



Full wwPDB EM Validation Report ⓘ

Mar 28, 2026 – 07:48 PM UTC

PDB ID : 7WQT / pdb_00007wqt
EMDB ID : EMD-32713
Title : Cryo-EM structure of VWF D'D3 dimer complexed with D1D2 at 4.3 angstrom resolution (VWF tube)
Authors : Zeng, J.W.; Shu, Z.M.; Zhou, A.W.
Deposited on : 2022-01-26
Resolution : 4.30 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.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

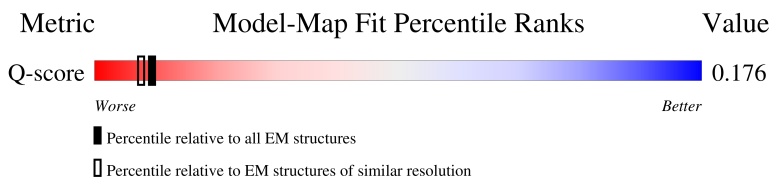
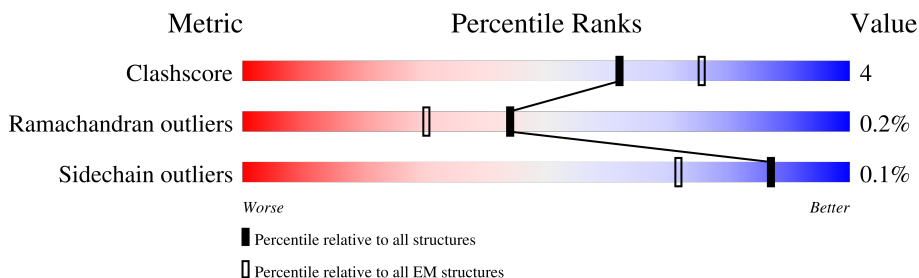
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.30 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	4585 (3.80 - 4.80)

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	 85% 11% .
1	B	741	 84% 12% .
1	E	741	 85% 11% .
1	F	741	 84% 12% .

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Mol	Chain	Length	Quality of chain
1	G	741	 84% 12% .
1	H	741	 86% 10% .
1	I	741	 85% 11% .
1	J	741	 14% 86% 10% .
1	K	741	 18% 83% 13% .
1	L	741	 86% 10% .
1	M	741	 85% 11% .
1	N	741	 84% 11% .
1	O	741	 82% 13% .
1	P	741	 85% 11% .
1	Q	741	 5% 86% 10% .
1	R	741	 32% 86% 10% .
2	C	490	 89% 8% .
2	D	490	 88% 10% .
2	S	490	 88% 9% .
2	T	490	 88% 9% .
2	U	490	 86% 10% ..
2	V	490	 7% 89% 8% .
2	W	490	 88% 9% ..
2	X	490	 20% 90% 8% .
2	Y	490	 28% 89% 8% .
2	Z	490	 85% 12% ..
2	a	490	 88% 9% .
2	b	490	 88% 10% .
2	c	490	 8% 90% 8% .

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Mol	Chain	Length	Quality of chain
2	d	490	
2	e	490	
2	f	490	

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

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
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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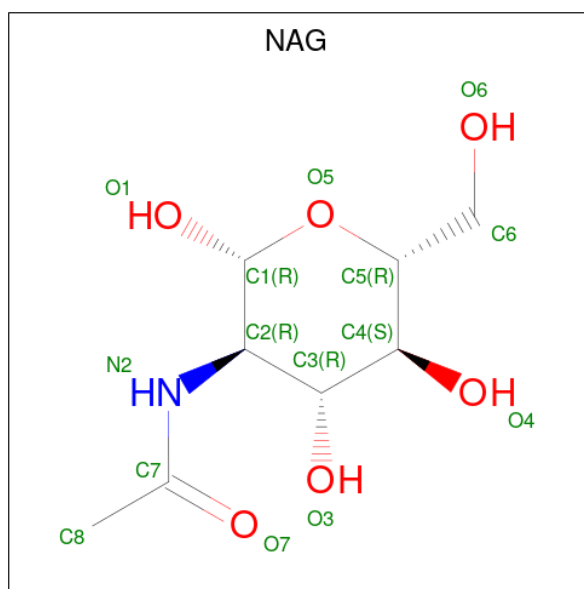
Chain	Residue	Modelled	Actual	Comment	Reference
V	1244	VAL	-	expression tag	UNP P04275
V	1245	VAL	-	expression tag	UNP P04275
V	1246	PRO	-	expression tag	UNP P04275
V	1247	PRO	-	expression tag	UNP P04275
V	1248	HIS	-	expression tag	UNP P04275
V	1249	HIS	-	expression tag	UNP P04275
V	1250	HIS	-	expression 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: $C_8H_{15}NO_6$) (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 14	C 8	N 1	O 5	0
3	B	1	Total 14	C 8	N 1	O 5	0
3	B	1	Total 14	C 8	N 1	O 5	0
3	b	1	Total 14	C 8	N 1	O 5	0
3	b	1	Total 14	C 8	N 1	O 5	0
3	C	1	Total 14	C 8	N 1	O 5	0
3	C	1	Total 14	C 8	N 1	O 5	0
3	D	1	Total 14	C 8	N 1	O 5	0
3	D	1	Total 14	C 8	N 1	O 5	0
3	d	1	Total 14	C 8	N 1	O 5	0
3	E	1	Total 14	C 8	N 1	O 5	0
3	E	1	Total 14	C 8	N 1	O 5	0
3	F	1	Total 14	C 8	N 1	O 5	0
3	F	1	Total 14	C 8	N 1	O 5	0
3	G	1	Total 14	C 8	N 1	O 5	0
3	G	1	Total 14	C 8	N 1	O 5	0
3	I	1	Total 14	C 8	N 1	O 5	0
3	I	1	Total 14	C 8	N 1	O 5	0
3	L	1	Total 14	C 8	N 1	O 5	0
3	L	1	Total 14	C 8	N 1	O 5	0
3	M	1	Total 14	C 8	N 1	O 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	

Continued on next page...

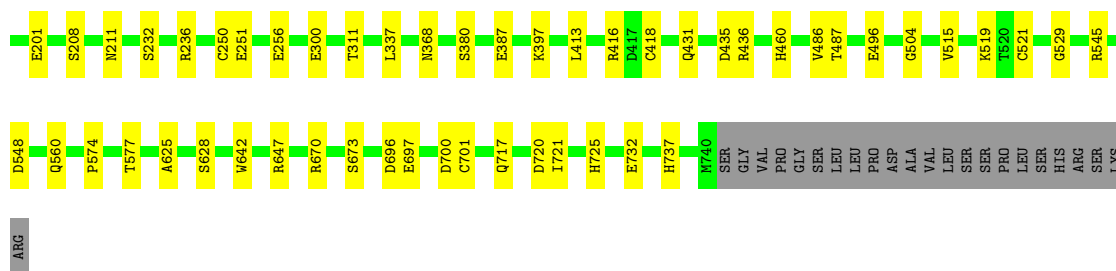
Continued from previous page...

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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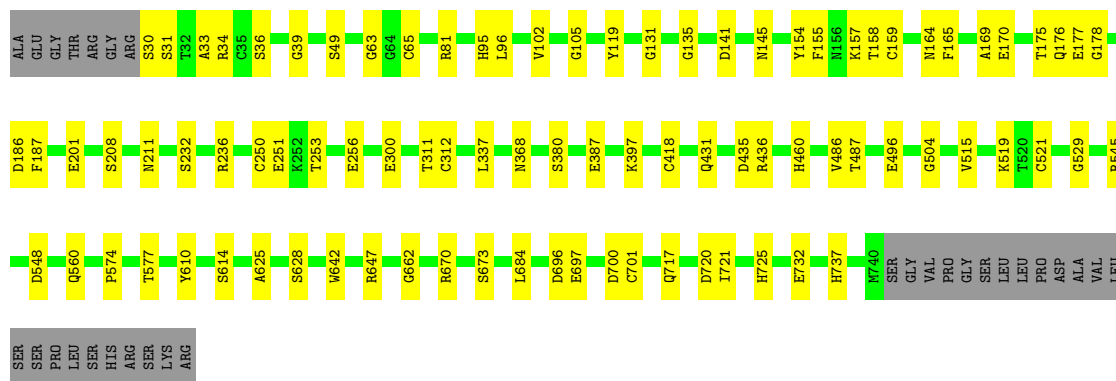
Continued from previous page...

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



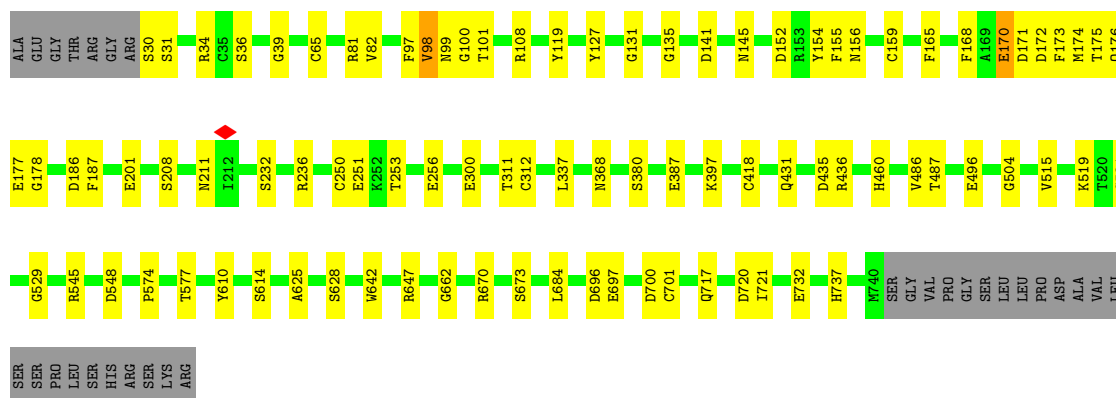
- Molecule 1: von Willebrand antigen 2

Chain F: 84% 12% .



- Molecule 1: von Willebrand antigen 2

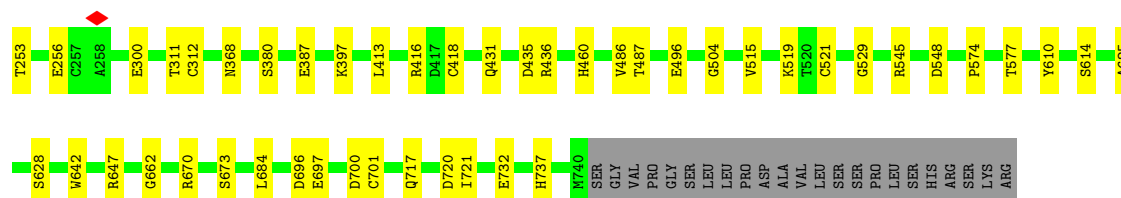
Chain G: 84% 12% .



- Molecule 1: von Willebrand antigen 2

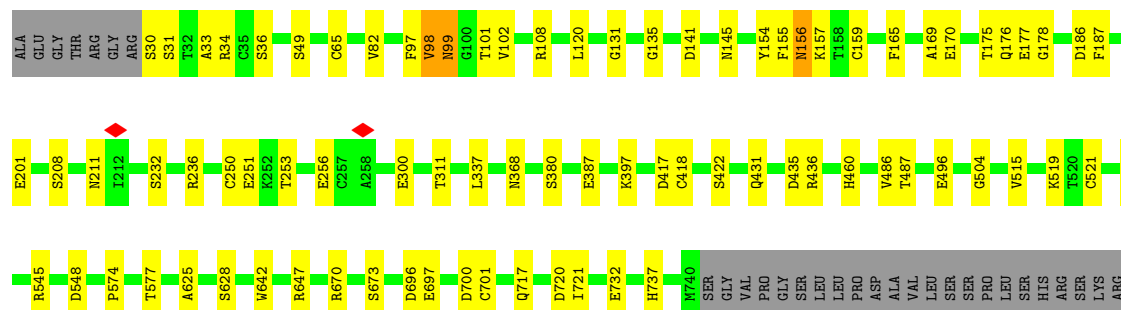
Chain H: 86% 10% .





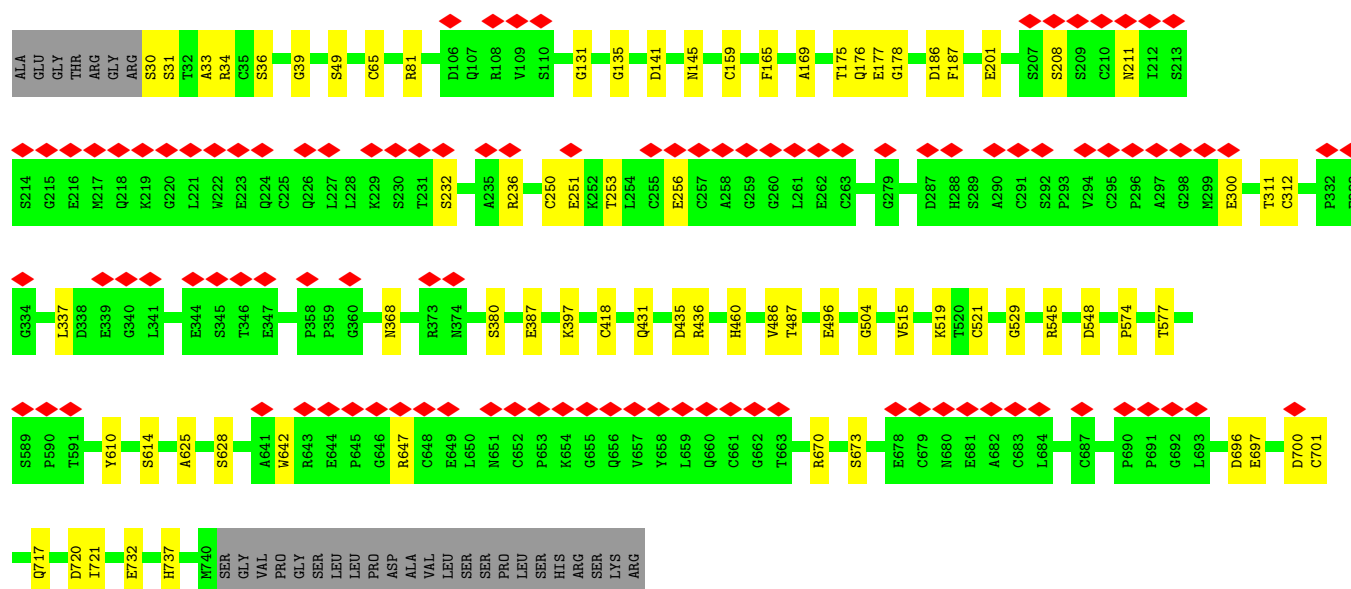
• Molecule 1: von Willebrand antigen 2

Chain I: 85% 11%



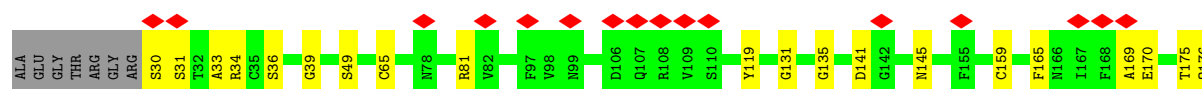
• Molecule 1: von Willebrand antigen 2

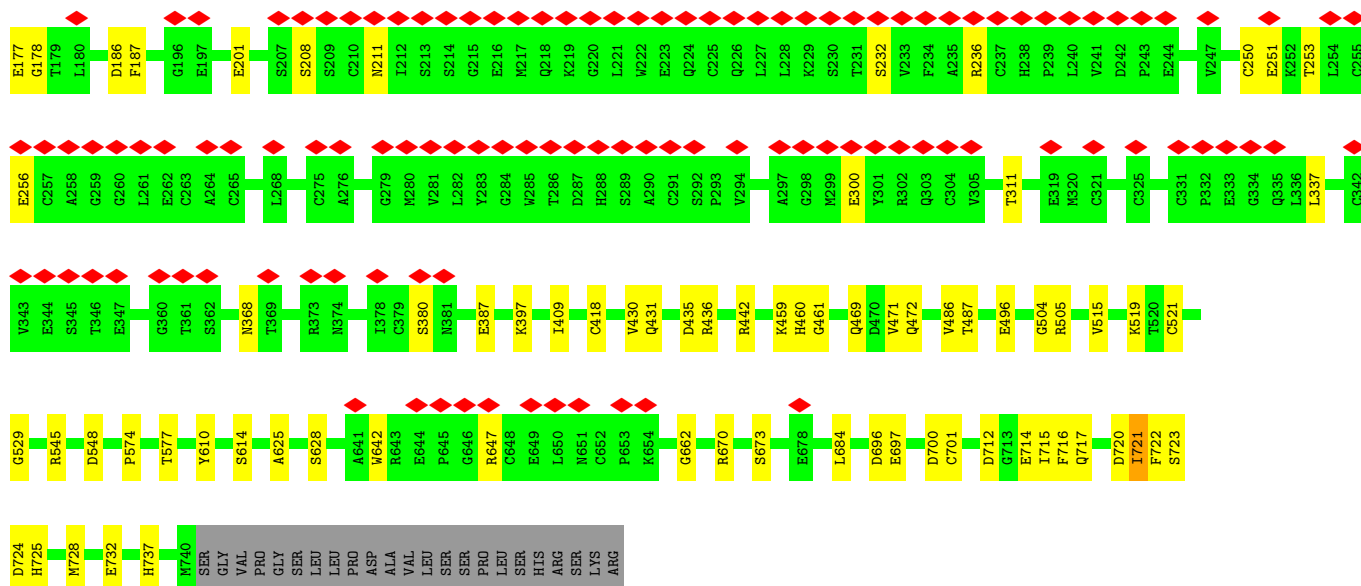
Chain J: 14% 86% 10%



• Molecule 1: von Willebrand antigen 2

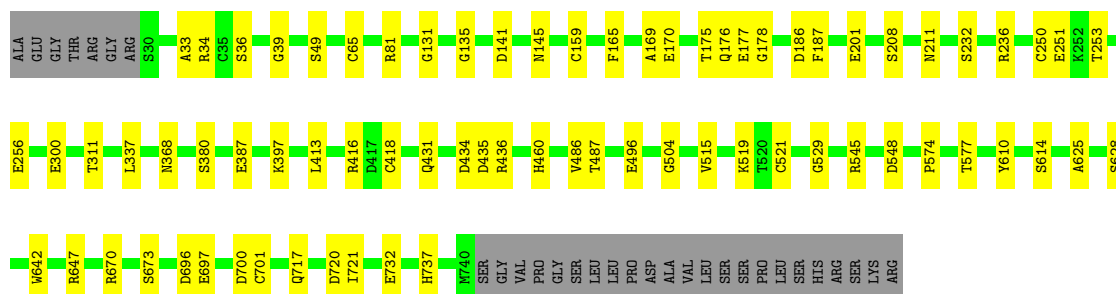
Chain K: 18% 83% 13%





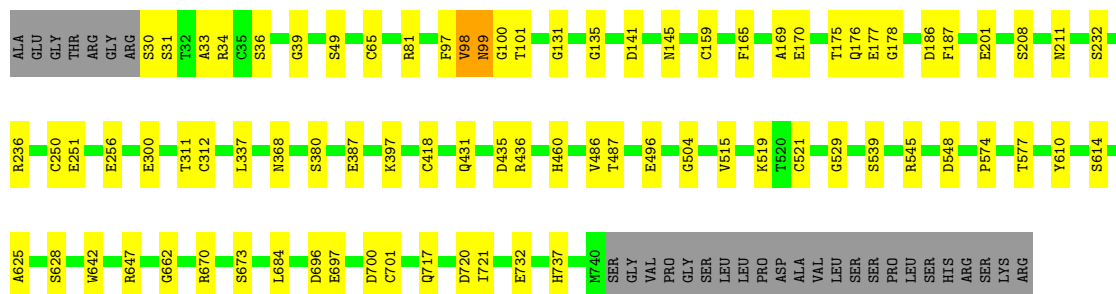
• Molecule 1: von Willebrand antigen 2

Chain L: 86% 10% .



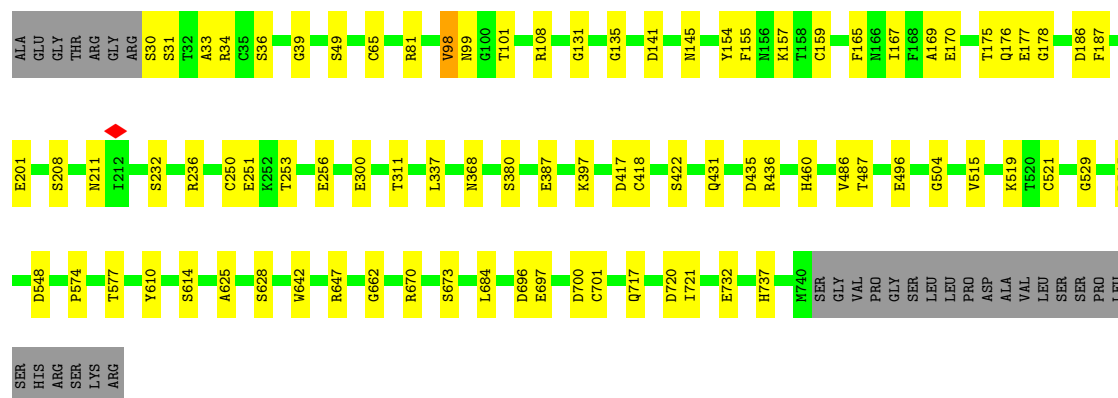
• Molecule 1: von Willebrand antigen 2

Chain M: 85% 11% .



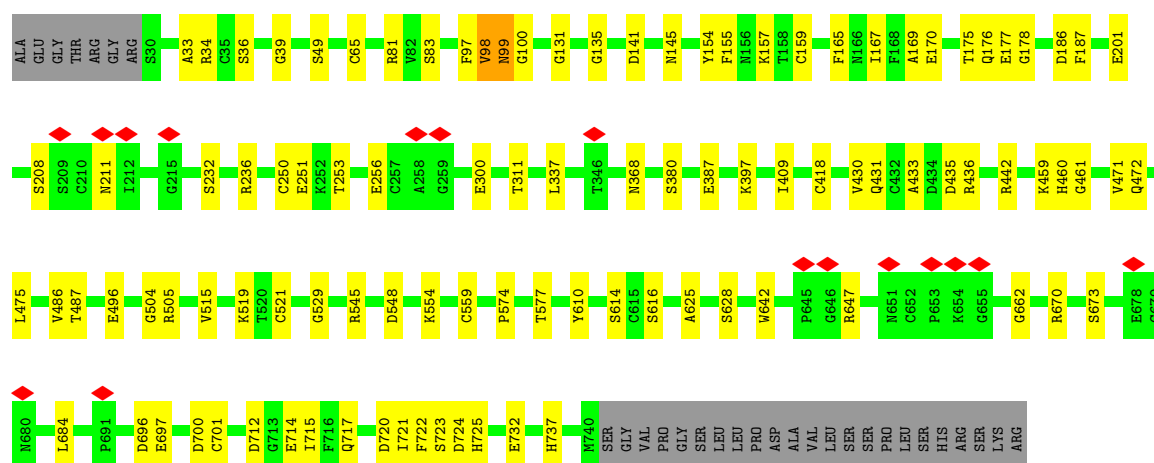
• Molecule 1: von Willebrand antigen 2

Chain N: 84% 11% .



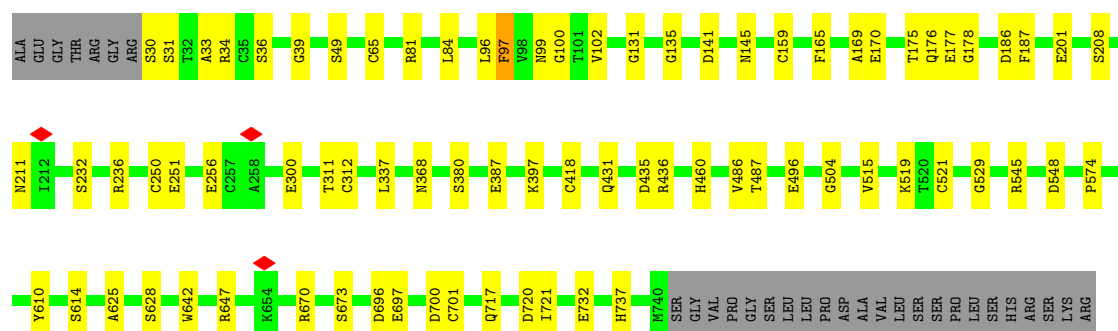
• Molecule 1: von Willebrand antigen 2

Chain O: 82% 13% .



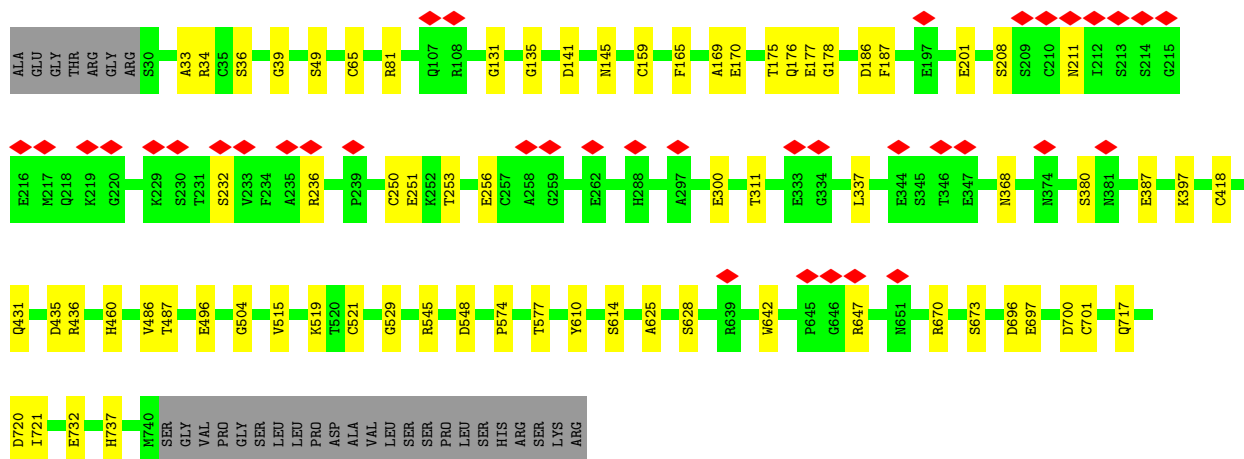
• Molecule 1: von Willebrand antigen 2

Chain P: 85% 11% .

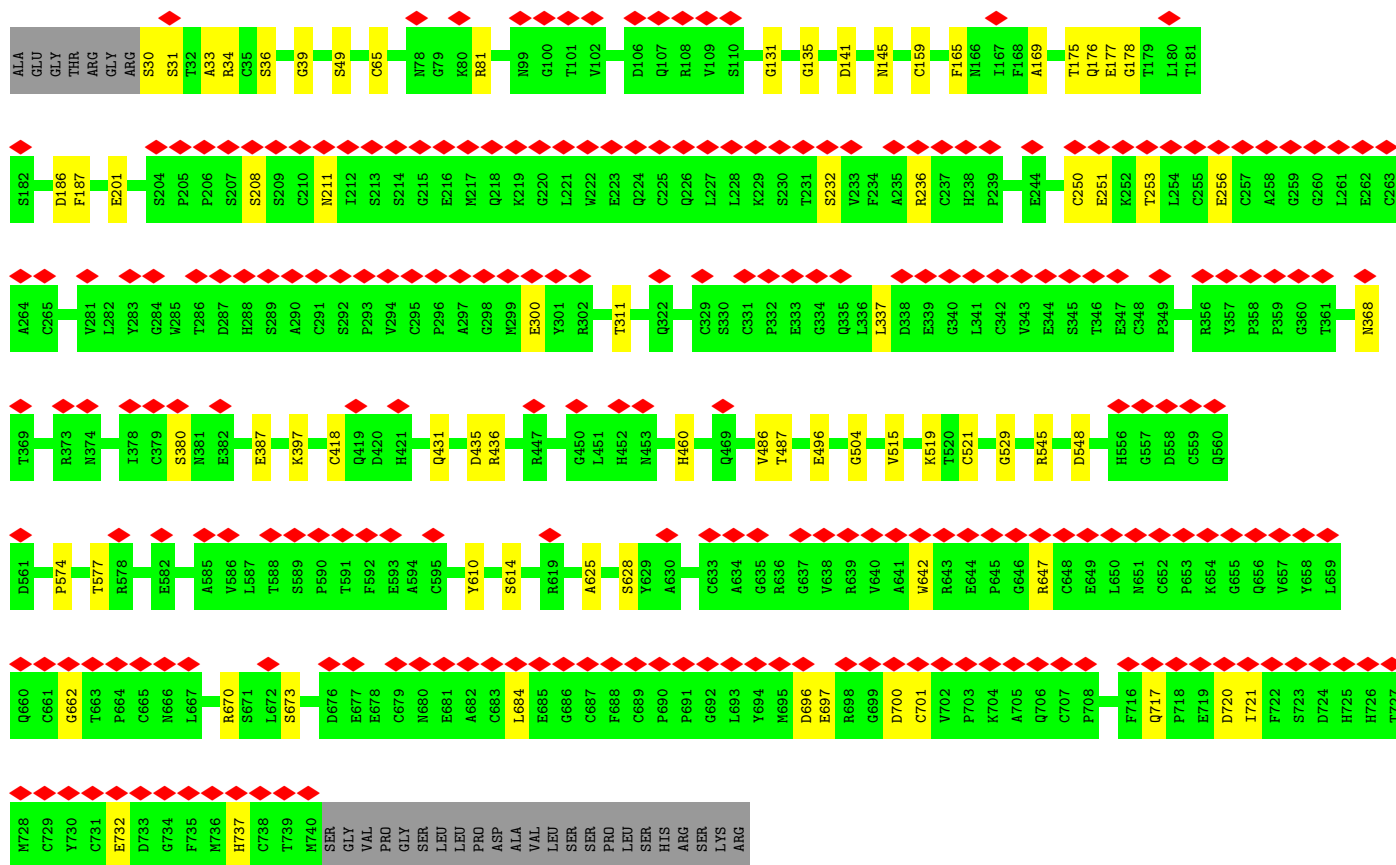
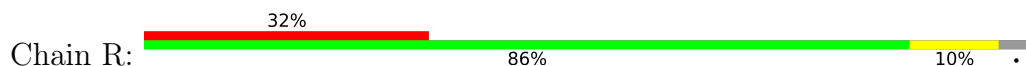


• Molecule 1: von Willebrand antigen 2

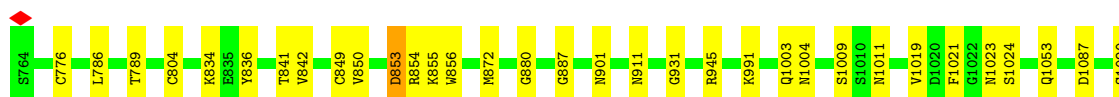
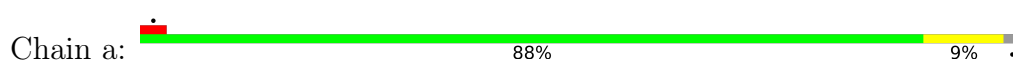
Chain Q: 5% 86% 10% .

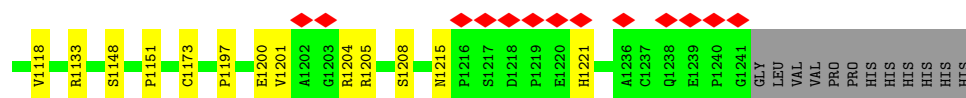


• Molecule 1: von Willebrand antigen 2



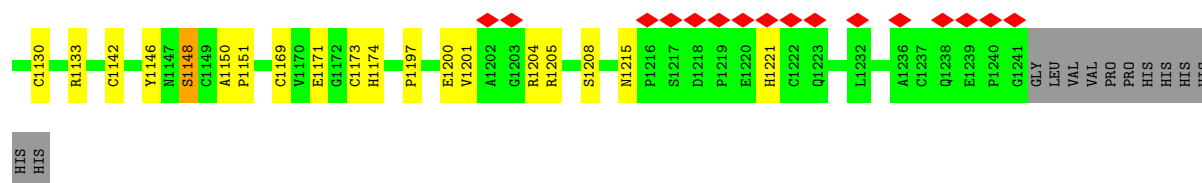
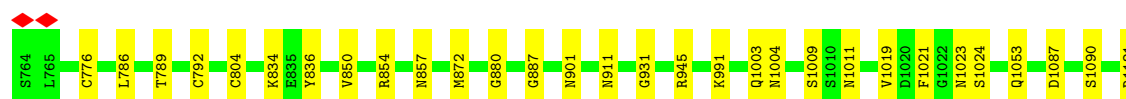
• Molecule 2: von Willebrand factor





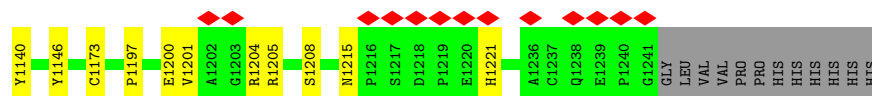
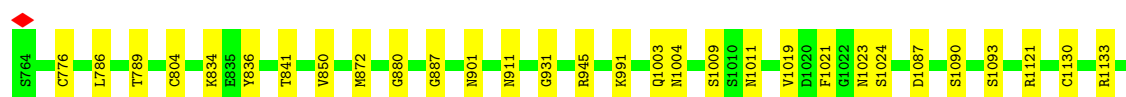
• Molecule 2: von Willebrand factor

Chain b: 88% 10% .



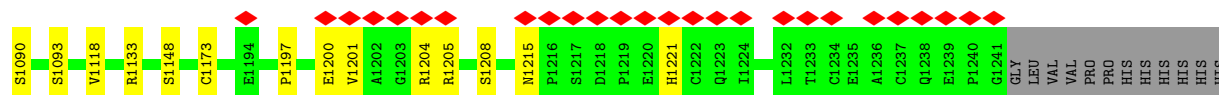
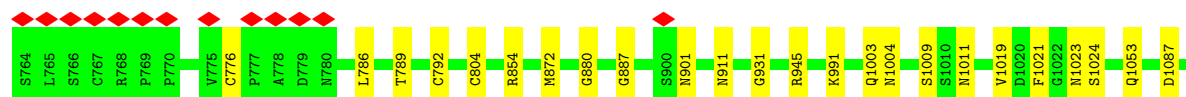
• Molecule 2: von Willebrand factor

Chain C: 89% 8% .



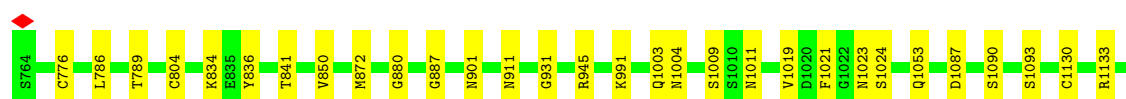
• Molecule 2: von Willebrand factor

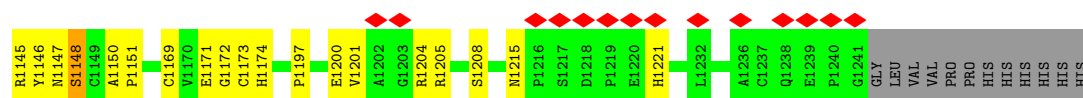
Chain c: 8% 90% 8% .



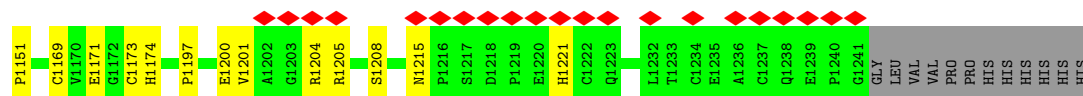
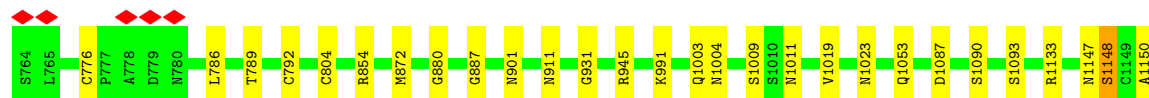
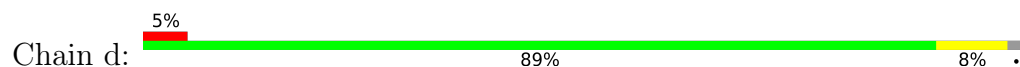
• Molecule 2: von Willebrand factor

Chain D: 88% 10% .

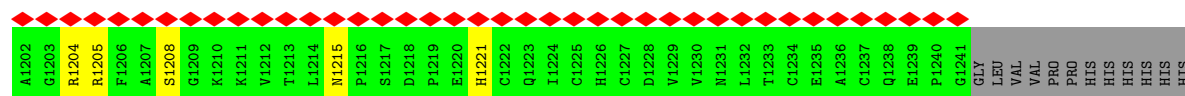
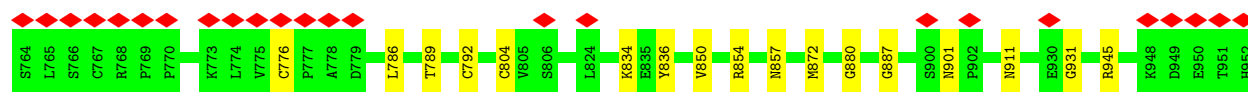
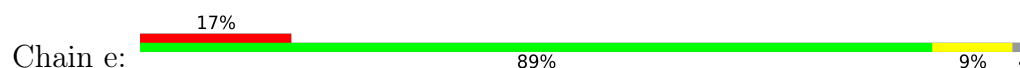




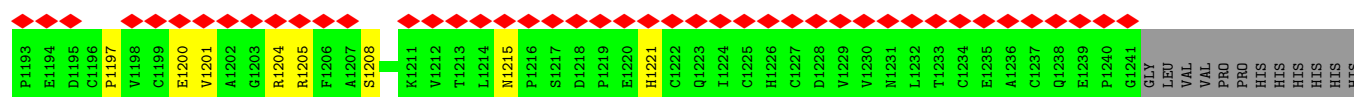
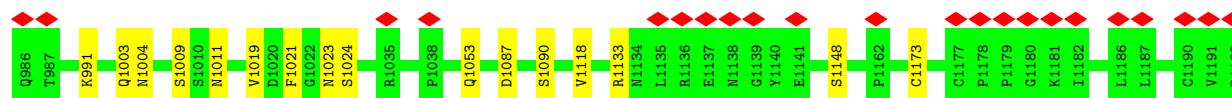
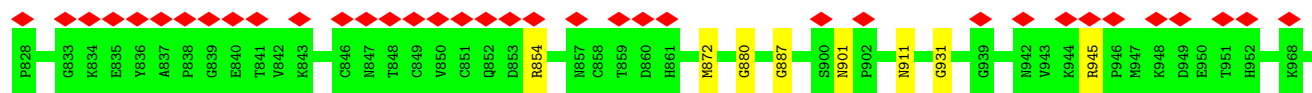
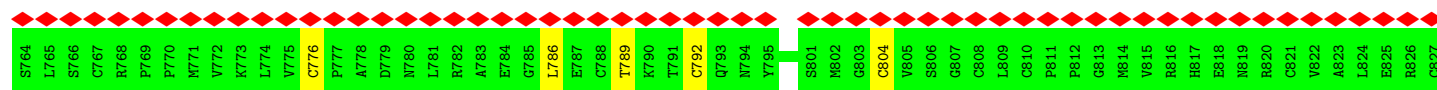
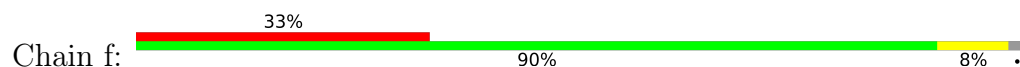
- Molecule 2: von Willebrand factor



- Molecule 2: von Willebrand factor

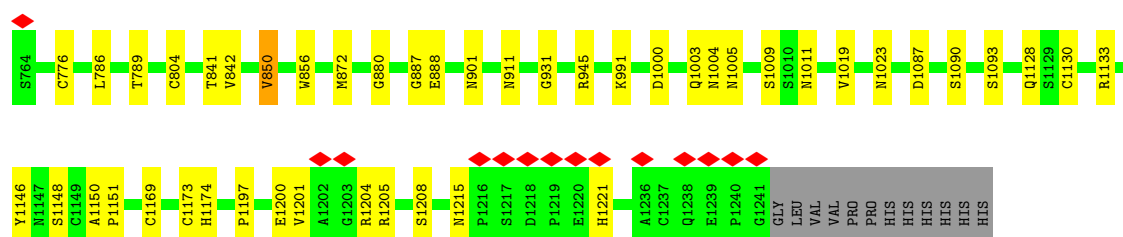


- Molecule 2: von Willebrand factor



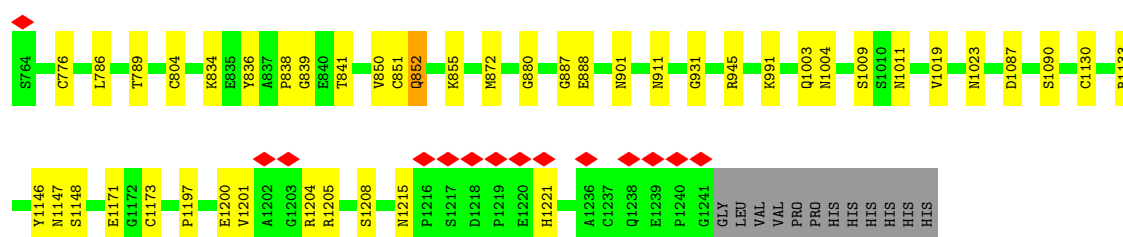
- Molecule 2: von Willebrand factor

Chain S:  88% 9% .



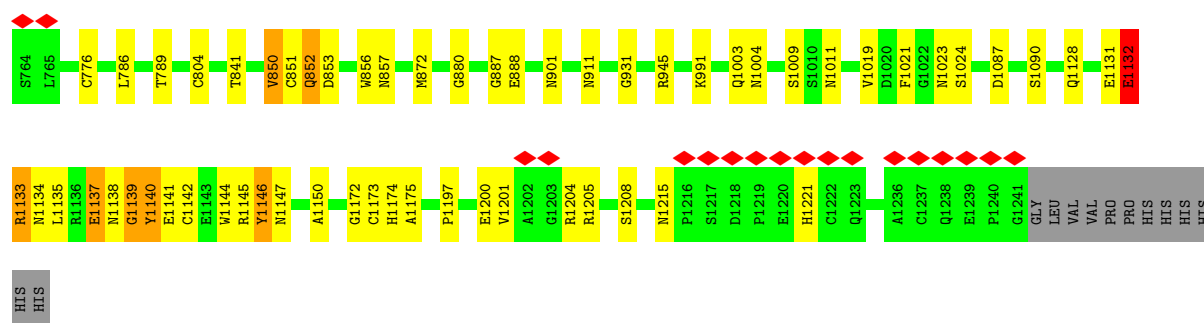
- Molecule 2: von Willebrand factor

Chain T:  88% 9% .

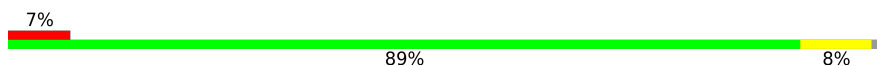


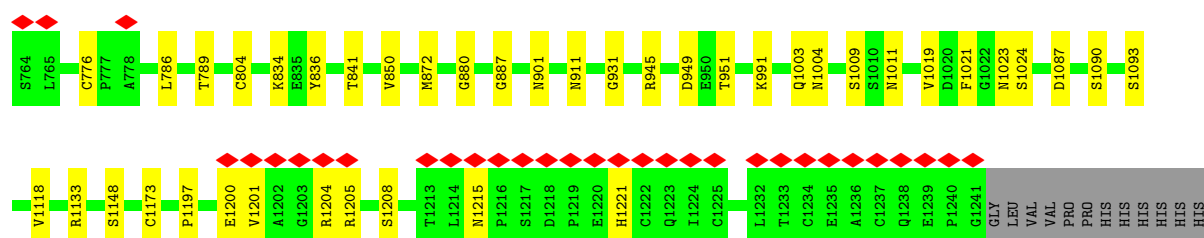
- Molecule 2: von Willebrand factor

Chain U:  86% 10% ..



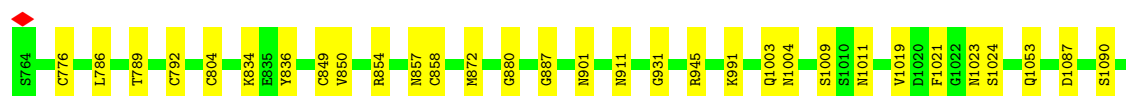
- Molecule 2: von Willebrand factor

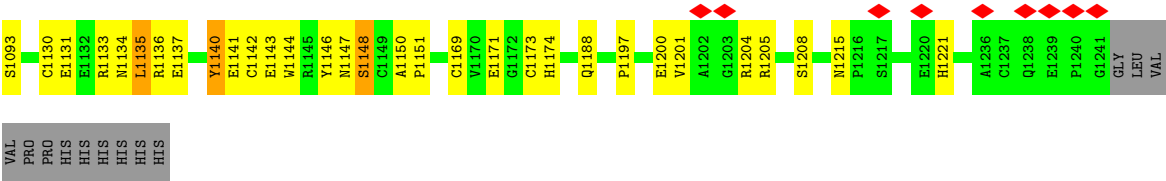
Chain V:  7% 89% 8% .



- Molecule 2: von Willebrand factor

Chain W:  88% 9% ..





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	220564	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	0.037	Depositor
Minimum map value	-0.010	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.003	Depositor
Map size (Å)	329.37, 345.8385, 425.9852	wwPDB
Map dimensions	300, 315, 388	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0979, 1.0979, 1.0979	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	0.35	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	0.36	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	0.31	0/3728	0.50	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.

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

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Mol	Chain	Res	Type	Group
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 [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	49	0
1	B	5421	0	5001	61	0
1	E	5421	0	5000	53	0
1	F	5421	0	5001	54	0
1	G	5421	0	5000	60	0
1	H	5421	0	5003	45	0
1	I	5421	0	5001	49	0
1	J	5421	0	5003	42	0
1	K	5421	0	5003	110	0
1	L	5421	0	5000	42	0
1	M	5421	0	5001	49	0
1	N	5421	0	5001	48	0
1	O	5421	0	5001	117	0
1	P	5421	0	5001	47	0
1	Q	5421	0	5003	41	0
1	R	5421	0	5003	42	0
2	C	3649	0	3442	23	0
2	D	3649	0	3442	31	0
2	S	3649	0	3441	25	0
2	T	3649	0	3442	26	0
2	U	3649	0	3443	46	0
2	V	3649	0	3443	22	0
2	W	3649	0	3442	30	0
2	X	3649	0	3444	20	0
2	Y	3649	0	3444	22	0
2	Z	3649	0	3442	40	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	a	3649	0	3442	31	0
2	b	3649	0	3443	28	0
2	c	3649	0	3444	21	0
2	d	3649	0	3443	23	0
2	e	3649	0	3444	23	0
2	f	3649	0	3444	20	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
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	3	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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
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	135653	1208	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.

All (1208) 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	1.11
2:a:1151:PRO:HD3	3:a:1302:NAG:H62	1.32	1.10
1:K:723:SER:O	1:O:431:GLN:N	1.87	1.07
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	1.00
1:K:472:GLN:HG3	1:O:472:GLN:HA	1.41	0.97
2:D:1151:PRO:HA	2:D:1169:CYS:HA	1.48	0.94
1:K:472:GLN:HA	1:O:472:GLN:HG3	1.48	0.92
1:B:101:THR:HG21	3:B:801:NAG:C7	2.02	0.89
1:K:472:GLN:CA	1:O:472:GLN:HG3	2.04	0.87
2:a:1151:PRO:HD2	3:a:1302:NAG:H62	1.57	0.86
1:K:724:ASP:OD1	1:O:430:VAL:HG12	1.77	0.85
1:K:471:VAL:C	1:O:472:GLN:HG3	2.02	0.85
1:B:101:THR:HG22	3:B:801:NAG:H82	1.60	0.84
1:K:725:HIS:CD2	1:O:409:ILE:HB	2.12	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:472:GLN:HG3	1:O:472:GLN:CA	2.07	0.83
1:B:101:THR:HG21	3:B:801:NAG:C8	2.09	0.82
1:K:472:GLN:N	1:O:472:GLN:HG3	1.94	0.82
1:E:154:TYR:HA	1:E:157:LYS:HD2	1.60	0.82
1:N:101:THR:HB	1:N:108:ARG:HD2	1.58	0.82
1:B:101:THR:HG21	3:B:801:NAG:H82	1.61	0.80
2:U:841:THR:HG22	2:U:850:VAL:HB	1.64	0.80
2:D:1009:SER:OG	2:D:1011:ASN:OD1	2.03	0.77
2:Y:1009:SER:OG	2:Y:1011:ASN:OD1	2.03	0.77
2:S:1009:SER:OG	2:S:1011:ASN:OD1	2.03	0.77
2:U:1009:SER:OG	2:U:1011:ASN:OD1	2.03	0.77
2:U:1147:ASN:HB2	2:U:1174:HIS:HB2	1.64	0.77
2:b:1009:SER:OG	2:b:1011:ASN:OD1	2.03	0.77
1:K:387:GLU:O	1:K:397:LYS:NZ	2.18	0.77
1:K:472:GLN:HA	1:O:472:GLN:CG	2.14	0.77
1:N:387:GLU:O	1:N:397:LYS:NZ	2.18	0.77
1:F:387:GLU:O	1:F:397:LYS:NZ	2.19	0.76
1:G:387:GLU:O	1:G:397:LYS:NZ	2.19	0.76
2:V:1009:SER:OG	2:V:1011:ASN:OD1	2.03	0.76
1:E:387:GLU:O	1:E:397:LYS:NZ	2.19	0.76
1:M:387:GLU:O	1:M:397:LYS:NZ	2.19	0.76
1:O:387:GLU:O	1:O:397:LYS:NZ	2.19	0.76
2:X:1009:SER:OG	2:X:1011:ASN:OD1	2.03	0.76
2:a:1009:SER:OG	2:a:1011:ASN:OD1	2.03	0.76
2:d:1009:SER:OG	2:d:1011:ASN:OD1	2.03	0.76
2:c:1009:SER:OG	2:c:1011:ASN:OD1	2.03	0.76
2:W:1009:SER:OG	2:W:1011:ASN:OD1	2.03	0.76
2:Z:1009:SER:OG	2:Z:1011:ASN:OD1	2.03	0.76
1:Q:625:ALA:O	1:Q:628:SER:OG	2.04	0.75
2:S:841:THR:HG22	2:S:850:VAL:HB	1.69	0.75
2:f:1009:SER:OG	2:f:1011:ASN:OD1	2.03	0.75
1:P:387:GLU:O	1:P:397:LYS:NZ	2.19	0.75
2:C:1009:SER:OG	2:C:1011:ASN:OD1	2.03	0.75
2:e:1009:SER:OG	2:e:1011:ASN:OD1	2.03	0.75
1:H:387:GLU:O	1:H:397:LYS:NZ	2.19	0.75
1:Q:387:GLU:O	1:Q:397:LYS:NZ	2.19	0.75
2:a:1151:PRO:CD	3:a:1302:NAG:C6	2.63	0.75
2:T:1009:SER:OG	2:T:1011:ASN:OD1	2.03	0.75
1:H:625:ALA:O	1:H:628:SER:OG	2.04	0.75
1:I:387:GLU:O	1:I:397:LYS:NZ	2.19	0.75
1:J:387:GLU:O	1:J:397:LYS:NZ	2.19	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:387:GLU:O	1:R:397:LYS:NZ	2.18	0.75
1:G:625:ALA:O	1:G:628:SER:OG	2.04	0.74
1:K:723:SER:N	1:O:431:GLN:O	2.20	0.74
1:R:625:ALA:O	1:R:628:SER:OG	2.04	0.74
1:B:387:GLU:O	1:B:397:LYS:NZ	2.19	0.74
1:A:387:GLU:O	1:A:397:LYS:NZ	2.19	0.74
2:a:841:THR:HG22	2:a:850:VAL:HB	1.70	0.74
2:W:1200:GLU:OE2	2:W:1205:ARG:NH1	2.21	0.74
2:Z:1200:GLU:OE2	2:Z:1205:ARG:NH1	2.21	0.74
1:K:723:SER:C	1:O:430:VAL:HB	2.13	0.74
2:T:1200:GLU:OE2	2:T:1205:ARG:NH1	2.21	0.74
2:c:1200:GLU:OE2	2:c:1205:ARG:NH1	2.21	0.74
2:U:1200:GLU:OE2	2:U:1205:ARG:NH1	2.21	0.73
2:b:1200:GLU:OE2	2:b:1205:ARG:NH1	2.21	0.73
2:W:841:THR:HG22	2:W:850:VAL:HB	1.70	0.73
2:e:1200:GLU:OE2	2:e:1205:ARG:NH1	2.21	0.73
2:f:1200:GLU:OE2	2:f:1205:ARG:NH1	2.21	0.73
1:K:714:GLU:HB3	1:O:460:HIS:HB3	1.70	0.73
2:b:1130:CYS:SG	2:b:1146:TYR:HB2	2.28	0.73
1:L:387:GLU:O	1:L:397:LYS:NZ	2.19	0.73
1:Q:49:SER:OG	1:Q:169:ALA:O	2.07	0.73
1:P:49:SER:OG	1:P:169:ALA:O	2.07	0.73
1:A:49:SER:OG	1:A:169:ALA:O	2.07	0.73
2:C:1200:GLU:OE2	2:C:1205:ARG:NH1	2.21	0.73
2:D:1200:GLU:OE2	2:D:1205:ARG:NH1	2.21	0.73
2:S:1200:GLU:OE2	2:S:1205:ARG:NH1	2.21	0.73
2:a:1200:GLU:OE2	2:a:1205:ARG:NH1	2.21	0.73
1:K:49:SER:OG	1:K:169:ALA:O	2.07	0.73
2:X:1200:GLU:OE2	2:X:1205:ARG:NH1	2.21	0.73
1:M:49:SER:OG	1:M:169:ALA:O	2.07	0.73
1:K:472:GLN:CG	1:O:472:GLN:HA	2.17	0.73
1:F:625:ALA:O	1:F:628:SER:OG	2.04	0.73
1:L:49:SER:OG	1:L:169:ALA:O	2.07	0.73
1:J:49:SER:OG	1:J:169:ALA:O	2.06	0.72
2:d:1200:GLU:OE2	2:d:1205:ARG:NH1	2.21	0.72
2:U:1147:ASN:HB3	2:U:1150:ALA:HB2	1.70	0.72
1:H:49:SER:OG	1:H:169:ALA:O	2.07	0.72
1:M:625:ALA:O	1:M:628:SER:OG	2.04	0.72
2:V:1200:GLU:OE2	2:V:1205:ARG:NH1	2.21	0.72
2:Y:1200:GLU:OE2	2:Y:1205:ARG:NH1	2.21	0.72
1:O:49:SER:OG	1:O:169:ALA:O	2.07	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:49:SER:OG	1:R:169:ALA:O	2.07	0.72
1:E:49:SER:OG	1:E:169:ALA:O	2.06	0.72
1:K:625:ALA:O	1:K:628:SER:OG	2.04	0.72
2:d:1151:PRO:HA	2:d:1169:CYS:HA	1.70	0.72
1:B:49:SER:OG	1:B:169:ALA:O	2.06	0.72
2:D:841:THR:HG22	2:D:850:VAL:HB	1.72	0.72
1:E:625:ALA:O	1:E:628:SER:OG	2.04	0.72
1:I:49:SER:OG	1:I:169:ALA:O	2.07	0.72
1:K:472:GLN:HG2	1:O:472:GLN:HG2	1.70	0.72
1:F:49:SER:OG	1:F:169:ALA:O	2.07	0.71
1:I:625:ALA:O	1:I:628:SER:OG	2.04	0.71
1:L:625:ALA:O	1:L:628:SER:OG	2.04	0.71
1:O:625:ALA:O	1:O:628:SER:OG	2.04	0.71
1:P:625:ALA:O	1:P:628:SER:OG	2.04	0.71
1:B:102:VAL:HG11	1:B:120:LEU:HD21	1.71	0.71
1:J:625:ALA:O	1:J:628:SER:OG	2.04	0.71
1:A:625:ALA:O	1:A:628:SER:OG	2.04	0.71
1:P:717:GLN:N	1:P:720:ASP:OD2	2.24	0.71
1:G:717:GLN:N	1:G:720:ASP:OD2	2.24	0.71
1:I:717:GLN:N	1:I:720:ASP:OD2	2.24	0.71
1:K:717:GLN:N	1:K:720:ASP:OD2	2.24	0.71
1:M:717:GLN:N	1:M:720:ASP:OD2	2.24	0.71
1:N:49:SER:OG	1:N:169:ALA:O	2.07	0.71
1:R:717:GLN:N	1:R:720:ASP:OD2	2.24	0.71
2:Z:1197:PRO:O	2:Z:1208:SER:OG	2.09	0.71
1:B:101:THR:HG21	3:B:801:NAG:HN2	1.54	0.70
2:C:1197:PRO:O	2:C:1208:SER:OG	2.10	0.70
1:G:97:PHE:CZ	1:G:101:THR:HB	2.26	0.70
1:N:625:ALA:O	1:N:628:SER:OG	2.04	0.70
1:N:717:GLN:N	1:N:720:ASP:OD2	2.24	0.70
2:c:1197:PRO:O	2:c:1208:SER:OG	2.09	0.70
2:e:1197:PRO:O	2:e:1208:SER:OG	2.09	0.70
1:J:717:GLN:N	1:J:720:ASP:OD2	2.24	0.70
2:Y:1197:PRO:O	2:Y:1208:SER:OG	2.09	0.70
1:L:717:GLN:N	1:L:720:ASP:OD2	2.24	0.70
1:O:717:GLN:N	1:O:720:ASP:OD2	2.24	0.70
2:V:841:THR:HG22	2:V:850:VAL:HB	1.74	0.70
2:d:1197:PRO:O	2:d:1208:SER:OG	2.10	0.70
2:f:1197:PRO:O	2:f:1208:SER:OG	2.09	0.70
2:a:1197:PRO:O	2:a:1208:SER:OG	2.10	0.70
1:H:717:GLN:N	1:H:720:ASP:OD2	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:U:1197:PRO:O	2:U:1208:SER:OG	2.09	0.70
2:T:1197:PRO:O	2:T:1208:SER:OG	2.10	0.70
1:Q:717:GLN:N	1:Q:720:ASP:OD2	2.24	0.70
1:A:717:GLN:N	1:A:720:ASP:OD2	2.24	0.69
1:E:717:GLN:N	1:E:720:ASP:OD2	2.24	0.69
1:B:717:GLN:N	1:B:720:ASP:OD2	2.24	0.69
2:S:1197:PRO:O	2:S:1208:SER:OG	2.09	0.69
1:B:625:ALA:O	1:B:628:SER:OG	2.04	0.69
1:F:717:GLN:N	1:F:720:ASP:OD2	2.24	0.69
2:X:1197:PRO:O	2:X:1208:SER:OG	2.09	0.69
2:D:1197:PRO:O	2:D:1208:SER:OG	2.09	0.69
2:V:1197:PRO:O	2:V:1208:SER:OG	2.10	0.69
2:b:1197:PRO:O	2:b:1208:SER:OG	2.10	0.69
2:W:1197:PRO:O	2:W:1208:SER:OG	2.09	0.68
1:K:725:HIS:NE2	1:O:409:ILE:HB	2.07	0.68
1:K:725:HIS:H	1:O:409:ILE:HG21	1.58	0.68
1:P:515:VAL:O	1:P:519:LYS:NZ	2.27	0.68
1:B:515:VAL:O	1:B:519:LYS:NZ	2.27	0.67
1:G:515:VAL:O	1:G:519:LYS:NZ	2.27	0.67
1:K:725:HIS:N	1:O:409:ILE:HG21	2.09	0.67
1:M:515:VAL:O	1:M:519:LYS:NZ	2.27	0.67
1:E:725:HIS:CE1	1:F:560:GLN:HB2	2.29	0.67
1:H:515:VAL:O	1:H:519:LYS:NZ	2.27	0.67
1:I:515:VAL:O	1:I:519:LYS:NZ	2.27	0.67
1:L:515:VAL:O	1:L:519:LYS:NZ	2.27	0.67
2:X:1021:PHE:O	2:X:1024:SER:OG	2.13	0.67
1:F:515:VAL:O	1:F:519:LYS:NZ	2.27	0.67
1:G:82:VAL:HA	1:G:98:VAL:HG23	1.77	0.67
2:S:1151:PRO:HA	2:S:1169:CYS:HA	1.77	0.67
1:E:515:VAL:O	1:E:519:LYS:NZ	2.27	0.67
2:W:1021:PHE:O	2:W:1024:SER:OG	2.13	0.67
1:K:515:VAL:O	1:K:519:LYS:NZ	2.27	0.66
2:a:1151:PRO:HD2	3:a:1302:NAG:C6	2.25	0.66
1:K:712:ASP:O	1:O:459:LYS:NZ	2.27	0.66
1:Q:515:VAL:O	1:Q:519:LYS:NZ	2.27	0.66
2:b:1151:PRO:HA	2:b:1169:CYS:HA	1.78	0.66
1:O:515:VAL:O	1:O:519:LYS:NZ	2.27	0.66
1:J:515:VAL:O	1:J:519:LYS:NZ	2.27	0.65
1:A:515:VAL:O	1:A:519:LYS:NZ	2.27	0.65
1:F:95:HIS:HE1	1:F:105:GLY:H	1.42	0.65
1:R:515:VAL:O	1:R:519:LYS:NZ	2.27	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:65:CYS:SG	1:B:159:CYS:N	2.70	0.65
1:H:65:CYS:SG	1:H:159:CYS:N	2.70	0.65
1:A:155:PHE:HA	1:A:165:PHE:HD2	1.62	0.65
1:G:65:CYS:SG	1:G:159:CYS:N	2.70	0.65
1:I:418:CYS:SG	1:I:521:CYS:N	2.71	0.65
1:L:418:CYS:SG	1:L:521:CYS:N	2.70	0.65
1:O:65:CYS:SG	1:O:159:CYS:N	2.70	0.65
1:Q:65:CYS:SG	1:Q:159:CYS:N	2.70	0.65
1:F:65:CYS:SG	1:F:159:CYS:N	2.70	0.64
1:J:418:CYS:SG	1:J:521:CYS:N	2.71	0.64
1:B:418:CYS:SG	1:B:521:CYS:N	2.70	0.64
2:b:1019:VAL:O	2:b:1023:ASN:ND2	2.31	0.64
2:C:1021:PHE:O	2:C:1024:SER:OG	2.13	0.64
1:E:65:CYS:SG	1:E:159:CYS:N	2.70	0.64
1:E:418:CYS:SG	1:E:521:CYS:N	2.71	0.64
1:F:418:CYS:SG	1:F:521:CYS:N	2.70	0.64
1:K:65:CYS:SG	1:K:159:CYS:N	2.70	0.64
1:N:515:VAL:O	1:N:519:LYS:NZ	2.27	0.64
1:P:65:CYS:SG	1:P:159:CYS:N	2.70	0.64
1:R:65:CYS:SG	1:R:159:CYS:N	2.70	0.64
2:T:1019:VAL:O	2:T:1023:ASN:ND2	2.31	0.64
1:A:418:CYS:SG	1:A:521:CYS:N	2.71	0.64
2:a:1019:VAL:O	2:a:1023:ASN:ND2	2.31	0.64
2:d:1019:VAL:O	2:d:1023:ASN:ND2	2.31	0.64
2:c:1019:VAL:O	2:c:1023:ASN:ND2	2.31	0.64
1:P:418:CYS:SG	1:P:521:CYS:N	2.71	0.64
1:A:65:CYS:SG	1:A:159:CYS:N	2.70	0.64
2:a:1151:PRO:HD3	3:a:1302:NAG:C6	2.19	0.64
2:C:1019:VAL:O	2:C:1023:ASN:ND2	2.31	0.64
1:H:418:CYS:SG	1:H:521:CYS:N	2.71	0.64
2:Z:1019:VAL:O	2:Z:1023:ASN:ND2	2.31	0.64
1:I:65:CYS:SG	1:I:159:CYS:N	2.70	0.64
1:J:65:CYS:SG	1:J:159:CYS:N	2.70	0.64
1:K:431:GLN:N	1:O:723:SER:O	2.31	0.64
1:R:418:CYS:SG	1:R:521:CYS:N	2.71	0.64
1:G:418:CYS:SG	1:G:521:CYS:N	2.71	0.64
1:L:65:CYS:SG	1:L:159:CYS:N	2.70	0.64
1:M:65:CYS:SG	1:M:159:CYS:N	2.70	0.64
1:N:418:CYS:SG	1:N:521:CYS:N	2.71	0.64
2:U:1019:VAL:O	2:U:1023:ASN:ND2	2.31	0.64
2:W:1019:VAL:O	2:W:1023:ASN:ND2	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:418:CYS:SG	1:Q:521:CYS:N	2.70	0.64
2:S:1019:VAL:O	2:S:1023:ASN:ND2	2.31	0.64
2:V:1019:VAL:O	2:V:1023:ASN:ND2	2.31	0.64
2:X:1019:VAL:O	2:X:1023:ASN:ND2	2.31	0.64
2:e:1019:VAL:O	2:e:1023:ASN:ND2	2.31	0.64
1:O:418:CYS:SG	1:O:521:CYS:N	2.71	0.64
2:b:1004:ASN:ND2	1:N:529:GLY:O	2.31	0.64
2:D:1019:VAL:O	2:D:1023:ASN:ND2	2.31	0.63
1:I:101:THR:HB	1:I:108:ARG:HD2	1.80	0.63
1:K:418:CYS:SG	1:K:521:CYS:N	2.71	0.63
1:K:723:SER:OG	1:O:431:GLN:HB3	1.98	0.63
2:f:1004:ASN:ND2	1:R:529:GLY:O	2.31	0.63
1:M:418:CYS:SG	1:M:521:CYS:N	2.71	0.63
2:f:1019:VAL:O	2:f:1023:ASN:ND2	2.31	0.63
1:N:65:CYS:SG	1:N:159:CYS:N	2.70	0.63
2:Y:1019:VAL:O	2:Y:1023:ASN:ND2	2.31	0.63
1:K:723:SER:O	1:O:430:VAL:HB	1.97	0.63
2:a:1004:ASN:ND2	1:M:529:GLY:O	2.31	0.63
1:B:529:GLY:O	2:D:1004:ASN:ND2	2.31	0.63
2:c:1004:ASN:ND2	1:O:529:GLY:O	2.31	0.63
2:W:1176:HIS:CD2	3:W:1302:NAG:H81	2.34	0.63
2:e:1021:PHE:O	2:e:1024:SER:OG	2.13	0.63
1:K:472:GLN:HG3	1:O:472:GLN:N	2.14	0.63
2:d:1004:ASN:ND2	1:P:529:GLY:O	2.31	0.63
2:b:1021:PHE:O	2:b:1024:SER:OG	2.12	0.62
2:e:1004:ASN:ND2	1:Q:529:GLY:O	2.31	0.62
1:P:84:LEU:HB3	1:P:96:LEU:HD11	1.82	0.62
2:Y:1021:PHE:O	2:Y:1024:SER:OG	2.13	0.62
1:O:642:TRP:O	1:O:647:ARG:NH1	2.33	0.62
2:W:852:GLN:NE2	2:W:857:ASN:HB2	2.14	0.62
1:P:642:TRP:O	1:P:647:ARG:NH1	2.33	0.62
2:f:1021:PHE:O	2:f:1024:SER:OG	2.13	0.62
1:K:642:TRP:O	1:K:647:ARG:NH1	2.33	0.62
1:Q:642:TRP:O	1:Q:647:ARG:NH1	2.33	0.62
1:A:642:TRP:O	1:A:647:ARG:NH1	2.33	0.61
2:d:792:CYS:O	2:d:854:ARG:NH2	2.33	0.61
1:G:642:TRP:O	1:G:647:ARG:NH1	2.33	0.61
1:B:642:TRP:O	1:B:647:ARG:NH1	2.33	0.61
1:E:431:GLN:NE2	1:E:435:ASP:O	2.34	0.61
1:E:642:TRP:O	1:E:647:ARG:NH1	2.33	0.61
1:J:435:ASP:OD1	1:Q:176:GLN:NE2	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:472:GLN:HG3	1:O:471:VAL:C	2.25	0.61
1:L:529:GLY:O	2:Z:1004:ASN:ND2	2.31	0.61
2:X:792:CYS:O	2:X:854:ARG:NH2	2.33	0.61
1:F:431:GLN:NE2	1:F:435:ASP:O	2.34	0.61
1:I:435:ASP:OD1	1:P:176:GLN:NE2	2.34	0.61
1:K:469:GLN:HE21	1:O:475:LEU:HD11	1.66	0.61
1:M:642:TRP:O	1:M:647:ARG:NH1	2.33	0.61
1:O:431:GLN:NE2	1:O:435:ASP:O	2.34	0.61
1:Q:431:GLN:NE2	1:Q:435:ASP:O	2.34	0.61
1:R:642:TRP:O	1:R:647:ARG:NH1	2.33	0.61
2:c:792:CYS:O	2:c:854:ARG:NH2	2.34	0.61
2:e:792:CYS:O	2:e:854:ARG:NH2	2.33	0.61
1:L:642:TRP:O	1:L:647:ARG:NH1	2.33	0.61
1:E:435:ASP:OD1	1:L:176:GLN:NE2	2.34	0.61
1:A:431:GLN:NE2	1:A:435:ASP:O	2.34	0.61
1:G:431:GLN:NE2	1:G:435:ASP:O	2.34	0.61
1:J:431:GLN:NE2	1:J:435:ASP:O	2.34	0.61
1:I:642:TRP:O	1:I:647:ARG:NH1	2.33	0.61
1:K:431:GLN:NE2	1:K:435:ASP:O	2.34	0.61
1:N:642:TRP:O	1:N:647:ARG:NH1	2.33	0.61
1:R:431:GLN:NE2	1:R:435:ASP:O	2.34	0.61
2:b:792:CYS:O	2:b:854:ARG:NH2	2.33	0.61
1:N:431:GLN:NE2	1:N:435:ASP:O	2.34	0.61
1:P:431:GLN:NE2	1:P:435:ASP:O	2.34	0.61
2:Z:792:CYS:O	2:Z:854:ARG:NH2	2.34	0.61
1:H:642:TRP:O	1:H:647:ARG:NH1	2.33	0.60
1:I:431:GLN:NE2	1:I:435:ASP:O	2.34	0.60
1:L:431:GLN:NE2	1:L:435:ASP:O	2.34	0.60
1:A:435:ASP:OD1	1:B:176:GLN:NE2	2.34	0.60
1:J:642:TRP:O	1:J:647:ARG:NH1	2.33	0.60
1:K:435:ASP:OD1	1:R:176:GLN:NE2	2.34	0.60
1:G:435:ASP:OD1	1:N:176:GLN:NE2	2.34	0.60
1:H:435:ASP:OD1	1:O:176:GLN:NE2	2.34	0.60
1:N:101:THR:HB	1:N:108:ARG:CD	2.31	0.60
1:B:431:GLN:NE2	1:B:435:ASP:O	2.34	0.60
2:f:792:CYS:O	2:f:854:ARG:NH2	2.33	0.60
1:F:642:TRP:O	1:F:647:ARG:NH1	2.33	0.60
2:Y:792:CYS:O	2:Y:854:ARG:NH2	2.34	0.60
1:M:431:GLN:NE2	1:M:435:ASP:O	2.34	0.60
1:F:435:ASP:OD1	1:M:176:GLN:NE2	2.34	0.60
2:W:852:GLN:HE21	2:W:857:ASN:HB2	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:ASN:C	1:A:101:THR:H	2.10	0.60
2:C:841:THR:HG22	2:C:850:VAL:HB	1.84	0.60
1:E:156:ASN:HA	1:E:166:ASN:ND2	2.16	0.60
1:H:431:GLN:NE2	1:H:435:ASP:O	2.34	0.60
1:F:176:GLN:NE2	1:M:435:ASP:OD1	2.35	0.60
1:O:97:PHE:O	1:O:98:VAL:C	2.45	0.60
1:H:176:GLN:NE2	1:O:435:ASP:OD1	2.35	0.59
1:I:176:GLN:NE2	1:P:435:ASP:OD1	2.35	0.59
1:G:176:GLN:NE2	1:N:435:ASP:OD1	2.35	0.59
1:J:176:GLN:NE2	1:Q:435:ASP:OD1	2.35	0.59
1:A:176:GLN:NE2	1:B:435:ASP:OD1	2.35	0.59
1:K:716:PHE:CD1	1:O:460:HIS:CD2	2.90	0.59
1:K:442:ARG:CD	1:O:722:PHE:HZ	2.15	0.59
1:B:155:PHE:HA	1:B:165:PHE:HD2	1.67	0.59
2:W:1147:ASN:O	2:W:1148:SER:C	2.45	0.59
1:E:176:GLN:NE2	1:L:435:ASP:OD1	2.35	0.58
1:B:156:ASN:CG	3:B:802:NAG:C1	2.69	0.58
1:E:560:GLN:HB2	1:F:725:HIS:CE1	2.38	0.58
1:K:722:PHE:CZ	1:O:442:ARG:HG3	2.37	0.58
1:K:722:PHE:HZ	1:O:442:ARG:HG3	1.68	0.58
1:K:176:GLN:NE2	1:R:435:ASP:OD1	2.35	0.58
1:G:101:THR:HG21	1:G:108:ARG:HD2	1.85	0.57
1:M:496:GLU:N	1:M:496:GLU:OE1	2.37	0.57
2:U:1147:ASN:H	2:U:1174:HIS:HB2	1.68	0.57
2:C:1130:CYS:SG	2:C:1146:TYR:HB2	2.44	0.57
1:J:486:VAL:O	1:J:487:THR:OG1	2.20	0.57
1:Q:496:GLU:OE1	1:Q:496:GLU:N	2.38	0.57
2:Z:1021:PHE:O	2:Z:1024:SER:OG	2.13	0.57
1:A:496:GLU:N	1:A:496:GLU:OE1	2.38	0.57
1:F:496:GLU:N	1:F:496:GLU:OE1	2.38	0.57
1:O:496:GLU:OE1	1:O:496:GLU:N	2.38	0.57
1:P:496:GLU:N	1:P:496:GLU:OE1	2.38	0.57
2:D:1021:PHE:O	2:D:1024:SER:OG	2.13	0.57
1:E:496:GLU:OE1	1:E:496:GLU:N	2.38	0.57
1:H:496:GLU:OE1	1:H:496:GLU:N	2.38	0.57
1:K:496:GLU:N	1:K:496:GLU:OE1	2.38	0.57
1:O:98:VAL:O	1:O:99:ASN:C	2.47	0.57
2:U:1131:GLU:O	2:U:1132:GLU:C	2.47	0.57
2:U:1147:ASN:CB	2:U:1174:HIS:HB2	2.35	0.57
1:G:496:GLU:N	1:G:496:GLU:OE1	2.38	0.57
1:N:496:GLU:N	1:N:496:GLU:OE1	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:a:855:LYS:HG2	1:M:539:SER:HA	1.86	0.57
1:I:496:GLU:N	1:I:496:GLU:OE1	2.38	0.57
1:J:496:GLU:OE1	1:J:496:GLU:N	2.38	0.57
1:R:496:GLU:N	1:R:496:GLU:OE1	2.38	0.57
1:G:545:ARG:NH2	1:G:548:ASP:OD1	2.37	0.57
1:I:155:PHE:O	1:I:157:LYS:HD3	2.05	0.57
1:O:486:VAL:O	1:O:487:THR:OG1	2.20	0.57
2:d:1147:ASN:O	2:d:1148:SER:C	2.48	0.56
1:F:545:ARG:NH2	1:F:548:ASP:OD1	2.37	0.56
1:M:97:PHE:O	1:M:98:VAL:C	2.48	0.56
1:H:208:SER:OG	1:H:211:ASN:OD1	2.24	0.56
1:L:208:SER:OG	1:L:211:ASN:OD1	2.24	0.56
1:L:496:GLU:N	1:L:496:GLU:OE1	2.37	0.56
1:M:208:SER:OG	1:M:211:ASN:OD1	2.24	0.56
1:R:545:ARG:NH2	1:R:548:ASP:OD1	2.37	0.56
1:B:496:GLU:N	1:B:496:GLU:OE1	2.38	0.56
1:F:253:THR:OG1	1:F:256:GLU:OE2	2.22	0.56
1:K:486:VAL:O	1:K:487:THR:OG1	2.20	0.56
1:K:545:ARG:NH2	1:K:548:ASP:OD1	2.37	0.56
1:Q:670:ARG:O	1:Q:673:SER:OG	2.18	0.56
2:V:1021:PHE:O	2:V:1024:SER:OG	2.13	0.56
1:B:208:SER:OG	1:B:211:ASN:OD1	2.24	0.56
2:b:1142:CYS:HB2	2:U:1145:ARG:HH21	1.70	0.56
1:F:155:PHE:HA	1:F:165:PHE:HD2	1.71	0.56
1:J:545:ARG:NH2	1:J:548:ASP:OD1	2.37	0.56
1:E:208:SER:OG	1:E:211:ASN:OD1	2.24	0.56
1:G:98:VAL:O	1:G:99:ASN:C	2.49	0.56
2:U:1146:TYR:HA	2:U:1173:CYS:HA	1.86	0.56
2:T:841:THR:HG22	2:T:850:VAL:HB	1.87	0.55
1:A:208:SER:OG	1:A:211:ASN:OD1	2.24	0.55
2:f:1215:ASN:ND2	2:f:1221:HIS:O	2.40	0.55
1:Q:545:ARG:NH2	1:Q:548:ASP:OD1	2.37	0.55
2:T:1215:ASN:ND2	2:T:1221:HIS:O	2.39	0.55
2:U:1215:ASN:ND2	2:U:1221:HIS:O	2.39	0.55
2:Z:1215:ASN:ND2	2:Z:1221:HIS:O	2.39	0.55
1:K:208:SER:OG	1:K:211:ASN:OD1	2.24	0.55
1:M:545:ARG:NH2	1:M:548:ASP:OD1	2.37	0.55
1:O:208:SER:OG	1:O:211:ASN:OD1	2.24	0.55
1:P:545:ARG:NH2	1:P:548:ASP:OD1	2.37	0.55
1:Q:486:VAL:O	1:Q:487:THR:OG1	2.20	0.55
1:R:208:SER:OG	1:R:211:ASN:OD1	2.24	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Z:1135:LEU:HA	2:Z:1140:TYR:CD1	2.41	0.55
1:A:486:VAL:O	1:A:487:THR:OG1	2.20	0.55
1:G:208:SER:OG	1:G:211:ASN:OD1	2.24	0.55
1:I:545:ARG:NH2	1:I:548:ASP:OD1	2.37	0.55
2:e:1093:SER:O	2:X:1093:SER:OG	2.21	0.55
1:P:208:SER:OG	1:P:211:ASN:OD1	2.24	0.55
1:J:208:SER:OG	1:J:211:ASN:OD1	2.24	0.55
1:M:98:VAL:O	1:M:99:ASN:C	2.48	0.55
2:d:1215:ASN:ND2	2:d:1221:HIS:O	2.39	0.55
2:a:1215:ASN:ND2	2:a:1221:HIS:O	2.39	0.55
1:I:208:SER:OG	1:I:211:ASN:OD1	2.24	0.55
1:K:714:GLU:HG2	1:O:459:LYS:HB3	1.88	0.55
1:Q:208:SER:OG	1:Q:211:ASN:OD1	2.24	0.55
1:H:545:ARG:NH2	1:H:548:ASP:OD1	2.37	0.55
1:F:208:SER:OG	1:F:211:ASN:OD1	2.24	0.55
1:B:732:GLU:OE1	1:B:737:HIS:NE2	2.41	0.54
1:L:253:THR:OG1	1:L:256:GLU:OE2	2.22	0.54
1:Q:732:GLU:OE1	1:Q:737:HIS:NE2	2.41	0.54
2:b:1215:ASN:ND2	2:b:1221:HIS:O	2.39	0.54
2:d:1150:ALA:HB3	2:d:1174:HIS:CD2	2.43	0.54
2:V:1215:ASN:ND2	2:V:1221:HIS:O	2.39	0.54
2:Y:1215:ASN:ND2	2:Y:1221:HIS:O	2.39	0.54
2:D:1215:ASN:ND2	2:D:1221:HIS:O	2.39	0.54
1:E:732:GLU:OE1	1:E:737:HIS:NE2	2.41	0.54
1:J:732:GLU:OE1	1:J:737:HIS:NE2	2.41	0.54
1:L:545:ARG:NH2	1:L:548:ASP:OD1	2.37	0.54
1:N:208:SER:OG	1:N:211:ASN:OD1	2.24	0.54
1:P:732:GLU:OE1	1:P:737:HIS:NE2	2.41	0.54
2:X:1215:ASN:ND2	2:X:1221:HIS:O	2.40	0.54
2:e:1215:ASN:ND2	2:e:1221:HIS:O	2.39	0.54
1:I:732:GLU:OE1	1:I:737:HIS:NE2	2.41	0.54
1:R:486:VAL:O	1:R:487:THR:OG1	2.20	0.54
2:S:1215:ASN:ND2	2:S:1221:HIS:O	2.39	0.54
2:U:1135:LEU:HA	2:U:1140:TYR:CE2	2.43	0.54
2:D:1147:ASN:O	2:D:1148:SER:C	2.49	0.54
1:F:96:LEU:HD23	1:F:96:LEU:H	1.72	0.54
1:H:732:GLU:OE1	1:H:737:HIS:NE2	2.41	0.54
1:B:141:ASP:OD2	1:B:145:ASN:ND2	2.41	0.54
1:M:670:ARG:O	1:M:673:SER:OG	2.18	0.54
1:N:545:ARG:NH2	1:N:548:ASP:OD1	2.37	0.54
1:O:732:GLU:OE1	1:O:737:HIS:NE2	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:732:GLU:OE1	1:R:737:HIS:NE2	2.41	0.54
1:A:545:ARG:NH2	1:A:548:ASP:OD1	2.37	0.54
1:E:460:HIS:ND1	1:E:504:GLY:O	2.41	0.54
1:K:430:VAL:HB	1:O:723:SER:O	2.08	0.54
1:O:141:ASP:OD2	1:O:145:ASN:ND2	2.41	0.54
2:T:1130:CYS:SG	2:T:1146:TYR:HB2	2.48	0.54
1:G:732:GLU:OE1	1:G:737:HIS:NE2	2.41	0.54
1:K:469:GLN:NE2	1:O:475:LEU:HD11	2.22	0.54
1:L:732:GLU:OE1	1:L:737:HIS:NE2	2.41	0.54
1:B:545:ARG:NH2	1:B:548:ASP:OD1	2.37	0.54
2:c:1021:PHE:O	2:c:1024:SER:OG	2.13	0.54
1:K:721:ILE:CG2	1:O:433:ALA:HA	2.38	0.54
1:M:732:GLU:OE1	1:M:737:HIS:NE2	2.41	0.54
1:P:486:VAL:O	1:P:487:THR:OG1	2.20	0.54
2:W:1215:ASN:ND2	2:W:1221:HIS:O	2.40	0.54
1:B:460:HIS:ND1	1:B:504:GLY:O	2.41	0.53
1:F:460:HIS:ND1	1:F:504:GLY:O	2.41	0.53
1:O:460:HIS:ND1	1:O:504:GLY:O	2.41	0.53
2:Z:1137:GLU:H	2:Z:1188:GLN:HE22	1.55	0.53
1:I:253:THR:OG1	1:I:256:GLU:OE2	2.23	0.53
1:I:460:HIS:ND1	1:I:504:GLY:O	2.41	0.53
1:Q:141:ASP:OD2	1:Q:145:ASN:ND2	2.41	0.53
2:U:1145:ARG:O	2:U:1146:TYR:C	2.50	0.53
2:a:1087:ASP:O	2:a:1090:SER:OG	2.27	0.53
1:H:141:ASP:OD2	1:H:145:ASN:ND2	2.41	0.53
1:N:732:GLU:OE1	1:N:737:HIS:NE2	2.41	0.53
2:S:1150:ALA:HB3	2:S:1174:HIS:CD2	2.43	0.53
1:A:732:GLU:OE1	1:A:737:HIS:NE2	2.41	0.53
2:C:1215:ASN:ND2	2:C:1221:HIS:O	2.39	0.53
1:K:732:GLU:OE1	1:K:737:HIS:NE2	2.41	0.53
2:S:1087:ASP:O	2:S:1090:SER:OG	2.27	0.53
1:O:545:ARG:NH2	1:O:548:ASP:OD1	2.37	0.53
2:V:931:GLY:O	2:V:945:ARG:NH1	2.42	0.53
2:Z:1147:ASN:O	2:Z:1148:SER:C	2.52	0.53
2:c:1215:ASN:ND2	2:c:1221:HIS:O	2.39	0.53
1:E:545:ARG:NH2	1:E:548:ASP:OD1	2.37	0.53
1:L:460:HIS:ND1	1:L:504:GLY:O	2.41	0.53
1:P:460:HIS:ND1	1:P:504:GLY:O	2.41	0.53
2:Y:1087:ASP:O	2:Y:1090:SER:OG	2.27	0.53
2:D:1147:ASN:HB3	2:D:1174:HIS:CD2	2.44	0.53
2:U:901:ASN:OD1	2:U:991:LYS:NZ	2.29	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:b:1150:ALA:HB3	2:b:1174:HIS:CD2	2.43	0.53
1:F:732:GLU:OE1	1:F:737:HIS:NE2	2.41	0.53
1:G:460:HIS:ND1	1:G:504:GLY:O	2.41	0.53
1:K:460:HIS:ND1	1:K:504:GLY:O	2.42	0.53
2:e:931:GLY:O	2:e:945:ARG:NH1	2.42	0.53
1:I:141:ASP:OD2	1:I:145:ASN:ND2	2.41	0.53
1:J:253:THR:OG1	1:J:256:GLU:OE2	2.23	0.53
1:K:442:ARG:CD	1:O:722:PHE:CZ	2.91	0.53
1:N:460:HIS:ND1	1:N:504:GLY:O	2.41	0.53
1:J:460:HIS:ND1	1:J:504:GLY:O	2.41	0.52
1:M:460:HIS:ND1	1:M:504:GLY:O	2.41	0.52
1:R:141:ASP:OD2	1:R:145:ASN:ND2	2.41	0.52
2:U:1087:ASP:O	2:U:1090:SER:OG	2.27	0.52
2:Y:931:GLY:O	2:Y:945:ARG:NH1	2.42	0.52
2:Z:1130:CYS:SG	2:Z:1146:TYR:HB2	2.50	0.52
1:G:253:THR:OG1	1:G:256:GLU:OE2	2.22	0.52
1:G:486:VAL:O	1:G:487:THR:OG1	2.20	0.52
1:J:141:ASP:OD2	1:J:145:ASN:ND2	2.41	0.52
1:L:486:VAL:O	1:L:487:THR:OG1	2.20	0.52
1:A:141:ASP:OD2	1:A:145:ASN:ND2	2.41	0.52
1:A:460:HIS:ND1	1:A:504:GLY:O	2.41	0.52
1:K:461:GLY:HA3	1:O:715:ILE:HB	1.91	0.52
1:M:486:VAL:O	1:M:487:THR:OG1	2.20	0.52
2:V:1087:ASP:O	2:V:1090:SER:OG	2.27	0.52
1:J:186:ASP:OD1	1:J:187:PHE:N	2.43	0.52
1:K:186:ASP:OD1	1:K:187:PHE:N	2.43	0.52
1:R:186:ASP:OD1	1:R:187:PHE:N	2.43	0.52
1:R:460:HIS:ND1	1:R:504:GLY:O	2.41	0.52
2:T:931:GLY:O	2:T:945:ARG:NH1	2.42	0.52
2:b:931:GLY:O	2:b:945:ARG:NH1	2.42	0.52
2:c:931:GLY:O	2:c:945:ARG:NH1	2.42	0.52
2:D:931:GLY:O	2:D:945:ARG:NH1	2.42	0.52
1:I:186:ASP:OD1	1:I:187:PHE:N	2.43	0.52
1:H:460:HIS:ND1	1:H:504:GLY:O	2.42	0.52
1:I:82:VAL:HA	1:I:98:VAL:HG23	1.91	0.52
1:K:670:ARG:O	1:K:673:SER:OG	2.18	0.52
1:N:141:ASP:OD2	1:N:145:ASN:ND2	2.41	0.52
1:O:186:ASP:OD1	1:O:187:PHE:N	2.43	0.52
1:Q:460:HIS:ND1	1:Q:504:GLY:O	2.41	0.52
2:f:931:GLY:O	2:f:945:ARG:NH1	2.42	0.52
1:H:186:ASP:OD1	1:H:187:PHE:N	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:471:VAL:O	1:O:472:GLN:HG3	2.09	0.52
1:N:186:ASP:OD1	1:N:187:PHE:N	2.43	0.52
1:P:96:LEU:HD12	1:P:96:LEU:C	2.35	0.52
2:W:852:GLN:HG2	3:W:1301:NAG:O7	2.09	0.52
2:C:786:LEU:O	2:C:789:THR:OG1	2.28	0.52
1:E:186:ASP:OD1	1:E:187:PHE:N	2.43	0.52
1:M:186:ASP:OD1	1:M:187:PHE:N	2.43	0.52
2:W:931:GLY:O	2:W:945:ARG:NH1	2.42	0.52
2:X:931:GLY:O	2:X:945:ARG:NH1	2.42	0.52
2:Z:931:GLY:O	2:Z:945:ARG:NH1	2.42	0.52
1:P:141:ASP:OD2	1:P:145:ASN:ND2	2.41	0.52
2:U:931:GLY:O	2:U:945:ARG:NH1	2.42	0.52
2:U:1147:ASN:HB2	2:U:1174:HIS:CB	2.35	0.52
1:E:486:VAL:O	1:E:487:THR:OG1	2.20	0.51
1:F:186:ASP:OD1	1:F:187:PHE:N	2.43	0.51
1:G:186:ASP:OD1	1:G:187:PHE:N	2.43	0.51
1:P:670:ARG:O	1:P:673:SER:OG	2.18	0.51
2:Y:1201:VAL:O	2:Y:1204:ARG:NH1	2.44	0.51
1:E:141:ASP:OD2	1:E:145:ASN:ND2	2.41	0.51
2:e:1201:VAL:O	2:e:1204:ARG:NH1	2.44	0.51
1:M:141:ASP:OD2	1:M:145:ASN:ND2	2.41	0.51
2:d:1201:VAL:O	2:d:1204:ARG:NH1	2.44	0.51
1:L:186:ASP:OD1	1:L:187:PHE:N	2.43	0.51
1:Q:186:ASP:OD1	1:Q:187:PHE:N	2.43	0.51
2:T:1201:VAL:O	2:T:1204:ARG:NH1	2.44	0.51
2:W:1201:VAL:O	2:W:1204:ARG:NH1	2.44	0.51
2:Z:1201:VAL:O	2:Z:1204:ARG:NH1	2.44	0.51
2:b:1201:VAL:O	2:b:1204:ARG:NH1	2.44	0.51
2:d:1087:ASP:O	2:d:1090:SER:OG	2.27	0.51
1:P:97:PHE:HD1	1:P:100:GLY:H	1.58	0.51
2:U:880:GLY:O	2:U:1003:GLN:NE2	2.42	0.51
2:V:1201:VAL:O	2:V:1204:ARG:NH1	2.44	0.51
2:X:1201:VAL:O	2:X:1204:ARG:NH1	2.44	0.51
2:Z:1087:ASP:O	2:Z:1090:SER:OG	2.27	0.51
2:b:1087:ASP:O	2:b:1090:SER:OG	2.27	0.51
2:D:901:ASN:OD1	2:D:991:LYS:NZ	2.29	0.51
1:G:171:ASP:C	1:G:173:PHE:H	2.18	0.51
1:K:724:ASP:HA	1:O:409:ILE:HG21	1.90	0.51
2:U:1201:VAL:O	2:U:1204:ARG:NH1	2.44	0.51
2:D:1201:VAL:O	2:D:1204:ARG:NH1	2.44	0.51
2:f:1087:ASP:O	2:f:1090:SER:OG	2.27	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:186:ASP:OD1	1:P:187:PHE:N	2.43	0.51
1:A:186:ASP:OD1	1:A:187:PHE:N	2.43	0.51
2:c:1201:VAL:O	2:c:1204:ARG:NH1	2.44	0.51
2:a:880:GLY:O	2:a:1003:GLN:NE2	2.42	0.51
1:B:186:ASP:OD1	1:B:187:PHE:N	2.43	0.51
2:D:880:GLY:O	2:D:1003:GLN:NE2	2.42	0.51
1:H:486:VAL:O	1:H:487:THR:OG1	2.20	0.51
2:S:1201:VAL:O	2:S:1204:ARG:NH1	2.44	0.51
2:T:1087:ASP:O	2:T:1090:SER:OG	2.27	0.51
2:a:1201:VAL:O	2:a:1204:ARG:NH1	2.44	0.51
2:C:1201:VAL:O	2:C:1204:ARG:NH1	2.44	0.51
2:d:931:GLY:O	2:d:945:ARG:NH1	2.42	0.51
1:K:529:GLY:O	2:Y:1004:ASN:ND2	2.44	0.51
2:c:1087:ASP:O	2:c:1090:SER:OG	2.27	0.50
2:f:1201:VAL:O	2:f:1204:ARG:NH1	2.44	0.50
1:G:529:GLY:O	2:U:1004:ASN:ND2	2.44	0.50
1:K:460:HIS:HB3	1:O:714:GLU:HB3	1.93	0.50
2:S:880:GLY:O	2:S:1003:GLN:NE2	2.42	0.50
1:K:721:ILE:HG21	1:O:433:ALA:HA	1.93	0.50
2:a:931:GLY:O	2:a:945:ARG:NH1	2.42	0.50
1:E:529:GLY:O	2:S:1004:ASN:ND2	2.44	0.50
1:K:723:SER:O	1:O:430:VAL:C	2.54	0.50
1:K:724:ASP:CA	1:O:409:ILE:HG21	2.41	0.50
1:J:529:GLY:O	2:X:1004:ASN:ND2	2.44	0.50
1:K:712:ASP:O	1:O:459:LYS:CE	2.60	0.50
1:I:529:GLY:O	2:W:1004:ASN:ND2	2.44	0.50
1:K:141:ASP:OD2	1:K:145:ASN:ND2	2.41	0.50
2:Y:786:LEU:O	2:Y:789:THR:OG1	2.27	0.50
2:Z:1141:GLU:HB2	2:Z:1143:GLU:OE1	2.12	0.50
1:H:529:GLY:O	2:V:1004:ASN:ND2	2.44	0.50
2:W:1087:ASP:O	2:W:1090:SER:OG	2.27	0.50
1:I:436:ARG:NH1	1:P:177:GLU:O	2.45	0.50
1:L:670:ARG:O	1:L:673:SER:OG	2.18	0.50
2:Z:1140:TYR:C	2:Z:1142:CYS:H	2.18	0.50
1:F:436:ARG:NH1	1:M:177:GLU:O	2.45	0.50
1:K:409:ILE:HB	1:O:725:HIS:NE2	2.26	0.50
1:K:720:ASP:CG	1:O:505:ARG:NH1	2.70	0.50
1:R:253:THR:OG1	1:R:256:GLU:OE2	2.22	0.50
2:C:1087:ASP:O	2:C:1090:SER:OG	2.27	0.50
1:G:141:ASP:OD2	1:G:145:ASN:ND2	2.41	0.50
1:H:436:ARG:NH1	1:O:177:GLU:O	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:436:ARG:NH1	1:L:177:GLU:O	2.45	0.49
2:f:880:GLY:O	2:f:1003:GLN:NE2	2.42	0.49
1:A:529:GLY:O	2:C:1004:ASN:ND2	2.44	0.49
2:c:1093:SER:OG	2:V:1093:SER:O	2.25	0.49
2:e:1087:ASP:O	2:e:1090:SER:OG	2.27	0.49
1:N:98:VAL:O	1:N:99:ASN:C	2.55	0.49
1:G:436:ARG:NH1	1:N:177:GLU:O	2.45	0.49
1:K:442:ARG:HG3	1:O:722:PHE:CZ	2.47	0.49
2:X:1087:ASP:O	2:X:1090:SER:OG	2.27	0.49
1:B:101:THR:CG2	3:B:801:NAG:C8	2.67	0.49
2:T:786:LEU:O	2:T:789:THR:OG1	2.27	0.49
2:U:1133:ARG:HD3	2:U:1144:TRP:CD2	2.46	0.49
1:A:99:ASN:C	1:A:101:THR:N	2.71	0.49
2:S:931:GLY:O	2:S:945:ARG:NH1	2.42	0.49
1:A:436:ARG:NH1	1:B:177:GLU:O	2.45	0.49
1:B:156:ASN:ND2	3:B:802:NAG:O5	2.40	0.49
1:B:696:ASP:OD1	1:B:697:GLU:N	2.46	0.49
1:N:486:VAL:O	1:N:487:THR:OG1	2.20	0.49
1:P:696:ASP:OD1	1:P:697:GLU:N	2.46	0.49
1:Q:696:ASP:OD1	1:Q:697:GLU:N	2.46	0.49
1:A:696:ASP:OD1	1:A:697:GLU:N	2.46	0.49
1:B:100:GLY:HA3	1:B:127:TYR:CE2	2.48	0.49
2:D:1146:TYR:HA	2:D:1173:CYS:HA	1.95	0.49
1:F:141:ASP:OD2	1:F:145:ASN:ND2	2.41	0.49
2:f:901:ASN:OD1	2:f:991:LYS:NZ	2.29	0.49
1:K:430:VAL:HG12	1:O:724:ASP:OD1	2.13	0.49
1:B:486:VAL:O	1:B:487:THR:OG1	2.20	0.49
2:C:931:GLY:O	2:C:945:ARG:NH1	2.42	0.49
2:d:880:GLY:O	2:d:1003:GLN:NE2	2.42	0.49
1:K:436:ARG:NH1	1:R:177:GLU:O	2.45	0.49
2:T:838:PRO:HA	2:T:851:CYS:O	2.13	0.49
2:U:852:GLN:HG3	2:U:857:ASN:HD22	1.78	0.49
2:Z:1131:GLU:O	2:Z:1135:LEU:HB2	2.13	0.49
2:b:901:ASN:OD1	2:b:991:LYS:NZ	2.29	0.49
2:b:1148:SER:O	2:b:1171:GLU:HG2	2.13	0.49
1:I:486:VAL:O	1:I:487:THR:OG1	2.20	0.49
1:J:436:ARG:NH1	1:Q:177:GLU:O	2.45	0.49
1:N:670:ARG:O	1:N:673:SER:OG	2.18	0.49
1:L:141:ASP:OD2	1:L:145:ASN:ND2	2.41	0.49
1:P:97:PHE:CD1	1:P:99:ASN:HB3	2.48	0.49
1:A:670:ARG:O	1:A:673:SER:OG	2.18	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:670:ARG:O	1:O:673:SER:OG	2.18	0.48
1:Q:131:GLY:O	1:Q:135:GLY:N	2.47	0.48
2:d:1148:SER:O	2:d:1171:GLU:HA	2.12	0.48
2:e:786:LEU:O	2:e:789:THR:OG1	2.28	0.48
1:G:670:ARG:O	1:G:673:SER:OG	2.18	0.48
1:I:102:VAL:HG11	1:I:120:LEU:HD21	1.95	0.48
1:J:696:ASP:OD1	1:J:697:GLU:N	2.46	0.48
1:K:131:GLY:O	1:K:135:GLY:N	2.47	0.48
1:L:131:GLY:O	1:L:135:GLY:N	2.46	0.48
1:O:131:GLY:O	1:O:135:GLY:N	2.46	0.48
2:a:853:ASP:CG	2:a:854:ARG:H	2.22	0.48
2:d:786:LEU:O	2:d:789:THR:OG1	2.28	0.48
1:E:696:ASP:OD1	1:E:697:GLU:N	2.46	0.48
1:F:670:ARG:O	1:F:673:SER:OG	2.18	0.48
1:G:155:PHE:O	1:G:156:ASN:C	2.56	0.48
1:A:131:GLY:O	1:A:135:GLY:N	2.46	0.48
2:c:1133:ARG:NH1	2:c:1173:CYS:SG	2.87	0.48
2:d:1133:ARG:NH1	2:d:1173:CYS:SG	2.87	0.48
2:X:1133:ARG:NH1	2:X:1173:CYS:SG	2.87	0.48
2:Z:880:GLY:O	2:Z:1003:GLN:NE2	2.42	0.48
2:C:901:ASN:OD1	2:C:991:LYS:NZ	2.29	0.48
2:e:880:GLY:O	2:e:1003:GLN:NE2	2.42	0.48
1:G:34:ARG:HE	1:G:36:SER:HB2	1.79	0.48
1:H:39:GLY:O	1:H:81:ARG:NH2	2.45	0.48
1:L:34:ARG:HE	1:L:36:SER:HB2	1.79	0.48
1:P:34:ARG:HE	1:P:36:SER:HB2	1.79	0.48
2:T:1133:ARG:NH1	2:T:1173:CYS:SG	2.87	0.48
2:Z:1133:ARG:HB3	2:Z:1144:TRP:CD1	2.49	0.48
2:a:1133:ARG:NH1	2:a:1173:CYS:SG	2.87	0.48
1:B:166:ASN:HD22	3:B:802:NAG:H81	1.79	0.48
1:M:34:ARG:HE	1:M:36:SER:HB2	1.79	0.48
1:R:131:GLY:O	1:R:135:GLY:N	2.47	0.48
2:S:1093:SER:O	2:Z:1093:SER:OG	2.25	0.48
2:W:852:GLN:CD	2:W:853:ASP:H	2.21	0.48
2:Z:786:LEU:O	2:Z:789:THR:OG1	2.28	0.48
2:b:1133:ARG:NH1	2:b:1173:CYS:SG	2.87	0.48
2:C:880:GLY:O	2:C:1003:GLN:NE2	2.42	0.48
2:c:786:LEU:O	2:c:789:THR:OG1	2.28	0.48
2:c:880:GLY:O	2:c:1003:GLN:NE2	2.42	0.48
1:E:131:GLY:O	1:E:135:GLY:N	2.47	0.48
1:F:34:ARG:HE	1:F:36:SER:HB2	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:610:TYR:O	1:H:614:SER:OG	2.31	0.48
1:M:131:GLY:O	1:M:135:GLY:N	2.46	0.48
1:N:253:THR:OG1	1:N:256:GLU:OE2	2.23	0.48
1:P:131:GLY:O	1:P:135:GLY:N	2.46	0.48
2:V:880:GLY:O	2:V:1003:GLN:NE2	2.42	0.48
1:F:95:HIS:HE1	1:F:105:GLY:N	2.11	0.48
1:F:529:GLY:O	2:T:1004:ASN:ND2	2.44	0.48
1:G:131:GLY:O	1:G:135:GLY:N	2.46	0.48
1:K:459:LYS:HB3	1:O:714:GLU:HG2	1.95	0.48
2:V:901:ASN:OD1	2:V:991:LYS:NZ	2.29	0.48
2:Z:850:VAL:O	2:Z:857:ASN:N	2.45	0.48
1:H:696:ASP:OD1	1:H:697:GLU:N	2.46	0.48
1:I:696:ASP:OD1	1:I:697:GLU:N	2.46	0.48
2:S:1133:ARG:NH1	2:S:1173:CYS:SG	2.87	0.48
2:U:1128:GLN:HG2	2:U:1146:TYR:HE2	1.79	0.48
2:U:1134:ASN:HD21	2:U:1144:TRP:N	2.12	0.48
2:V:1133:ARG:NH1	2:V:1173:CYS:SG	2.87	0.48
2:Y:1133:ARG:NH1	2:Y:1173:CYS:SG	2.87	0.48
1:A:34:ARG:HE	1:A:36:SER:HB2	1.79	0.48
2:e:1133:ARG:NH1	2:e:1173:CYS:SG	2.87	0.48
1:F:131:GLY:O	1:F:135:GLY:N	2.47	0.48
2:f:1133:ARG:NH1	2:f:1173:CYS:SG	2.87	0.48
1:H:34:ARG:HE	1:H:36:SER:HB2	1.79	0.48
1:K:39:GLY:O	1:K:81:ARG:NH2	2.45	0.48
1:M:696:ASP:OD1	1:M:697:GLU:N	2.46	0.48
1:Q:34:ARG:HE	1:Q:36:SER:HB2	1.79	0.48
2:W:1133:ARG:NH1	2:W:1173:CYS:SG	2.87	0.48
2:C:1133:ARG:NH1	2:C:1173:CYS:SG	2.87	0.47
2:D:1133:ARG:NH1	2:D:1173:CYS:SG	2.87	0.47
1:H:131:GLY:O	1:H:135:GLY:N	2.46	0.47
1:N:34:ARG:HE	1:N:36:SER:HB2	1.79	0.47
1:Q:39:GLY:O	1:Q:81:ARG:NH2	2.45	0.47
2:b:776:CYS:SG	2:b:804:CYS:N	2.88	0.47
1:E:99:ASN:OD1	1:E:99:ASN:N	2.45	0.47
1:H:253:THR:OG1	1:H:256:GLU:OE2	2.23	0.47
1:J:39:GLY:O	1:J:81:ARG:NH2	2.45	0.47
2:U:776:CYS:SG	2:U:804:CYS:N	2.88	0.47
2:X:776:CYS:SG	2:X:804:CYS:N	2.88	0.47
2:Z:1146:TYR:HA	2:Z:1173:CYS:HA	1.95	0.47
1:A:97:PHE:HE2	1:A:99:ASN:ND2	2.12	0.47
1:B:131:GLY:O	1:B:135:GLY:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:834:LYS:NZ	2:C:836:TYR:OH	2.35	0.47
2:c:901:ASN:OD1	2:c:991:LYS:NZ	2.29	0.47
1:E:34:ARG:HE	1:E:36:SER:HB2	1.79	0.47
1:G:168:PHE:HB3	1:G:170:GLU:OE2	2.14	0.47
1:G:696:ASP:OD1	1:G:697:GLU:N	2.46	0.47
1:N:131:GLY:O	1:N:135:GLY:N	2.47	0.47
1:B:34:ARG:HE	1:B:36:SER:HB2	1.79	0.47
2:e:776:CYS:SG	2:e:804:CYS:N	2.88	0.47
2:f:776:CYS:SG	2:f:804:CYS:N	2.88	0.47
1:J:131:GLY:O	1:J:135:GLY:N	2.47	0.47
2:T:776:CYS:SG	2:T:804:CYS:N	2.88	0.47
2:W:776:CYS:SG	2:W:804:CYS:N	2.88	0.47
2:a:776:CYS:SG	2:a:804:CYS:N	2.88	0.47
2:d:776:CYS:SG	2:d:804:CYS:N	2.88	0.47
1:F:201:GLU:N	1:F:201:GLU:OE1	2.48	0.47
1:F:486:VAL:O	1:F:487:THR:OG1	2.20	0.47
1:H:232:SER:O	1:H:236:ARG:NE	2.47	0.47
1:I:131:GLY:O	1:I:135:GLY:N	2.47	0.47
1:I:201:GLU:N	1:I:201:GLU:OE1	2.48	0.47
1:N:201:GLU:N	1:N:201:GLU:OE1	2.48	0.47
1:O:34:ARG:HE	1:O:36:SER:HB2	1.79	0.47
1:B:155:PHE:HD1	1:B:165:PHE:CE2	2.33	0.47
1:B:232:SER:O	1:B:236:ARG:NE	2.47	0.47
2:f:786:LEU:O	2:f:789:THR:OG1	2.28	0.47
2:S:776:CYS:SG	2:S:804:CYS:N	2.88	0.47
2:T:880:GLY:O	2:T:1003:GLN:NE2	2.42	0.47
2:a:1021:PHE:O	2:a:1024:SER:OG	2.13	0.47
1:E:155:PHE:HA	1:E:165:PHE:HD2	1.80	0.47
1:F:39:GLY:O	1:F:81:ARG:NH2	2.45	0.47
1:G:99:ASN:OD1	3:G:801:NAG:C7	2.63	0.47
1:I:34:ARG:HE	1:I:36:SER:HB2	1.79	0.47
1:J:34:ARG:HE	1:J:36:SER:HB2	1.79	0.47
1:K:34:ARG:HE	1:K:36:SER:HB2	1.79	0.47
1:L:201:GLU:OE1	1:L:201:GLU:N	2.48	0.47
1:O:201:GLU:OE1	1:O:201:GLU:N	2.48	0.47
1:P:311:THR:HG1	1:P:312:CYS:H	1.63	0.47
1:R:201:GLU:N	1:R:201:GLU:OE1	2.48	0.47
2:Z:776:CYS:SG	2:Z:804:CYS:N	2.88	0.47
2:b:880:GLY:O	2:b:1003:GLN:NE2	2.42	0.47
2:D:1087:ASP:O	2:D:1090:SER:OG	2.27	0.47
1:E:368:ASN:ND2	1:E:380:SER:OG	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:34:ARG:HE	1:R:36:SER:HB2	1.79	0.47
2:U:1021:PHE:O	2:U:1024:SER:OG	2.13	0.47
1:A:368:ASN:ND2	1:A:380:SER:OG	2.48	0.47
1:B:175:THR:O	1:B:178:GLY:N	2.48	0.47
1:F:175:THR:O	1:F:178:GLY:N	2.48	0.47
1:G:201:GLU:OE1	1:G:201:GLU:N	2.48	0.47
1:G:311:THR:HG1	1:G:312:CYS:H	1.63	0.47
1:K:201:GLU:N	1:K:201:GLU:OE1	2.48	0.47
2:T:839:GLY:N	2:T:852:GLN:HA	2.30	0.47
1:H:175:THR:O	1:H:178:GLY:N	2.48	0.47
1:I:154:TYR:C	1:I:157:LYS:HB2	2.39	0.47
1:O:368:ASN:ND2	1:O:380:SER:OG	2.48	0.47
1:Q:201:GLU:OE1	1:Q:201:GLU:N	2.48	0.47
2:X:880:GLY:O	2:X:1003:GLN:NE2	2.42	0.47
1:A:175:THR:O	1:A:178:GLY:N	2.48	0.46
1:K:696:ASP:OD1	1:K:697:GLU:N	2.46	0.46
1:O:253:THR:OG1	1:O:256:GLU:OE2	2.22	0.46
1:R:232:SER:O	1:R:236:ARG:NE	2.47	0.46
2:S:901:ASN:OD1	2:S:991:LYS:NZ	2.29	0.46
1:A:201:GLU:N	1:A:201:GLU:OE1	2.48	0.46
1:I:175:THR:O	1:I:178:GLY:N	2.48	0.46
1:I:670:ARG:O	1:I:673:SER:OG	2.18	0.46
1:L:232:SER:O	1:L:236:ARG:NE	2.47	0.46
1:L:368:ASN:ND2	1:L:380:SER:OG	2.48	0.46
2:X:901:ASN:OD1	2:X:991:LYS:NZ	2.29	0.46
2:D:776:CYS:SG	2:D:804:CYS:N	2.88	0.46
1:F:158:THR:O	1:F:164:ASN:HA	2.16	0.46
1:F:250:CYS:SG	1:F:251:GLU:N	2.89	0.46
1:I:154:TYR:HA	1:I:157:LYS:HB2	1.98	0.46
1:L:175:THR:O	1:L:178:GLY:N	2.48	0.46
1:P:175:THR:O	1:P:178:GLY:N	2.48	0.46
1:P:368:ASN:ND2	1:P:380:SER:OG	2.48	0.46
1:Q:175:THR:O	1:Q:178:GLY:N	2.48	0.46
2:U:1137:GLU:OE2	2:U:1141:GLU:HB2	2.15	0.46
2:U:1141:GLU:O	2:U:1142:CYS:C	2.59	0.46
2:Y:776:CYS:SG	2:Y:804:CYS:N	2.88	0.46
1:B:368:ASN:ND2	1:B:380:SER:OG	2.48	0.46
1:H:368:ASN:ND2	1:H:380:SER:OG	2.48	0.46
1:K:368:ASN:ND2	1:K:380:SER:OG	2.48	0.46
1:M:201:GLU:N	1:M:201:GLU:OE1	2.48	0.46
1:N:250:CYS:SG	1:N:251:GLU:N	2.89	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:c:776:CYS:SG	2:c:804:CYS:N	2.88	0.46
1:E:166:ASN:N	1:E:166:ASN:HD22	2.11	0.46
1:F:232:SER:O	1:F:236:ARG:NE	2.47	0.46
1:G:175:THR:O	1:G:178:GLY:N	2.48	0.46
1:O:155:PHE:HZ	1:O:167:ILE:HG12	1.80	0.46
2:U:1146:TYR:HA	2:U:1172:GLY:O	2.16	0.46
1:E:119:TYR:OH	2:S:888:GLU:O	2.30	0.46
1:G:250:CYS:SG	1:G:251:GLU:N	2.89	0.46
1:H:201:GLU:N	1:H:201:GLU:OE1	2.48	0.46
1:J:610:TYR:O	1:J:614:SER:OG	2.31	0.46
1:Q:368:ASN:ND2	1:Q:380:SER:OG	2.48	0.46
1:I:250:CYS:SG	1:I:251:GLU:N	2.89	0.46
1:J:175:THR:O	1:J:178:GLY:N	2.48	0.46
1:N:610:TYR:O	1:N:614:SER:OG	2.31	0.46
1:O:175:THR:O	1:O:178:GLY:N	2.48	0.46
1:O:250:CYS:SG	1:O:251:GLU:N	2.89	0.46
2:D:834:LYS:NZ	2:D:836:TYR:OH	2.35	0.46
1:M:39:GLY:O	1:M:81:ARG:NH2	2.45	0.46
1:M:101:THR:HG21	3:M:801:NAG:H62	1.98	0.46
1:P:201:GLU:N	1:P:201:GLU:OE1	2.48	0.46
1:P:250:CYS:SG	1:P:251:GLU:N	2.89	0.46
2:V:776:CYS:SG	2:V:804:CYS:N	2.88	0.46
1:B:201:GLU:N	1:B:201:GLU:OE1	2.48	0.46
1:E:99:ASN:O	1:E:101:THR:N	2.49	0.46
1:F:368:ASN:ND2	1:F:380:SER:OG	2.48	0.46
1:J:201:GLU:OE1	1:J:201:GLU:N	2.48	0.46
1:K:610:TYR:O	1:K:614:SER:OG	2.31	0.46
1:N:175:THR:O	1:N:178:GLY:N	2.48	0.46
1:R:175:THR:O	1:R:178:GLY:N	2.48	0.46
1:R:368:ASN:ND2	1:R:380:SER:OG	2.48	0.46
1:R:696:ASP:OD1	1:R:697:GLU:N	2.46	0.46
2:Y:880:GLY:O	2:Y:1003:GLN:NE2	2.42	0.46
1:E:201:GLU:OE1	1:E:201:GLU:N	2.48	0.46
1:G:368:ASN:ND2	1:G:380:SER:OG	2.48	0.46
1:H:250:CYS:SG	1:H:251:GLU:N	2.89	0.46
1:K:250:CYS:SG	1:K:251:GLU:N	2.89	0.46
1:M:250:CYS:SG	1:M:251:GLU:N	2.89	0.46
1:P:232:SER:O	1:P:236:ARG:NE	2.47	0.46
1:R:250:CYS:SG	1:R:251:GLU:N	2.89	0.46
2:Z:834:LYS:NZ	2:Z:836:TYR:OH	2.35	0.46
1:B:250:CYS:SG	1:B:251:GLU:N	2.89	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:c:872:MET:SD	2:c:872:MET:N	2.89	0.45
1:E:175:THR:O	1:E:178:GLY:N	2.48	0.45
1:E:250:CYS:SG	1:E:251:GLU:N	2.89	0.45
1:I:232:SER:O	1:I:236:ARG:NE	2.47	0.45
1:J:368:ASN:ND2	1:J:380:SER:OG	2.48	0.45
1:M:368:ASN:ND2	1:M:380:SER:OG	2.48	0.45
1:O:154:TYR:HA	1:O:157:LYS:HB2	1.98	0.45
1:Q:250:CYS:SG	1:Q:251:GLU:N	2.89	0.45
2:T:872:MET:SD	2:T:872:MET:N	2.89	0.45
2:W:786:LEU:O	2:W:789:THR:OG1	2.27	0.45
2:X:872:MET:SD	2:X:872:MET:N	2.89	0.45
2:Z:1150:ALA:HB3	2:Z:1174:HIS:CD2	2.51	0.45
1:E:670:ARG:O	1:E:673:SER:OG	2.18	0.45
2:f:872:MET:SD	2:f:872:MET:N	2.89	0.45
1:I:97:PHE:HE1	1:I:99:ASN:HB2	1.81	0.45
1:K:712:ASP:C	1:O:459:LYS:HZ1	2.22	0.45
1:N:696:ASP:OD1	1:N:697:GLU:N	2.46	0.45
2:W:901:ASN:OD1	2:W:991:LYS:NZ	2.29	0.45
2:Y:872:MET:SD	2:Y:872:MET:N	2.90	0.45
1:A:250:CYS:SG	1:A:251:GLU:N	2.89	0.45
1:G:119:TYR:OH	2:U:888:GLU:O	2.30	0.45
1:G:168:PHE:HB2	1:G:171:ASP:OD1	2.16	0.45
1:O:610:TYR:O	1:O:614:SER:OG	2.31	0.45
2:U:872:MET:SD	2:U:872:MET:N	2.89	0.45
2:D:872:MET:SD	2:D:872:MET:N	2.89	0.45
1:G:39:GLY:O	1:G:81:ARG:NH2	2.45	0.45
1:K:472:GLN:CG	1:O:472:GLN:HG2	2.43	0.45
1:M:175:THR:O	1:M:178:GLY:N	2.48	0.45
1:N:368:ASN:ND2	1:N:380:SER:OG	2.48	0.45
1:O:155:PHE:HA	1:O:165:PHE:HD2	1.82	0.45
1:O:696:ASP:OD1	1:O:697:GLU:N	2.46	0.45
2:U:1134:ASN:ND2	2:U:1142:CYS:SG	2.90	0.45
1:B:96:LEU:HB3	1:B:102:VAL:HG12	1.99	0.45
2:C:776:CYS:SG	2:C:804:CYS:N	2.88	0.45
2:d:872:MET:SD	2:d:872:MET:N	2.89	0.45
2:e:872:MET:SD	2:e:872:MET:N	2.89	0.45
1:I:154:TYR:CA	1:I:157:LYS:HB2	2.46	0.45
1:K:175:THR:O	1:K:178:GLY:N	2.48	0.45
1:O:232:SER:O	1:O:236:ARG:NE	2.47	0.45
1:P:39:GLY:O	1:P:81:ARG:NH2	2.45	0.45
2:T:901:ASN:OD1	2:T:991:LYS:NZ	2.29	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:W:872:MET:SD	2:W:872:MET:N	2.89	0.45
1:J:250:CYS:SG	1:J:251:GLU:N	2.89	0.45
2:V:872:MET:SD	2:V:872:MET:N	2.89	0.45
2:Z:872:MET:SD	2:Z:872:MET:N	2.89	0.45
2:a:872:MET:SD	2:a:872:MET:N	2.89	0.45
2:b:872:MET:SD	2:b:872:MET:N	2.89	0.45
2:b:1142:CYS:SG	2:U:1142:CYS:CB	3.04	0.45
1:F:696:ASP:OD1	1:F:697:GLU:N	2.46	0.45
1:L:610:TYR:O	1:L:614:SER:OG	2.31	0.45
1:P:33:ALA:HB2	1:P:165:PHE:CD1	2.52	0.45
1:R:39:GLY:O	1:R:81:ARG:NH2	2.45	0.45
2:T:839:GLY:H	2:T:852:GLN:HA	1.80	0.45
2:U:1133:ARG:HB3	2:U:1144:TRP:CD1	2.52	0.45
2:Z:1134:ASN:CG	2:Z:1142:CYS:HA	2.42	0.45
1:A:232:SER:O	1:A:236:ARG:NE	2.47	0.45
2:C:872:MET:SD	2:C:872:MET:N	2.90	0.45
1:E:311:THR:OG1	1:E:337:LEU:O	2.35	0.45
1:I:368:ASN:ND2	1:I:380:SER:OG	2.48	0.45
1:L:250:CYS:SG	1:L:251:GLU:N	2.89	0.45
1:Q:232:SER:O	1:Q:236:ARG:NE	2.47	0.45
2:S:872:MET:SD	2:S:872:MET:N	2.90	0.45
1:B:39:GLY:O	1:B:81:ARG:NH2	2.45	0.45
1:E:33:ALA:HB2	1:E:165:PHE:CD1	2.52	0.45
1:F:96:LEU:HA	1:F:102:VAL:HG12	1.99	0.45
1:K:33:ALA:HB2	1:K:165:PHE:CD1	2.52	0.45
1:K:722:PHE:HZ	1:O:442:ARG:CD	2.30	0.45
1:R:670:ARG:O	1:R:673:SER:OG	2.18	0.45
1:A:33:ALA:HB2	1:A:165:PHE:CD1	2.52	0.45
2:d:901:ASN:OD1	2:d:991:LYS:NZ	2.29	0.45
1:J:232:SER:O	1:J:236:ARG:NE	2.47	0.45
1:L:33:ALA:HB2	1:L:165:PHE:CD1	2.52	0.45
1:M:33:ALA:HB2	1:M:165:PHE:CD1	2.52	0.45
1:M:232:SER:O	1:M:236:ARG:NE	2.47	0.45
1:P:256:GLU:OE1	1:P:256:GLU:N	2.44	0.45
1:Q:33:ALA:HB2	1:Q:165:PHE:CD1	2.52	0.45
1:R:33:ALA:HB2	1:R:165:PHE:CD1	2.52	0.45
1:B:156:ASN:C	1:B:157:LYS:HD2	2.42	0.44
1:B:670:ARG:O	1:B:673:SER:OG	2.18	0.44
1:F:311:THR:OG1	1:F:337:LEU:O	2.35	0.44
1:I:311:THR:OG1	1:I:337:LEU:O	2.35	0.44
1:J:670:ARG:O	1:J:673:SER:OG	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:33:ALA:HB2	1:N:165:PHE:CD1	2.52	0.44
1:N:232:SER:O	1:N:236:ARG:NE	2.47	0.44
1:O:155:PHE:HD2	1:O:165:PHE:CE2	2.35	0.44
1:R:256:GLU:OE1	1:R:256:GLU:N	2.44	0.44
1:J:33:ALA:HB2	1:J:165:PHE:CD1	2.52	0.44
1:L:39:GLY:O	1:L:81:ARG:NH2	2.45	0.44
1:F:154:TYR:C	1:F:157:LYS:HD3	2.42	0.44
1:H:33:ALA:HB2	1:H:165:PHE:CD1	2.52	0.44
1:O:33:ALA:HB2	1:O:165:PHE:CD1	2.52	0.44
2:W:880:GLY:O	2:W:1003:GLN:NE2	2.42	0.44
1:A:170:GLU:OE1	1:A:170:GLU:N	2.50	0.44
1:E:256:GLU:OE1	1:E:256:GLU:N	2.44	0.44
1:K:724:ASP:HA	1:O:409:ILE:CG2	2.48	0.44
2:X:786:LEU:O	2:X:789:THR:OG1	2.27	0.44
2:Z:849:CYS:HA	2:Z:858:CYS:HA	2.00	0.44
1:B:610:TYR:O	1:B:614:SER:OG	2.31	0.44
1:E:39:GLY:O	1:E:81:ARG:NH2	2.45	0.44
2:e:834:LYS:NZ	2:e:836:TYR:OH	2.35	0.44
1:G:232:SER:O	1:G:236:ARG:NE	2.47	0.44
1:I:33:ALA:HB2	1:I:165:PHE:CD1	2.52	0.44
1:K:505:ARG:NH1	1:O:720:ASP:OD1	2.51	0.44
1:P:170:GLU:OE1	1:P:170:GLU:N	2.51	0.44
1:F:63:GLY:O	1:F:158:THR:HA	2.17	0.44
1:F:119:TYR:OH	2:T:888:GLU:O	2.30	0.44
1:K:721:ILE:HD13	1:O:616:SER:CB	2.48	0.44
1:R:30:SER:OG	1:R:31:SER:N	2.51	0.44
1:B:33:ALA:HB2	1:B:165:PHE:CD1	2.52	0.44
1:E:232:SER:O	1:E:236:ARG:NE	2.47	0.44
1:G:152:ASP:HA	1:G:165:PHE:CE2	2.53	0.44
1:M:256:GLU:OE1	1:M:256:GLU:N	2.44	0.44
1:N:311:THR:OG1	1:N:337:LEU:O	2.35	0.44
2:U:1137:GLU:O	2:U:1138:ASN:C	2.61	0.44
2:Z:1151:PRO:HA	2:Z:1169:CYS:HA	1.99	0.44
2:D:1146:TYR:HA	2:D:1172:GLY:O	2.18	0.44
1:F:300:GLU:N	1:F:300:GLU:OE1	2.51	0.44
1:J:300:GLU:N	1:J:300:GLU:OE1	2.51	0.44
1:K:700:ASP:OD1	1:K:701:CYS:N	2.51	0.44
1:M:98:VAL:O	1:M:100:GLY:N	2.51	0.44
1:M:170:GLU:OE1	1:M:170:GLU:N	2.51	0.44
1:O:98:VAL:O	1:O:100:GLY:N	2.51	0.44
2:U:1150:ALA:HB3	2:U:1174:HIS:CE1	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:700:ASP:OD1	1:B:701:CYS:N	2.51	0.43
1:F:33:ALA:HB2	1:F:165:PHE:CD1	2.52	0.43
1:G:300:GLU:N	1:G:300:GLU:OE1	2.51	0.43
1:N:700:ASP:OD1	1:N:701:CYS:N	2.51	0.43
1:R:300:GLU:N	1:R:300:GLU:OE1	2.51	0.43
2:a:901:ASN:OD1	2:a:991:LYS:NZ	2.29	0.43
1:F:610:TYR:O	1:F:614:SER:OG	2.31	0.43
1:J:700:ASP:OD1	1:J:701:CYS:N	2.51	0.43
1:M:300:GLU:N	1:M:300:GLU:OE1	2.51	0.43
1:M:700:ASP:OD1	1:M:701:CYS:N	2.51	0.43
2:T:851:CYS:SG	2:T:855:LYS:N	2.92	0.43
1:A:700:ASP:OD1	1:A:701:CYS:N	2.51	0.43
2:a:786:LEU:O	2:a:789:THR:OG1	2.28	0.43
1:B:170:GLU:OE1	1:B:170:GLU:N	2.51	0.43
1:E:700:ASP:OD1	1:E:701:CYS:N	2.51	0.43
1:I:300:GLU:OE1	1:I:300:GLU:N	2.51	0.43
1:K:300:GLU:N	1:K:300:GLU:OE1	2.51	0.43
1:M:311:THR:HG1	1:M:312:CYS:H	1.66	0.43
1:O:311:THR:OG1	1:O:337:LEU:O	2.35	0.43
1:E:170:GLU:OE1	1:E:170:GLU:N	2.51	0.43
1:H:700:ASP:OD1	1:H:701:CYS:N	2.51	0.43
1:I:700:ASP:OD1	1:I:701:CYS:N	2.51	0.43
1:N:300:GLU:OE1	1:N:300:GLU:N	2.51	0.43
1:P:700:ASP:OD1	1:P:701:CYS:N	2.51	0.43
2:Z:1135:LEU:O	2:Z:1136:ARG:C	2.61	0.43
1:A:300:GLU:N	1:A:300:GLU:OE1	2.51	0.43
2:a:834:LYS:NZ	2:a:836:TYR:OH	2.35	0.43
1:E:300:GLU:N	1:E:300:GLU:OE1	2.51	0.43
1:K:311:THR:OG1	1:K:337:LEU:O	2.35	0.43
1:O:300:GLU:N	1:O:300:GLU:OE1	2.51	0.43
1:P:300:GLU:OE1	1:P:300:GLU:N	2.51	0.43
1:Q:300:GLU:N	1:Q:300:GLU:OE1	2.51	0.43
1:A:311:THR:OG1	1:A:337:LEU:O	2.35	0.43
2:b:834:LYS:NZ	2:b:836:TYR:OH	2.35	0.43
1:F:30:SER:OG	1:F:31:SER:N	2.51	0.43
1:H:177:GLU:OE2	1:K:728:MET:SD	2.76	0.43
1:J:311:THR:OG1	1:J:337:LEU:O	2.35	0.43
1:K:459:LYS:NZ	1:O:714:GLU:N	2.66	0.43
2:U:1144:TRP:HA	2:U:1175:ALA:HA	2.01	0.43
2:Z:901:ASN:OD1	2:Z:991:LYS:NZ	2.29	0.43
1:G:30:SER:OG	1:G:31:SER:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:311:THR:OG1	1:L:337:LEU:O	2.35	0.43
1:L:696:ASP:OD1	1:L:697:GLU:N	2.46	0.43
1:L:700:ASP:OD1	1:L:701:CYS:N	2.51	0.43
1:N:39:GLY:O	1:N:81:ARG:NH2	2.45	0.43
1:O:154:TYR:CA	1:O:157:LYS:HB2	2.48	0.43
1:P:30:SER:OG	1:P:31:SER:N	2.51	0.43
1:Q:256:GLU:OE1	1:Q:256:GLU:N	2.44	0.43
1:R:700:ASP:OD1	1:R:701:CYS:N	2.51	0.43
2:Z:1133:ARG:HD3	2:Z:1144:TRP:CE3	2.53	0.43
1:A:39:GLY:O	1:A:81:ARG:NH2	2.45	0.43
2:C:1121:ARG:HD2	2:C:1146:TYR:CE2	2.54	0.43
1:E:164:ASN:ND2	1:E:166:ASN:OD1	2.52	0.43
1:G:700:ASP:OD1	1:G:701:CYS:N	2.51	0.43
1:K:722:PHE:HZ	1:O:442:ARG:CG	2.30	0.43
2:Z:1140:TYR:C	2:Z:1142:CYS:N	2.75	0.43
1:B:300:GLU:OE1	1:B:300:GLU:N	2.51	0.43
1:H:170:GLU:OE1	1:H:170:GLU:N	2.51	0.43
1:H:300:GLU:N	1:H:300:GLU:OE1	2.51	0.43
1:H:574:PRO:HA	1:H:577:THR:HG23	2.01	0.43
1:I:30:SER:OG	1:I:31:SER:N	2.51	0.43
1:N:30:SER:OG	1:N:31:SER:N	2.51	0.43
1:O:700:ASP:OD1	1:O:701:CYS:N	2.51	0.43
1:Q:311:THR:OG1	1:Q:337:LEU:O	2.35	0.43
1:Q:700:ASP:OD1	1:Q:701:CYS:N	2.51	0.43
2:U:852:GLN:CG	2:U:857:ASN:HD22	2.31	0.43
1:L:300:GLU:N	1:L:300:GLU:OE1	2.51	0.43
1:O:170:GLU:OE1	1:O:170:GLU:N	2.51	0.43
1:P:574:PRO:HA	1:P:577:THR:HG23	2.01	0.43
2:S:1130:CYS:SG	2:S:1146:TYR:HB2	2.58	0.43
2:V:834:LYS:NZ	2:V:836:TYR:OH	2.35	0.43
2:C:1140:TYR:HD2	2:D:1145:ARG:NH1	2.17	0.42
1:F:700:ASP:OD1	1:F:701:CYS:N	2.51	0.42
1:K:170:GLU:OE1	1:K:170:GLU:N	2.51	0.42
1:K:430:VAL:HB	1:O:723:SER:C	2.44	0.42
1:O:39:GLY:O	1:O:81:ARG:NH2	2.45	0.42
2:Y:1118:VAL:O	2:Y:1148:SER:OG	2.37	0.42
2:D:786:LEU:O	2:D:789:THR:OG1	2.28	0.42
1:K:574:PRO:HA	1:K:577:THR:HG23	2.01	0.42
1:N:574:PRO:HA	1:N:577:THR:HG23	2.01	0.42
2:a:836:TYR:CD2	2:a:856:TRP:HZ2	2.37	0.42
1:E:155:PHE:C	1:E:157:LYS:H	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:e:901:ASN:OD1	2:e:991:LYS:NZ	2.29	0.42
1:G:574:PRO:HA	1:G:577:THR:HG23	2.01	0.42
1:H:256:GLU:OE1	1:H:256:GLU:N	2.44	0.42
1:K:442:ARG:HD2	1:O:722:PHE:HZ	1.83	0.42
1:M:574:PRO:HA	1:M:577:THR:HG23	2.01	0.42
2:U:1139:GLY:O	2:U:1141:GLU:N	2.51	0.42
2:V:1118:VAL:O	2:V:1148:SER:OG	2.37	0.42
2:a:1118:VAL:O	2:a:1148:SER:OG	2.37	0.42
2:D:1147:ASN:HB3	2:D:1174:HIS:HD2	1.85	0.42
1:R:311:THR:OG1	1:R:337:LEU:O	2.35	0.42
2:V:786:LEU:O	2:V:789:THR:OG1	2.28	0.42
2:W:1130:CYS:SG	2:W:1146:TYR:HB2	2.59	0.42
1:A:610:TYR:O	1:A:614:SER:OG	2.31	0.42
1:B:154:TYR:C	1:B:157:LYS:HD3	2.45	0.42
1:H:670:ARG:O	1:H:673:SER:OG	2.18	0.42
1:P:311:THR:OG1	1:P:337:LEU:O	2.35	0.42
1:P:610:TYR:O	1:P:614:SER:OG	2.31	0.42
2:V:887:GLY:O	2:V:911:ASN:ND2	2.53	0.42
2:X:887:GLY:O	2:X:911:ASN:ND2	2.53	0.42
2:c:887:GLY:O	2:c:911:ASN:ND2	2.53	0.42
2:e:887:GLY:O	2:e:911:ASN:ND2	2.53	0.42
2:S:887:GLY:O	2:S:911:ASN:ND2	2.53	0.42
2:U:786:LEU:O	2:U:789:THR:OG1	2.28	0.42
2:b:887:GLY:O	2:b:911:ASN:ND2	2.53	0.42
2:C:887:GLY:O	2:C:911:ASN:ND2	2.53	0.42
1:H:30:SER:OG	1:H:31:SER:N	2.51	0.42
1:K:232:SER:O	1:K:236:ARG:NE	2.47	0.42
1:K:720:ASP:OD1	1:O:505:ARG:NH1	2.53	0.42
2:W:887:GLY:O	2:W:911:ASN:ND2	2.53	0.42
2:Y:887:GLY:O	2:Y:911:ASN:ND2	2.53	0.42
2:Y:949:ASP:OD1	2:Y:951:THR:OG1	2.23	0.42
2:a:842:VAL:HG22	2:a:849:CYS:O	2.19	0.42
2:b:786:LEU:O	2:b:789:THR:OG1	2.27	0.42
2:D:887:GLY:O	2:D:911:ASN:ND2	2.53	0.42
1:F:574:PRO:HA	1:F:577:THR:HG23	2.01	0.42
1:P:96:LEU:HA	1:P:102:VAL:HG12	2.02	0.42
2:Y:850:VAL:O	2:Y:857:ASN:N	2.46	0.42
2:Z:1133:ARG:HD3	2:Z:1144:TRP:CD2	2.54	0.42
2:Z:1135:LEU:HA	2:Z:1140:TYR:CE1	2.55	0.42
1:A:155:PHE:HD2	1:A:165:PHE:CE2	2.38	0.42
2:a:887:GLY:O	2:a:911:ASN:ND2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:30:SER:OG	1:M:31:SER:N	2.51	0.42
1:G:171:ASP:O	1:G:173:PHE:N	2.53	0.42
1:I:417:ASP:OD2	1:I:422:SER:OG	2.36	0.42
1:J:30:SER:OG	1:J:31:SER:N	2.51	0.42
1:K:253:THR:OG1	1:K:256:GLU:OE2	2.23	0.42
1:K:725:HIS:CE1	1:O:409:ILE:HB	2.55	0.42
1:Q:170:GLU:OE1	1:Q:170:GLU:N	2.51	0.42
1:B:253:THR:OG1	1:B:256:GLU:OE2	2.22	0.41
2:D:1148:SER:O	2:D:1171:GLU:HG2	2.20	0.41
2:d:887:GLY:O	2:d:911:ASN:ND2	2.53	0.41
1:G:168:PHE:HB2	1:G:171:ASP:CG	2.45	0.41
1:G:256:GLU:OE1	1:G:256:GLU:N	2.44	0.41
1:K:442:ARG:HG3	1:O:722:PHE:CE1	2.55	0.41
2:T:887:GLY:O	2:T:911:ASN:ND2	2.53	0.41
2:b:1121:ARG:HD2	2:b:1146:TYR:CE2	2.55	0.41
2:D:1130:CYS:SG	2:D:1146:TYR:HB2	2.60	0.41
2:e:1118:VAL:O	2:e:1148:SER:OG	2.37	0.41
1:K:119:TYR:OH	2:Y:888:GLU:O	2.30	0.41
1:N:154:TYR:C	1:N:157:LYS:HD3	2.45	0.41
1:R:574:PRO:HA	1:R:577:THR:HG23	2.01	0.41
2:T:834:LYS:NZ	2:T:836:TYR:OH	2.35	0.41
2:X:1118:VAL:O	2:X:1148:SER:OG	2.38	0.41
1:B:30:SER:OG	1:B:31:SER:N	2.51	0.41
2:e:850:VAL:O	2:e:857:ASN:N	2.46	0.41
1:K:715:ILE:HB	1:O:461:GLY:HA3	2.01	0.41
1:O:83:SER:HA	1:O:97:PHE:HB3	2.01	0.41
1:Q:574:PRO:HA	1:Q:577:THR:HG23	2.01	0.41
2:Y:901:ASN:OD1	2:Y:991:LYS:NZ	2.29	0.41
1:B:574:PRO:HA	1:B:577:THR:HG23	2.01	0.41
2:C:1093:SER:O	2:D:1093:SER:OG	2.25	0.41
2:c:1118:VAL:O	2:c:1148:SER:OG	2.37	0.41
1:E:177:GLU:O	1:L:436:ARG:NH1	2.53	0.41
1:E:574:PRO:HA	1:E:577:THR:HG23	2.01	0.41
1:G:101:THR:CG2	1:G:108:ARG:HD2	2.51	0.41
1:G:171:ASP:HB2	1:G:174:MET:HE2	2.02	0.41
1:J:177:GLU:O	1:Q:436:ARG:NH1	2.53	0.41
1:M:97:PHE:CD2	1:M:99:ASN:HB3	2.55	0.41
1:A:30:SER:OG	1:A:31:SER:N	2.51	0.41
1:J:311:THR:HG1	1:J:312:CYS:H	1.68	0.41
1:K:724:ASP:C	1:O:409:ILE:HG21	2.44	0.41
1:N:170:GLU:OE1	1:N:170:GLU:N	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:W:851:CYS:O	2:W:852:GLN:C	2.62	0.41
2:Z:887:GLY:O	2:Z:911:ASN:ND2	2.53	0.41
1:A:574:PRO:HA	1:A:577:THR:HG23	2.01	0.41
1:A:721:ILE:HG21	1:L:434:ASP:OD1	2.20	0.41
2:D:1150:ALA:HB3	2:D:1174:HIS:CD2	2.55	0.41
1:F:311:THR:HG1	1:F:312:CYS:H	1.69	0.41
1:G:97:PHE:HZ	1:G:101:THR:HB	1.78	0.41
1:G:610:TYR:O	1:G:614:SER:OG	2.31	0.41
1:H:177:GLU:O	1:O:436:ARG:NH1	2.53	0.41
1:I:170:GLU:OE1	1:I:170:GLU:N	2.51	0.41
1:K:459:LYS:HZ3	1:O:714:GLU:CG	2.34	0.41
1:M:610:TYR:O	1:M:614:SER:OG	2.31	0.41
2:U:887:GLY:O	2:U:911:ASN:ND2	2.53	0.41
1:A:177:GLU:O	1:B:436:ARG:NH1	2.53	0.41
1:A:554:LYS:NZ	1:A:559:CYS:O	2.51	0.41
1:M:311:THR:OG1	1:M:337:LEU:O	2.35	0.41
1:O:554:LYS:NZ	1:O:559:CYS:O	2.51	0.41
1:Q:253:THR:OG1	1:Q:256:GLU:OE2	2.22	0.41
1:R:610:TYR:O	1:R:614:SER:OG	2.31	0.41
2:S:1000:ASP:OD2	2:S:1005:ASN:ND2	2.50	0.41
2:U:851:CYS:HA	2:U:856:TRP:HA	2.02	0.41
2:W:834:LYS:NZ	2:W:836:TYR:OH	2.35	0.41
2:Z:1148:SER:O	2:Z:1171:GLU:HG2	2.20	0.41
2:f:1118:VAL:O	2:f:1148:SER:OG	2.37	0.41
1:H:311:THR:HG1	1:H:312:CYS:H	1.67	0.41
1:I:574:PRO:HA	1:I:577:THR:HG23	2.01	0.41
1:K:177:GLU:O	1:R:436:ARG:NH1	2.53	0.41
1:K:662:GLY:O	1:K:684:LEU:N	2.54	0.41
1:O:574:PRO:HA	1:O:577:THR:HG23	2.01	0.41
2:T:1148:SER:O	2:T:1171:GLU:HG2	2.20	0.41
1:A:723:SER:OG	1:E:177:GLU:OE2	2.38	0.41
2:b:850:VAL:O	2:b:857:ASN:N	2.47	0.41
1:F:170:GLU:OE1	1:F:170:GLU:N	2.51	0.41
1:F:662:GLY:O	1:F:684:LEU:N	2.54	0.41
1:G:100:GLY:CA	1:G:127:TYR:HE2	2.34	0.41
1:G:154:TYR:O	1:G:165:PHE:HB3	2.21	0.41
1:G:171:ASP:C	1:G:173:PHE:N	2.79	0.41
1:G:177:GLU:O	1:N:436:ARG:NH1	2.53	0.41
1:J:256:GLU:OE1	1:J:256:GLU:N	2.44	0.41
1:J:574:PRO:HA	1:J:577:THR:HG23	2.01	0.41
1:K:459:LYS:NZ	1:O:712:ASP:O	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:170:GLU:OE1	1:L:170:GLU:N	2.51	0.41
1:L:574:PRO:HA	1:L:577:THR:HG23	2.01	0.41
1:N:417:ASP:OD2	1:N:422:SER:OG	2.36	0.41
1:N:662:GLY:O	1:N:684:LEU:N	2.54	0.41
2:S:842:VAL:HG13	2:S:856:TRP:CH2	2.56	0.41
2:S:1128:GLN:HG2	2:S:1146:TYR:CE1	2.56	0.41
2:T:1147:ASN:O	2:T:1148:SER:C	2.64	0.41
2:W:1146:TYR:HA	2:W:1172:GLY:O	2.21	0.41
2:f:887:GLY:O	2:f:911:ASN:ND2	2.53	0.41
1:G:662:GLY:O	1:G:684:LEU:N	2.54	0.41
1:I:177:GLU:O	1:P:436:ARG:NH1	2.53	0.41
1:K:30:SER:OG	1:K:31:SER:N	2.51	0.41
1:K:461:GLY:CA	1:O:715:ILE:HB	2.51	0.41
1:N:155:PHE:HZ	1:N:167:ILE:HG12	1.84	0.41
1:B:413:LEU:HD11	1:B:416:ARG:HD2	2.04	0.40
2:d:1093:SER:O	2:W:1093:SER:OG	2.21	0.40
1:G:311:THR:OG1	1:G:337:LEU:O	2.35	0.40
1:I:155:PHE:O	1:I:156:ASN:C	2.64	0.40
1:O:662:GLY:O	1:O:684:LEU:N	2.54	0.40
1:Q:610:TYR:O	1:Q:614:SER:OG	2.31	0.40
2:U:1145:ARG:O	2:U:1147:ASN:N	2.53	0.40
1:A:155:PHE:HZ	1:A:167:ILE:HG12	1.86	0.40
1:B:36:SER:O	1:B:44:ASN:N	2.54	0.40
1:E:36:SER:O	1:E:44:ASN:N	2.54	0.40
1:E:413:LEU:HD11	1:E:416:ARG:HD2	2.04	0.40
1:F:177:GLU:O	1:M:436:ARG:NH1	2.53	0.40
1:H:662:GLY:O	1:H:684:LEU:N	2.54	0.40
1:M:662:GLY:O	1:M:684:LEU:N	2.54	0.40
2:V:949:ASP:OD1	2:V:951:THR:OG1	2.23	0.40
1:H:413:LEU:HD11	1:H:416:ARG:HD2	2.04	0.40
1:K:472:GLN:CA	1:O:472:GLN:CG	2.85	0.40
1:L:413:LEU:HD11	1:L:416:ARG:HD2	2.04	0.40
1:R:662:GLY:O	1:R:684:LEU:N	2.54	0.40
2:U:1147:ASN:N	2:U:1174:HIS:HB2	2.33	0.40
1:B:311:THR:HG1	1:B:312:CYS:H	1.69	0.40
2:S:786:LEU:O	2:S:789:THR:OG1	2.28	0.40
2:W:1117:VAL:HG21	3:W:1302:NAG:O6	2.21	0.40

There are no symmetry-related clashes.

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%)	646 (91%)	61 (9%)	2 (0%)	36	71
1	E	709/741 (96%)	643 (91%)	63 (9%)	3 (0%)	30	66
1	F	709/741 (96%)	644 (91%)	65 (9%)	0	100	100
1	G	709/741 (96%)	640 (90%)	66 (9%)	3 (0%)	30	66
1	H	709/741 (96%)	647 (91%)	62 (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%)	648 (91%)	61 (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%)	647 (91%)	62 (9%)	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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	17116 (90%)	1829 (10%)	31 (0%)	44	77

All (31) 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
2	U	1137	GLU
2	Z	1148	SER
2	a	853	ASP
2	U	853	ASP
2	U	1133	ARG
1	B	101	THR

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Mol	Chain	Res	Type
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%)	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
2	U	423/436 (97%)	420 (99%)	3 (1%)	76	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	97	PHE
1	I	99	ASN
1	P	97	PHE
2	S	850	VAL
2	T	852	GLN
2	U	850	VAL
2	U	1132	GLU
2	U	1140	TYR
2	W	850	VAL
2	W	852	GLN
2	Z	1135	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (121) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	368	ASN
1	A	563	GLN
1	A	725	HIS
2	a	780	ASN
2	a	852	GLN
2	a	916	HIS

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Mol	Chain	Res	Type
2	a	1109	HIS
2	a	1113	GLN
1	B	95	HIS
1	B	368	ASN
1	B	566	HIS
2	b	780	ASN
2	b	916	HIS
2	b	1109	HIS
2	b	1113	GLN
2	C	780	ASN
2	C	916	HIS
2	C	1013	GLN
2	C	1109	HIS
2	C	1113	GLN
2	c	780	ASN
2	c	857	ASN
2	c	916	HIS
2	c	1109	HIS
2	c	1113	GLN
2	D	780	ASN
2	D	852	GLN
2	D	916	HIS
2	D	1109	HIS
2	D	1113	GLN
2	d	780	ASN
2	d	857	ASN
2	d	916	HIS
2	d	1109	HIS
2	d	1113	GLN
1	E	166	ASN
1	E	368	ASN
1	E	725	HIS
2	e	780	ASN
2	e	857	ASN
2	e	916	HIS
2	e	1109	HIS
2	e	1113	GLN
1	F	368	ASN
1	F	725	HIS
2	f	780	ASN
2	f	857	ASN
2	f	916	HIS

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Mol	Chain	Res	Type
2	f	1109	HIS
2	f	1113	GLN
1	G	368	ASN
1	G	725	HIS
1	H	95	HIS
1	H	368	ASN
1	I	95	HIS
1	I	368	ASN
1	J	368	ASN
1	K	368	ASN
1	K	469	GLN
1	L	368	ASN
1	L	566	HIS
1	M	368	ASN
1	M	725	HIS
1	N	368	ASN
1	N	563	GLN
1	N	725	HIS
1	O	368	ASN
1	O	469	GLN
1	P	368	ASN
1	P	725	HIS
1	Q	368	ASN
1	Q	469	GLN
1	R	368	ASN
1	R	563	GLN
1	R	566	HIS
2	S	780	ASN
2	S	916	HIS
2	S	1013	GLN
2	S	1109	HIS
2	S	1113	GLN
2	T	780	ASN
2	T	852	GLN
2	T	916	HIS
2	T	1013	GLN
2	T	1109	HIS
2	T	1113	GLN
2	U	780	ASN
2	U	916	HIS
2	U	1013	GLN
2	U	1109	HIS

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Mol	Chain	Res	Type
2	U	1113	GLN
2	U	1138	ASN
2	V	780	ASN
2	V	916	HIS
2	V	1109	HIS
2	V	1113	GLN
2	W	780	ASN
2	W	852	GLN
2	W	916	HIS
2	W	1013	GLN
2	W	1109	HIS
2	W	1113	GLN
2	W	1176	HIS
2	X	780	ASN
2	X	857	ASN
2	X	916	HIS
2	X	1013	GLN
2	X	1109	HIS
2	X	1113	GLN
2	Y	780	ASN
2	Y	857	ASN
2	Y	916	HIS
2	Y	1013	GLN
2	Y	1109	HIS
2	Y	1113	GLN
2	Z	780	ASN
2	Z	916	HIS
2	Z	1109	HIS
2	Z	1113	GLN
2	Z	1138	ASN
2	Z	1188	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates [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	F	802	1	14,14,15	0.40	0	17,19,21	0.76	0
3	NAG	M	801	1	14,14,15	0.40	0	17,19,21	0.76	0
3	NAG	C	1301	2	14,14,15	0.40	0	17,19,21	0.75	0
3	NAG	C	1302	2	14,14,15	0.39	0	17,19,21	0.75	0
3	NAG	d	1301	2	14,14,15	0.39	0	17,19,21	0.76	0
3	NAG	W	1301	2	14,14,15	0.40	0	17,19,21	0.76	0
3	NAG	F	801	1	14,14,15	0.41	0	17,19,21	0.75	0
3	NAG	Z	1301	2	14,14,15	0.28	0	17,19,21	0.61	0
3	NAG	N	804	1	14,14,15	0.40	0	17,19,21	0.75	0
3	NAG	T	1301	2	14,14,15	0.28	0	17,19,21	0.56	0
3	NAG	O	802	1	14,14,15	0.41	0	17,19,21	0.76	0
3	NAG	W	1302	2	14,14,15	0.39	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	a	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	G	802	1	14,14,15	0.41	0	17,19,21	0.75	0
3	NAG	S	1302	2	14,14,15	0.39	0	17,19,21	0.76	0
3	NAG	T	1302	2	14,14,15	0.41	0	17,19,21	0.75	0
3	NAG	G	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	V	1301	2	14,14,15	0.40	0	17,19,21	0.75	0
3	NAG	D	1301	2	14,14,15	0.40	0	17,19,21	0.76	0
3	NAG	A	802	1	14,14,15	0.28	0	17,19,21	0.63	0
3	NAG	B	802	1	14,14,15	0.30	0	17,19,21	0.64	0
3	NAG	L	802	1	14,14,15	0.41	0	17,19,21	0.76	0
3	NAG	b	1301	2	14,14,15	0.40	0	17,19,21	0.75	0
3	NAG	S	1301	2	14,14,15	0.41	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	I	802	1	14,14,15	0.40	0	17,19,21	0.75	0
3	NAG	L	801	1	14,14,15	0.41	0	17,19,21	0.75	0
3	NAG	P	802	1	14,14,15	0.39	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	P	801	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	E	801	1	14,14,15	0.30	0	17,19,21	0.63	0
3	NAG	I	801	1	14,14,15	0.38	0	17,19,21	0.75	0
3	NAG	b	1302	2	14,14,15	0.40	0	17,19,21	0.76	0
3	NAG	N	801	1	14,14,15	0.40	0	17,19,21	0.75	0
3	NAG	U	1302	2	14,14,15	0.41	0	17,19,21	0.76	0
3	NAG	A	801	1	14,14,15	0.41	0	17,19,21	0.75	0
3	NAG	D	1302	2	14,14,15	0.40	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	a	1301	2	14,14,15	0.26	0	17,19,21	0.68	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	F	802	1	-	1/6/23/26	0/1/1/1
3	NAG	M	801	1	-	1/6/23/26	0/1/1/1
3	NAG	C	1301	2	-	1/6/23/26	0/1/1/1
3	NAG	C	1302	2	-	1/6/23/26	0/1/1/1
3	NAG	d	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	F	801	1	-	1/6/23/26	0/1/1/1
3	NAG	Z	1301	2	-	0/6/23/26	0/1/1/1
3	NAG	N	804	1	-	1/6/23/26	0/1/1/1
3	NAG	T	1301	2	-	1/6/23/26	0/1/1/1
3	NAG	O	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	Z	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	E	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	S	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	G	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	V	1301	2	-	1/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	D	1301	2	-	1/6/23/26	0/1/1/1
3	NAG	A	802	1	-	2/6/23/26	0/1/1/1
3	NAG	B	802	1	-	2/6/23/26	0/1/1/1
3	NAG	L	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	S	1301	2	-	1/6/23/26	0/1/1/1
3	NAG	I	802	1	-	1/6/23/26	0/1/1/1
3	NAG	L	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	U	1303	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	801	1	-	1/6/23/26	0/1/1/1
3	NAG	E	801	1	-	3/6/23/26	0/1/1/1
3	NAG	I	801	1	-	1/6/23/26	0/1/1/1
3	NAG	b	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	U	1302	2	-	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	M	802	1	-	1/6/23/26	0/1/1/1
3	NAG	a	1301	2	-	3/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (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
3	T	1301	NAG	O5-C5-C6-O6
3	A	802	NAG	C8-C7-N2-C2
3	A	802	NAG	O7-C7-N2-C2
3	B	802	NAG	C8-C7-N2-C2
3	A	801	NAG	C1-C2-N2-C7
3	a	1302	NAG	C1-C2-N2-C7
3	B	801	NAG	C1-C2-N2-C7

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Mol	Chain	Res	Type	Atoms
3	b	1301	NAG	C1-C2-N2-C7
3	b	1302	NAG	C1-C2-N2-C7
3	C	1301	NAG	C1-C2-N2-C7
3	C	1302	NAG	C1-C2-N2-C7
3	D	1301	NAG	C1-C2-N2-C7
3	D	1302	NAG	C1-C2-N2-C7
3	d	1301	NAG	C1-C2-N2-C7
3	E	801	NAG	C1-C2-N2-C7
3	E	802	NAG	C1-C2-N2-C7
3	F	801	NAG	C1-C2-N2-C7
3	F	802	NAG	C1-C2-N2-C7
3	G	801	NAG	C1-C2-N2-C7
3	G	802	NAG	C1-C2-N2-C7
3	I	801	NAG	C1-C2-N2-C7
3	I	802	NAG	C1-C2-N2-C7
3	L	801	NAG	C1-C2-N2-C7
3	L	802	NAG	C1-C2-N2-C7
3	M	801	NAG	C1-C2-N2-C7
3	M	802	NAG	C1-C2-N2-C7
3	N	801	NAG	C1-C2-N2-C7
3	N	804	NAG	C1-C2-N2-C7
3	O	801	NAG	C1-C2-N2-C7
3	O	802	NAG	C1-C2-N2-C7
3	P	801	NAG	C1-C2-N2-C7
3	P	802	NAG	C1-C2-N2-C7
3	S	1301	NAG	C1-C2-N2-C7
3	S	1302	NAG	C1-C2-N2-C7
3	T	1302	NAG	C1-C2-N2-C7
3	U	1302	NAG	C1-C2-N2-C7
3	U	1303	NAG	C1-C2-N2-C7
3	V	1301	NAG	C1-C2-N2-C7
3	W	1301	NAG	C1-C2-N2-C7
3	W	1302	NAG	C1-C2-N2-C7
3	Z	1302	NAG	C1-C2-N2-C7
3	B	802	NAG	O7-C7-N2-C2

There are no ring outliers.

7 monomers are involved in 22 short contacts:

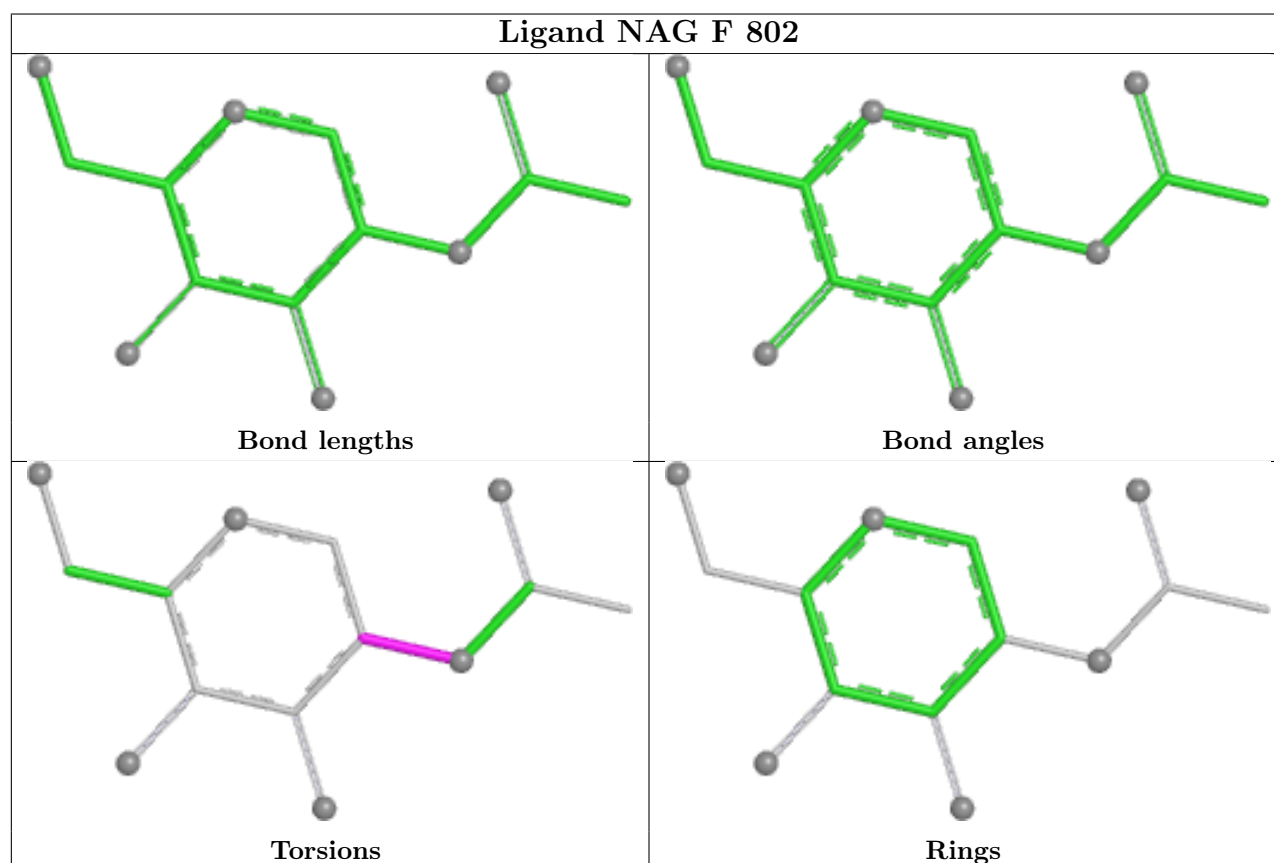
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	M	801	NAG	1	0
3	W	1301	NAG	1	0

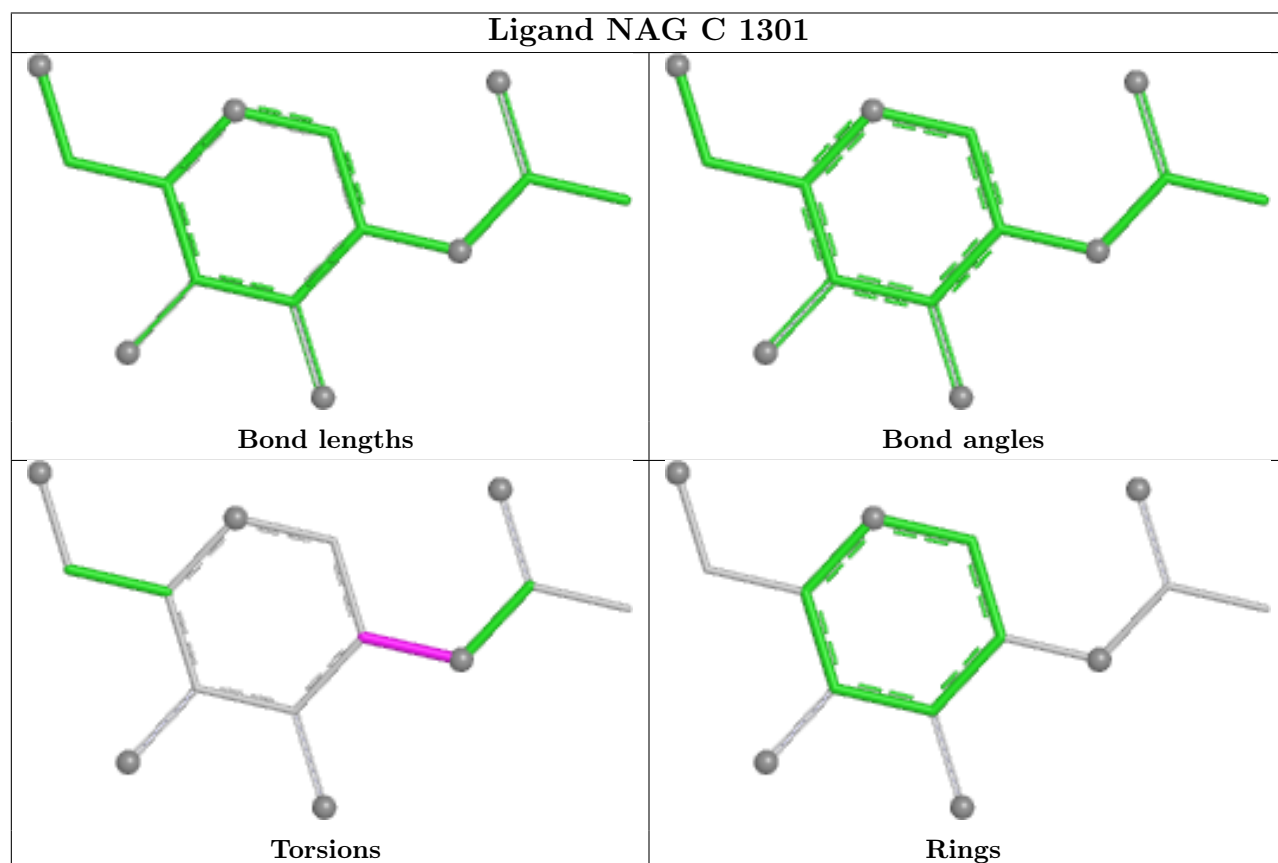
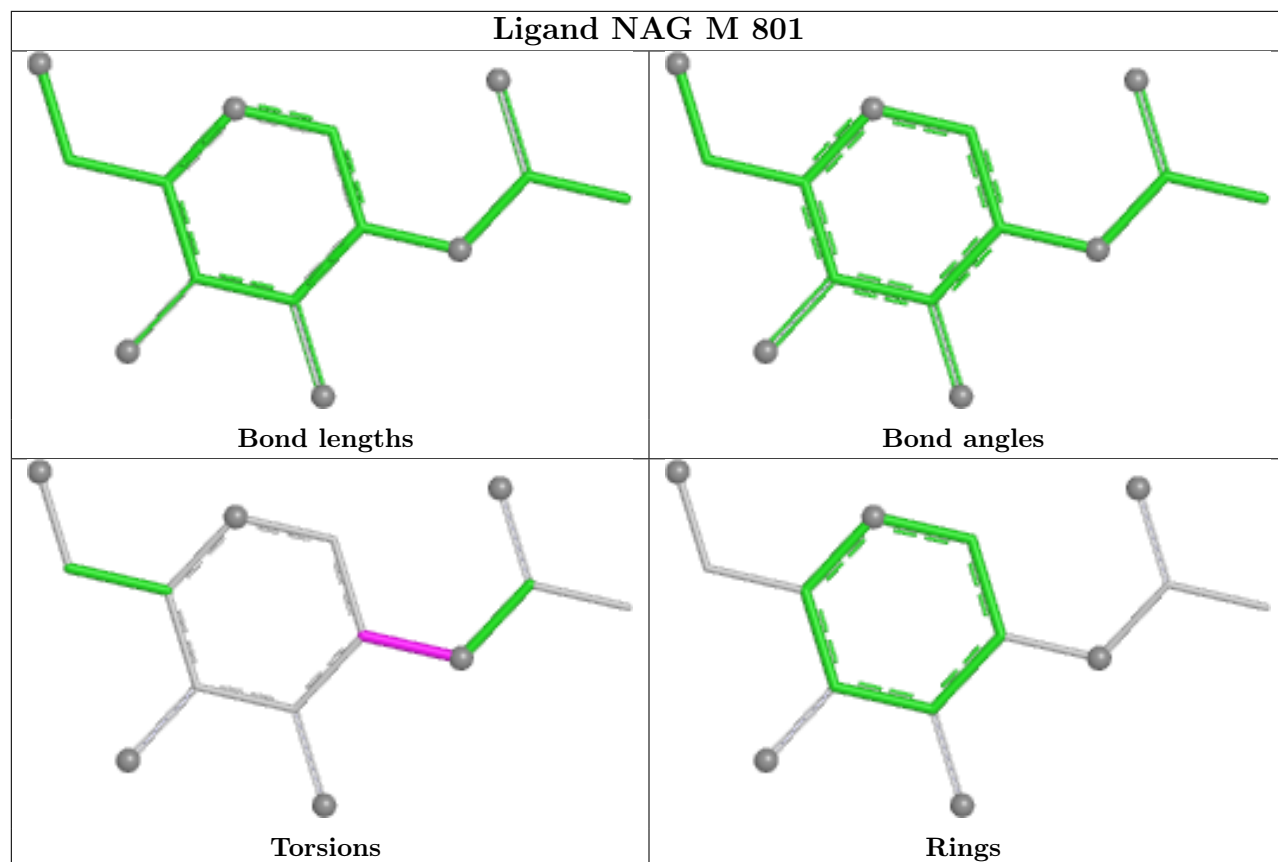
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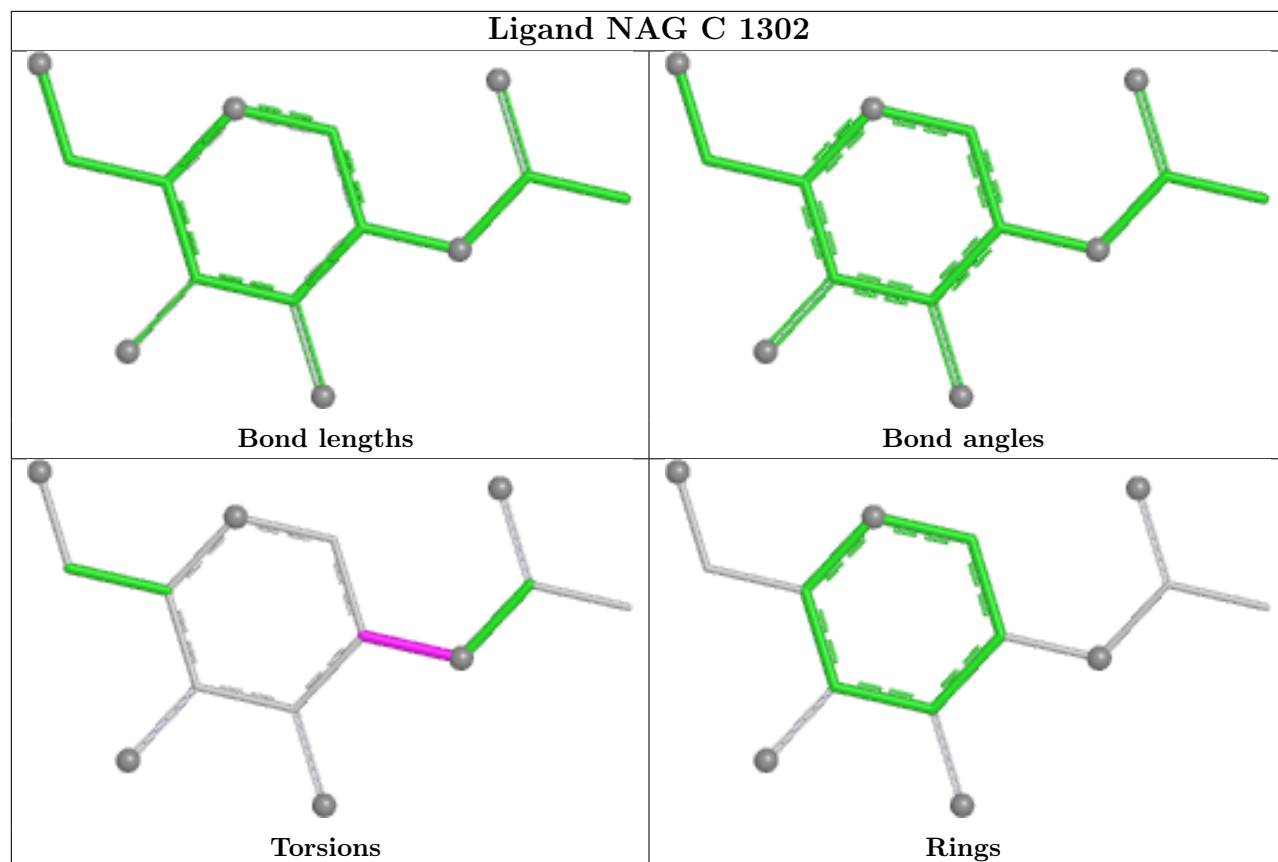
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	W	1302	NAG	2	0
3	a	1302	NAG	6	0
3	G	801	NAG	1	0
3	B	802	NAG	3	0
3	B	801	NAG	8	0

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

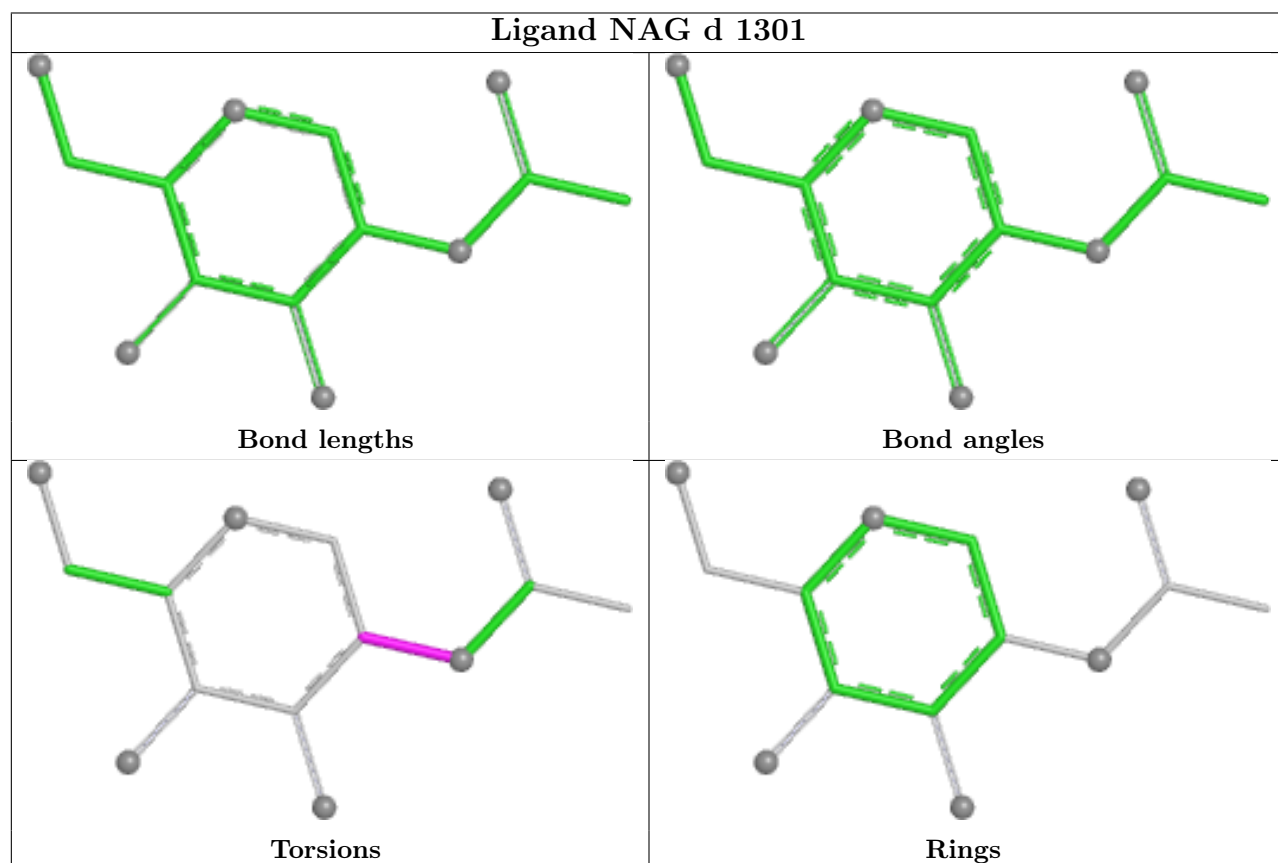




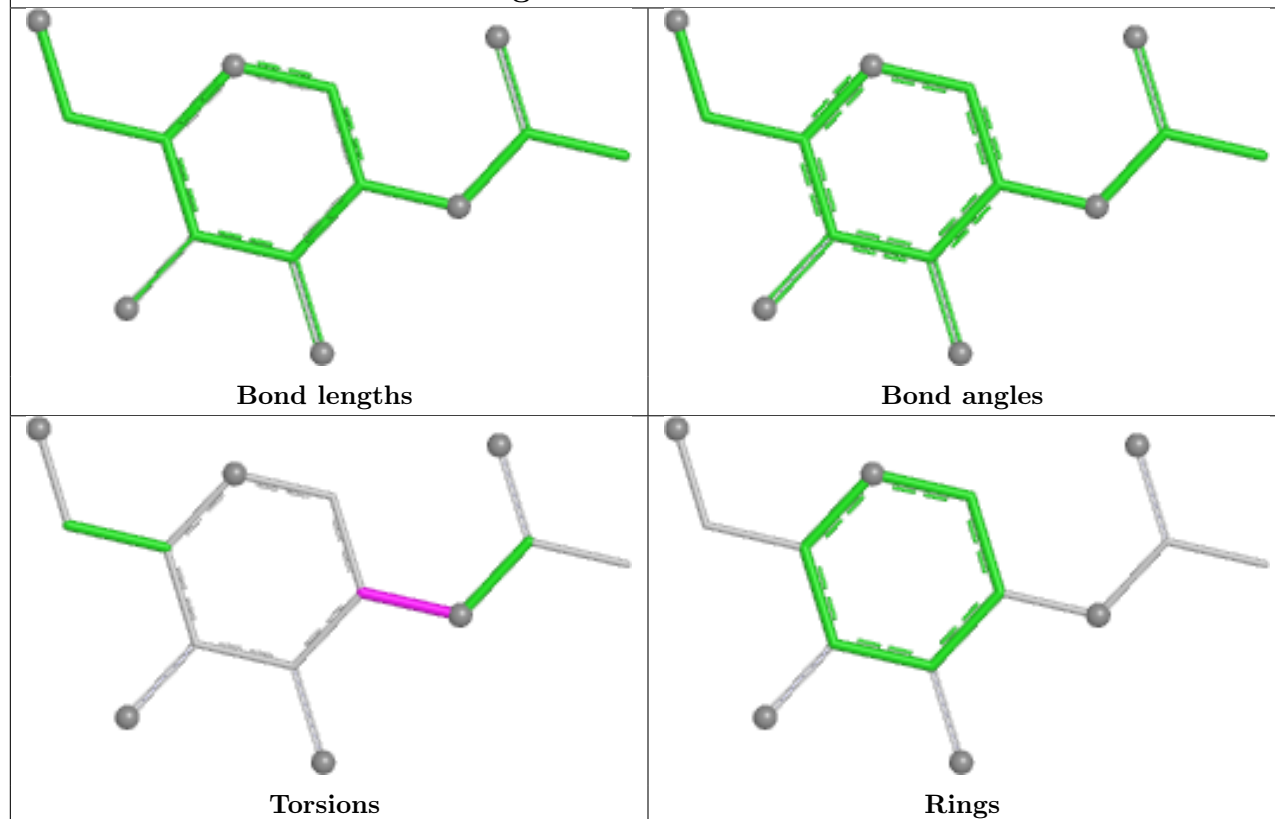
Ligand NAG C 1302



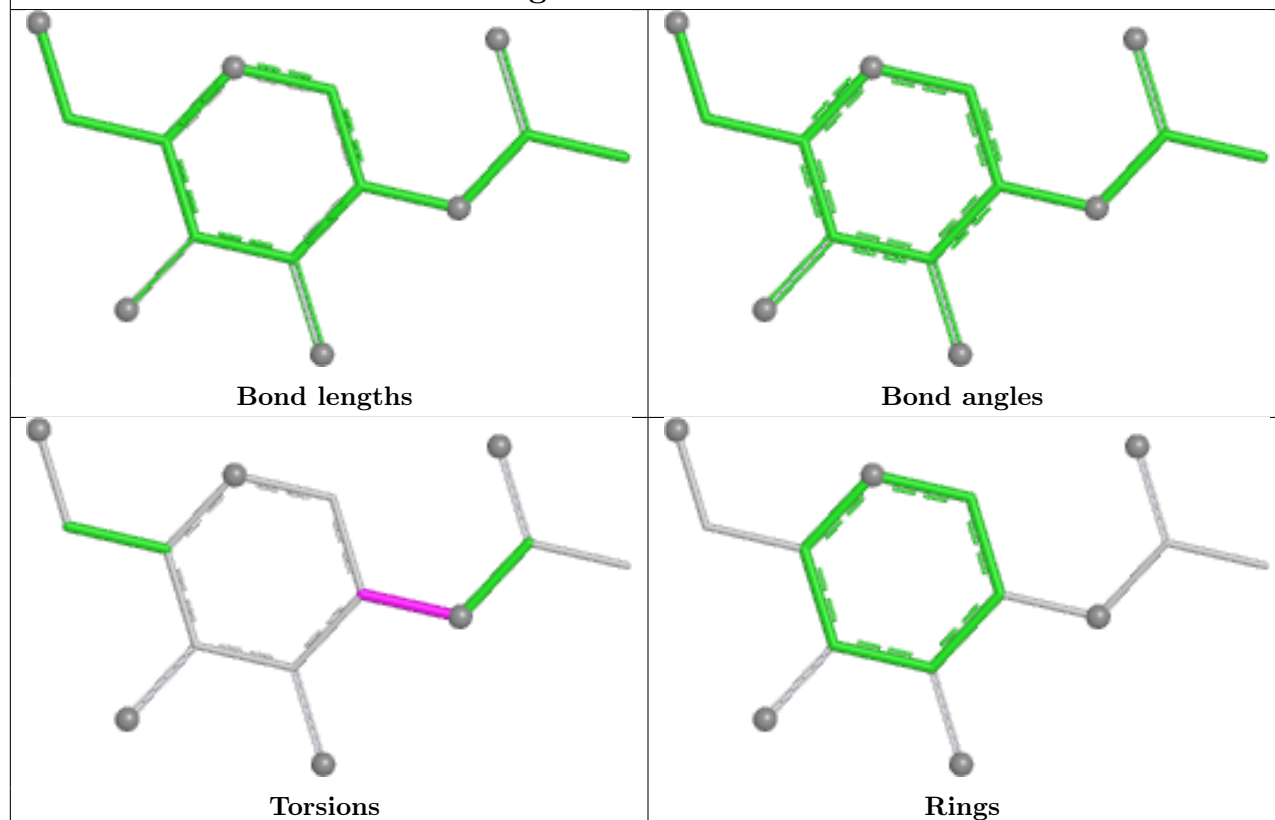
Ligand NAG d 1301

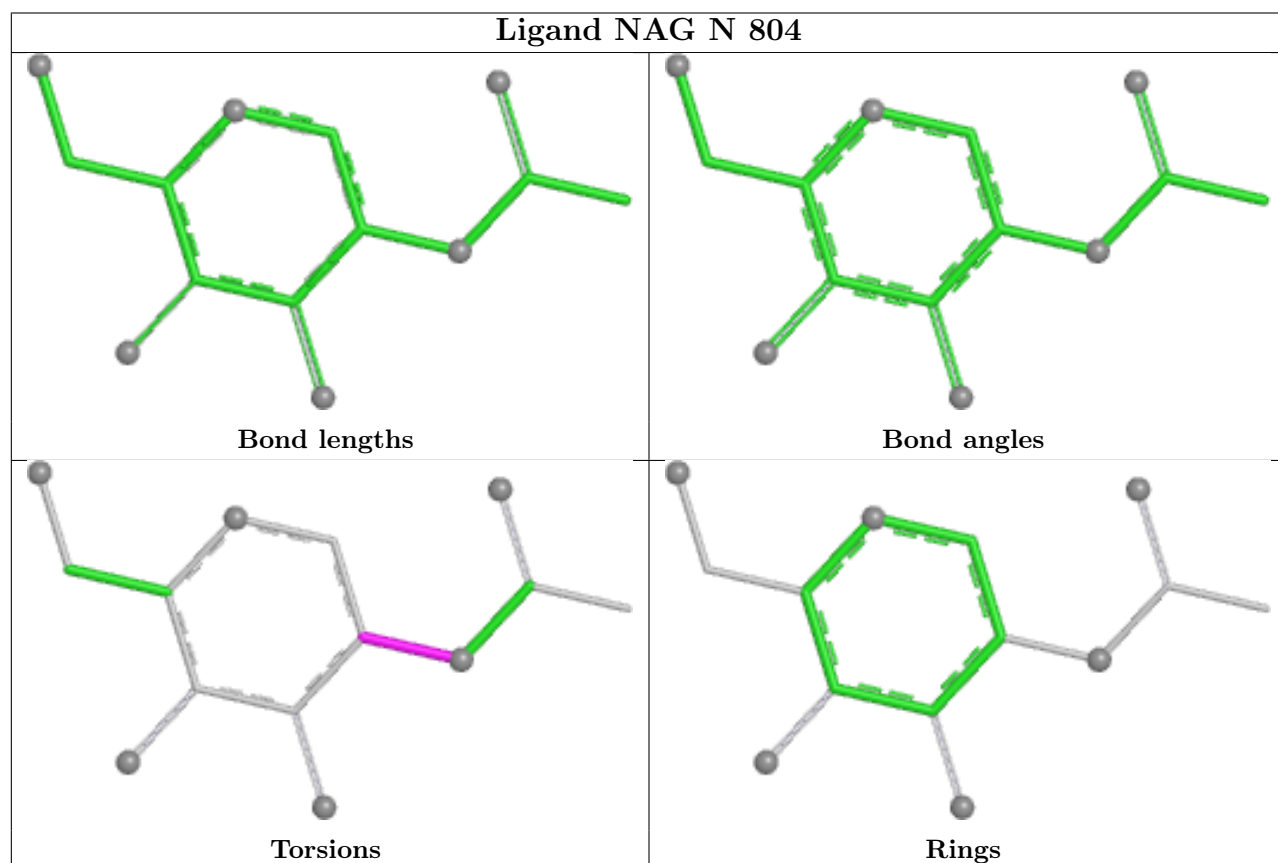
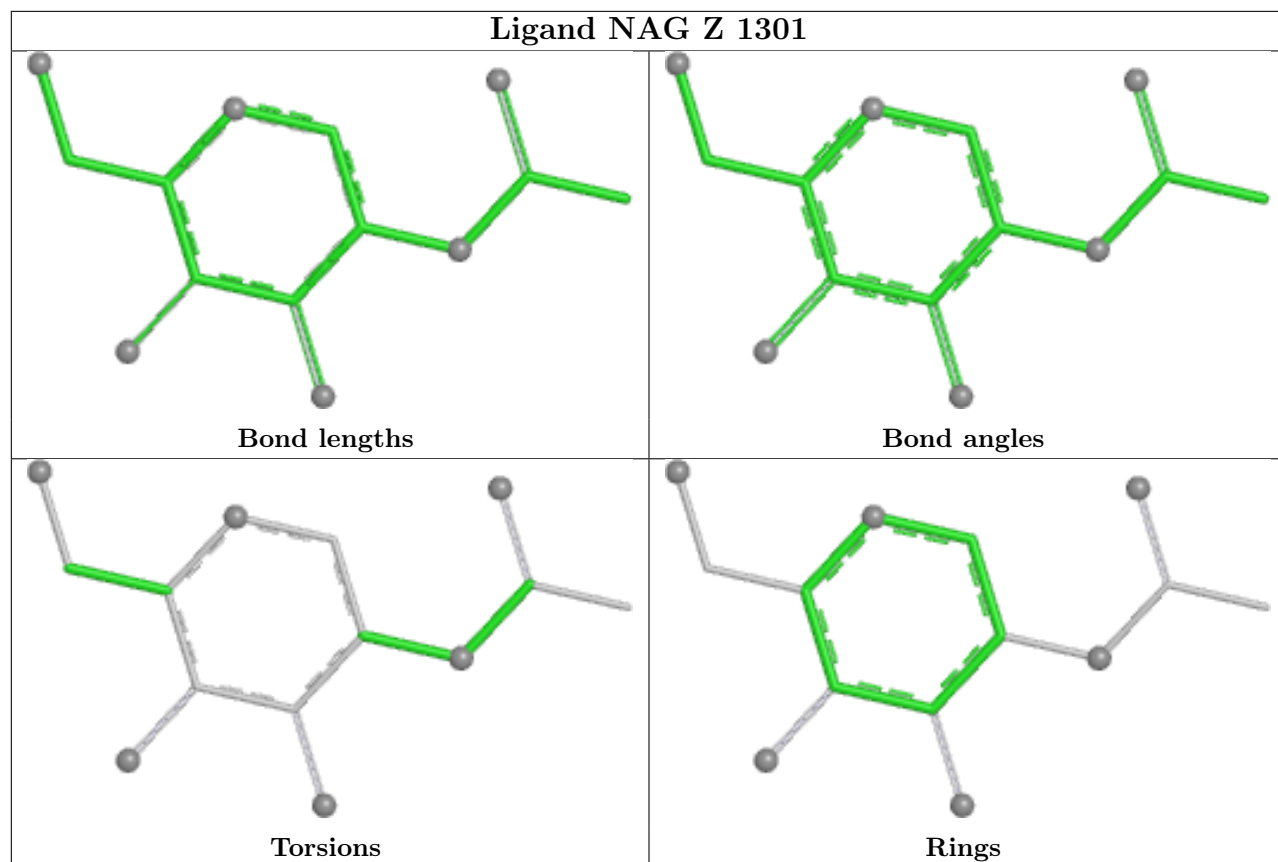


Ligand NAG W 1301

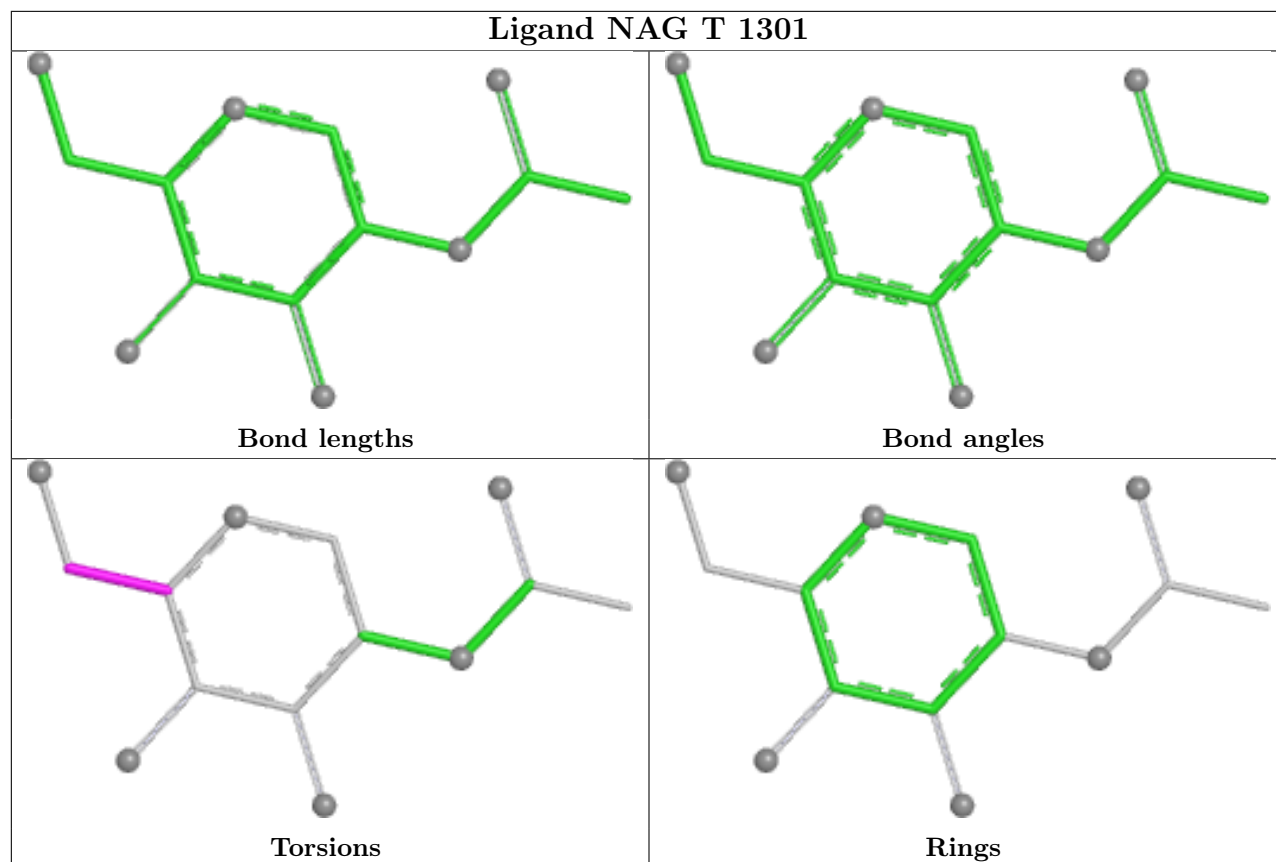


Ligand NAG F 801

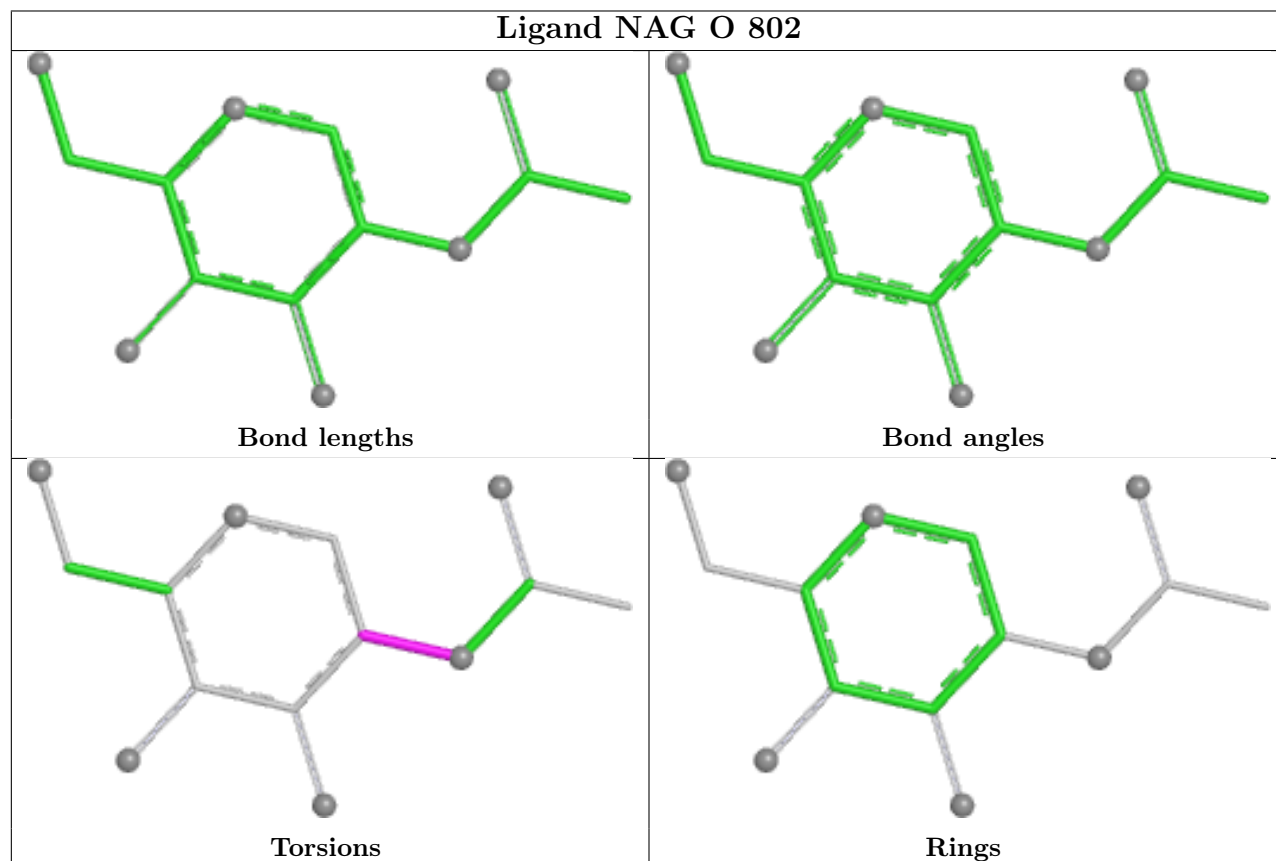




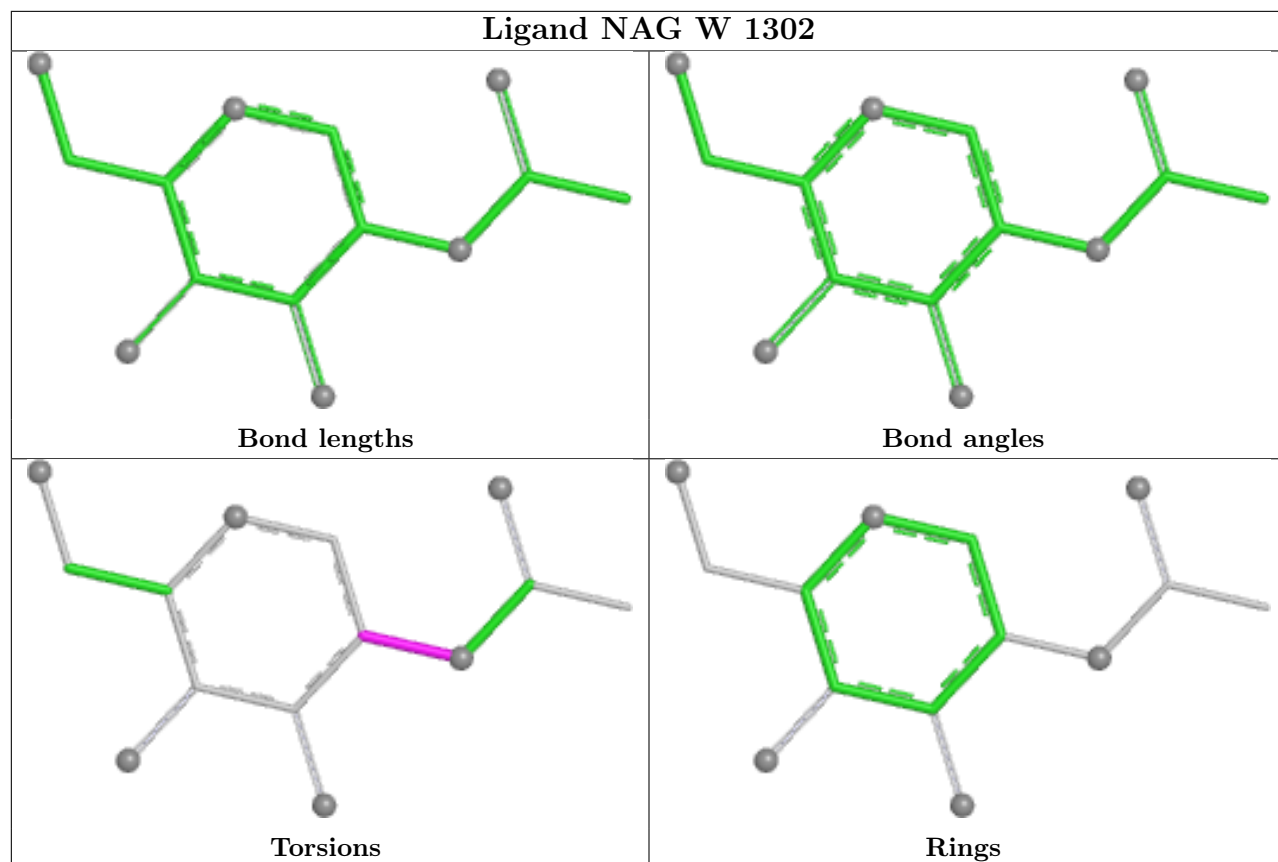
Ligand NAG T 1301



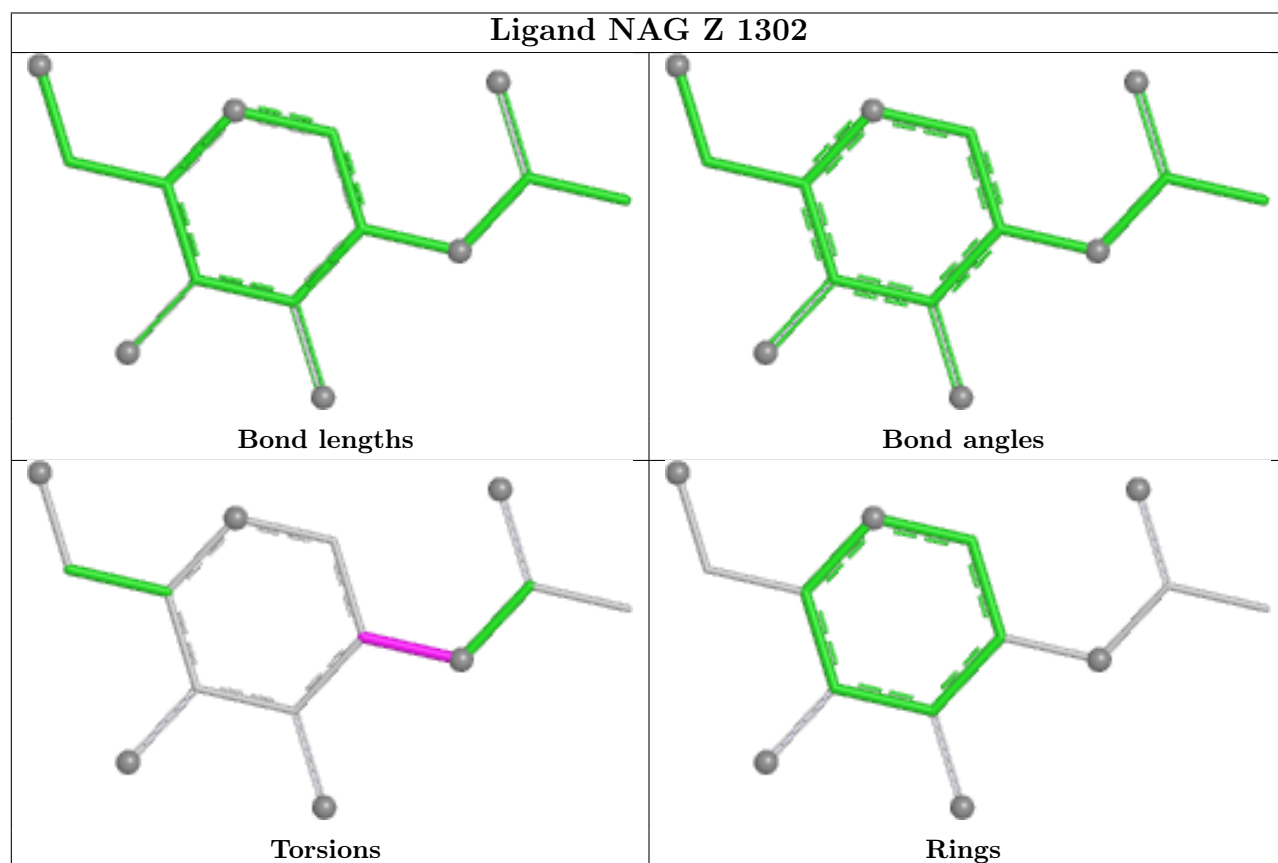
Ligand NAG O 802

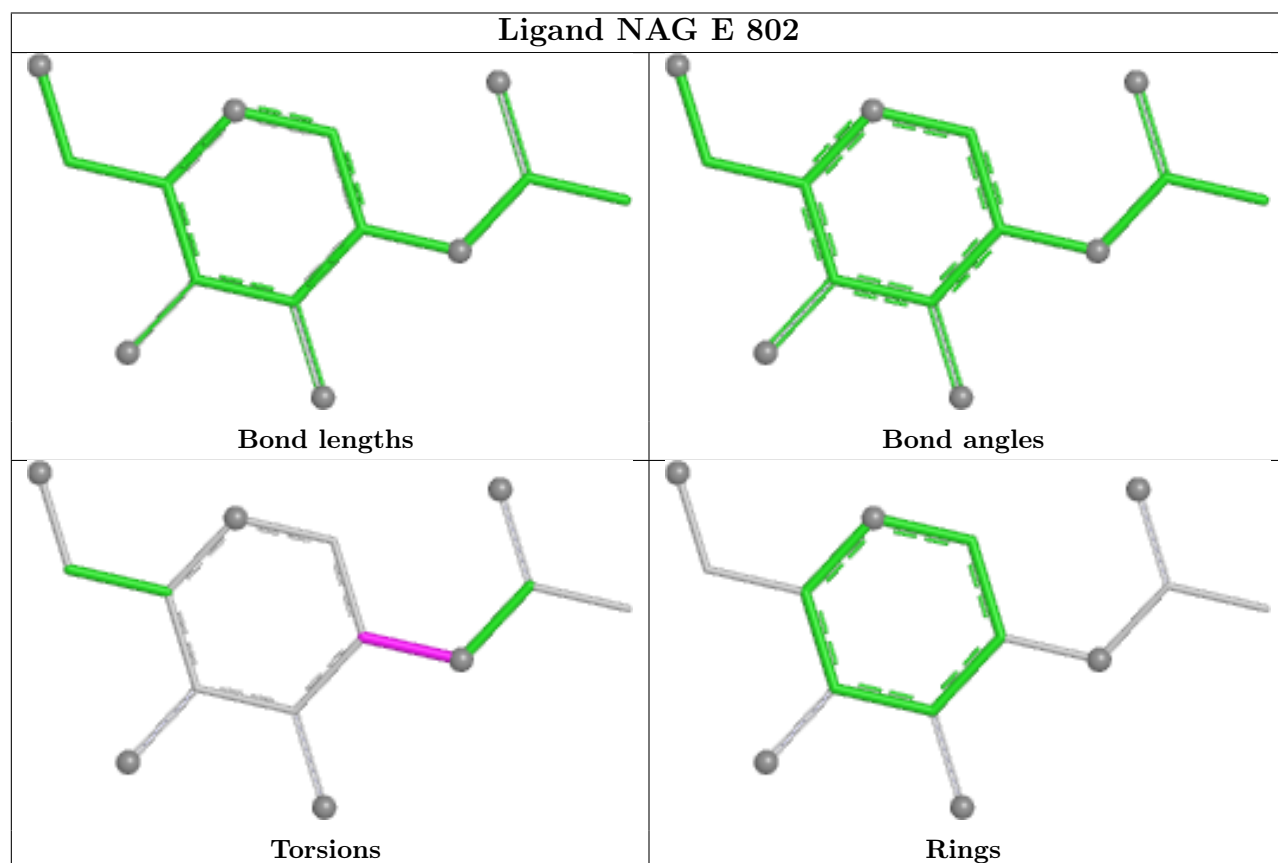
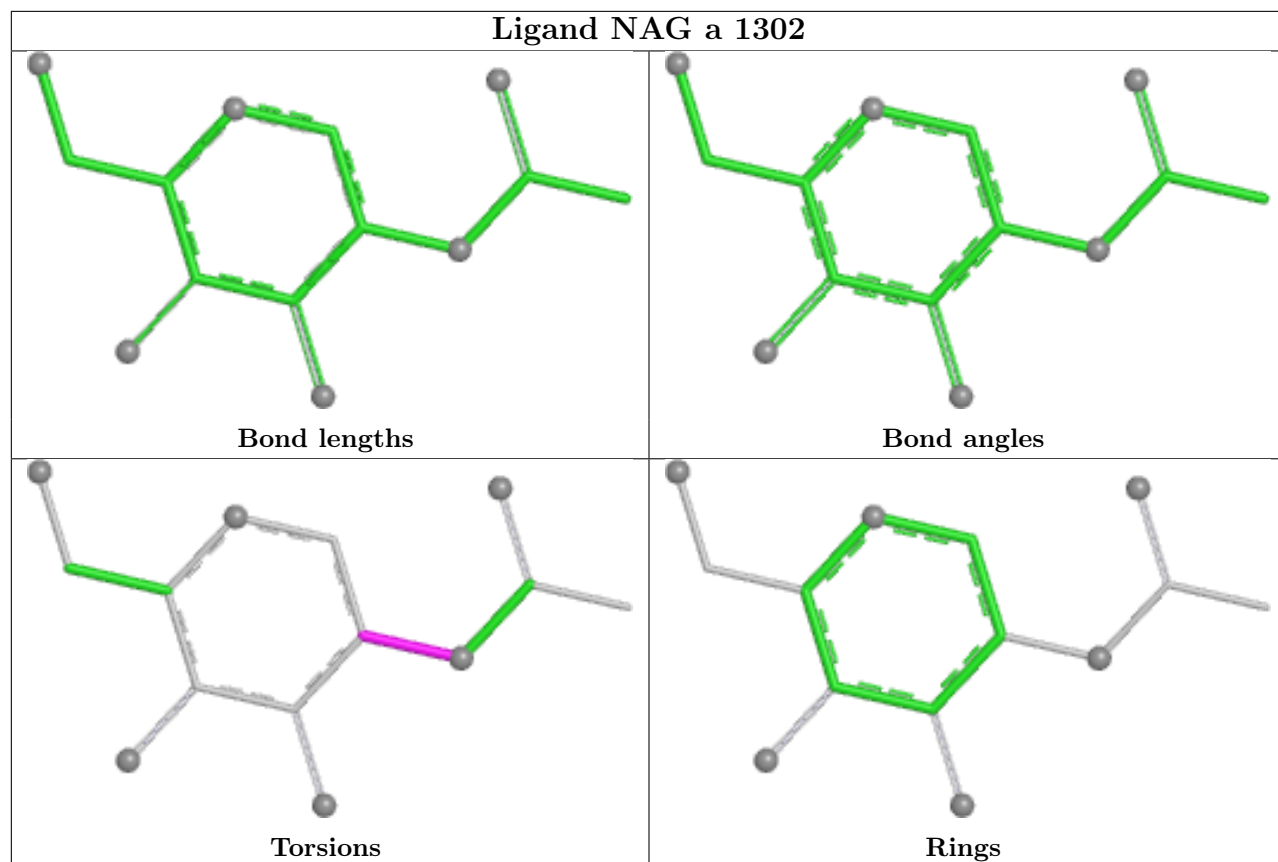


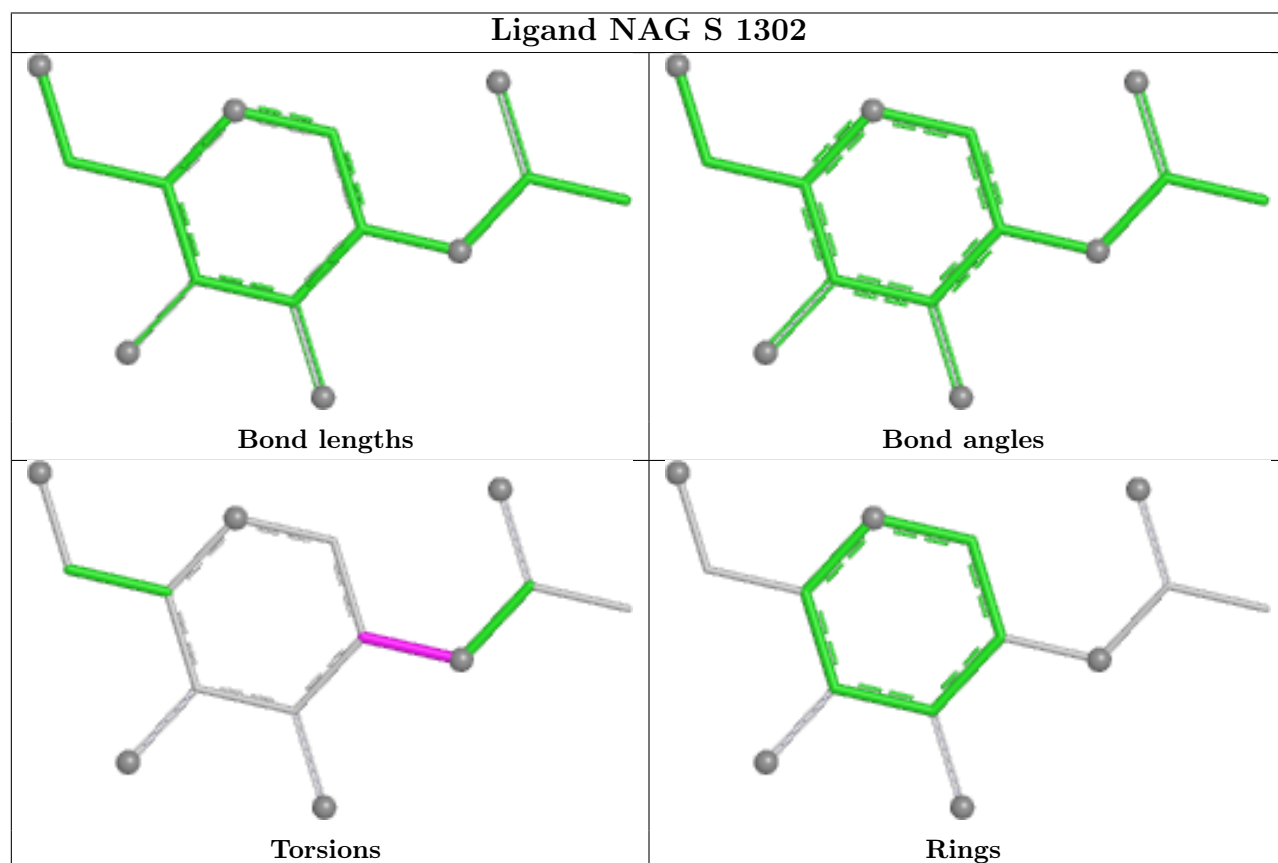
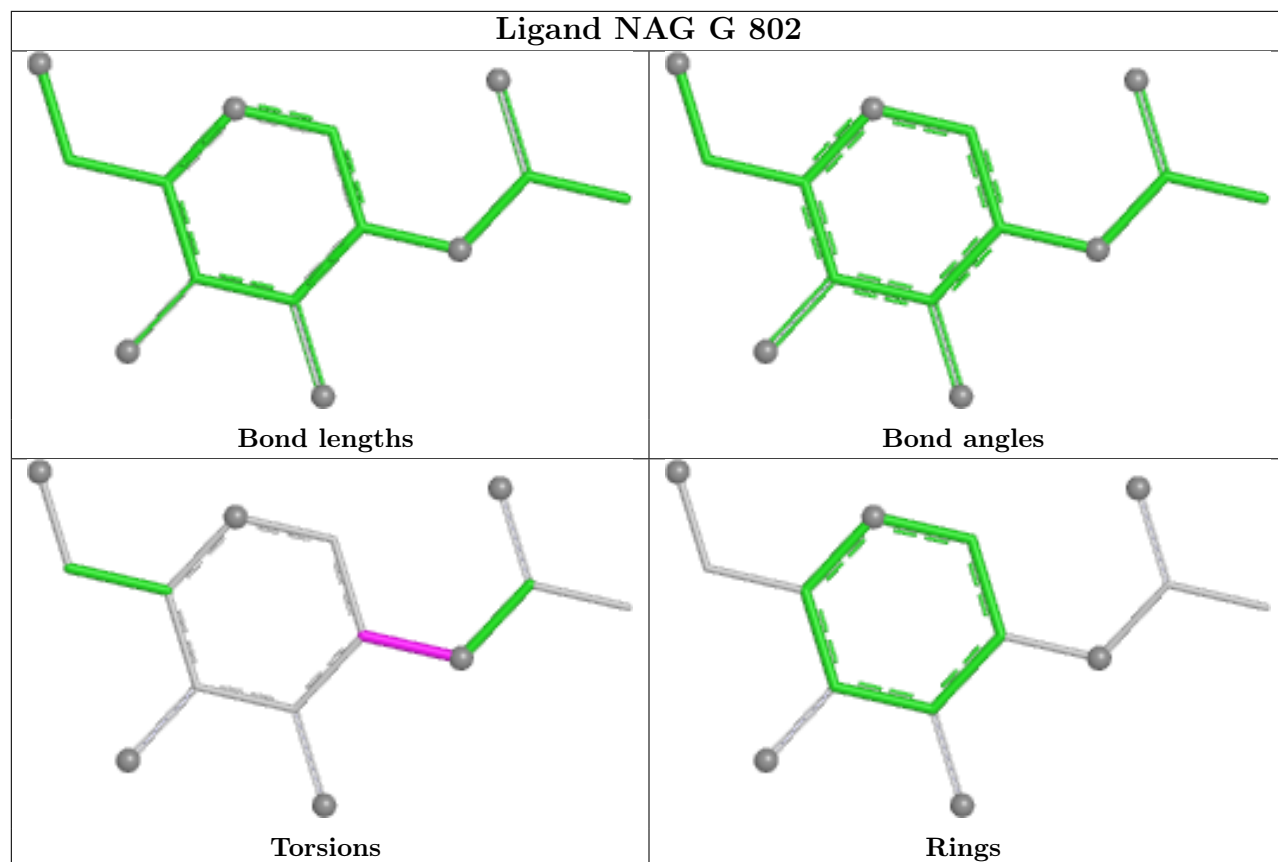
Ligand NAG W 1302



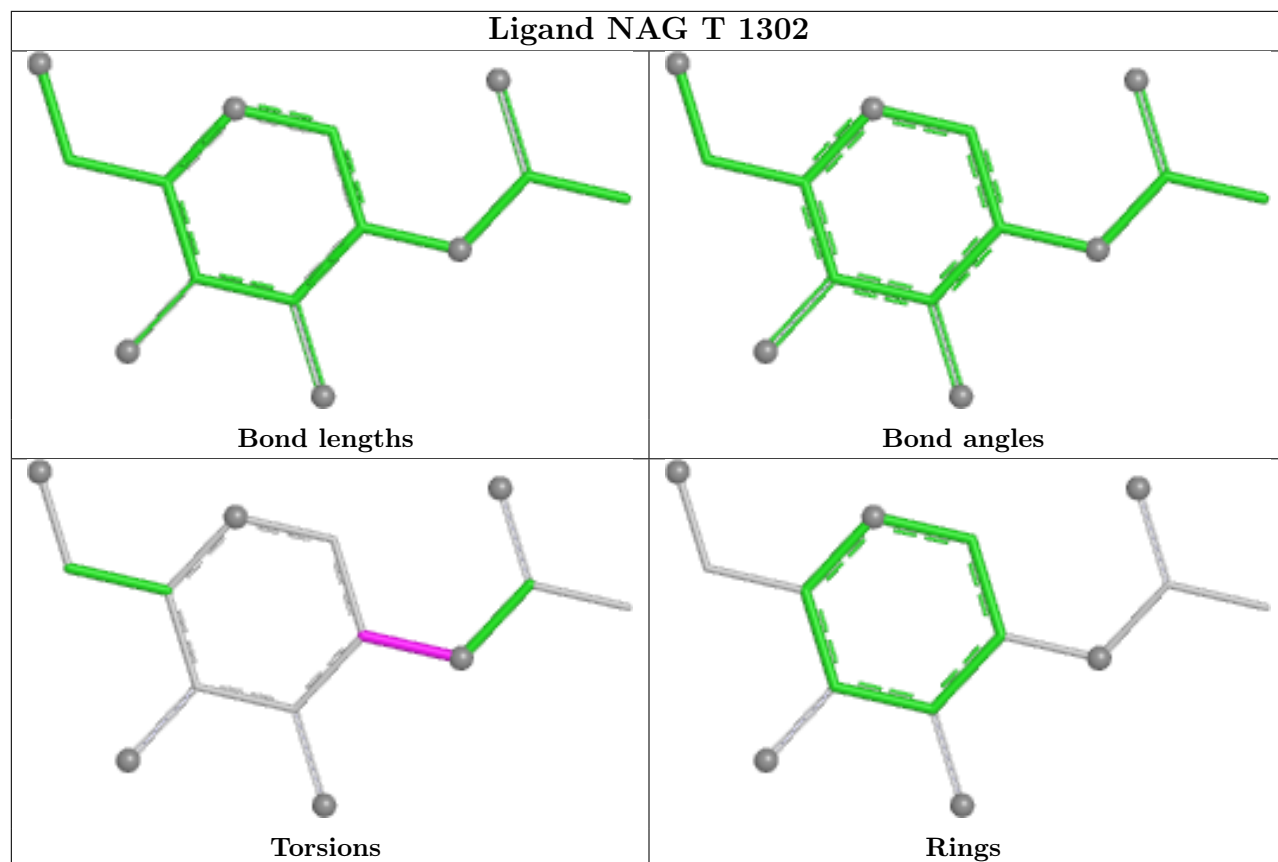
Ligand NAG Z 1302



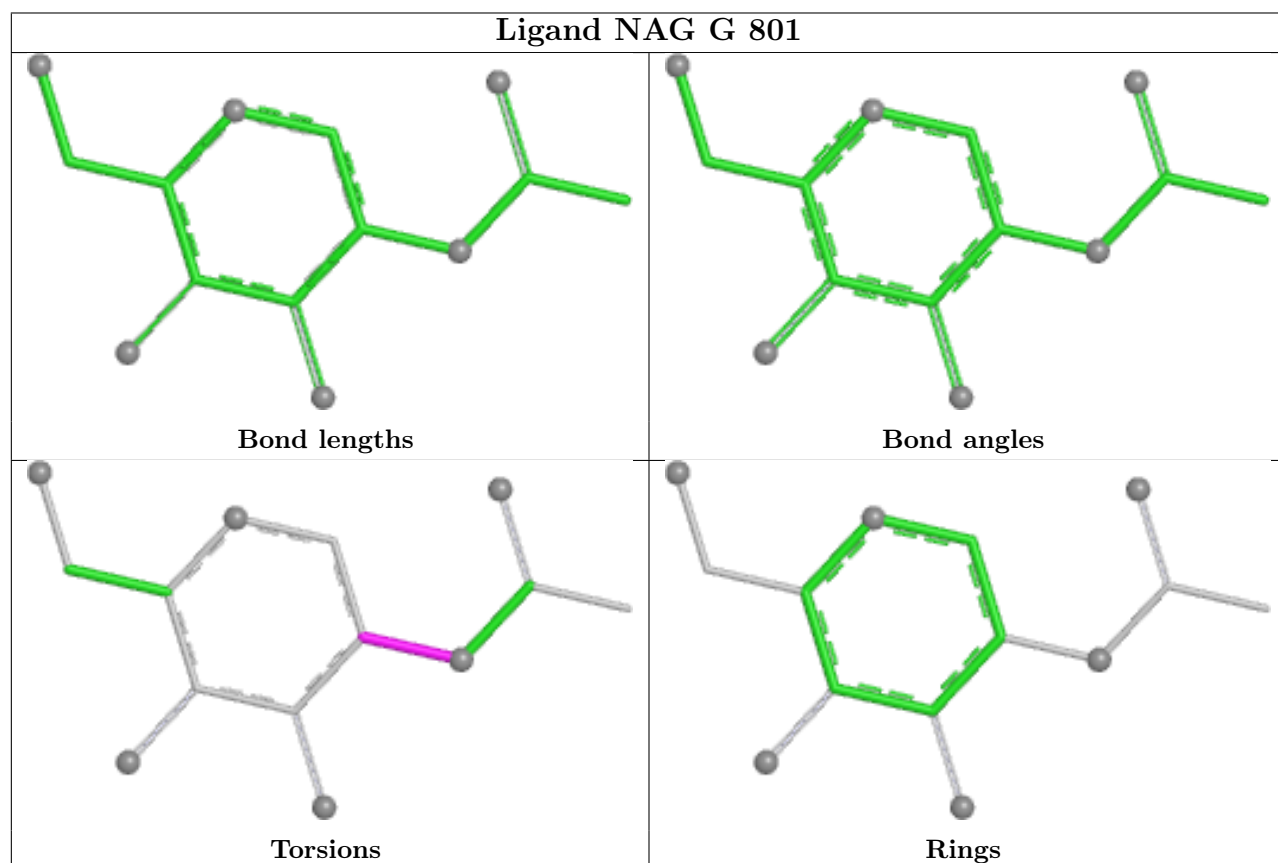


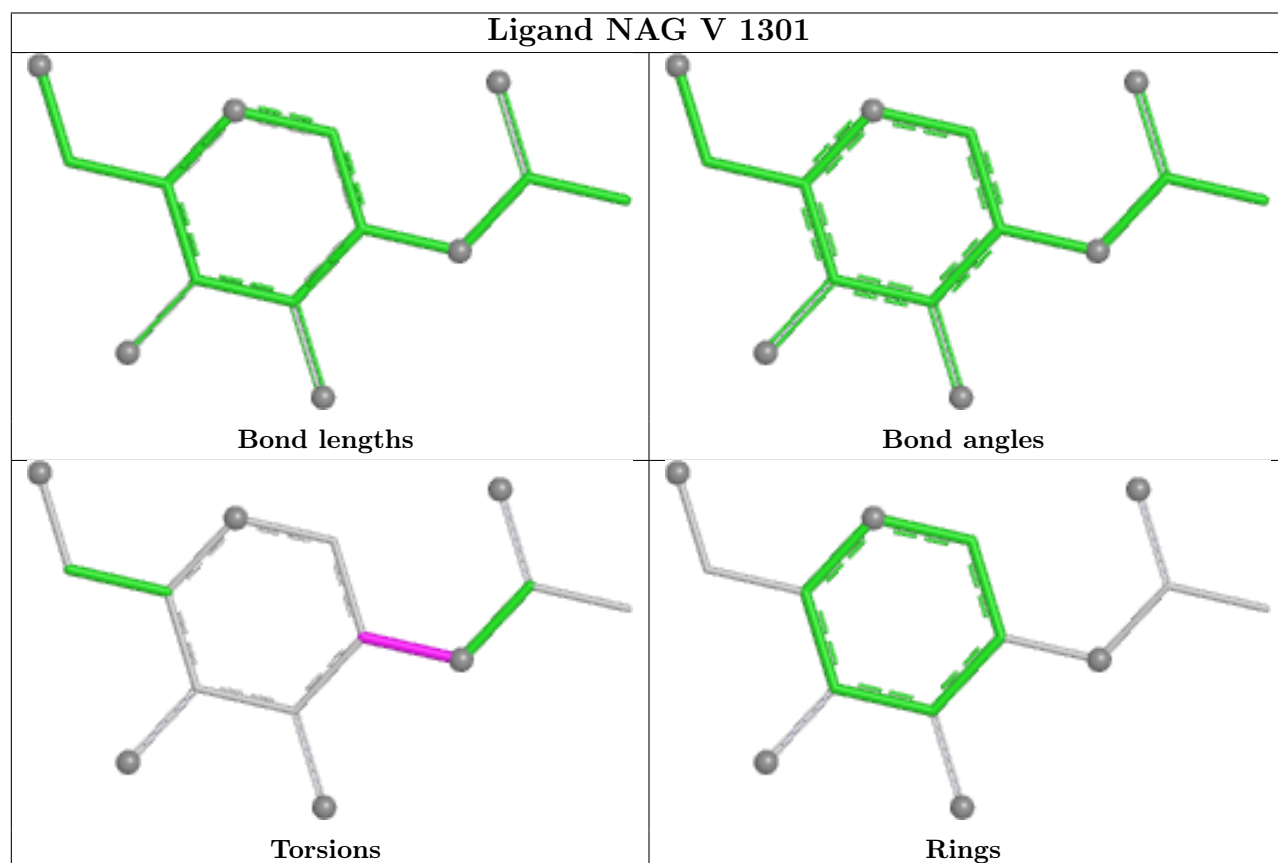
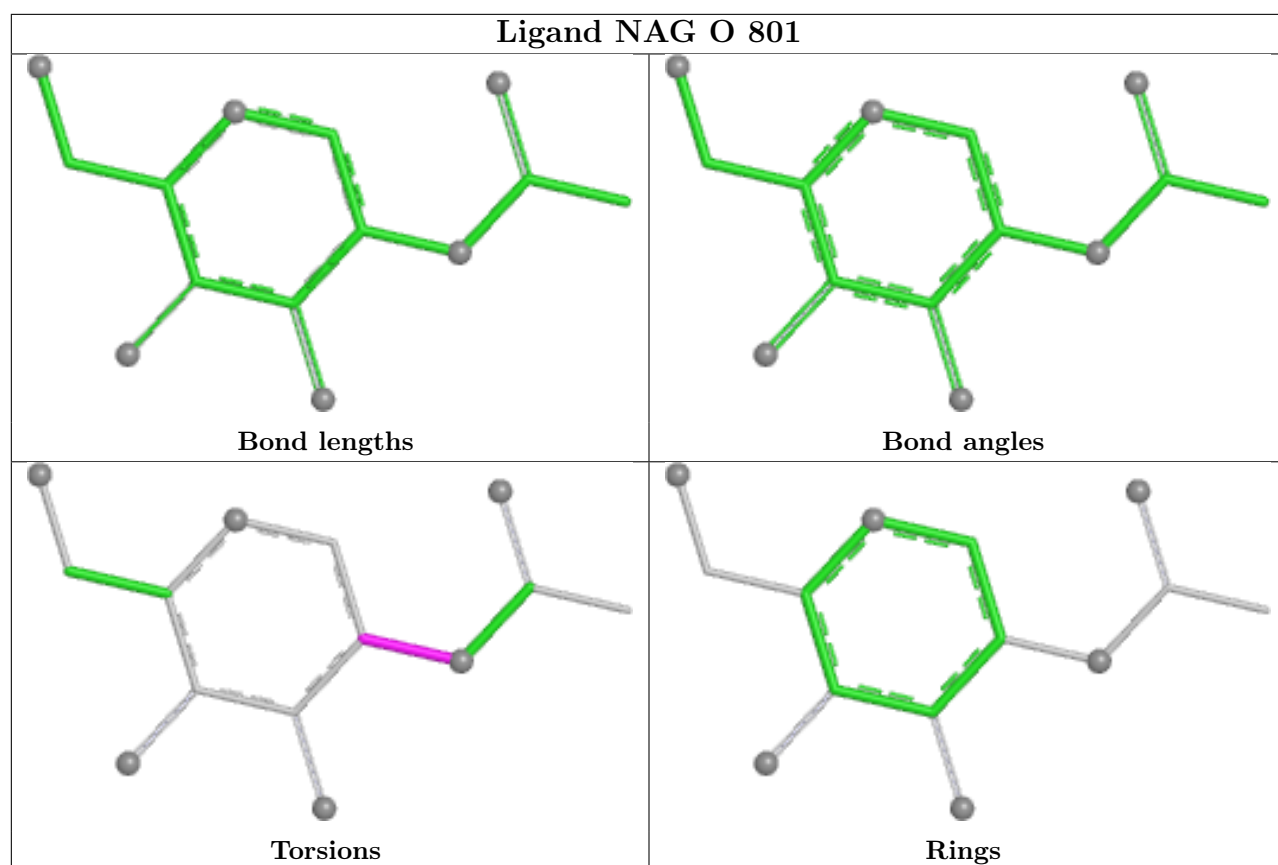


Ligand NAG T 1302

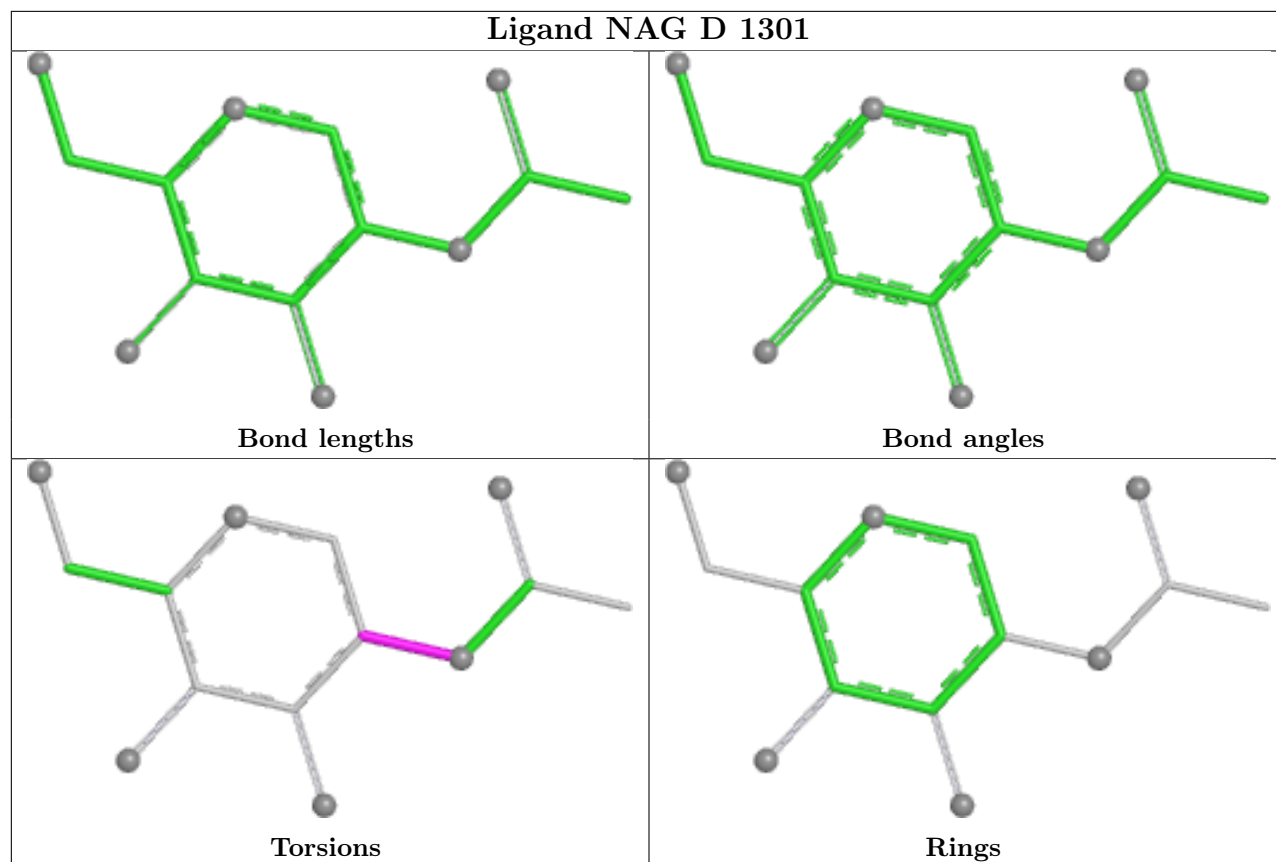


Ligand NAG G 801

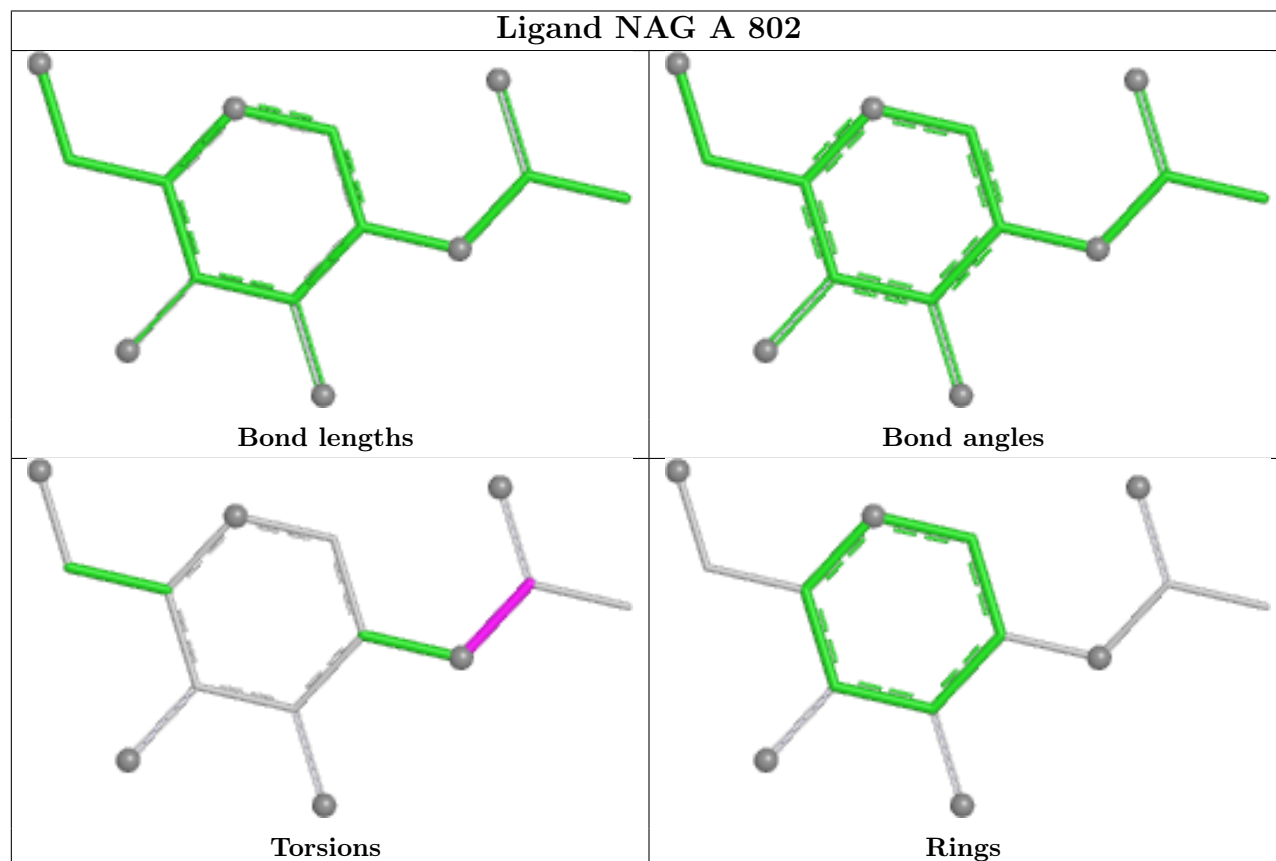


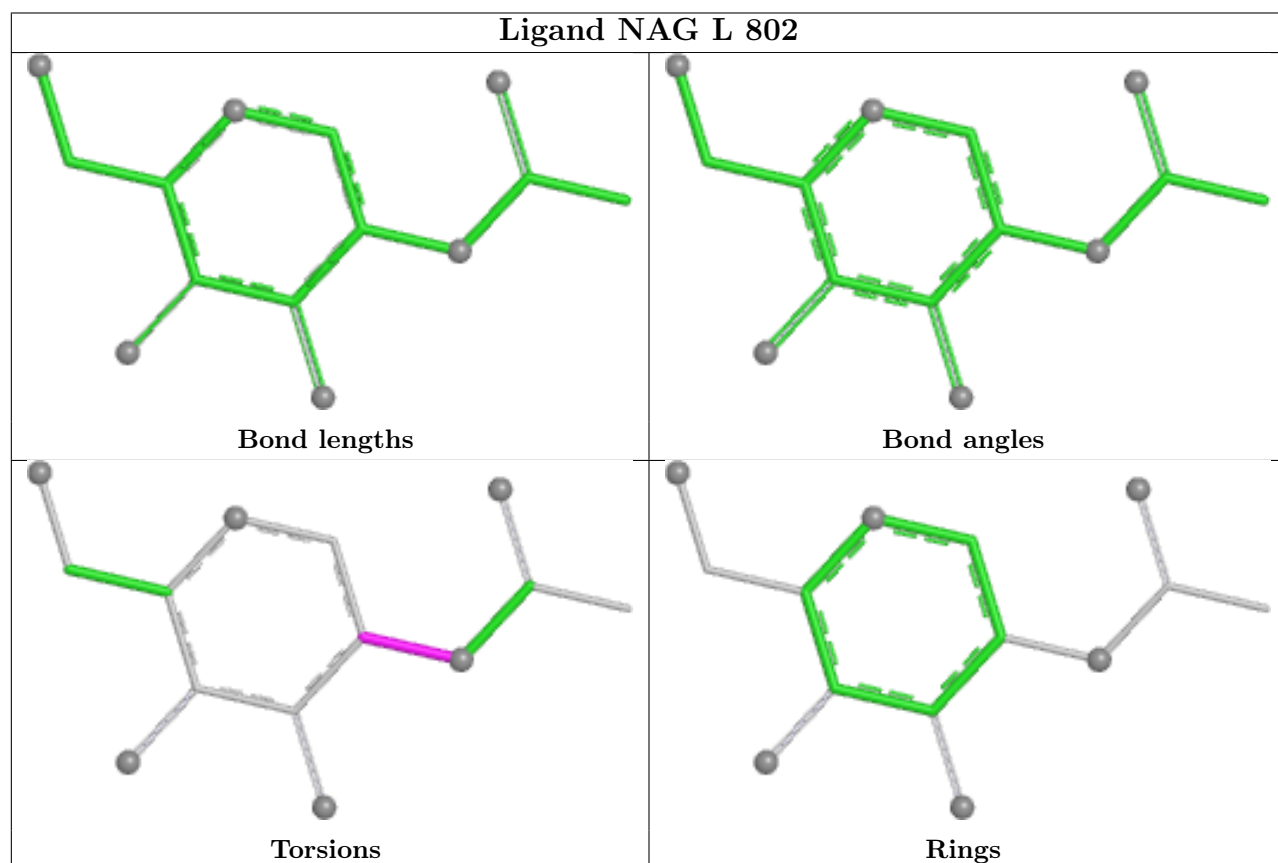
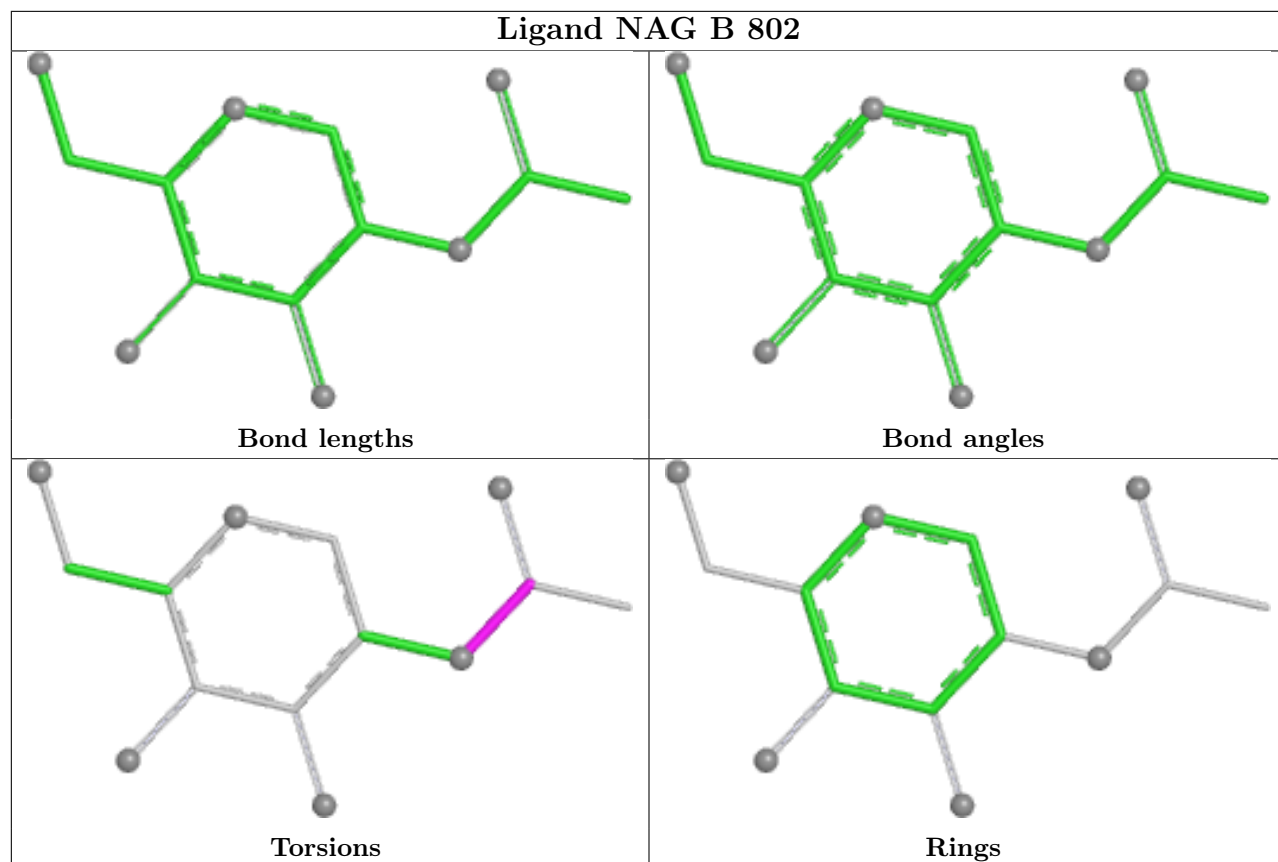


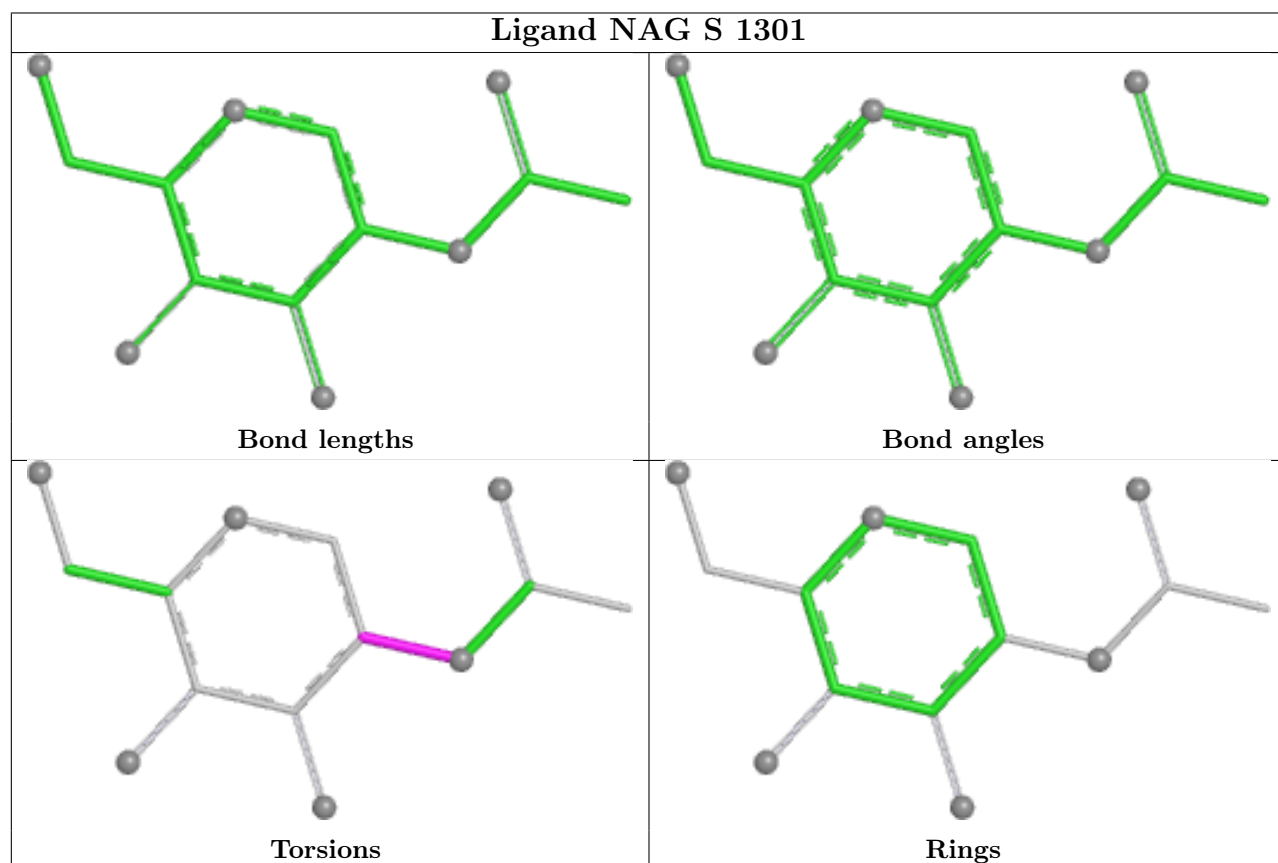
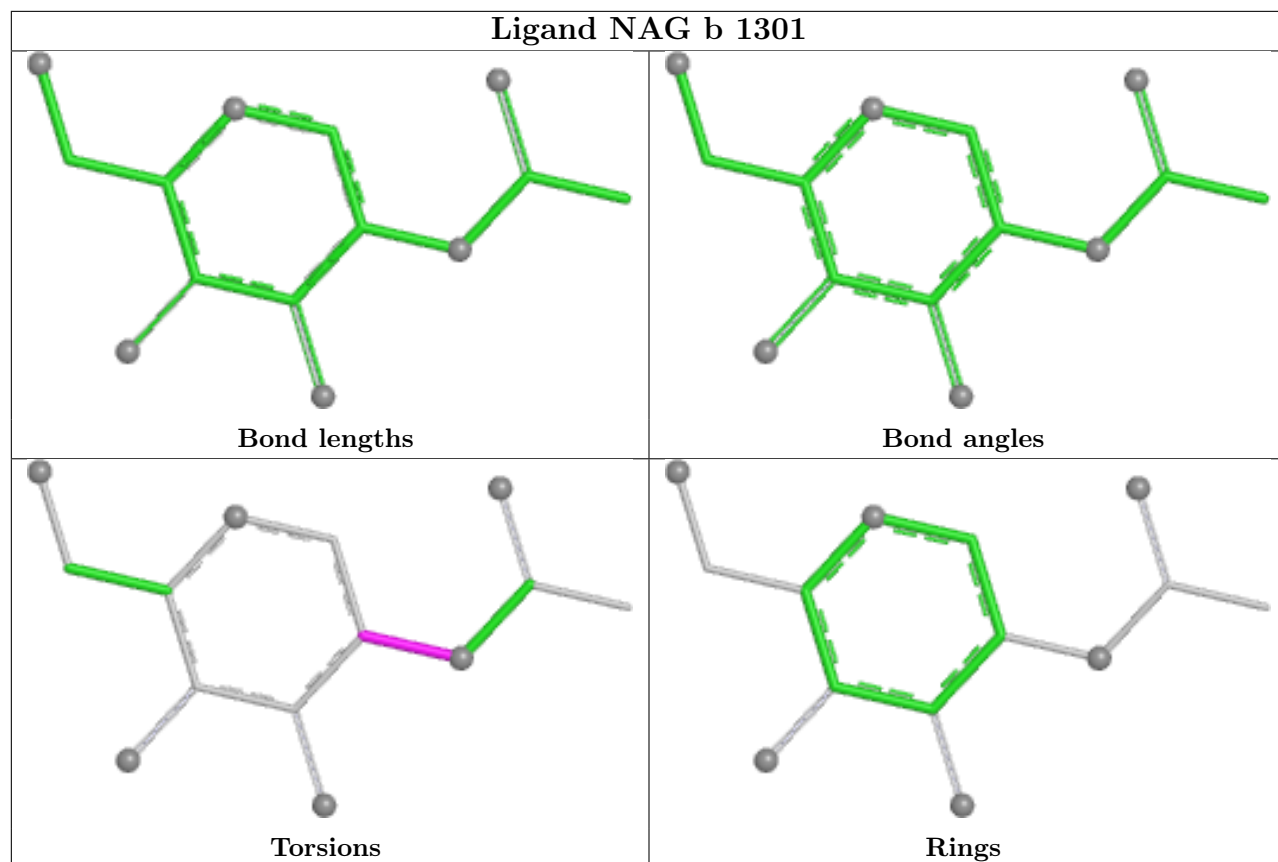
Ligand NAG D 1301

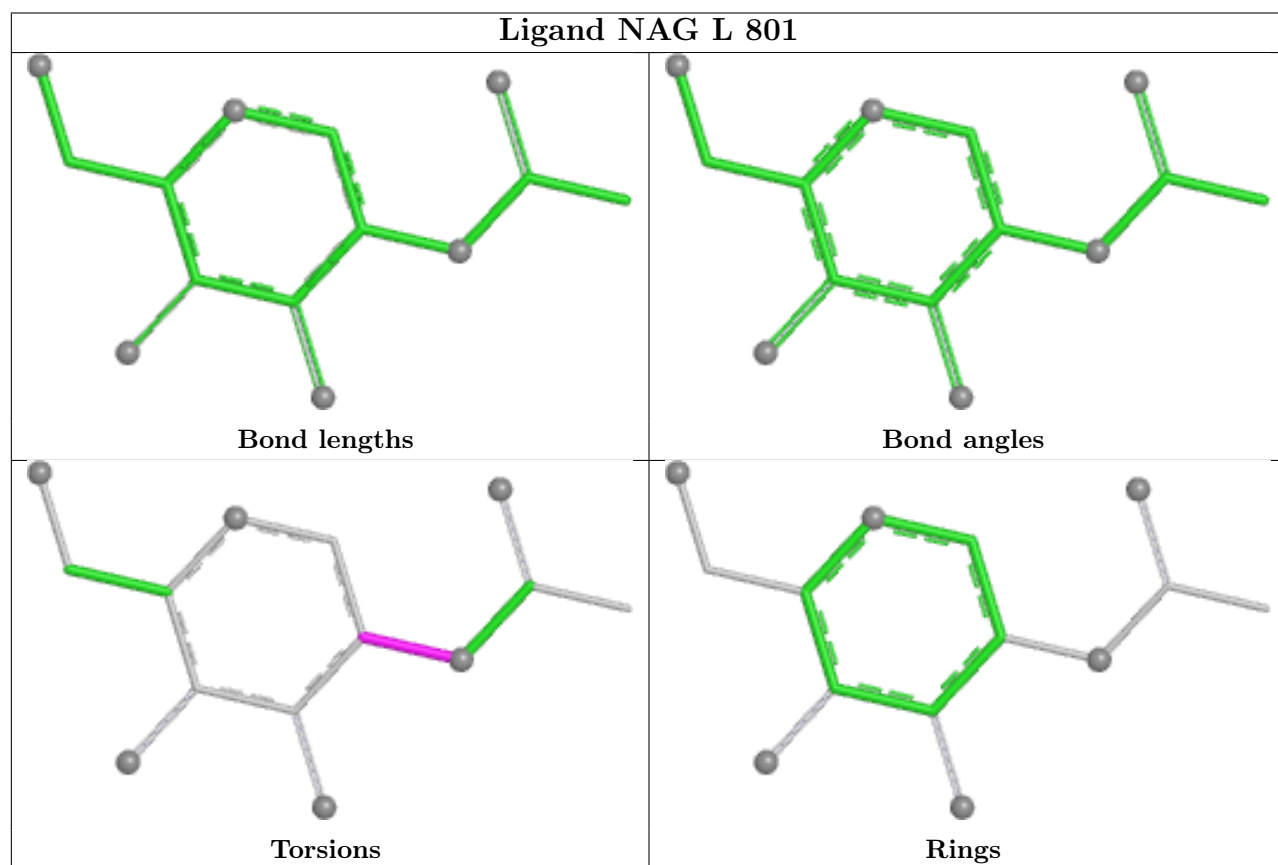
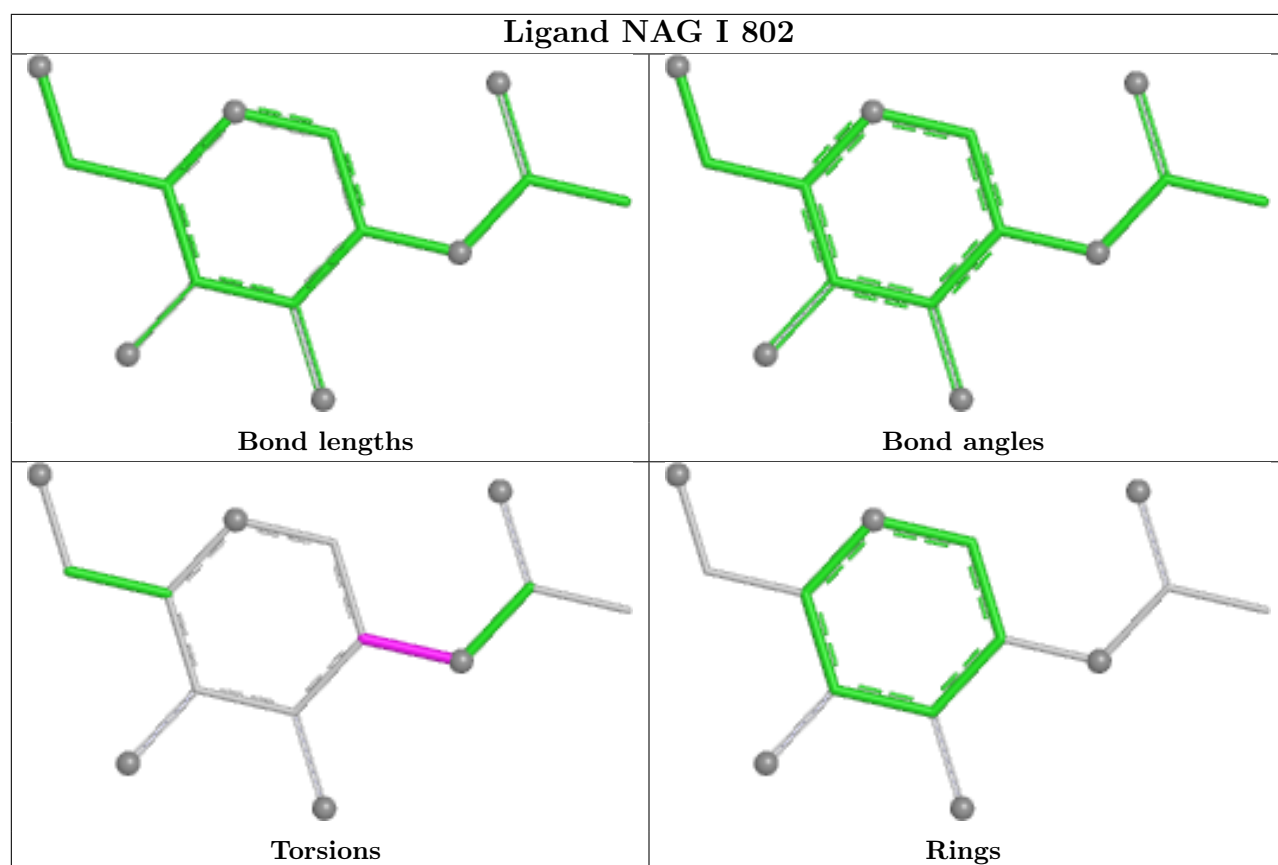


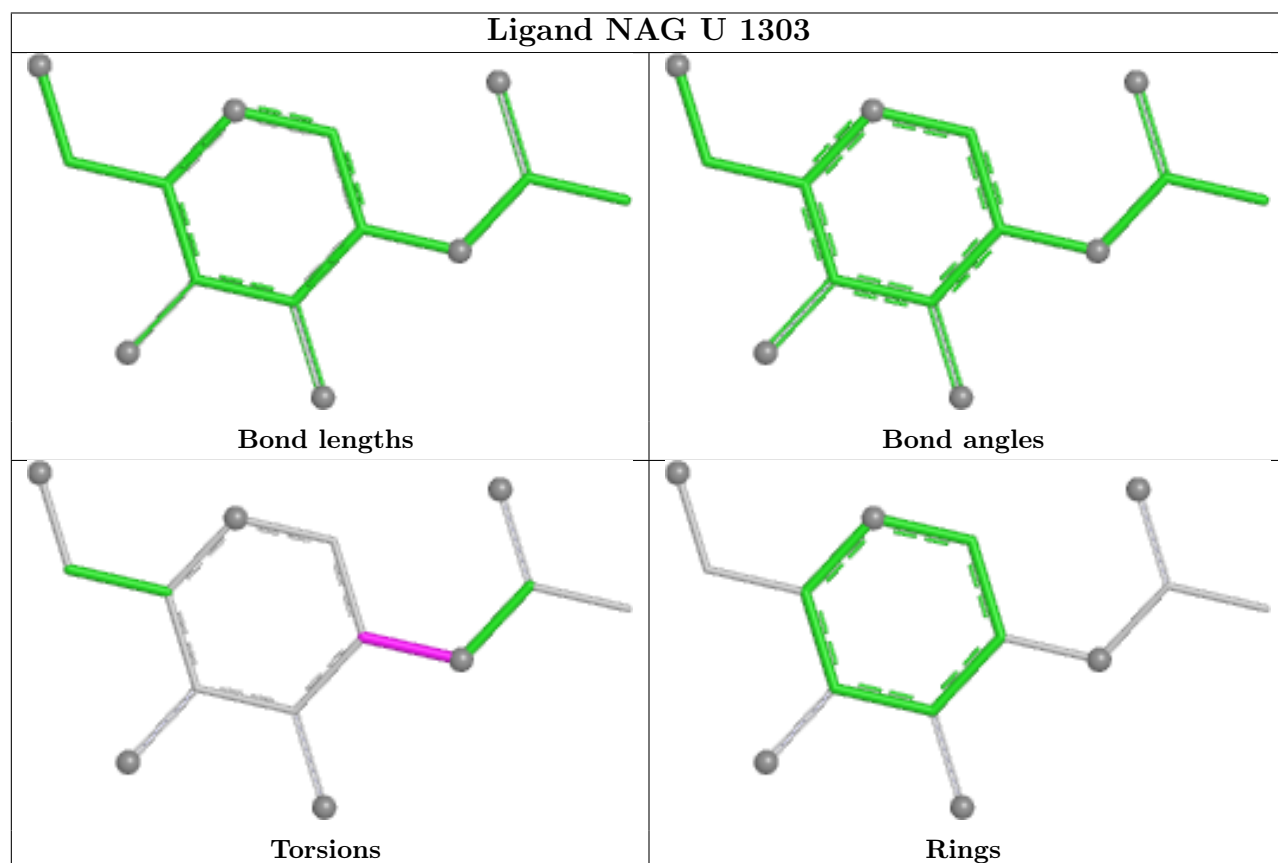
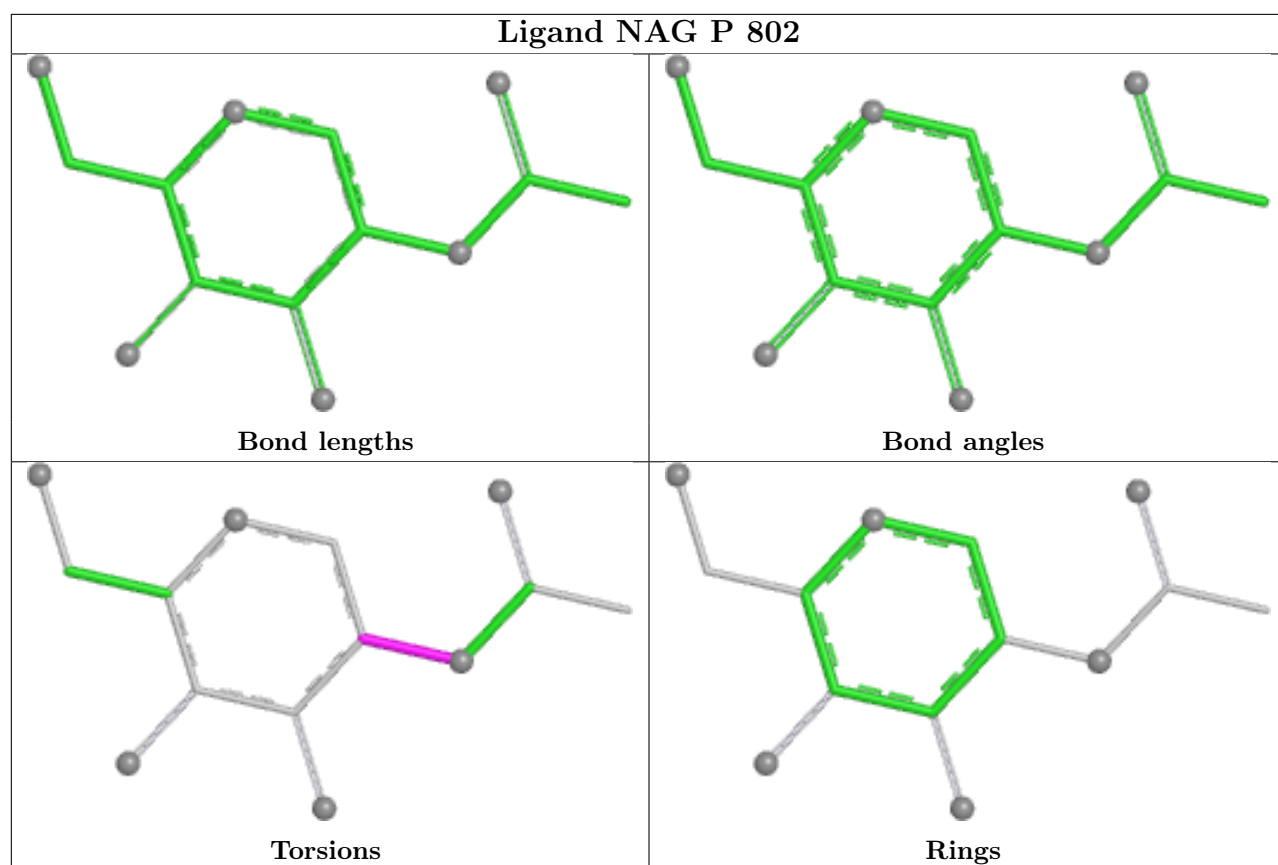
Ligand NAG A 802

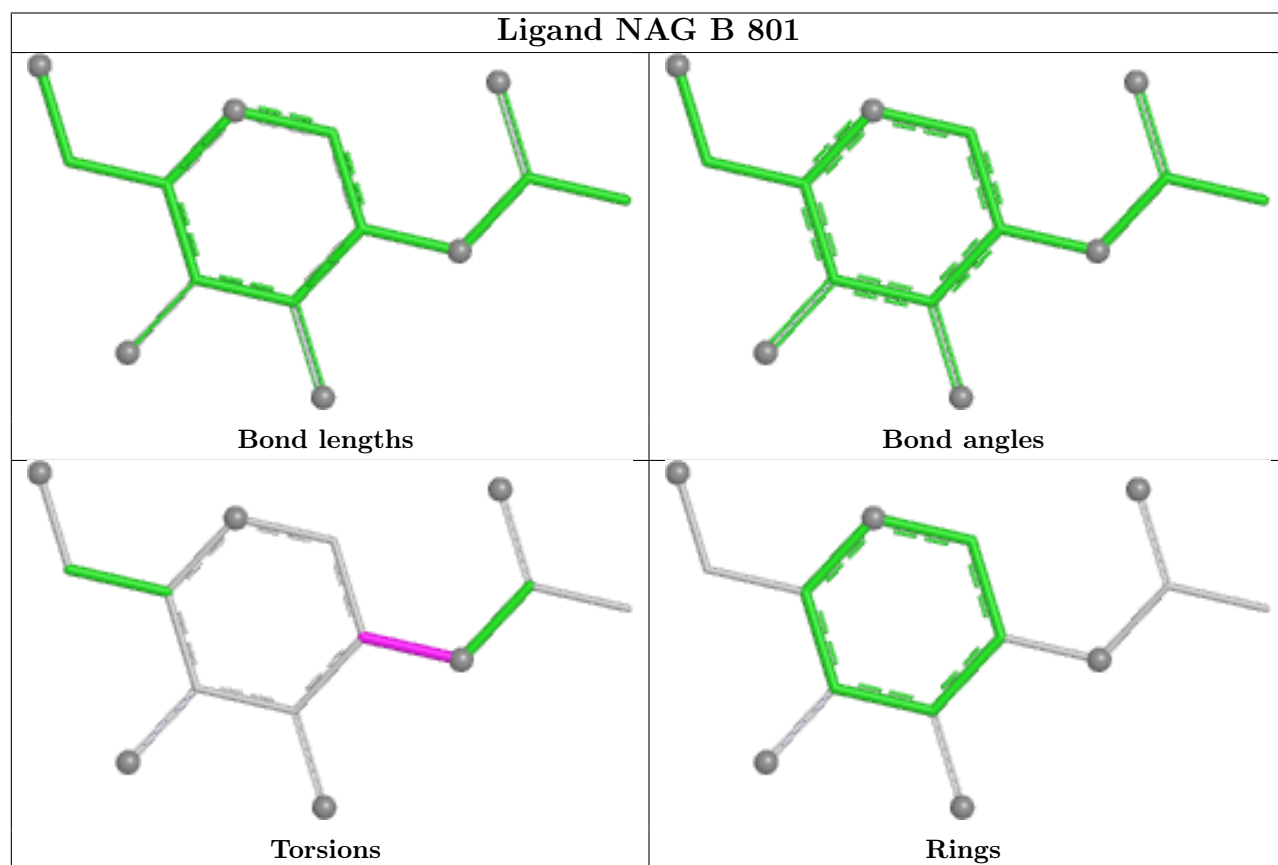
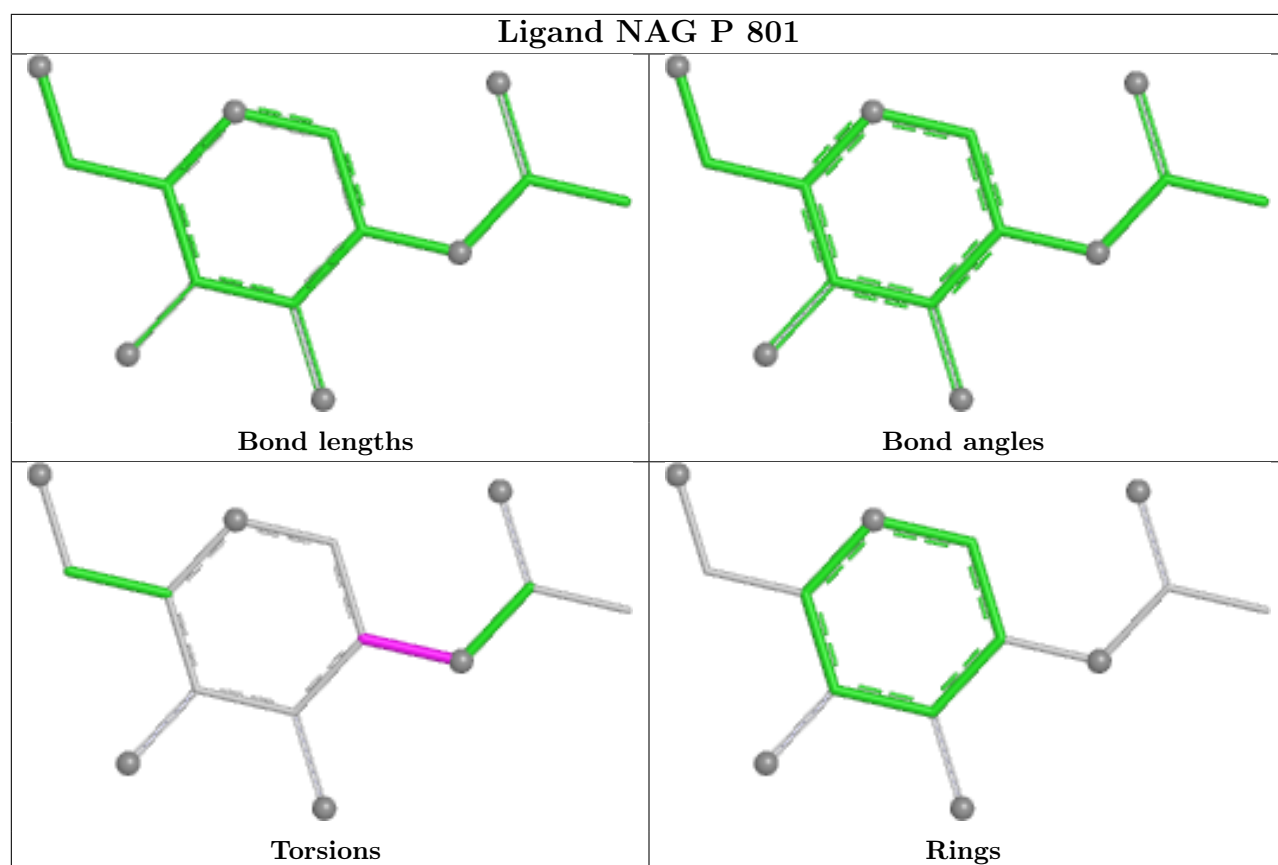


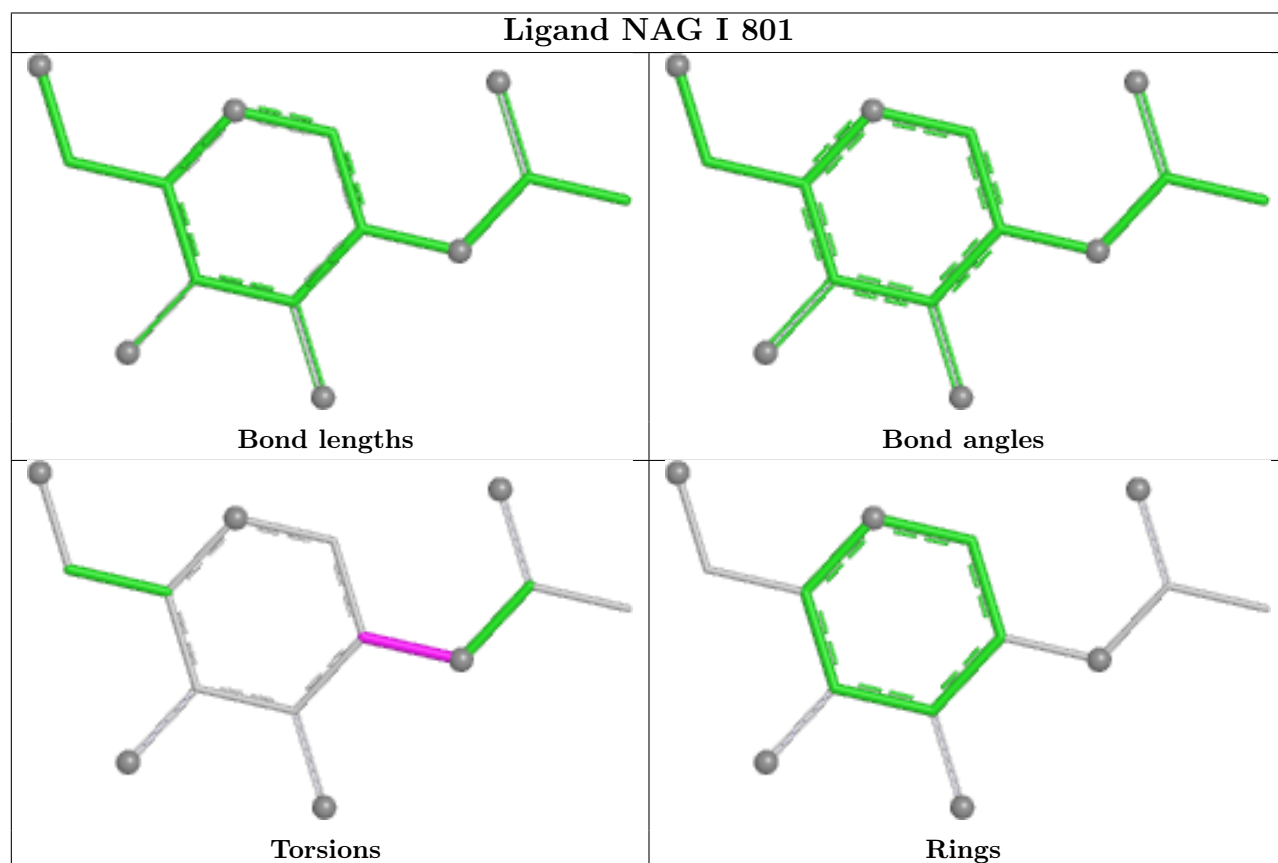
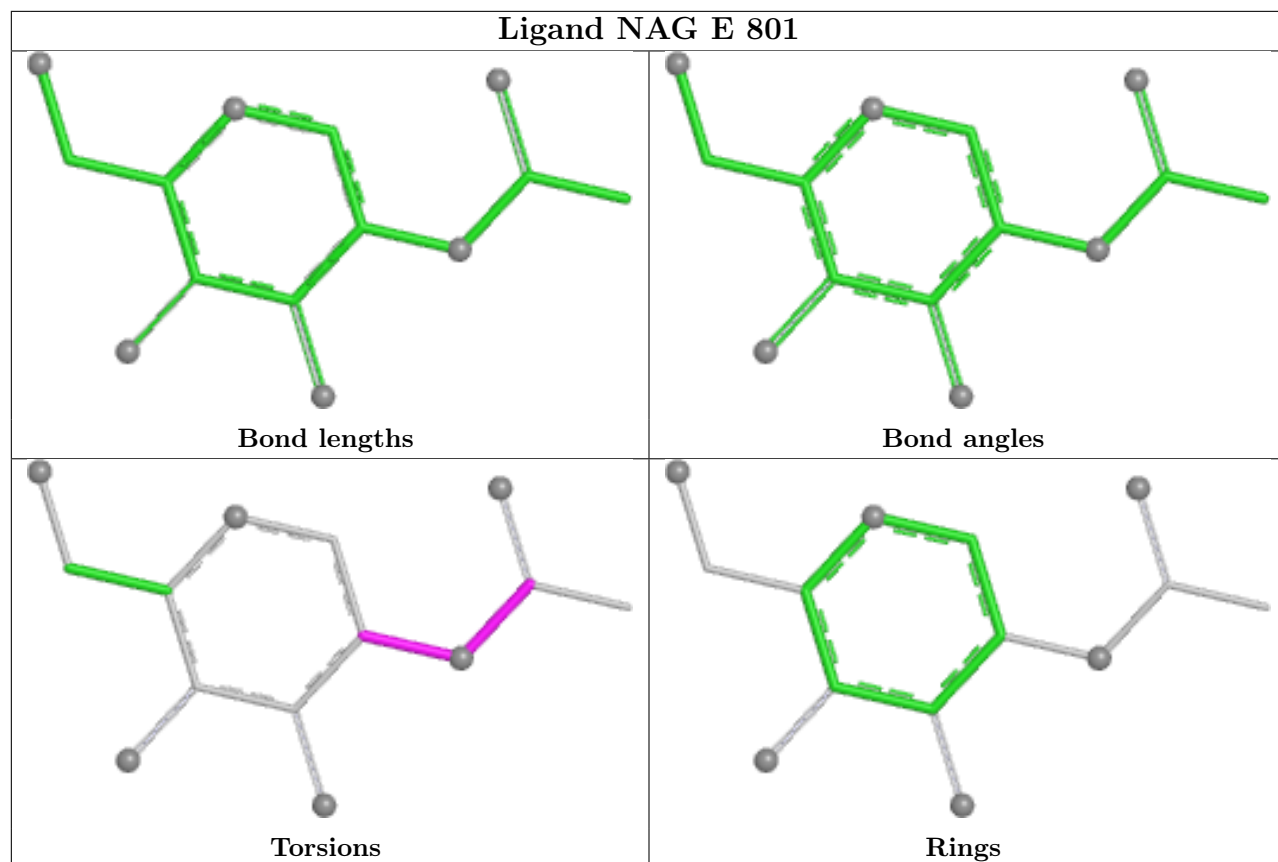


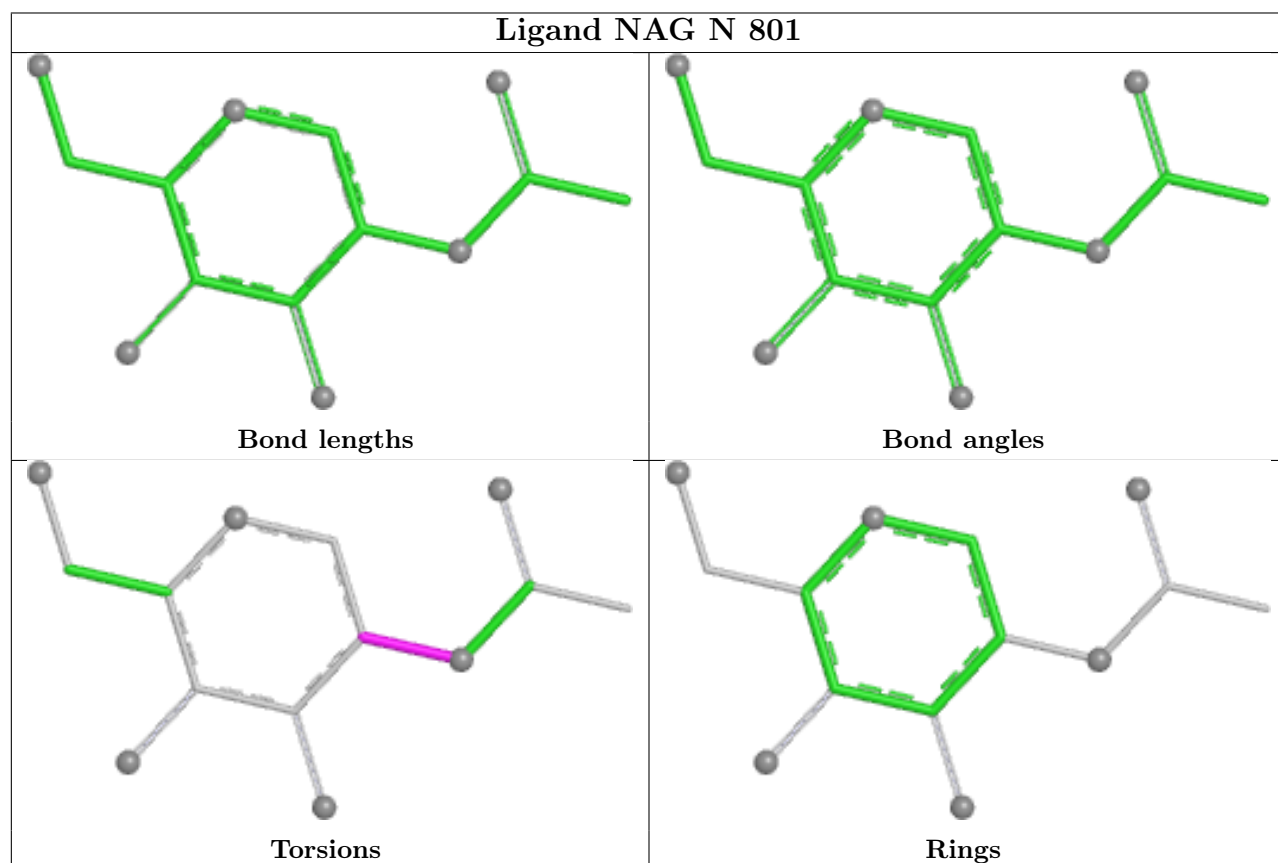
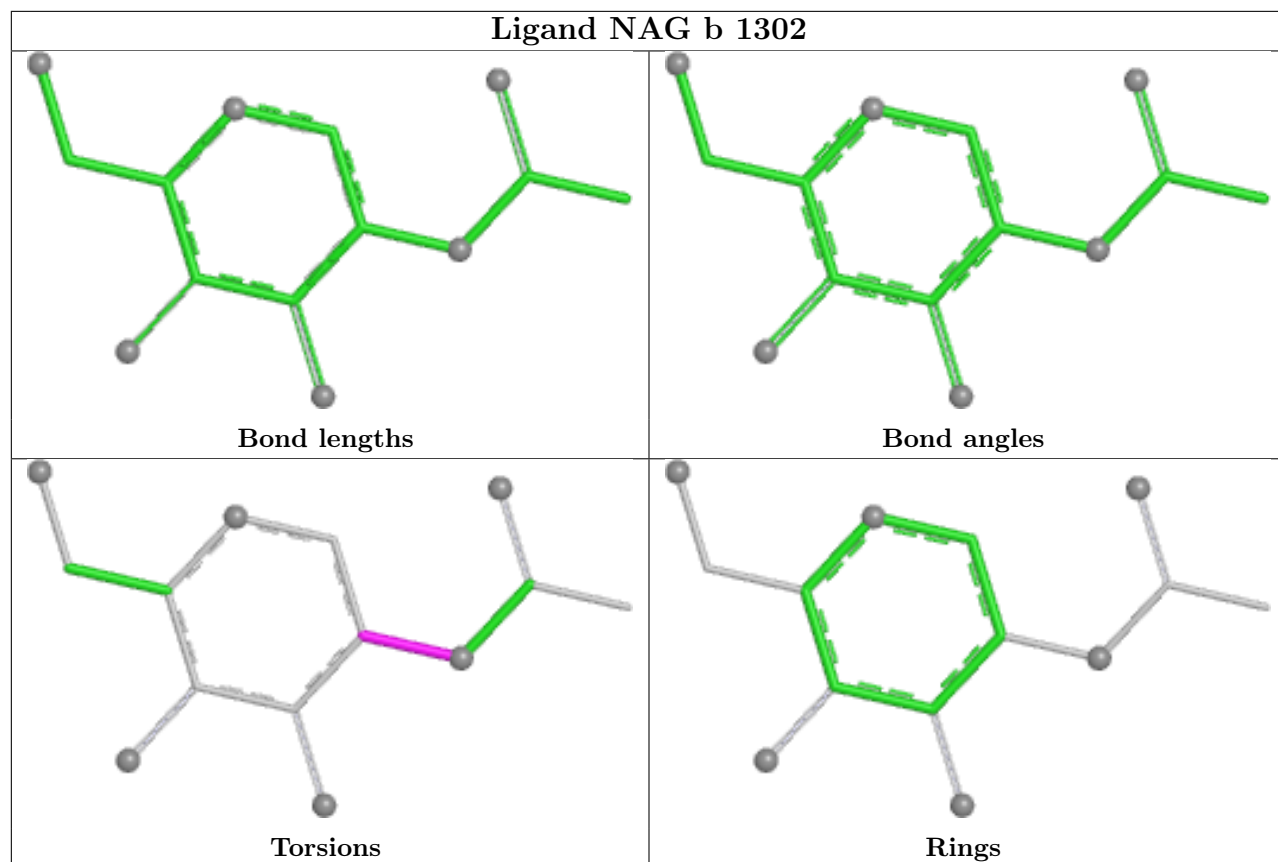




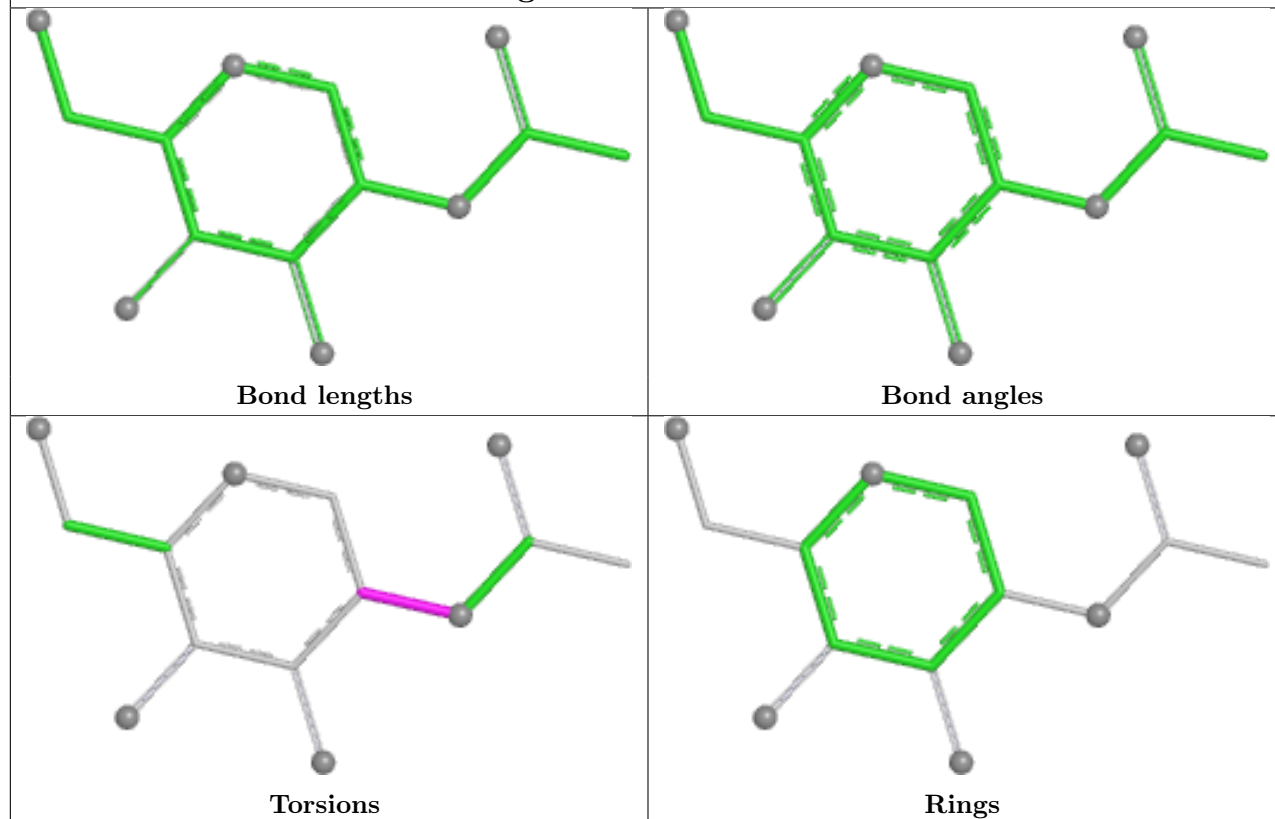




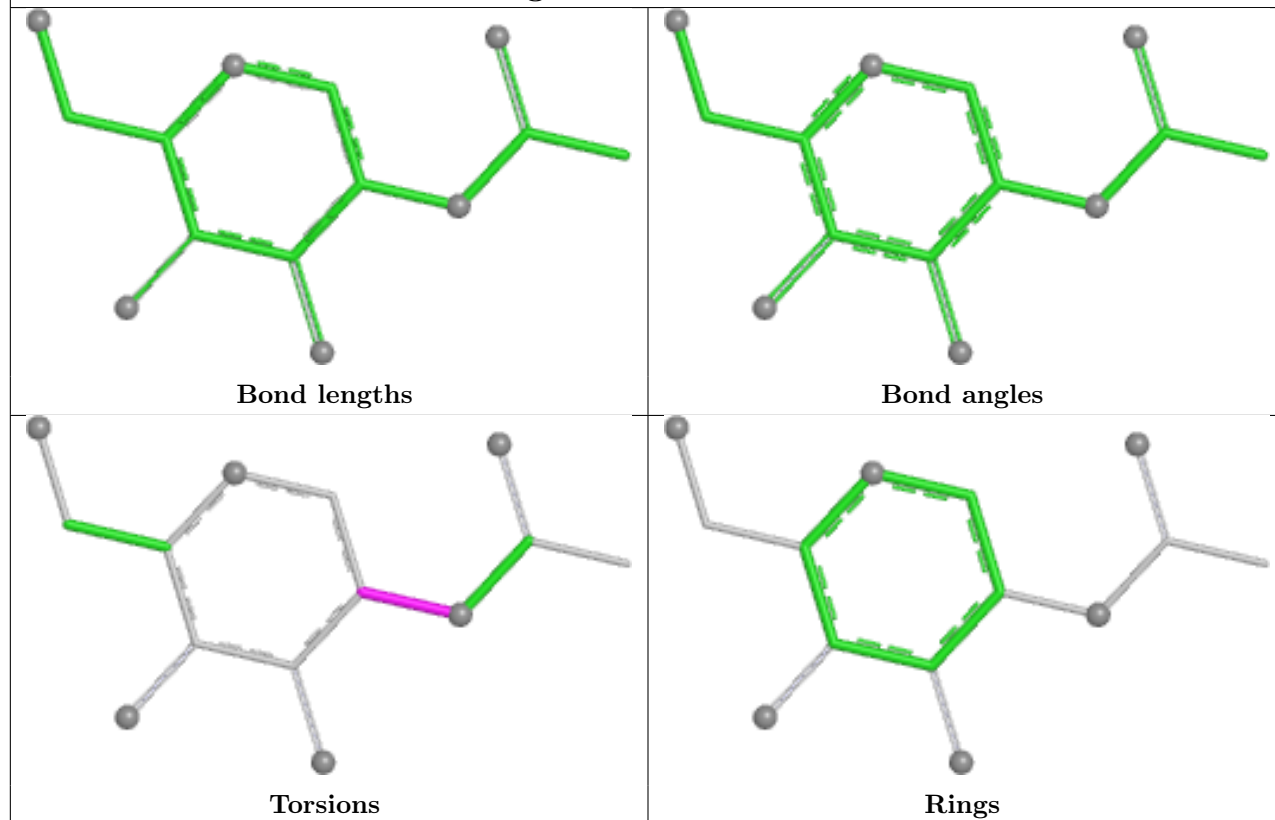




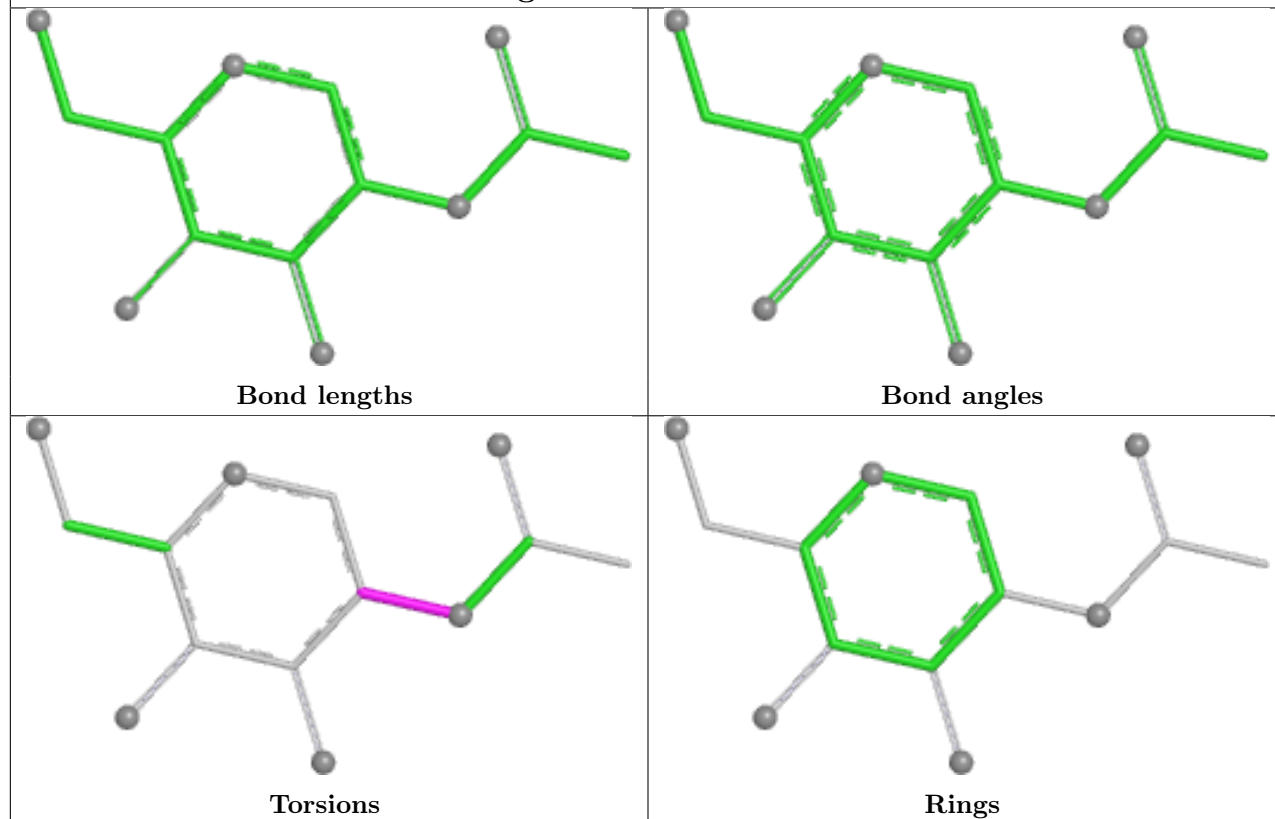
Ligand NAG U 1302



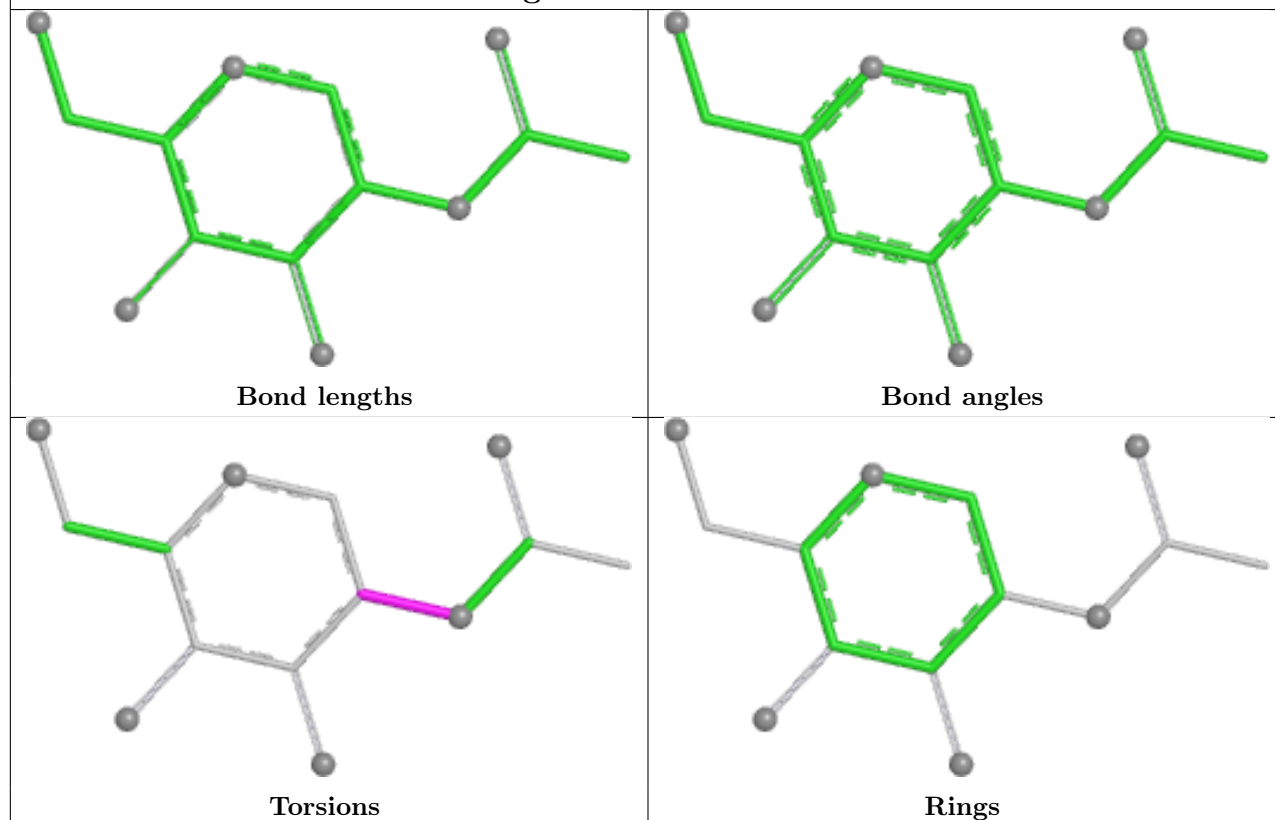
Ligand NAG A 801

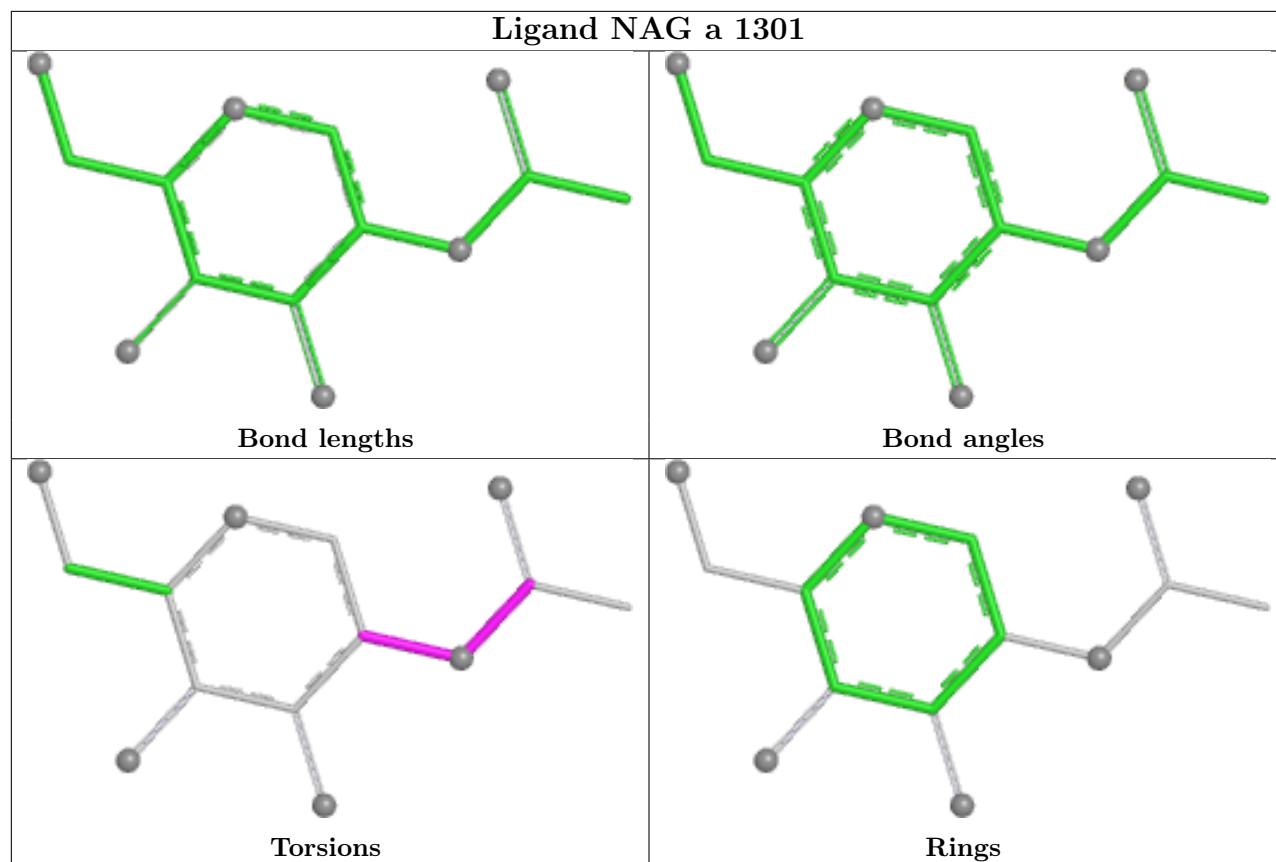


Ligand NAG D 1302



Ligand NAG M 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.

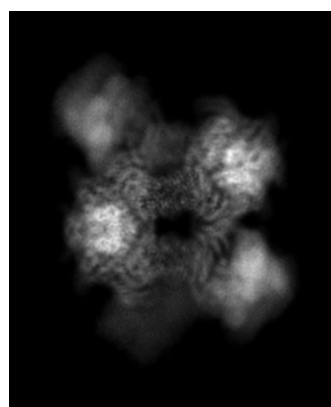
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32713. These allow visual inspection of the internal detail of the map and identification of artifacts.

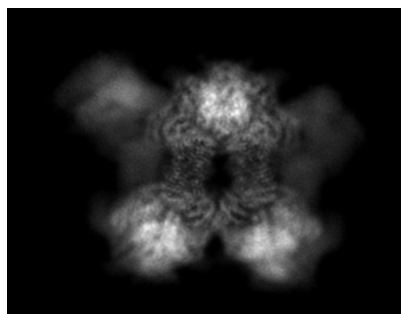
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

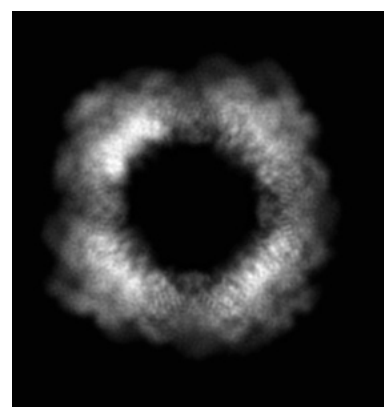
6.1.1 Primary map



X



Y

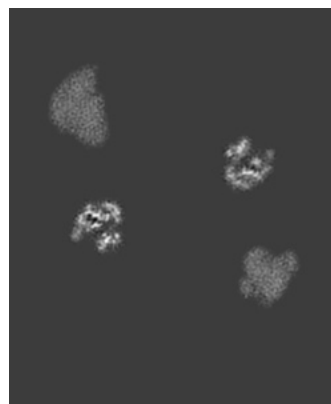


Z

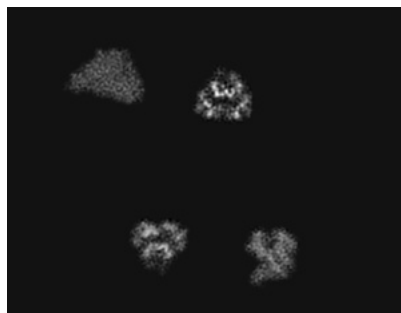
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

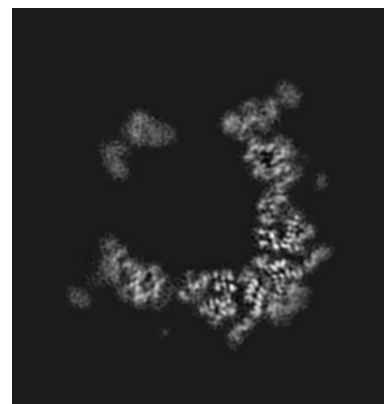
6.2.1 Primary map



X Index: 150



Y Index: 157

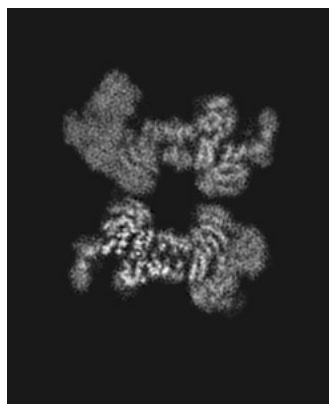


Z Index: 194

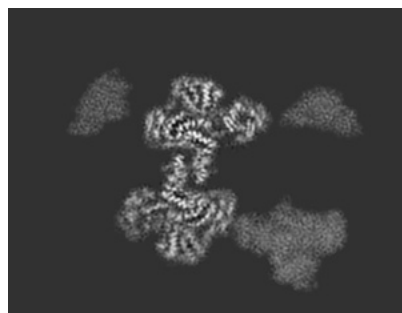
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

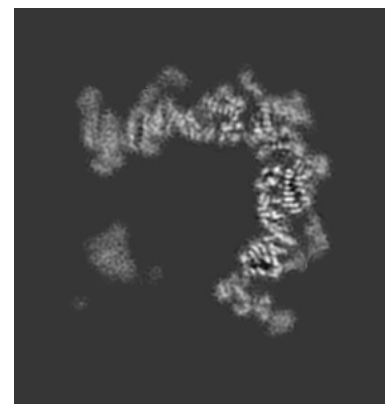
6.3.1 Primary map



X Index: 77



Y Index: 104

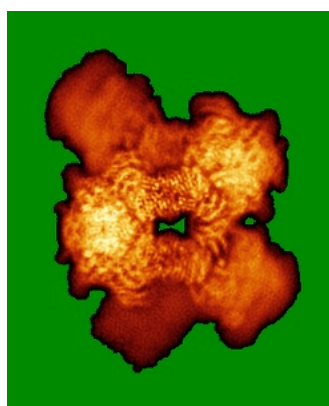


Z Index: 222

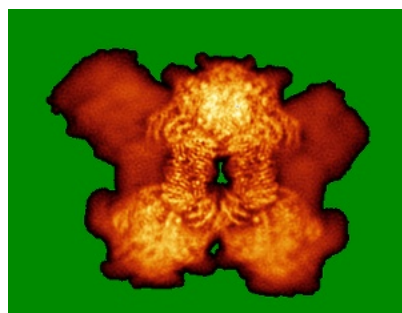
The images above show the largest variance slices of the map in three orthogonal directions.

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

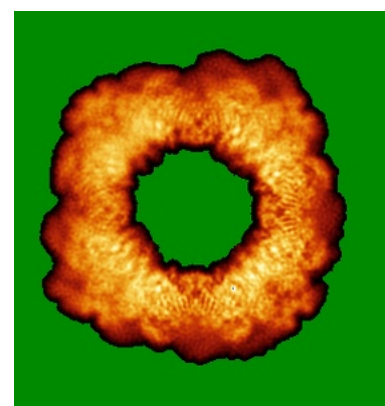
6.4.1 Primary map



X



Y

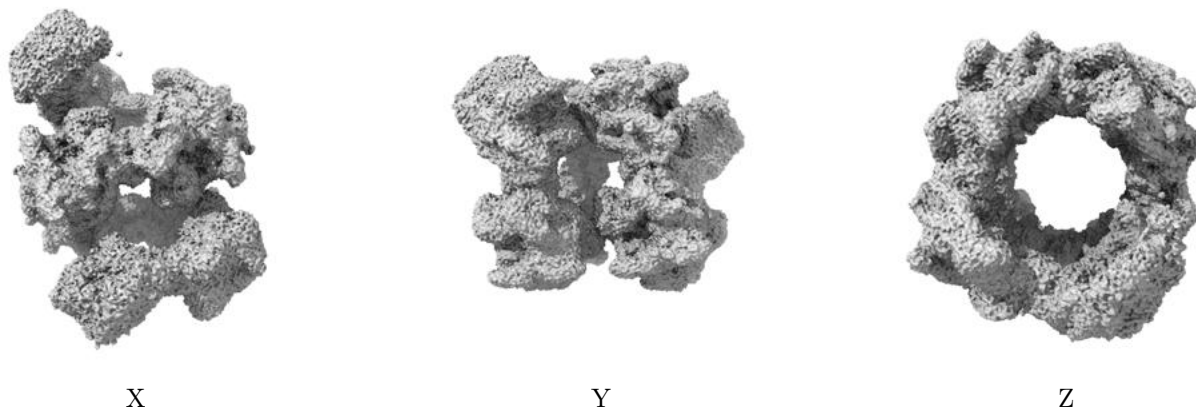


Z

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 0.003. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

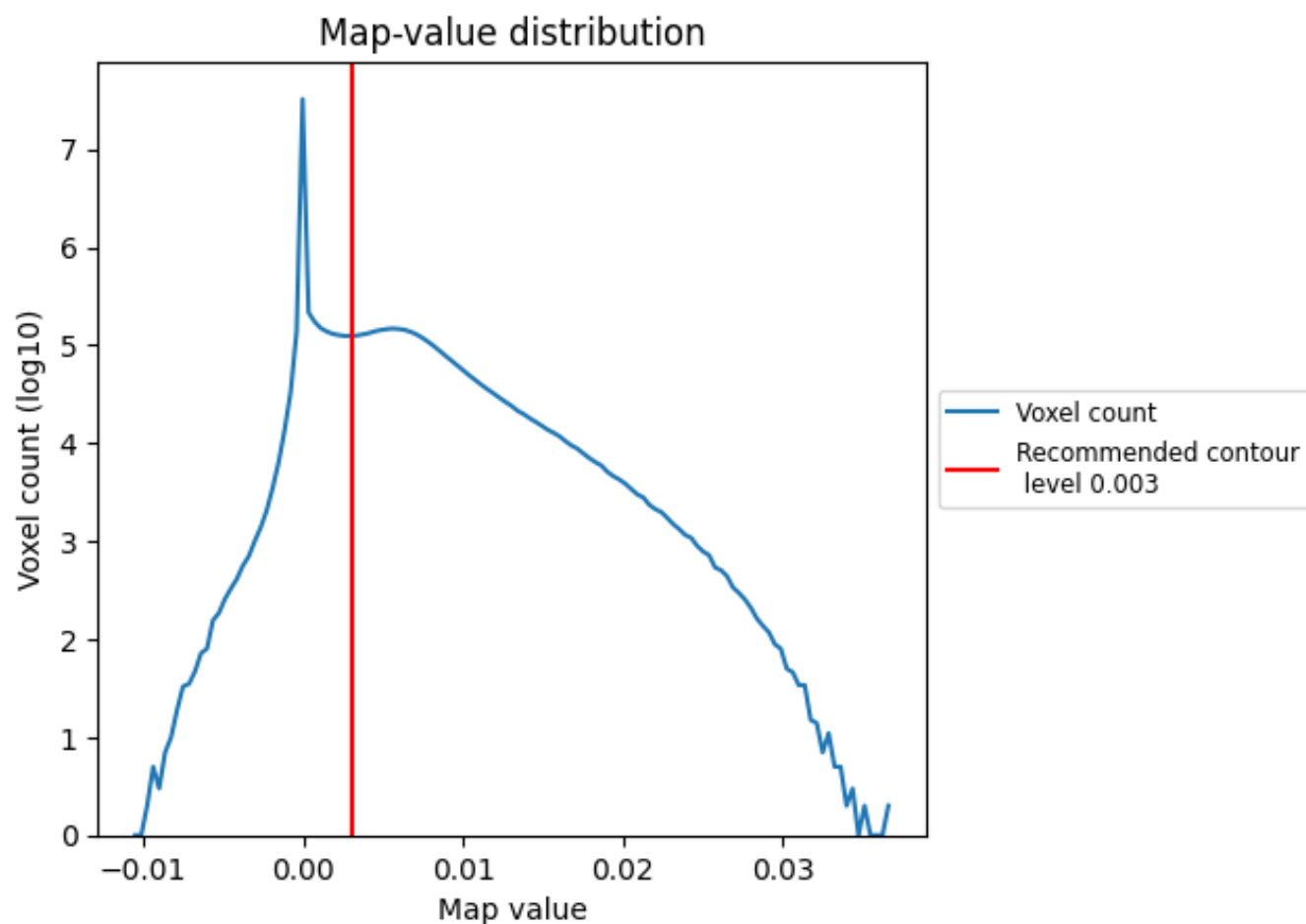
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

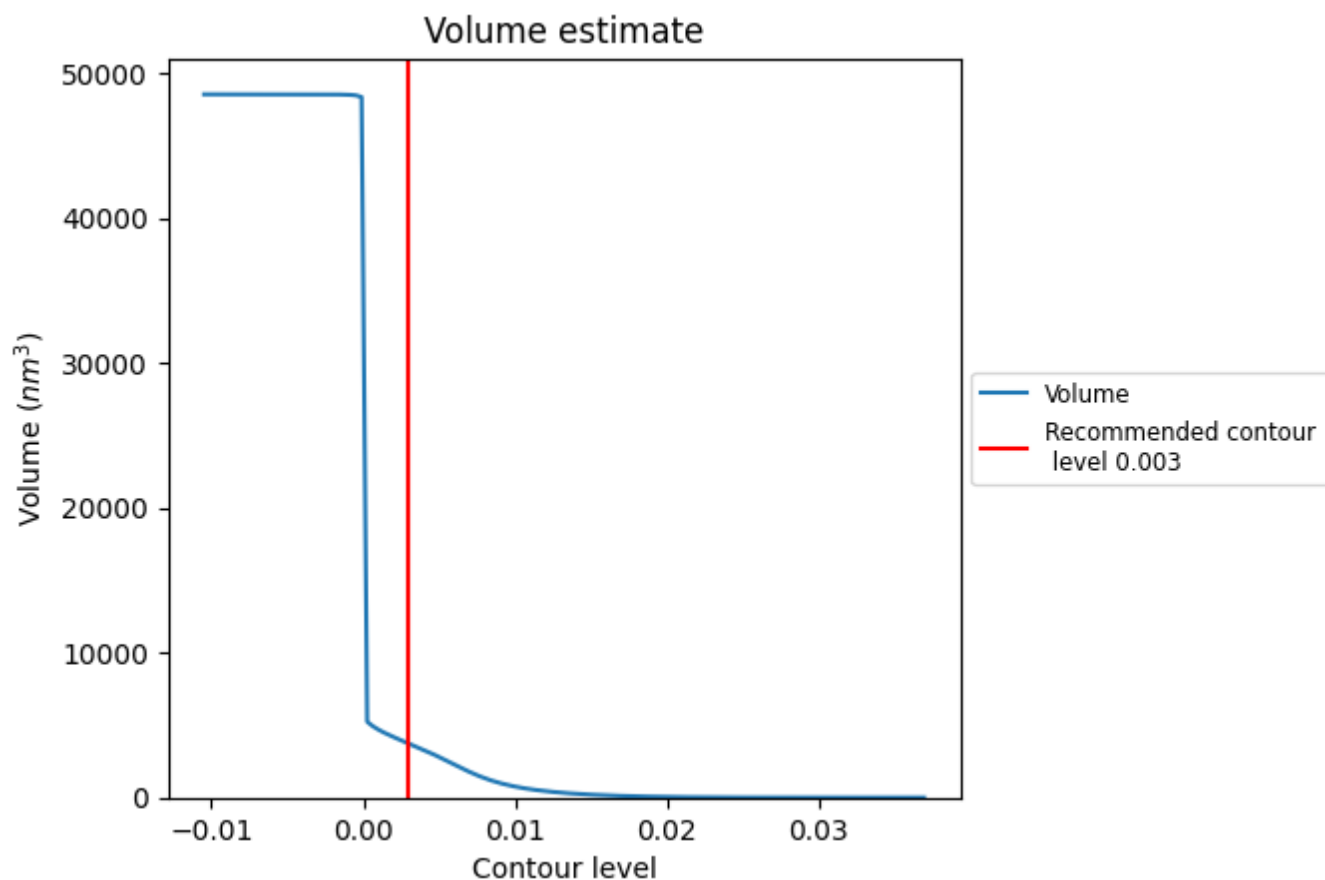
This section contains the results of statistical analysis of the map.

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 3728 nm³; this corresponds to an approximate mass of 3368 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](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

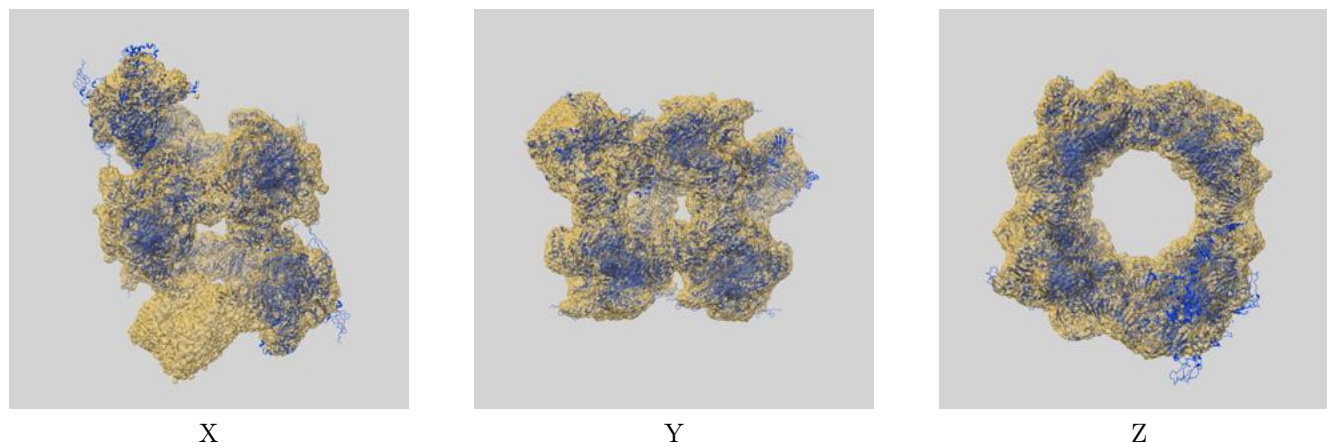
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

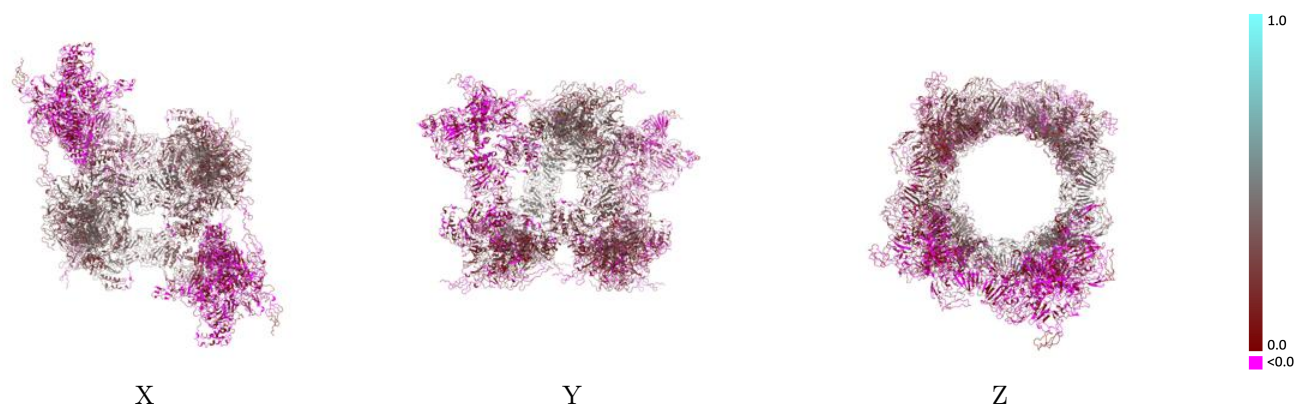
This section contains information regarding the fit between EMDB map EMD-32713 and PDB model 7WQT. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



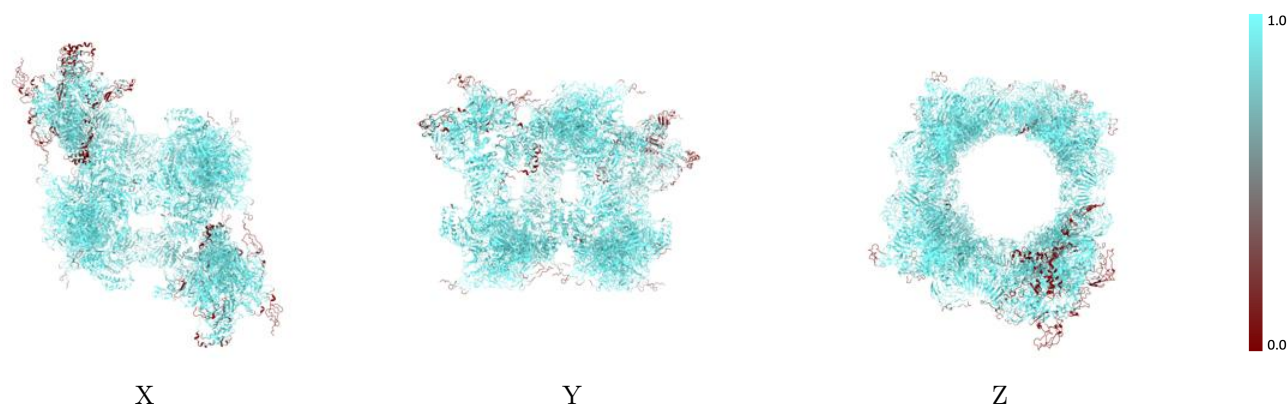
The images above show the 3D surface view of the map at the recommended contour level 0.003 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



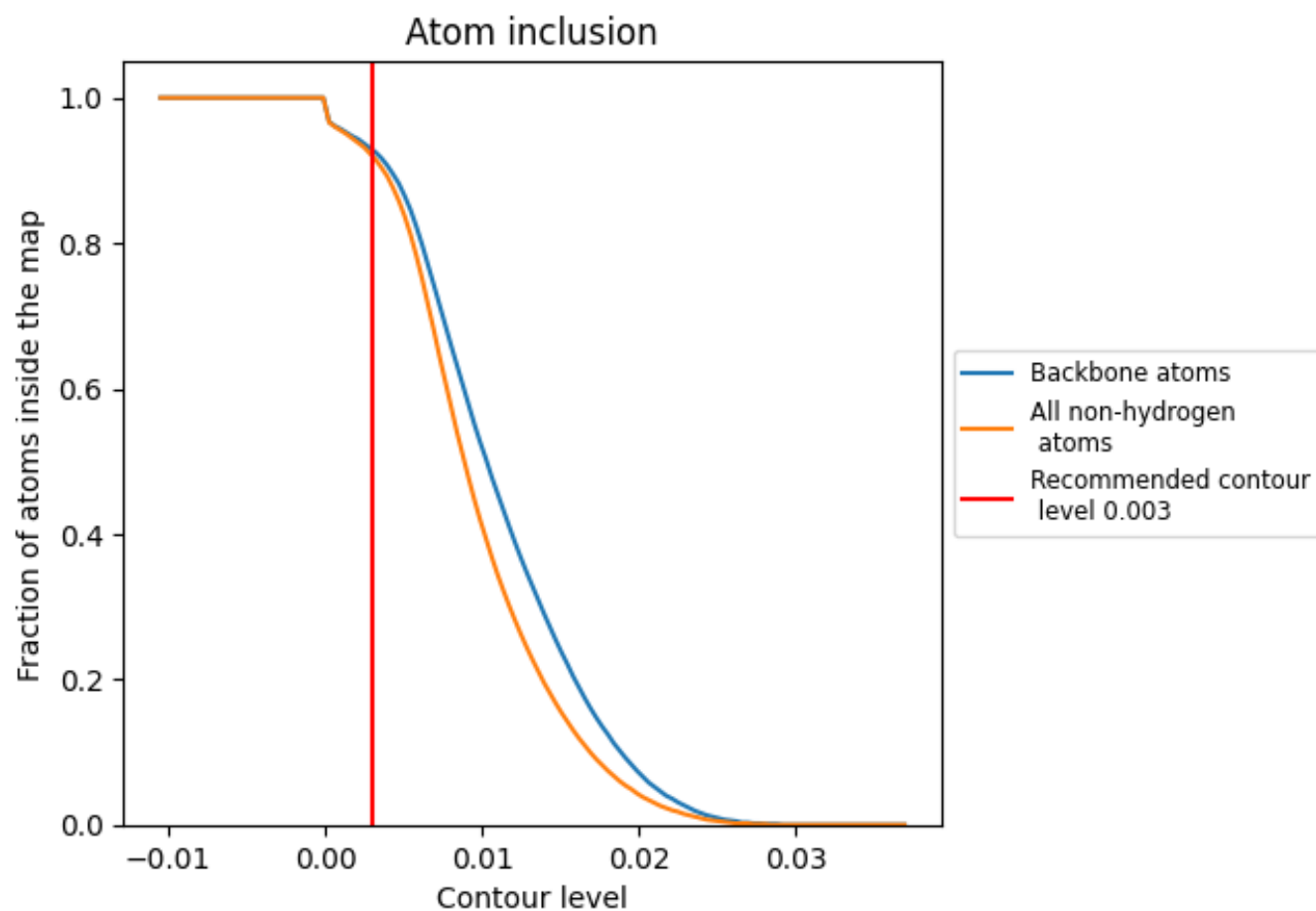
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.003).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 92% 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 (0.003) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9200	 0.1760
A	 0.9930	 0.3460
B	 0.9940	 0.3080
C	 0.9660	 0.2820
D	 0.9580	 0.2550
E	 0.9920	 0.3540
F	 0.9910	 0.3450
G	 0.9920	 0.2830
H	 0.9840	 0.1110
I	 0.9890	 0.1990
J	 0.8310	 0.0240
K	 0.7850	 0.0100
L	 0.9910	 0.3510
M	 0.9900	 0.3220
N	 0.9920	 0.2060
O	 0.9620	 0.0580
P	 0.9830	 0.1070
Q	 0.9240	 0.0410
R	 0.6260	 -0.0040
S	 0.9620	 0.3020
T	 0.9570	 0.2830
U	 0.9530	 0.2180
V	 0.9170	 0.0730
W	 0.9530	 0.1480
X	 0.7700	 -0.0020
Y	 0.6830	 0.0040
Z	 0.9680	 0.3040
a	 0.9610	 0.2660
b	 0.9530	 0.1570
c	 0.9020	 0.0480
d	 0.9370	 0.0990
e	 0.8070	 0.0110
f	 0.6390	 -0.0180

