



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 21, 2022 – 02:22 PM EDT

PDB ID : 7SFD
Title : Human DNMT1(729-1600) Bound to Zebularine-Containing 12mer dsDNA and Inhibitor GSK3543105A
Authors : Horton, J.R.; Pathuri, S.; Cheng, X.
Deposited on : 2021-10-03
Resolution : 2.09 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) : 1.13
EDS : 2.27
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) : 2.27

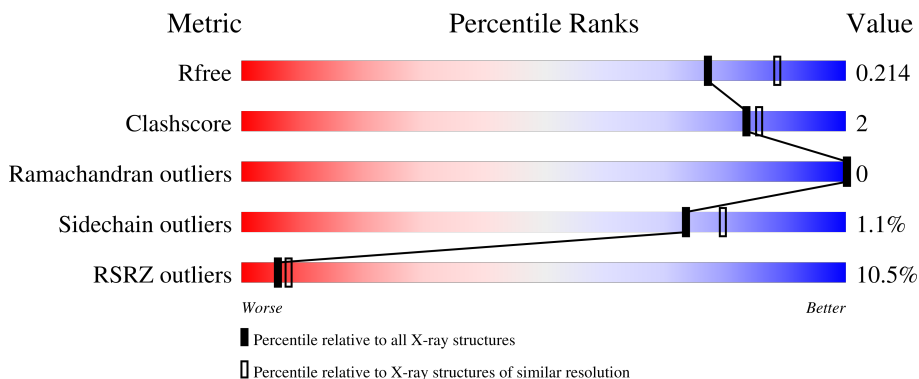
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.09 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))
R_{free}	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 $\leq 5\%$. 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	874	<div> <div>10%</div> <div>90%</div> <div>6%</div> <div>.</div> </div>
2	C	12	<div> <div>8%</div> <div>75%</div> <div>25%</div> </div>
3	D	12	<div> <div>33%</div> <div>67%</div> <div>33%</div> </div>

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 7262 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 DNA (cytosine-5)-methyltransferase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	842	Total	C	N	O	S	0	4	0
			6439	4093	1127	1177	42			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	727	HIS	-	expression tag	UNP P26358
A	728	MET	-	expression tag	UNP P26358

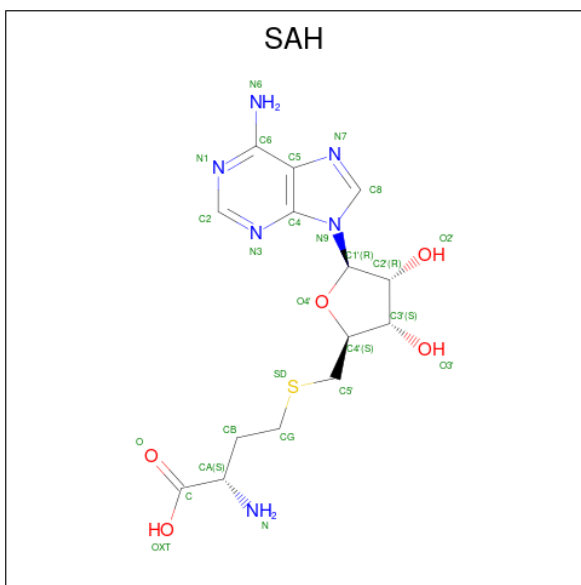
- Molecule 2 is a DNA chain called DNA (12-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	12	Total	C	N	O	P	0	0	0
			244	116	47	70	11			

- Molecule 3 is a DNA chain called DNA (12-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	12	Total	C	N	O	P	0	0	0
			243	115	46	71	11			

- Molecule 4 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: C₁₄H₂₀N₆O₅S).

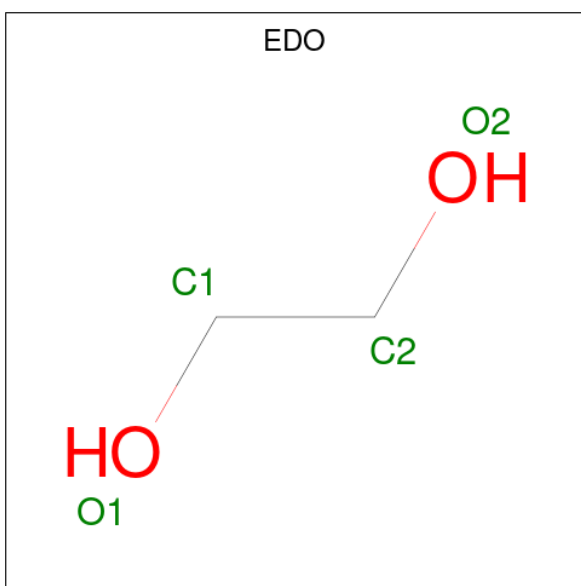


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			26	14	6	5	1		

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

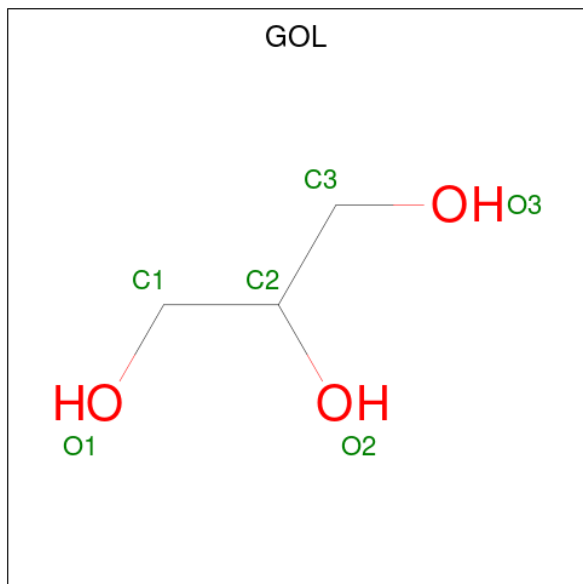
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	2	Total Zn 2 2	0	0

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $\text{C}_2\text{H}_6\text{O}_2$).



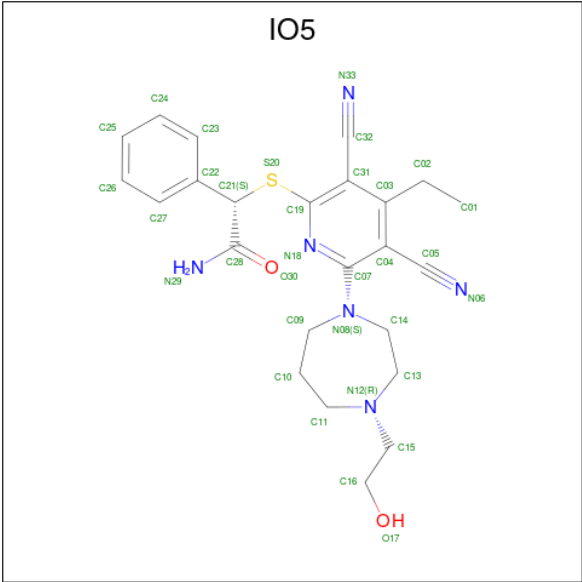
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

- Molecule 8 is (2S)-2-({3,5-dicyano-4-ethyl-6-[4-(2-hydroxyethyl)-1,4-diazepan-1-yl]pyridin-2-yl}sulfanyl)-2-phenylacetamide (three-letter code: IO5) (formula: C₂₄H₂₈N₆O₂S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
8	C	1	Total	C	N	O	S	0	0
			33	24	6	2	1		

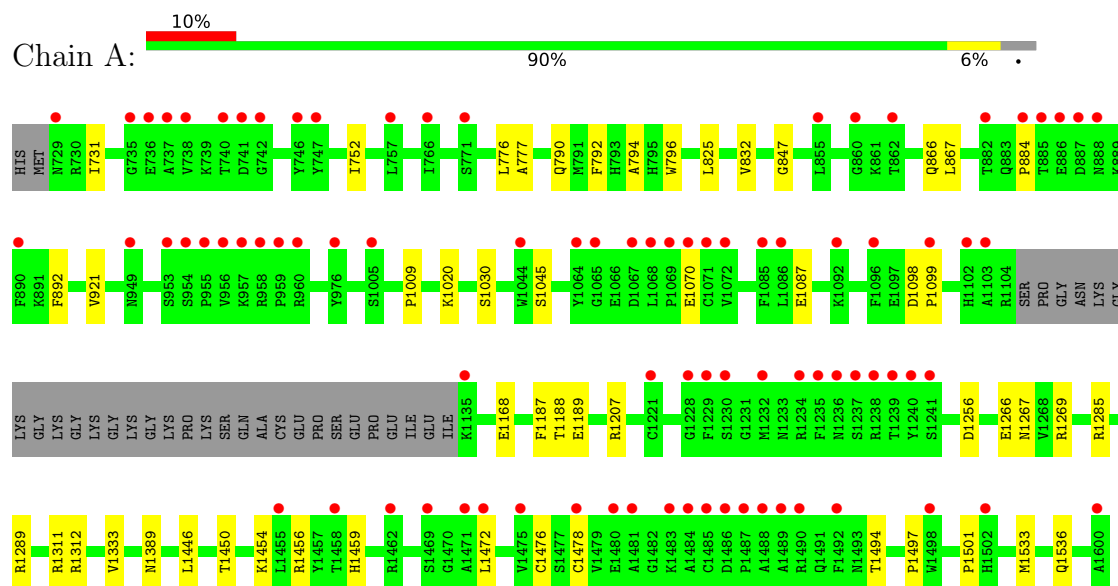
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	248	Total	O	0	0
			248	248		
9	C	2	Total	O	0	0
			2	2		
9	D	1	Total	O	0	0
			1	1		

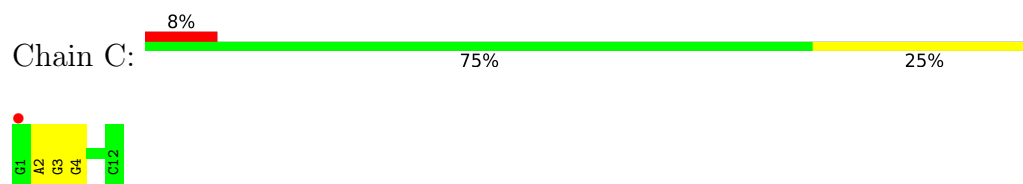
3 Residue-property plots [i](#)

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.

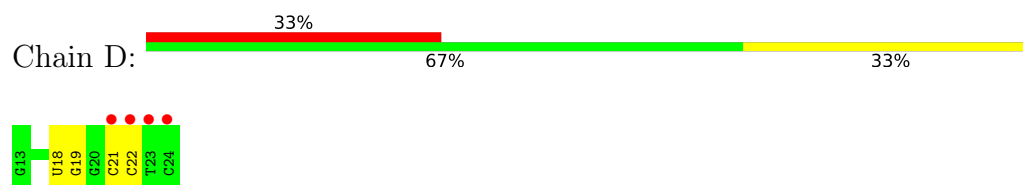
- Molecule 1: DNA (cytosine-5)-methyltransferase 1



- Molecule 2: DNA (12-MER)



- Molecule 3: DNA (12-MER)



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	161.60Å 77.42Å 116.51Å 90.00° 125.76° 90.00°	Depositor
Resolution (Å)	41.81 – 2.09 47.27 – 2.09	Depositor EDS
% Data completeness (in resolution range)	96.1 (41.81-2.09) 88.6 (47.27-2.09)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.30 (at 2.08Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.185 , 0.216 0.184 , 0.214	Depositor DCC
R_{free} test set	1968 reflections (2.97%)	wwPDB-VP
Wilson B-factor (Å ²)	34.0	Xtriage
Anisotropy	0.151	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 51.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7262	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.13% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PYO, SAH, 5CM, GOL, IO5, ZN, EDO

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	0.32	0/6617	0.55	0/9013
2	C	0.59	0/250	0.79	0/382
3	D	0.54	0/250	0.80	0/382
All	All	0.34	0/7117	0.57	0/9777

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

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	6439	0	6079	28	0
2	C	244	0	137	2	0
3	D	243	0	134	2	0
4	A	26	0	19	0	0
5	A	2	0	0	0	0
6	A	12	0	18	1	0
7	A	12	0	16	3	0
8	C	33	0	0	1	0
9	A	248	0	0	3	0
9	C	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	D	1	0	0	0	0
All	All	7262	0	6403	32	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.

All (32) 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:1446:LEU:HD12	1:A:1450:THR:HB	1.71	0.71
1:A:1266:GLU:OE2	1:A:1312[B]:ARG:HD2	2.00	0.60
1:A:1476:CYS:HB3	1:A:1478:CYS:SG	2.42	0.59
1:A:790:GLN:HB3	1:A:825:LEU:HD12	1.86	0.58
1:A:731:ILE:HG13	1:A:752:ILE:HG12	1.86	0.58
1:A:1187:PHE:HB3	1:A:1189:GLU:HG3	1.88	0.55
1:A:777:ALA:HB2	1:A:796:TRP:CE3	2.43	0.54
1:A:884:PRO:HB3	1:A:892:PHE:CG	2.43	0.54
2:C:2:DA:H2'	2:C:3:DG:C8	2.43	0.53
1:A:1497:PRO:O	1:A:1501:PRO:HD2	2.11	0.50
1:A:1333:VAL:HA	7:A:1707:GOL:H12	1.93	0.50
8:C:101:IO5:C05	8:C:101:IO5:C09	2.90	0.50
1:A:1207[B]:ARG:NH1	9:A:1811:HOH:O	2.43	0.49
6:A:1704:EDO:H12	3:D:19:DG:H5'	1.94	0.49
1:A:1311:ARG:O	1:A:1312[A]:ARG:NH1	2.35	0.49
3:D:21:DC:H2''	3:D:22:DC:O5'	2.12	0.49
1:A:1533:MET:HE1	2:C:4:DG:H2'	1.96	0.48
1:A:921:VAL:HG21	1:A:1009:PRO:HG3	1.97	0.46
1:A:1168:GLU:O	1:A:1188:THR:HA	2.16	0.46
1:A:866:GLN:HG3	1:A:867:LEU:HG	1.98	0.46
1:A:1312[B]:ARG:HH22	7:A:1708:GOL:H31	1.80	0.46
1:A:847:GLY:HA3	1:A:1256:ASP:O	2.17	0.45
1:A:1454:LYS:HD2	1:A:1456:ARG:HH21	1.81	0.45
1:A:1459:HIS:O	1:A:1472:LEU:HB3	2.17	0.44
1:A:1020:LYS:O	1:A:1045:SER:HB3	2.17	0.43
1:A:1098:ASP:CG	1:A:1099:PRO:HD2	2.39	0.43
1:A:1333:VAL:HA	7:A:1707:GOL:C1	2.48	0.43
1:A:1389:ASN:ND2	9:A:1812:HOH:O	2.43	0.43
1:A:1285:ARG:NE	9:A:1822:HOH:O	2.51	0.43
1:A:1087:GLU:HA	1:A:1099:PRO:HD3	2.00	0.42
1:A:776:LEU:HD22	1:A:832:VAL:HG21	2.02	0.41
1:A:792:PHE:CE2	1:A:794:ALA:HB2	2.56	0.40

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	A	842/874 (96%)	817 (97%)	25 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	657/753 (87%)	650 (99%)	7 (1%)	73	79

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1030	SER
1	A	1070	GLU
1	A	1267	ASN
1	A	1269	ARG
1	A	1289	ARG
1	A	1494	THR
1	A	1536	GLN

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 ⓘ

2 non-standard protein/DNA/RNA residues 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$
3	PYO	D	18	2,3	14,20,21	0.73	1 (7%)	16,28,31	0.70	0
2	5CM	C	6	3,2	15,21,22	0.61	0	19,30,33	0.79	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	PYO	D	18	2,3	-	1/5/25/26	0/2/2/2
2	5CM	C	6	3,2	-	1/4/21/22	0/2/2/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	18	PYO	C6-N1	-2.19	1.33	1.35

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	6	5CM	O4'-C1'-N1-C6
3	D	18	PYO	O4'-C1'-N1-C6

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 2 are monoatomic - leaving 7 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	$\# Z > 2$
4	SAH	A	1701	-	21,28,28	0.75	0	20,40,40	0.66	0
6	EDO	A	1706	-	3,3,3	0.47	0	2,2,2	0.32	0
7	GOL	A	1708	-	5,5,5	1.01	0	5,5,5	0.91	0
7	GOL	A	1707	-	5,5,5	0.76	0	5,5,5	1.06	0
8	IO5	C	101	-	34,35,35	0.91	1 (2%)	35,47,47	1.19	4 (11%)
6	EDO	A	1705	-	3,3,3	0.53	0	2,2,2	0.23	0
6	EDO	A	1704	-	3,3,3	0.43	0	2,2,2	0.34	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
4	SAH	A	1701	-	-	0/7/31/31	0/3/3/3
6	EDO	A	1706	-	-	0/1/1/1	-
7	GOL	A	1708	-	-	2/4/4/4	-
7	GOL	A	1707	-	-	0/4/4/4	-
8	IO5	C	101	-	-	2/19/36/36	0/3/3/3
6	EDO	A	1705	-	-	0/1/1/1	-
6	EDO	A	1704	-	-	0/1/1/1	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	C	101	IO5	C04-C03	-2.93	1.37	1.40

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	C	101	IO5	N18-C07-N08	-3.65	110.88	116.80
8	C	101	IO5	C19-C31-C32	2.88	123.00	119.79
8	C	101	IO5	C04-C07-N08	2.26	127.55	123.15
8	C	101	IO5	C27-C22-C23	2.02	120.81	118.29

There are no chirality outliers.

All (4) torsion outliers are listed below:

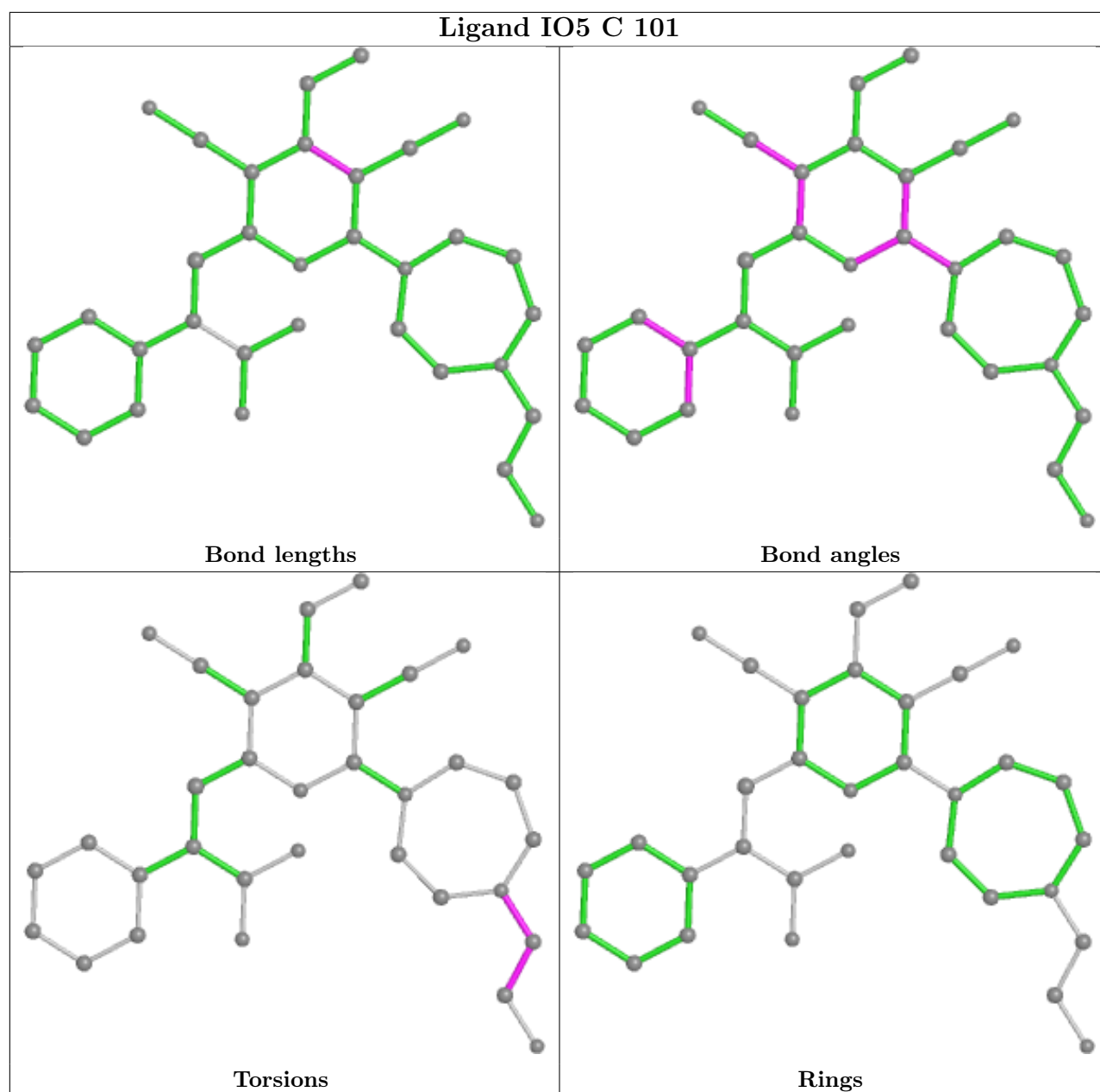
Mol	Chain	Res	Type	Atoms
8	C	101	IO5	C16-C15-N12-C13
8	C	101	IO5	N12-C15-C16-O17
7	A	1708	GOL	C1-C2-C3-O3
7	A	1708	GOL	O2-C2-C3-O3

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	1708	GOL	1	0
7	A	1707	GOL	2	0
8	C	101	IO5	1	0
6	A	1704	EDO	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

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, 95th 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	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	842/874 (96%)	0.46	86 (10%) 6 8	23, 52, 106, 142	0
2	C	11/12 (91%)	0.76	1 (9%) 9 12	82, 99, 150, 153	0
3	D	11/12 (91%)	1.23	4 (36%) 0 0	94, 107, 158, 174	0
All	All	864/898 (96%)	0.47	91 (10%) 6 8	23, 53, 109, 174	0

All (91) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	738	VAL	6.9
1	A	956	VAL	6.5
1	A	1064	TYR	5.4
1	A	1229	PHE	5.3
1	A	1600	ALA	5.1
1	A	1485	CYS	4.8
1	A	1484	ALA	4.8
1	A	890	PHE	4.8
1	A	1241	SER	4.7
1	A	1232	MET	4.7
3	D	24	DC	4.6
1	A	954	SER	4.6
1	A	1068	LEU	4.5
1	A	737	ALA	4.5
1	A	885	THR	4.3
1	A	955	PRO	4.1
1	A	729	ASN	4.0
1	A	1235	PHE	3.9
1	A	886	GLU	3.8
1	A	1069	PRO	3.7
1	A	1044	TRP	3.7
1	A	1099	PRO	3.7
1	A	1230	SER	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	1236	ASN	3.6
1	A	742	GLY	3.5
1	A	746	TYR	3.5
1	A	1086	LEU	3.5
1	A	1498	TRP	3.4
1	A	1489	ALA	3.4
1	A	953	SER	3.4
1	A	957	LYS	3.3
1	A	1480	GLU	3.3
1	A	888	ASN	3.3
1	A	1228	GLY	3.3
3	D	23	DT	3.2
1	A	1238	ARG	3.2
1	A	1492	PHE	3.2
1	A	735	GLY	3.1
1	A	887	ASP	3.1
1	A	1472	LEU	3.1
1	A	1071	CYS	3.1
2	C	1	DG	3.0
1	A	1469	SER	3.0
1	A	959	PRO	3.0
1	A	1103	ALA	2.9
1	A	1486	ASP	2.9
1	A	771	SER	2.9
1	A	1072	VAL	2.9
1	A	1483	LYS	2.9
1	A	1085	PHE	2.8
1	A	1005	SER	2.8
1	A	884	PRO	2.8
1	A	976	TYR	2.8
1	A	860	GLY	2.8
1	A	1070	GLU	2.8
1	A	1471	ALA	2.7
1	A	1240	TYR	2.6
3	D	21	DC	2.6
1	A	741	ASP	2.6
1	A	1458	THR	2.6
3	D	22	DC	2.6
1	A	1487	PRO	2.6
1	A	1475	VAL	2.5
1	A	958	ARG	2.5
1	A	1135	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	882	THR	2.4
1	A	1237	SER	2.4
1	A	949	ASN	2.4
1	A	1490	ARG	2.4
1	A	757	LEU	2.3
1	A	1455	LEU	2.3
1	A	1502	HIS	2.3
1	A	1478	CYS	2.3
1	A	1065	GLY	2.3
1	A	740	THR	2.3
1	A	1096	PHE	2.2
1	A	1067	ASP	2.2
1	A	862	THR	2.2
1	A	1102	HIS	2.2
1	A	1234	ARG	2.2
1	A	1462	ARG	2.2
1	A	960	ARG	2.1
1	A	1239	THR	2.1
1	A	1481	ALA	2.1
1	A	1488	ALA	2.1
1	A	747	TYR	2.1
1	A	736	GLU	2.1
1	A	766	ILE	2.1
1	A	1092	LYS	2.1
1	A	1221	CYS	2.1
1	A	855	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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, 95th 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	B-factors(Å ²)	Q<0.9
3	PYO	D	18	19/20	0.74	0.18	111,119,131,136	0
2	5CM	C	6	20/21	0.92	0.16	73,81,87,92	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands

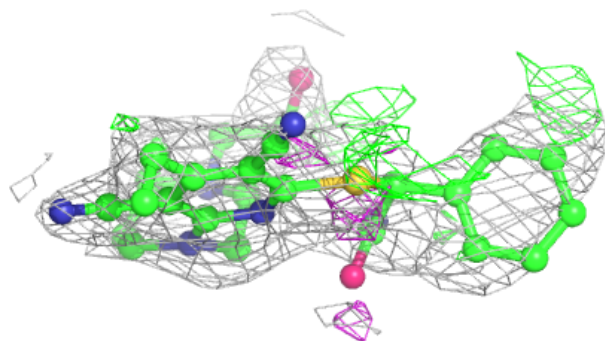
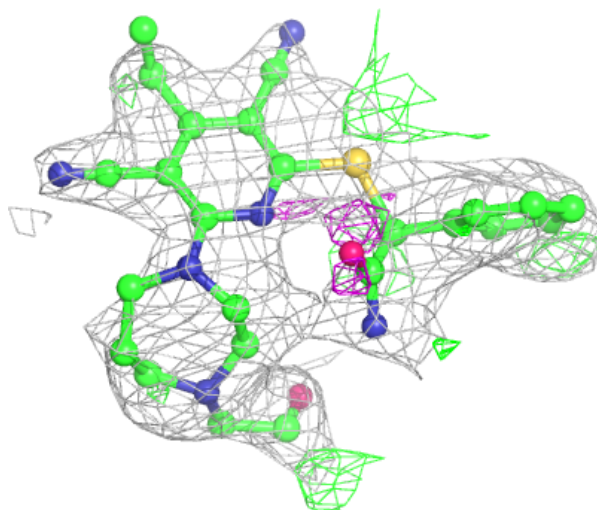
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
8	IO5	C	101	33/33	0.72	0.25	69,86,102,104	0
7	GOL	A	1708	6/6	0.74	0.23	58,60,65,72	0
7	GOL	A	1707	6/6	0.78	0.18	45,53,63,70	0
6	EDO	A	1706	4/4	0.79	0.25	79,88,88,91	0
6	EDO	A	1705	4/4	0.88	0.14	46,54,55,55	0
6	EDO	A	1704	4/4	0.89	0.15	57,59,66,69	0
5	ZN	A	1702	1/1	0.94	0.07	102,102,102,102	0
5	ZN	A	1703	1/1	0.95	0.06	49,49,49,49	0
4	SAH	A	1701	26/26	0.96	0.14	25,34,39,41	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 IO5 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.