

wwPDB X-ray Structure Validation Summary Report (i)

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PDB ID : 8EPD

Title : Engineering Crystals with Tunable Symmetries from 14- or 16-Base-Long DNA

Strands

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Deposited on : 2022-10-05

Resolution : 2.42 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 Xtriage (Phenix): 1.13

EDS : 2.36.1

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

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

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

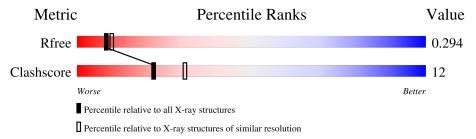
Validation Pipeline (wwPDB-VP) : 2.36.1

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 2.42 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 $(\# \mathrm{Entries})$	Similar resolution $(\#\text{Entries, resolution range}(\mathring{A}))$				
R_{free}	130704	4647 (2.44-2.40)				
Clashscore	141614	5161 (2.44-2.40)				

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%

Mol	Chain	Length	Quality of chain				
1	С	6	33%	67%			
2	A	5	20%	80%			
3	В	5	609	6 40%			



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 325 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(P*CP*GP*TP*TP*CP*C)-3').

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	С	6	Total	С	N	О	Р	0	0	0
1		U	119	57	18	38	6		U	U

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

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
9	Λ	5	Total	С	N	О	Р	0	0	0
	Λ	9	100	48	21	27	4	0	U	U

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

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
3	В	5	Total 106	C 49	N 23	O 29	P 5	0	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.

Molecule 1: DNA (5'-D(P*CP*GP*TP*TP*CP*C)-3')
Chain C: 33% 67%
■ Molecule 2: DNA (5'-D(*CP*GP*AP*CP*G)-3')
Chain A: 20% 80%
■ Molecule 3: DNA (5'-D(P*GP*GP*AP*GP*C)-3')
Chain B: 60% 40%



4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 43 2 2	Depositor	
Cell constants	34.17Å 34.17Å 104.32Å	Donogitor	
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	17.81 - 2.42	Depositor	
rtesolution (A)	17.81 - 2.42	EDS	
% Data completeness	41.5 (17.81-2.42)	Depositor	
(in resolution range)	41.6 (17.81-2.42)	EDS	
R_{merge}	(Not available)	Depositor	
R_{sym}	(Not available)	Depositor	
$< I/\sigma(I) > 1$	1.73 (at 2.43Å)	Xtriage	
Refinement program	PHENIX 1.20.1_4487	Depositor	
D D.	0.246 , 0.298	Depositor	
R, R_{free}	0.245 , 0.294	DCC	
R_{free} test set	49 reflections (3.73%)	wwPDB-VP	
Wilson B-factor (Å ²)	22.5	Xtriage	
Anisotropy	5.053	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.08 , -10.0	EDS	
L-test for twinning ²	$ < L >=0.51, < L^2>=0.35$	Xtriage	
Estimated twinning fraction	No twinning to report.	Xtriage	
F_o, F_c correlation	0.79	EDS	
Total number of atoms	325	wwPDB-VP	
Average B, all atoms (Å ²)	51.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 16.42% of the height of the origin peak. No significant pseudotranslation is detected.

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)

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		
MIOI	Chain	RMSZ	# Z >5	RMSZ	# Z > 5	
1	С	1.15	0/131	1.37	$2/199 \ (1.0\%)$	
2	A	1.28	0/112	1.12	0/171	
3	В	0.99	0/119	0.90	0/182	
All	All	1.14	0/362	1.16	2/552 (0.4%)	

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	С	3	DT	N3-C4-O4	5.78	123.37	119.90
1	С	3	DT	C5-C4-O4	-5.61	120.97	124.90

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	С	119	0	69	2	4
2	A	100	0	57	3	2
3	В	106	0	56	1	2
All	All	325	0	182	6	4

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 12.

The worst 5 of 6 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)
3:B:1:DG:H2"	3:B:2:DG:C8	2.30	0.67
2:A:1:DC:C2'	2:A:2:DG:H5'	2.35	0.56
1:C:1:DC:H2"	1:C:2:DG:C8	2.48	0.48
1:C:1:DC:H2"	1:C:2:DG:OP2	2.15	0.46
2:A:1:DC:H2'	2:A:2:DG:H5'	1.97	0.45

All (4) 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	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
1:C:1:DC:P	2:A:5:DG:O3'[7_555]	1.59	0.61
1:C:6:DC:O3'	3:B:1:DG:P[7_555]	1.61	0.59
1:C:1:DC:O5'	2:A:5:DG:O3'[7_555]	1.74	0.46
1:C:6:DC:O3'	3:B:1:DG:OP2[7_555]	2.14	0.06

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)

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)

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)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

