Full wwPDB X-ray Structure Validation Report (i)

Aug 16, 2023 – 07:17 AM EDT

PDB ID	:	1YRJ
Title	:	Crystal Structure of Apramycin bound to a Ribosomal RNA A site oligonucleotide
Authors	:	Han, Q.; Zhao, Q.; Fish, S.; Simonsen, K.B.; Vourloumis, D.; Froelich, J.M.; Wall, D.; Hermann, T.
Deposited on	:	2005-02-03
Resolution	:	2.70 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

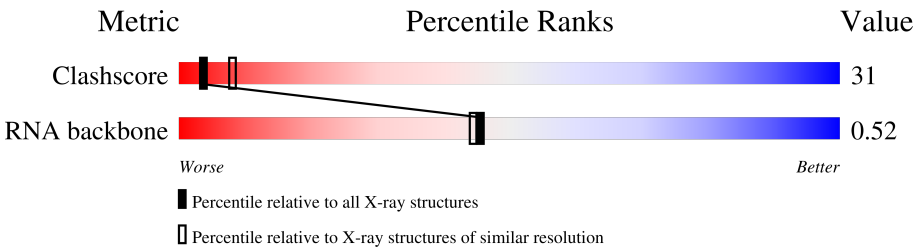
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	3122 (2.70-2.70)
RNA backbone	3102	1159 (3.00-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	23	26% 52% 13% 9%
1	B	23	22% 39% 30% . .

2 Entry composition (i)

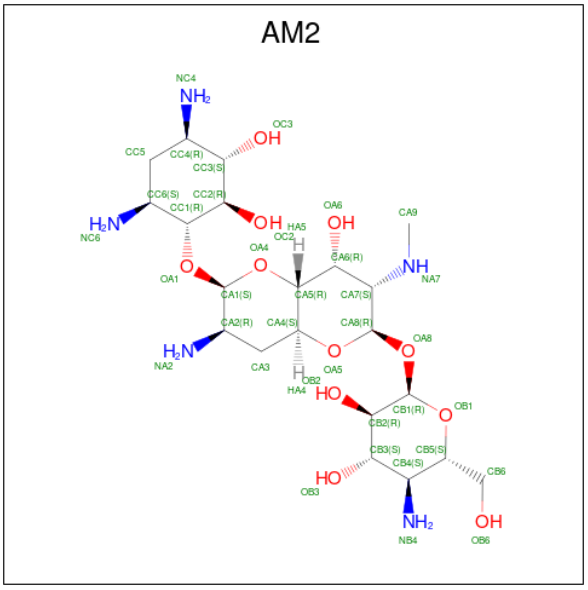
There are 5 unique types of molecules in this entry. The entry contains 1093 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 RNA chain called Bacterial 16 S Ribosomal RNA A Site Oligonucleotide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	A	23	486	218	86	160	22	0	0	0
1	B	22	466	209	84	152	21	0	0	0

- Molecule 2 is APRAMYCIN (three-letter code: AM2) (formula: $C_{21}H_{41}N_5O_{11}$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	37	21	5	11	0	0
2	B	1	37	21	5	11	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mg 1 1	0	0

- Molecule 4 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total K 1 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	34	Total O 34 34	0	0
5	B	31	Total O 31 31	0	0

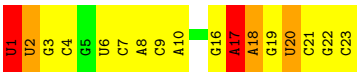
3 Residue-property plots (i)

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

Note EDS was not executed.

• Molecule 1: Bacterial 16 S Ribosomal RNA A Site Oligonucleotide

Chain A: 26% 52% 13% 9%



• Molecule 1: Bacterial 16 S Ribosomal RNA A Site Oligonucleotide

Chain B: 22% 39% 30%

4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	92.25Å 30.90Å 45.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.70	Depositor
% Data completeness (in resolution range)	99.0 (8.00-2.70)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.246 , 0.307	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1093	wwPDB-VP
Average B, all atoms (Å^2)	37.0	wwPDB-VP

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: AM2, K, MG

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	0.95	0/542	0.97	2/843 (0.2%)
1	B	0.82	0/520	0.97	1/809 (0.1%)
All	All	0.89	0/1062	0.97	3/1652 (0.2%)

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	3
1	B	0	3
All	All	0	6

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	17	A	N9-C1'-C2'	8.00	124.40	114.00
1	A	1	U	N1-C1'-C2'	6.94	123.03	114.00
1	B	25	U	N1-C1'-C2'	5.46	121.10	114.00

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1	U	Sidechain
1	A	17	A	Sidechain
1	A	20	U	Sidechain

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Mol	Chain	Res	Type	Group
1	B	38	U	Sidechain
1	B	43	U	Sidechain
1	B	45	G	Sidechain

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	486	0	250	20	0
1	B	466	0	240	24	0
2	A	37	0	41	5	0
2	B	37	0	41	4	0
3	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	34	0	0	5	0
5	B	31	0	0	2	0
All	All	1093	0	572	45	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 31.

All (45) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:41:A:OP1	2:B:150:AM2:HA7	1.64	0.96
1:B:28:G:H2'	1:B:29:U:H5"	1.62	0.81
1:B:28:G:C2'	1:B:29:U:H5"	2.14	0.77
1:B:40:A:C5'	2:B:150:AM2:HA32	2.21	0.71
1:A:22:G:O2'	1:A:23:C:H5'	1.91	0.70
1:B:28:G:C3'	1:B:29:U:H5"	2.25	0.65
1:B:40:A:H5'	2:B:150:AM2:HA32	1.80	0.64
1:B:29:U:H5'	1:B:29:U:H6	1.65	0.62
1:A:7:C:O2'	1:A:8:A:H5'	2.00	0.61
1:B:40:A:H5"	2:B:150:AM2:HA32	1.82	0.61
1:B:35:C:H2'	1:B:36:G:H8	1.67	0.60
1:B:44:C:H2'	1:B:45:G:H8	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:26:G:C2'	1:B:27:C:H5'	2.34	0.57
1:B:29:U:H2'	1:B:30:C:O4'	2.05	0.56
1:B:35:C:H2'	1:B:36:G:C8	2.42	0.55
1:B:26:G:O2'	1:B:27:C:H5'	2.07	0.54
1:A:22:G:OP2	5:A:167:HOH:O	2.19	0.53
1:A:1:U:C5'	1:A:2:U:H5"	2.38	0.53
1:A:16:G:H1'	5:A:169:HOH:O	2.08	0.53
1:B:25:U:H5"	5:B:175:HOH:O	2.08	0.52
1:B:25:U:O5'	1:B:26:G:H5'	2.10	0.52
1:A:4:C:H5	5:A:157:HOH:O	1.93	0.52
1:A:20:U:H2'	1:A:21:C:C6	2.45	0.51
1:A:20:U:O4	2:A:151:AM2:NC4	2.42	0.51
1:A:1:U:H5"	1:A:2:U:H5"	1.94	0.49
1:A:9:C:H2'	1:A:10:A:C8	2.48	0.49
1:A:18:A:OP2	2:A:151:AM2:NC6	2.45	0.49
1:B:36:G:O3'	5:B:154:HOH:O	2.20	0.49
1:A:21:C:H1'	5:A:155:HOH:O	2.11	0.48
1:B:44:C:H2'	1:B:45:G:C8	2.48	0.47
1:B:43:U:C4	1:B:44:C:N4	2.83	0.46
1:A:16:G:H21	2:A:151:AM2:HB61	1.80	0.46
2:A:151:AM2:OC2	2:A:151:AM2:HA1	2.16	0.46
1:A:22:G:P	5:A:167:HOH:O	2.74	0.45
1:A:8:A:O2'	1:A:9:C:H5'	2.18	0.44
1:A:19:G:N7	2:A:151:AM2:NC6	2.66	0.44
1:B:26:G:H2'	1:B:27:C:H5'	2.00	0.44
1:B:44:C:O2'	1:B:45:G:C5'	2.66	0.43
1:A:8:A:H2'	1:A:9:C:O5'	2.18	0.43
1:A:6:U:C4	1:A:7:C:C4	3.07	0.43
1:A:22:G:C2'	1:A:23:C:H5'	2.48	0.43
1:B:45:G:H2'	1:B:46:C:O5'	2.19	0.42
1:B:44:C:O2'	1:B:45:G:O5'	2.37	0.42
1:A:1:U:H5"	1:A:2:U:C5'	2.50	0.41
1:B:43:U:N3	1:B:44:C:N4	2.68	0.41

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

There are no protein molecules in this entry.

5.3.2 Protein sidechains (i)

There are no protein molecules in this entry.

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	23/23 (100%)	3 (13%)	2 (8%)
1	B	21/23 (91%)	7 (33%)	2 (9%)
All	All	44/46 (95%)	10 (22%)	4 (9%)

All (10) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	3	G
1	A	17	A
1	A	18	A
1	B	29	U
1	B	37	G
1	B	40	A
1	B	41	A
1	B	42	G
1	B	45	G
1	B	46	C

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1	U
1	A	2	U
1	B	41	A
1	B	44	C

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	$\#\|Z\| > 2$
2	AM2	B	150	-	40,40,40	1.35	5 (12%)	53,60,60	1.07	5 (9%)
2	AM2	A	151	-	40,40,40	1.77	8 (20%)	53,60,60	1.06	5 (9%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	AM2	B	150	-	-	0/12/84/84	0/4/4/4
2	AM2	A	151	-	-	3/12/84/84	0/4/4/4

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	151	AM2	CA8-CA7	4.48	1.60	1.53
2	A	151	AM2	CB5-CB4	3.79	1.59	1.52
2	A	151	AM2	OB1-CB1	3.44	1.50	1.41
2	B	150	AM2	OA1-CC1	3.35	1.52	1.43
2	A	151	AM2	OA5-CA8	3.03	1.49	1.41
2	A	151	AM2	OA4-CA5	3.03	1.48	1.44
2	B	150	AM2	OA4-CA5	2.68	1.48	1.44
2	B	150	AM2	OB1-CB1	2.65	1.48	1.41
2	B	150	AM2	CA6-CA5	2.53	1.59	1.52
2	A	151	AM2	CA7-NA7	2.52	1.51	1.47
2	B	150	AM2	OA4-CA1	2.44	1.48	1.41
2	A	151	AM2	CB3-CB4	2.32	1.56	1.53
2	A	151	AM2	CA5-CA4	2.05	1.58	1.52

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	150	AM2	OA1-CA1-CA2	3.23	113.64	108.23
2	A	151	AM2	OA1-CA1-CA2	3.18	113.55	108.23
2	A	151	AM2	OA8-CA8-CA7	2.64	112.80	108.24
2	A	151	AM2	OA8-CB1-CB2	2.55	114.70	108.10
2	B	150	AM2	CA1-OA1-CC1	2.40	123.91	117.96
2	B	150	AM2	CA1-OA4-CA5	2.21	116.61	113.06
2	A	151	AM2	CA9-NA7-CA7	2.13	117.49	114.38
2	B	150	AM2	OA8-CA8-CA7	2.12	111.90	108.24
2	B	150	AM2	OA8-CB1-CB2	2.02	113.34	108.10
2	A	151	AM2	CA8-CA7-NA7	2.01	114.60	111.00

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	151	AM2	OB1-CB5-CB6-OB6
2	A	151	AM2	CB4-CB5-CB6-OB6
2	A	151	AM2	CC2-CC1-OA1-CA1

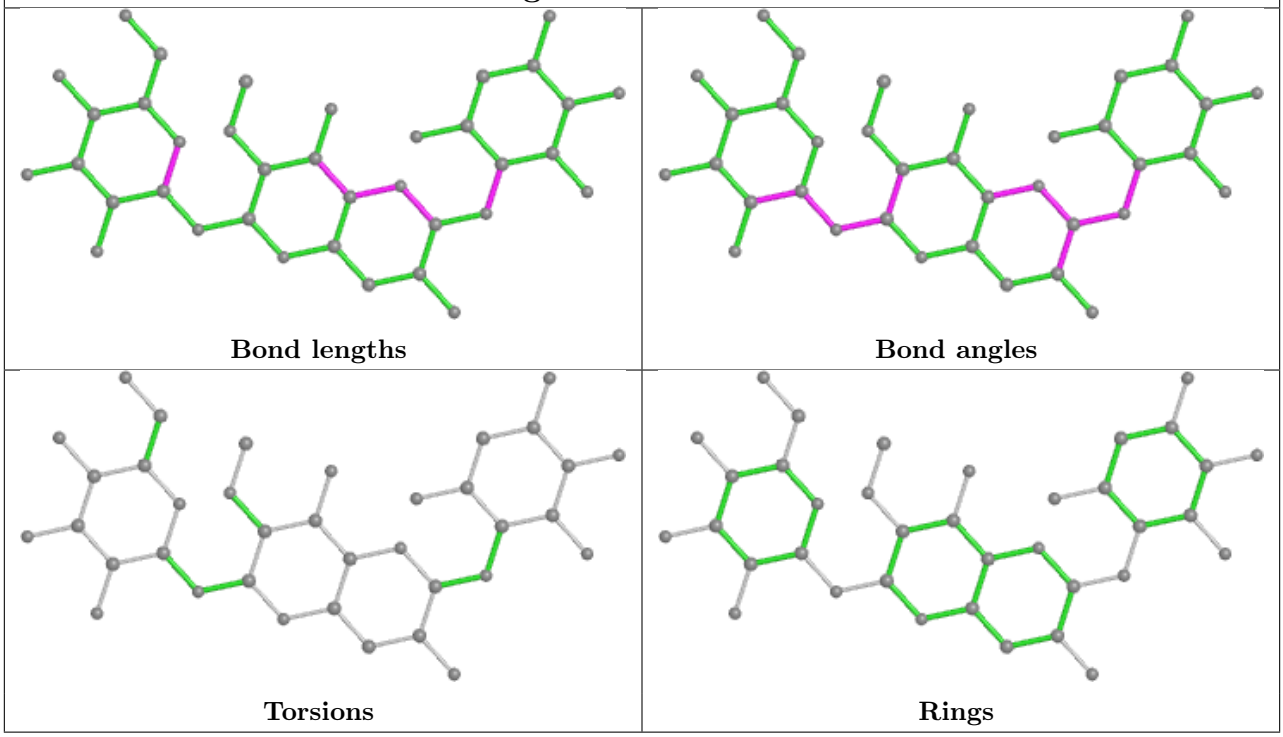
There are no ring outliers.

2 monomers are involved in 9 short contacts:

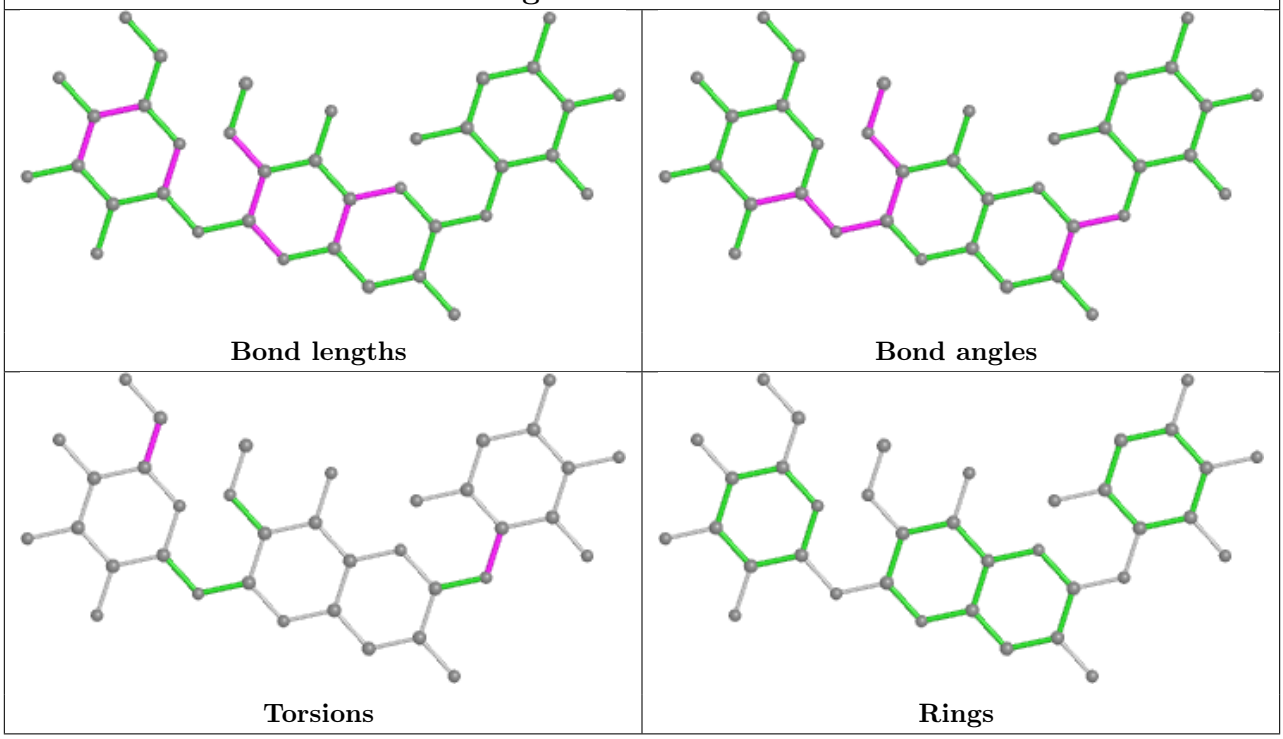
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	150	AM2	4	0
2	A	151	AM2	5	0

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 then 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 AM2 B 150



Ligand AM2 A 151



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 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.