



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 16, 2021 – 02:02 pm BST

PDB ID : 7AU9
Title : Structure of P. aeruginosa PBP3 in complex with a benzoxaborole (Compound 14)
Authors : Newman, H.; Bellini, B.; Dowson, C.G.
Deposited on : 2020-11-02
Resolution : 2.14 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) 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) : 2.23.1

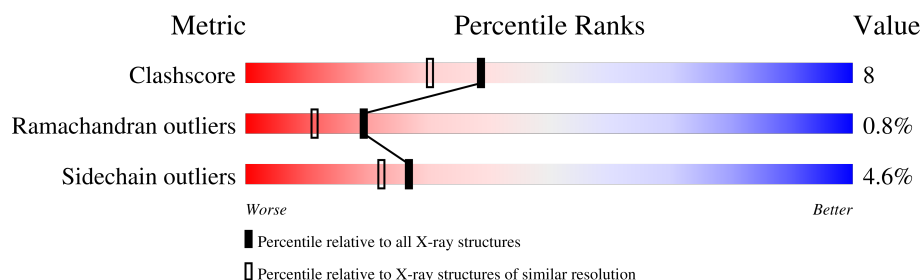
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.14 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	2653 (2.16-2.12)
Ramachandran outliers	138981	2618 (2.16-2.12)
Sidechain outliers	138945	2617 (2.16-2.12)

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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	537	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3871 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.

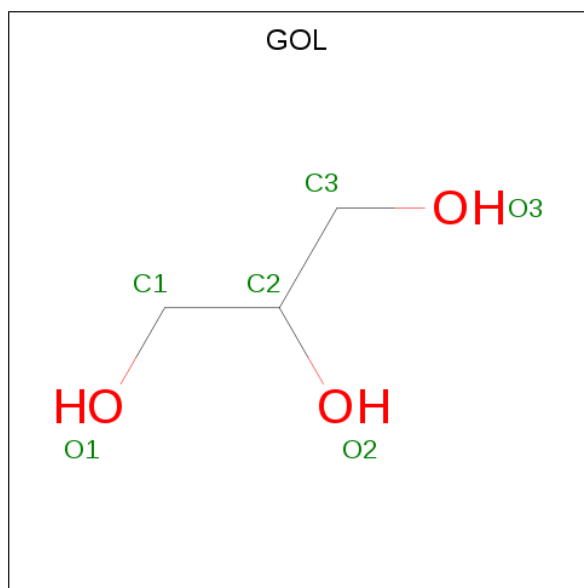
- Molecule 1 is a protein called Peptidoglycan D,D-transpeptidase FtsI.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	489	3739	2358	678	691	12	0	1	0

There are 7 discrepancies between the modelled and reference sequences:

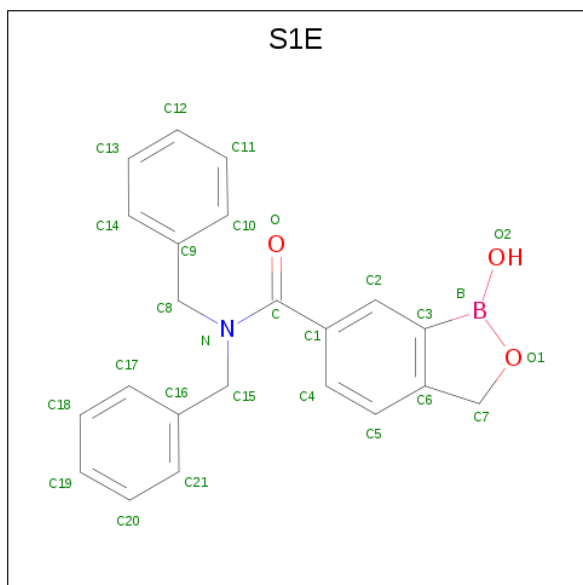
Chain	Residue	Modelled	Actual	Comment	Reference
A	43	GLY	-	expression tag	UNP G3XD46
A	44	PRO	-	expression tag	UNP G3XD46
A	45	GLY	-	expression tag	UNP G3XD46
A	46	TYR	-	expression tag	UNP G3XD46
A	47	GLN	-	expression tag	UNP G3XD46
A	48	ASP	-	expression tag	UNP G3XD46
A	49	PRO	-	expression tag	UNP G3XD46

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 3 is N,N-dibenzyl-1-hydroxy-1,3-dihydrobenzo[c][1,2]oxaborole-6-carboxamide (three-letter code: S1E) (formula: $C_{22}H_{20}BNO_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	B	C	N	O	0	0
			26	1	22	1	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	97	Total	O	0	3
			100	100		

4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	68.70 Å 82.72 Å 88.54 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	60.45 – 2.14	Depositor
% Data completeness (in resolution range)	73.5 (60.45-2.14)	Depositor
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.192 , 0.274	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3871	wwPDB-VP
Average B, all atoms (Å ²)	52.0	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: S1E, GOL

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	0.69	0/3813	0.86	1/5170 (0.0%)

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

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	409	TYR	CB-CA-C	6.38	123.17	110.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	410	GLY	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	3739	0	3784	57	0
2	A	6	0	8	1	0
3	A	26	0	0	0	0
4	A	100	0	0	2	0
All	All	3871	0	3792	57	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 8.

All (57) 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:A:83:TRP:CZ2	1:A:146:TYR:HD1	2.10	0.69
1:A:186:LEU:O	1:A:216:GLY:HA3	1.92	0.69
1:A:505:SER:OG	1:A:534:GLY:HA2	1.99	0.62
1:A:471:VAL:HG21	4:A:720:HOH:O	2.02	0.58
1:A:288:ASP:HB3	1:A:504:ARG:NH2	2.19	0.58
1:A:126:VAL:HG21	1:A:129:LEU:HD21	1.88	0.55
1:A:404:THR:HA	1:A:407:TYR:CE1	2.42	0.55
1:A:81:THR:HG23	1:A:148:ILE:HB	1.89	0.54
1:A:297:LYS:N	1:A:298:PRO:CD	2.71	0.53
1:A:282:ARG:NH2	1:A:288:ASP:OD2	2.42	0.53
1:A:325:ILE:O	1:A:325:ILE:HG22	2.08	0.53
1:A:193:ARG:HG2	1:A:209:VAL:HG22	1.90	0.52
1:A:135:GLU:O	1:A:139:ALA:N	2.38	0.52
1:A:325:ILE:HD12	1:A:399:LYS:HD3	1.92	0.52
1:A:83:TRP:CZ2	1:A:146:TYR:CD1	2.97	0.51
1:A:85:ASN:ND2	1:A:88:GLU:HG3	2.25	0.51
1:A:55:HIS:HA	1:A:193:ARG:O	2.11	0.50
1:A:489:ARG:HA	1:A:502:ALA:O	2.11	0.50
1:A:383:PHE:HB3	1:A:384:PRO:HD2	1.95	0.49
1:A:83:TRP:NE1	1:A:146:TYR:HB2	2.28	0.48
1:A:284:ARG:HD3	4:A:733:HOH:O	2.14	0.48
1:A:81:THR:CG2	1:A:148:ILE:HB	2.44	0.48
1:A:84:ALA:HB2	1:A:125:LEU:HD11	1.96	0.48
1:A:311:LYS:O	1:A:342:LEU:HD22	2.14	0.48
1:A:84:ALA:HA	1:A:144:GLY:O	2.14	0.48
1:A:520:MET:HE1	1:A:545:VAL:HG12	1.95	0.47
1:A:82:LEU:HD13	1:A:137:VAL:HG11	1.95	0.47
1:A:174:GLY:N	1:A:183:ASP:OD1	2.47	0.47
1:A:83:TRP:CE3	1:A:122:PHE:CD1	3.03	0.46
1:A:414:THR:OG1	1:A:416:ILE:HG22	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:346:LEU:O	1:A:484:LYS:HE2	2.16	0.46
1:A:54:ARG:HB2	1:A:195:VAL:CG2	2.47	0.45
1:A:276:LEU:O	1:A:276:LEU:HD13	2.17	0.45
1:A:363:ALA:HB2	1:A:402:THR:HG23	1.97	0.45
1:A:64:LEU:HD11	1:A:72:PRO:HB3	1.99	0.44
1:A:160:VAL:HG21	1:A:229:TYR:CE2	2.52	0.44
1:A:249:LEU:C	1:A:249:LEU:HD23	2.37	0.44
1:A:304:ALA:HA	1:A:361:ILE:HD13	2.00	0.44
1:A:126:VAL:CG2	1:A:129:LEU:HD21	2.48	0.43
1:A:96:TRP:HB2	1:A:97:PRO:HD3	2.01	0.43
1:A:430:LYS:CG	1:A:445:GLY:HA3	2.48	0.43
1:A:103:LEU:C	1:A:105:GLN:H	2.23	0.42
1:A:159:GLU:HA	1:A:268:TYR:O	2.19	0.42
1:A:86:PRO:HD3	1:A:123:ILE:HG22	2.02	0.41
1:A:411:LEU:HD23	1:A:411:LEU:N	2.36	0.41
1:A:314:ASP:O	1:A:341:ASP:HA	2.20	0.41
1:A:489:ARG:HH12	1:A:503:TYR:HB2	1.85	0.41
1:A:54:ARG:HB2	1:A:195:VAL:HG22	2.02	0.41
1:A:83:TRP:CZ3	1:A:122:PHE:HD1	2.38	0.41
1:A:135:GLU:OE2	1:A:135:GLU:HA	2.21	0.41
1:A:288:ASP:HB3	1:A:504:ARG:HH22	1.86	0.41
1:A:319:TYR:HA	1:A:320:PRO:HA	1.86	0.41
1:A:111:ALA:O	1:A:115:GLU:HG2	2.21	0.40
1:A:450:SER:HA	2:A:601:GOL:C1	2.51	0.40
1:A:503:TYR:CE2	1:A:527:PRO:HD2	2.56	0.40
1:A:476:VAL:O	1:A:479:TYR:O	2.38	0.40
1:A:537:VAL:O	1:A:540:PRO:HD2	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 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	A	482/537 (90%)	453 (94%)	25 (5%)	4 (1%)	19 11

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	100	ALA
1	A	326	GLY
1	A	128	GLY
1	A	384	PRO

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	A	391/424 (92%)	373 (95%)	18 (5%)	27 22

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	67	ASP
1	A	76	SER
1	A	146	TYR
1	A	149	GLU
1	A	175	ARG
1	A	189	VAL
1	A	212	ASN
1	A	276	LEU
1	A	287	ILE
1	A	325	ILE
1	A	328	TYR
1	A	334	SER
1	A	371	GLN
1	A	390	ASN
1	A	489	ARG
1	A	503	TYR
1	A	504	ARG

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Mol	Chain	Res	Type
1	A	525	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	69	ASN
1	A	98	GLN
1	A	116	GLN
1	A	277	GLN
1	A	336	ASN
1	A	390	ASN
1	A	394	HIS

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](#)

2 ligands are modelled in this entry.

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	GOL	A	601	-	5,5,5	0.13	0	5,5,5	0.36	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	S1E	A	602	1	27,29,30	1.26	1 (3%)	37,39,41	0.95	3 (8%)

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	GOL	A	601	-	-	2/4/4/4	-
3	S1E	A	602	1	-	0/16/22/25	0/4/4/4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	602	S1E	O1-C7	-6.19	1.39	1.44

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	S1E	C7-C6-C3	3.24	112.15	110.50
3	A	602	S1E	B-O1-C7	2.48	113.78	109.93
3	A	602	S1E	C16-C15-N	2.07	116.47	113.13

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	GOL	O1-C1-C2-O2
2	A	601	GOL	O1-C1-C2-C3

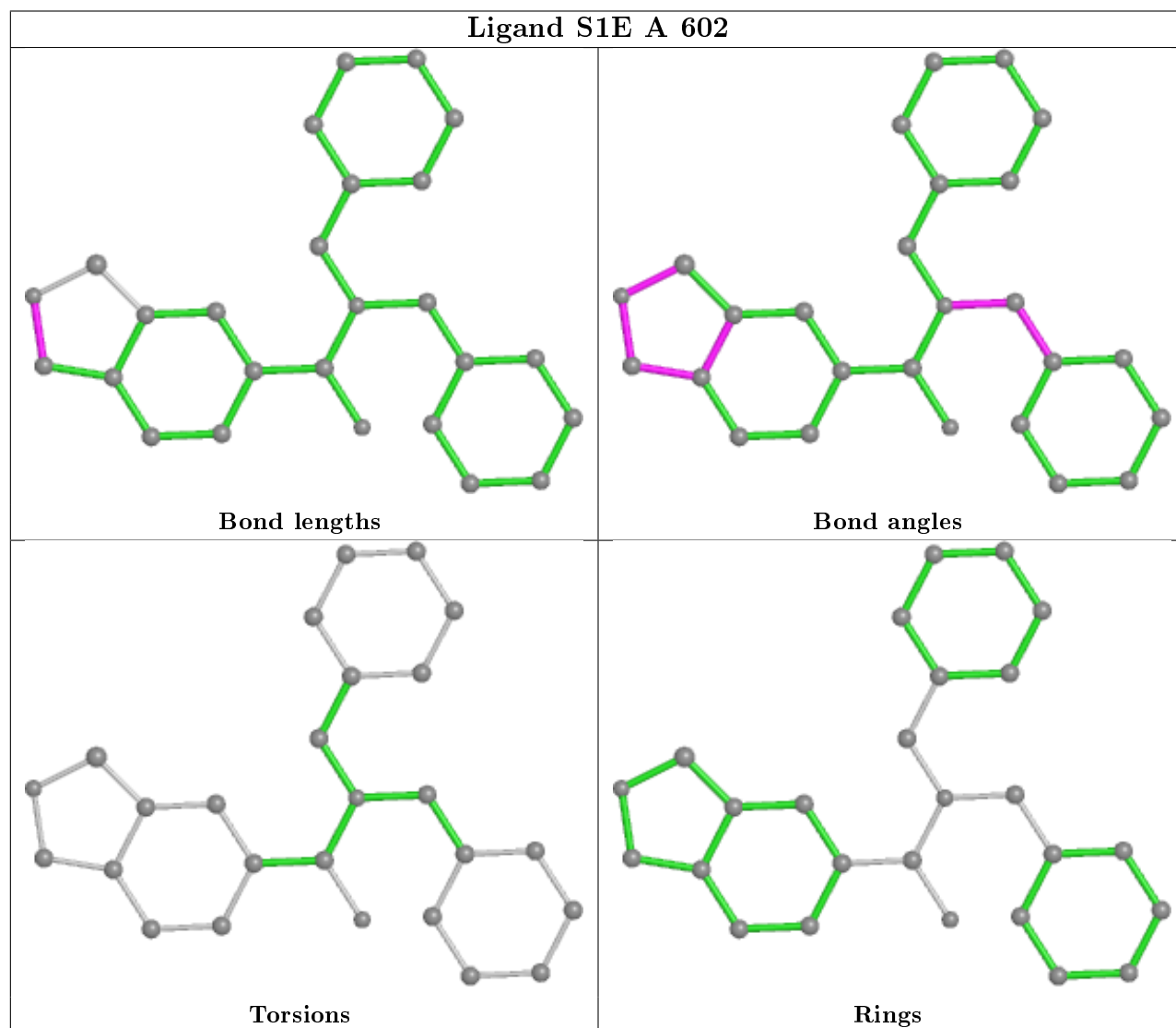
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	GOL	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 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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.