



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 07:38 PM UTC

PDB ID : 7WPR / pdb_00007wpr
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 wwPDB EM Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

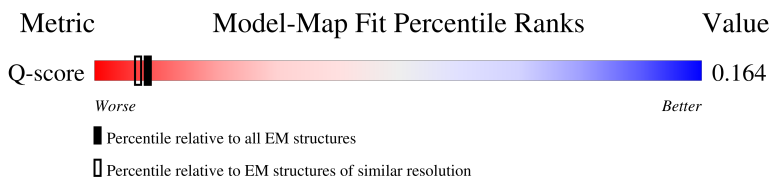
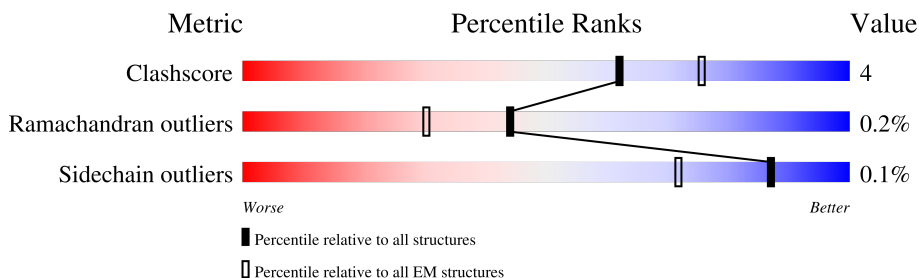
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	3667 (3.89 - 4.88)

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	
1	B	741	
1	E	741	
1	F	741	

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Mol	Chain	Length	Quality of chain
1	G	741	 84% 11% .
1	H	741	 86% 10% .
1	I	741	 84% 11% .
1	J	741	 9% 86% 10% .
1	K	741	 16% 84% 12% .
1	L	741	 85% 11% .
1	M	741	 85% 10% .
1	N	741	 84% 11% .
1	O	741	 82% 13% .
1	P	741	 85% 11% .
1	Q	741	 86% 10% .
1	R	741	 30% 86% 10% .
2	C	490	 89% 9% .
2	D	490	 88% 10% .
2	S	490	 87% 10% .
2	T	490	 88% 10% .
2	U	490	 85% 11% ..
2	V	490	 6% 89% 9% .
2	W	490	 88% 9% ..
2	X	490	 16% 89% 8% .
2	Y	490	 23% 89% 9% .
2	Z	490	 85% 12% ..
2	a	490	 88% 10% .
2	b	490	 88% 10% .
2	c	490	 6% 90% 8% .

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Mol	Chain	Length	Quality of chain
2	d	490	 88% 9%
2	e	490	 14% 89% 9%
2	f	490	 30% 89% 8%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAG	B	801	-	-	X	-

2 Entry composition [i](#)

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

- Molecule 2 is a protein called von Willebrand factor.

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

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
f	1250	HIS	-	expression tag	UNP P04275
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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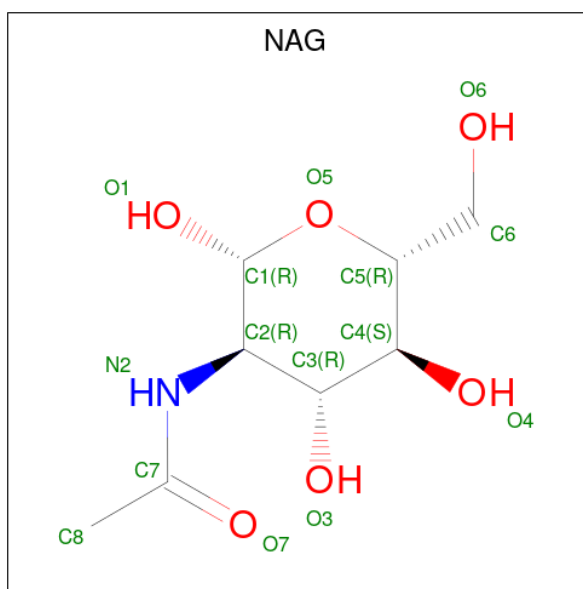
Chain	Residue	Modelled	Actual	Comment	Reference
V	1244	VAL	-	expression tag	UNP P04275
V	1245	VAL	-	expression tag	UNP P04275
V	1246	PRO	-	expression tag	UNP P04275
V	1247	PRO	-	expression tag	UNP P04275
V	1248	HIS	-	expression tag	UNP P04275
V	1249	HIS	-	expression tag	UNP P04275
V	1250	HIS	-	expression 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 (CCD ID: NAG) (formula: C₈H₁₅NO₆) (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
			Total	C	N	O	
3	a	1	Total 14	8	1	5	0
3	B	1	Total 14	8	1	5	0
3	B	1	Total 14	8	1	5	0
3	b	1	Total 14	8	1	5	0
3	b	1	Total 14	8	1	5	0
3	C	1	Total 14	8	1	5	0
3	C	1	Total 14	8	1	5	0
3	D	1	Total 14	8	1	5	0
3	D	1	Total 14	8	1	5	0
3	d	1	Total 14	8	1	5	0
3	E	1	Total 14	8	1	5	0
3	E	1	Total 14	8	1	5	0
3	F	1	Total 14	8	1	5	0
3	F	1	Total 14	8	1	5	0
3	G	1	Total 14	8	1	5	0
3	G	1	Total 14	8	1	5	0
3	I	1	Total 14	8	1	5	0
3	I	1	Total 14	8	1	5	0
3	L	1	Total 14	8	1	5	0
3	L	1	Total 14	8	1	5	0
3	M	1	Total 14	8	1	5	0

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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 (CCD ID: 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

Continued on next page...

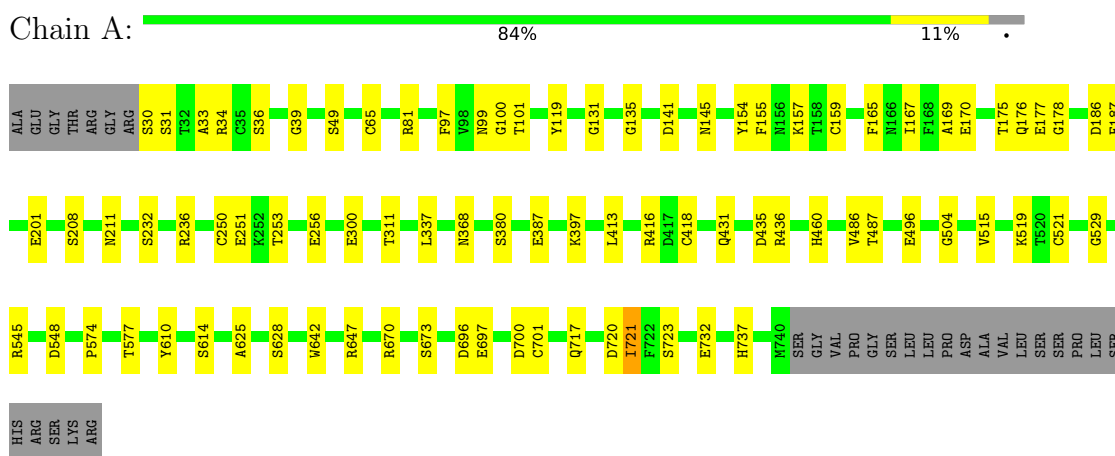
Continued from previous page...

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

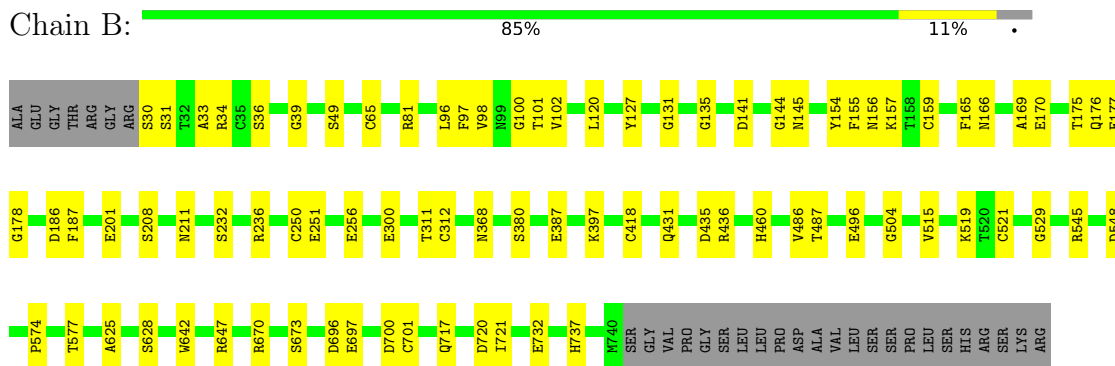
3 Residue-property plots [i](#)

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.

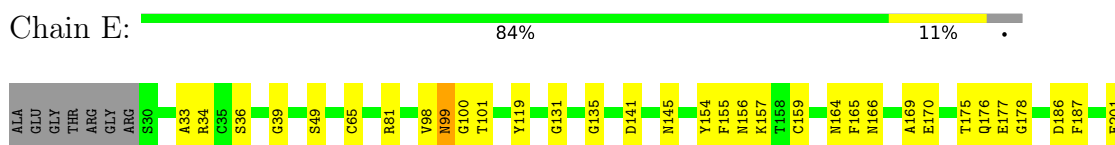
- Molecule 1: von Willebrand antigen 2

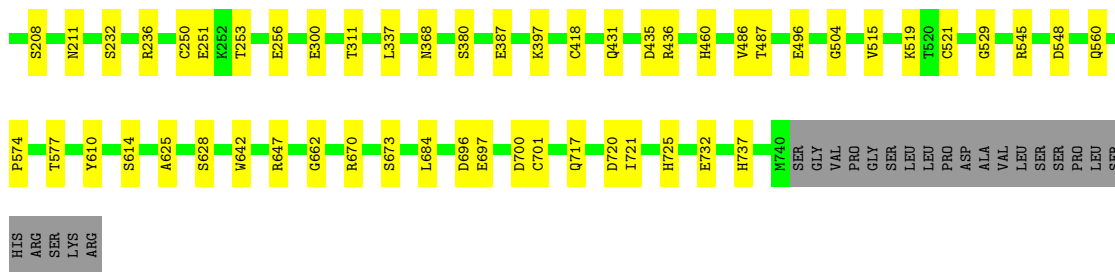


- Molecule 1: von Willebrand antigen 2

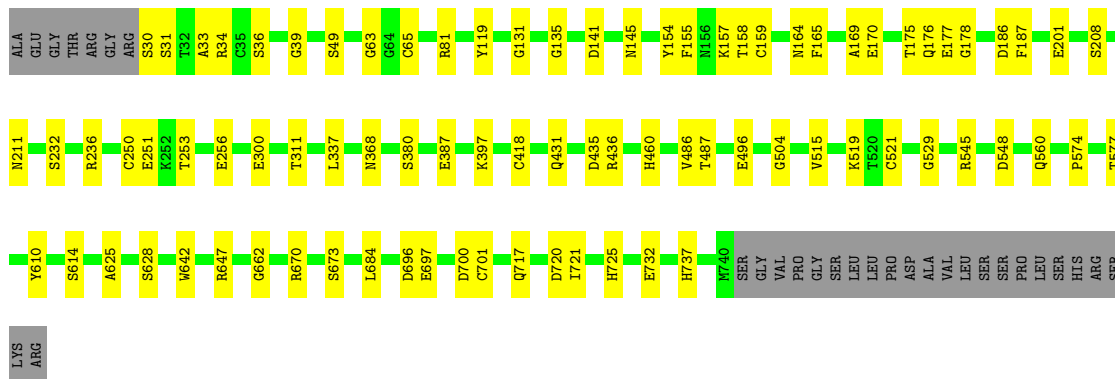
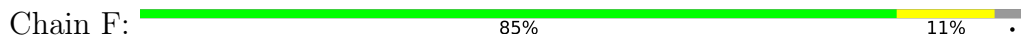


- Molecule 1: von Willebrand antigen 2

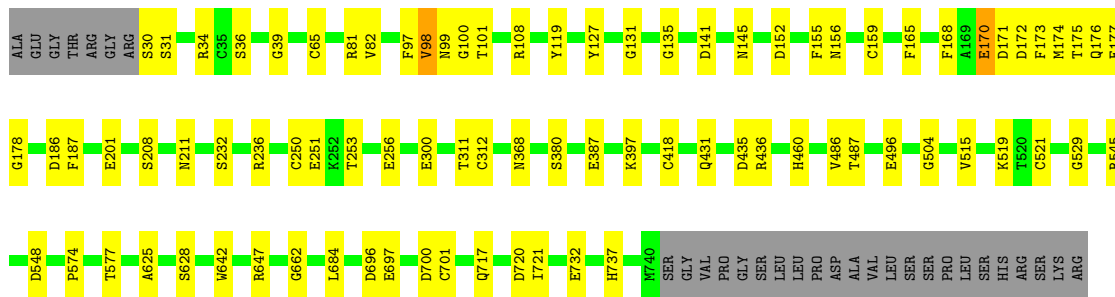
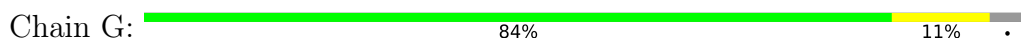




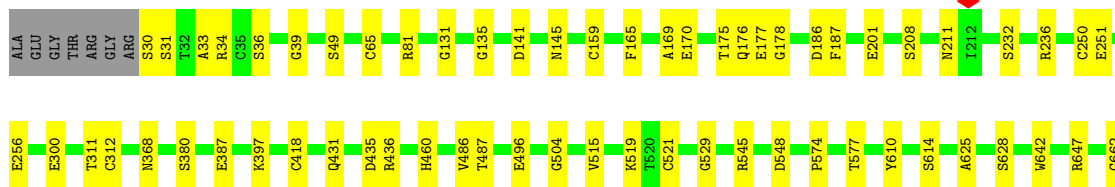
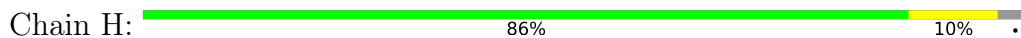
- Molecule 1: von Willebrand antigen 2

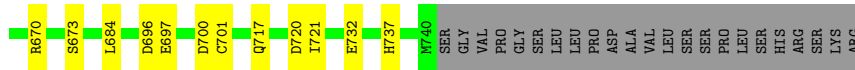


- Molecule 1: von Willebrand antigen 2

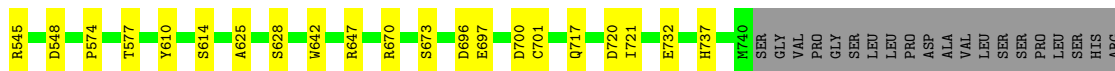
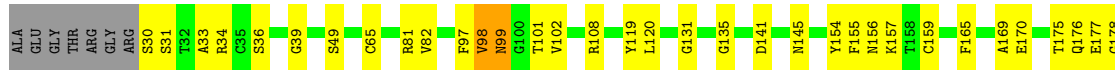
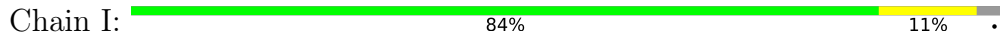


- Molecule 1: von Willebrand antigen 2

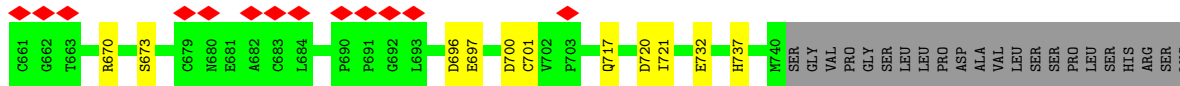
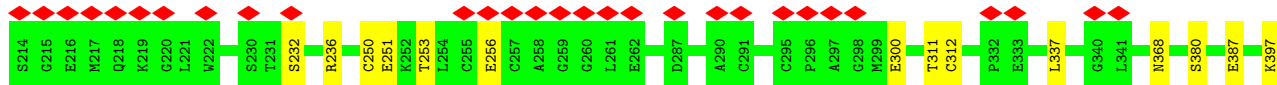
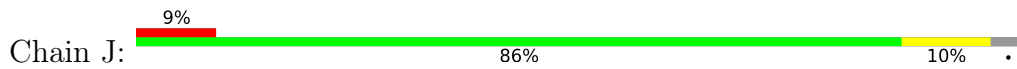




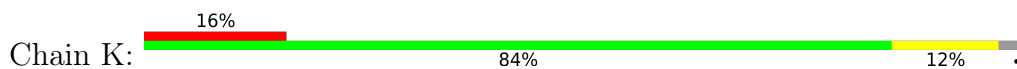
• Molecule 1: von Willebrand antigen 2

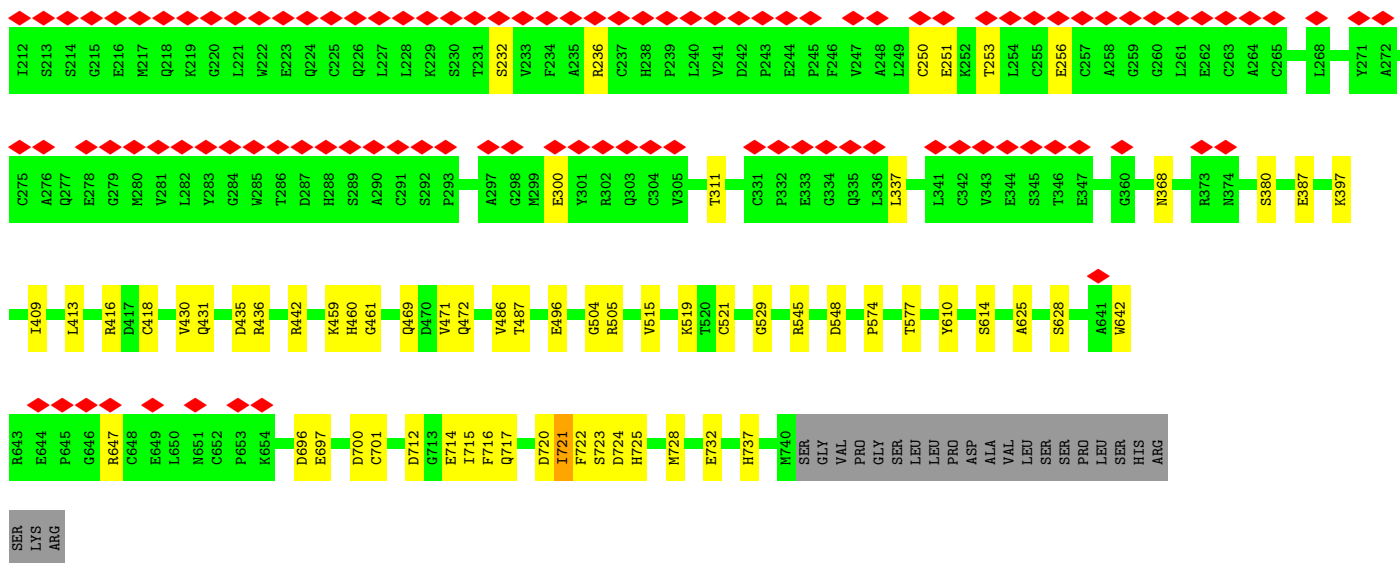


• Molecule 1: von Willebrand antigen 2

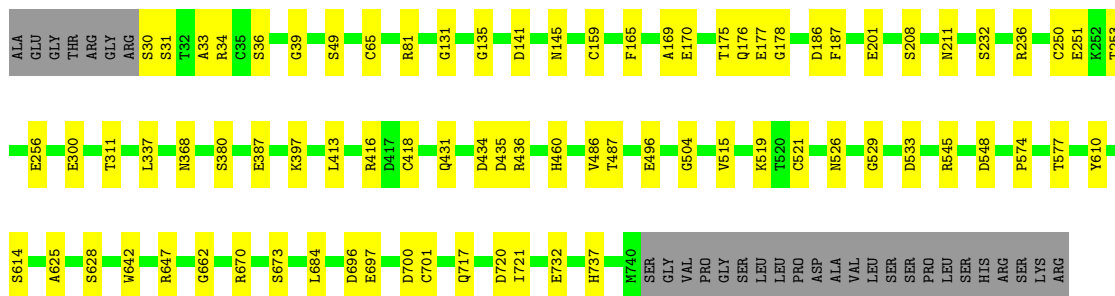
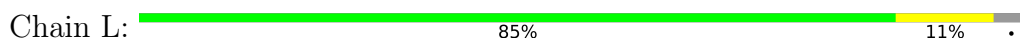


• Molecule 1: von Willebrand antigen 2

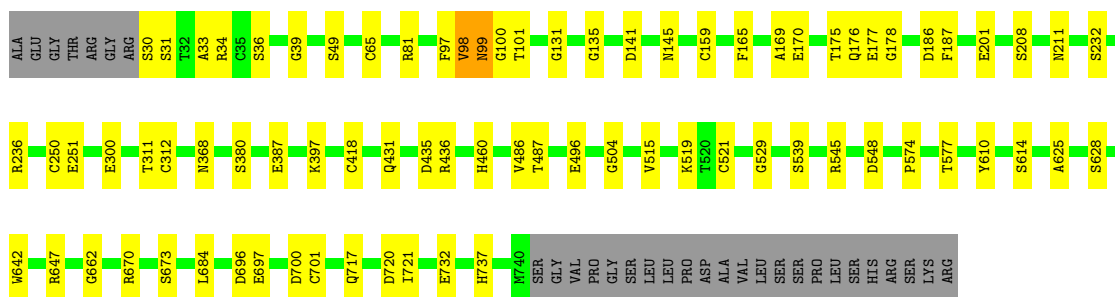
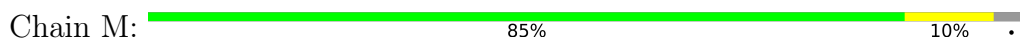




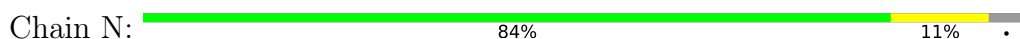
• Molecule 1: von Willebrand antigen 2

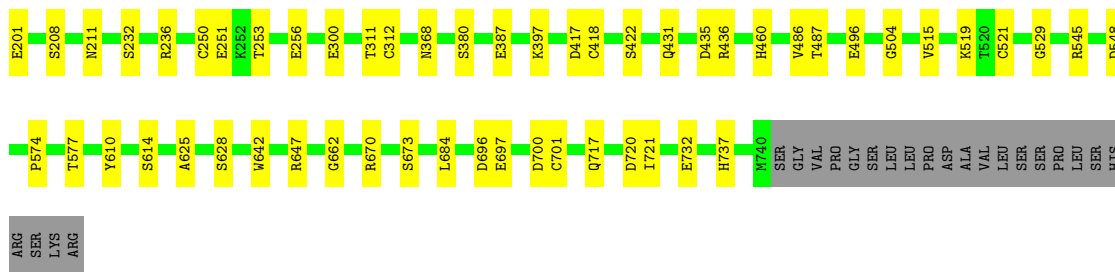


• Molecule 1: von Willebrand antigen 2

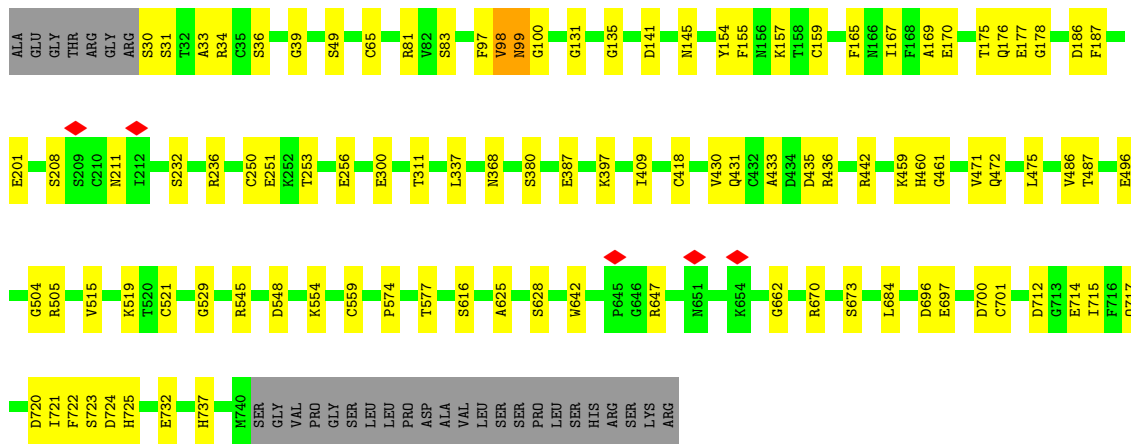
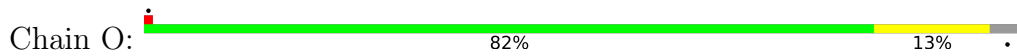


• Molecule 1: von Willebrand antigen 2

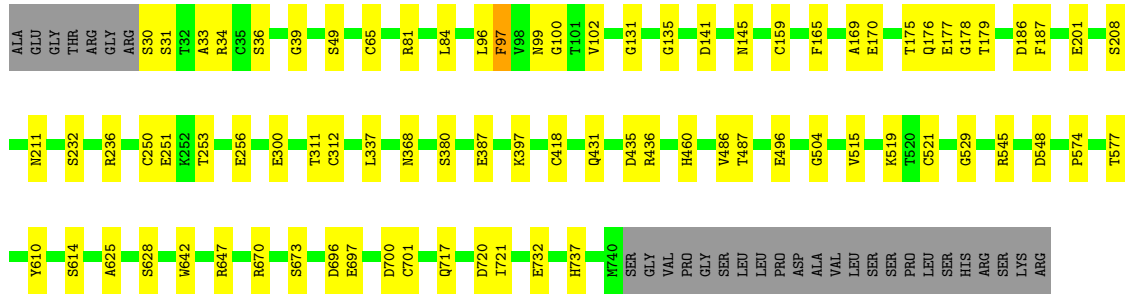
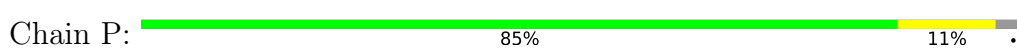




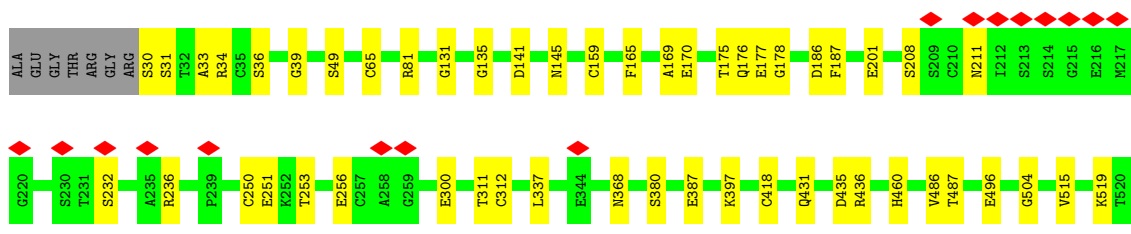
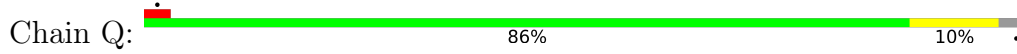
• Molecule 1: von Willebrand antigen 2

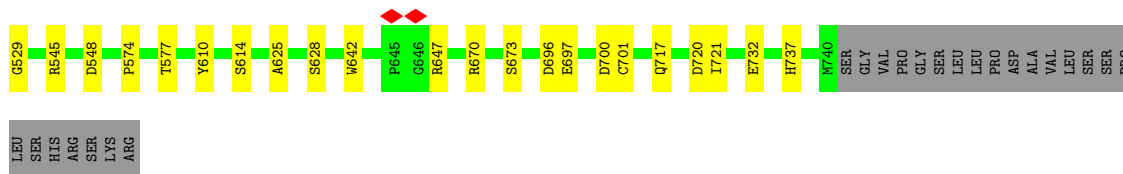


• Molecule 1: von Willebrand antigen 2

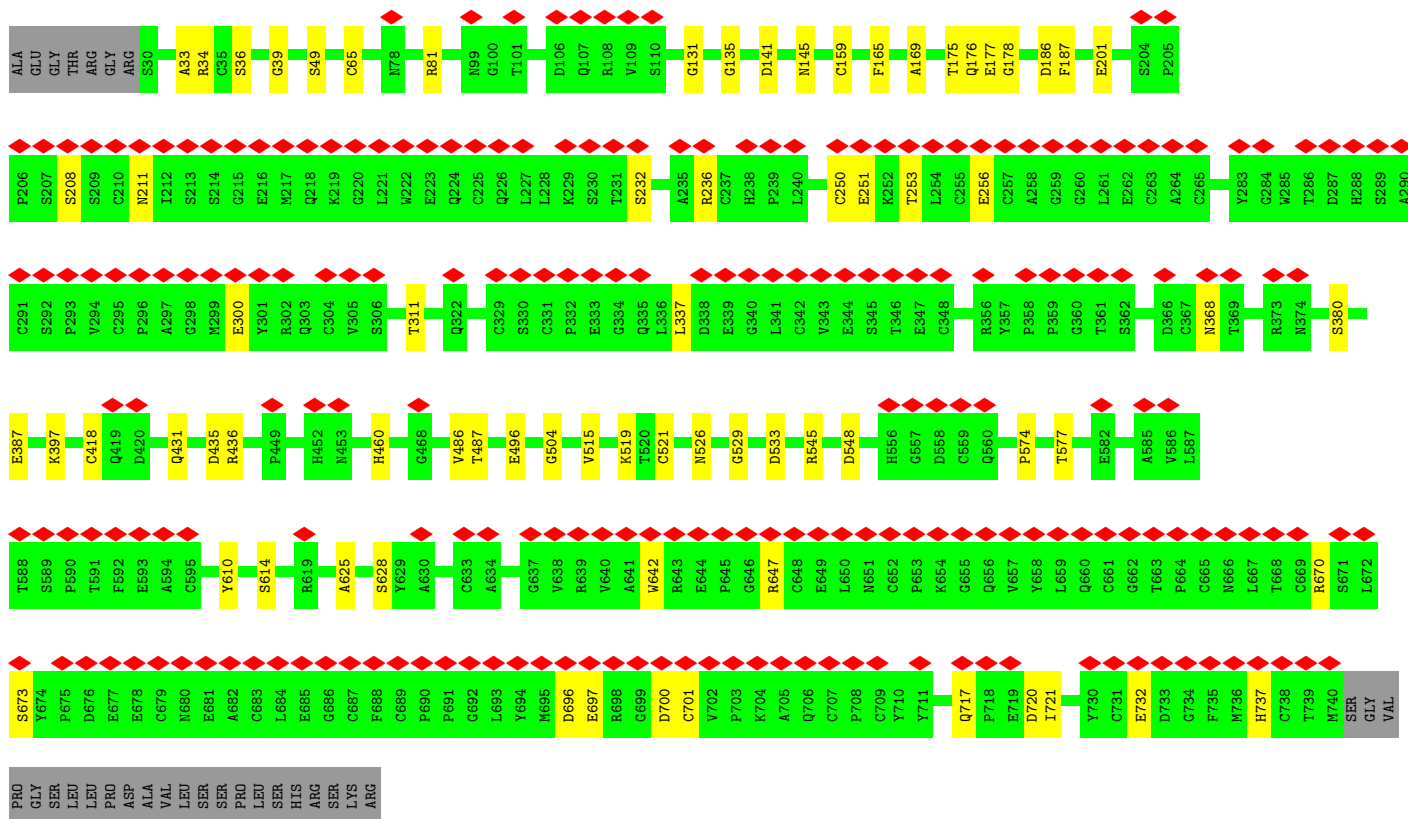
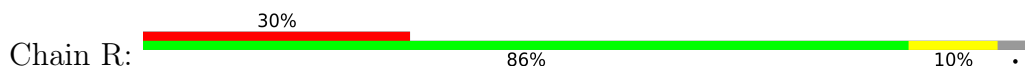


• Molecule 1: von Willebrand antigen 2

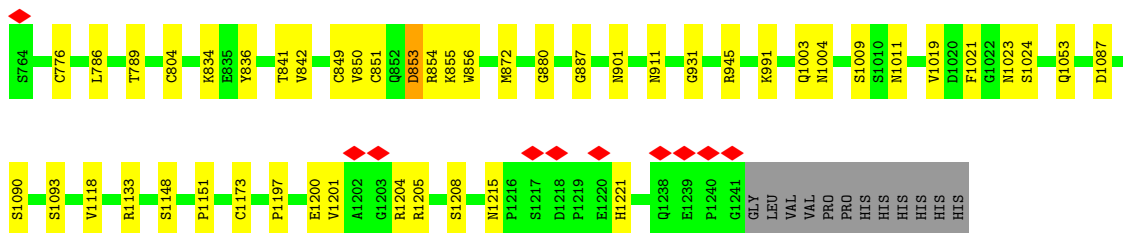
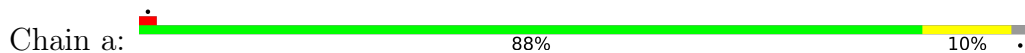




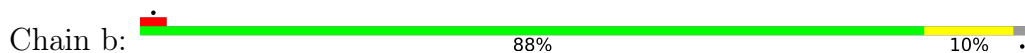
• Molecule 1: von Willebrand antigen 2

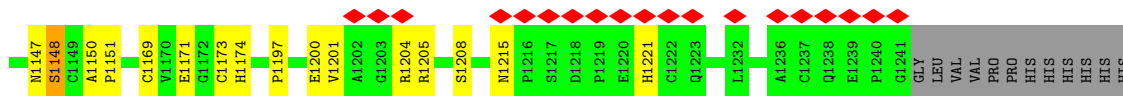


• Molecule 2: von Willebrand factor

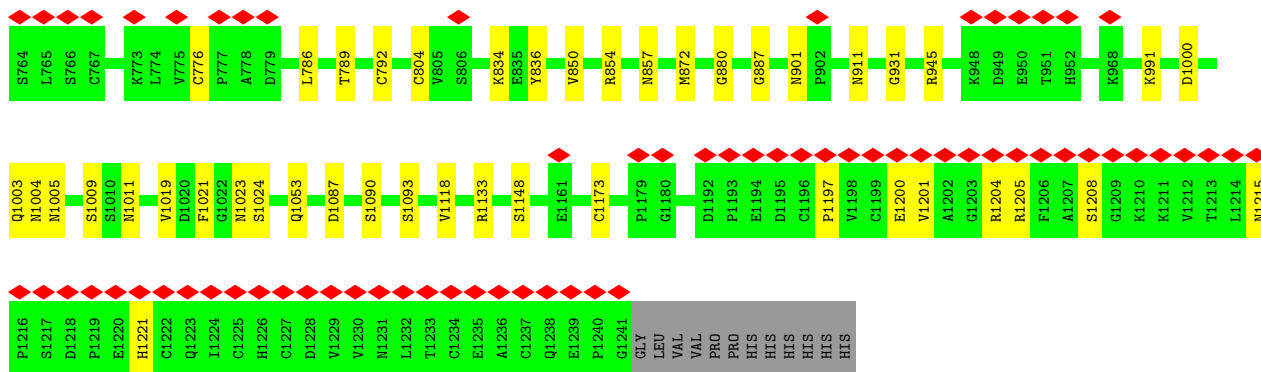
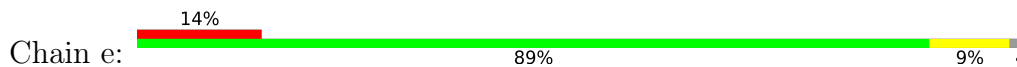


• Molecule 2: von Willebrand factor

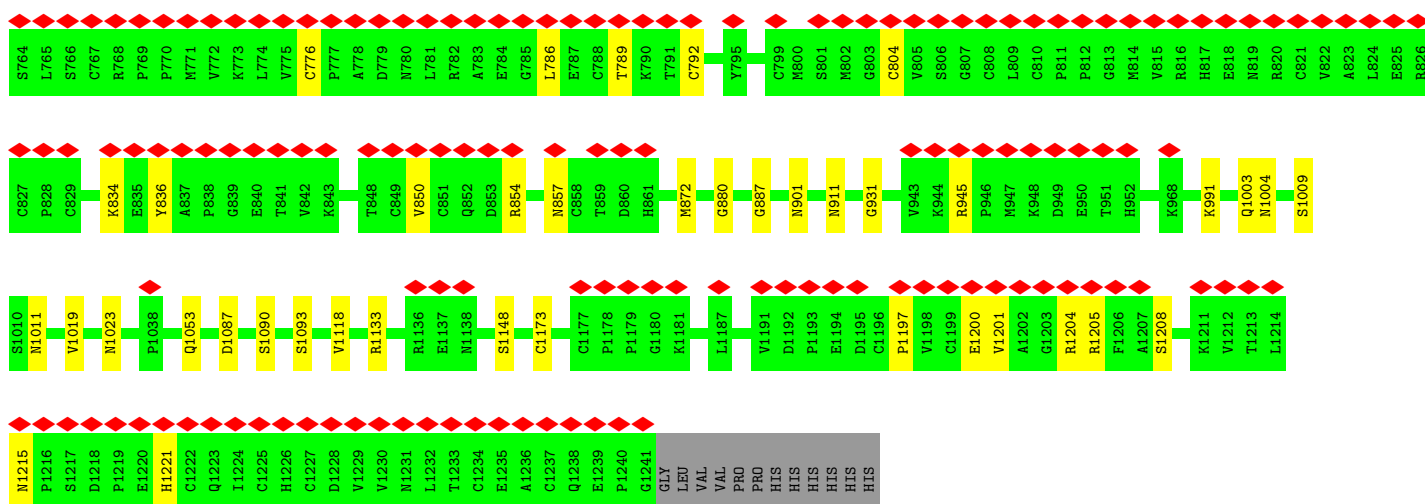
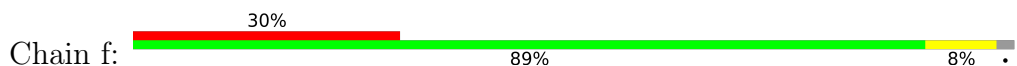




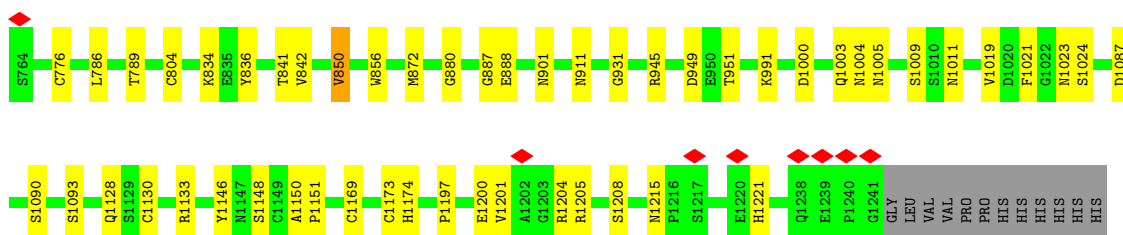
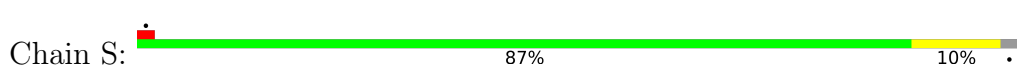
• Molecule 2: von Willebrand factor



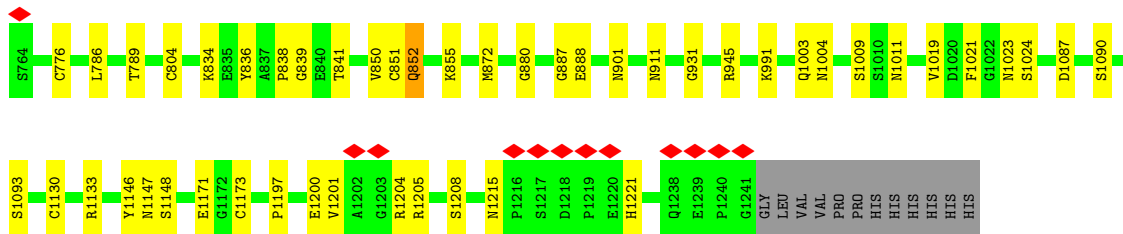
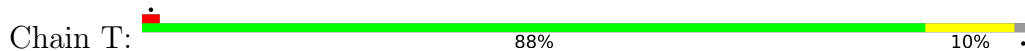
• Molecule 2: von Willebrand factor



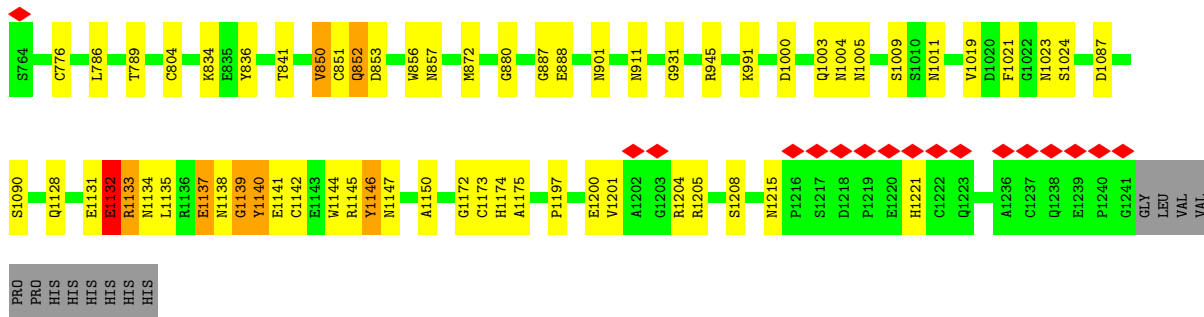
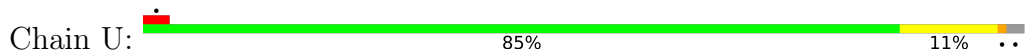
• Molecule 2: von Willebrand factor



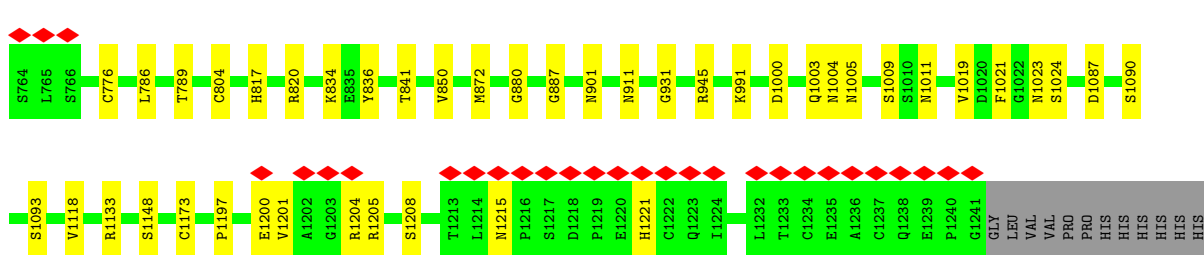
• Molecule 2: von Willebrand factor



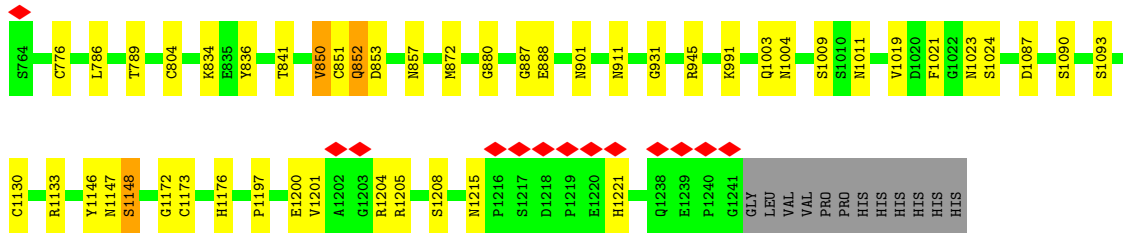
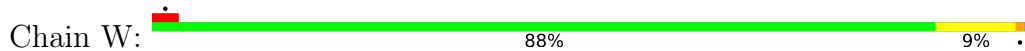
• Molecule 2: von Willebrand factor



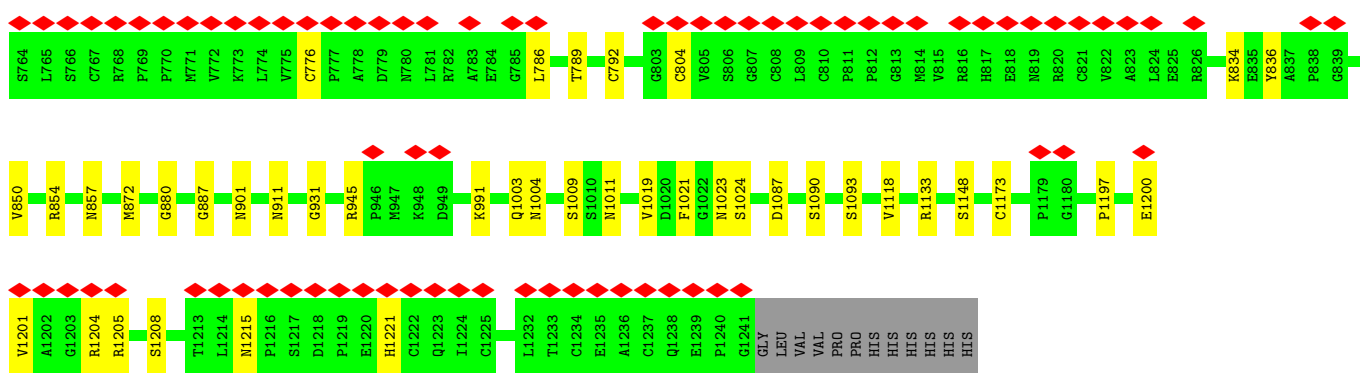
• Molecule 2: von Willebrand factor



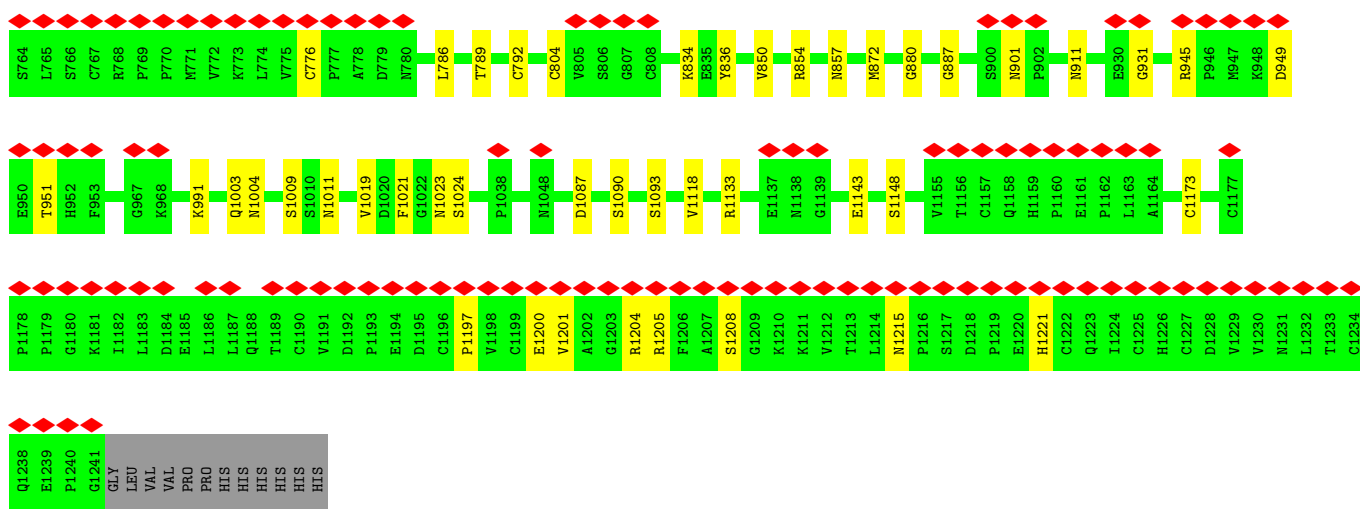
• Molecule 2: von Willebrand factor



• Molecule 2: von Willebrand factor



• Molecule 2: von Willebrand factor



• 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	0.36	0/5547	0.55	0/7520
1	B	0.36	0/5547	0.55	0/7520
1	E	0.36	0/5547	0.55	0/7520
1	F	0.35	0/5547	0.55	0/7520
1	G	0.37	0/5547	0.56	0/7520
1	H	0.35	0/5547	0.54	0/7520
1	I	0.36	0/5547	0.55	0/7520
1	J	0.35	0/5547	0.54	0/7520
1	K	0.35	0/5547	0.54	0/7520
1	L	0.35	0/5547	0.54	0/7520
1	M	0.36	0/5547	0.55	0/7520
1	N	0.36	0/5547	0.55	0/7520
1	O	0.36	0/5547	0.55	0/7520
1	P	0.36	0/5547	0.55	0/7520
1	Q	0.35	0/5547	0.54	0/7520
1	R	0.35	0/5547	0.54	0/7520
2	C	0.32	0/3728	0.51	0/5066
2	D	0.33	0/3728	0.52	0/5066
2	S	0.33	0/3728	0.52	0/5066
2	T	0.33	0/3728	0.51	0/5066
2	U	0.35	0/3728	0.53	0/5066
2	V	0.30	0/3728	0.50	0/5066
2	W	0.32	0/3728	0.51	0/5066
2	X	0.29	0/3728	0.49	0/5066
2	Y	0.29	0/3728	0.49	0/5066
2	Z	0.35	0/3728	0.53	0/5066
2	a	0.33	0/3728	0.51	0/5066
2	b	0.32	0/3728	0.51	0/5066
2	c	0.29	0/3728	0.49	0/5066
2	d	0.31	0/3728	0.50	0/5066
2	e	0.29	0/3728	0.49	0/5066
2	f	0.29	0/3728	0.49	0/5066

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.34	0/148400	0.53	0/201376

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.

There are no bond angle outliers.

There are no chirality outliers.

5 of 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

5.2 Too-close contacts [i](#)

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	5421	0	5000	52	0
1	B	5421	0	5001	59	0
1	E	5421	0	5000	54	0
1	F	5421	0	5000	49	0
1	G	5421	0	5000	56	0
1	H	5421	0	5003	43	0
1	I	5421	0	5001	50	0
1	J	5421	0	5003	42	0
1	K	5421	0	5003	105	0
1	L	5421	0	5000	45	0
1	M	5421	0	5001	47	0
1	N	5421	0	5001	49	0
1	O	5421	0	5001	115	0
1	P	5421	0	5001	48	0
1	Q	5421	0	5003	42	0
1	R	5421	0	5003	40	0
2	C	3649	0	3442	24	0
2	D	3649	0	3442	31	0
2	S	3649	0	3441	28	0
2	T	3649	0	3442	28	0
2	U	3649	0	3443	48	0
2	V	3649	0	3443	23	0
2	W	3649	0	3442	31	0
2	X	3649	0	3444	22	0
2	Y	3649	0	3444	24	0
2	Z	3649	0	3442	40	0
2	a	3649	0	3442	33	0
2	b	3649	0	3443	28	0
2	c	3649	0	3444	21	0
2	d	3649	0	3443	26	0
2	e	3649	0	3444	24	0
2	f	3649	0	3444	22	0
3	A	28	0	26	0	0
3	B	28	0	26	11	0
3	C	28	0	26	0	0
3	D	28	0	26	0	0
3	E	28	0	26	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	28	0	26	0	0
3	G	28	0	26	1	0
3	I	28	0	26	0	0
3	L	28	0	26	0	0
3	M	28	0	26	1	0
3	N	28	0	26	0	0
3	O	28	0	26	0	0
3	P	28	0	26	0	0
3	S	28	0	26	0	0
3	T	28	0	26	0	0
3	U	28	0	26	0	0
3	V	14	0	13	0	0
3	W	28	0	26	2	0
3	Z	28	0	26	0	0
3	a	28	0	26	6	0
3	b	28	0	26	0	0
3	d	14	0	13	0	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
4	D	1	0	0	0	0
4	E	2	0	0	0	0
4	F	2	0	0	0	0
4	G	2	0	0	0	0
4	H	2	0	0	0	0
4	I	2	0	0	0	0
4	J	2	0	0	0	0
4	K	2	0	0	0	0
4	L	2	0	0	0	0
4	M	2	0	0	0	0
4	N	2	0	0	0	0
4	O	2	0	0	0	0
4	P	2	0	0	0	0
4	Q	2	0	0	0	0
4	R	2	0	0	0	0
4	S	2	0	0	0	0
4	T	2	0	0	0	0
4	U	2	0	0	0	0
4	V	2	0	0	0	0
4	W	2	0	0	0	0
4	X	2	0	0	0	0
4	Y	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	Z	1	0	0	0	0
4	a	1	0	0	0	0
4	b	1	0	0	0	0
4	c	1	0	0	0	0
4	d	1	0	0	0	0
4	e	1	0	0	0	0
4	f	1	0	0	0	0
All	All	145764	0	135652	1215	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 4.

The worst 5 of 1215 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)
2:a:1151:PRO:CD	3:a:1302:NAG:H62	1.79	1.12
1:K:723:SER:O	1:O:431:GLN:N	1.86	1.08
2:a:1151:PRO:HD3	3:a:1302:NAG:H62	1.32	1.06
1:B:101:THR:CG2	3:B:801:NAG:H82	1.88	1.03
1:B:101:THR:HG21	3:B:801:NAG:N2	1.75	1.02

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	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 66
1	F	709/741 (96%)	646 (91%)	63 (9%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	709/741 (96%)	638 (90%)	68 (10%)	3 (0%)	30	66
1	H	709/741 (96%)	646 (91%)	63 (9%)	0	100	100
1	I	709/741 (96%)	643 (91%)	64 (9%)	2 (0%)	36	71
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%)	36	71
1	N	709/741 (96%)	643 (91%)	65 (9%)	1 (0%)	48	83
1	O	709/741 (96%)	644 (91%)	63 (9%)	2 (0%)	36	71
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%)	43	77
2	S	477/490 (97%)	425 (89%)	51 (11%)	1 (0%)	43	77
2	T	477/490 (97%)	425 (89%)	52 (11%)	0	100	100
2	U	477/490 (97%)	415 (87%)	55 (12%)	7 (2%)	8	38
2	V	477/490 (97%)	427 (90%)	50 (10%)	0	100	100
2	W	477/490 (97%)	426 (89%)	50 (10%)	1 (0%)	43	77
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	66
2	a	477/490 (97%)	427 (90%)	49 (10%)	1 (0%)	43	77
2	b	477/490 (97%)	425 (89%)	51 (11%)	1 (0%)	43	77
2	c	477/490 (97%)	425 (89%)	52 (11%)	0	100	100
2	d	477/490 (97%)	424 (89%)	52 (11%)	1 (0%)	43	77
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%)	44	77

5 of 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

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	599/628 (95%)	599 (100%)	0	100	100
1	B	599/628 (95%)	598 (100%)	1 (0%)	87	85
1	E	599/628 (95%)	599 (100%)	0	100	100
1	F	599/628 (95%)	599 (100%)	0	100	100
1	G	599/628 (95%)	599 (100%)	0	100	100
1	H	599/628 (95%)	599 (100%)	0	100	100
1	I	599/628 (95%)	598 (100%)	1 (0%)	87	85
1	J	599/628 (95%)	599 (100%)	0	100	100
1	K	599/628 (95%)	599 (100%)	0	100	100
1	L	599/628 (95%)	599 (100%)	0	100	100
1	M	599/628 (95%)	599 (100%)	0	100	100
1	N	599/628 (95%)	599 (100%)	0	100	100
1	O	599/628 (95%)	599 (100%)	0	100	100
1	P	599/628 (95%)	598 (100%)	1 (0%)	87	85
1	Q	599/628 (95%)	599 (100%)	0	100	100
1	R	599/628 (95%)	599 (100%)	0	100	100
2	C	423/436 (97%)	423 (100%)	0	100	100
2	D	423/436 (97%)	423 (100%)	0	100	100
2	S	423/436 (97%)	422 (100%)	1 (0%)	87	85
2	T	423/436 (97%)	422 (100%)	1 (0%)	87	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	U	423/436 (97%)	420 (99%)	3 (1%)	76	79
2	V	423/436 (97%)	423 (100%)	0	100	100
2	W	423/436 (97%)	421 (100%)	2 (0%)	81	81
2	X	423/436 (97%)	423 (100%)	0	100	100
2	Y	423/436 (97%)	423 (100%)	0	100	100
2	Z	423/436 (97%)	422 (100%)	1 (0%)	87	85
2	a	423/436 (97%)	423 (100%)	0	100	100
2	b	423/436 (97%)	423 (100%)	0	100	100
2	c	423/436 (97%)	423 (100%)	0	100	100
2	d	423/436 (97%)	423 (100%)	0	100	100
2	e	423/436 (97%)	423 (100%)	0	100	100
2	f	423/436 (97%)	423 (100%)	0	100	100
All	All	16352/17024 (96%)	16341 (100%)	11 (0%)	87	88

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	U	1140	TYR
2	W	850	VAL
2	Z	1135	LEU
2	W	852	GLN
2	T	852	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 114 such sidechains are listed below:

Mol	Chain	Res	Type
1	M	368	ASN
2	Z	916	HIS
2	S	1109	HIS
2	Z	780	ASN
2	X	916	HIS

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	A	802	1	14,14,15	0.27	0	17,19,21	0.63	0
3	NAG	I	802	1	14,14,15	0.39	0	17,19,21	0.75	0
3	NAG	b	1301	2	14,14,15	0.39	0	17,19,21	0.75	0
3	NAG	M	801	1	14,14,15	0.40	0	17,19,21	0.76	0
3	NAG	d	1301	2	14,14,15	0.40	0	17,19,21	0.76	0
3	NAG	D	1301	2	14,14,15	0.39	0	17,19,21	0.76	0
3	NAG	F	801	1	14,14,15	0.39	0	17,19,21	0.76	0
3	NAG	C	1302	2	14,14,15	0.39	0	17,19,21	0.76	0
3	NAG	a	1302	2	14,14,15	0.41	0	17,19,21	0.75	0
3	NAG	O	802	1	14,14,15	0.41	0	17,19,21	0.76	0
3	NAG	U	1303	2	14,14,15	0.42	0	17,19,21	0.75	0
3	NAG	C	1301	2	14,14,15	0.40	0	17,19,21	0.75	0
3	NAG	L	802	1	14,14,15	0.42	0	17,19,21	0.76	0
3	NAG	V	1301	2	14,14,15	0.42	0	17,19,21	0.76	0
3	NAG	a	1301	2	14,14,15	0.27	0	17,19,21	0.68	0
3	NAG	U	1302	2	14,14,15	0.40	0	17,19,21	0.76	0
3	NAG	T	1302	2	14,14,15	0.40	0	17,19,21	0.75	0
3	NAG	Z	1302	2	14,14,15	0.40	0	17,19,21	0.75	0
3	NAG	E	802	1	14,14,15	0.40	0	17,19,21	0.75	0
3	NAG	T	1301	2	14,14,15	0.29	0	17,19,21	0.56	0
3	NAG	Z	1301	2	14,14,15	0.28	0	17,19,21	0.62	0
3	NAG	S	1302	2	14,14,15	0.39	0	17,19,21	0.76	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	N	801	1	14,14,15	0.40	0	17,19,21	0.75	0
3	NAG	P	802	1	14,14,15	0.39	0	17,19,21	0.75	0
3	NAG	B	801	1	14,14,15	0.40	0	17,19,21	0.75	0
3	NAG	O	801	1	14,14,15	0.39	0	17,19,21	0.76	0
3	NAG	S	1301	2	14,14,15	0.40	0	17,19,21	0.76	0
3	NAG	W	1301	2	14,14,15	0.41	0	17,19,21	0.75	0
3	NAG	I	801	1	14,14,15	0.37	0	17,19,21	0.76	0
3	NAG	N	804	1	14,14,15	0.40	0	17,19,21	0.75	0
3	NAG	A	801	1	14,14,15	0.40	0	17,19,21	0.75	0
3	NAG	D	1302	2	14,14,15	0.39	0	17,19,21	0.76	0
3	NAG	B	802	1	14,14,15	0.29	0	17,19,21	0.63	0
3	NAG	G	801	1	14,14,15	0.41	0	17,19,21	0.75	0
3	NAG	L	801	1	14,14,15	0.42	0	17,19,21	0.75	0
3	NAG	M	802	1	14,14,15	0.40	0	17,19,21	0.76	0
3	NAG	G	802	1	14,14,15	0.40	0	17,19,21	0.76	0
3	NAG	E	801	1	14,14,15	0.30	0	17,19,21	0.62	0
3	NAG	F	802	1	14,14,15	0.39	0	17,19,21	0.76	0
3	NAG	W	1302	2	14,14,15	0.40	0	17,19,21	0.75	0
3	NAG	P	801	1	14,14,15	0.39	0	17,19,21	0.75	0
3	NAG	b	1302	2	14,14,15	0.40	0	17,19,21	0.76	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	A	802	1	-	2/6/23/26	0/1/1/1
3	NAG	I	802	1	-	1/6/23/26	0/1/1/1
3	NAG	b	1301	2	-	1/6/23/26	0/1/1/1
3	NAG	M	801	1	-	1/6/23/26	0/1/1/1
3	NAG	d	1301	2	-	1/6/23/26	0/1/1/1
3	NAG	D	1301	2	-	1/6/23/26	0/1/1/1
3	NAG	F	801	1	-	1/6/23/26	0/1/1/1
3	NAG	C	1302	2	-	1/6/23/26	0/1/1/1
3	NAG	a	1302	2	-	1/6/23/26	0/1/1/1
3	NAG	O	802	1	-	1/6/23/26	0/1/1/1
3	NAG	U	1303	2	-	1/6/23/26	0/1/1/1
3	NAG	C	1301	2	-	1/6/23/26	0/1/1/1
3	NAG	L	802	1	-	1/6/23/26	0/1/1/1
3	NAG	V	1301	2	-	1/6/23/26	0/1/1/1
3	NAG	a	1301	2	-	3/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	U	1302	2	-	1/6/23/26	0/1/1/1
3	NAG	T	1302	2	-	1/6/23/26	0/1/1/1
3	NAG	Z	1302	2	-	1/6/23/26	0/1/1/1
3	NAG	E	802	1	-	1/6/23/26	0/1/1/1
3	NAG	T	1301	2	-	1/6/23/26	0/1/1/1
3	NAG	Z	1301	2	-	0/6/23/26	0/1/1/1
3	NAG	S	1302	2	-	1/6/23/26	0/1/1/1
3	NAG	N	801	1	-	1/6/23/26	0/1/1/1
3	NAG	P	802	1	-	1/6/23/26	0/1/1/1
3	NAG	B	801	1	-	1/6/23/26	0/1/1/1
3	NAG	O	801	1	-	1/6/23/26	0/1/1/1
3	NAG	S	1301	2	-	1/6/23/26	0/1/1/1
3	NAG	W	1301	2	-	1/6/23/26	0/1/1/1
3	NAG	I	801	1	-	1/6/23/26	0/1/1/1
3	NAG	N	804	1	-	1/6/23/26	0/1/1/1
3	NAG	A	801	1	-	1/6/23/26	0/1/1/1
3	NAG	D	1302	2	-	1/6/23/26	0/1/1/1
3	NAG	B	802	1	-	2/6/23/26	0/1/1/1
3	NAG	G	801	1	-	1/6/23/26	0/1/1/1
3	NAG	L	801	1	-	1/6/23/26	0/1/1/1
3	NAG	M	802	1	-	1/6/23/26	0/1/1/1
3	NAG	G	802	1	-	1/6/23/26	0/1/1/1
3	NAG	E	801	1	-	3/6/23/26	0/1/1/1
3	NAG	F	802	1	-	1/6/23/26	0/1/1/1
3	NAG	W	1302	2	-	1/6/23/26	0/1/1/1
3	NAG	P	801	1	-	1/6/23/26	0/1/1/1
3	NAG	b	1302	2	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 47 torsion outliers are listed below:

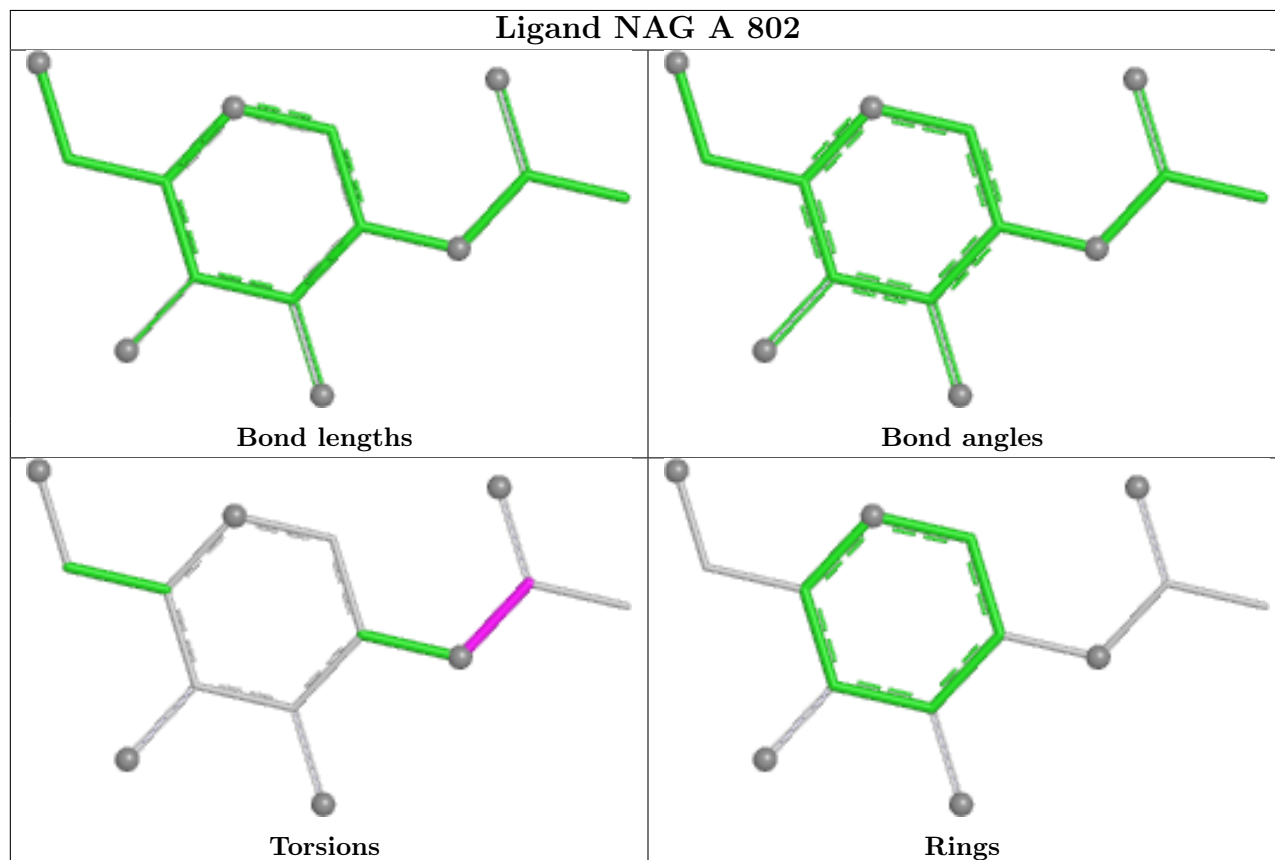
Mol	Chain	Res	Type	Atoms
3	a	1301	NAG	C3-C2-N2-C7
3	a	1301	NAG	C8-C7-N2-C2
3	a	1301	NAG	O7-C7-N2-C2
3	E	801	NAG	C8-C7-N2-C2
3	E	801	NAG	O7-C7-N2-C2

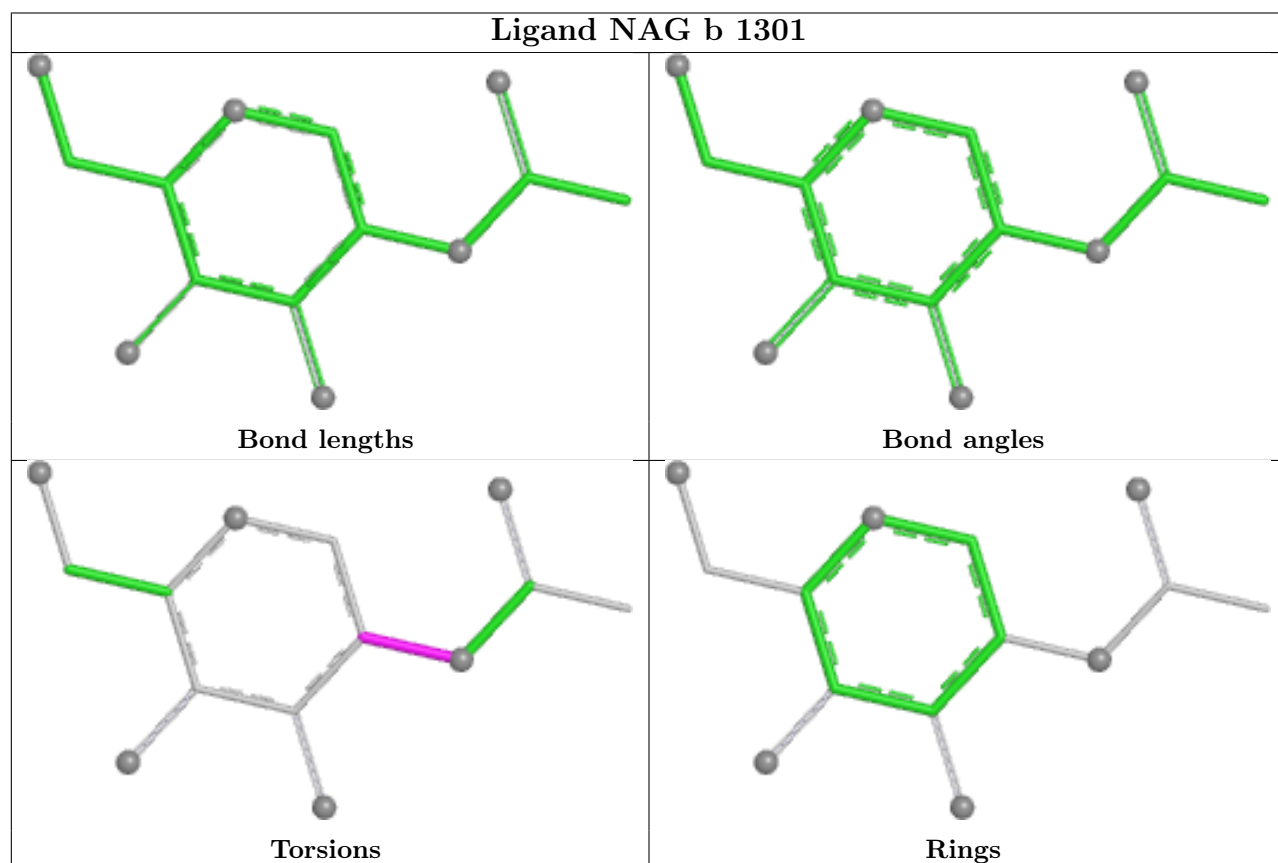
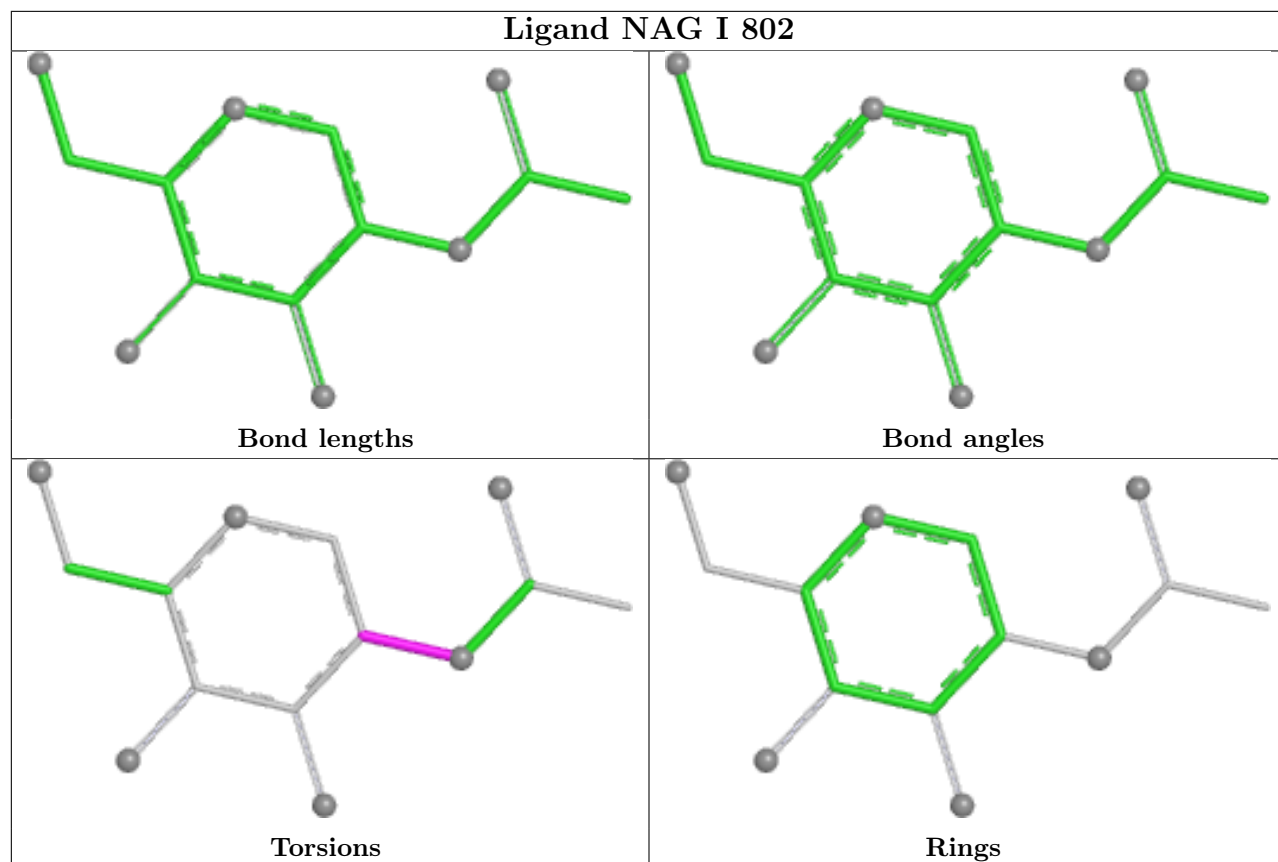
There are no ring outliers.

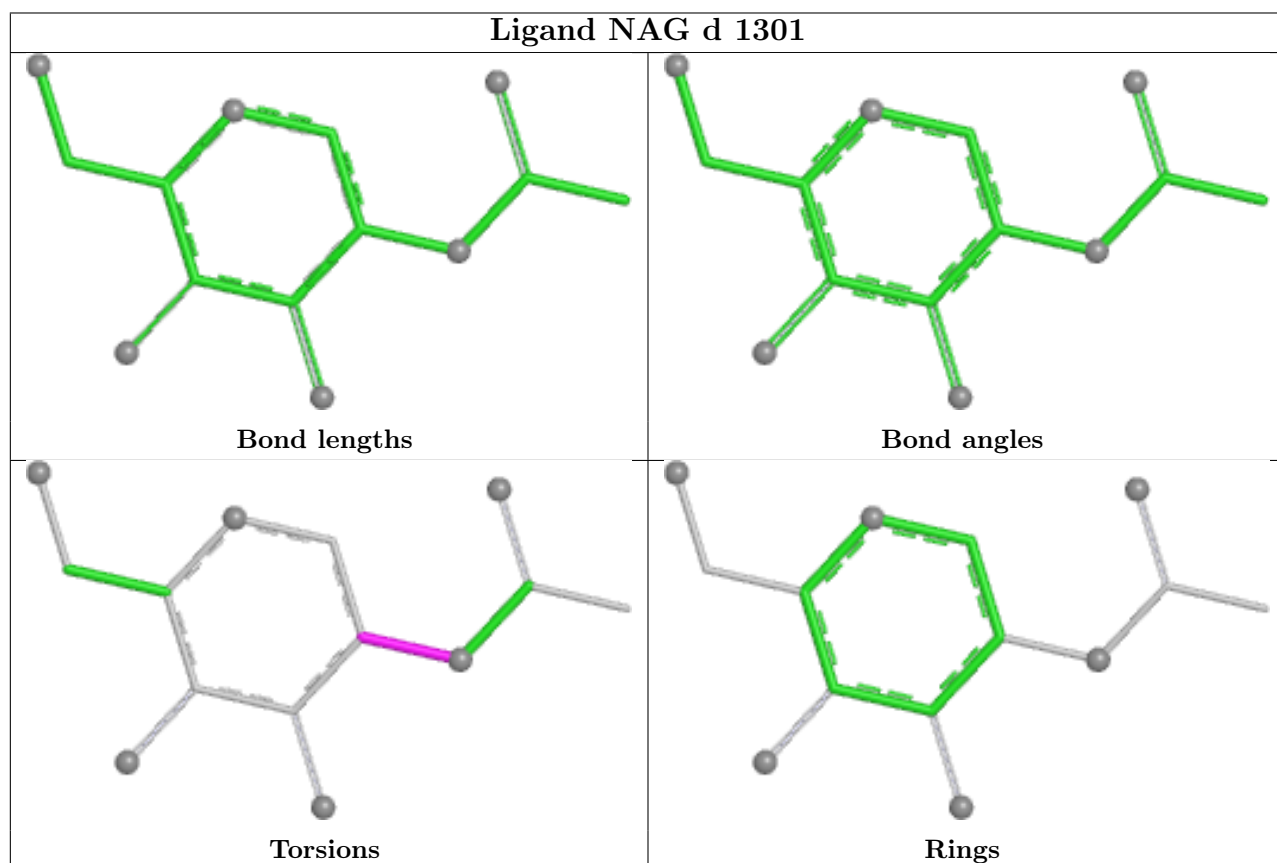
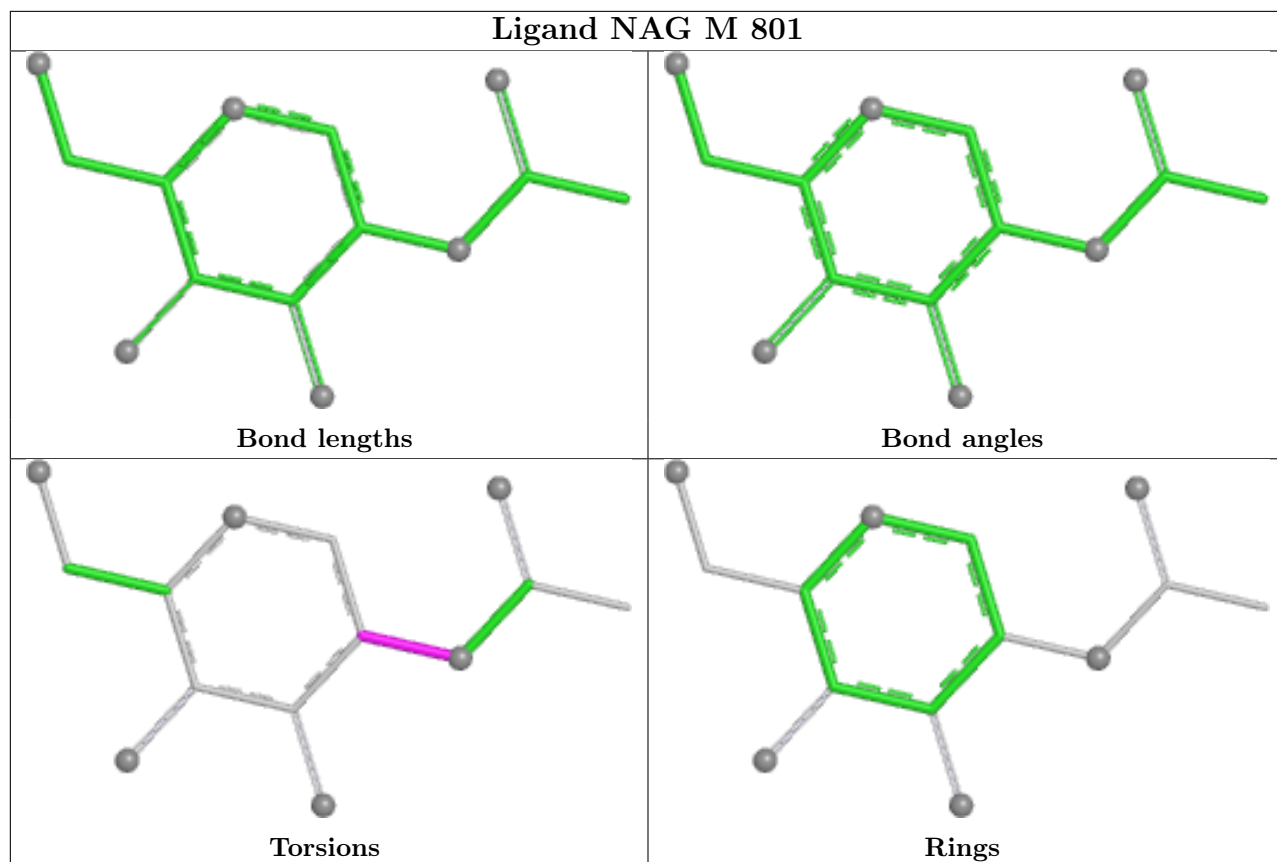
7 monomers are involved in 21 short contacts:

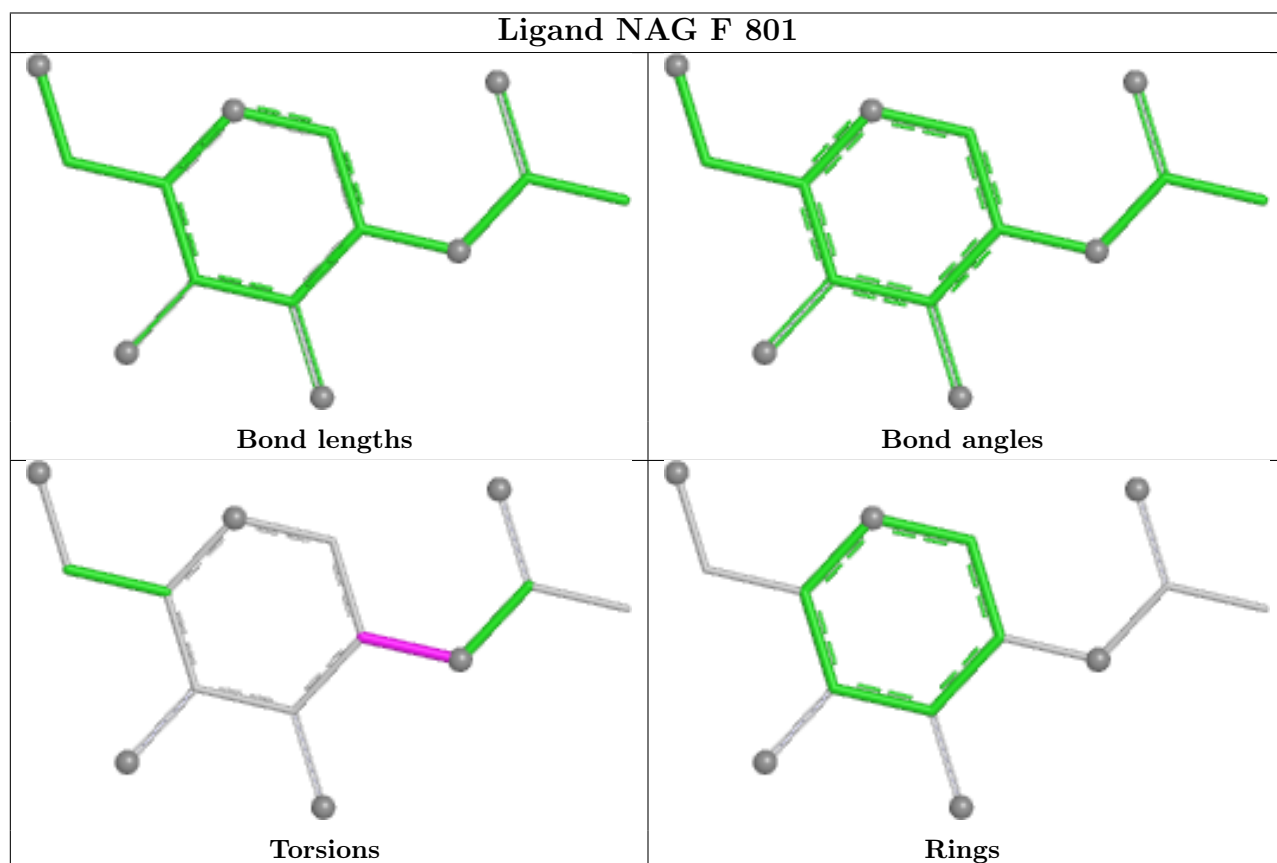
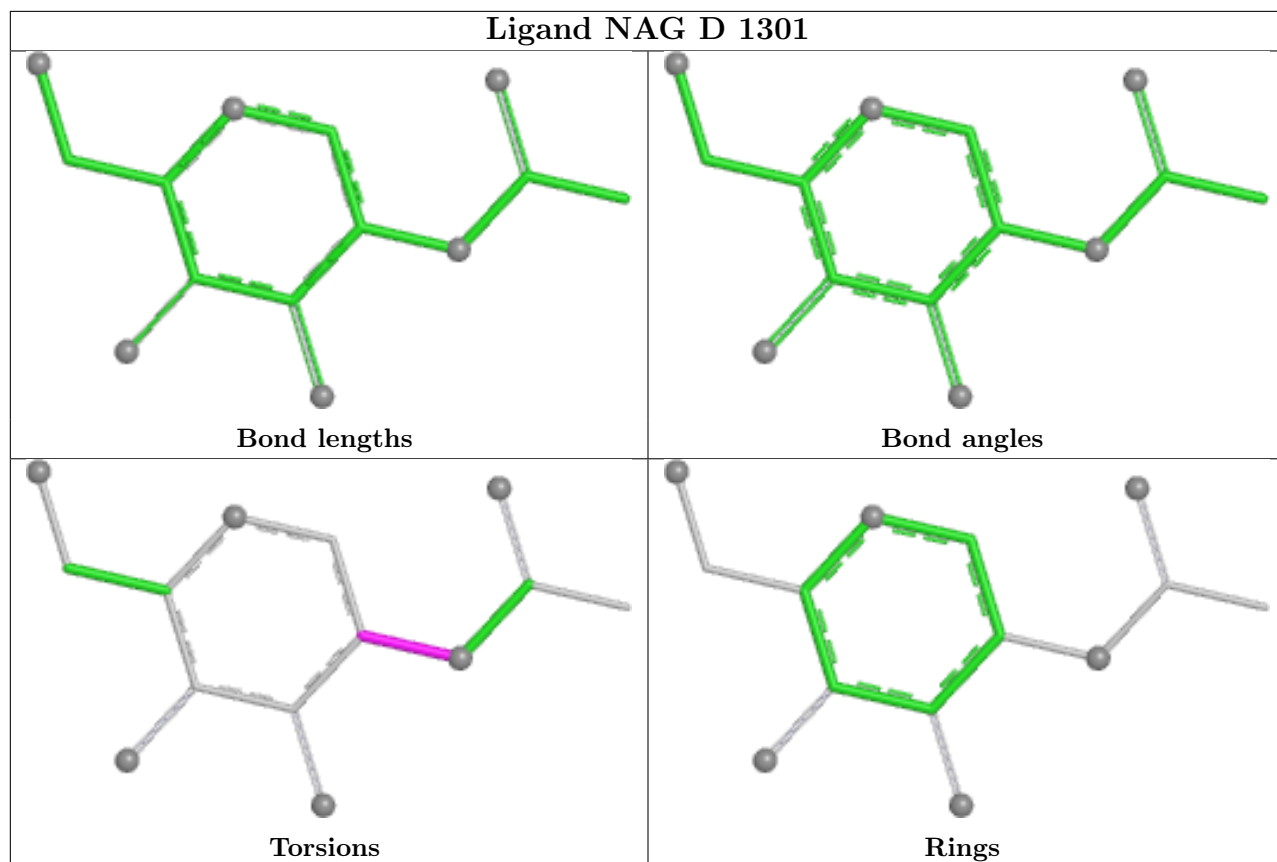
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	M	801	NAG	1	0
3	a	1302	NAG	6	0
3	B	801	NAG	8	0
3	W	1301	NAG	1	0
3	B	802	NAG	3	0
3	G	801	NAG	1	0
3	W	1302	NAG	1	0

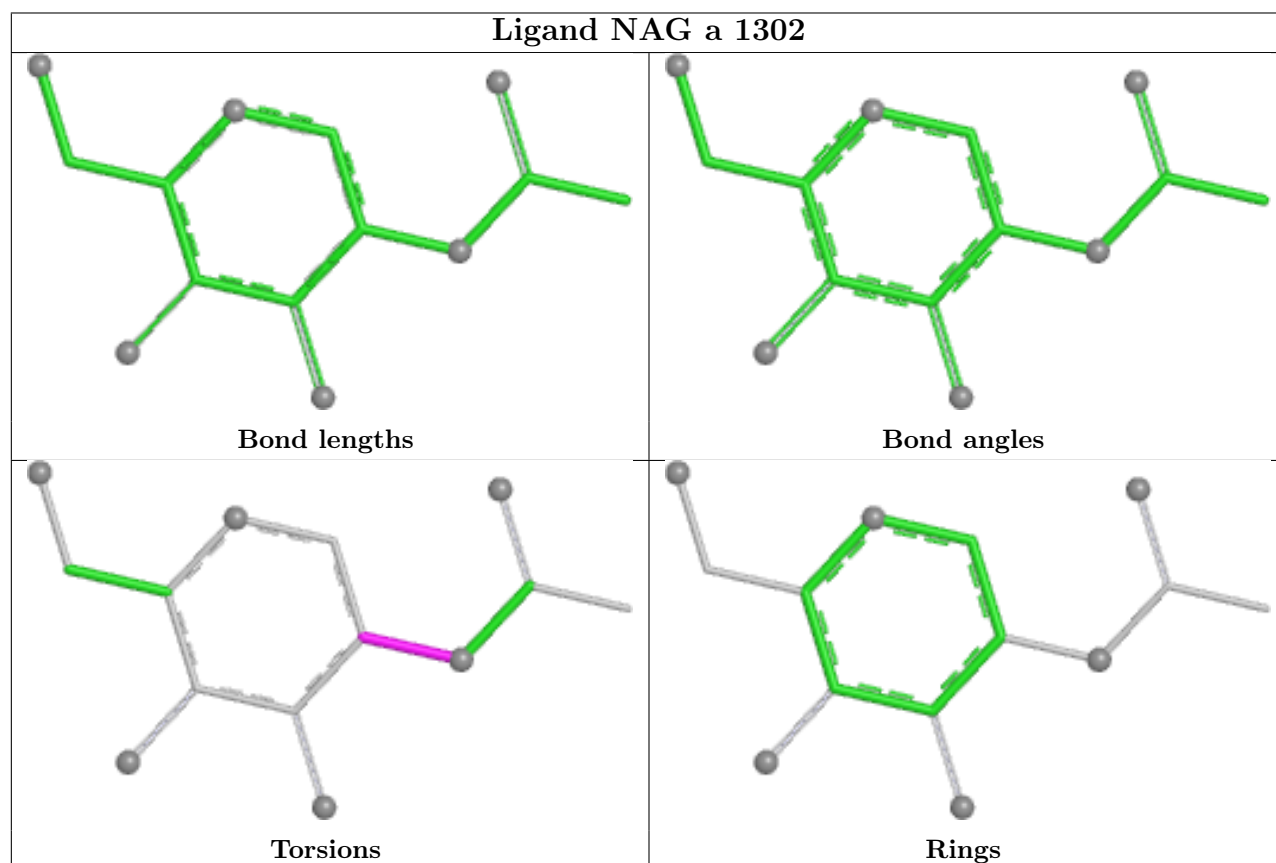
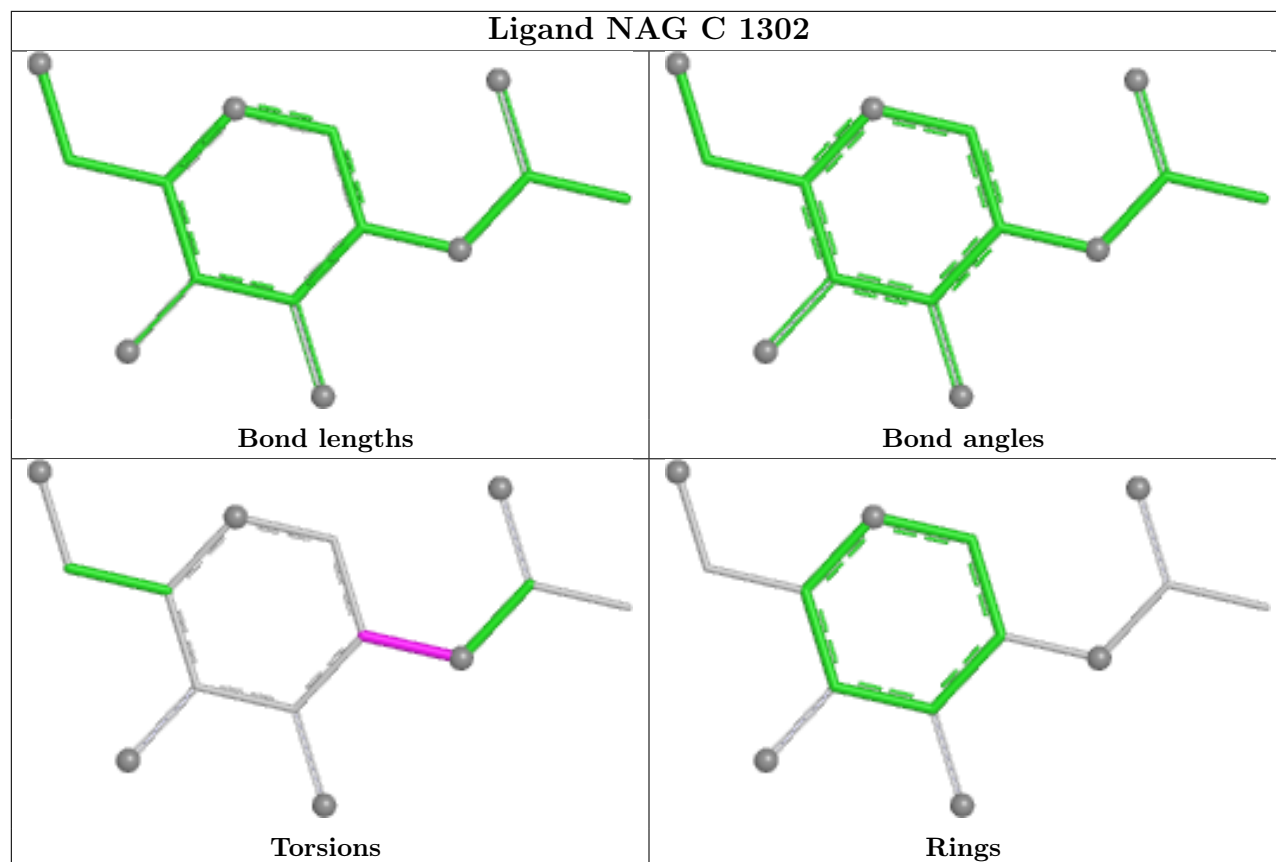
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

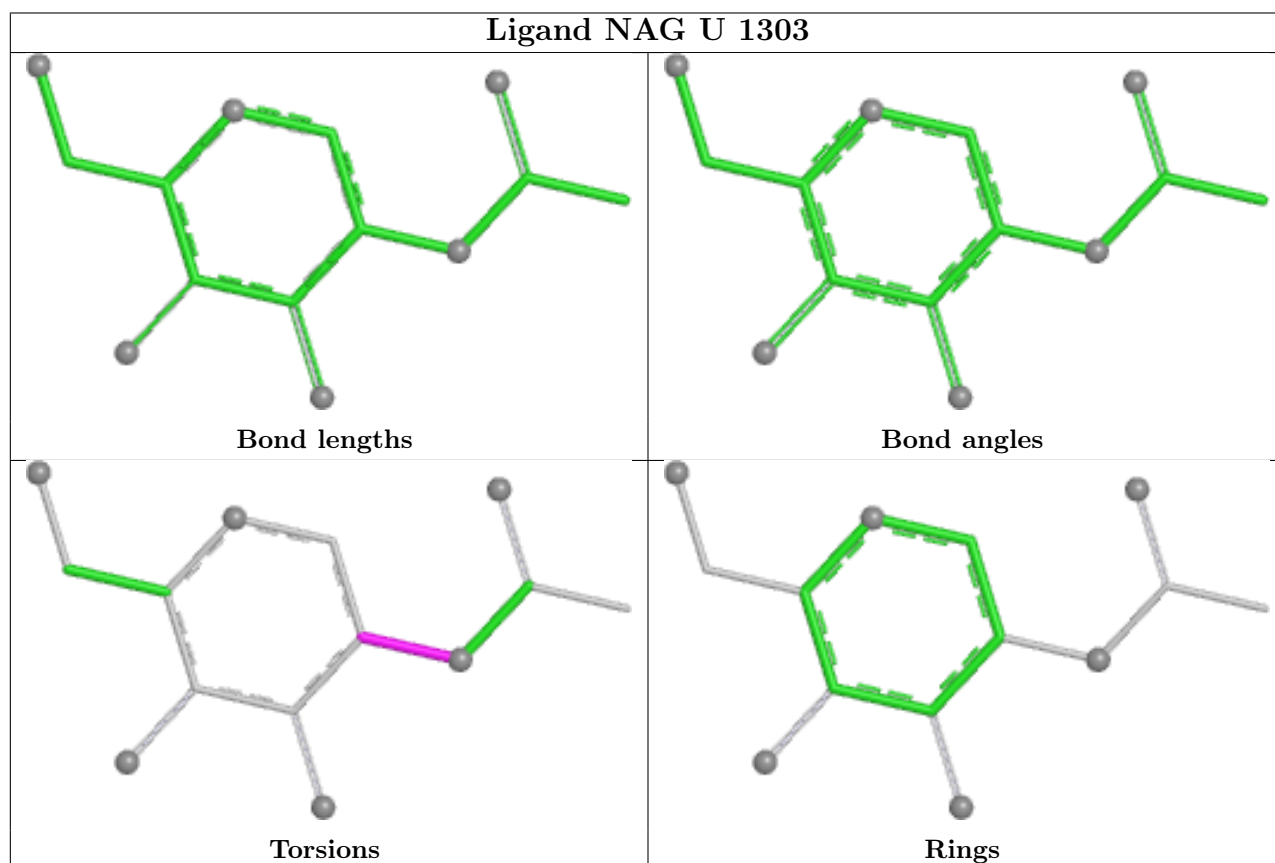
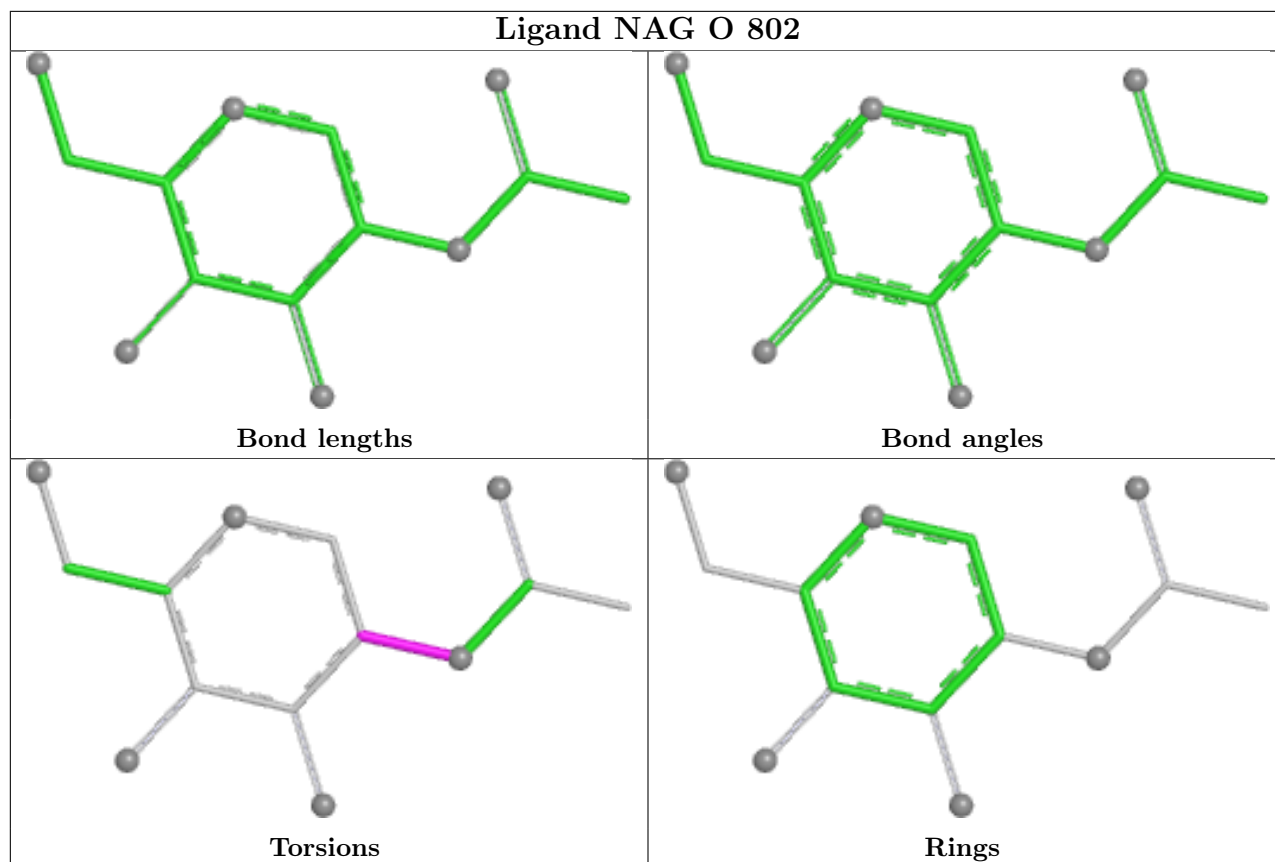


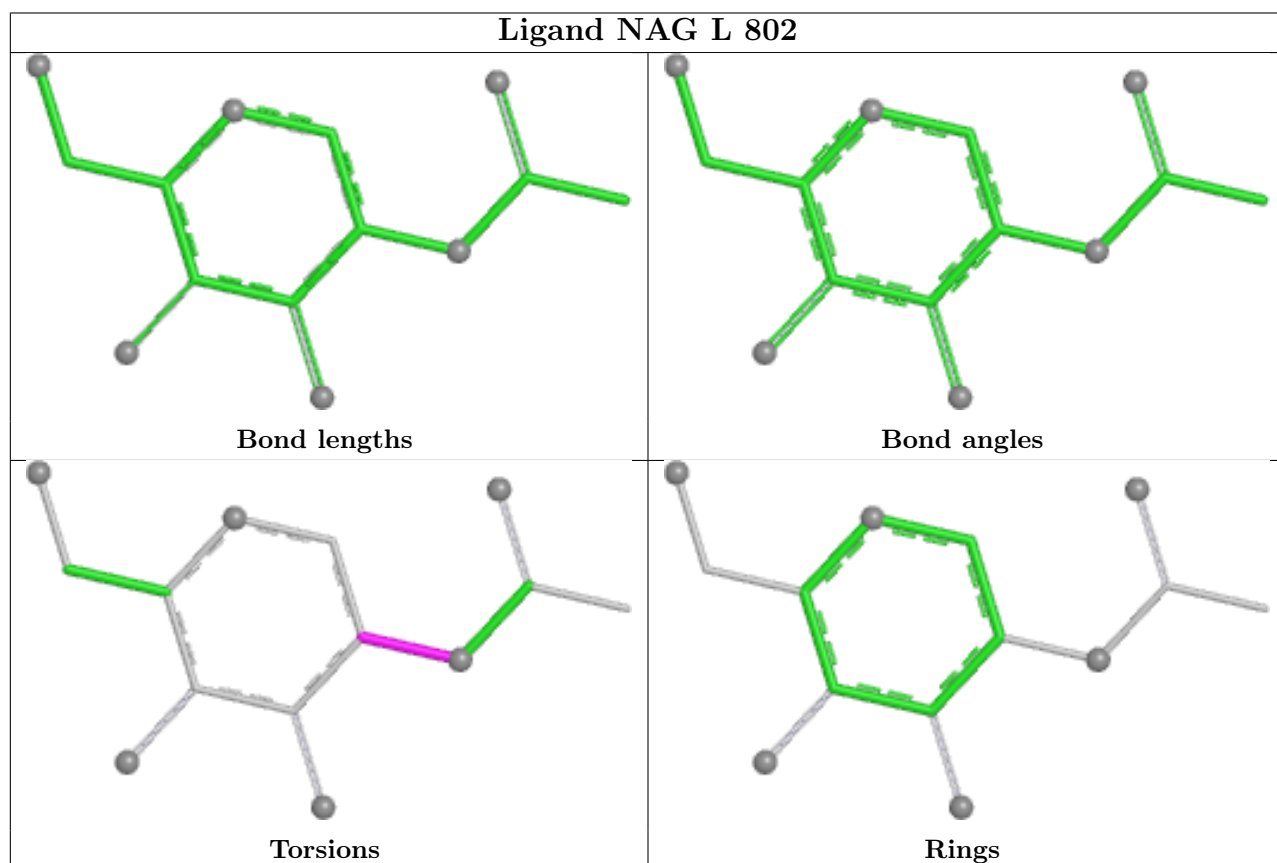
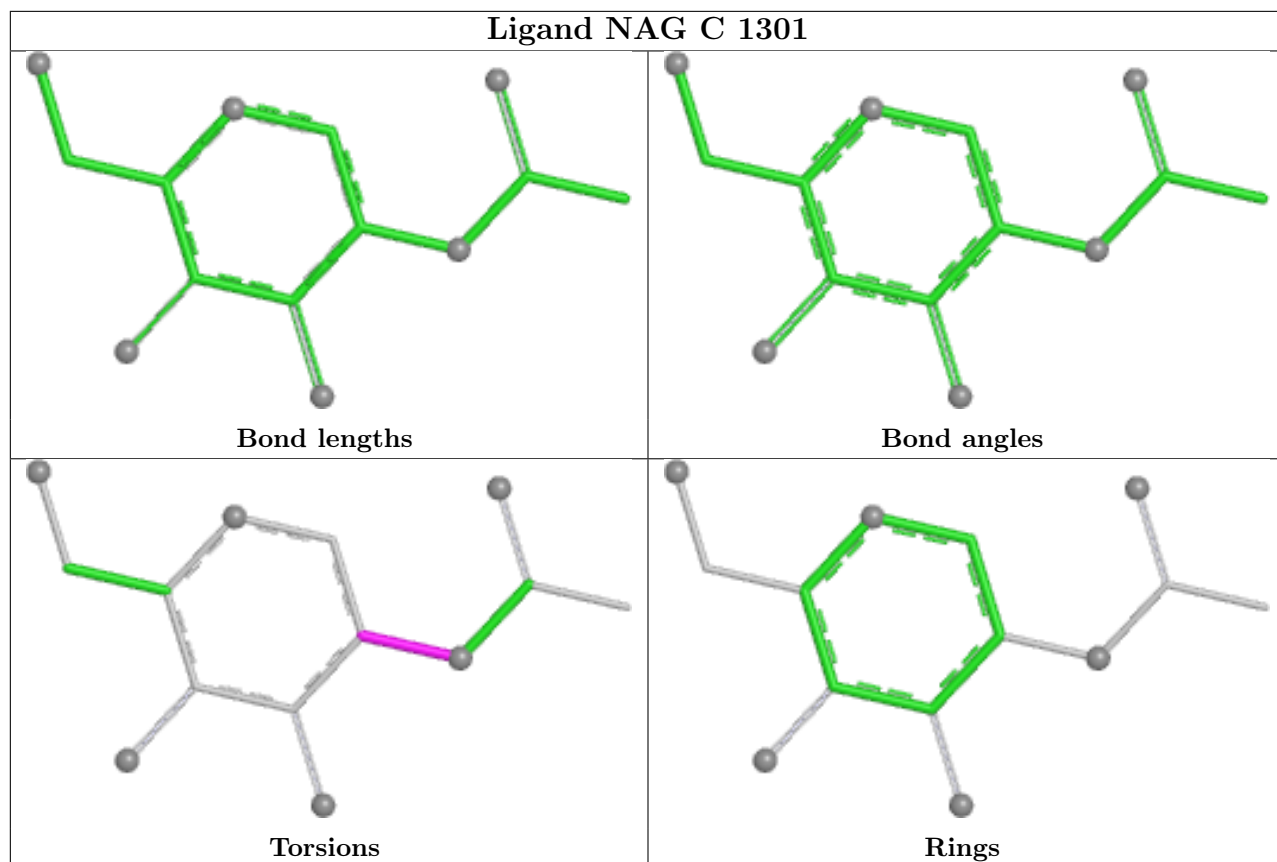


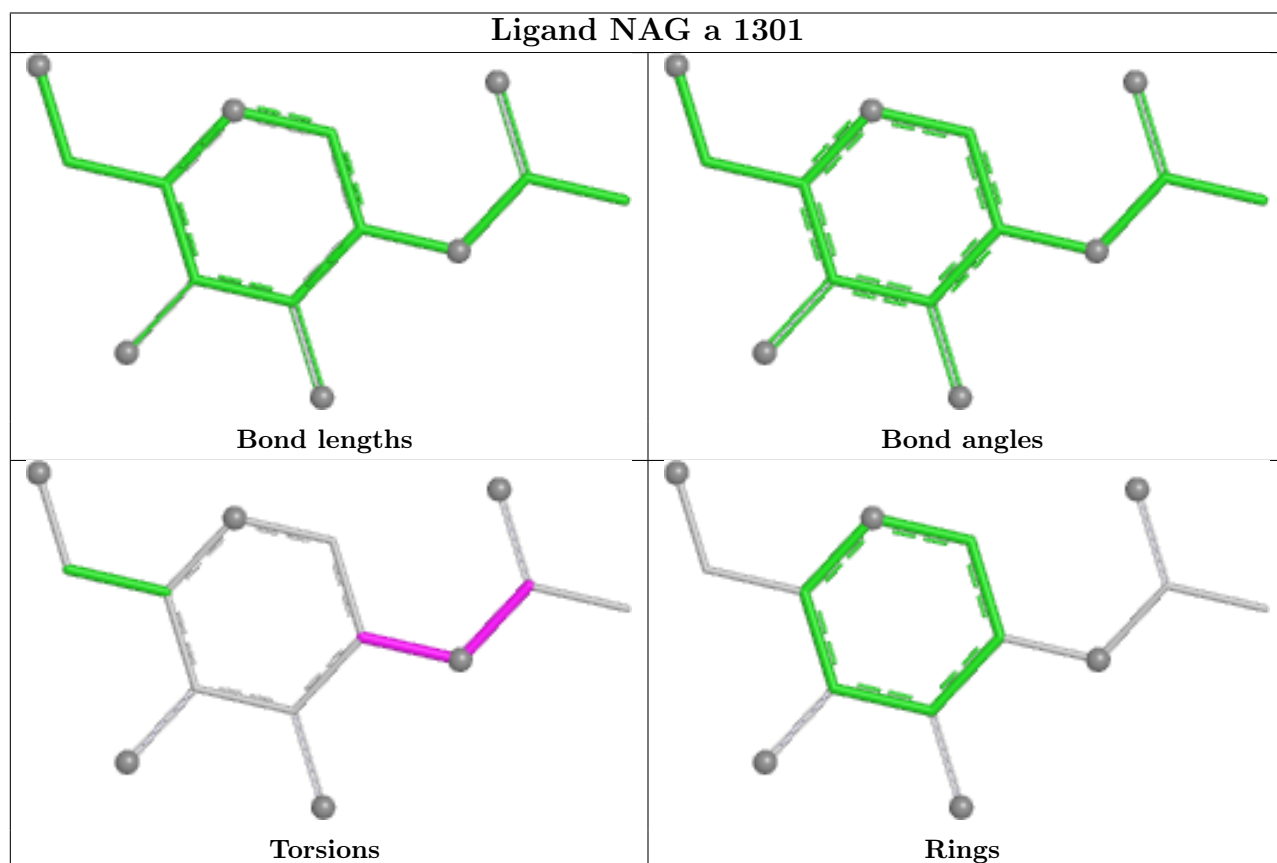
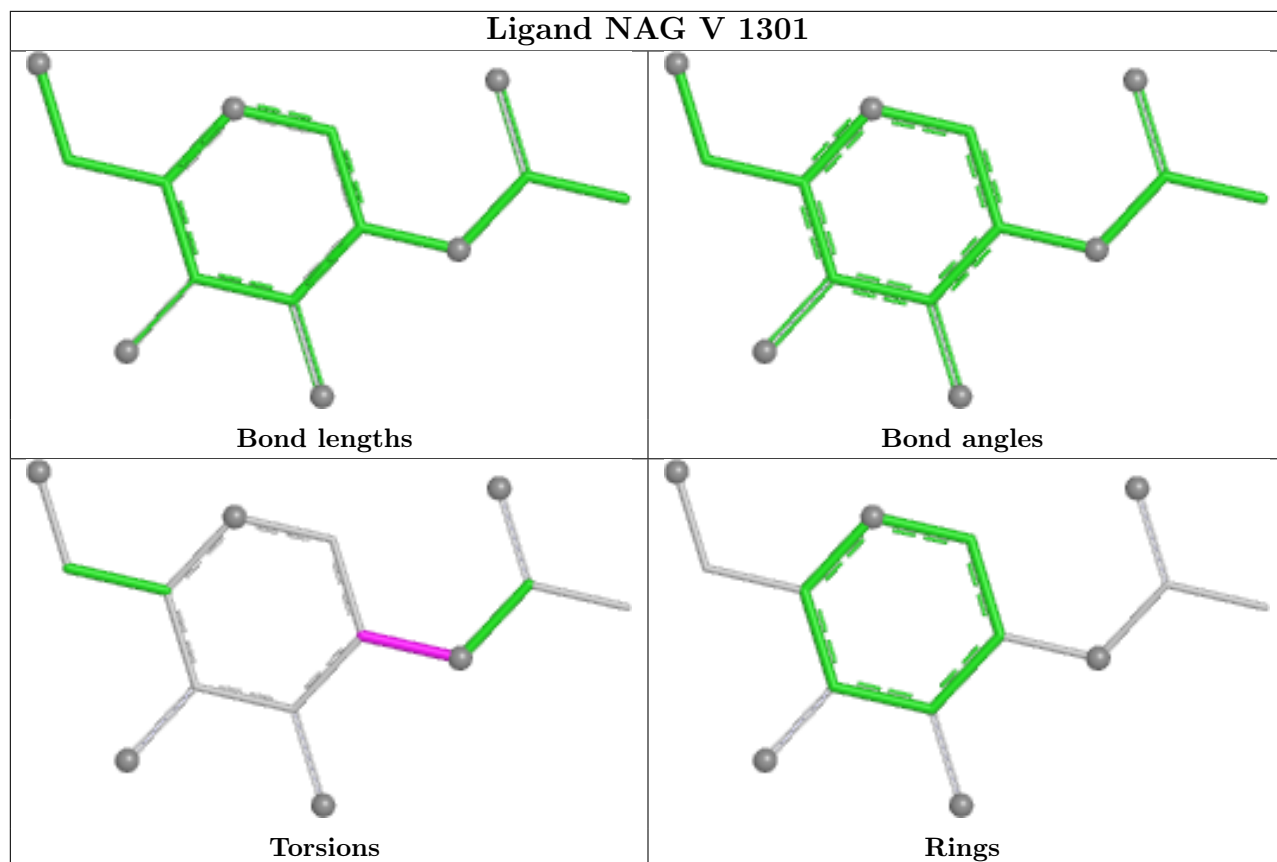


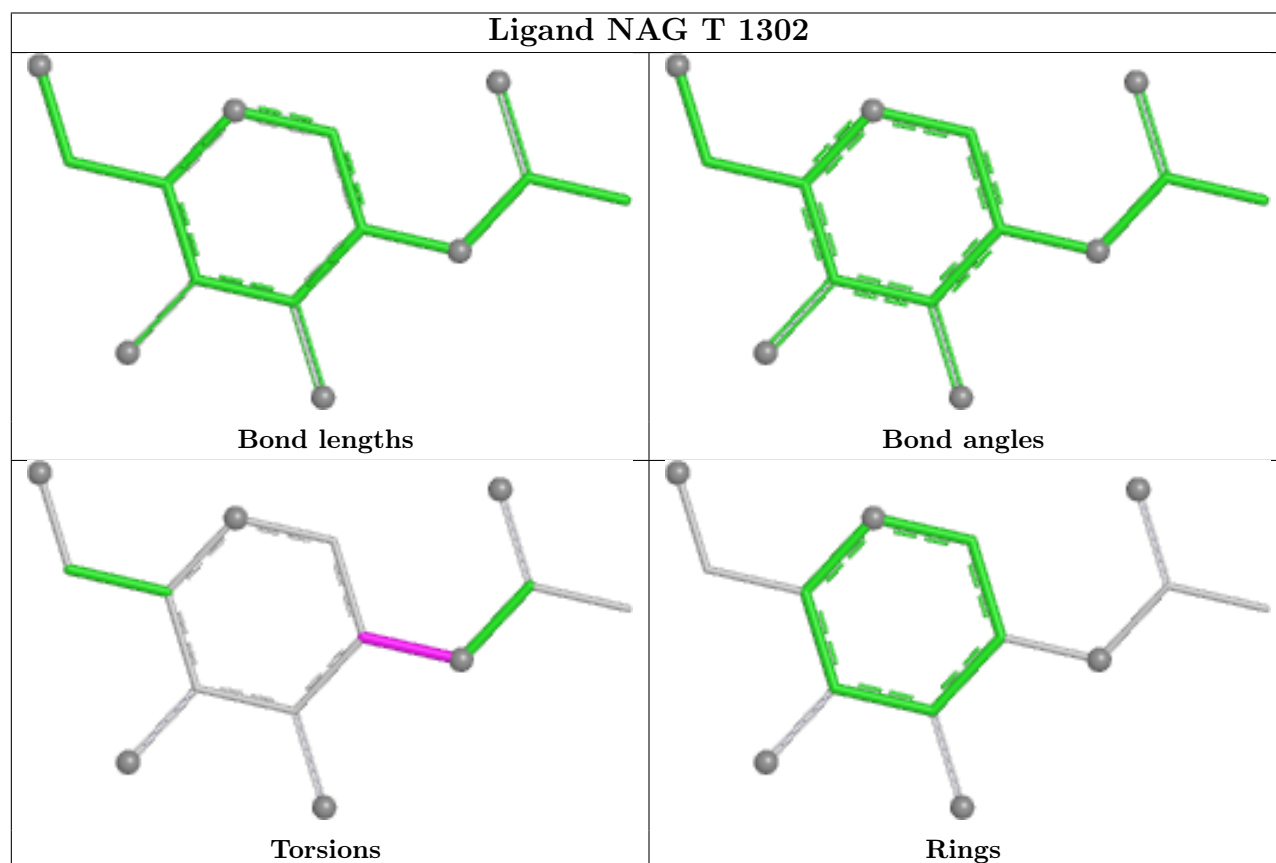
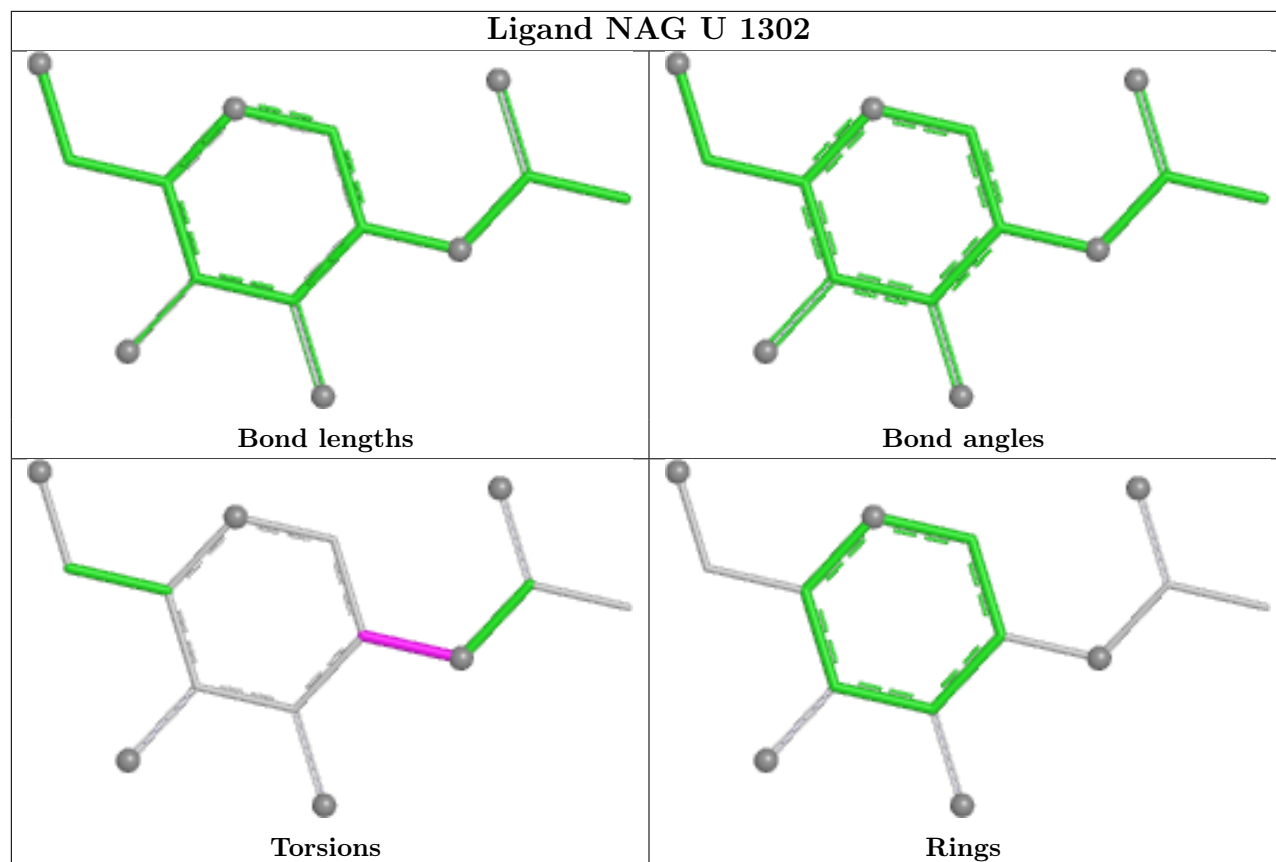


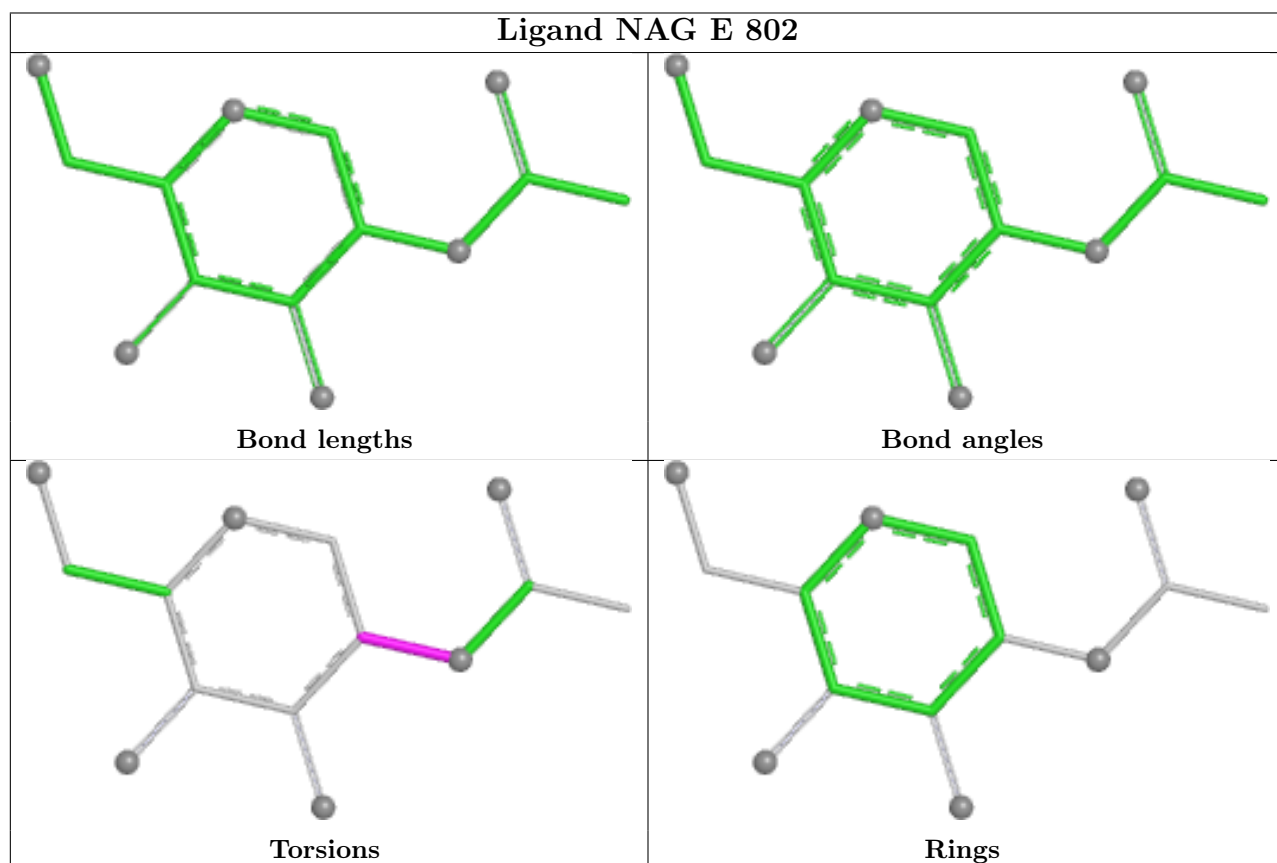
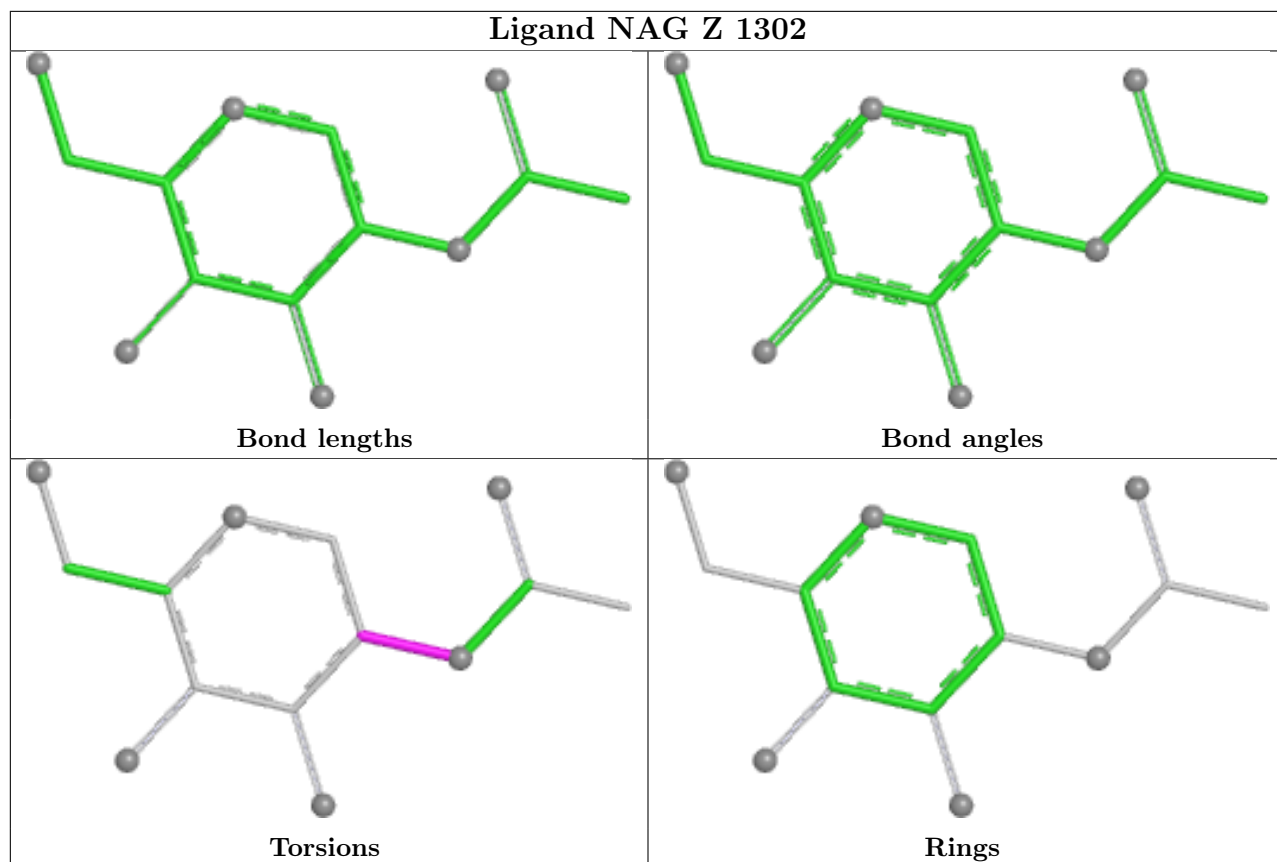


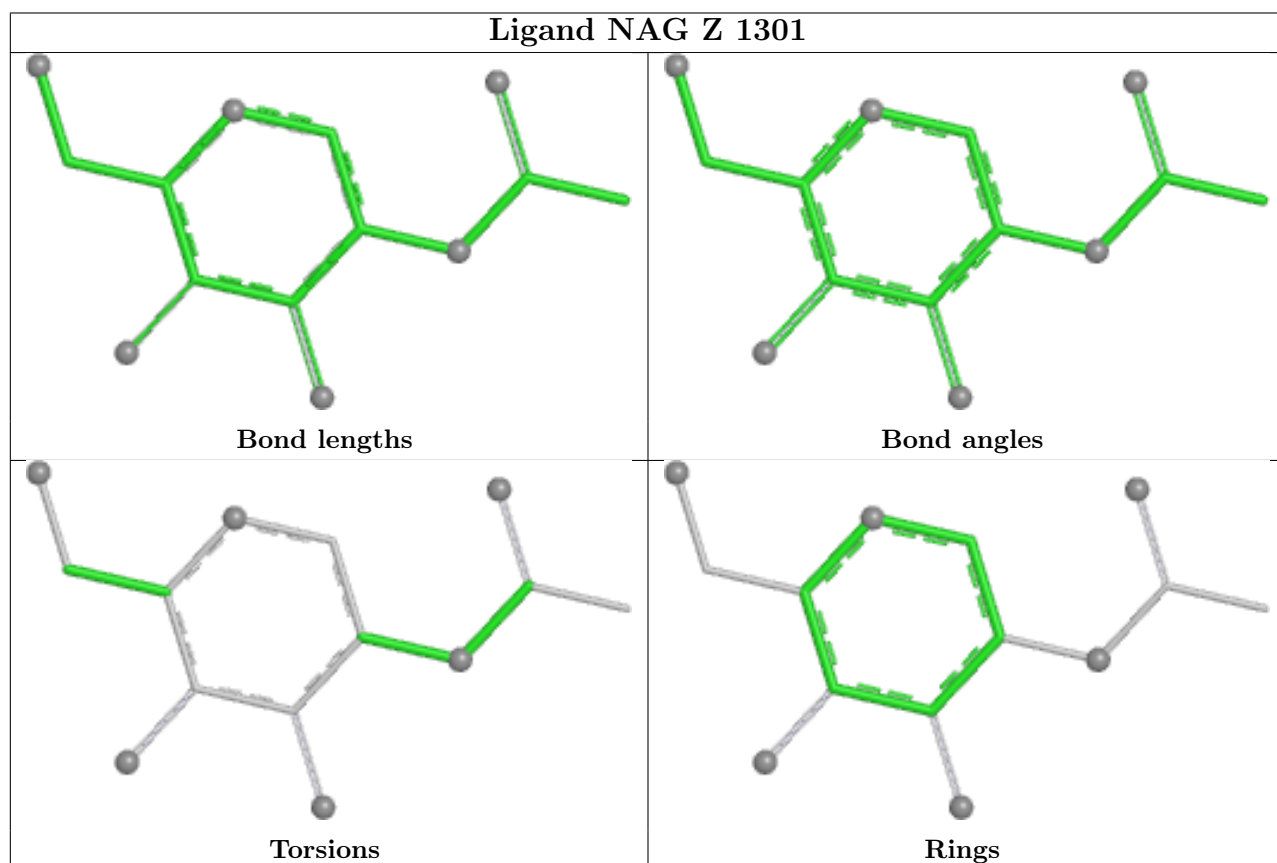
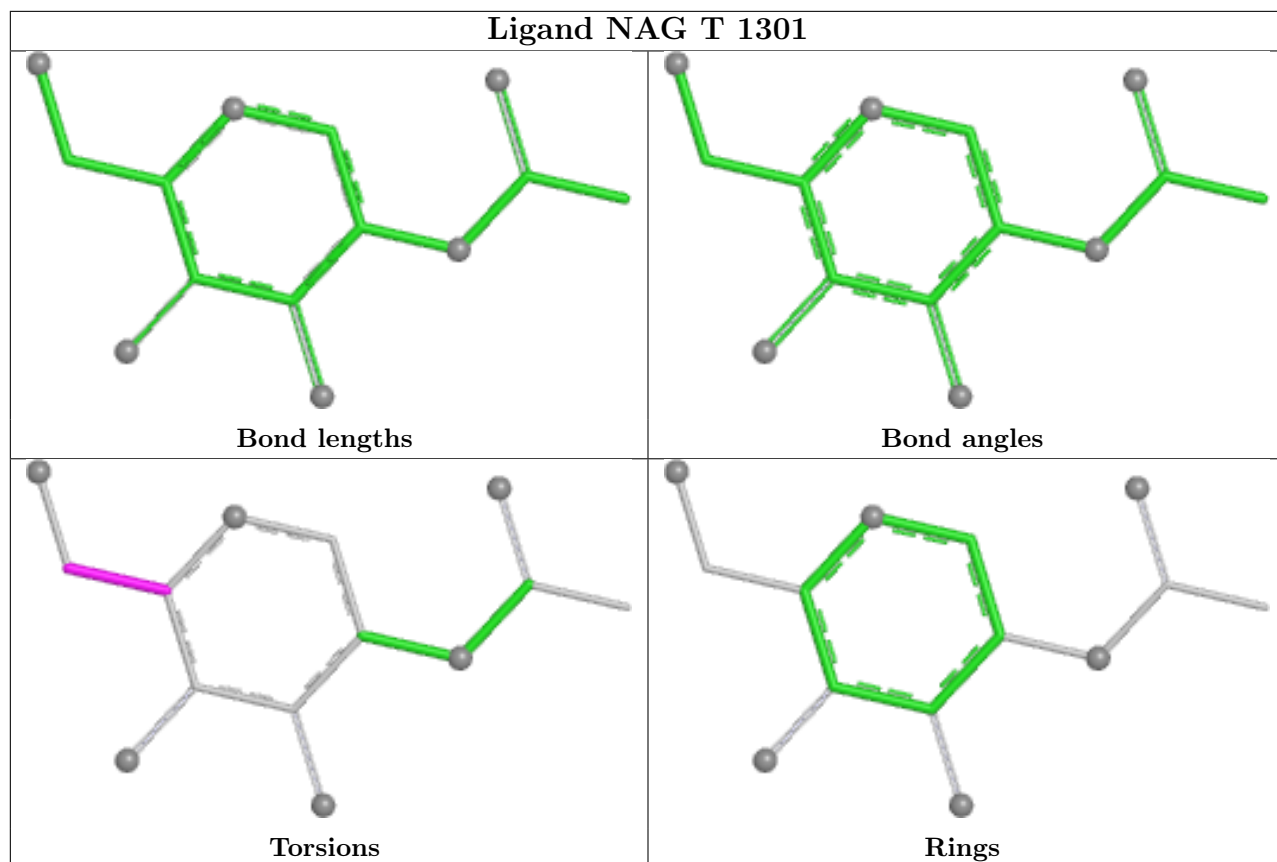


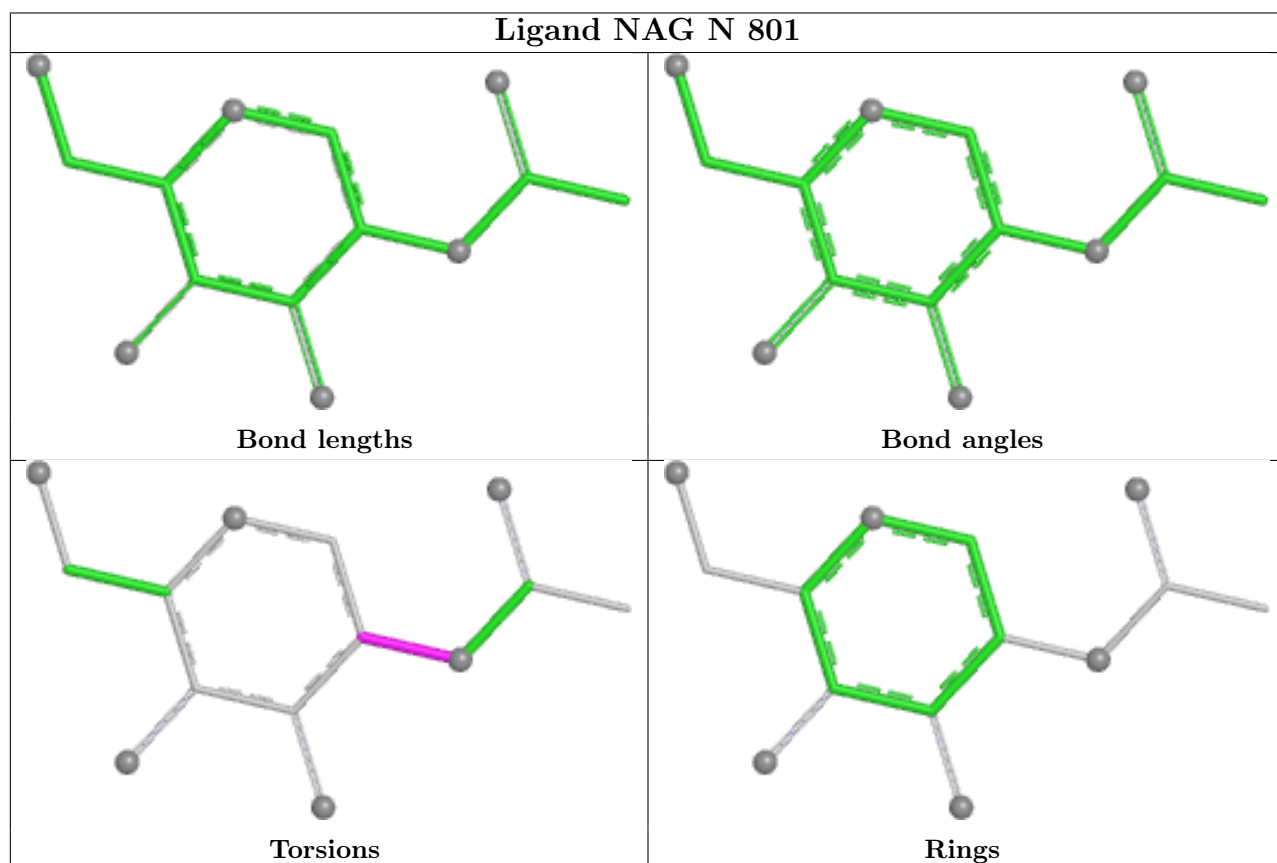
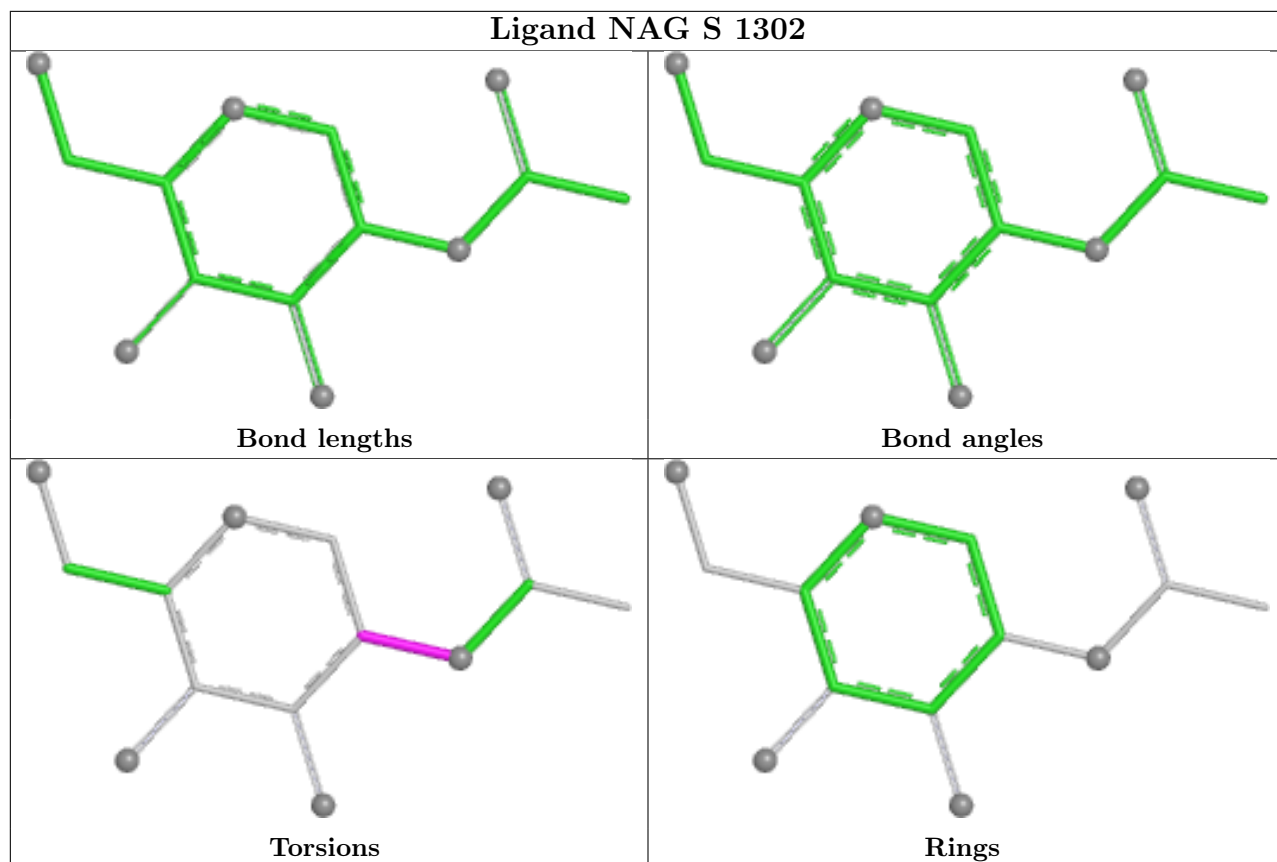


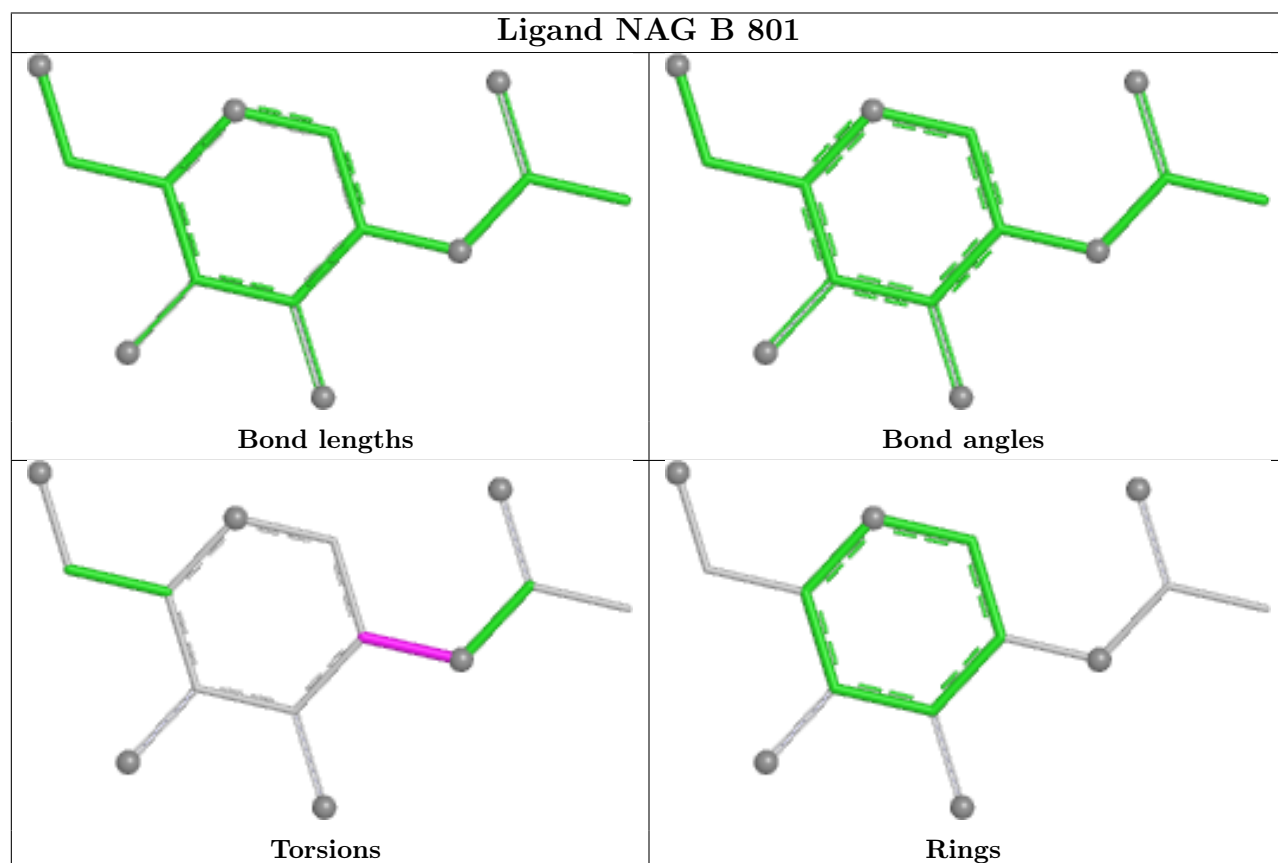
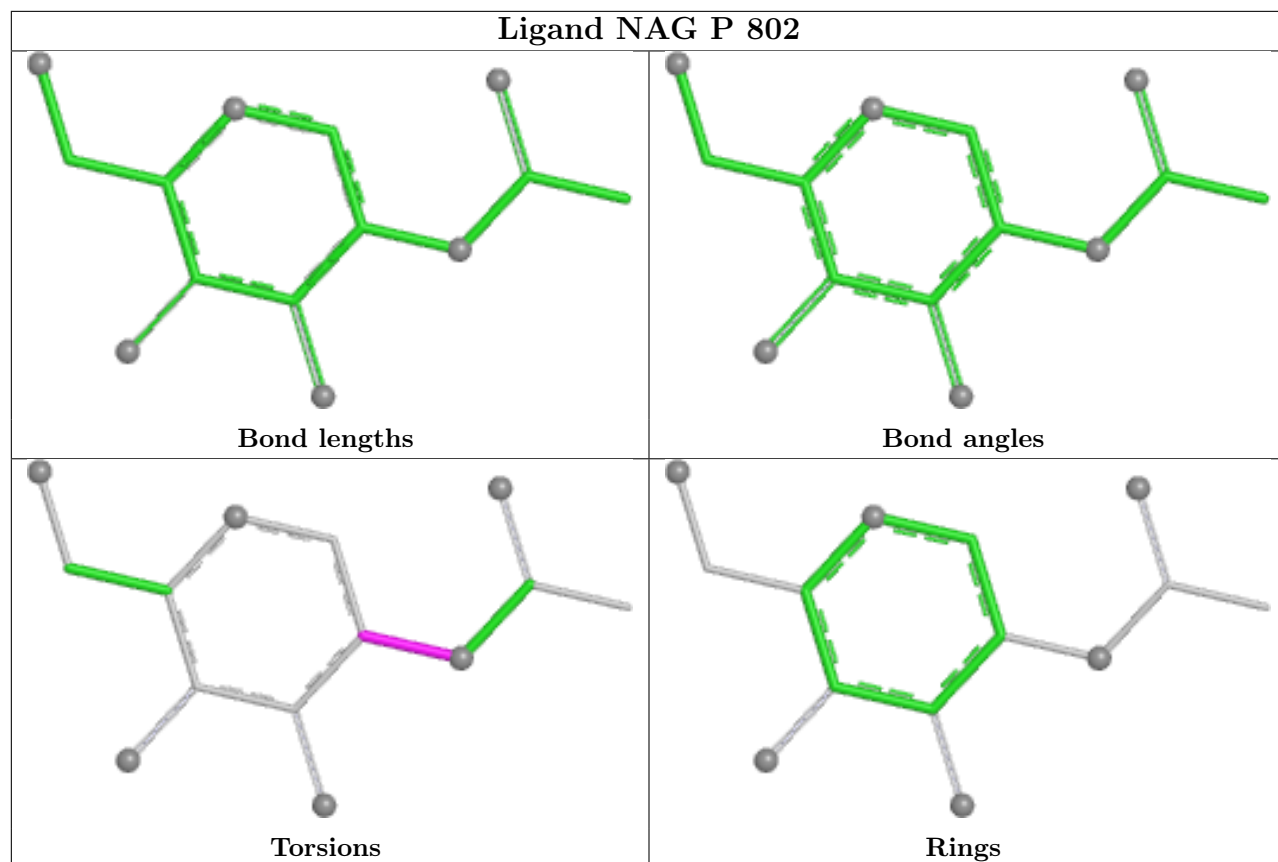


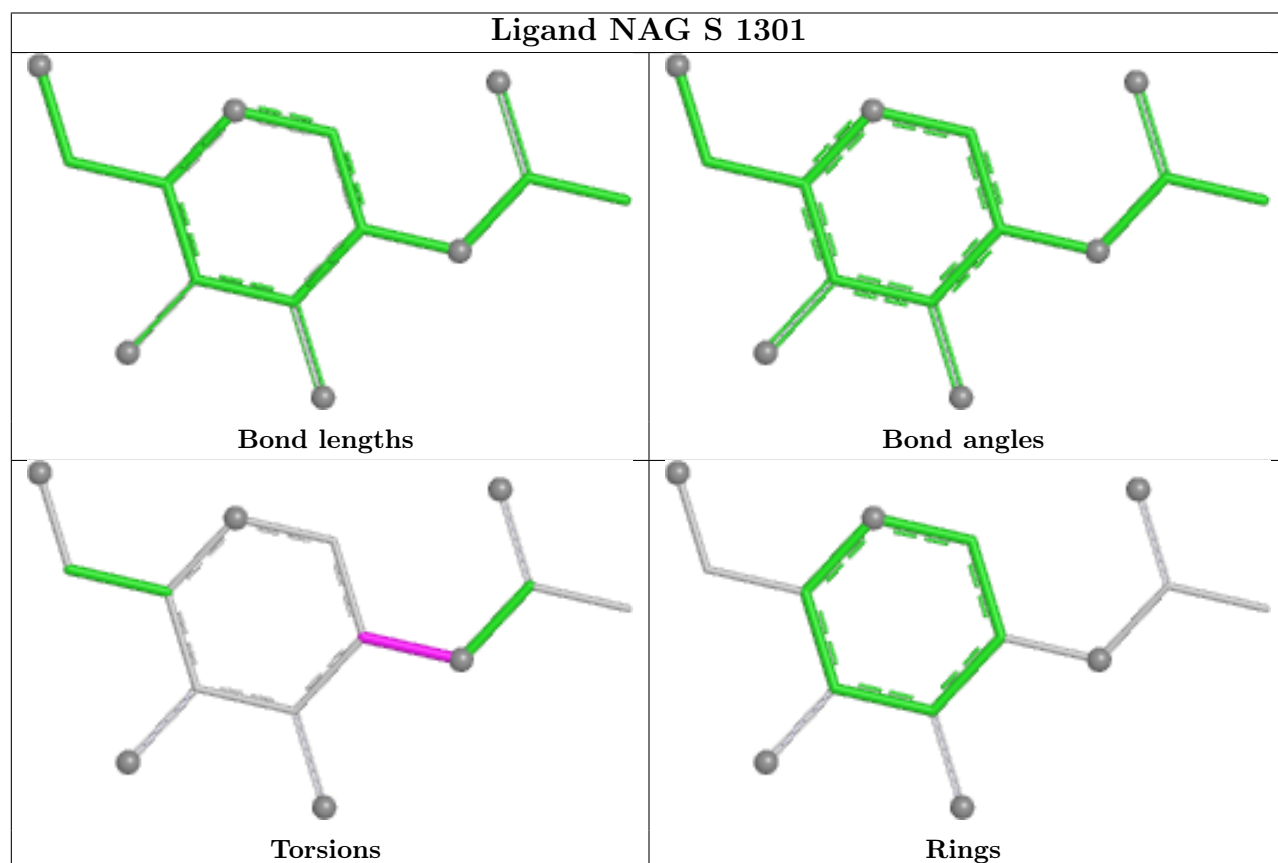
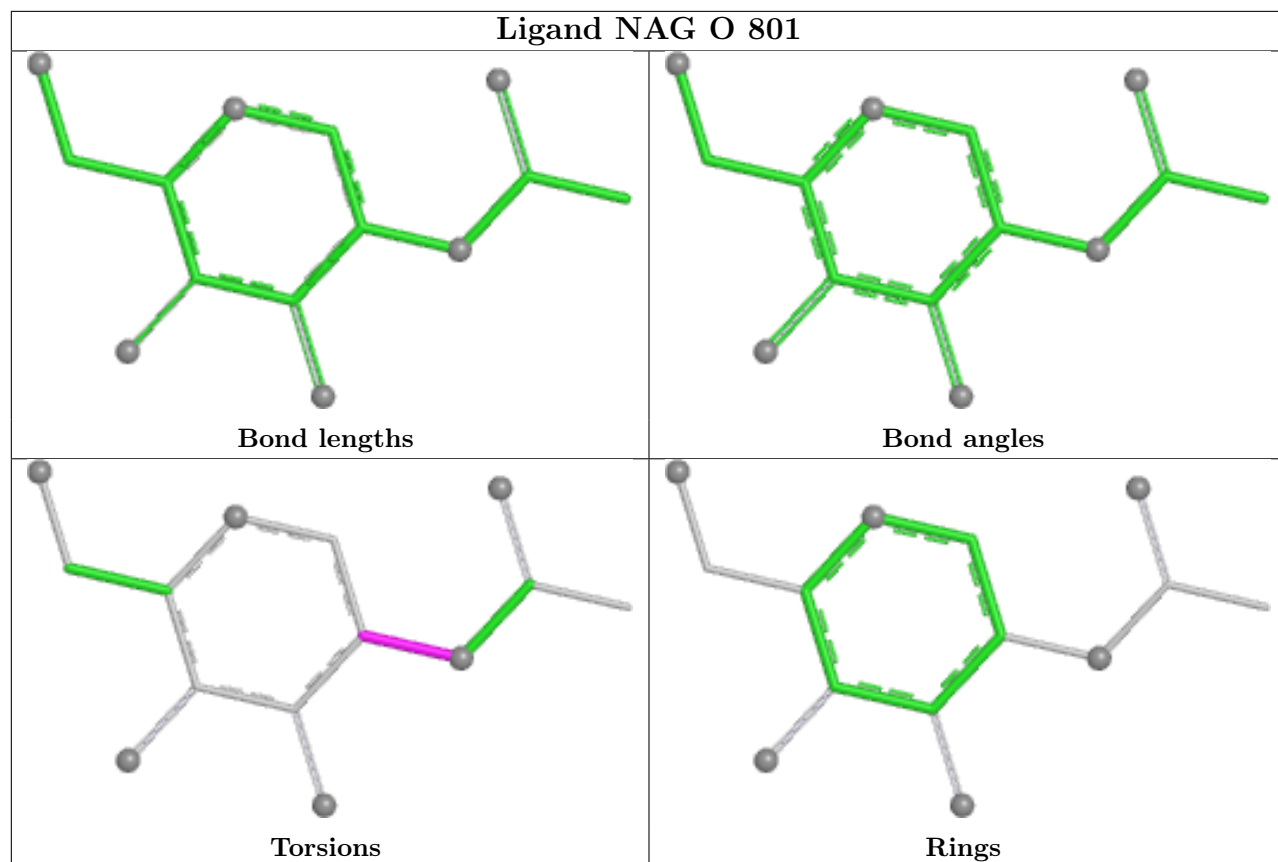


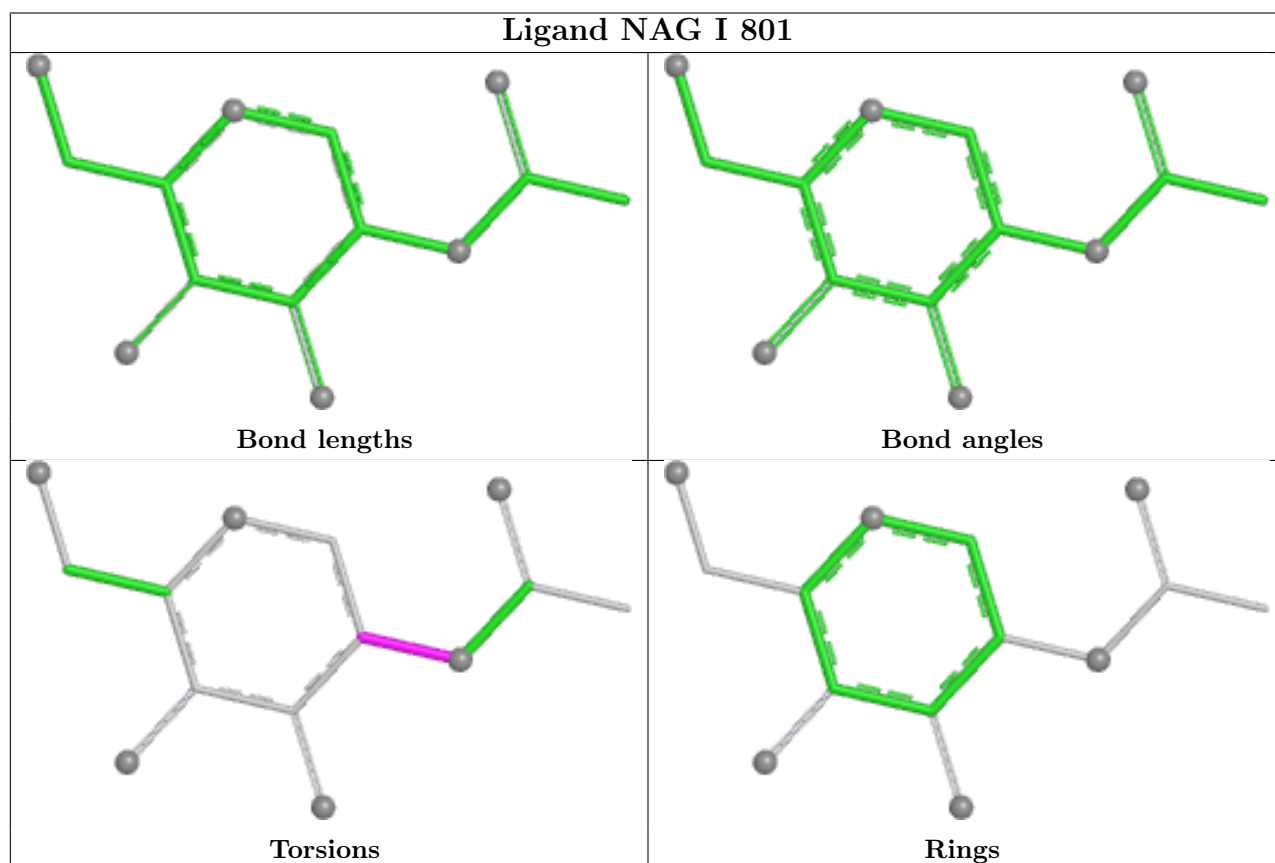
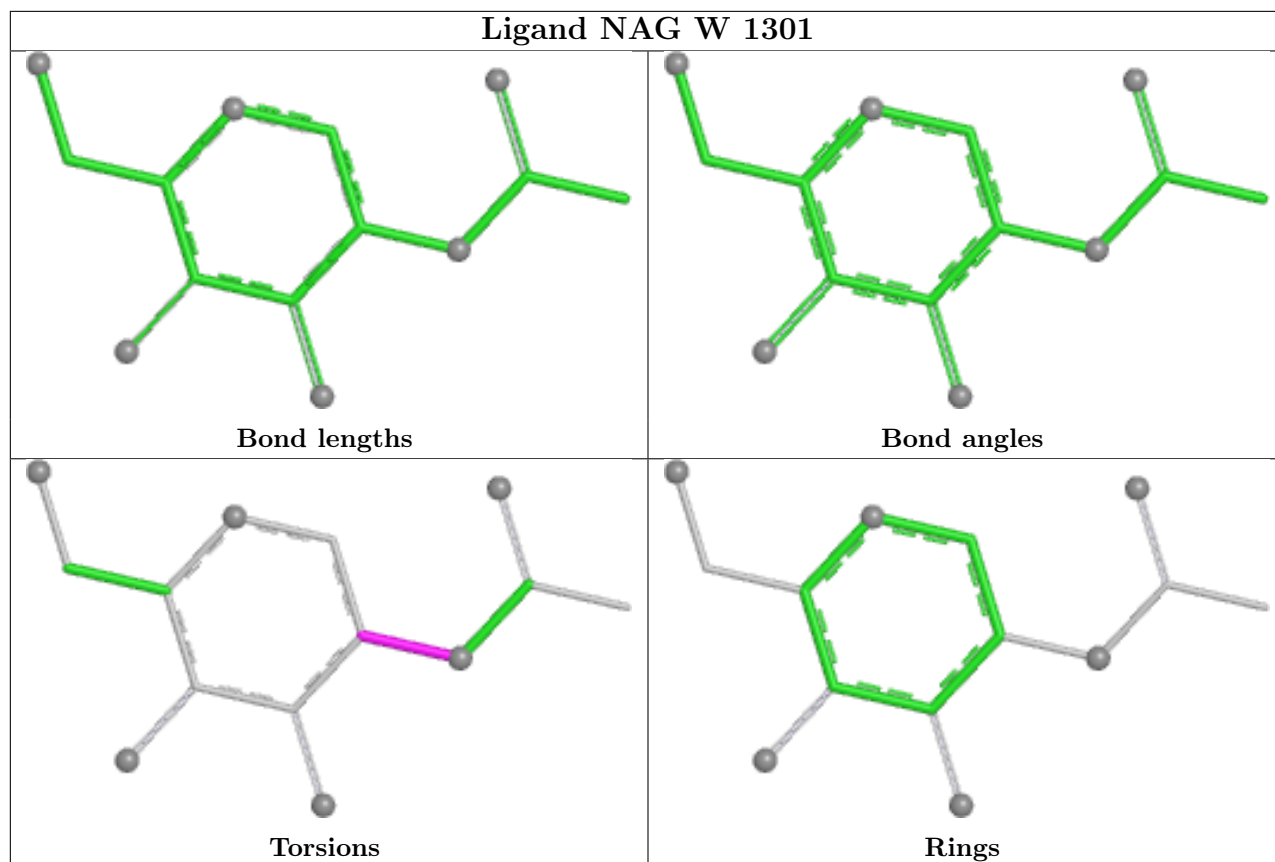


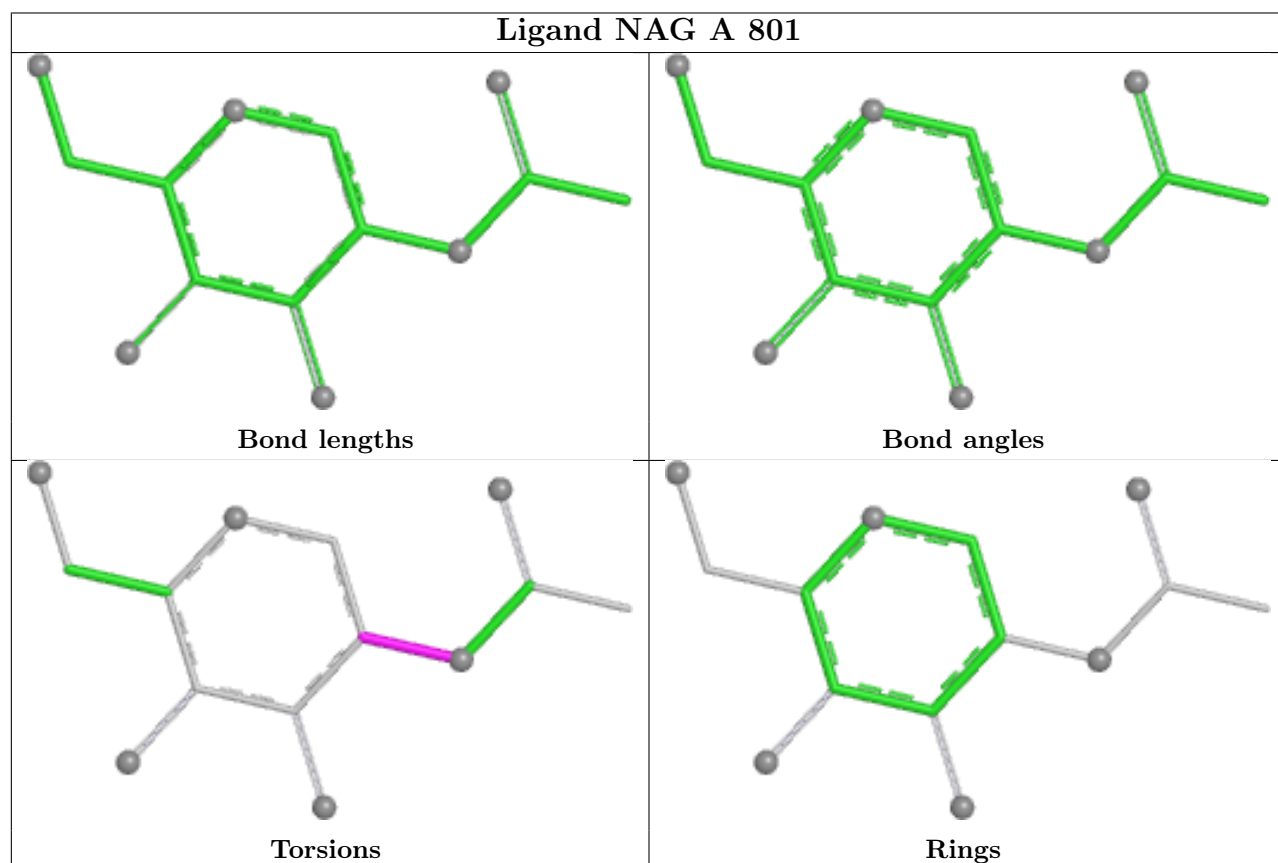
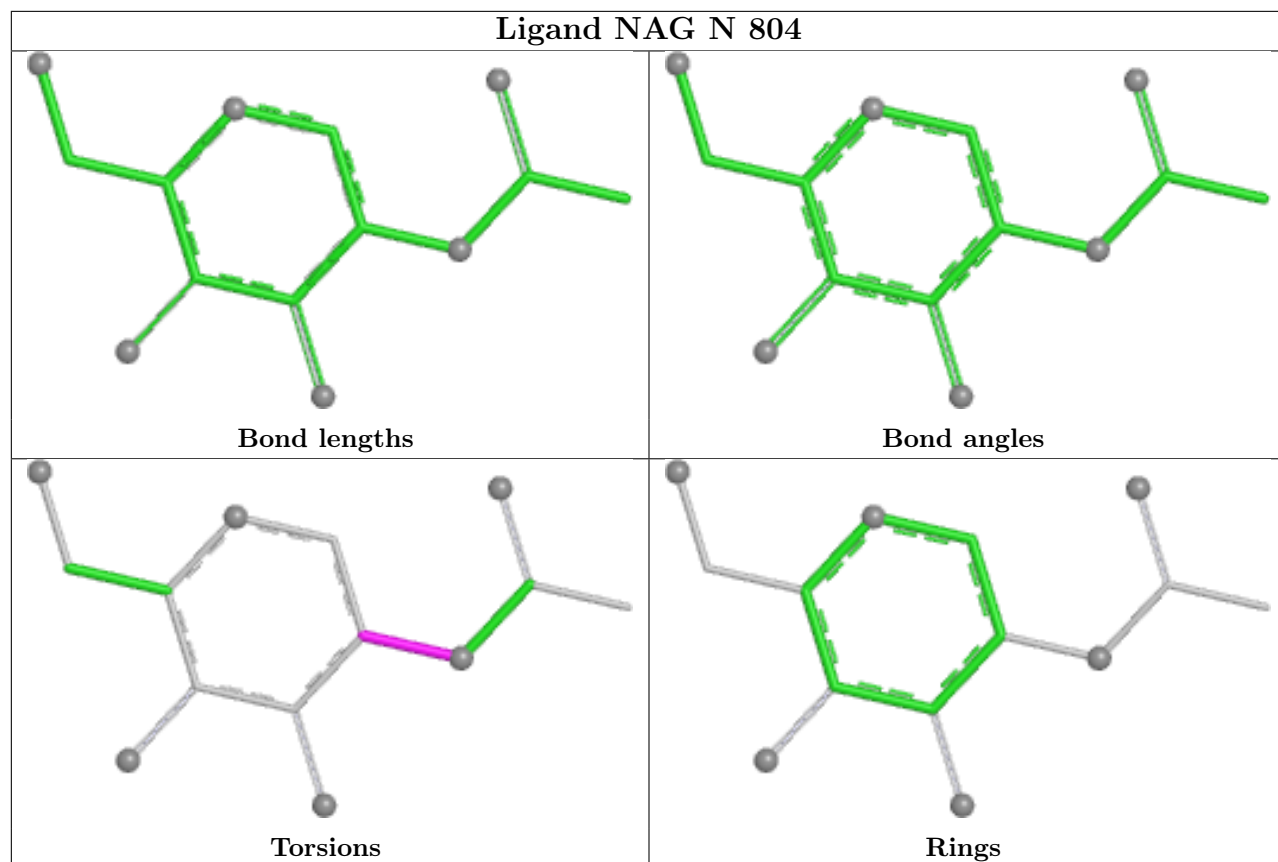


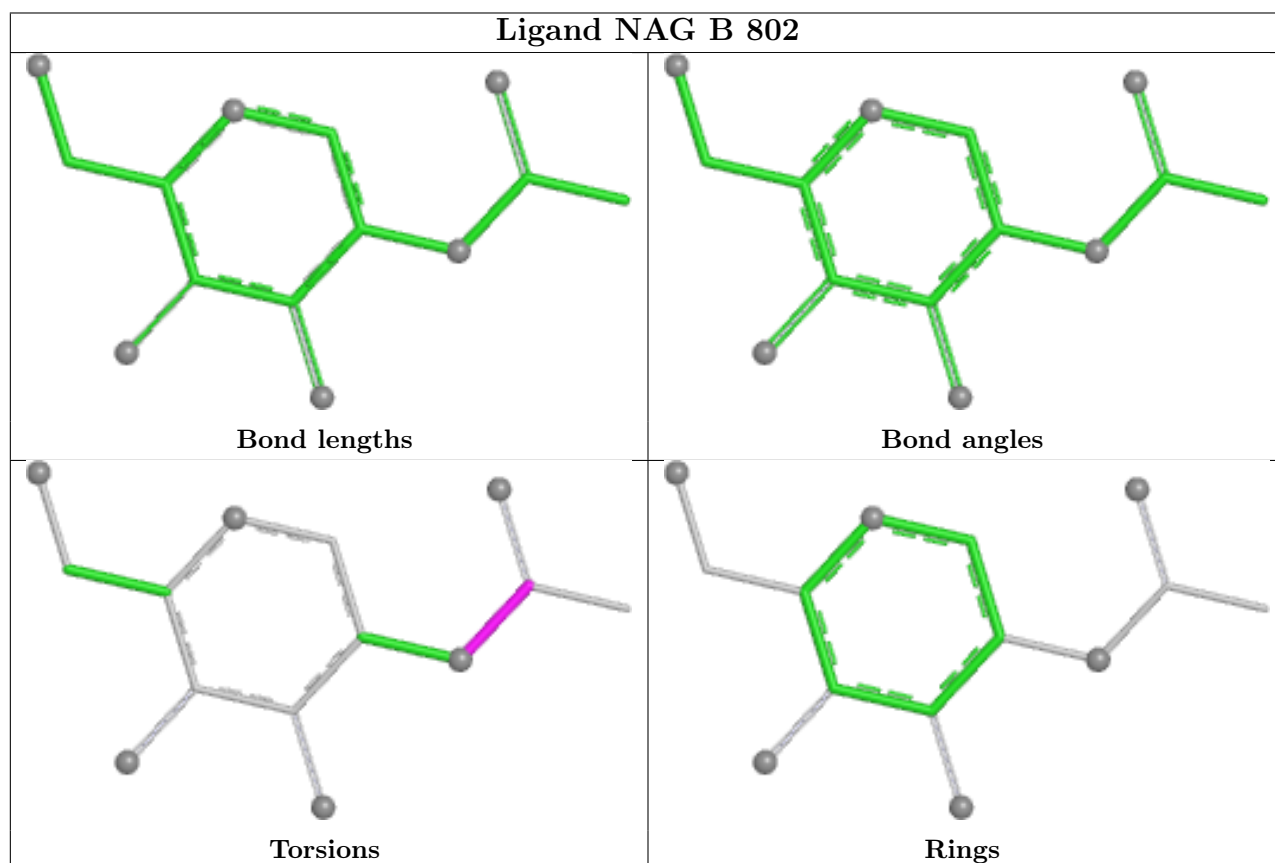
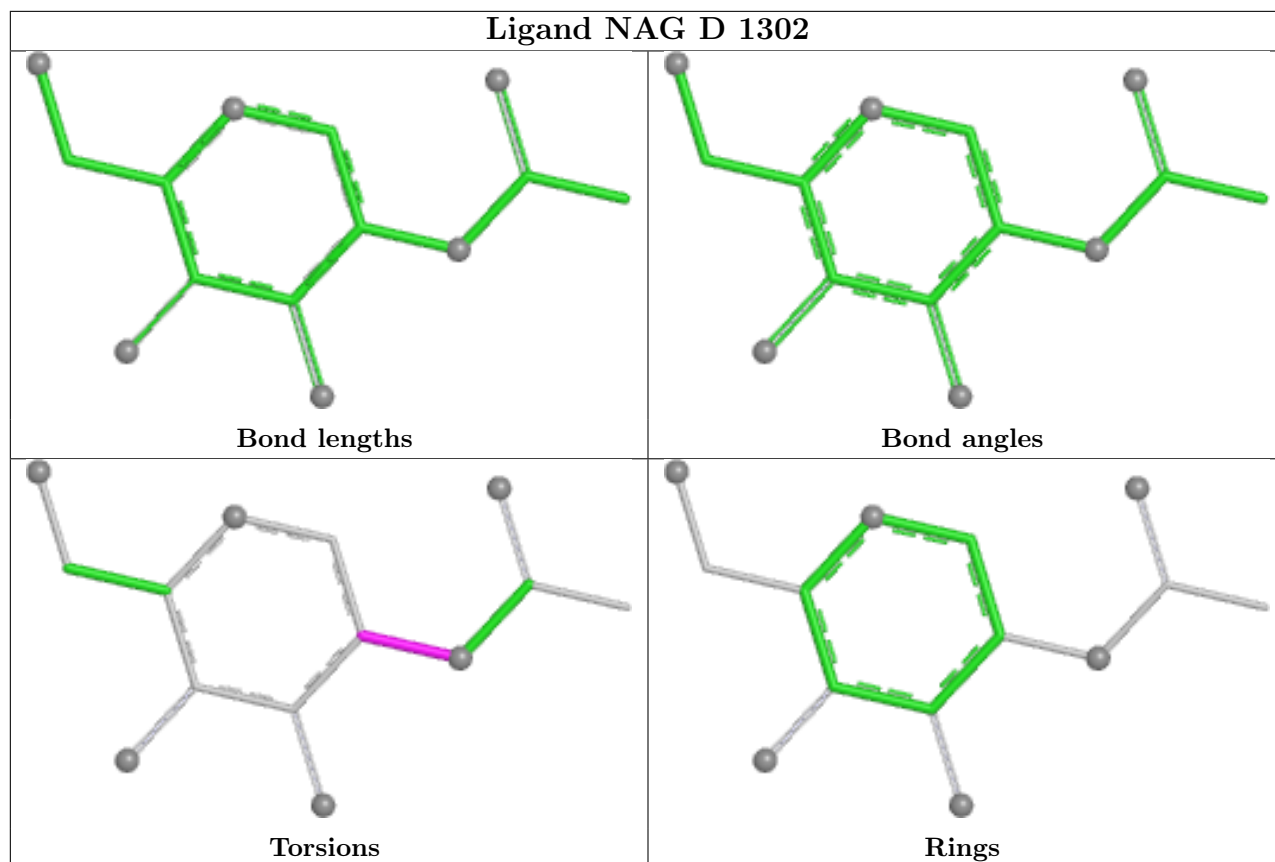


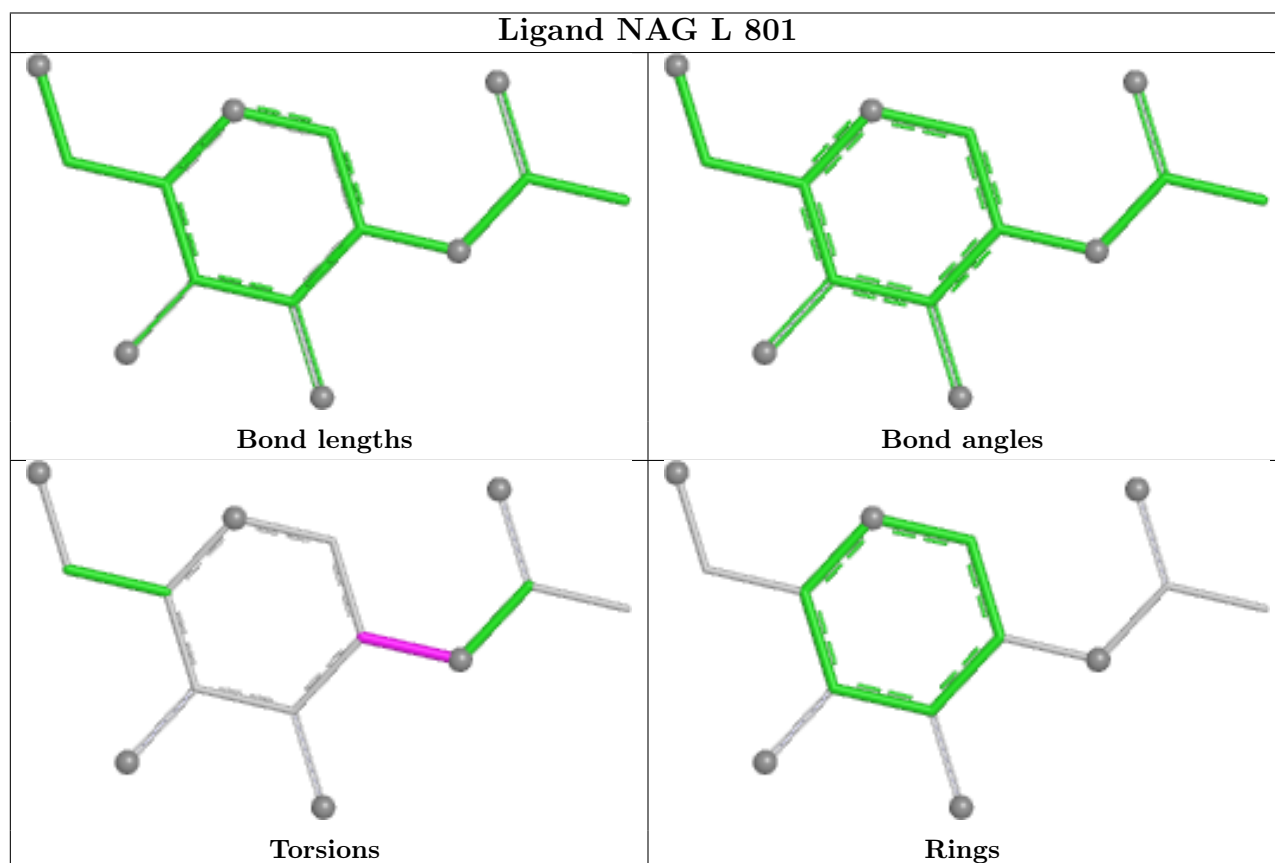
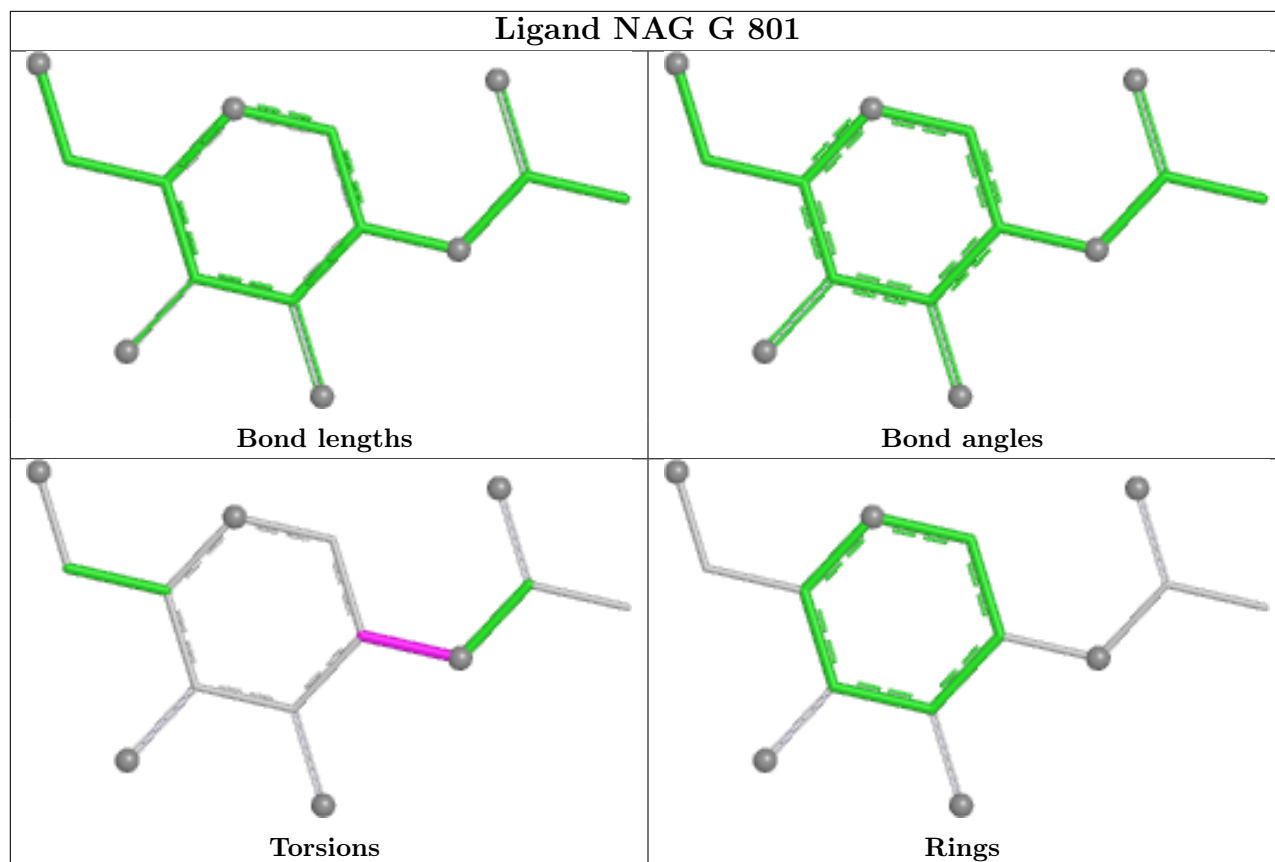


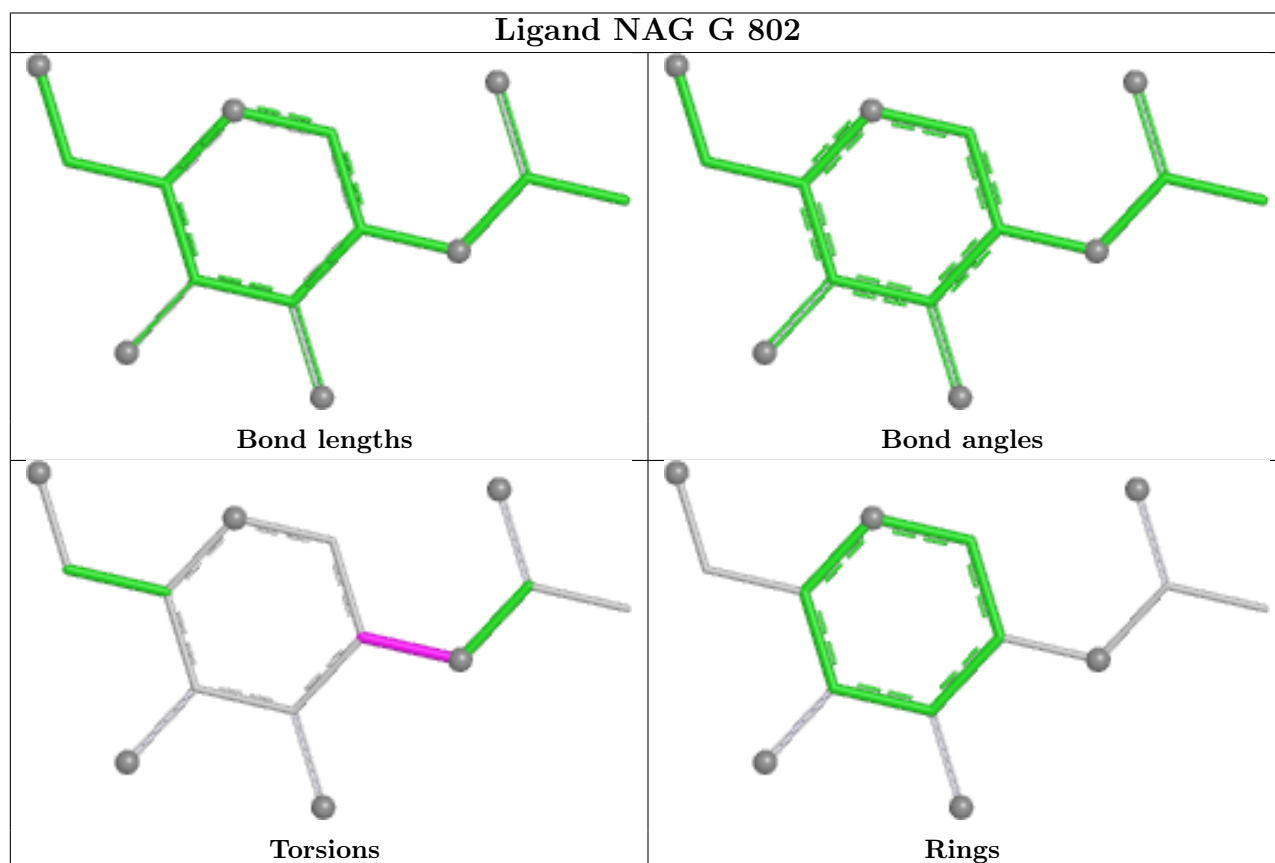
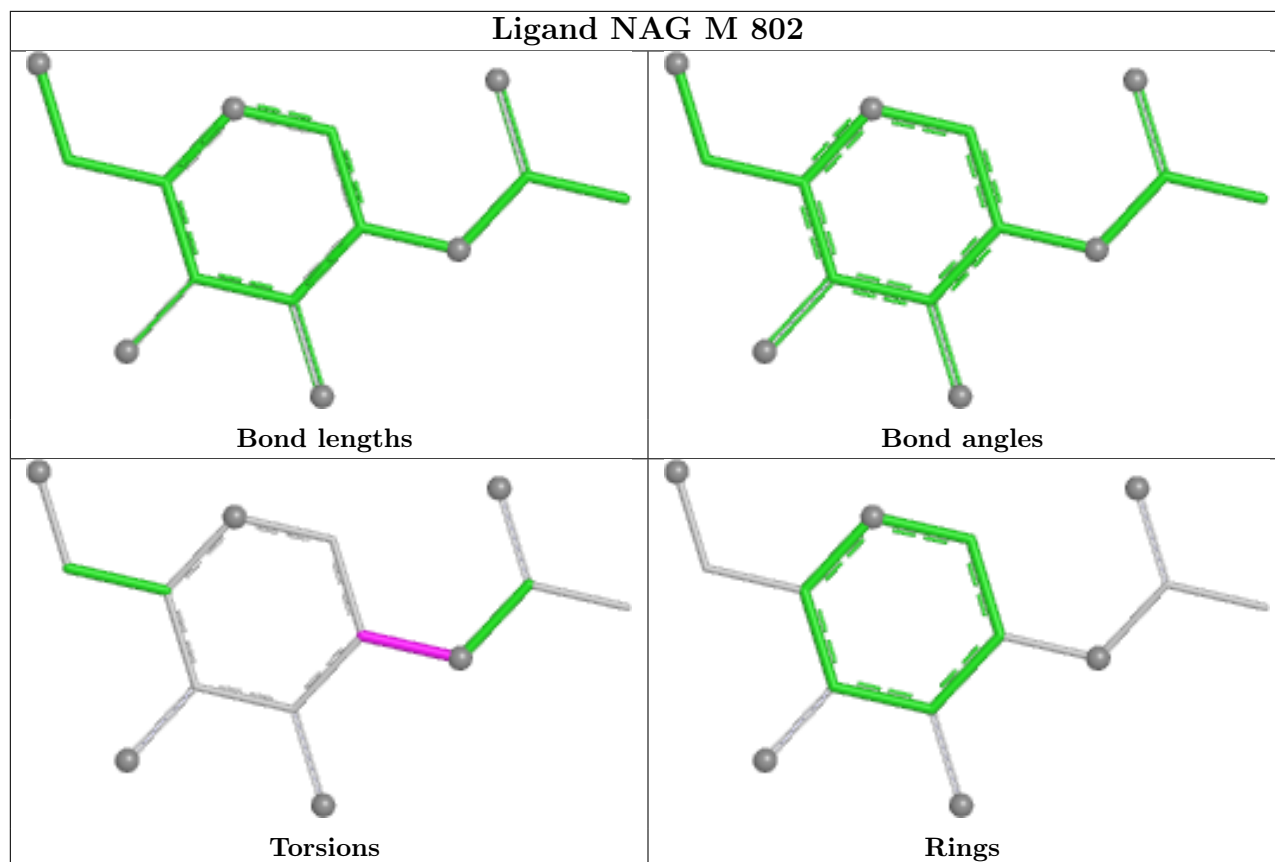


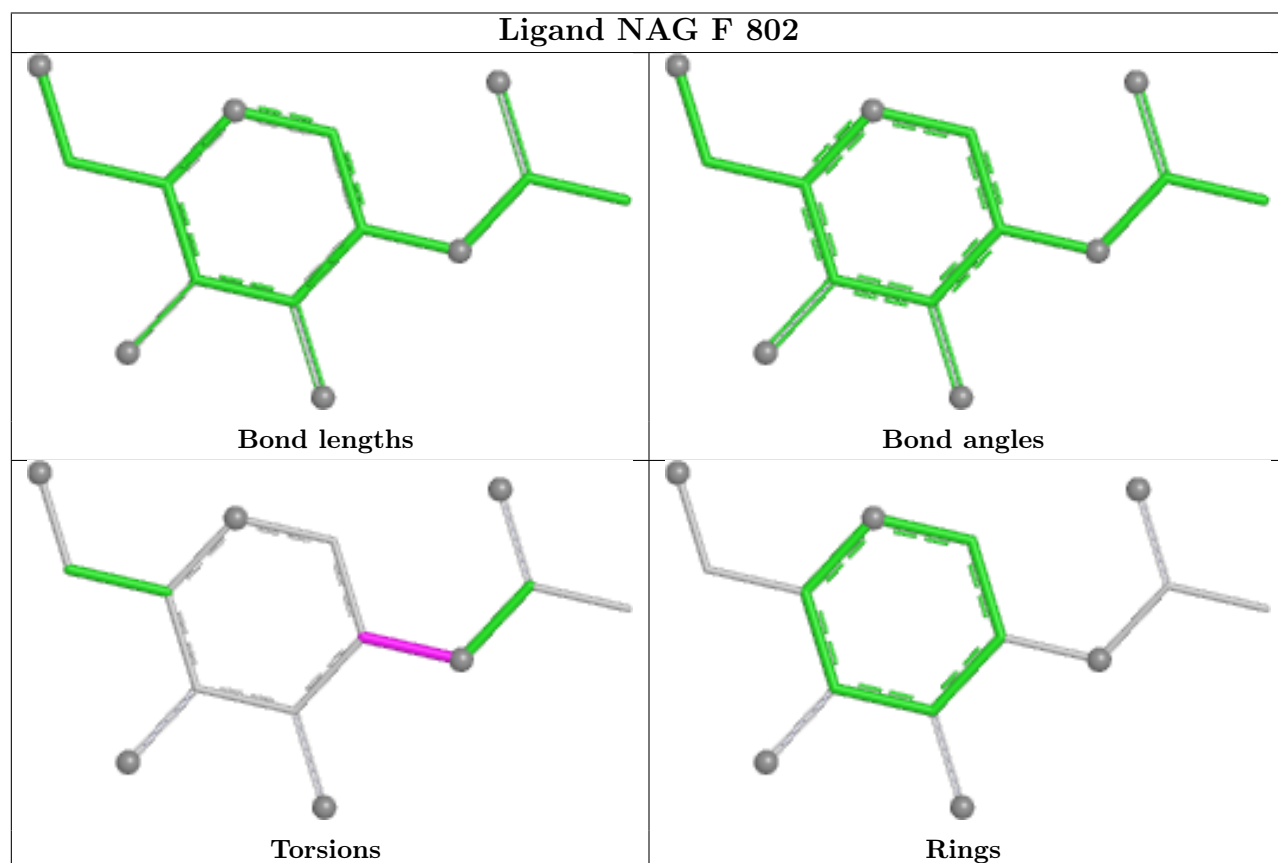
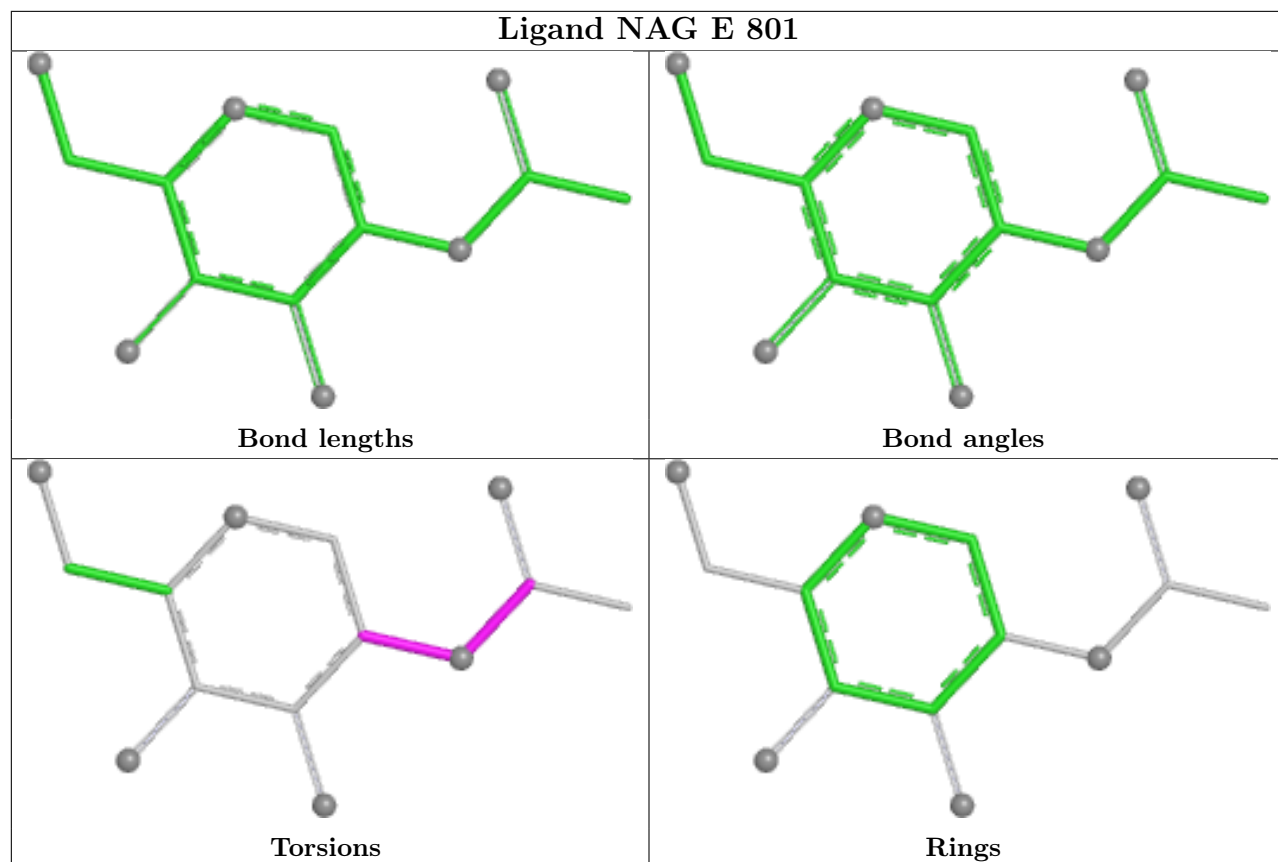


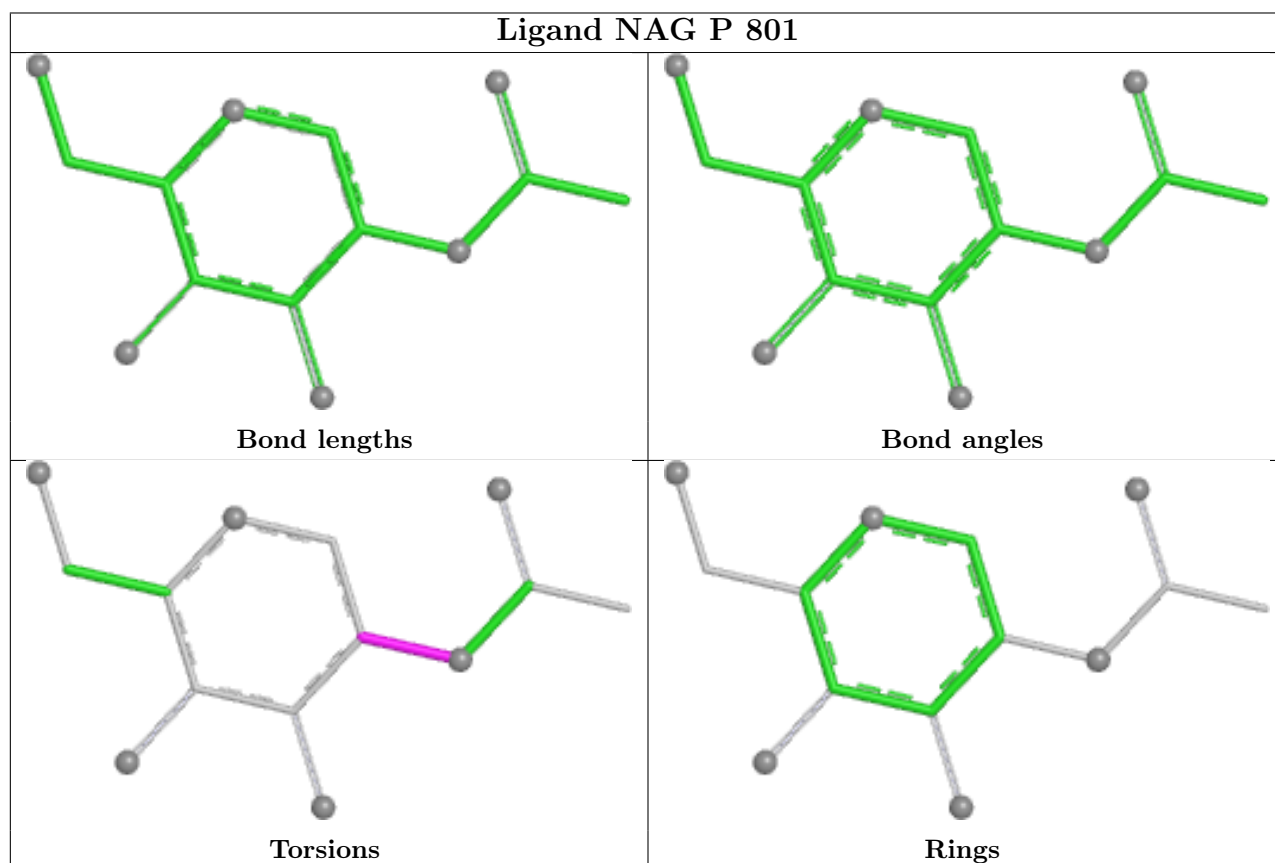
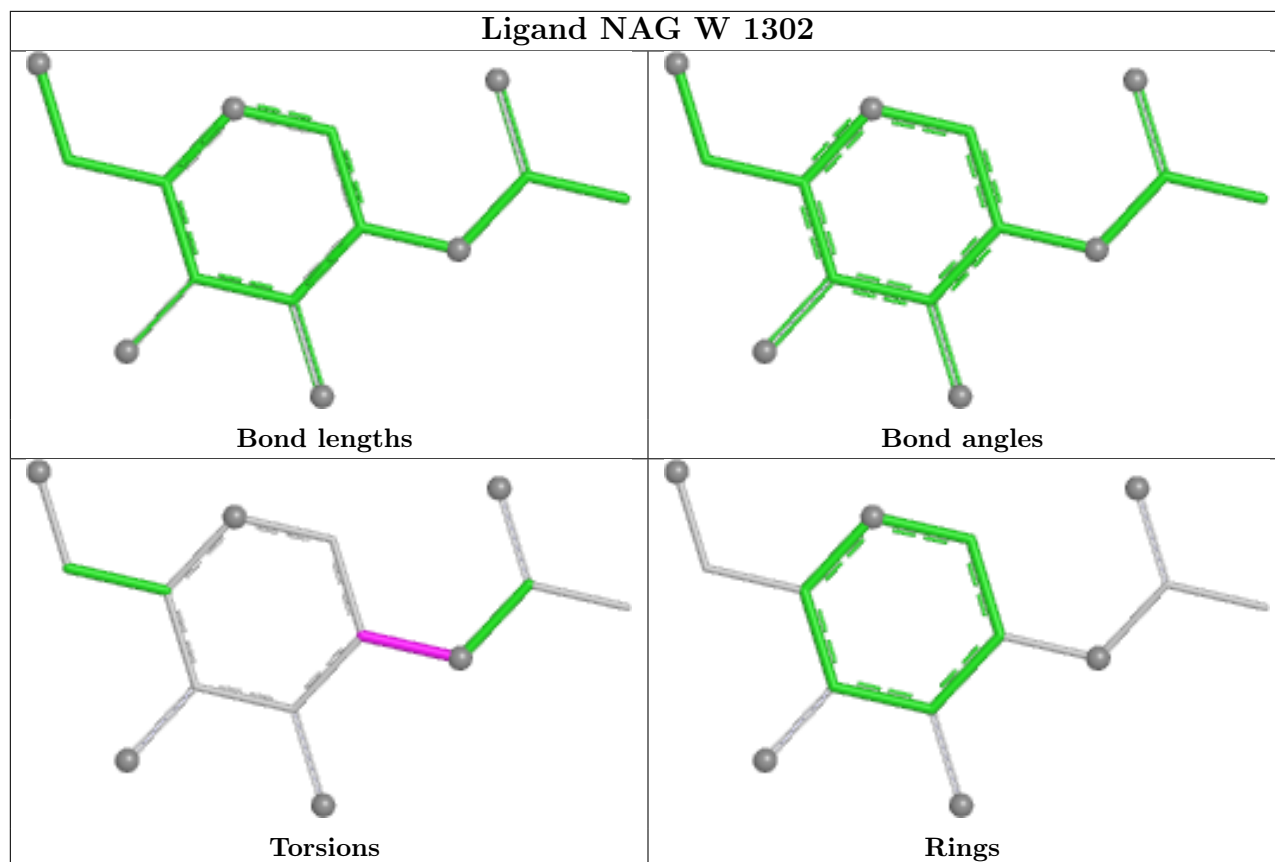


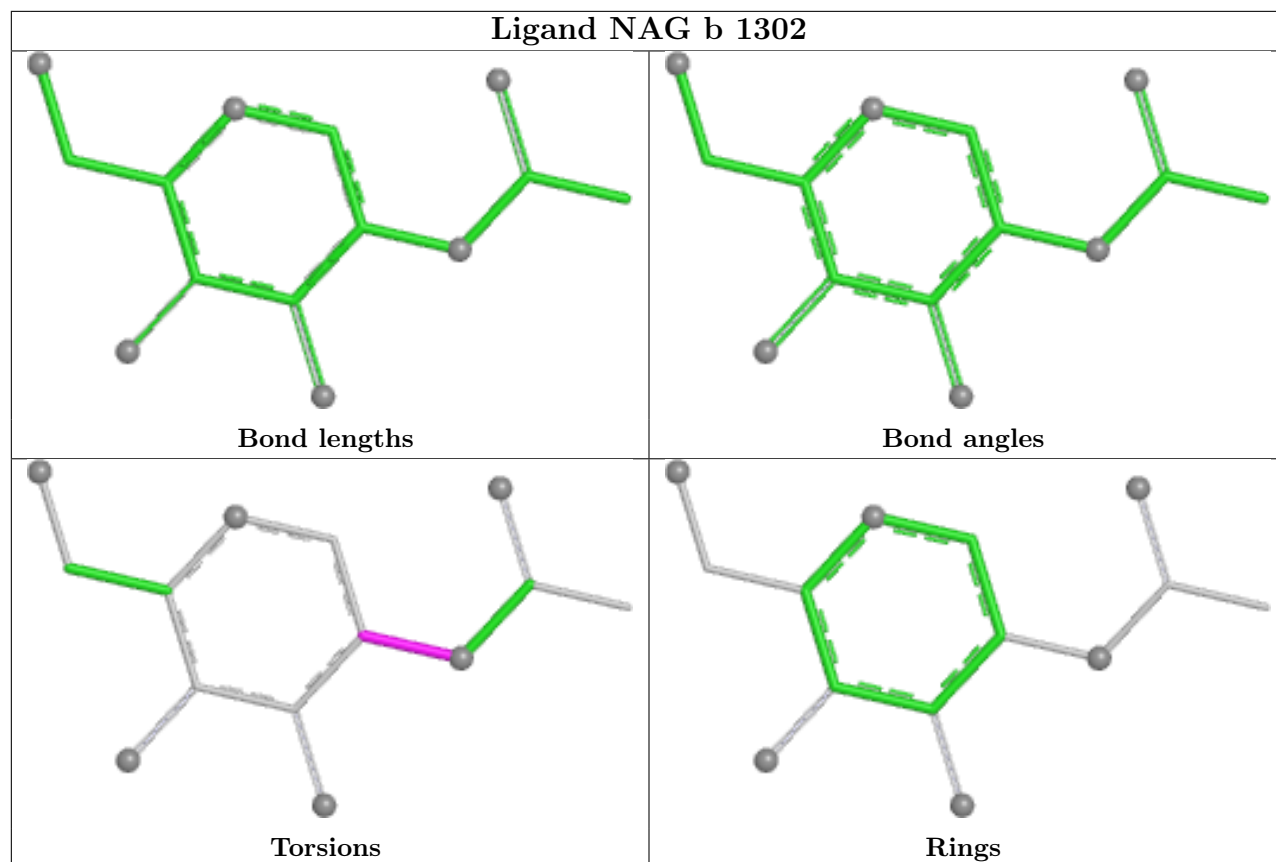












5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [\(i\)](#)

There are no chain breaks in this entry.

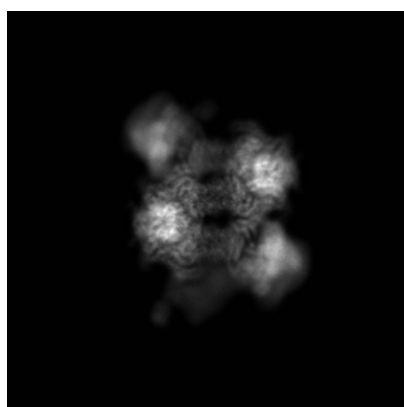
6 Map visualisation [i](#)

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.

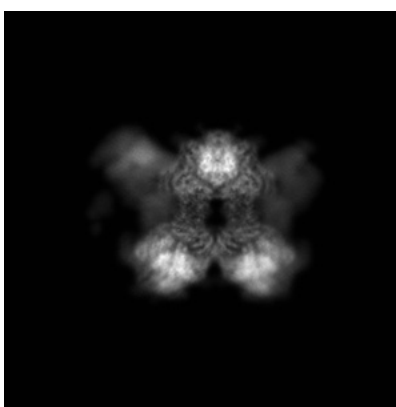
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

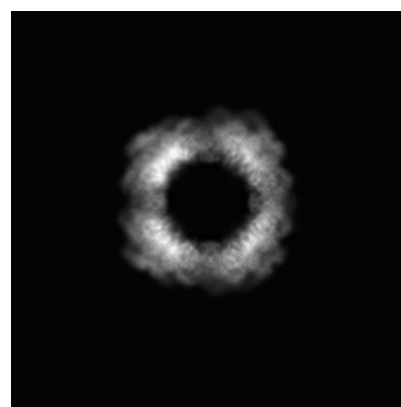
6.1.1 Primary map



X



Y

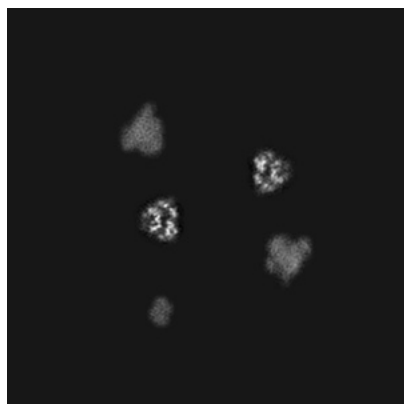


Z

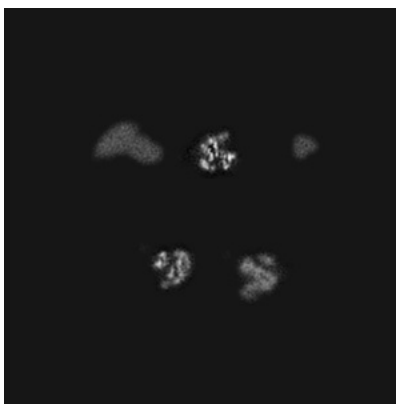
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

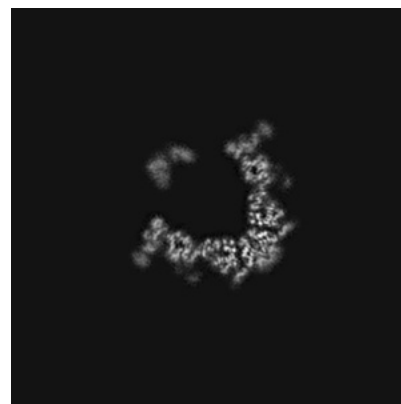
6.2.1 Primary map



X Index: 128



Y Index: 128

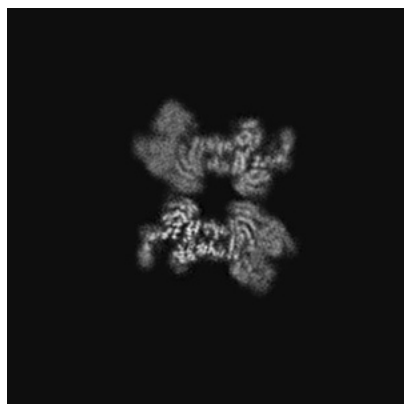


Z Index: 128

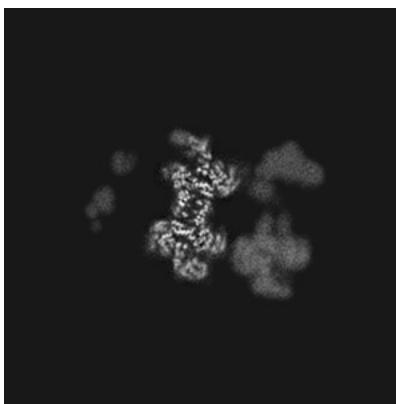
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [\(i\)](#)

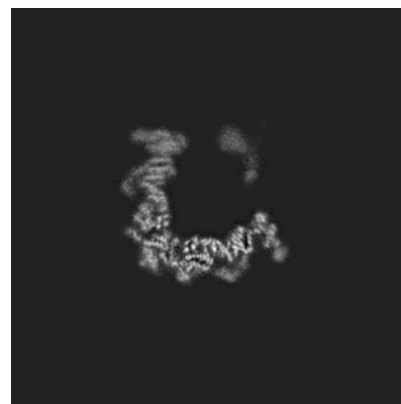
6.3.1 Primary map



X Index: 94



Y Index: 101

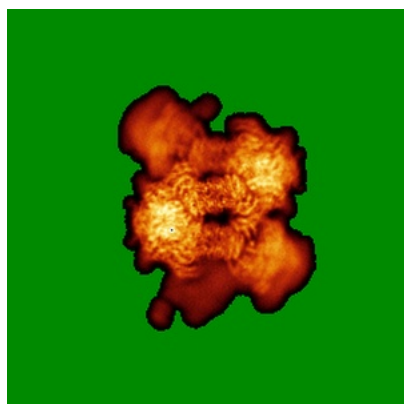


Z Index: 114

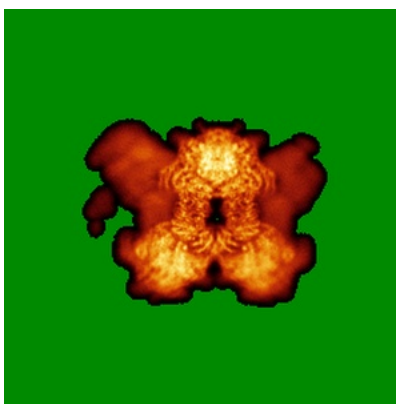
The images above show the largest variance slices of the map in three orthogonal directions.

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

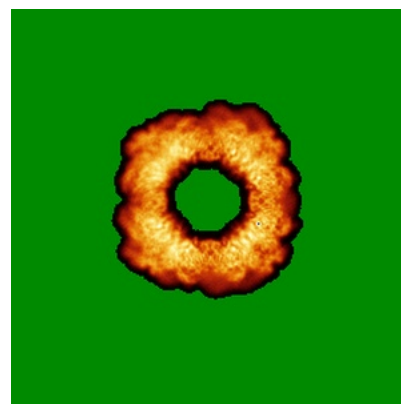
6.4.1 Primary map



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

This section was not generated.

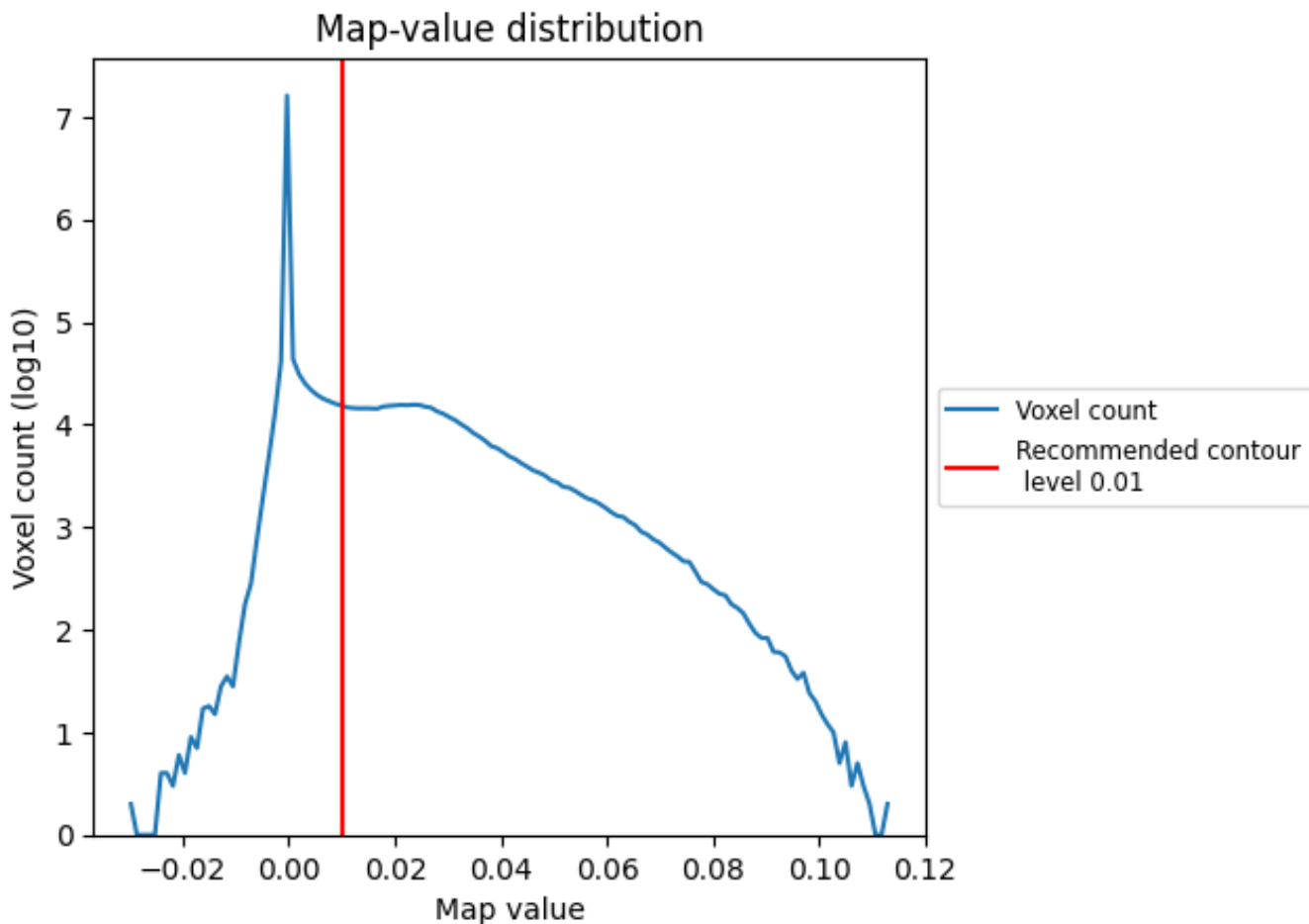
6.6 Mask visualisation

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

7 Map analysis [i](#)

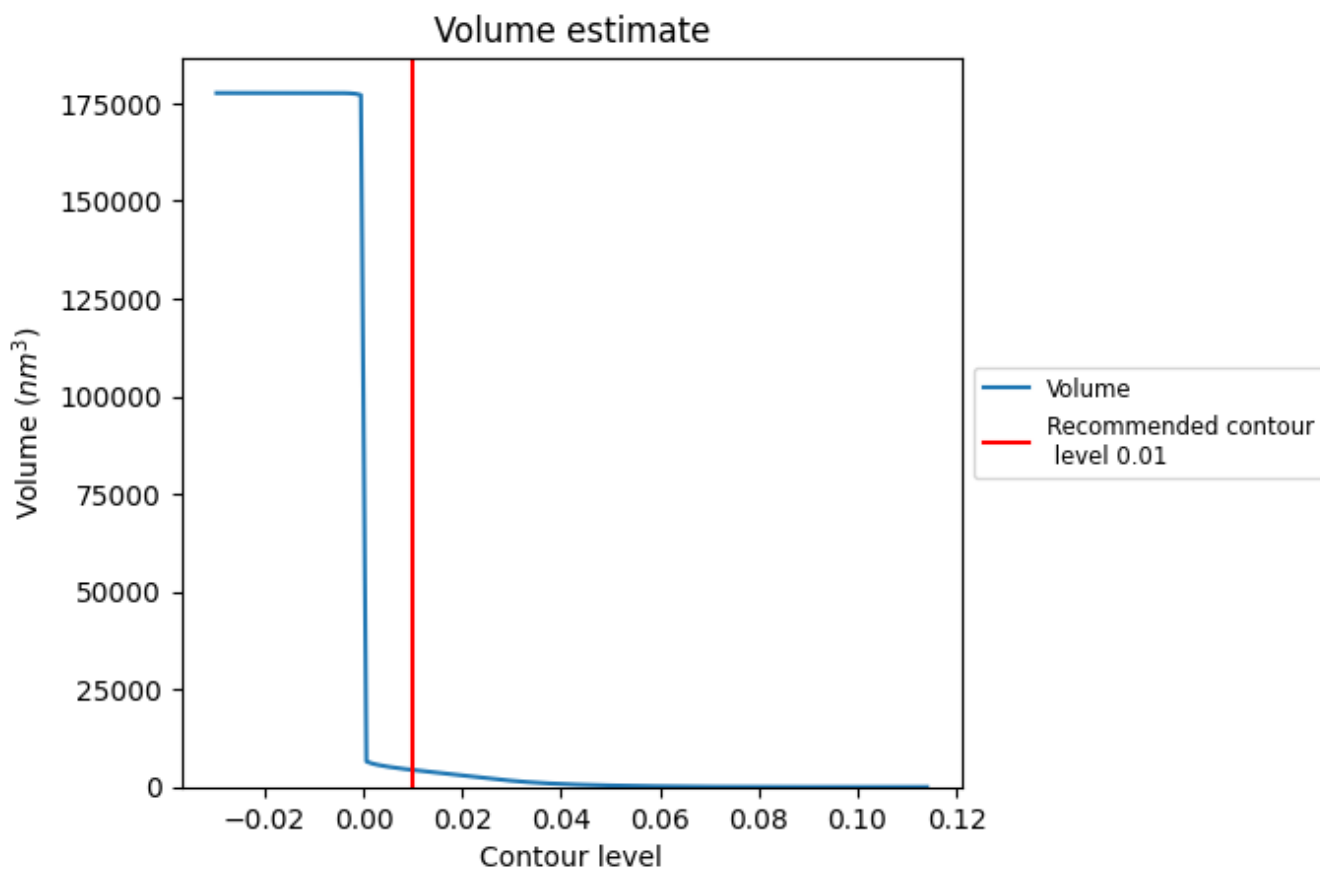
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

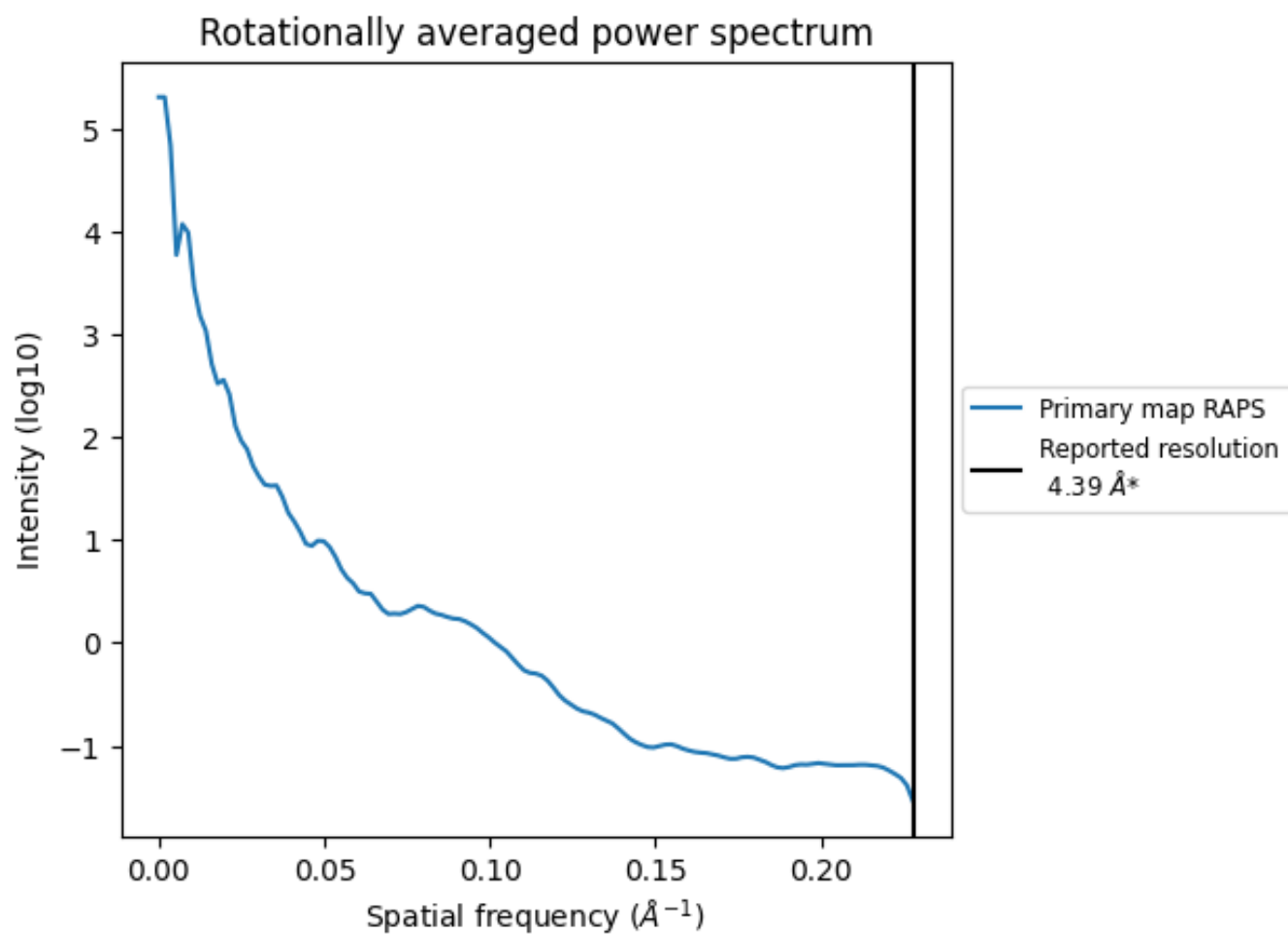
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 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 i



*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.

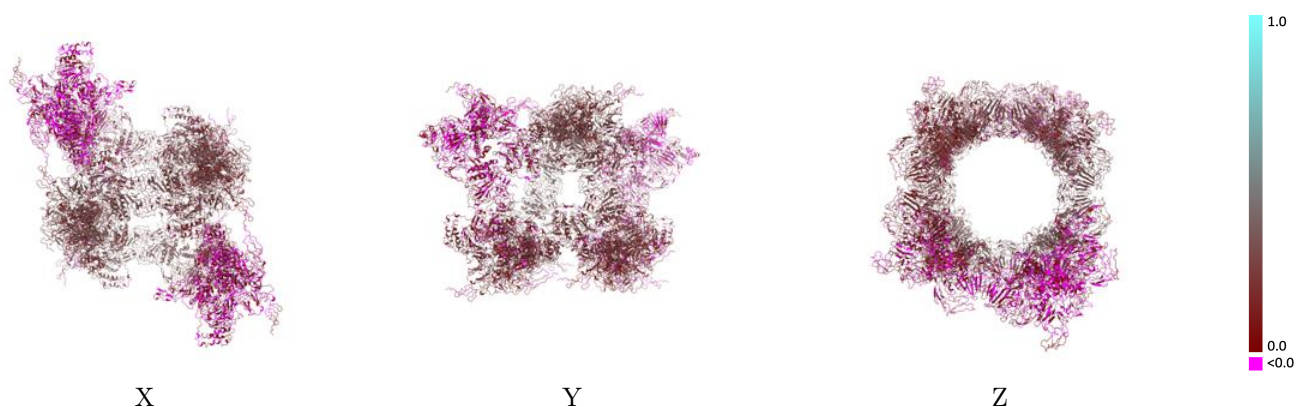
9 Map-model fit [i](#)

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 16.

9.1 Map-model overlay [i](#)

This section was not generated.

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

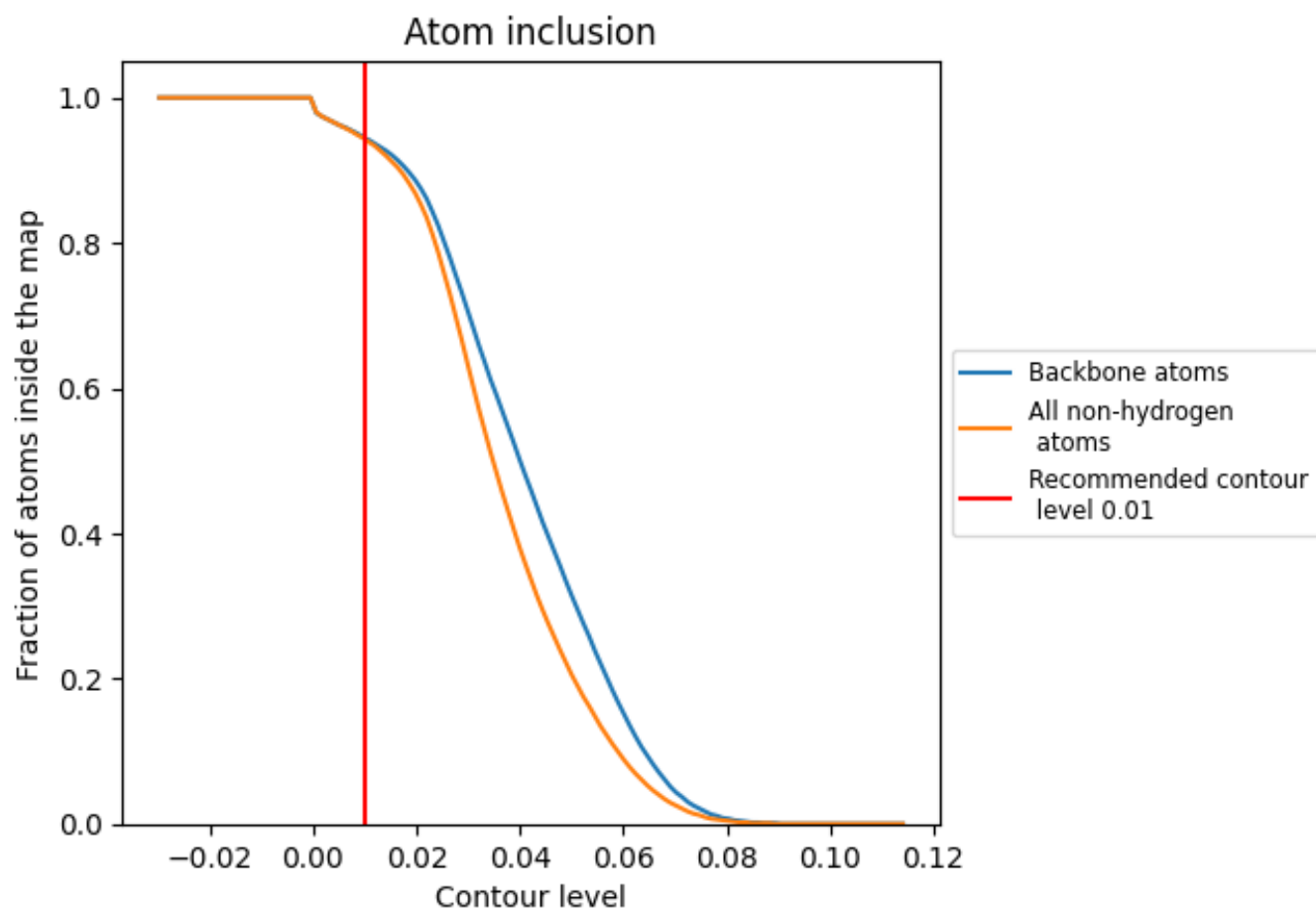


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.



































































9.4 Atom inclusion [i](#)



At the recommended contour level, 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

