

wwPDB X-ray Structure Validation Summary Report (i)

Oct 24, 2022 – 10:22 am BST

PDB ID : 7Q1D

Title: Acetyltrasferase(3) type IIIa in complex with 3-N-methyl-nemycin B

Authors: Pontillo, N.; Guskov, A.

Deposited on : 2021-10-18

Resolution : 1.43 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
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 : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : 2.31.2buster-report : 1.1.7 (2018)

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

Refmac : 5.8.0267

CCP4 : 7.1.010 (Gargrove)

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

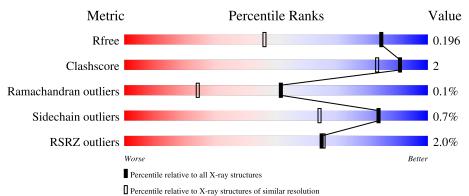
Validation Pipeline (wwPDB-VP) : 2.31.2

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 1.43 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},{\rm resolution\ range}({\rm \AA})) \end{array}$
R_{free}	130704	2021 (1.46-1.42)
Clashscore	141614	2086 (1.46-1.42)
Ramachandran outliers	138981	2047 (1.46-1.42)
Sidechain outliers	138945	2047 (1.46-1.42)
RSRZ outliers	127900	1993 (1.46-1.42)

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	287		6%	8%
1	В	287	87%		9%
1	С	287	87%		9%
1	D	287	91%		• 5%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard



residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density	
3	8I8	A	304	X	-	-	-	
3	8I8	В	303	X	-	-	-	
3	8I8	С	303	X	-	-	-	
3	8I8	D	302	X	-	-	-	



2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 9888 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 Aminoglycoside N(3)-acetyltransferase III.

Mol	Chain	Residues		Atoms					AltConf	Trace
1	Λ	263	Total	С	N	О	S	0	9	0
1 A	203	2096	1332	371	382	11	U	9		
1	В	261	Total	С	N	О	S	0	5	0
1	Б	201	2051	1307	359	374	11	U		
1	C	261	Total	С	N	О	S	0	6	0
1		201	2053	1310	356	376	11	U		
1	D	272	Total	С	N	О	S	0	5	0
1	D	272	2131	1357	374	388	12	U	9	

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	5	HIS	-	expression tag	UNP P29808
A	6	HIS	-	expression tag	UNP P29808
A	7	HIS	-	expression tag	UNP P29808
A	8	HIS	-	expression tag	UNP P29808
A	9	HIS	-	expression tag	UNP P29808
A	10	HIS	-	expression tag	UNP P29808
A	11	SER	-	expression tag	UNP P29808
A	12	SER	-	expression tag	UNP P29808
A	13	GLY	-	expression tag	UNP P29808
A	14	LEU	-	expression tag	UNP P29808
A	15	VAL	-	expression tag	UNP P29808
A	16	PRO	_	expression tag	UNP P29808
A	17	ARG	-	expression tag	UNP P29808
A	18	GLY	-	expression tag	UNP P29808
A	19	SER	-	expression tag	UNP P29808
A	20	HIS	-	expression tag	UNP P29808
В	5	HIS		expression tag	UNP P29808
В	6	HIS	-	expression tag	UNP P29808
В	7	HIS	-	expression tag	UNP P29808
В	8	HIS	-	expression tag	UNP P29808
В	9	HIS	-	expression tag	UNP P29808



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В		Modelled	Actual	Comment	Reference
	10	HIS	-	expression tag	UNP P29808
В	11	SER	-	expression tag	UNP P29808
В	12	SER	-	expression tag	UNP P29808
В	13	GLY	-	expression tag	UNP P29808
В	14	LEU	-	expression tag	UNP P29808
В	15	VAL	-	expression tag	UNP P29808
В	16	PRO	-	expression tag	UNP P29808
В	17	ARG	-	expression tag	UNP P29808
В	18	GLY	-	expression tag	UNP P29808
В	19	SER	-	expression tag	UNP P29808
В	20	HIS	-	expression tag	UNP P29808
С	5	HIS	-	expression tag	UNP P29808
С	6	HIS	-	expression tag	UNP P29808
С	7	HIS	-	expression tag	UNP P29808
С	8	HIS	-	expression tag	UNP P29808
С	9	HIS	-	expression tag	UNP P29808
С	10	HIS	-	expression tag	UNP P29808
С	11	SER	-	expression tag	UNP P29808
С	12	SER	-	expression tag	UNP P29808
С	13	GLY	-	expression tag	UNP P29808
С	14	LEU	-	expression tag	UNP P29808
С	15	VAL	-	expression tag	UNP P29808
С	16	PRO	-	expression tag	UNP P29808
С	17	ARG	-	expression tag	UNP P29808
С	18	GLY	-	expression tag	UNP P29808
С	19	SER	-	expression tag	UNP P29808
С	20	HIS	-	expression tag	UNP P29808
D	5	HIS	-	expression tag	UNP P29808
D	6	HIS	-	expression tag	UNP P29808
D	7	HIS	-	expression tag	UNP P29808
D	8	HIS	-	expression tag	UNP P29808
D	9	HIS	-	expression tag	UNP P29808
D	10	HIS	-	expression tag	UNP P29808
D	11	SER	-	expression tag	UNP P29808
D	12	SER	-	expression tag	UNP P29808
D	13	GLY	-	expression tag	UNP P29808
D	14	LEU	-	expression tag	UNP P29808
D	15	VAL	-	expression tag	UNP P29808
D	16	PRO	-	expression tag	UNP P29808
D	17	ARG	-	expression tag	UNP P29808
D	18	GLY	-	expression tag	UNP P29808
D	19	SER	-	expression tag	UNP P29808



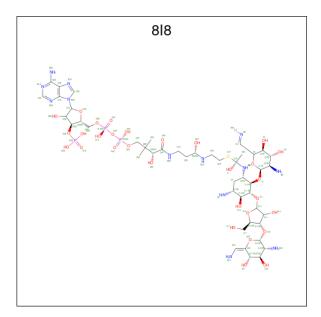
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Chain	Residue	Modelled	Actual	Comment	Reference
D	20	HIS	-	expression tag	UNP P29808

• Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	3	Total Na 3 3	0	0

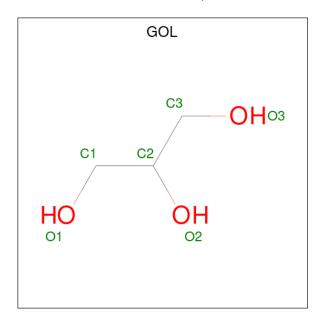
• Molecule 3 is [[(2 {R},3 {S})-5-(6-aminopurin-9-yl)-4-oxidanyl-3-phosphonooxy-oxolan-2-yl] methoxy-oxidanyl-phosphoryl] [(3 {R})-4-[[(3 {S})-3-[2-[(1 {S})-1-[[(1 {S}),2 {R}),3 {R},4 {S} {S},5 {R})-5-azanyl-3-[(4 {S},5 {R})-4-[(2 {S},3 {R},4 {R},5 {S},6 {E})-3-azanyl-6-(azanylm ethylidene)-4,5-bis(oxidanyl)oxan-2-yl]oxy-5-(hydroxymethyl)-3-oxidanyl-oxolan-2-yl]oxy-2-[(2 {S},3 {R},4 {R},5 {S})-3-azanyl-6-(iminomethyl)-4,5-bis(oxidanyl)oxan-2-yl]oxy-4-ox idanyl-cyclohexyl]amino]-1-oxidanyl-ethyl]sulfanylethylamino]-3-oxidanyl-propyl]amino]-2,2-dimethyl-3-oxidanyl-4-oxidanylidene-butyl] hydrogen phosphate (three-letter code: 8I8) (formula: $C_{46}H_{82}N_{13}O_{30}P_3S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	
3	Λ	1	Total	С	N	О	Р	S	0	0	
3 A	1	93	46	13	30	3	1	U	0		
3	В	1	Total	С	N	О	Р	S	0	0	
3	Б	1	93	46	13	30	3	1			
3	С	1	Total	С	N	О	Р	S	0	0	
3		1	93	46	13	30	3	1	U		
3	D	D 1	Total	С	N	О	Р	S	0	0	
3	ע	1	93	46	13	30	3	1	U	0	



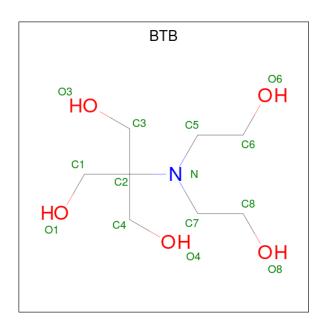
• Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0
4	В	1	Total C O 6 3 3	0	0
4	С	1	Total C O 6 3 3	0	0
4	С	1	Total C O 6 3 3	0	0

• Molecule 5 is 2-[BIS-(2-HYDROXY-ETHYL)-AMINO]-2-HYDROXYMETHYL-PROPAN E-1,3-DIOL (three-letter code: BTB) (formula: $C_8H_{19}NO_5$).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	В	1	Total 14	C 8	N 1	O 5	0	0

• Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	D	1	Total Cl 1 1	0	0

• Molecule 7 is water.

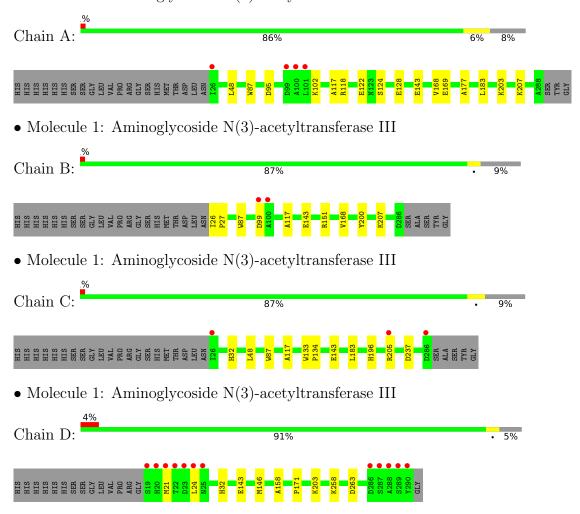
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	287	Total O 287 287	0	0
7	В	283	Total O 283 283	0	1
7	С	289	Total O 289 289	0	2
7	D	284	Total O 284 284	0	1



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: Aminoglycoside N(3)-acetyltransferase III





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 2 21	Depositor
Cell constants	90.96Å 100.49Å 131.91Å	Donositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.15 - 1.43	Depositor
Resolution (A)	47.15 - 1.43	EDS
% Data completeness	95.3 (47.15-1.43)	Depositor
(in resolution range)	98.6 (47.15-1.43)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.56 (at 1.43Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
D D.	0.176 , 0.200	Depositor
R, R_{free}	0.172 , 0.196	DCC
R_{free} test set	10954 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	18.3	Xtriage
Anisotropy	0.389	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	(Not available), (Not available)	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	0.97	EDS
Total number of atoms	9888	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The analyses of the Patterson function reveals a significant off-origin peak that is 34.99 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.2580e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

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: BTB, NA, 8I8, CL, 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	
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	A	0.33	0/2163	0.59	0/2945
1	В	0.33	0/2113	0.60	0/2880
1	С	0.34	0/2118	0.59	0/2888
1	D	0.31	0/2200	0.59	0/2997
All	All	0.33	0/8594	0.59	0/11710

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	2096	0	2061	9	0
1	В	2051	0	2009	5	0
1	С	2053	0	2011	8	0
1	D	2131	0	2100	6	0
2	A	3	0	0	0	0
3	A	93	0	0	1	0
3	В	93	0	0	1	0
3	С	93	0	0	2	0
3	D	93	0	0	2	0



Continued	trom	mmoninonic	maaa
COHABABACA		DIEUIUU	DUIUE
0 0 1000100000			

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	6	0	8	0	0
4	В	6	0	8	0	0
4	С	12	0	16	0	0
5	В	14	0	19	0	0
6	D	1	0	0	0	0
7	A	287	0	0	1	0
7	В	283	0	0	1	0
7	С	289	0	0	2	0
7	D	284	0	0	1	0
All	All	9888	0	8232	28	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 28 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
1:A:95[B]:ASP:HA	1:A:102:LYS:HE3	1.65	0.79
1:A:95[A]:ASP:HA	1:A:102:LYS:HE3	1.69	0.72
1:A:207:LYS:NZ	7:A:401:HOH:O	2.26	0.66
1:C:205:ARG:NH1	7:C:401:HOH:O	2.31	0.63
1:B:207:LYS:NZ	7:B:401:HOH:O	2.33	0.62

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	\mathbf{s}
1	A	270/287~(94%)	264 (98%)	5 (2%)	1 (0%)	34 13	
1	В	$264/287 \ (92\%)$	257 (97%)	7 (3%)	0	100 100	



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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	\mathbf{ntiles}
1	С	$265/287 \; (92\%)$	258 (97%)	7 (3%)	0	100	100
1	D	275/287 (96%)	269 (98%)	6 (2%)	0	100	100
All	All	1074/1148 (94%)	1048 (98%)	25 (2%)	1 (0%)	51	24

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	124	SER

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	Perce	ntiles
1	A	215/227~(95%)	213 (99%)	2 (1%)	78	54
1	В	$210/227 \ (92\%)$	207 (99%)	3 (1%)	67	37
1	С	211/227 (93%)	211 (100%)	0	100	100
1	D	$220/227 \ (97\%)$	218 (99%)	2 (1%)	78	54
All	All	856/908 (94%)	849 (99%)	7 (1%)	84	61

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	151[A]	ARG
1	В	151[B]	ARG
1	D	24	LEU
1	D	21	MET
1	В	99	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	32	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)

Of 13 ligands modelled in this entry, 4 are monoatomic - leaving 9 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	Bo	Bond lengths			Bond angles		
MIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
4	GOL	A	305	-	5,5,5	0.82	0	5,5,5	1.00	0	
4	GOL	С	301	-	5,5,5	0.95	0	5,5,5	0.96	0	
3	8I8	D	302	-	85,99,99	2.12	9 (10%)	103,150,150	2.53	18 (17%)	
5	BTB	В	302	-	13,13,13	0.40	0	7,16,16	0.55	0	
3	8I8	С	303	-	85,99,99	2.09	8 (9%)	103,150,150	2.49	18 (17%)	
3	8I8	В	303	-	85,99,99	2.13	9 (10%)	103,150,150	2.58	18 (17%)	
4	GOL	С	302	-	5,5,5	0.95	0	5,5,5	1.01	0	
3	8I8	A	304	-	85,99,99	2.12	9 (10%)	103,150,150	2.51	17 (16%)	
4	GOL	В	301	-	5,5,5	0.86	0	5,5,5	0.93	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	GOL	A	305	-	-	2/4/4/4	-
4	GOL	С	301	-	-	2/4/4/4	-
3	8I8	D	302	-	5/5/31/36	6/60/167/167	0/7/7/7
5	BTB	В	302	-	-	2/21/21/21	-
3	8I8	С	303	-	5/5/31/36	5/60/167/167	0/7/7/7
3	8I8	В	303	-	5/5/31/36	8/60/167/167	0/7/7/7
4	GOL	С	302	-	-	2/4/4/4	-
3	8I8	A	304	-	5/5/31/36	8/60/167/167	0/7/7/7
4	GOL	В	301	-	-	2/4/4/4	-

The worst 5 of 35 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(\text{\AA})$
3	В	303	8I8	C2B-C1B	-13.80	1.32	1.53
3	A	304	8I8	C2B-C1B	-13.56	1.33	1.53
3	D	302	8I8	C2B-C1B	-13.54	1.33	1.53
3	С	303	8I8	C2B-C1B	-13.23	1.33	1.53
3	С	303	8I8	C23-C22	9.00	1.53	1.35

The worst 5 of 71 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
3	В	303	8I8	O11-C13-O16	15.74	128.46	111.43
3	D	302	8I8	O11-C13-O16	15.73	128.46	111.43
3	С	303	8I8	O11-C13-O16	15.53	128.25	111.43
3	A	304	8I8	O11-C13-O16	15.07	127.74	111.43
3	A	304	8I8	O11-C13-C14	7.69	123.91	107.96

5 of 20 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	304	8I8	C14
3	A	304	8I8	C2B
3	A	304	8I8	C5
3	A	304	8I8	C13
3	A	304	8I8	C1B

5 of 37 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	304	8I8	C14-C13-O11-C11



Continued from previous page...

Mol	Chain	Res	Type	Atoms
3	A	304	8I8	S1P-C2P-C3P-N4P
3	В	303	8I8	C14-C13-O11-C11
3	В	303	8I8	S1P-C2P-C3P-N4P
3	С	303	8I8	C14-C13-O11-C11

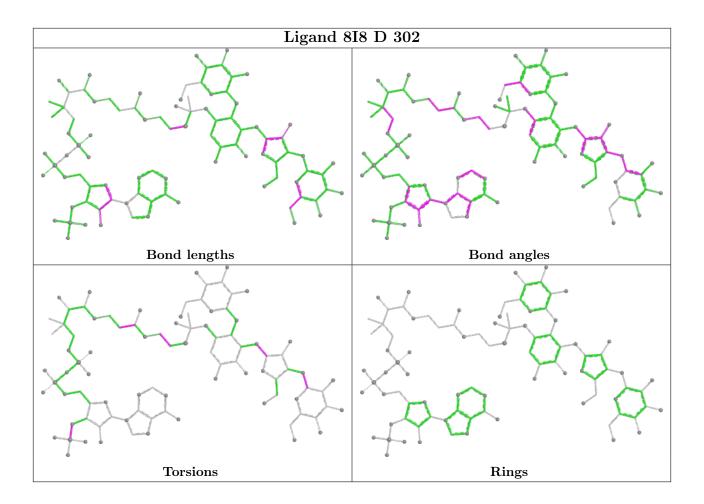
There are no ring outliers.

4 monomers are involved in 6 short contacts:

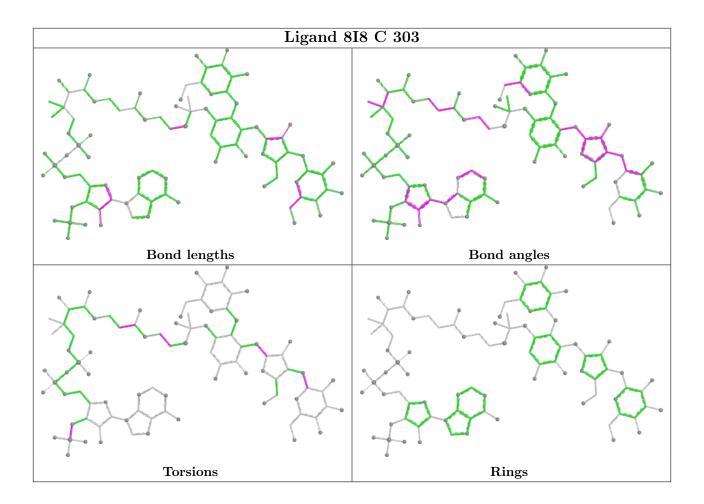
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	302	8I8	2	0
3	С	303	8I8	2	0
3	В	303	8I8	1	0
3	A	304	8I8	1	0

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.

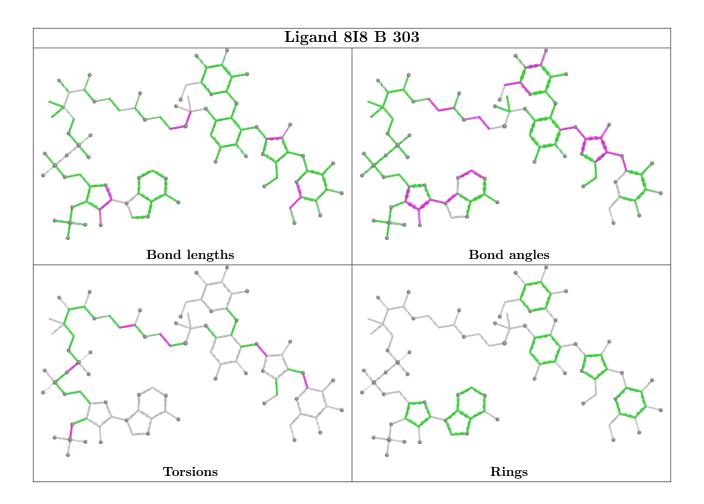




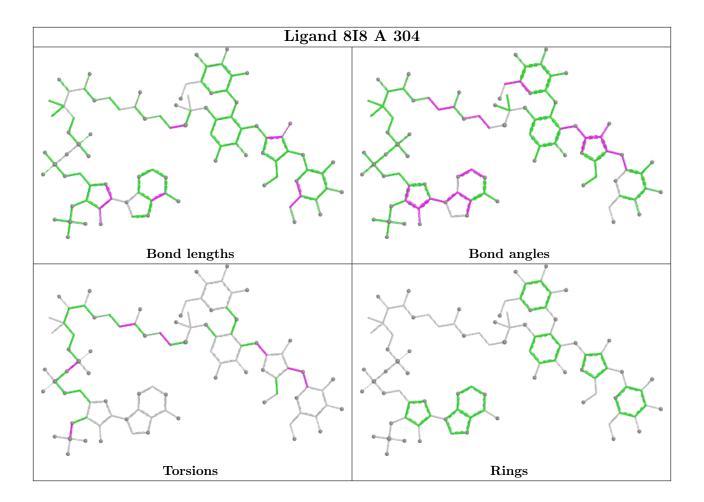












5.7 Other polymers (i)

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	Analysed	$\langle { m RSRZ} \rangle$	$\#\mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q<0.9
1	A	263/287 (91%)	-0.37	4 (1%) 73 73	15, 21, 39, 58	0
1	В	261/287 (90%)	-0.40	2 (0%) 86 86	14, 20, 36, 59	0
1	С	261/287 (90%)	-0.35	3 (1%) 80 81	13, 20, 34, 48	0
1	D	272/287 (94%)	-0.13	12 (4%) 34 35	15, 22, 41, 79	0
All	All	$1057/1148 \ (92\%)$	-0.31	21 (1%) 65 65	13, 21, 38, 79	0

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	289	SER	7.7
1	D	288	ALA	7.1
1	D	290	TYR	7.0
1	D	24	LEU	6.5
1	D	287	SER	6.4

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.

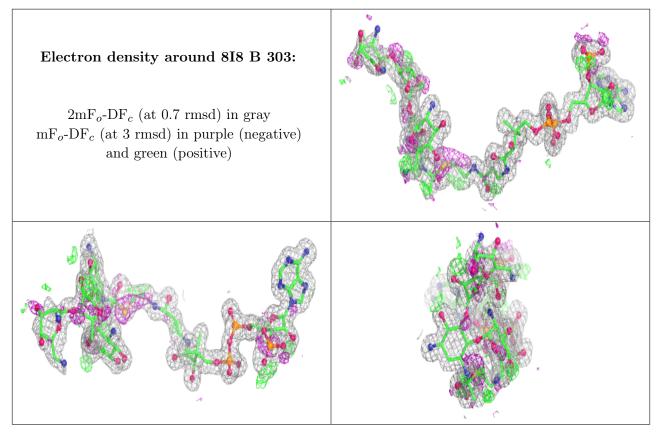
6.4 Ligands (i)

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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
2	NA	A	301	1/1	0.62	0.30	49,49,49,49	0
4	GOL	С	302	6/6	0.70	0.27	35,41,45,50	0
4	GOL	В	301	6/6	0.76	0.20	33,36,42,52	0
4	GOL	A	305	6/6	0.81	0.14	37,43,46,49	0
5	BTB	В	302	14/14	0.81	0.14	21,26,30,36	14
6	CL	D	301	1/1	0.87	0.15	58,58,58,58	0
4	GOL	С	301	6/6	0.89	0.31	45,47,49,53	0
2	NA	A	302	1/1	0.93	0.23	45,45,45,45	0
3	8I8	В	303	93/93	0.93	0.11	15,24,51,58	0
3	8I8	A	304	93/93	0.94	0.11	18,26,56,64	0
3	8I8	С	303	93/93	0.94	0.12	16,29,70,79	0
3	8I8	D	302	93/93	0.94	0.11	18,28,70,77	0
2	NA	A	303	1/1	0.97	0.07	39,39,39,39	0

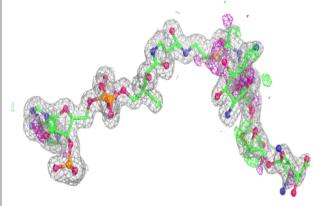
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

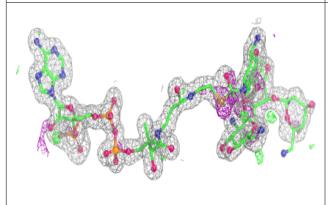


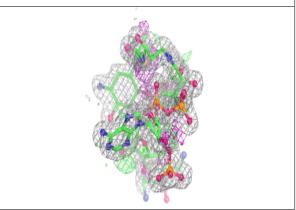


Electron density around 8I8 A 304:

 $2 \mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 0.7 rmsd) in gray $\mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)

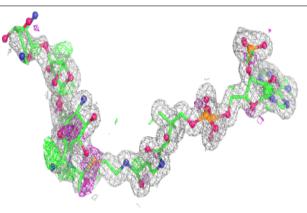


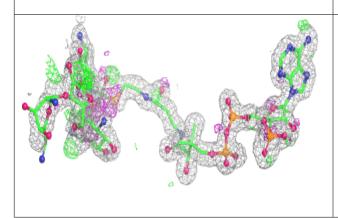


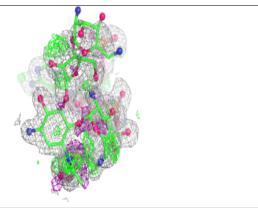


Electron density around 8I8 C 303:

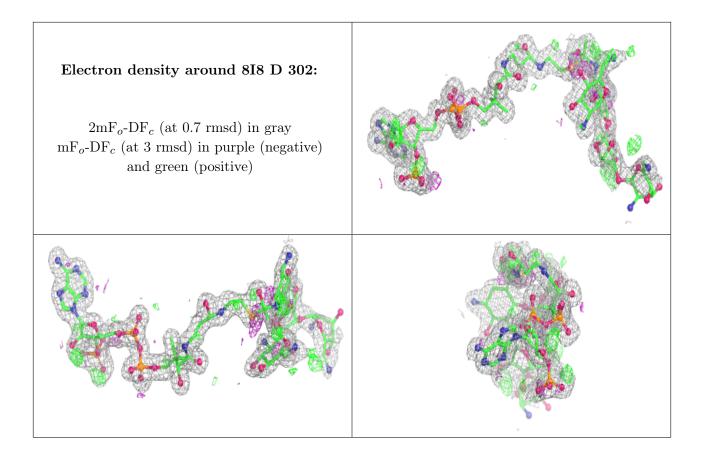
 $2 {\rm mF}_o\text{-}{\rm DF}_c$ (at 0.7 rmsd) in gray ${\rm mF}_o\text{-}{\rm DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)











6.5 Other polymers (i)

There are no such residues in this entry.

