



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2026 – 07:26 PM UTC

PDB ID : 1D21 / pdb\_00001d21  
Title : BINDING OF THE ANTITUMOR DRUG NOGALAMYCIN AND ITS DERIVATIVES TO DNA: STRUCTURAL COMPARISON  
Authors : Gao, Y.-G.; Liaw, Y.-C.; Robinson, H.; Wang, A.H.-J.  
Deposited on : 1990-08-08  
Resolution : 1.70 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtrriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

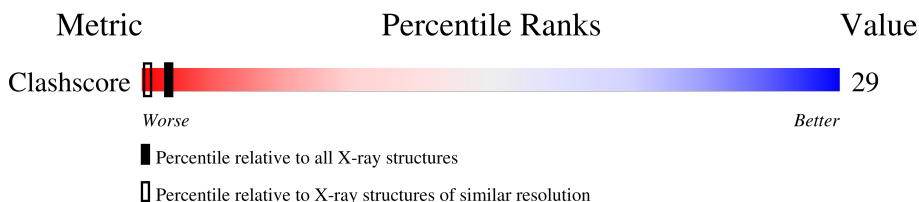
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.70 Å.



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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	5924 (1.70-1.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	6	
1	B	6	

## 2 Entry composition [i](#)

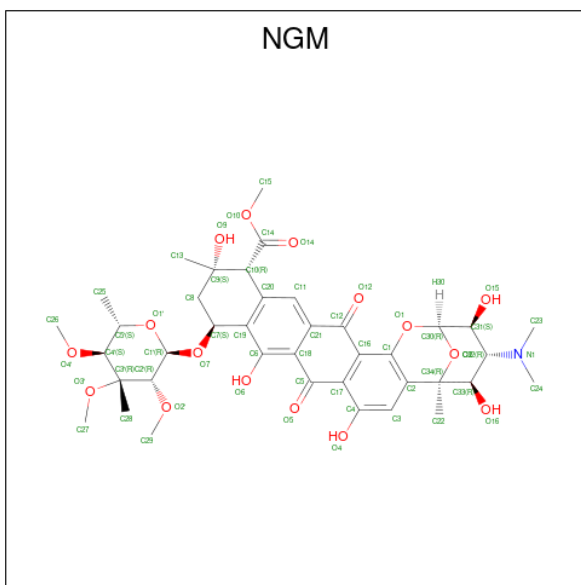
There are 3 unique types of molecules in this entry. The entry contains 433 atoms, of which 0 are hydrogens and 0 are deuteriums.

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\*(5CM)P\*GP\*TP\*(AS)P\*(5CM)P\*(G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	N	O	P				S
1	A	6	Total	C	N	O	P	S	0	0	0
			122	60	23	33	5	1			
1	B	6	Total	C	N	O	P	S	0	0	0
			122	60	23	33	5	1			

- Molecule 2 is NOGALAMYCIN (CCD ID: NGM) (formula: C<sub>39</sub>H<sub>49</sub>NO<sub>16</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
			Total	C	N			O
2	A	1	Total	C	N	O	0	0
			56	39	1	16		
2	B	1	Total	C	N	O	0	0
			56	39	1	16		

- Molecule 3 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
3	A	45	Total 45	O 45	0	0
3	B	32	Total 32	O 32	0	0

### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

- Molecule 1: DNA (5'-D\*(5CM)P\*GP\*TP\*(AS)P\*(5CM)P\*G)-3')

Chain A:  67% 33%



- Molecule 1: DNA (5'-D\*(5CM)P\*GP\*TP\*(AS)P\*(5CM)P\*G)-3')

Chain B:  17% 83%



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	26.31Å 26.31Å 100.25Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	(Not available) – 1.70	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-1.70)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	NUCLSQ	Depositor
R, $R_{free}$	0.208 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	433	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	21.0	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: AS, NGM, 5CM

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	2.03	4/70 (5.7%)	4.56	15/104 (14.4%)
1	B	1.99	2/70 (2.9%)	2.86	10/104 (9.6%)
All	All	2.01	6/140 (4.3%)	3.81	25/208 (12.0%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	12	DG	O4'-C1'	8.79	1.59	1.41
1	A	6	DG	P-OP2	6.36	1.61	1.48
1	A	2	DG	O4'-C1'	6.18	1.54	1.41
1	A	3	DT	O4'-C1'	5.50	1.52	1.41
1	B	12	DG	P-O5'	5.40	1.71	1.60
1	A	2	DG	O3'-P	5.20	1.69	1.61

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2	DG	P-O5'-C5'	26.86	160.30	120.00
1	A	3	DT	P-O5'-C5'	13.01	139.51	120.00
1	A	6	DG	P-O5'-C5'	-11.70	102.45	120.00
1	A	2	DG	P-O3'-C3'	9.29	134.13	120.20
1	A	2	DG	O5'-C5'-C4'	-8.71	97.73	110.80
1	A	2	DG	O4'-C1'-C2'	-8.67	93.39	106.40
1	A	3	DT	O4'-C1'-C2'	-8.24	94.04	106.40
1	B	8	DG	P-O5'-C5'	-8.19	107.72	120.00
1	B	12	DG	OP1-P-OP2	-8.01	95.98	120.00
1	A	6	DG	N9-C1'-C2'	-7.10	102.85	113.50
1	B	12	DG	O4'-C1'-C2'	-6.73	96.30	106.40
1	A	2	DG	C3'-C2'-C1'	-6.55	91.78	101.60
1	A	2	DG	C1'-O4'-C4'	-6.29	100.26	109.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	6	DG	N3-C2-N2	-6.22	110.38	119.70
1	B	9	DT	O5'-P-OP2	6.19	126.57	108.00
1	A	2	DG	O5'-P-OP2	6.13	126.39	108.00
1	B	12	DG	O4'-C1'-N9	-6.04	99.35	108.40
1	A	3	DT	O5'-C5'-C4'	-5.73	102.20	110.80
1	B	12	DG	O5'-P-OP1	5.69	126.07	109.00
1	A	3	DT	C6-C5-C7	-5.49	115.76	124.00
1	B	9	DT	C5'-C4'-O4'	5.42	117.53	109.40
1	B	8	DG	O5'-C5'-C4'	-5.40	102.71	110.80
1	A	3	DT	C1'-O4'-C4'	-5.34	101.69	109.70
1	B	12	DG	N9-C1'-C2'	5.27	121.40	113.50
1	B	12	DG	O5'-C5'-C4'	-5.25	102.92	110.80

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	122	0	72	2	0
1	B	122	0	72	9	0
2	A	56	0	47	4	0
2	B	56	0	47	10	1
3	A	45	0	0	0	1
3	B	32	0	0	1	0
All	All	433	0	238	17	1

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 29.

All (17) 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:B:11:5CM:H5A3	3:B:59:HOH:O	1.72	0.88
1:B:7:5CM:O2	2:B:13:NGM:H153	1.90	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:10:AS:O4'	2:B:13:NGM:H272	1.95	0.66
2:B:13:NGM:H282	2:B:13:NGM:H132	1.77	0.66
1:B:9:DT:H2''	1:B:10:AS:H5'	1.86	0.58
1:A:4:AS:H5'	2:A:14:NGM:H263	1.88	0.55
1:B:9:DT:H1'	2:B:13:NGM:C28	2.37	0.55
1:B:7:5CM:H2''	2:B:13:NGM:H151	1.90	0.54
2:A:14:NGM:H293	1:B:12:DG:H4'	1.90	0.52
1:B:9:DT:H1'	2:B:13:NGM:H281	1.94	0.50
2:B:13:NGM:H133	2:B:13:NGM:H5'	1.95	0.47
2:B:13:NGM:H282	2:B:13:NGM:C13	2.44	0.47
2:B:13:NGM:H132	2:B:13:NGM:O7	2.16	0.45
1:B:9:DT:C2'	1:B:10:AS:H5'	2.47	0.44
2:B:13:NGM:C25	2:B:13:NGM:H263	2.48	0.44
1:A:2:DG:O6	2:A:14:NGM:H32	2.19	0.43
2:A:14:NGM:H282	2:A:14:NGM:O7	2.19	0.42

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:13:NGM:C24	3:A:52:HOH:O[1_445]	1.99	0.21

### 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

6 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
1	AS	A	4	1	20,23,24	1.65	4 (20%)	28,33,36	2.47	8 (28%)
1	5CM	B	11	1	18,21,22	0.98	0	24,30,33	2.58	9 (37%)
1	5CM	B	7	1	18,18,22	1.90	4 (22%)	25,26,33	1.81	6 (24%)
1	5CM	A	5	1	18,21,22	0.99	0	24,30,33	1.98	6 (25%)
1	5CM	A	1	1	18,18,22	2.07	2 (11%)	25,26,33	2.88	15 (60%)
1	AS	B	10	1	20,23,24	1.52	5 (25%)	28,33,36	1.79	5 (17%)

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
1	AS	A	4	1	-	0/7/21/22	0/3/3/3
1	5CM	B	11	1	-	0/7/21/22	0/2/2/2
1	5CM	B	7	1	-	2/6/18/22	0/2/2/2
1	5CM	A	5	1	-	0/7/21/22	0/2/2/2
1	5CM	A	1	1	-	0/6/18/22	0/2/2/2
1	AS	B	10	1	-	2/7/21/22	0/3/3/3

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1	5CM	C5-C4	-7.63	1.38	1.44
1	B	7	5CM	C5-C4	-4.53	1.40	1.44
1	B	7	5CM	O4'-C1'	4.02	1.51	1.42
1	A	4	AS	O4'-C1'	3.86	1.51	1.42
1	B	10	AS	C8-N9	-3.44	1.31	1.37
1	B	7	5CM	C2'-C1'	-3.28	1.43	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	7	5CM	O3'-C3'	2.81	1.49	1.43
1	A	4	AS	C2'-C3'	-2.67	1.46	1.52
1	A	4	AS	O4'-C4'	-2.62	1.39	1.45
1	A	4	AS	C2'-C1'	2.45	1.59	1.52
1	B	10	AS	O4'-C4'	-2.44	1.39	1.45
1	B	10	AS	C6-N6	-2.36	1.28	1.34
1	B	10	AS	C5-N7	2.18	1.43	1.39
1	A	1	5CM	C2'-C1'	-2.16	1.46	1.52
1	B	10	AS	C4-N9	2.07	1.42	1.37

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	4	AS	C2-N1-C6	7.50	131.05	118.73
1	B	11	5CM	O4'-C1'-N1	7.46	121.10	107.86
1	A	5	5CM	O4'-C1'-N1	6.49	119.39	107.86
1	A	1	5CM	O2-C2-N3	6.00	131.79	122.33
1	A	1	5CM	O4'-C4'-C3'	-5.92	92.16	105.65
1	B	10	AS	C2-N1-C6	5.55	127.86	118.73
1	A	4	AS	O3'-C3'-C2'	4.95	128.07	110.88
1	A	4	AS	N3-C2-N1	-4.79	121.33	128.58
1	B	7	5CM	C5'-C4'-C3'	4.69	126.51	114.82
1	B	11	5CM	C2'-C1'-N1	-4.40	102.80	113.81
1	A	1	5CM	C1'-N1-C2	-4.30	110.44	117.83
1	A	4	AS	O4'-C1'-C2'	-4.30	98.22	106.25
1	A	1	5CM	C4'-O4'-C1'	-4.25	99.41	109.51
1	B	10	AS	N3-C2-N1	-4.08	122.41	128.58
1	A	4	AS	O4'-C1'-N9	-4.02	100.73	107.96
1	B	11	5CM	C5-C6-N1	-3.84	119.14	123.31
1	A	1	5CM	C5-C6-N1	-3.80	119.19	123.31
1	A	1	5CM	C2'-C3'-C4'	-3.61	95.47	102.80
1	A	1	5CM	C1'-N1-C6	3.42	126.48	120.74
1	B	11	5CM	O4'-C1'-C2'	3.40	112.60	106.25
1	B	11	5CM	C5A-C5-C6	-3.31	118.37	122.85
1	B	7	5CM	C2'-C3'-C4'	3.28	109.45	102.80
1	B	11	5CM	C1'-N1-C2	-3.24	112.27	117.83
1	A	5	5CM	C5-C4-N3	-3.19	118.49	121.75
1	A	1	5CM	O4'-C4'-C5'	-3.04	102.79	109.22
1	B	10	AS	N6-C6-N1	2.99	125.03	118.38
1	A	5	5CM	O3'-C3'-C2'	-2.92	100.74	110.88
1	B	11	5CM	C5-C4-N3	-2.90	118.78	121.75
1	B	7	5CM	O5'-C5'-C4'	2.89	121.19	111.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1	5CM	O2-C2-N1	-2.84	113.33	118.90
1	B	11	5CM	C1'-N1-C6	2.82	125.47	120.74
1	A	4	AS	C5-C6-N1	-2.73	110.58	117.51
1	A	1	5CM	C4-N3-C2	2.72	124.59	120.81
1	B	11	5CM	O3'-C3'-C4'	2.65	120.10	110.07
1	B	7	5CM	C5-C4-N3	-2.61	119.08	121.75
1	A	1	5CM	C5'-C4'-C3'	2.58	121.25	114.82
1	B	10	AS	N9-C8-N7	2.46	117.43	113.94
1	B	7	5CM	O3'-C3'-C2'	-2.45	102.38	110.88
1	A	4	AS	C5-C6-N6	2.37	129.16	123.29
1	B	10	AS	C5-C4-N9	-2.36	103.24	105.81
1	A	1	5CM	C5A-C5-C6	-2.32	119.71	122.85
1	A	1	5CM	N1-C2-N3	-2.28	114.84	118.80
1	A	4	AS	O4'-C4'-C5'	2.25	116.55	109.33
1	A	1	5CM	C2'-C1'-N1	2.24	119.40	113.81
1	A	5	5CM	N4-C4-N3	2.23	122.55	118.51
1	A	1	5CM	O5'-C5'-C4'	-2.23	103.73	111.33
1	A	5	5CM	C4-N3-C2	2.15	123.79	120.81
1	A	5	5CM	C2'-C3'-C4'	2.03	106.92	102.80
1	B	7	5CM	O2-C2-N1	2.01	122.83	118.90

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	10	AS	O4'-C4'-C5'-O5'
1	B	10	AS	C3'-C4'-C5'-O5'
1	B	7	5CM	C2'-C1'-N1-C6
1	B	7	5CM	C2'-C1'-N1-C2

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	4	AS	1	0
1	B	11	5CM	1	0
1	B	7	5CM	2	0
1	B	10	AS	3	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides 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	NGM	A	14	-	59,62,62	2.36	20 (33%)	72,101,101	2.27	26 (36%)
2	NGM	B	13	-	59,62,62	2.42	23 (38%)	72,101,101	2.37	25 (34%)

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	NGM	A	14	-	-	7/21/113/113	0/1/7/7
2	NGM	B	13	-	-	3/21/113/113	0/1/7/7

All (43) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	14	NGM	O2-C30	7.14	1.55	1.42
2	B	13	NGM	C13-C9	-6.24	1.42	1.52
2	B	13	NGM	C28-C3'	5.39	1.64	1.52
2	B	13	NGM	C1'-C2'	5.29	1.61	1.53
2	A	14	NGM	C13-C9	-5.24	1.44	1.52
2	B	13	NGM	C6-C19	5.14	1.48	1.40
2	A	14	NGM	C24-N1	5.12	1.64	1.46
2	A	14	NGM	C20-C10	4.46	1.57	1.52
2	B	13	NGM	O2-C30	4.20	1.49	1.42
2	A	14	NGM	C28-C3'	4.16	1.61	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	13	NGM	C20-C10	3.94	1.57	1.52
2	A	14	NGM	C11-C21	3.77	1.45	1.39
2	B	13	NGM	C18-C6	-3.51	1.35	1.41
2	A	14	NGM	C8-C7	3.47	1.58	1.52
2	B	13	NGM	O1'-C5'	3.46	1.52	1.44
2	A	14	NGM	O4-C4	-3.44	1.29	1.36
2	A	14	NGM	C3-C2	3.43	1.44	1.39
2	B	13	NGM	O1-C1	-3.41	1.32	1.37
2	B	13	NGM	C11-C21	3.34	1.45	1.39
2	A	14	NGM	C25-C5'	3.23	1.59	1.51
2	B	13	NGM	O1-C30	3.21	1.49	1.42
2	B	13	NGM	C8-C7	3.19	1.58	1.52
2	B	13	NGM	C8-C9	3.17	1.59	1.53
2	A	14	NGM	C1'-C2'	3.06	1.57	1.53
2	B	13	NGM	C24-N1	3.03	1.56	1.46
2	B	13	NGM	C3-C2	3.00	1.43	1.39
2	B	13	NGM	O9-C9	2.94	1.49	1.44
2	B	13	NGM	C22-C34	2.92	1.57	1.52
2	B	13	NGM	O3'-C3'	-2.86	1.33	1.45
2	B	13	NGM	C23-N1	-2.76	1.36	1.46
2	A	14	NGM	C21-C18	2.76	1.45	1.41
2	A	14	NGM	O9-C9	2.74	1.48	1.44
2	A	14	NGM	C1-C2	-2.73	1.36	1.41
2	B	13	NGM	C16-C12	2.69	1.54	1.47
2	A	14	NGM	C6-C19	2.59	1.44	1.40
2	A	14	NGM	C8-C9	2.49	1.58	1.53
2	B	13	NGM	C4'-C5'	-2.37	1.45	1.52
2	A	14	NGM	C22-C34	2.31	1.56	1.52
2	A	14	NGM	C18-C5	-2.29	1.42	1.47
2	A	14	NGM	C34-C2	2.27	1.56	1.52
2	B	13	NGM	C32-N1	2.20	1.55	1.48
2	B	13	NGM	O12-C12	2.12	1.26	1.22
2	A	14	NGM	C18-C6	-2.00	1.37	1.41

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	13	NGM	C26-O4'-C4'	-9.52	98.36	114.46
2	A	14	NGM	O10-C14-O14	-6.58	111.04	123.85
2	B	13	NGM	C27-O3'-C3'	6.07	133.13	117.70
2	B	13	NGM	C31-C32-C33	5.36	118.71	110.57
2	A	14	NGM	C29-O2'-C2'	4.57	122.18	114.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	14	NGM	C11-C20-C19	4.53	126.24	119.70
2	A	14	NGM	C28-C3'-C2'	-4.28	102.80	111.55
2	B	13	NGM	C3-C2-C1	4.23	123.06	117.15
2	B	13	NGM	O16-C33-C34	4.23	119.56	110.23
2	A	14	NGM	C24-N1-C23	-4.01	98.70	110.49
2	A	14	NGM	C27-O3'-C3'	3.98	127.83	117.70
2	A	14	NGM	C3-C2-C1	3.90	122.60	117.15
2	B	13	NGM	O1'-C1'-C2'	-3.82	104.85	112.33
2	B	13	NGM	C11-C20-C19	3.64	124.96	119.70
2	A	14	NGM	C30-C31-C32	3.63	115.04	109.20
2	A	14	NGM	O7-C1'-O1'	3.61	120.18	110.69
2	A	14	NGM	O10-C14-C10	3.58	117.62	110.74
2	A	14	NGM	C34-C33-C32	3.55	115.81	110.50
2	B	13	NGM	O10-C14-C10	-3.51	103.98	110.74
2	A	14	NGM	O14-C14-C10	3.45	131.04	125.22
2	A	14	NGM	C6-C19-C20	-3.41	115.06	118.84
2	A	14	NGM	C26-O4'-C4'	3.39	120.18	114.46
2	B	13	NGM	O9-C9-C8	-3.32	100.66	108.05
2	A	14	NGM	O1'-C5'-C25	-3.31	99.39	106.74
2	B	13	NGM	C6-C19-C20	-3.22	115.28	118.84
2	B	13	NGM	O2'-C2'-C1'	-3.17	102.03	110.98
2	A	14	NGM	O15-C31-C32	3.06	117.07	109.14
2	A	14	NGM	O7-C1'-C2'	3.04	115.01	109.09
2	A	14	NGM	C11-C20-C10	-2.99	114.56	121.16
2	B	13	NGM	C34-C33-C32	2.92	114.87	110.50
2	A	14	NGM	O5-C5-C18	-2.92	116.56	121.44
2	B	13	NGM	O15-C31-C32	2.91	116.68	109.14
2	B	13	NGM	O12-C12-C21	-2.89	116.82	120.99
2	A	14	NGM	O12-C12-C21	-2.71	117.07	120.99
2	A	14	NGM	C4-C3-C2	-2.71	116.50	120.16
2	B	13	NGM	C11-C21-C12	-2.66	114.44	119.21
2	B	13	NGM	C23-N1-C32	2.62	120.92	113.25
2	B	13	NGM	O14-C14-C10	2.54	129.52	125.22
2	B	13	NGM	O1'-C5'-C25	-2.45	101.31	106.74
2	A	14	NGM	C3-C4-C17	2.44	123.65	120.92
2	B	13	NGM	O4-C4-C3	-2.44	112.88	119.45
2	B	13	NGM	O4-C4-C17	2.39	125.57	121.14
2	B	13	NGM	C29-O2'-C2'	-2.31	110.55	114.46
2	B	13	NGM	C20-C10-C14	-2.30	104.86	110.17
2	B	13	NGM	O12-C12-C16	2.25	125.19	121.44
2	A	14	NGM	O1'-C1'-C2'	-2.17	108.09	112.33
2	B	13	NGM	C1'-O1'-C5'	-2.17	109.94	113.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	14	NGM	O12-C12-C16	2.09	124.93	121.44
2	A	14	NGM	C16-C17-C5	2.03	122.74	120.00
2	A	14	NGM	C25-C5'-C4'	-2.03	109.52	113.55
2	B	13	NGM	C11-C21-C18	2.02	122.92	120.33

There are no chirality outliers.

All (10) torsion outliers are listed below:

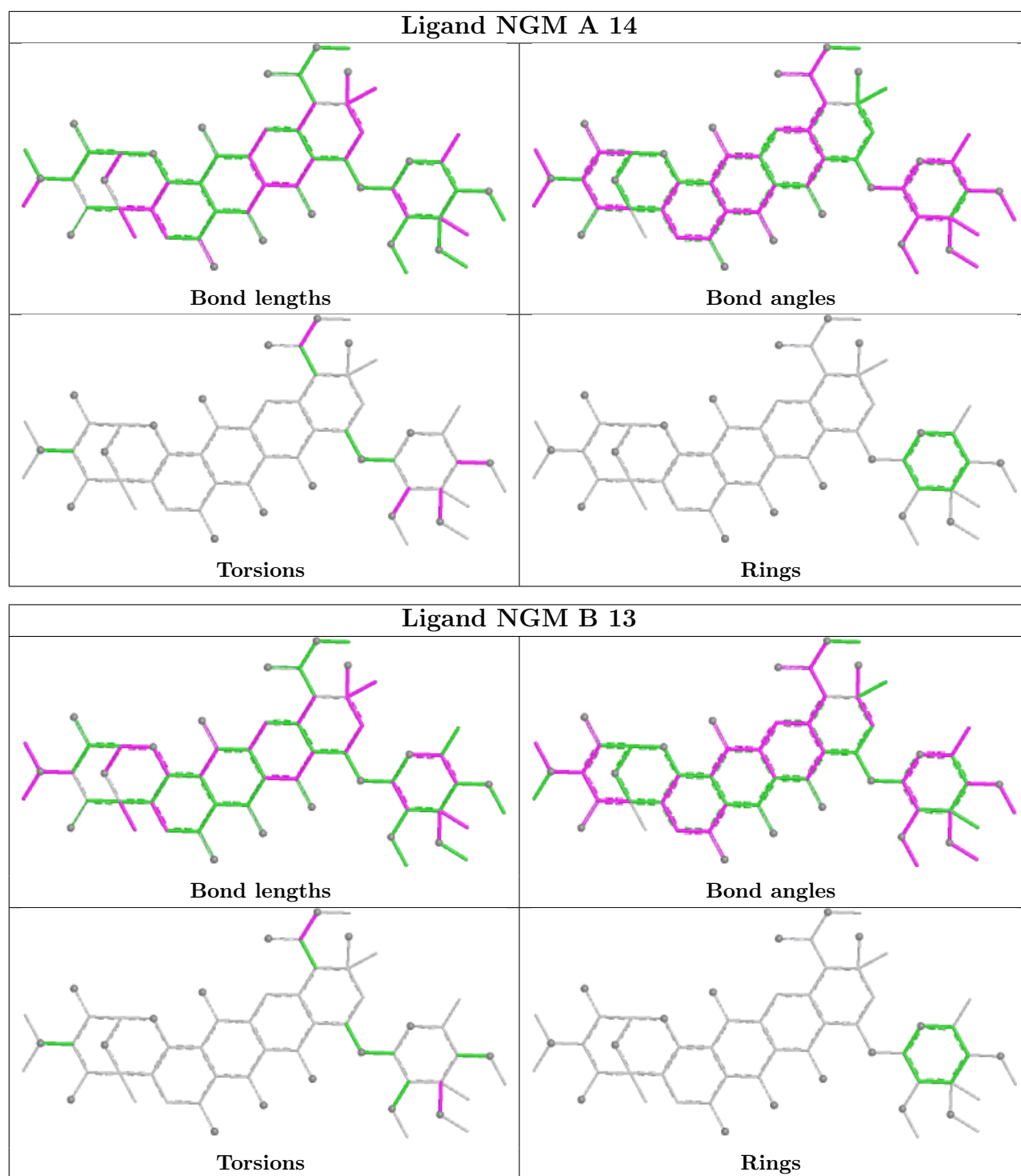
Mol	Chain	Res	Type	Atoms
2	B	13	NGM	C10-C14-O10-C15
2	A	14	NGM	C10-C14-O10-C15
2	B	13	NGM	C28-C3'-O3'-C27
2	A	14	NGM	O14-C14-O10-C15
2	A	14	NGM	C3'-C4'-O4'-C26
2	A	14	NGM	C5'-C4'-O4'-C26
2	A	14	NGM	C3'-C2'-O2'-C29
2	A	14	NGM	C1'-C2'-O2'-C29
2	A	14	NGM	C4'-C3'-O3'-C27
2	B	13	NGM	C4'-C3'-O3'-C27

There are no ring outliers.

2 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	14	NGM	4	0
2	B	13	NGM	10	1

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

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.