



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2022 – 03:13 am GMT

PDB ID : 7OM1  
Title : Tankyrase 2 in complex with an inhibitor (OUL220)  
Authors : Sowa, S.T.; Lehtio, L.  
Deposited on : 2021-05-21  
Resolution : 1.70 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](mailto: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.

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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 : **FAILED**  
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) : 2.27

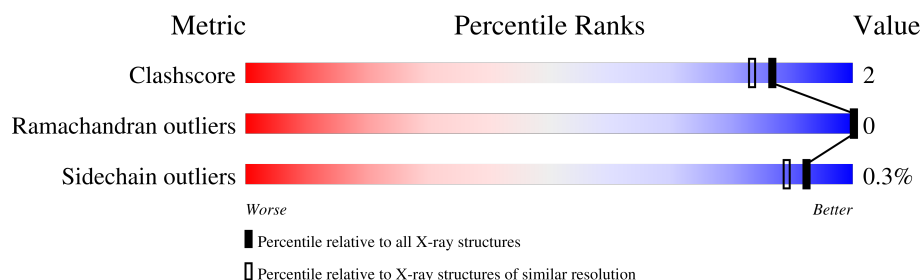
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.70 Å.


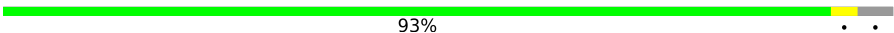


Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)

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  $\geq 3$ , 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  $\leq 5\%$ .

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	AAA	171	 91% 5%
1	BBB	171	 93%
2	A	48	 94%
2	B	48	 88% 10%

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 3811 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 protein called Poly [ADP-ribose] polymerase tankyrase-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	162	Total	C	N	O	S	0	3	0
			1323	830	245	240	8			
1	BBB	164	Total	C	N	O	S	0	2	0
			1317	824	242	242	9			

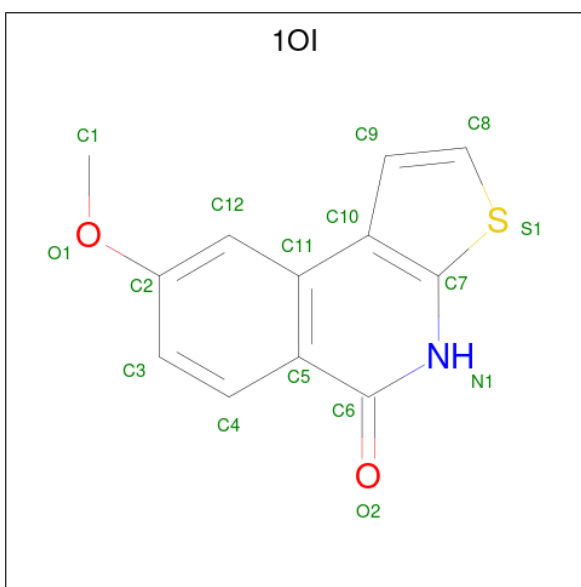
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	944	SER	-	expression tag	UNP Q9H2K2
AAA	945	MET	-	expression tag	UNP Q9H2K2
BBB	944	SER	-	expression tag	UNP Q9H2K2
BBB	945	MET	-	expression tag	UNP Q9H2K2

- Molecule 2 is a protein called Poly [ADP-ribose] polymerase tankyrase-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	46	Total	C	N	O	S	0	0	0
			367	235	64	66	2			
2	B	47	Total	C	N	O	S	0	1	0
			381	243	66	69	3			

- Molecule 3 is 8-methoxy-4 {H}-thieno[2,3-c]isoquinolin-5-one (three-letter code: 1OI) (formula: C<sub>12</sub>H<sub>9</sub>NO<sub>2</sub>S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	AAA	1	Total	C	N	O	S	0	0
			16	12	1	2	1		
3	BBB	1	Total	C	N	O	S	0	0
			16	12	1	2	1		

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

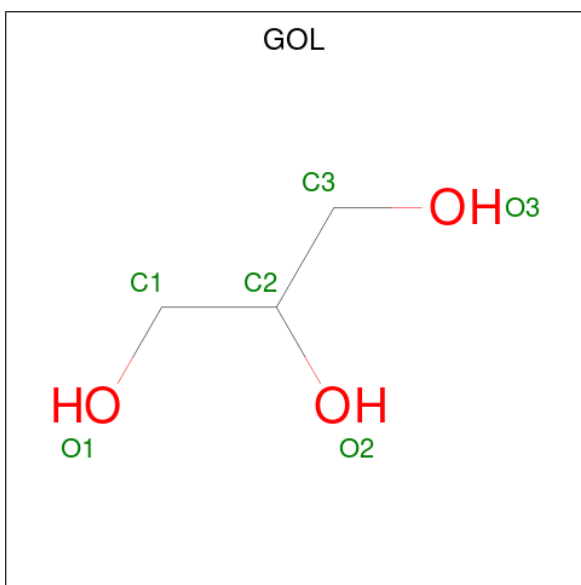
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	AAA	1	Total	Zn	0	0
			1	1		
4	BBB	1	Total	Zn	0	0
			1	1		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	AAA	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	BBB	1	Total	O	S	0	0
			5	4	1		
5	BBB	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			6	3	3		
6	BBB	1	Total	C	O	0	0
			6	3	3		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	AAA	161	Total	O	0	0
			161	161		
7	A	26	Total	O	0	0
			26	26		
7	BBB	148	Total	O	0	0
			148	148		
7	B	22	Total	O	0	0
			22	22		

### 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 failed to run properly.

- Molecule 1: Poly [ADP-ribose] polymerase tankyrase-2

Chain AAA:  91% 5%



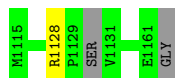
- Molecule 1: Poly [ADP-ribose] polymerase tankyrase-2

Chain BBB:  93%




- Molecule 2: Poly [ADP-ribose] polymerase tankyrase-2

Chain A:  94%



- Molecule 2: Poly [ADP-ribose] polymerase tankyrase-2

Chain B:  88% 10%



## 4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	91.21Å 98.30Å 118.27Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.43 – 1.70	Depositor
% Data completeness (in resolution range)	99.9 (45.43-1.70)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.04 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, $R_{free}$	0.182 , 0.197	Depositor
Wilson B-factor (Å <sup>2</sup> )	27.7	Xtriage
Anisotropy	0.527	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3811	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.58% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



## 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: 1OI, GOL, SO4, ZN

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	AAA	0.63	0/1357	0.72	0/1818
1	BBB	0.64	0/1351	0.72	0/1813
2	A	0.61	0/378	0.69	0/514
2	B	0.61	0/393	0.68	0/535
All	All	0.63	0/3479	0.71	0/4680

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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	AAA	1323	0	1272	9	0
1	BBB	1317	0	1247	4	0
2	A	367	0	351	2	0
2	B	381	0	365	4	0
3	AAA	16	0	0	0	0
3	BBB	16	0	0	0	0
4	AAA	1	0	0	0	0
4	BBB	1	0	0	0	0
5	A	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	AAA	5	0	0	0	0
5	BBB	10	0	0	0	0
6	A	6	0	8	0	0
6	BBB	6	0	8	0	0
7	A	26	0	0	0	0
7	AAA	161	0	0	5	0
7	B	22	0	0	0	0
7	BBB	148	0	0	0	0
All	All	3811	0	3251	14	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 2.

The worst 5 of 14 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:AAA:1108[B]:LEU:HD21	7:AAA:1397:HOH:O	1.20	1.34
1:AAA:1108[B]:LEU:CD2	7:AAA:1397:HOH:O	1.83	1.02
2:B:1118:SER:HG	2:B:1142:TYR:HD2	1.55	0.54
1:AAA:1108[B]:LEU:CG	7:AAA:1397:HOH:O	2.35	0.52
1:AAA:1108[A]:LEU:HD21	2:A:1128:ARG:HD2	1.93	0.50

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	AAA	163/171 (95%)	160 (98%)	3 (2%)	0	100	100
1	BBB	164/171 (96%)	162 (99%)	2 (1%)	0	100	100
2	A	42/48 (88%)	41 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	46/48 (96%)	45 (98%)	1 (2%)	0	100	100
All	All	415/438 (95%)	408 (98%)	7 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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 X-ray entries followed by that with respect to entries of similar resolution.

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	AAA	141/146 (97%)	140 (99%)	1 (1%)	84	77
1	BBB	139/146 (95%)	139 (100%)	0	100	100
2	A	38/39 (97%)	38 (100%)	0	100	100
2	B	40/39 (103%)	40 (100%)	0	100	100
All	All	358/370 (97%)	357 (100%)	1 (0%)	92	89

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	1037	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 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
6	GOL	A	1201	-	5,5,5	0.10	0	5,5,5	0.27	0
5	SO4	BBB	1205	-	4,4,4	0.40	0	6,6,6	0.08	0
3	1OI	BBB	1202	-	15,18,18	1.03	1 (6%)	19,26,26	2.21	2 (10%)
6	GOL	BBB	1201	-	5,5,5	0.08	0	5,5,5	0.27	0
5	SO4	AAA	1203	-	4,4,4	0.47	0	6,6,6	0.14	0
5	SO4	BBB	1204	-	4,4,4	0.40	0	6,6,6	0.18	0
3	1OI	AAA	1201	-	15,18,18	1.07	2 (13%)	19,26,26	2.23	2 (10%)
5	SO4	A	1202	-	4,4,4	0.39	0	6,6,6	0.08	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	1OI	AAA	1201	-	-	0/2/2/2	0/3/3/3
6	GOL	BBB	1201	-	-	2/4/4/4	-
6	GOL	A	1201	-	-	2/4/4/4	-
3	1OI	BBB	1202	-	-	0/2/2/2	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	BBB	1202	1OI	C6-N1	2.94	1.38	1.33
3	AAA	1201	1OI	C6-N1	2.88	1.38	1.33
3	AAA	1201	1OI	C7-C10	-2.01	1.39	1.42

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	AAA	1201	1OI	C5-C6-N1	-8.45	118.51	124.40
3	BBB	1202	1OI	C5-C6-N1	-8.43	118.53	124.40
3	AAA	1201	1OI	C7-N1-C6	3.42	121.99	116.88
3	BBB	1202	1OI	C7-N1-C6	3.28	121.78	116.88

There are no chirality outliers.

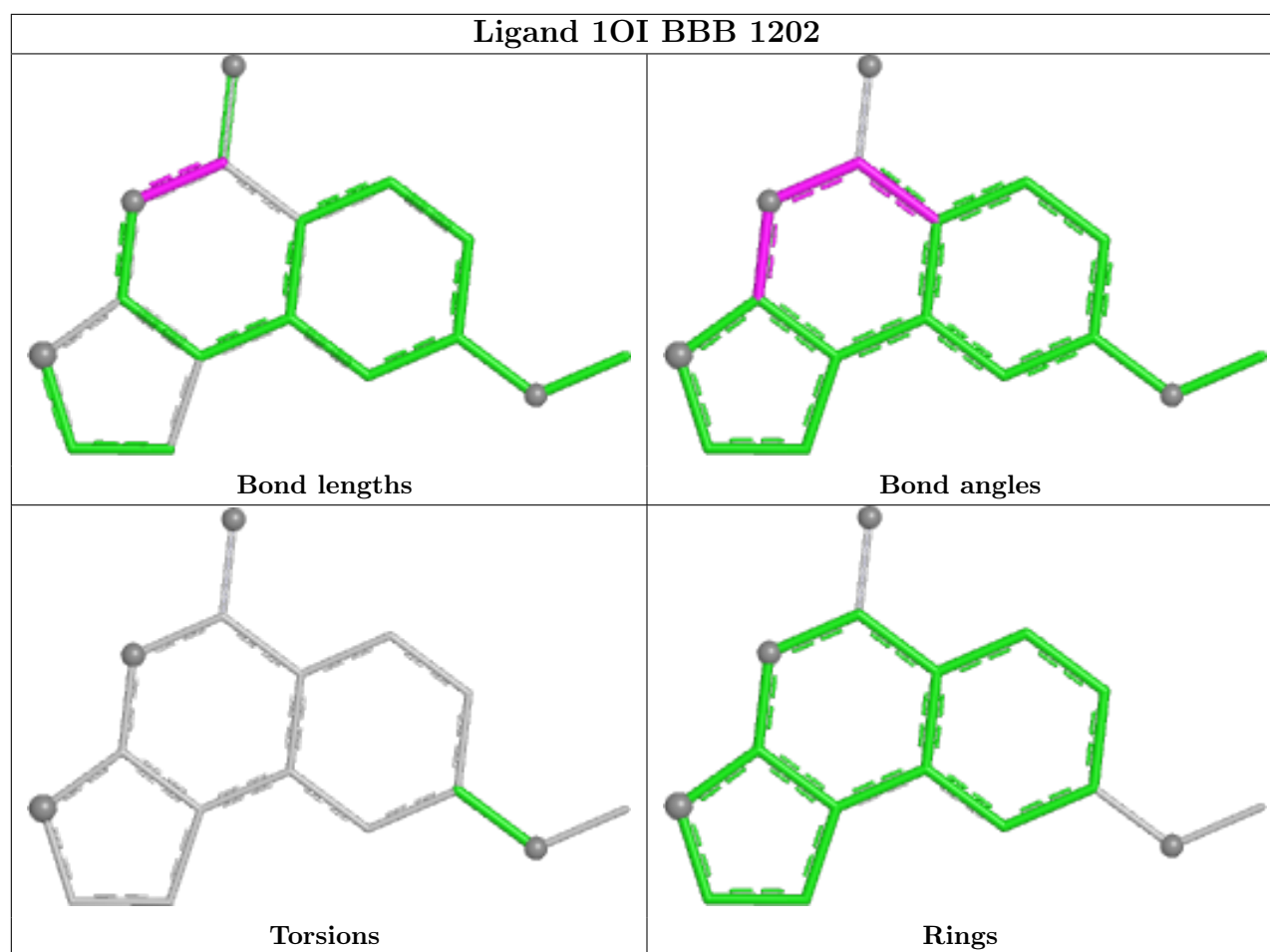
All (4) torsion outliers are listed below:

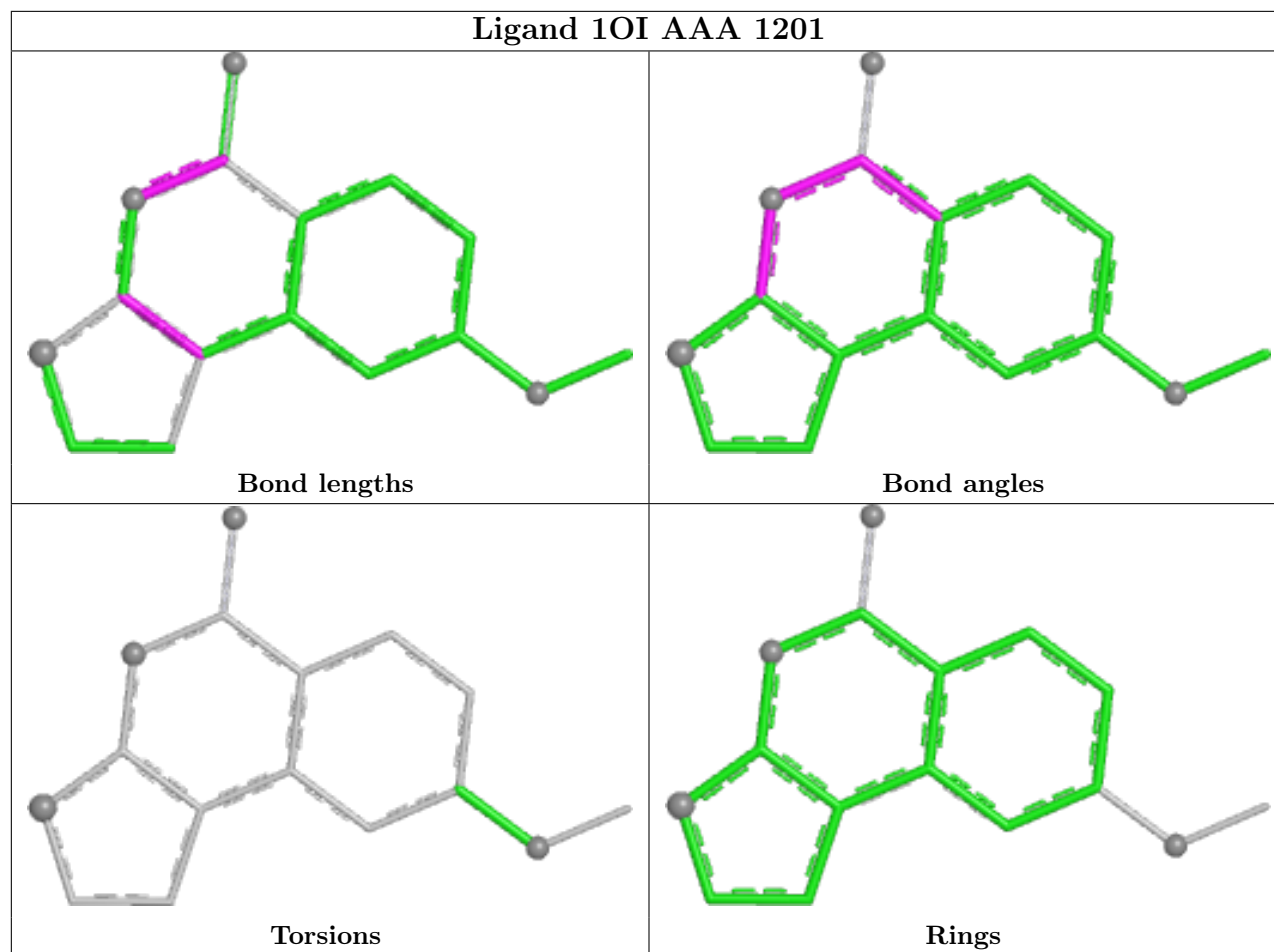
Mol	Chain	Res	Type	Atoms
6	A	1201	GOL	O1-C1-C2-O2
6	A	1201	GOL	O1-C1-C2-C3
6	BBB	1201	GOL	C1-C2-C3-O3
6	BBB	1201	GOL	O2-C2-C3-O3

There are no ring outliers.

No monomer is involved in short contacts.

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





## 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 failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

### 6.3 Carbohydrates [i](#)

EDS failed to run properly - this section is therefore empty.

### 6.4 Ligands [i](#)

EDS failed to run properly - this section is therefore empty.

### 6.5 Other polymers [i](#)

EDS failed to run properly - this section is therefore empty.