

wwPDB X-ray Structure Validation Summary Report (i)

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PDB ID	:	1D3R
Title	:	CRYSTAL STRUCTURE OF TRIPLEX DNA
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Deposited on		
Resolution	:	1.80 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	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
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)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 1.80 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	Percentile Rank	s Value
Clashscore		17
Worse		Better
Percentile relati	ive to all X-ray structures	
Percentile relati	ive to X-ray structures of similar resolution	1
Wh	ole archive	Similar resolution

	Matria	Whole archive	Similar resolution
Metric		$(\# {\rm Entries})$	$(\# {\rm Entries}, {\rm resolution} {\rm range}({ m \AA}))$
(Clashscore	141614	6793 (1.80-1.80)

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%

Note EDS was not executed.

Mol	Chain	Length		Quality of chain		
1	А	12	50%	17%	25%	8%
1	С	12	33%	33%	33%	
2	В	9	44%		56%	
2	D	9	44%	33%	11%	11%



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 980 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(*CP*(BRU)P*CP*CP*(BRU)P*CP*CP*GP *CP*GP)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
1	А	12	Total 236		C 111		-		0	0	0
1	С	12	Total 236		-		0 72	Р 11	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
0	В	0	Total	С	Ν	Ο	Р	0	0	0
	2 D	9	185	87	39	51	8	0		
0	Л	Q	Total	С	Ν	Ο	Р	0	0	0
	D	0	166	78	36	45	7	0		0

• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	46	Total O 46 46	0	0
3	В	22	Total O 22 22	0	0
3	С	47	Total O 47 47	0	0
3	D	42	$\begin{array}{cc} \text{Total} & \text{O} \\ 42 & 42 \end{array}$	0	0





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. 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(*CP*(BRU)P*CP*CP*(BRU)P*CP*CP*GP*CP*GP*CP*G)-3')

Chain A:	50%	17%	25%	8%
C 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2				
• Molecule	e 1: DNA (5'-D(*CP*(BRU)P*CP*CP*(BF	RU)P*CP*CP*C	GP*CF
Chain C:	33%	33%	33%	
C31 C32 C33 C34 C36 C36 C37 C37	650 67 7 7 7 7 7			
• Molecul	e 2: DNA (5'-D(*CP*	GP*CP*GP*CP*GP	*GP*AP*G)-3')
Chain B:	44%		56%	
C13 G14 G18 G19 G21 G21				
• Molecul	e 2: DNA (5'-D(*CP*	GP*CP*GP*CP*GP	*GP*AP*G)-3')
			, ,	, ,
Chain D:	44%	33%	11%	11%
DC 644 646 646 649 649 650				



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 42	Depositor
Cell constants	53.80Å 53.80Å 43.10Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 - 1.80	Depositor
% Data completeness	96.3 (20.00-1.80)	Depositor
(in resolution range)	30.3 (20.00-1.00)	Depositor
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.210 , 0.275	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	980	wwPDB-VP
Average B, all atoms $(Å^2)$	29.0	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: BRU

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	Bon	d lengths	Bond angles		
10101	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	1.07	0/216	1.43	3/325~(0.9%)	
1	С	1.12	1/216~(0.5%)	1.26	3/325~(0.9%)	
2	В	0.93	0/208	1.04	0/320	
2	D	1.08	0/187	1.24	1/288~(0.3%)	
All	All	1.05	1/827~(0.1%)	1.25	7/1258~(0.6%)	

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	А	1	1
1	С	0	1
2	В	0	1
2	D	0	1
All	All	1	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	С	42	DG	C5-C6	-5.07	1.37	1.42

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
2	D	44	DG	O5'-C5'-C4'	9.41	134.53	111.00
1	А	12	DG	C4'-C3'-O3'	8.79	131.68	109.70
1	С	40	DG	N9-C1'-C2'	5.40	122.85	112.60
1	С	37	DC	N1-C1'-C2'	5.31	122.69	112.60

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Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	1	DC	N1-C1'-C2'	-5.17	102.78	112.60

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	А	12	DG	C3'

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	А	12	DG	Sidechain
2	В	14	DG	Sidechain
1	С	39	DC	Sidechain
2	D	44	DG	Sidechain

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	А	236	0	130	5	0
1	С	236	0	130	8	0
2	В	185	0	101	6	0
2	D	166	0	90	5	0
3	А	46	0	0	2	2
3	В	22	0	0	0	0
3	С	47	0	0	1	2
3	D	42	0	0	0	0
All	All	980	0	451	22	2

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 17.

The worst 5 of 22 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)
2:B:20:DA:H2"	2:B:21:DG:H5'	1.40	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:31:DC:H6	1:C:31:DC:H5'	1.42	0.85
1:C:42:DG:OP1	3:C:119:HOH:O	2.01	0.78
1:C:31:DC:H5'	1:C:31:DC:C6	2.23	0.74
1:A:12:DG:OP2	3:A:306:HOH:O	2.07	0.72

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All (2) 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)
3:A:128:HOH:O	3:C:119:HOH:O[1_565]	2.09	0.11
3:A:309:HOH:O	3:C:119:HOH:O[1_565]	2.13	0.07

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 (i)

4 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	Mol Type Chain Res			Link	Bond lengths			Bond angles		
IVIOI	Type	Unam	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
1	BRU	А	5	1,2	18,21,22	<mark>3.83</mark>	2 (11%)	26,30,33	1.15	3 (11%)
1	BRU	С	32	1,2	18,21,22	3.62	2 (11%)	26,30,33	1.38	3 (11%)
1	BRU	С	35	1,2	18,21,22	3.72	2 (11%)	26,30,33	1.06	2 (7%)
1	BRU	А	2	1,2	18,21,22	3.51	2 (11%)	26,30,33	1.28	2 (7%)

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	BRU	А	5	1,2	-	6/7/21/22	0/2/2/2
1	BRU	С	32	1,2	-	0/7/21/22	0/2/2/2
1	BRU	С	35	1,2	-	6/7/21/22	0/2/2/2
1	BRU	А	2	1,2	-	0/7/21/22	0/2/2/2

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
1	А	5	BRU	BR-C5	-15.84	1.51	1.88
1	С	35	BRU	BR-C5	-15.33	1.52	1.88
1	С	32	BRU	BR-C5	-14.91	1.53	1.88
1	А	2	BRU	BR-C5	-14.41	1.54	1.88
1	А	5	BRU	C4-C5	2.95	1.50	1.45

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
1	А	2	BRU	C6-C5-C4	-4.49	116.11	120.67
1	С	32	BRU	C6-C5-C4	-4.47	116.13	120.67
1	А	5	BRU	C6-C5-C4	-3.54	117.08	120.67
1	С	32	BRU	BR-C5-C4	3.36	121.93	118.03
1	С	35	BRU	C6-C5-C4	-3.23	117.39	120.67

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	\mathbf{Res}	Type	Atoms
1	С	35	BRU	C3'-C4'-C5'-O5'
1	С	35	BRU	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
1	С	35	BRU	C2'-C1'-N1-C6
1	А	5	BRU	O4'-C4'-C5'-O5'
1	С	35	BRU	O4'-C1'-N1-C6

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	А	5	BRU	1	0
1	С	32	BRU	3	0
1	С	35	BRU	1	0
1	А	2	BRU	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

