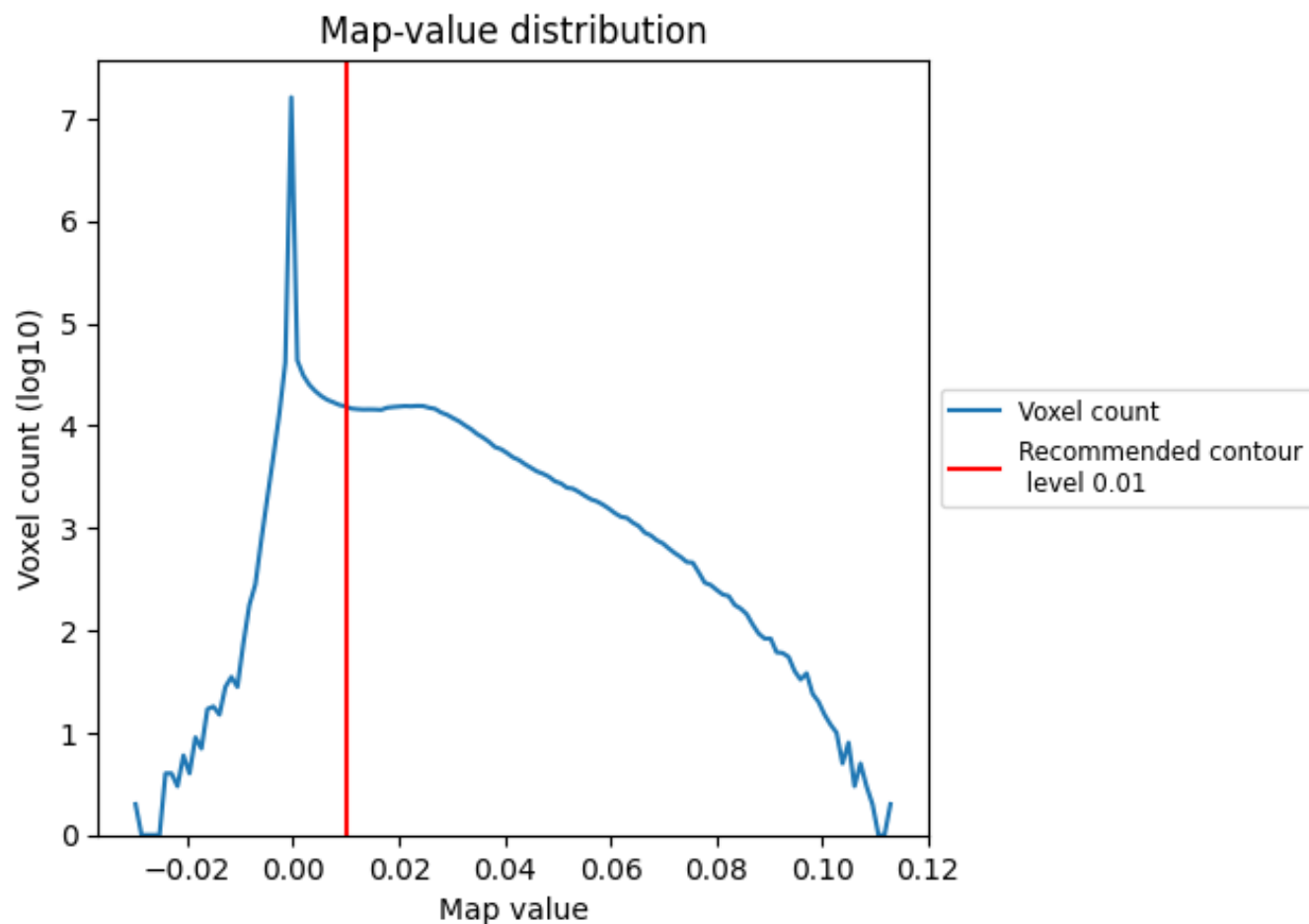
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

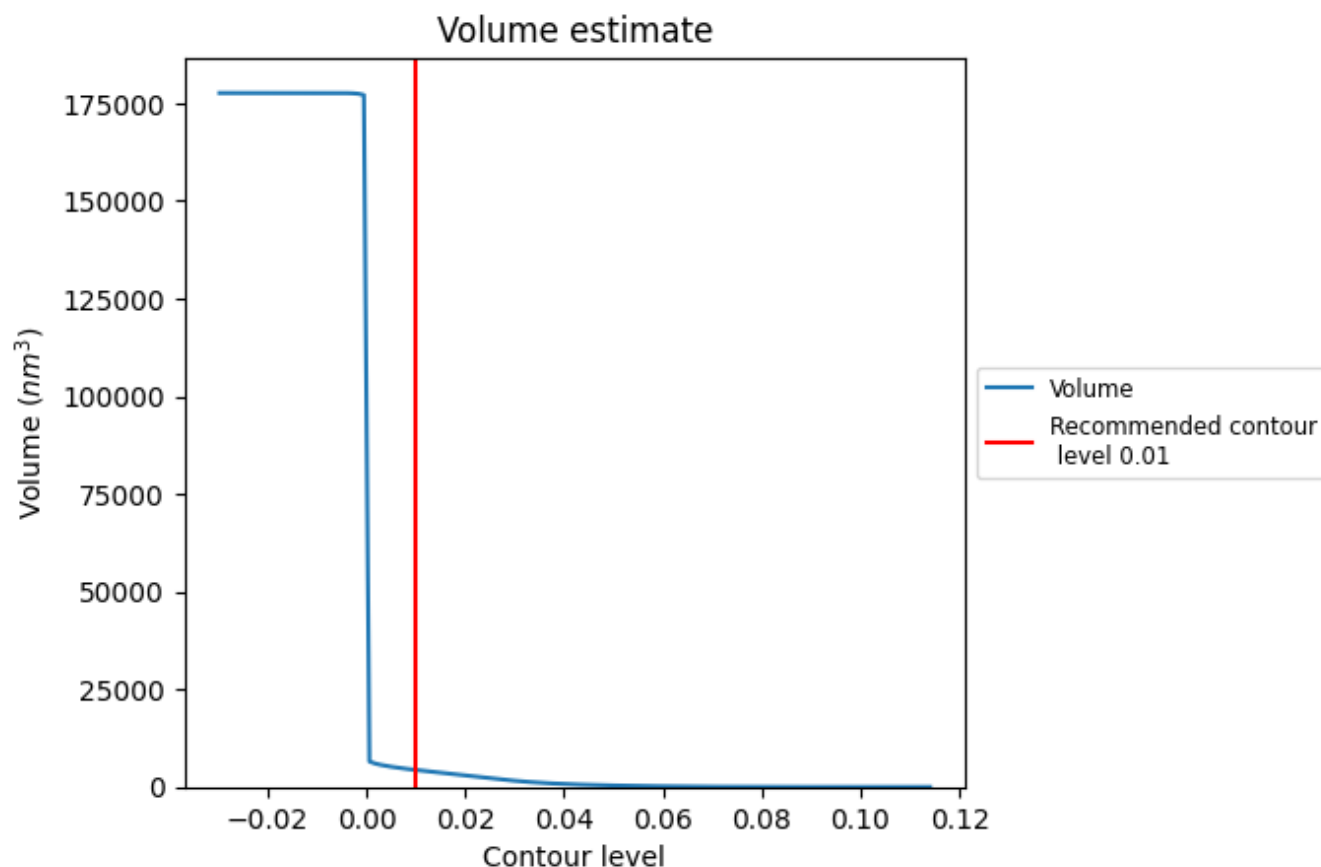
This section contains the results of statistical analysis of the map.

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.

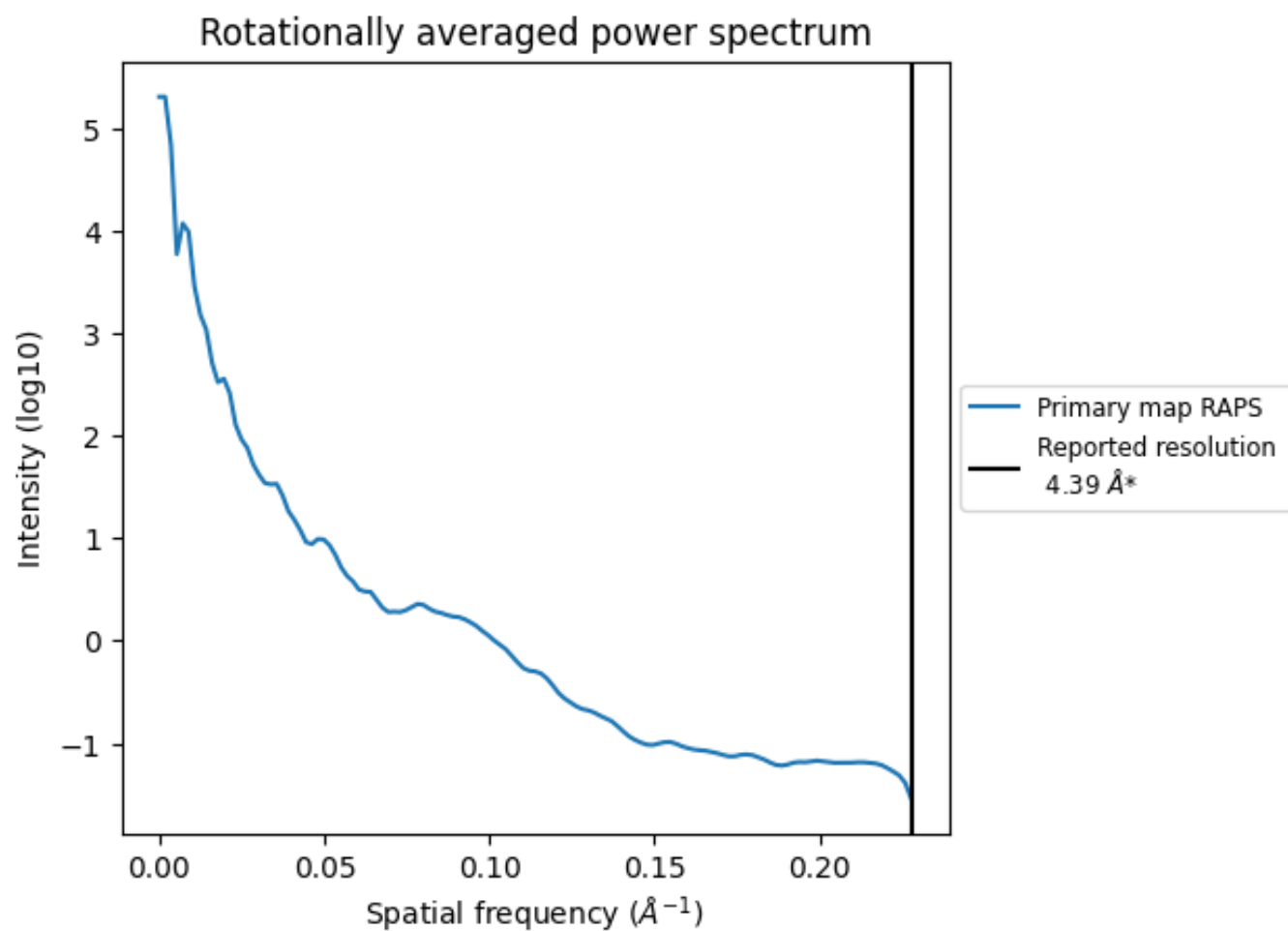
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4345 nm³; this corresponds to an approximate mass of 3925 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 0.228 Å⁻¹

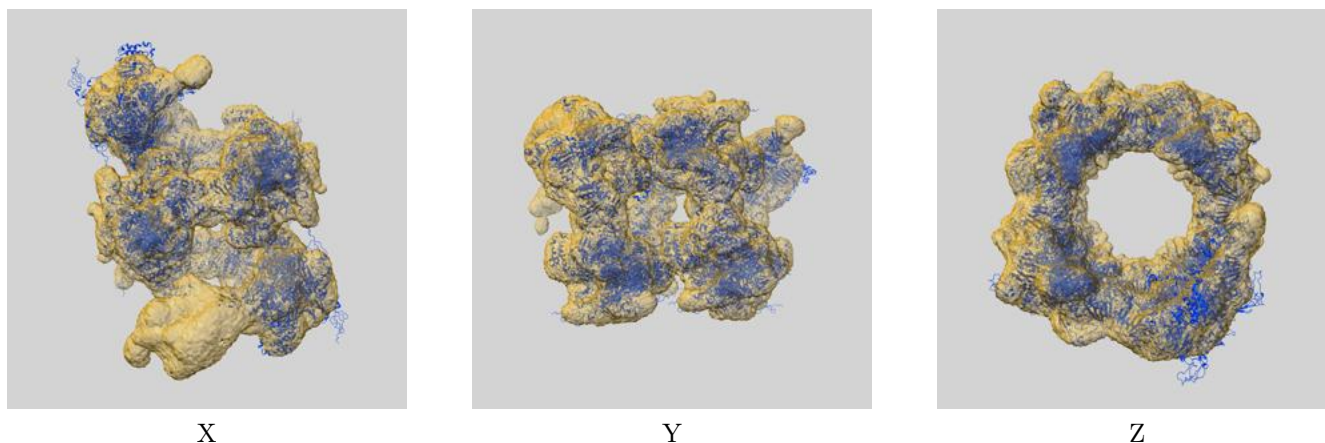
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

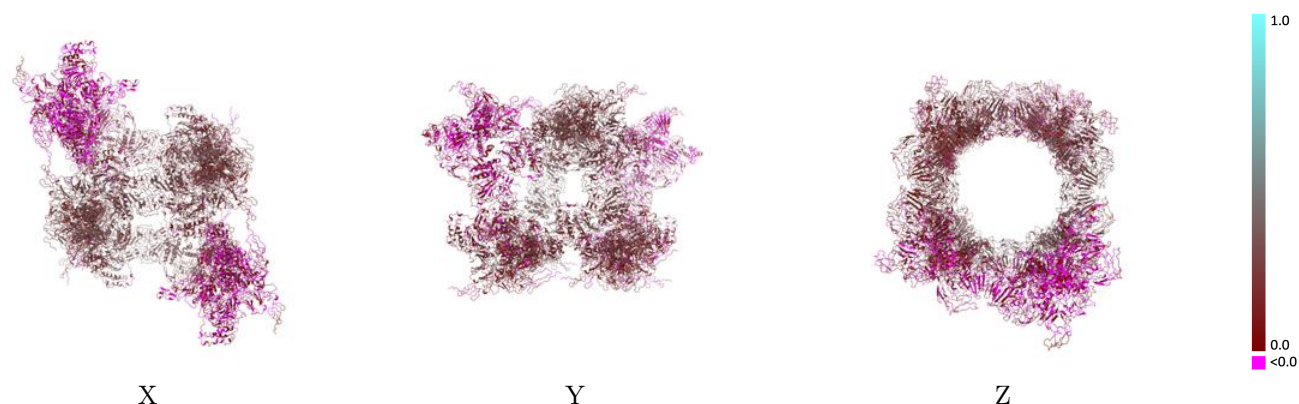
This section contains information regarding the fit between EMDB map EMD-32689 and PDB model 7WPR. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



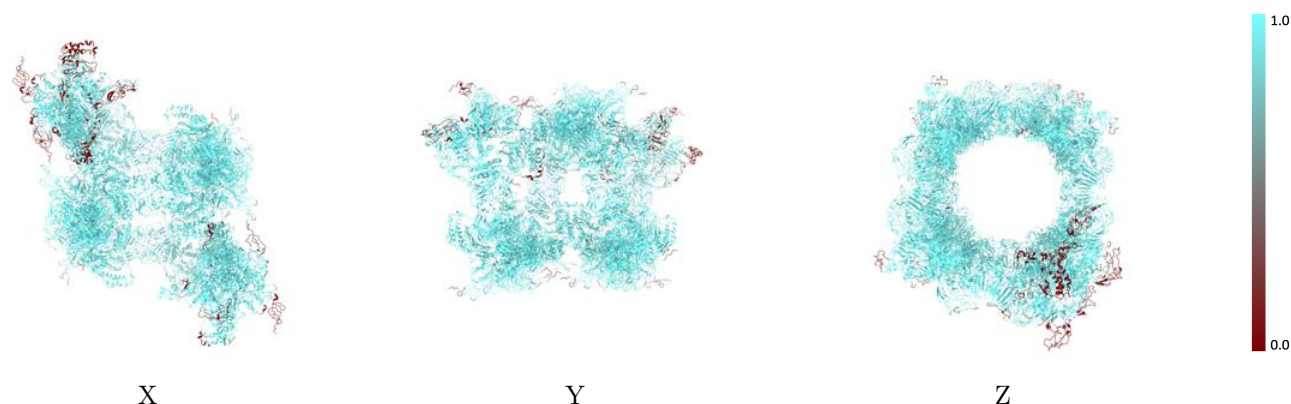
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



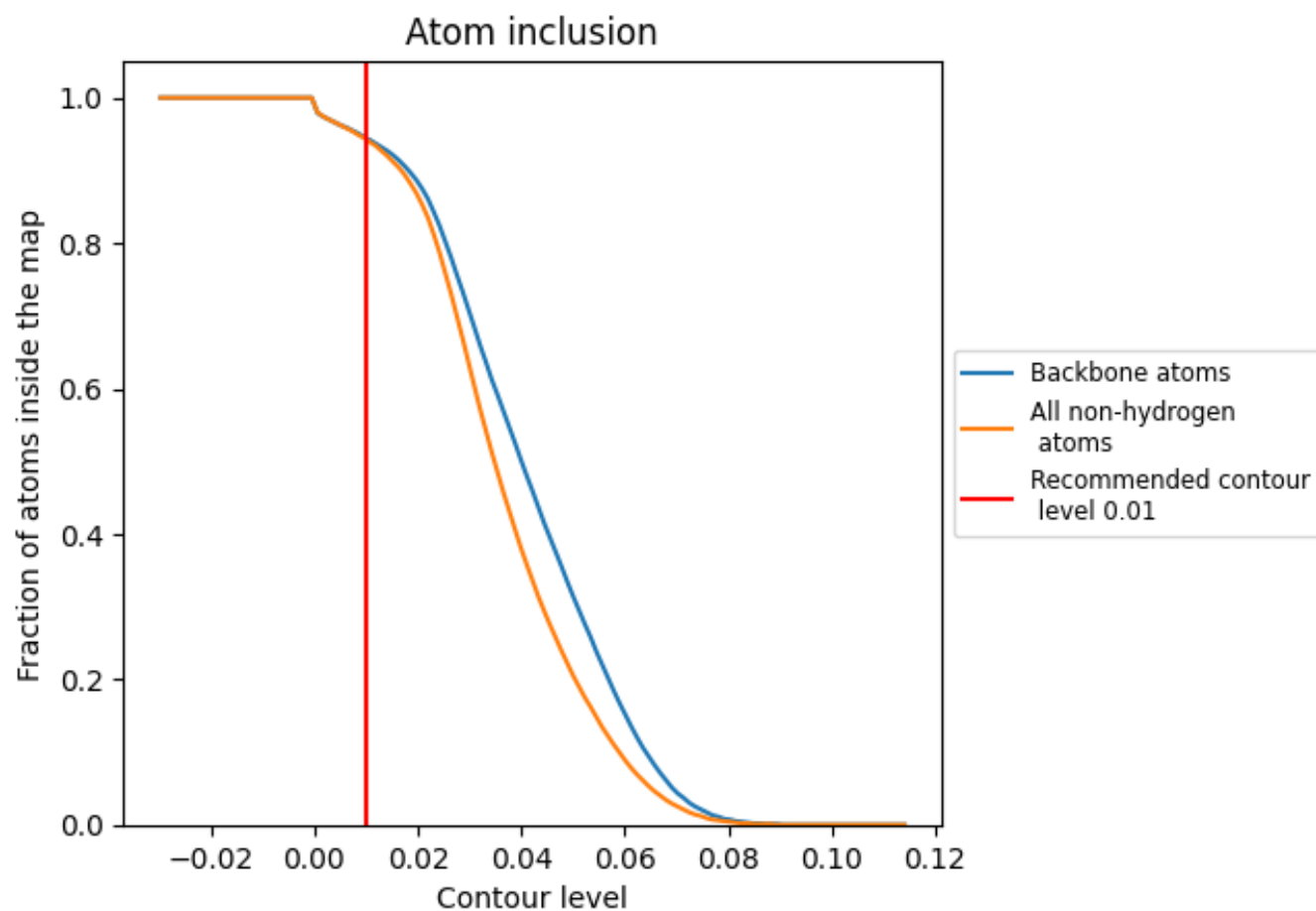
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).



































































9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 94% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9430	 0.1640
A	 0.9990	 0.2860
B	 0.9980	 0.2670
C	 0.9760	 0.2420
D	 0.9760	 0.2300
E	 0.9990	 0.2830
F	 0.9990	 0.2840
G	 0.9990	 0.2460
H	 0.9960	 0.1280
I	 0.9980	 0.2040
J	 0.9000	 0.0440
K	 0.8160	 0.0210
L	 0.9970	 0.2850
M	 0.9990	 0.2630
N	 0.9990	 0.2030
O	 0.9860	 0.0830
P	 0.9970	 0.1410
Q	 0.9640	 0.0600
R	 0.6860	 0.0020
S	 0.9790	 0.2520
T	 0.9720	 0.2380
U	 0.9660	 0.2110
V	 0.9350	 0.1040
W	 0.9670	 0.1760
X	 0.8320	 0.0200
Y	 0.7500	 0.0140
Z	 0.9850	 0.2560
a	 0.9780	 0.2270
b	 0.9660	 0.1720
c	 0.9350	 0.0740
d	 0.9530	 0.1240
e	 0.8500	 0.0270
f	 0.6820	 -0.0060

