

Full wwPDB X-ray Structure Validation Report (i)

Feb 25, 2024 – 03:58 PM EST

PDB ID : 5JW0

Title : Crystal structure of mithramycin analogue MTM SA-Phe in complex with a

10-mer DNA AGGGTACCCT

Authors: Hou, C.; Rohr, J.; Tsodikov, O.V.

Deposited on : 2016-05-11

Resolution : 2.40 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) : 1.13

EDS : 2.36

buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

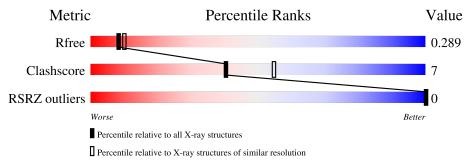
Validation Pipeline (wwPDB-VP) : 2.36

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 2.40 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	Similar resolution				
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$				
R_{free}	130704	3907 (2.40-2.40)				
Clashscore	141614	4398 (2.40-2.40)				
RSRZ outliers	127900	3811 (2.40-2.40)				

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% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain					
1	A	10	80%	20%				
1	В	10	80%	20%				



2 Entry composition (i)

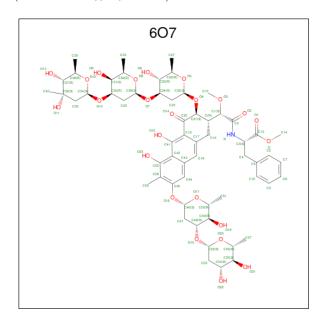
There are 4 unique types of molecules in this entry. The entry contains 759 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 DNA chain called DNA (5'-D(P*AP*GP*GP*GP*TP*AP*CP*CP*T)-3').

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	10	Total	С	N	О	Р	0	0	0
1	1 A	10	205	97	38	60	10	0		U
1	D	10	Total	С	N	О	Р	0	0	0
1	Б	10	202	97	38	58	9	U		U

• Molecule 2 is Plicamycin, mithramycin analogue MTM SA-Phe (three-letter code: 6O7) (formula: C₅₉H₈₁NO₂₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2 A	Λ	1	Total	С	N	О	0	0	
	A	1	84	59	1	24	0	0	
2	Λ	1	Total	С	N	О	0	0	
	Α	1	84	59 1 24	24	0	0		
9	Λ	1	Total	С	N	О	0	0	
2	A	A 1	84	59	1	24	0	0	



 $Continued\ from\ previous\ page...$

Mol	Chain	Residues	A	Ator	ns		ZeroOcc	AltConf
2	R	1	Total	С	N	О	0	0
	Б	1	84	59	1	24		0

• Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	5	Total Zn 5 5	0	0
3	В	1	Total Zn 1 1	0	0

• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	7	Total O 7 7	0	0
4	В	3	Total O 3 3	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 and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: DNA (5'-D(P*AP*GP*GP*GP*TP*AP*CP*CP*CP*T)-3')

Chain A: 80% 20%



• Molecule 1: DNA (5'-D(P*AP*GP*GP*GP*TP*AP*CP*CP*T)-3')

Chain B: 80% 20%





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants	50.56Å 50.56Å 125.24Å	Donogitor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 - 2.40	Depositor
resolution (A)	39.34 - 2.40	EDS
% Data completeness	98.2 (40.00-2.40)	Depositor
(in resolution range)	98.3 (39.34-2.40)	EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.55 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.8.0071	Depositor
P.P.	0.262 , 0.289	Depositor
R, R_{free}	0.266 , 0.289	DCC
R_{free} test set	373 reflections (5.55%)	wwPDB-VP
Wilson B-factor (Å ²)	49.3	Xtriage
Anisotropy	0.118	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.39, 36.1	EDS
L-test for twinning ²	$ < L > = 0.50, < L^2> = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	759	wwPDB-VP
Average B, all atoms $(Å^2)$	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.13% of the height of the origin peak. No significant pseudotranslation is detected.

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



¹Intensities estimated from amplitudes.

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: 6O7, 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	Bond angles		
MIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5		
1	A	0.45	0/229	0.70	0/351		
1	В	0.45	0/226	0.71	0/347		
All	All	0.45	0/455	0.70	0/698		

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	A	205	0	113	1	0
1	В	202	0	114	2	0
2	A	252	0	0	2	0
2	В	84	0	0	3	0
3	A	5	0	0	0	0
3	В	1	0	0	0	0
4	A	7	0	0	0	0
4	В	3	0	0	0	0
All	All	759	0	227	7	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 7.



All (7) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash	
Atom-1	Atom-2	${\rm distance} \ ({\rm \AA})$	$overlap(ext{Å})$	
2:B:101:6O7:O2	2:B:101:6O7:C15	2.44	0.65	
1:B:3:DA:H2'	1:B:4:DC:C6	2.35	0.62	
1:A:6:DG:H2'	1:A:7:DG:C8	2.48	0.49	
2:A:102:6O7:O15	2:A:102:6O7:O23	2.34	0.43	
2:B:101:6O7:O2	2:B:101:6O7:C4	2.64	0.42	
1:B:3:DA:N3	2:B:101:6O7:O11	2.53	0.42	
2:A:101:6O7:O23	2:A:101:6O7:O15	2.37	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)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.



5.6 Ligand geometry (i)

Of 10 ligands modelled in this entry, 6 are monoatomic - leaving 4 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	Tuno	Cl !	Das	Res Link	Bo	ond leng	ths	Bond angles		
MIOI	Type	Chain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	607	A	103	3	91,92,92	0.92	4 (4%)	128,138,138	1.46	20 (15%)
2	607	В	101	3	91,92,92	0.98	2 (2%)	128,138,138	1.49	20 (15%)
2	607	A	102	3	91,92,92	1.00	4 (4%)	128,138,138	1.24	13 (10%)
2	607	A	101	3	91,92,92	0.99	3 (3%)	128,138,138	1.34	17 (13%)

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	607	A	103	3	-	3/44/143/143	0/9/9/9
2	607	В	101	3	-	11/44/143/143	0/9/9/9
2	607	A	102	3	-	4/44/143/143	0/9/9/9
2	607	A	101	3	-	2/44/143/143	0/9/9/9

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(A)	Ideal(A)
2	A	101	607	O-C13	5.28	1.46	1.33
2	В	101	607	O-C13	5.20	1.45	1.33
2	A	102	607	O-C13	5.19	1.45	1.33
2	A	103	607	O-C13	4.90	1.45	1.33
2	A	101	607	O11-C36	-3.19	1.39	1.44
2	В	101	607	O14-C20	3.15	1.26	1.22
2	A	103	607	C19-C20	2.38	1.52	1.46
2	A	101	607	C44-C45	2.28	1.40	1.36
2	A	102	607	O14-C20	2.27	1.25	1.22
2	A	102	607	C44-C45	2.22	1.40	1.36



 $Continued\ from\ previous\ page...$

Mol	Chain	Res	Type	Atoms	${f Z}$	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(ext{\AA})$
2	A	103	607	O14-C20	2.10	1.25	1.22
2	A	102	607	C19-C20	2.05	1.51	1.46
2	A	103	607	C44-C45	2.01	1.40	1.36

All (70) bond angle outliers are listed below:

2 A 101 607 O16-C45-C58 6.22 120.15 114.19 2 A 103 607 O16-C45-C58 5.63 119.58 114.19 2 B 101 607 O16-C45-C58 5.05 119.02 114.19 2 A 103 607 C41-C19-C17 -4.50 117.03 119.77 2 A 102 607 O16-C45-C58 4.32 118.33 114.19 2 B 101 607 O19-C52-C53 4.23 116.58 108.41 2 B 101 607 C4-C3-N 4.14 119.50 110.79 2 B 101 607 C-C1-C2 3.89 119.19 111.55 2 A 103 607 O-C13-C3 3.84 121.35 111.52 2 A 102 607 O-C13-C3 3.64 120.84 111.52 2 A 102 <	Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\mathrm{Ideal}(^{o})$
2 B 101 607 O16-C45-C58 5.05 119.02 114.19 2 A 103 607 C41-C19-C17 -4.50 117.03 119.77 2 A 102 607 O16-C45-C58 4.32 118.33 114.19 2 B 101 607 O19-C52-C53 4.23 116.58 108.41 2 B 101 607 C4-C3-N 4.14 119.50 110.79 2 B 101 607 C-C1-C2 3.89 119.19 111.55 2 A 101 607 O-C13-C3 3.84 121.35 111.52 2 A 103 607 O-C13-C3 3.64 120.84 111.52 2 A 102 607 O-C13-C3 3.64 120.84 111.52 2 A 102 607 O-C13-C3 3.47 120.40 111.52 2 A 102 607	2	A	101	607	O16-C45-C58	6.22	120.15	114.19
2 A 103 6O7 C41-C19-C17 -4.50 117.03 119.77 2 A 102 6O7 O16-C45-C58 4.32 118.33 114.19 2 B 101 6O7 O19-C52-C53 4.23 116.58 108.41 2 B 101 6O7 C4-C3-N 4.14 119.50 110.79 2 B 101 6O7 C-C1-C2 3.89 119.19 111.55 2 A 101 6O7 O-C13-C3 3.84 121.35 111.52 2 A 103 6O7 O-C13-C3 3.77 121.16 111.52 2 A 102 6O7 O-C13-C3 3.64 120.84 111.52 2 A 102 6O7 C-G13-C3 3.47 120.40 111.52 2 B 101 6O7 C-G13-C13 3.21 102.40 111.52 2 A 102 6O7 </td <td>2</td> <td>A</td> <td>103</td> <td>607</td> <td>O16-C45-C58</td> <td>5.63</td> <td>119.58</td> <td>114.19</td>	2	A	103	607	O16-C45-C58	5.63	119.58	114.19
2 A 102 607 O16-C45-C58 4.32 118.33 114.19 2 B 101 607 O19-C52-C53 4.23 116.58 108.41 2 B 101 607 C4-C3-N 4.14 119.50 110.79 2 B 101 607 C-C1-C2 3.89 119.19 111.55 2 A 101 607 O-C13-C3 3.84 121.35 111.52 2 A 103 607 O-C13-C3 3.64 120.84 111.52 2 A 102 607 O-C13-C3 3.64 120.84 111.52 2 A 102 607 O-C13-C3 3.47 120.40 111.52 2 B 101 607 O-C13-C3 3.47 120.40 111.52 2 A 102 607 O-C13-C1 3.21 102.40 111.52 2 A 102 607	2	В	101	607	O16-C45-C58	5.05	119.02	114.19
2 B 101 607 O19-C52-C53 4.23 116.58 108.41 2 B 101 607 C4-C3-N 4.14 119.50 110.79 2 B 101 607 C-C1-C2 3.89 119.19 111.55 2 A 101 607 O-C13-C3 3.84 121.35 111.52 2 A 103 607 O-C13-C3 3.64 120.84 111.52 2 A 102 607 O-C13-C3 3.64 120.84 111.52 2 B 101 607 C16-C17-C19 3.59 124.14 118.03 2 B 101 607 O-C13-C3 3.47 120.40 111.52 2 A 102 607 O-C13-C13 3.21 102.40 111.52 2 A 102 607 C4-C3-C13 3.21 102.40 110.37 2 B 101 607	2	A	103	607	C41-C19-C17	-4.50	117.03	119.77
2 B 101 607 C4-C3-N 4.14 119.50 110.79 2 B 101 607 C-C1-C2 3.89 119.19 111.55 2 A 101 607 O-C13-C3 3.84 121.35 111.52 2 A 103 607 O-C13-C3 3.77 121.16 111.52 2 A 102 607 O-C13-C3 3.64 120.84 111.52 2 B 101 607 C16-C17-C19 3.59 124.14 118.03 2 B 101 607 O-C13-C3 3.47 120.40 111.52 2 A 102 607 O-C13-C13 -3.21 102.40 111.52 2 A 102 607 C4-C3-C13 -3.21 102.40 110.37 2 B 101 607 C4-C3-C13 -3.21 102.40 110.37 2 A 102 607 <td>2</td> <td>A</td> <td>102</td> <td>607</td> <td>O16-C45-C58</td> <td>4.32</td> <td>118.33</td> <td>114.19</td>	2	A	102	607	O16-C45-C58	4.32	118.33	114.19
2 B 101 607 C-C1-C2 3.89 119.19 111.55 2 A 101 607 O-C13-C3 3.84 121.35 111.52 2 A 103 607 O-C13-C3 3.77 121.16 111.52 2 A 102 607 O-C13-C3 3.64 120.84 111.52 2 B 101 607 C16-C17-C19 3.59 124.14 118.03 2 B 101 607 O-C13-C3 3.47 120.40 111.52 2 A 102 607 O-C13-O1 -3.28 117.43 123.84 2 B 101 607 C4-C3-C13 -3.21 102.40 110.37 2 B 101 607 C4-C3-C13 -3.21 102.40 110.37 2 B 101 607 C16-C17-C18 -3.15 115.62 121.05 2 A 102 607	2	В	101	607	O19-C52-C53	4.23	116.58	108.41
2 A 101 6O7 O-C13-C3 3.84 121.35 111.52 2 A 103 6O7 O-C13-C3 3.77 121.16 111.52 2 A 102 6O7 O-C13-C3 3.64 120.84 111.52 2 B 101 6O7 C16-C17-C19 3.59 124.14 118.03 2 B 101 6O7 O-C13-C3 3.47 120.40 111.52 2 A 102 6O7 O-C13-O1 -3.28 117.43 123.84 2 B 101 6O7 C4-C3-C13 -3.21 102.40 110.37 2 B 101 6O7 C16-C17-C18 -3.15 115.62 121.05 2 A 102 6O7 C60-C42-C43 3.12 120.90 118.11 2 B 101 6O7 O5-C26-C25 -3.03 104.08 109.52 2 A 103 <t< td=""><td>2</td><td>В</td><td>101</td><td>607</td><td>C4-C3-N</td><td>4.14</td><td>119.50</td><td>110.79</td></t<>	2	В	101	607	C4-C3-N	4.14	119.50	110.79
2 A 103 6O7 O-C13-C3 3.77 121.16 111.52 2 A 102 6O7 O-C13-C3 3.64 120.84 111.52 2 B 101 6O7 C16-C17-C19 3.59 124.14 118.03 2 B 101 6O7 O-C13-C3 3.47 120.40 111.52 2 A 102 6O7 O-C13-O1 -3.28 117.43 123.84 2 B 101 6O7 C4-C3-C13 -3.21 102.40 110.37 2 B 101 6O7 C4-C3-C13 -3.15 115.62 121.05 2 A 102 6O7 C60-C42-C43 3.12 120.90 118.11 2 B 101 6O7 O3-C1-C2 -3.05 105.16 111.51 2 A 103 6O7 O-C13-O1 -3.01 117.95 123.84 2 A 103 6	2	В	101	607	C-C1-C2	3.89	119.19	111.55
2 A 102 6O7 O-C13-C3 3.64 120.84 111.52 2 B 101 6O7 C16-C17-C19 3.59 124.14 118.03 2 B 101 6O7 O-C13-C3 3.47 120.40 111.52 2 A 102 6O7 O-C13-O1 -3.28 117.43 123.84 2 B 101 6O7 C4-C3-C13 -3.21 102.40 110.37 2 B 101 6O7 C4-C3-C13 -3.21 102.40 110.37 2 B 101 6O7 C4-C3-C13 -3.21 102.40 110.37 2 B 101 6O7 C16-C17-C18 -3.15 115.62 121.05 2 A 102 6O7 C60-C42-C43 3.12 120.90 118.11 2 A 103 6O7 O5-C26-C25 -3.03 104.08 109.52 2 A 103	2	A	101	607	O-C13-C3	3.84	121.35	111.52
2 B 101 6O7 C16-C17-C19 3.59 124.14 118.03 2 B 101 6O7 O-C13-C3 3.47 120.40 111.52 2 A 102 6O7 O-C13-O1 -3.28 117.43 123.84 2 B 101 6O7 C4-C3-C13 -3.21 102.40 110.37 2 B 101 6O7 C16-C17-C18 -3.15 115.62 121.05 2 A 102 6O7 C60-C42-C43 3.12 120.90 118.11 2 B 101 6O7 C3-C1-C2 -3.05 105.16 111.51 2 A 103 6O7 O5-C26-C25 -3.03 104.08 109.52 2 A 103 6O7 O-C13-O1 -3.01 117.95 123.84 2 A 103 6O7 C16-C17-C18 -3.00 115.88 121.05 2 A 101	2	A	103	607	O-C13-C3	3.77	121.16	111.52
2 B 101 6O7 O-C13-C3 3.47 120.40 111.52 2 A 102 6O7 O-C13-O1 -3.28 117.43 123.84 2 B 101 6O7 C4-C3-C13 -3.21 102.40 110.37 2 B 101 6O7 C16-C17-C18 -3.15 115.62 121.05 2 A 102 6O7 C60-C42-C43 3.12 120.90 118.11 2 B 101 6O7 C3-C1-C2 -3.05 105.16 111.51 2 A 103 6O7 O5-C26-C25 -3.03 104.08 109.52 2 A 103 6O7 O5-C26-C25 -3.03 104.08 109.52 2 A 103 6O7 O5-C26-C25 -3.03 104.08 109.52 2 A 103 6O7 C16-C17-C18 -3.00 115.88 121.05 2 A 101	2	A	102	607	O-C13-C3	3.64	120.84	111.52
2 A 102 6O7 O-C13-O1 -3.28 117.43 123.84 2 B 101 6O7 C4-C3-C13 -3.21 102.40 110.37 2 B 101 6O7 C16-C17-C18 -3.15 115.62 121.05 2 A 102 6O7 C60-C42-C43 3.12 120.90 118.11 2 A 102 6O7 C60-C42-C43 3.12 120.90 118.11 2 B 101 6O7 O3-C1-C2 -3.05 105.16 111.51 2 A 103 6O7 O5-C26-C25 -3.03 104.08 109.52 2 A 103 6O7 O-C13-O1 -3.01 117.95 123.84 2 A 103 6O7 C16-C17-C18 -3.00 115.88 121.05 2 A 101 6O7 C45-C58-C60 2.97 120.39 116.78 2 A 103	2	В	101	607	C16-C17-C19	3.59	124.14	118.03
2 B 101 6O7 C4-C3-C13 -3.21 102.40 110.37 2 B 101 6O7 C16-C17-C18 -3.15 115.62 121.05 2 A 102 6O7 C60-C42-C43 3.12 120.90 118.11 2 B 101 6O7 O3-C1-C2 -3.05 105.16 111.51 2 A 103 6O7 O5-C26-C25 -3.03 104.08 109.52 2 A 103 6O7 O-C13-O1 -3.01 117.95 123.84 2 A 103 6O7 C16-C17-C18 -3.00 115.88 121.05 2 A 101 6O7 C45-C58-C60 2.97 120.39 116.78 2 A 101 6O7 C45-C58-C60 2.89 120.30 116.78 2 A 103 6O7 C16-C17-C19 2.78 122.76 118.03 2 A 103	2	В	101	607	O-C13-C3	3.47	120.40	111.52
2 B 101 6O7 C16-C17-C18 -3.15 115.62 121.05 2 A 102 6O7 C60-C42-C43 3.12 120.90 118.11 2 B 101 6O7 O3-C1-C2 -3.05 105.16 111.51 2 A 103 6O7 O5-C26-C25 -3.03 104.08 109.52 2 A 103 6O7 O-C13-O1 -3.01 117.95 123.84 2 A 103 6O7 C16-C17-C18 -3.00 115.88 121.05 2 A 101 6O7 C45-C58-C60 2.97 120.39 116.78 2 A 103 6O7 C45-C58-C60 2.89 120.30 116.78 2 A 103 6O7 C45-C58-C60 2.87 120.27 116.78 2 A 103 6O7 C16-C17-C19 2.78 122.76 118.03 2 A 103 <td>2</td> <td>A</td> <td>102</td> <td>607</td> <td>O-C13-O1</td> <td>-3.28</td> <td>117.43</td> <td>123.84</td>	2	A	102	607	O-C13-O1	-3.28	117.43	123.84
2 A 102 607 C60-C42-C43 3.12 120.90 118.11 2 B 101 607 O3-C1-C2 -3.05 105.16 111.51 2 A 103 607 O5-C26-C25 -3.03 104.08 109.52 2 A 103 607 O-C13-O1 -3.01 117.95 123.84 2 A 103 607 C16-C17-C18 -3.00 115.88 121.05 2 A 101 607 C45-C58-C60 2.97 120.39 116.78 2 A 103 607 C45-C58-C60 2.89 120.30 116.78 2 B 101 607 C45-C58-C60 2.87 120.27 116.78 2 A 103 607 C16-C17-C19 2.78 122.76 118.03 2 A 103 607 O17-C46-C47 -2.70 106.80 110.87 2 A 103 <td>2</td> <td>В</td> <td>101</td> <td>607</td> <td>C4-C3-C13</td> <td>-3.21</td> <td>102.40</td> <td>110.37</td>	2	В	101	607	C4-C3-C13	-3.21	102.40	110.37
2 B 101 6O7 O3-C1-C2 -3.05 105.16 111.51 2 A 103 6O7 O5-C26-C25 -3.03 104.08 109.52 2 A 103 6O7 O-C13-O1 -3.01 117.95 123.84 2 A 103 6O7 C16-C17-C18 -3.00 115.88 121.05 2 A 101 6O7 C45-C58-C60 2.97 120.39 116.78 2 A 103 6O7 C45-C58-C60 2.89 120.30 116.78 2 B 101 6O7 C45-C58-C60 2.89 120.30 116.78 2 A 103 6O7 C16-C17-C19 2.78 122.76 118.03 2 A 103 6O7 O17-C46-C47 -2.70 106.80 110.87 2 A 103 6O7 C16-C17-C19 2.65 122.55 118.03 2 A 101 <td>2</td> <td>В</td> <td>101</td> <td>607</td> <td>C16-C17-C18</td> <td>-3.15</td> <td>115.62</td> <td>121.05</td>	2	В	101	607	C16-C17-C18	-3.15	115.62	121.05
2 A 103 6O7 O5-C26-C25 -3.03 104.08 109.52 2 A 103 6O7 O-C13-O1 -3.01 117.95 123.84 2 A 103 6O7 C16-C17-C18 -3.00 115.88 121.05 2 A 101 6O7 C45-C58-C60 2.97 120.39 116.78 2 A 103 6O7 C45-C58-C60 2.89 120.30 116.78 2 B 101 6O7 C45-C58-C60 2.89 120.30 116.78 2 A 103 6O7 C45-C58-C60 2.87 120.27 116.78 2 A 103 6O7 C16-C17-C19 2.78 122.76 118.03 2 A 103 6O7 O17-C46-C47 -2.70 106.80 110.87 2 A 103 6O7 O19-C52-C53 2.68 113.58 108.41 2 A 104 </td <td>2</td> <td>A</td> <td>102</td> <td>607</td> <td>C60-C42-C43</td> <td>3.12</td> <td>120.90</td> <td>118.11</td>	2	A	102	607	C60-C42-C43	3.12	120.90	118.11
2 A 103 6O7 O-C13-O1 -3.01 117.95 123.84 2 A 103 6O7 C16-C17-C18 -3.00 115.88 121.05 2 A 101 6O7 C45-C58-C60 2.97 120.39 116.78 2 A 103 6O7 C45-C58-C60 2.89 120.30 116.78 2 B 101 6O7 C45-C58-C60 2.87 120.27 116.78 2 A 103 6O7 C16-C17-C19 2.78 122.76 118.03 2 A 103 6O7 O17-C46-C47 -2.70 106.80 110.87 2 A 103 6O7 O19-C52-C53 2.68 113.58 108.41 2 A 101 6O7 C16-C17-C19 2.65 122.55 118.03 2 A 102 6O7 O14-C20-C19 -2.62 118.75 122.78 2 A 102<	2	В	101	607	O3-C1-C2	-3.05	105.16	111.51
2 A 103 6O7 C16-C17-C18 -3.00 115.88 121.05 2 A 101 6O7 C45-C58-C60 2.97 120.39 116.78 2 A 103 6O7 C45-C58-C60 2.89 120.30 116.78 2 B 101 6O7 C45-C58-C60 2.87 120.27 116.78 2 A 103 6O7 C16-C17-C19 2.78 122.76 118.03 2 A 103 6O7 O17-C46-C47 -2.70 106.80 110.87 2 A 103 6O7 O19-C52-C53 2.68 113.58 108.41 2 A 101 6O7 C16-C17-C19 2.65 122.55 118.03 2 A 101 6O7 C16-C17-C19 2.62 118.75 122.78 2 A 102 6O7 C45-C58-C60 2.60 119.94 116.78 2 A 101	2	A	103	607	O5-C26-C25	-3.03	104.08	109.52
2 A 101 6O7 C45-C58-C60 2.97 120.39 116.78 2 A 103 6O7 C45-C58-C60 2.89 120.30 116.78 2 B 101 6O7 C45-C58-C60 2.87 120.27 116.78 2 A 103 6O7 C16-C17-C19 2.78 122.76 118.03 2 A 103 6O7 O17-C46-C47 -2.70 106.80 110.87 2 A 103 6O7 O19-C52-C53 2.68 113.58 108.41 2 A 101 6O7 C16-C17-C19 2.65 122.55 118.03 2 A 101 6O7 C16-C17-C19 2.62 118.75 122.78 2 A 102 6O7 C45-C58-C60 2.60 119.94 116.78 2 A 101 6O7 O7-C24-C23 -2.59 104.62 109.62 2 A 101<	2	A	103	607	O-C13-O1	-3.01	117.95	123.84
2 A 103 6O7 C45-C58-C60 2.89 120.30 116.78 2 B 101 6O7 C45-C58-C60 2.87 120.27 116.78 2 A 103 6O7 C16-C17-C19 2.78 122.76 118.03 2 A 103 6O7 O17-C46-C47 -2.70 106.80 110.87 2 A 103 6O7 O19-C52-C53 2.68 113.58 108.41 2 A 101 6O7 C16-C17-C19 2.65 122.55 118.03 2 A 102 6O7 O14-C20-C19 -2.62 118.75 122.78 2 A 102 6O7 C45-C58-C60 2.60 119.94 116.78 2 A 101 6O7 O7-C24-C23 -2.59 104.62 109.62 2 A 101 6O7 O-C13-O1 -2.58 118.79 123.84 2 B 101 </td <td>2</td> <td>A</td> <td>103</td> <td>607</td> <td>C16-C17-C18</td> <td>-3.00</td> <td>115.88</td> <td>121.05</td>	2	A	103	607	C16-C17-C18	-3.00	115.88	121.05
2 B 101 6O7 C45-C58-C60 2.87 120.27 116.78 2 A 103 6O7 C16-C17-C19 2.78 122.76 118.03 2 A 103 6O7 O17-C46-C47 -2.70 106.80 110.87 2 A 103 6O7 O19-C52-C53 2.68 113.58 108.41 2 A 101 6O7 C16-C17-C19 2.65 122.55 118.03 2 A 102 6O7 O14-C20-C19 -2.62 118.75 122.78 2 A 102 6O7 C45-C58-C60 2.60 119.94 116.78 2 A 101 6O7 O7-C24-C23 -2.59 104.62 109.62 2 A 101 6O7 O-C13-O1 -2.58 118.79 123.84 2 B 101 6O7 O2-C2-N -2.58 118.16 122.93 2 A 103 6O7 O12-C34-C35 -2.56 107.25 112.12	2	A	101	607	C45-C58-C60	2.97	120.39	116.78
2 A 103 607 C16-C17-C19 2.78 122.76 118.03 2 A 103 607 O17-C46-C47 -2.70 106.80 110.87 2 A 103 607 O19-C52-C53 2.68 113.58 108.41 2 A 101 607 C16-C17-C19 2.65 122.55 118.03 2 A 102 607 O14-C20-C19 -2.62 118.75 122.78 2 A 102 607 C45-C58-C60 2.60 119.94 116.78 2 A 101 607 O7-C24-C23 -2.59 104.62 109.62 2 A 101 607 O-C13-O1 -2.58 118.79 123.84 2 B 101 607 O2-C2-N -2.58 118.16 122.93 2 A 103 607 O12-C34-C35 -2.56 107.25 112.12	2	A	103	607	C45-C58-C60	2.89	120.30	116.78
2 A 103 607 O17-C46-C47 -2.70 106.80 110.87 2 A 103 607 O19-C52-C53 2.68 113.58 108.41 2 A 101 607 C16-C17-C19 2.65 122.55 118.03 2 A 102 607 O14-C20-C19 -2.62 118.75 122.78 2 A 102 607 C45-C58-C60 2.60 119.94 116.78 2 A 101 607 O7-C24-C23 -2.59 104.62 109.62 2 A 101 607 O-C13-O1 -2.58 118.79 123.84 2 B 101 607 O2-C2-N -2.58 118.16 122.93 2 A 103 607 O12-C34-C35 -2.56 107.25 112.12	2	В	101	607	C45-C58-C60	2.87	120.27	116.78
2 A 103 6O7 O19-C52-C53 2.68 113.58 108.41 2 A 101 6O7 C16-C17-C19 2.65 122.55 118.03 2 A 102 6O7 O14-C20-C19 -2.62 118.75 122.78 2 A 102 6O7 C45-C58-C60 2.60 119.94 116.78 2 A 101 6O7 O7-C24-C23 -2.59 104.62 109.62 2 A 101 6O7 O-C13-O1 -2.58 118.79 123.84 2 B 101 6O7 O2-C2-N -2.58 118.16 122.93 2 A 103 6O7 O12-C34-C35 -2.56 107.25 112.12	2	A	103	607	C16-C17-C19	2.78	122.76	118.03
2 A 101 6O7 C16-C17-C19 2.65 122.55 118.03 2 A 102 6O7 O14-C20-C19 -2.62 118.75 122.78 2 A 102 6O7 C45-C58-C60 2.60 119.94 116.78 2 A 101 6O7 O7-C24-C23 -2.59 104.62 109.62 2 A 101 6O7 O-C13-O1 -2.58 118.79 123.84 2 B 101 6O7 O2-C2-N -2.58 118.16 122.93 2 A 103 6O7 O12-C34-C35 -2.56 107.25 112.12	2	A	103	607	O17-C46-C47	-2.70	106.80	110.87
2 A 102 6O7 O14-C20-C19 -2.62 118.75 122.78 2 A 102 6O7 C45-C58-C60 2.60 119.94 116.78 2 A 101 6O7 O7-C24-C23 -2.59 104.62 109.62 2 A 101 6O7 O-C13-O1 -2.58 118.79 123.84 2 B 101 6O7 O2-C2-N -2.58 118.16 122.93 2 A 103 6O7 O12-C34-C35 -2.56 107.25 112.12	2	A	103	607	O19-C52-C53	2.68	113.58	108.41
2 A 102 6O7 C45-C58-C60 2.60 119.94 116.78 2 A 101 6O7 O7-C24-C23 -2.59 104.62 109.62 2 A 101 6O7 O-C13-O1 -2.58 118.79 123.84 2 B 101 6O7 O2-C2-N -2.58 118.16 122.93 2 A 103 6O7 O12-C34-C35 -2.56 107.25 112.12	2	A	101	607	C16-C17-C19	2.65	122.55	118.03
2 A 101 6O7 O7-C24-C23 -2.59 104.62 109.62 2 A 101 6O7 O-C13-O1 -2.58 118.79 123.84 2 B 101 6O7 O2-C2-N -2.58 118.16 122.93 2 A 103 6O7 O12-C34-C35 -2.56 107.25 112.12	2	A	102	607	O14-C20-C19	-2.62	118.75	122.78
2 A 101 6O7 O-C13-O1 -2.58 118.79 123.84 2 B 101 6O7 O2-C2-N -2.58 118.16 122.93 2 A 103 6O7 O12-C34-C35 -2.56 107.25 112.12	2	A	102	607	C45-C58-C60	2.60	119.94	116.78
2 B 101 6O7 O2-C2-N -2.58 118.16 122.93 2 A 103 6O7 O12-C34-C35 -2.56 107.25 112.12	2	A	101	607	O7-C24-C23	-2.59	104.62	109.62
2 A 103 6O7 O12-C34-C35 -2.56 107.25 112.12	2	A	101	607	O-C13-O1	-2.58	118.79	123.84
	2	В	101	607	O2-C2-N	-2.58	118.16	122.93
2 A 102 6O7 O17-C50-C51 2.56 112.22 106.70	2	A	103	607	O12-C34-C35	-2.56	107.25	112.12
	2	A	102	607	O17-C50-C51	2.56	112.22	106.70



 $Continued\ from\ previous\ page...$

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$Ideal(^{o})$
2	A	102	607	O8-C32-C31	-2.54	104.97	109.52
2	A	102	607	O20-C56-C55	2.53	114.06	109.52
2	A	101	607	C60-C42-C43	2.51	120.36	118.11
2	A	103	607	C45-O16-C46	2.50	122.79	118.11
2	В	101	607	O12-C34-C35	-2.49	107.39	112.12
2	A	101	607	O14-C20-C19	-2.48	118.96	122.78
2	В	101	607	O20-C56-C57	2.46	112.01	106.70
2	A	103	607	O18-C49-C50	-2.44	104.25	109.67
2	A	101	607	C44-C45-C58	-2.44	119.56	122.52
2	A	102	607	C16-C17-C19	2.41	122.14	118.03
2	A	101	607	C16-C17-C18	-2.40	116.92	121.05
2	В	101	607	O17-C46-C47	2.40	114.49	110.87
2	A	102	607	C36-C35-C34	-2.36	110.30	114.82
2	В	101	607	C1-C2-N	2.34	122.74	117.73
2	A	103	607	C41-C19-C20	2.33	123.46	120.41
2	A	103	607	C48-C49-C50	2.32	113.97	110.04
2	A	102	607	C52-O19-C48	-2.29	111.03	116.27
2	В	101	607	C44-C45-C58	-2.27	119.77	122.52
2	A	101	607	C45-O16-C46	2.22	122.27	118.11
2	A	103	607	C44-C45-C58	-2.22	119.83	122.52
2	A	101	607	C5-C4-C3	-2.21	107.30	113.39
2	A	103	607	C19-C41-C42	2.17	122.81	121.09
2	A	103	607	C4-C3-C13	-2.15	105.01	110.37
2	A	101	607	C41-C42-C43	2.13	120.02	118.11
2	A	101	607	C30-C31-C32	2.12	113.64	110.04
2	A	103	607	C6-C5-C10	2.10	121.47	118.17
2	В	101	607	O7-C24-C23	-2.10	105.57	109.62
2	В	101	607	C52-O19-C48	2.08	121.02	116.27
2	В	101	607	O11-C36-C37	2.07	111.32	107.48
2	A	101	607	C52-O19-C48	-2.05	111.58	116.27
2	В	101	607	O20-C56-C55	-2.05	105.85	109.52
2	A	101	607	C23-C24-C25	-2.04	106.95	110.77
2	A	103	607	C28-O7-C24	-2.03	111.63	116.27
2	A	102	607	C57-C56-C55	-2.01	109.37	113.07
2	A	101	607	C19-C20-C21	2.00	120.06	116.00

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	101	607	C16-C-C1-O3
2	В	101	607	C16-C-C1-C2



Continued from previous page...

Mol	Chain	Res	Type	Atoms
2	В	101	607	C21-C-C1-O3
2	В	101	607	C47-C46-O16-C45
2	В	101	607	O20-C52-O19-C48
2	В	101	607	C53-C52-O19-C48
2	В	101	607	C-C1-O3-C15
2	В	101	607	C4-C3-N-C2
2	A	102	607	O1-C13-O-C14
2	В	101	607	O1-C13-O-C14
2	A	101	607	C3-C13-O-C14
2	A	102	607	C3-C13-O-C14
2	В	101	607	C3-C13-O-C14
2	A	101	607	O1-C13-O-C14
2	A	103	607	C3-C13-O-C14
2	A	103	607	O1-C13-O-C14
2	A	102	607	C-C1-O3-C15
2	В	101	607	C-C1-C2-O2
2	A	102	607	C2-C1-O3-C15
2	A	103	607	C16-C-C1-O3

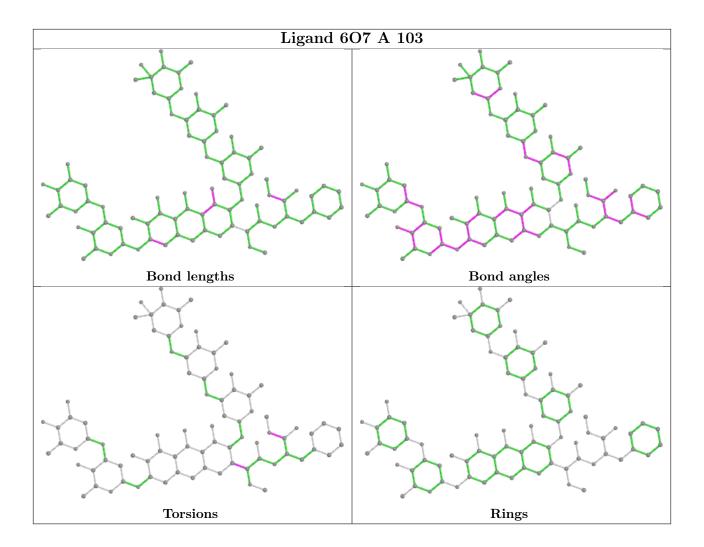
There are no ring outliers.

3 monomers are involved in 5 short contacts:

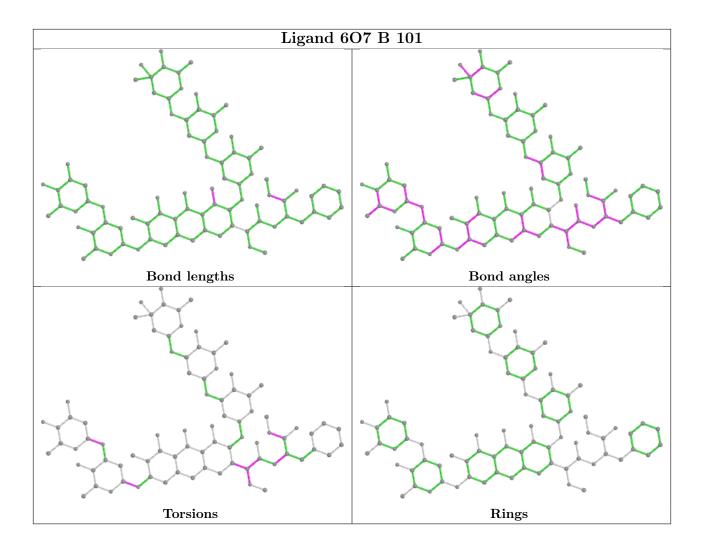
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	В	101	607	3	0
2	A	102	607	1	0
2	A	101	607	1	0

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

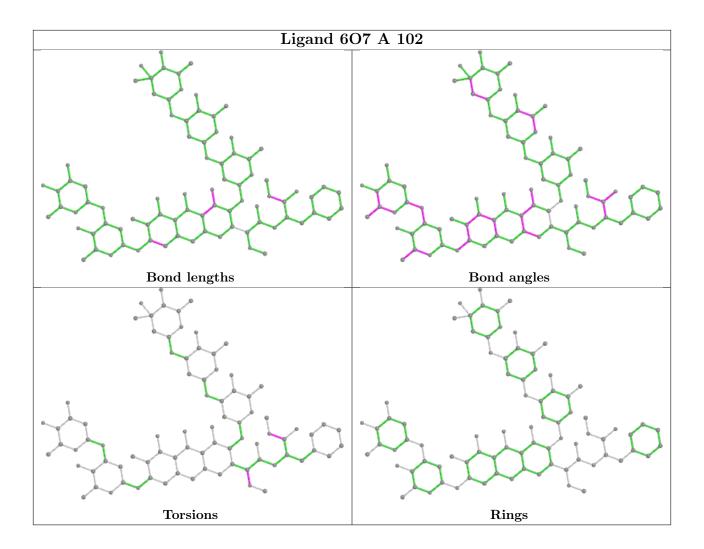




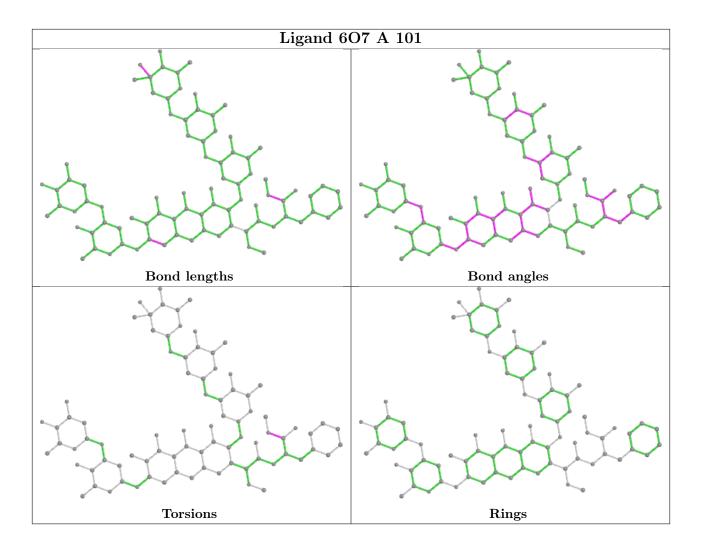












5.7 Other polymers (i)

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)

In the following table, the column labelled '#RSRZ>2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	${\bf Analysed} < \!\! {\rm RSRZ} \!\! > $		$\# \mathrm{RSRZ}{>}2$			$OWAB(A^2)$	Q<0.9
1	A	10/10 (100%)	0.25	0	100	100	38, 41, 45, 47	0
1	В	10/10 (100%)	0.37	0	100	100	40, 43, 49, 50	0
All	All	20/20 (100%)	0.31	0	100	100	38, 43, 49, 50	0

There are no RSRZ outliers to report.

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

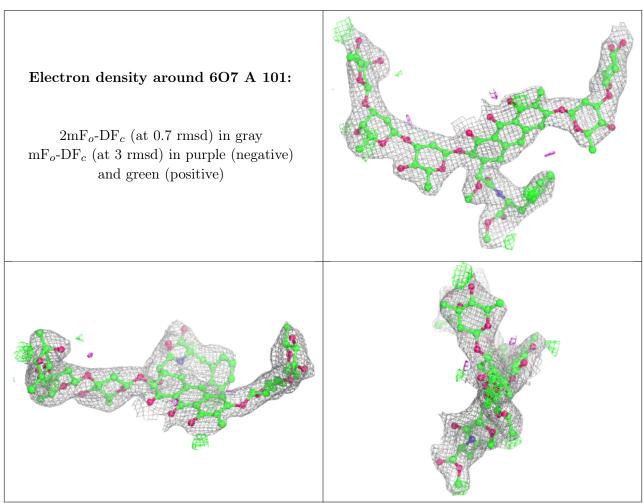
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\operatorname{B-factors}(\mathring{\mathrm{A}}^2)$	Q<0.9
3	ZN	A	108	1/1	0.57	0.28	36,36,36,36	1
3	ZN	A	107	1/1	0.66	0.28	26,26,26,26	1
2	607	A	101	84/84	0.90	0.20	31,48,63,66	0
2	607	В	101	84/84	0.92	0.19	35,47,54,57	0
2	607	A	102	84/84	0.92	0.15	31,45,54,58	0
2	607	A	103	84/84	0.92	0.17	31,40,55,58	0
3	ZN	A	105	1/1	0.95	0.07	65,65,65,65	1



Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
3	ZN	В	102	1/1	0.95	0.12	53,53,53,53	0
3	ZN	A	106	1/1	0.98	0.16	41,41,41,41	0
3	ZN	A	104	1/1	0.99	0.14	37,37,37,37	0

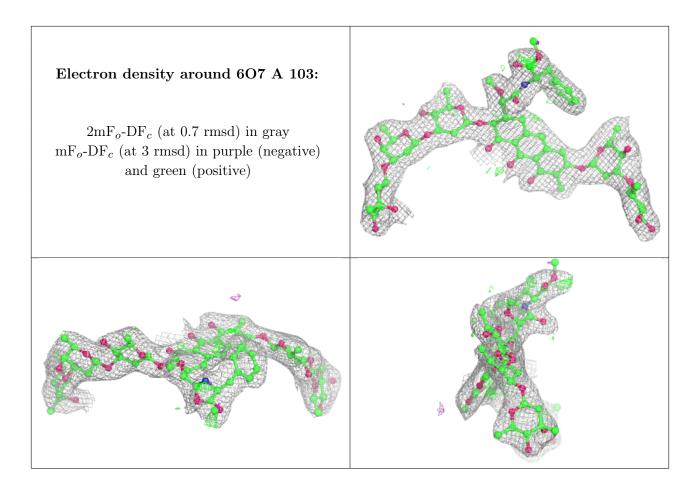
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





Electron density around 6O7 B 101: $2 \mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 0.7 rmsd) in gray ${\rm mF}_o\text{-}{\rm DF}_c$ (at 3 rmsd) in purple (negative) and green (positive) Electron density around 6O7 A 102: $2 \mathrm{mF}_o\text{-}\mathrm{DF}_c$ (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.

