



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 28, 2023 – 03:31 pm GMT

PDB ID : 6YMJ
Title : Crystal structure of the SAM-SAH riboswitch with adenosine.
Authors : Huang, L.; Lilley, D.M.J.
Deposited on : 2020-04-08
Resolution : 2.04 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

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

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:

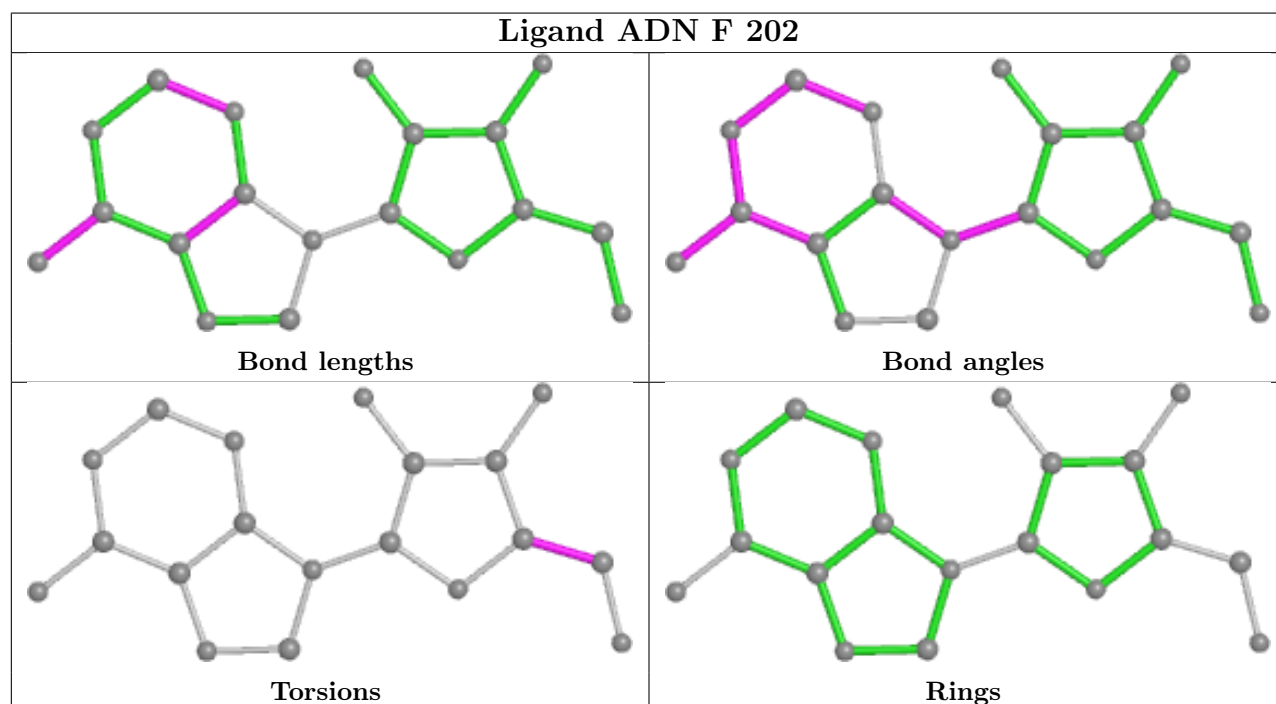
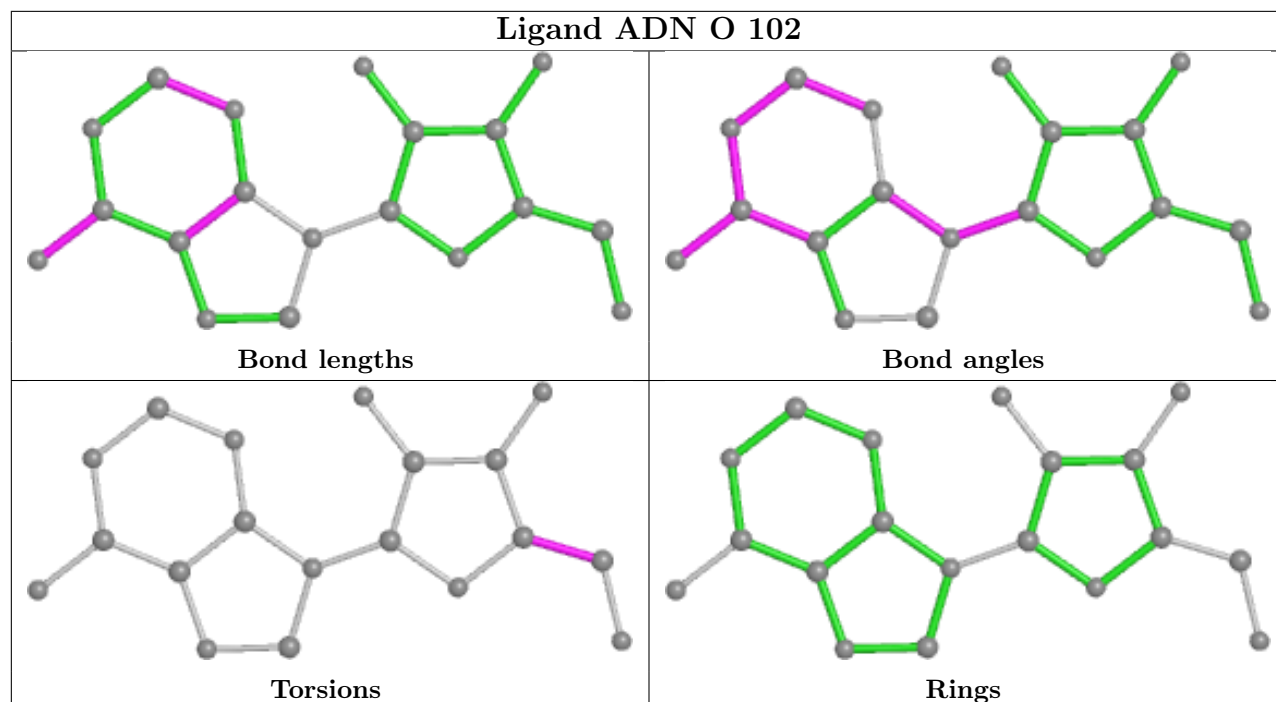
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.32.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.32.1

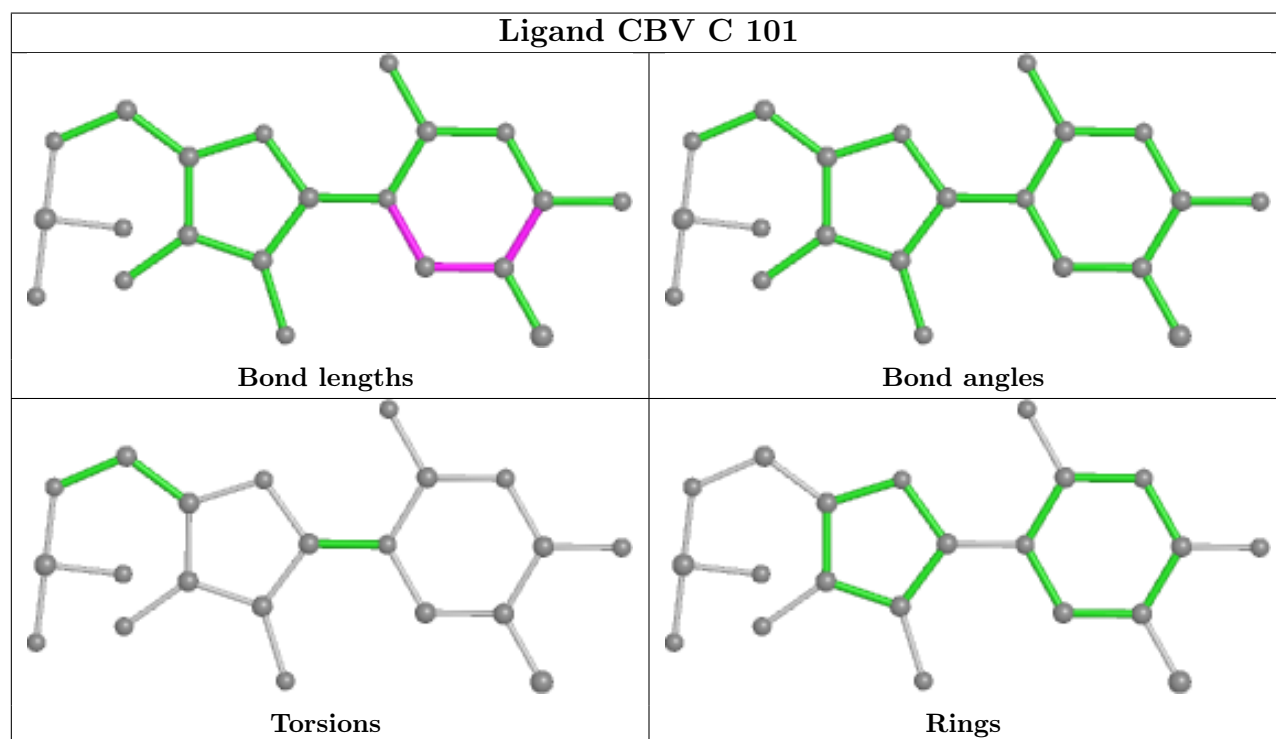
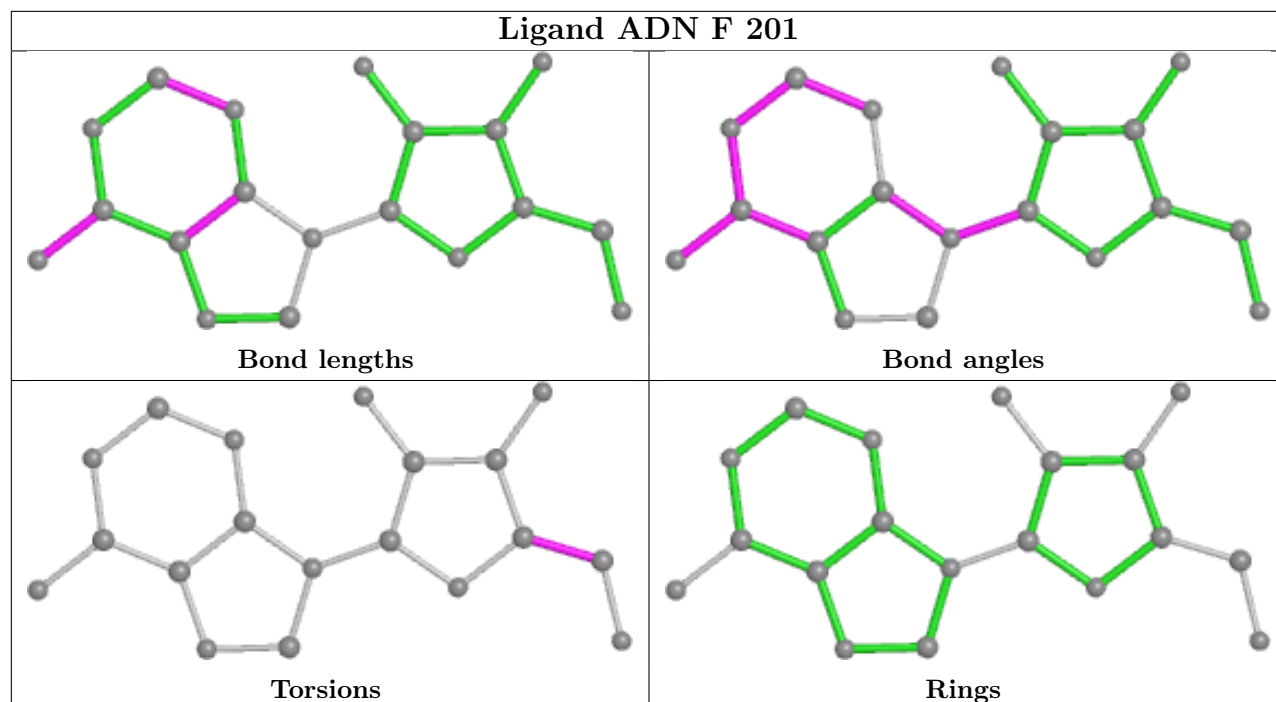
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Mol	Chain	Length	Quality of chain
2	B	9	 67%33%
2	D	9	 89%11%
2	G	9	 67%33%
2	J	9	 89%11%
2	N	9	 89%11%
2	P	9	 89%11%

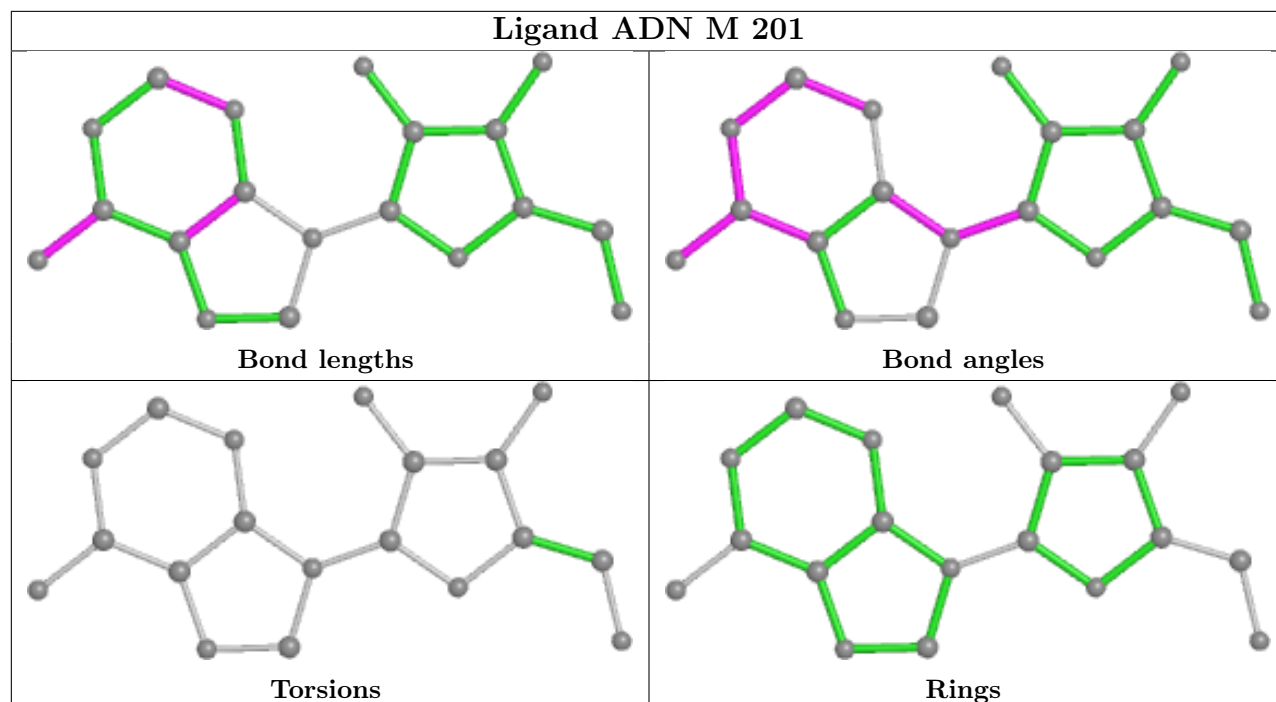
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	O	6	Total	O	0	0
			6	6		

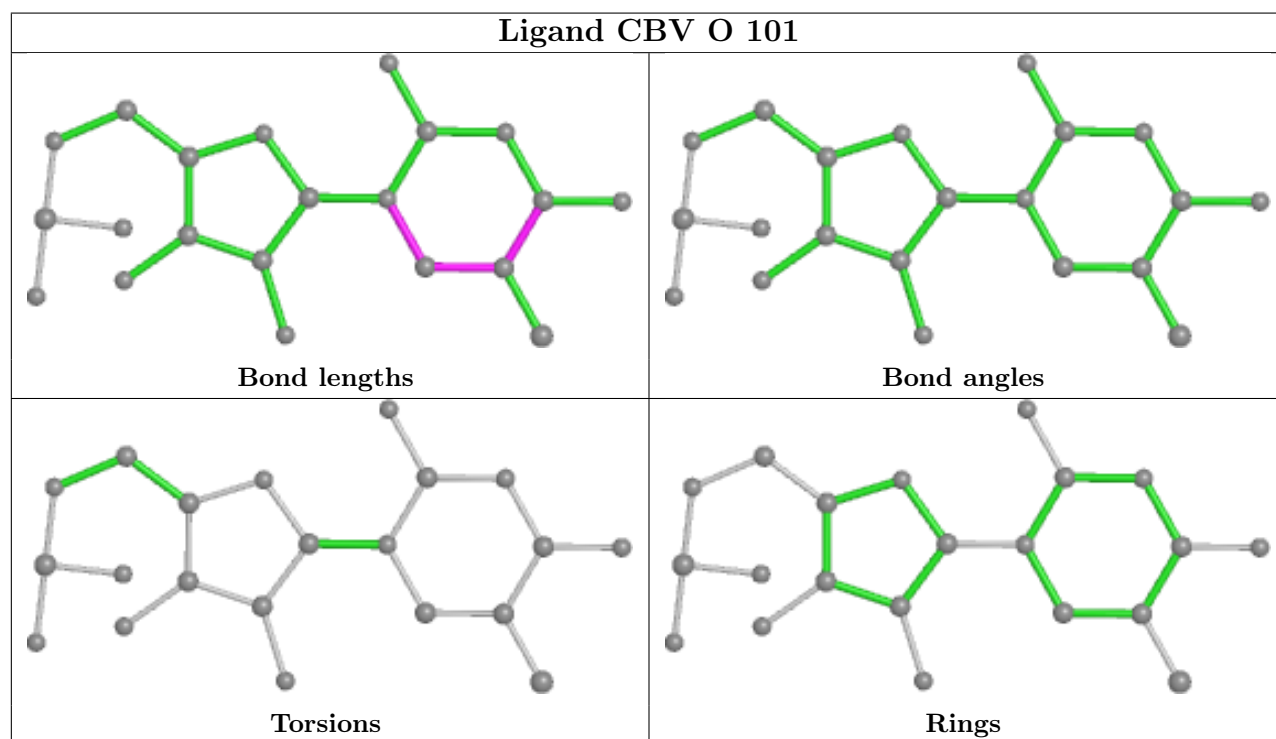


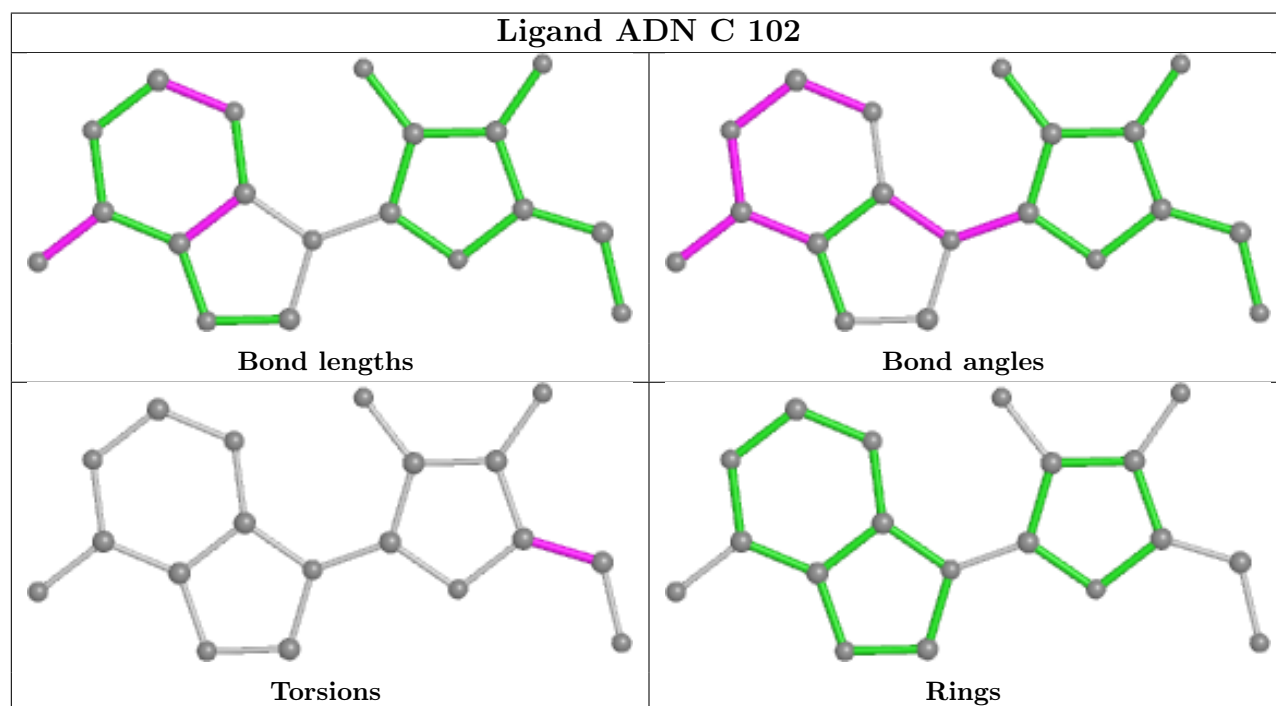
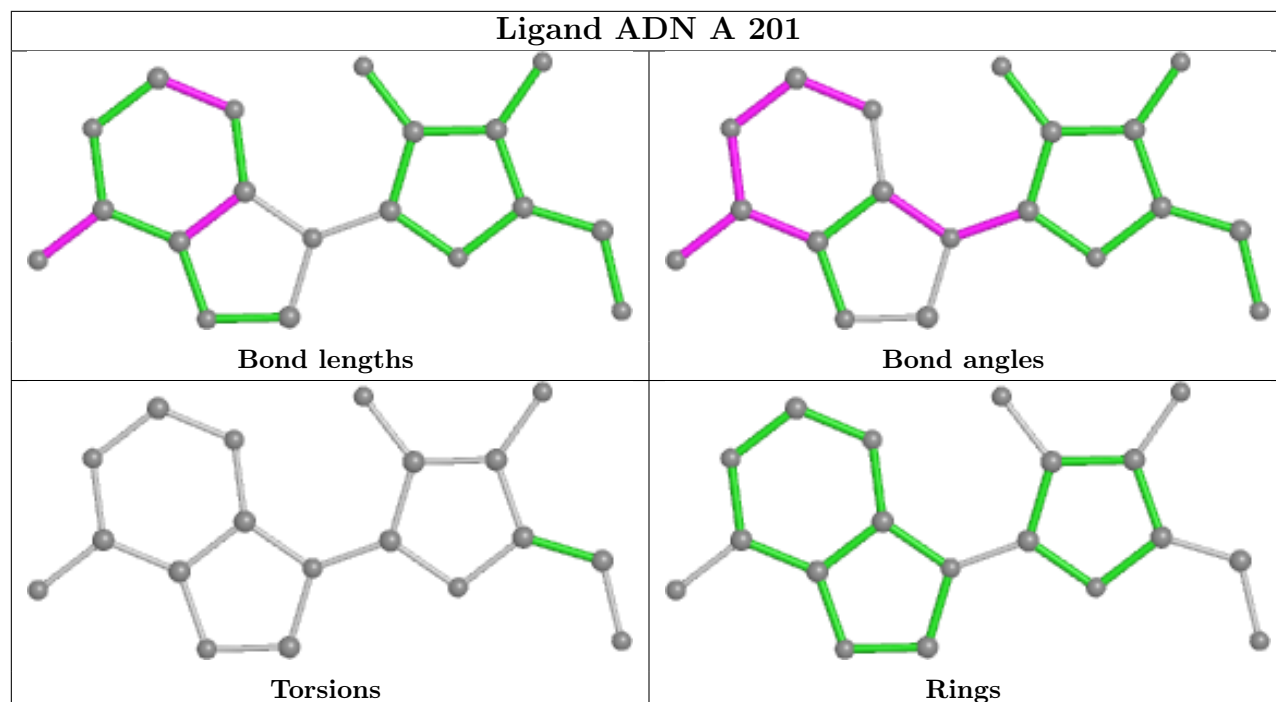


Ligand ADN M 201

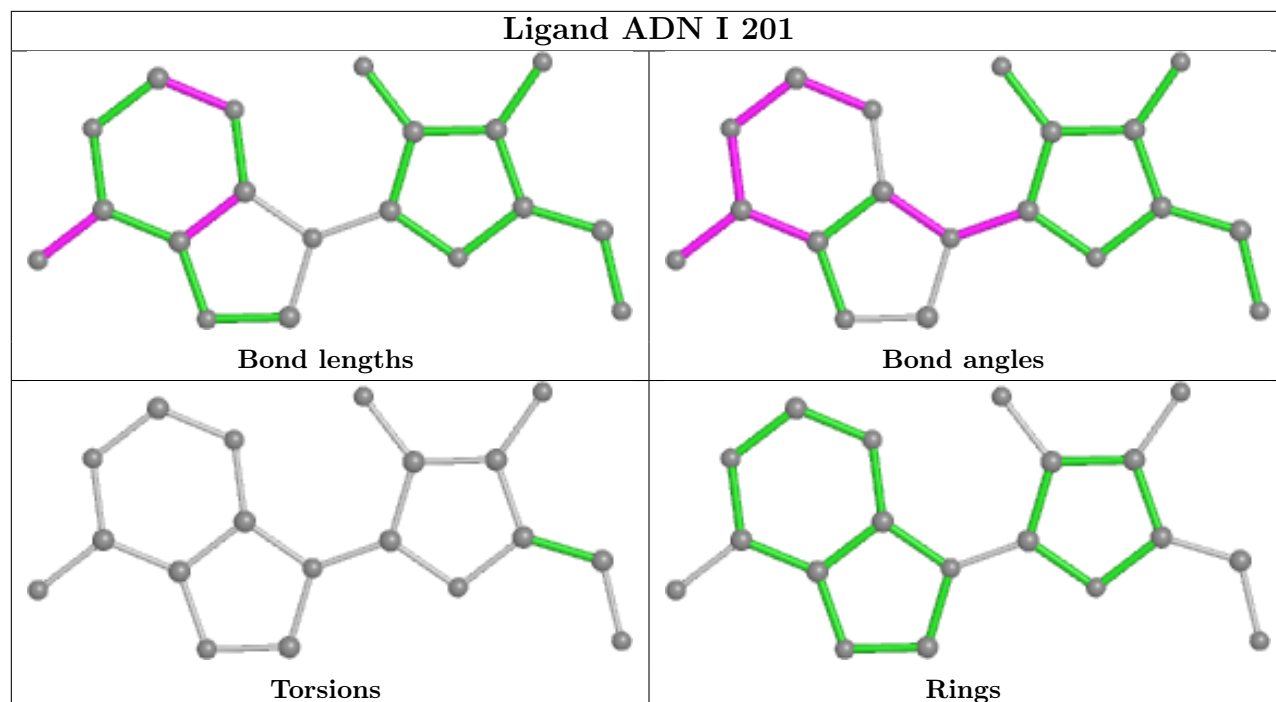


Ligand CBV O 101

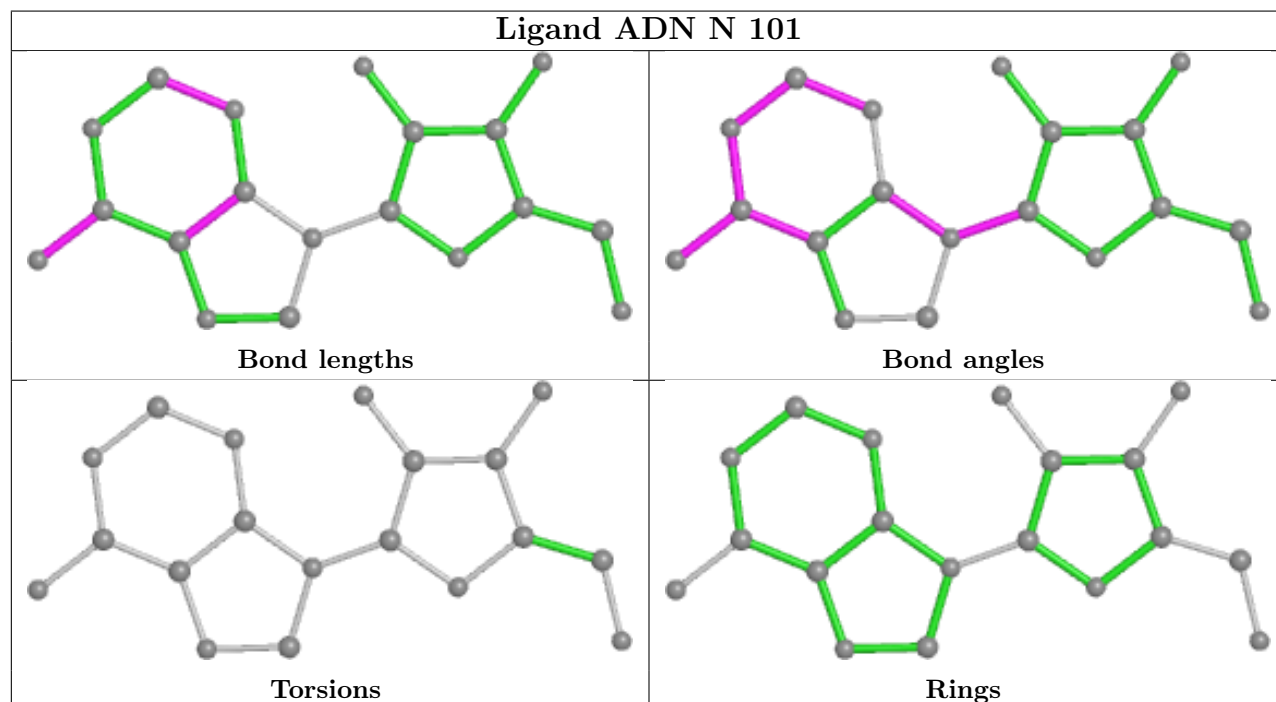


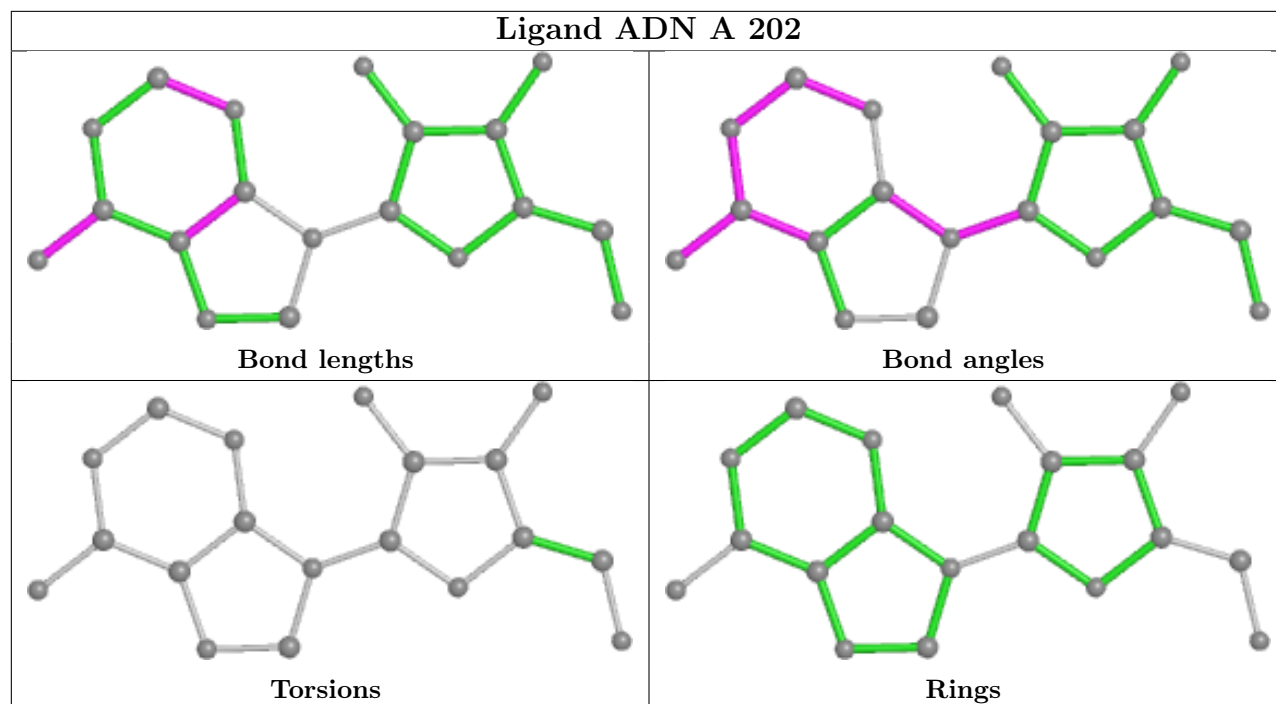


Ligand ADN I 201



Ligand ADN N 101





5.7 Other polymers [i](#)

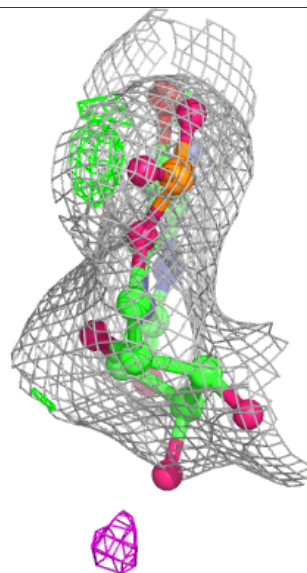
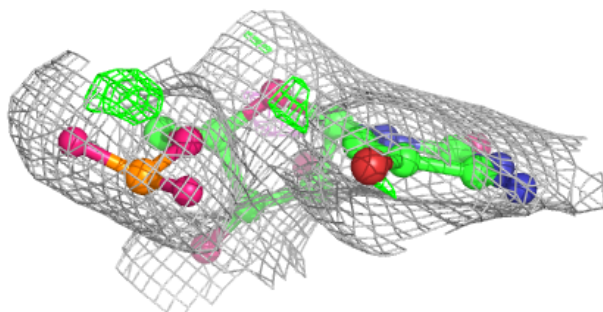
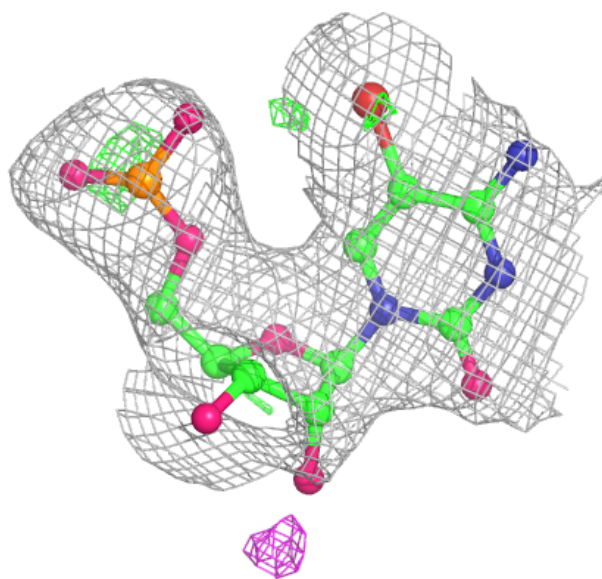
There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

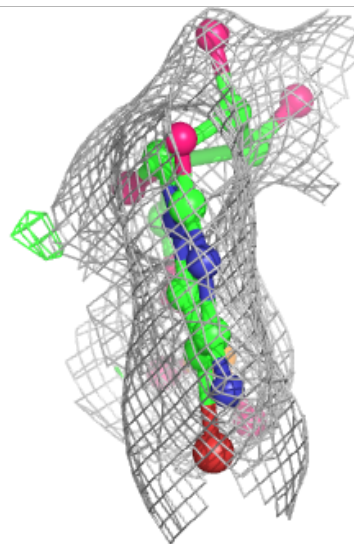
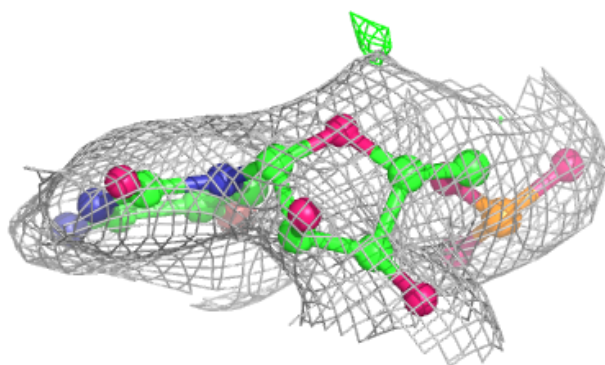
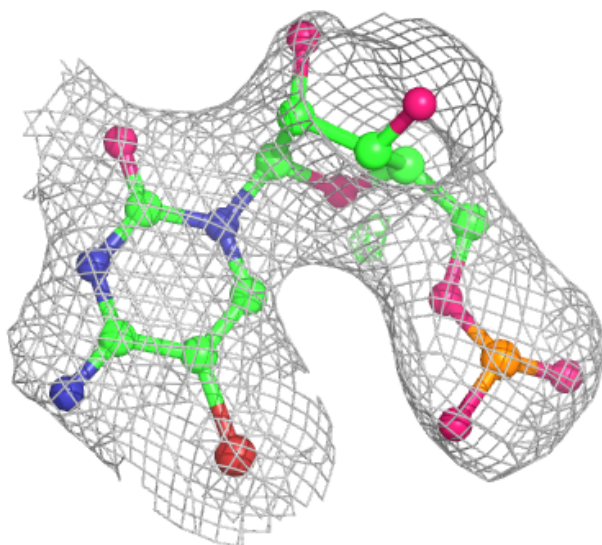
Electron density around CBV O 101:

2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



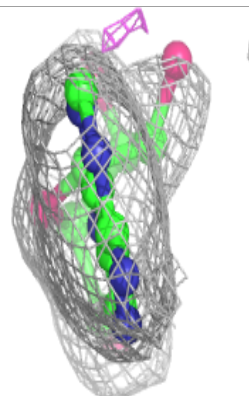
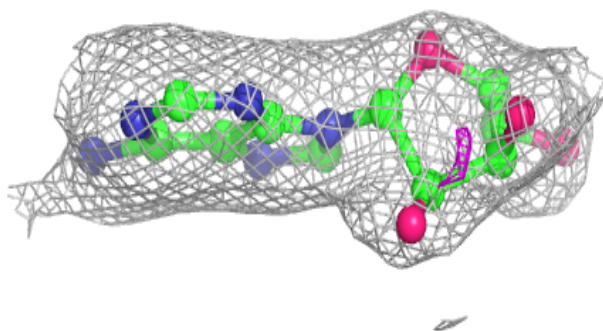
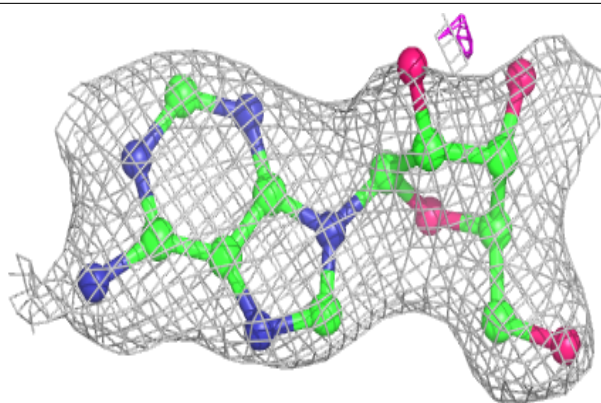
Electron density around CBV C 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

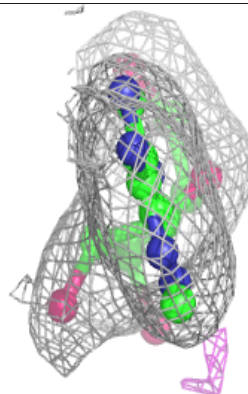
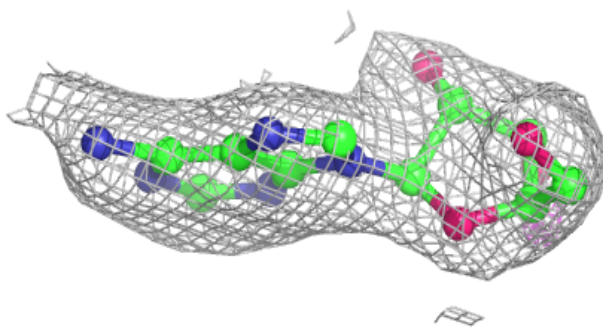
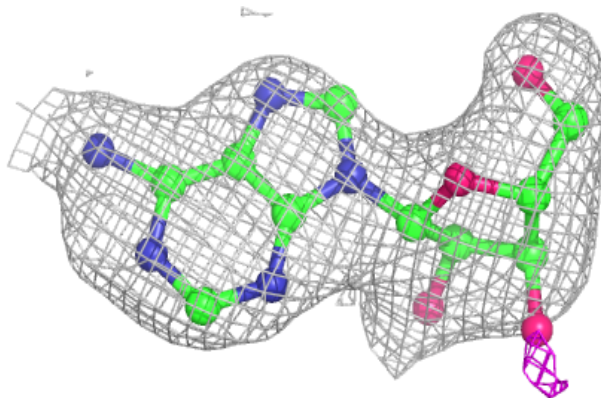


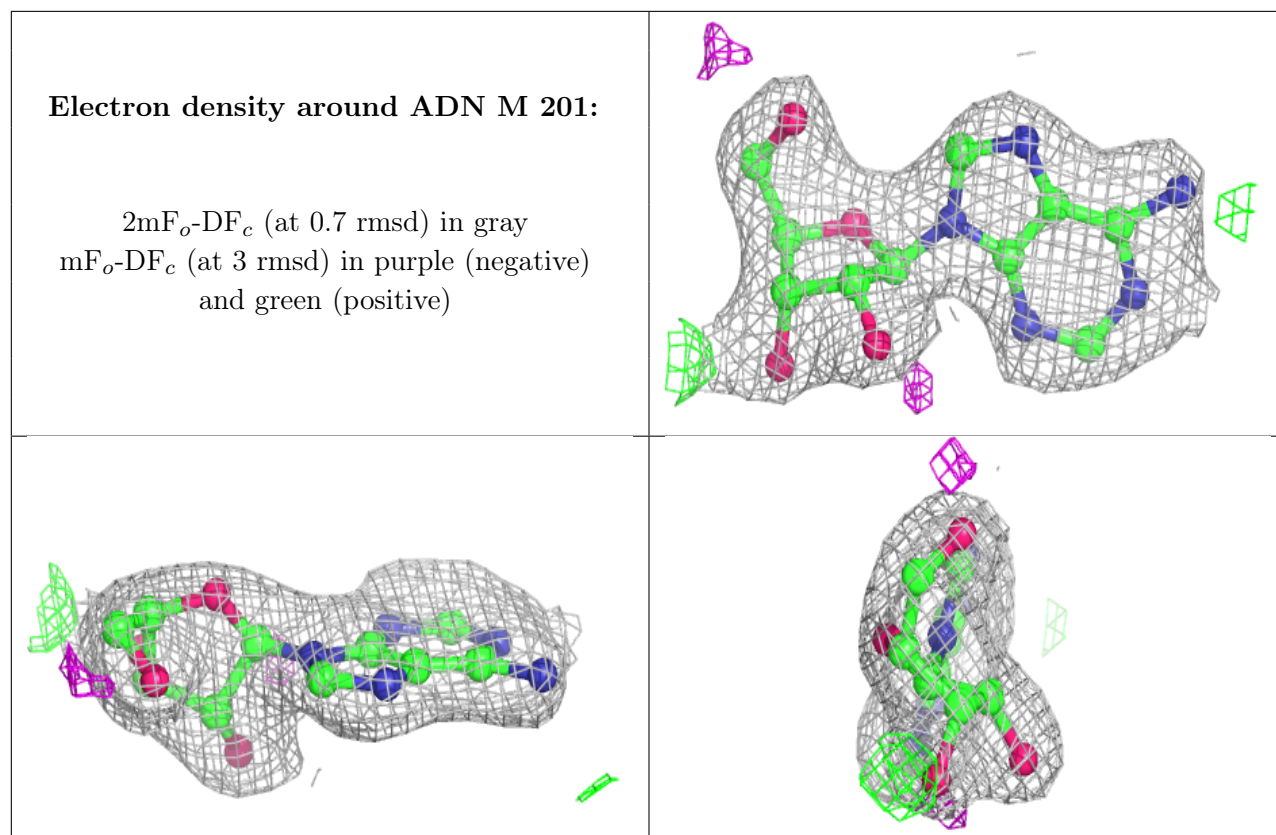
Electron density around ADN I 201:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around ADN C 102:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.5 Other polymers [i](#)

There are no such residues in this entry.