

Full wwPDB NMR Structure Validation Report (i)

May 28, 2020 – 08:39 pm BST

PDB ID : 1QMS

Title : Head-to-Tail Dimer of Calicheamicin gamma-1-I Oligosaccharide Bound to

DNA Duplex, NMR, 9 Structures

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Deposited on : 1999-10-06

This is a Full wwPDB NMR 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/NMRValidationReportHelp with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

Cyrange : Kirchner and Güntert (2011)

NmrClust : Kelley et al. (1996)

MolProbity: 4.02b-467

Mogul: 1.8.5 (274361), CSD as541be (2020)

buster-report : 1.1.7 (2018)

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

RCI : v 1n 11 5 13 A (Berjanski et al., 2005)

PANAV : Wang et al. (2010)

ShiftChecker : 2.11

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

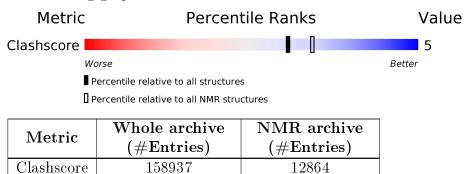
Validation Pipeline (wwPDB-VP) : 2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $SOLUTION\ NMR$

The overall completeness of chemical shifts assignment was not calculated.

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.



The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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%

Mol	Chain	Length	Quality of chain					
1	A	12	50%	42%	8%			
2	В	12	33%	50%	17%			



2 Ensemble composition and analysis (i)

This entry contains 9 models. This entry does not contain polypeptide chains, therefore identification of well-defined residues and clustering analysis are not possible. All residues are included in the validation scores.



3 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 1009 atoms, of which 401 are hydrogens and 0 are deuteriums.

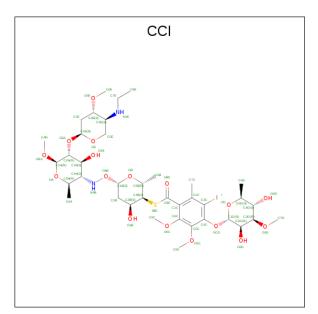
• Molecule 1 is a DNA chain called DNA (5'-D(*GP*CP*AP*CP*CP*TP*TP*CP*CP*TP* GP*C)-3').

Mol	Chain	Residues	Atoms					Trace	
1	Λ	19	Total	С	Н	Ν	О	Р	0
	A 12	373	114	137	39	72	11	. 0	

• Molecule 2 is a DNA chain called DNA (5'-D(*GP*CP*AP*GP*GP*AP*AP*GP*GP*TP*GP*C)-3').

Mol	Chain	Residues	Atoms					Trace	
9	D	10	Total	С	Н	Ν	О	Р	0
$\begin{vmatrix} 2 & B \end{vmatrix}$	12	385	118	135	53	68	11	U	

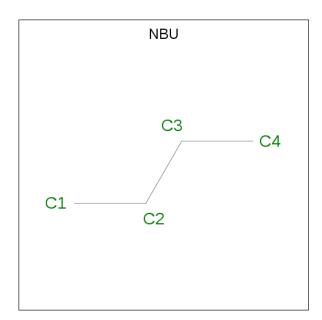
• Molecule 3 is CALICHEAMICIN GAMMA-1-OLIGOSACCHARIDE (three-letter code: CCI) (formula: C₃₈H₆₁IN₂O₁₇S).



Mol	Chain	Residues	Atoms						
3 B	1	Total	С	Н	I	N	О	S	
	Б	1	120	38	61	1	2	17	1
9	2 D	1	Total	С	Н	I	N	О	S
3	D		119	38	60	1	2	17	1

• Molecule 4 is N-BUTANE (three-letter code: NBU) (formula: C₄H₁₀).





Mol	Chain	Residues	Atoms		
4	D	1	Total	С	Н
4	Б	1	12	4	8

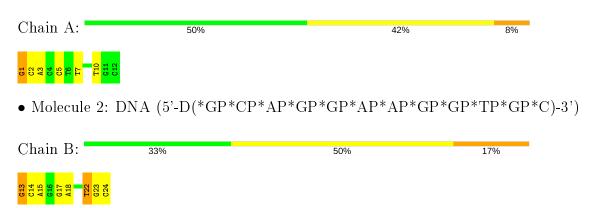


4 Residue-property plots (i)

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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 outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.





4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: DNA (5'-D(*GP*CP*AP*CP*CP*TP*TP*CP*CP*TP*GP*C)-3')

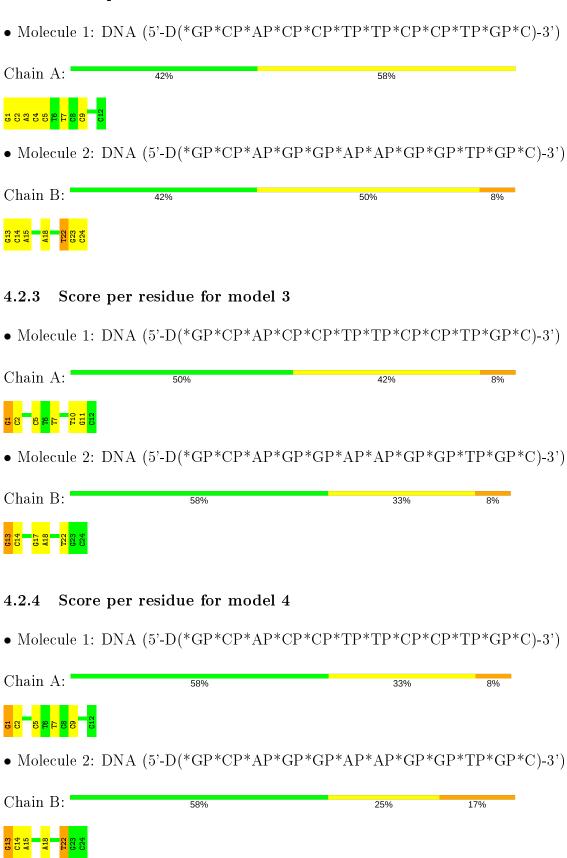


• Molecule 2: DNA (5'-D(*GP*CP*AP*GP*GP*AP*AP*AP*GP*GP*TP*GP*C)-3')





4.2.2 Score per residue for model 2





4.2.5 Score per residue for model 5

• Molecule 1: DNA (5'-D(*GP*CP*AP*CP*CP*TP*TP*CP*CP*TP*GP*C)-3')

Chain A: 58% 33% 8%

G1 C2 A3 T10 G11

• Molecule 2: DNA (5'-D(*GP*CP*AP*GP*GP*AP*AP*AP*GP*GP*TP*GP*C)-3')

Chain B: 42% 33% 25%

G13 C14 G17 A18 T22 G23 C24

4.2.6 Score per residue for model 6

• Molecule 1: DNA (5'-D(*GP*CP*AP*CP*CP*TP*TP*CP*CP*TP*GP*C)-3')

Chain A: 33% 50% 17%

G1 G2 G4 C4 C5 G5 G1 G11 G11 G11 G11

• Molecule 2: DNA (5'-D(*GP*CP*AP*GP*GP*AP*AP*AP*GP*GP*TP*GP*C)-3')

Chain B: 33% 42% 25%

613 C14 A15 G17 A18 T22 T22 C24

4.2.7 Score per residue for model 7

• Molecule 1: DNA (5'-D(*GP*CP*AP*CP*CP*TP*TP*CP*CP*TP*GP*C)-3')

Chain A: 50% 33% 17%

G1 C2 C2 C4 C4 C5 C5 T7 T7 T10 C12

• Molecule 2: DNA (5'-D(*GP*CP*AP*GP*GP*AP*AP*GP*GP*TP*GP*C)-3')

Chain B: 42% 33% 25%

613 C14 A15 A18 T22 G23 C24



4.2.8 Score per residue for model 8

 \bullet Molecule 1: DNA (5'-D(*GP*CP*AP*CP*CP*TP*TP*CP*CP*TP*GP*C)-3')

Chain A: 42% 50% 8%



• Molecule 2: DNA (5'-D(*GP*CP*AP*GP*GP*AP*AP*GP*GP*TP*GP*C)-3')

Chain B: 42% 42% 17%



4.2.9 Score per residue for model 9

• Molecule 1: DNA (5'-D(*GP*CP*AP*CP*CP*TP*TP*CP*CP*TP*GP*C)-3')

Chain A: 58% 33% 8%



• Molecule 2: DNA (5'-D(*GP*CP*AP*GP*GP*AP*AP*GP*GP*TP*GP*C)-3')

Chain B: 58% 25% 17%

613 C14 A18 T22 T22 C24



5 Refinement protocol and experimental data overview (i)



The models were refined using the following method: RESTRAINED MOLECULAR DYNAM-ICS.

Of the 20 calculated structures, 9 were deposited, based on the following criterion: LOWEST RESTRAINT VIOLATION.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
Amber	refinement	4.1
Amber	structure solution	4.1

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

COVALENT-GEOMETRY INFOmissingINFO

5.1Too-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 each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
2	В	250	135	135	0±0
3	В	118	121	120	5±1
All	All	5472	3609	3600	42

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 5.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	$Distance(\mathring{A})$	Models	
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total
3:B:27:CCI:C3C	3:B:27:CCI:I	0.79	3.01	8	5
3:B:27:CCI:I	3:B:27:CCI:C3C	0.78	3.02	3	4
3:B:27:CCI:H7C1	3:B:27:CCI:SBC	0.76	2.20	8	1
3:B:25:CCI:C3C	3:B:25:CCI:I	0.75	3.04	9	4
3:B:25:CCI:I	3:B:25:CCI:C3C	0.74	3.06	7	5
3:B:27:CCI:H7C1	3:B:27:CCI:OBC	0.66	1.91	4	6
3:B:25:CCI:H7C1	3:B:25:CCI:OBC	0.64	1.93	5	5
3:B:25:CCI:OBC	3:B:25:CCI:H7C1	0.64	1.93	6	4

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Atom-1	Atom-2	Clash(Å)	$\mathbf{Distance}(\mathbf{\mathring{A}})$	${f Models}$	
Atom-1			Distance(A)	Worst	Total
3:B:25:CCI:H7C2	3:B:27:CCI:H6E1	0.50	1.82	9	1
3:B:27:CCI:H2D	3:B:27:CCI:C8C	0.47	2.40	1	1
2:B:17:DG:H21	3:B:27:CCI:H7C1	0.47	1.70	6	1
3:B:27:CCI:OAB	3:B:27:CCI:H6A3	0.45	2.12	3	2
3:B:25:CCI:C6A	3:B:25:CCI:OAB	0.43	2.66	4	1
3:B:25:CCI:H7D2	3:B:27:CCI:H6E2	0.42	1.90	9	1
3:B:27:CCI:OAB	3:B:27:CCI:C6A	0.41	2.68	3	1

5.2 Torsion angles (i)

5.2.1 Protein backbone (i)

There are no protein molecules in this entry.

5.2.2 Protein sidechains (i)

There are no protein molecules in this entry.

5.2.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.4 Carbohydrates (i)

There are no carbohydrates in this entry.

 ${\bf LIGAND\text{-}GEOMETRY\ INFOmissing INFO}$

5.5 Other polymers (i)

There are no such molecules in this entry.



5.6 Polymer linkage issues (i)

There are no chain breaks in this entry.



6 Chemical shift validation (i)

No chemical shift data were provided

