Full wwPDB X-ray Structure Validation Report ⓘ

Sep 25, 2023 – 03:40 PM EDT

PDB ID	:	6AQX
Title	:	Crystal Structure of Z-DNA with 6-fold Twinning_Z4B
Authors	:	Luo, Z.; Dauter, Z.; Gilski, M.
Deposited on	:	2017-08-21
Resolution	:	1.55 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*
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.

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

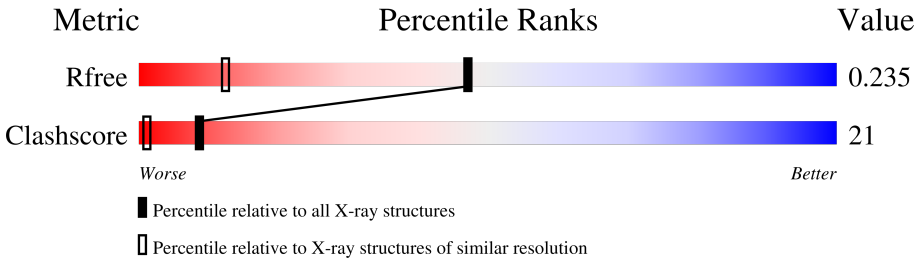
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 1.55 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))
R_{free}	130704	1483 (1.56-1.56)
Clashscore	141614	1529 (1.56-1.56)

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	A	6	17% 83%
1	B	6	67% 33%
1	C	6	33% 67%
1	D	6	100%
1	E	6	67% 33%
1	F	6	100%
1	G	6	67% 33%
1	H	6	100%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1001 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*GP*CP*GP*CP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	6	Total	C	N	O	P	0	0	0
			120	57	24	34	5			
1	B	6	Total	C	N	O	P	0	0	0
			120	57	24	34	5			
1	C	6	Total	C	N	O	P	0	0	0
			120	57	24	34	5			
1	D	6	Total	C	N	O	P	0	0	0
			120	57	24	34	5			
1	E	6	Total	C	N	O	P	0	0	0
			120	57	24	34	5			
1	F	6	Total	C	N	O	P	0	0	0
			120	57	24	34	5			
1	G	6	Total	C	N	O	P	0	0	0
			120	57	24	34	5			
1	H	6	Total	C	N	O	P	0	0	0
			120	57	24	34	5			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	4	Total	O	0	0
			4	4		
2	B	6	Total	O	0	0
			6	6		
2	C	6	Total	O	0	0
			6	6		
2	D	6	Total	O	0	0
			6	6		
2	E	4	Total	O	0	0
			4	4		
2	F	6	Total	O	0	0
			6	6		

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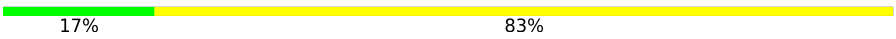
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	G	4	Total O 4 4	0	0
2	H	5	Total O 5 5	0	0

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.

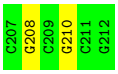
• Molecule 1: DNA (5'-D(*CP*GP*CP*GP*CP*G)-3')

Chain A:



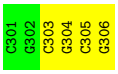
• Molecule 1: DNA (5'-D(*CP*GP*CP*GP*CP*G)-3')

Chain B:



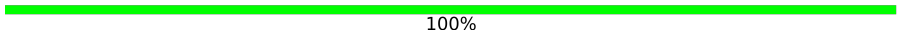
• Molecule 1: DNA (5'-D(*CP*GP*CP*GP*CP*G)-3')

Chain C:



• Molecule 1: DNA (5'-D(*CP*GP*CP*GP*CP*G)-3')

Chain D:



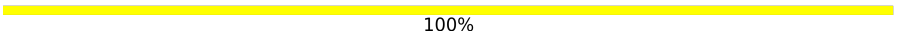
There are no outlier residues recorded for this chain.

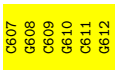
• Molecule 1: DNA (5'-D(*CP*GP*CP*GP*CP*G)-3')

Chain E:

• Molecule 1: DNA (5'-D(*CP*GP*CP*GP*CP*G)-3')

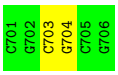
Chain F:





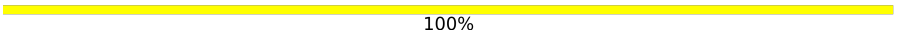
• Molecule 1: DNA (5'-D(*CP*GP*CP*GP*CP*G)-3')

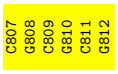
Chain G:



• Molecule 1: DNA (5'-D(*CP*GP*CP*GP*CP*G)-3')

Chain H:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	35.20Å 42.22Å 35.21Å 90.00° 119.83° 90.00°	Depositor
Resolution (Å)	30.54 – 1.55 30.54 – 1.55	Depositor EDS
% Data completeness (in resolution range)	99.2 (30.54-1.55) 99.7 (30.54-1.55)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.03 (at 1.54Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.209 , 0.227 0.216 , 0.235	Depositor DCC
R_{free} test set	657 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	15.2	Xtriage
Anisotropy	0.466	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 76.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.101 for -h-l,k,h 0.101 for l,k,-h-l 0.096 for h,-k,-h-l 0.108 for -h-l,-k,l 0.469 for l,-k,h	Xtriage
Reported twinning fraction	0.354 for H, K, L 0.375 for L, -K, H 0.073 for -H, -K, H+L 0.082 for L, K, -H-L 0.061 for -H-L, K, H 0.055 for H+L, -K, -L	Depositor
Outliers	0 of 13133 reflections	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	1001	wwPDB-VP
Average B, all atoms (Å^2)	36.0	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 90.08 % 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 2.6527e-08. The detected translational NCS is most*

[1] Intensities estimated from amplitudes.

[2] Theoretical 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.

likely also responsible for the elevated intensity ratio.

5 Model quality

5.1 Standard geometry

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	0.67	0/134	1.14	0/205
1	B	0.71	0/134	1.03	0/205
1	C	0.69	0/134	1.16	0/205
1	D	0.73	0/134	1.04	0/205
1	E	0.55	0/134	1.16	0/205
1	F	0.83	0/134	1.03	0/205
1	G	0.61	0/134	1.15	0/205
1	H	0.79	0/134	1.04	0/205
All	All	0.70	0/1072	1.09	0/1640

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

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	120	0	68	4	0
1	B	120	0	68	7	0
1	C	120	0	68	7	0
1	D	120	0	68	0	0
1	E	120	0	68	1	0
1	F	120	0	68	7	1
1	G	120	0	68	6	0
1	H	120	0	68	6	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	4	0	0	0	0
2	B	6	0	0	0	0
2	C	6	0	0	0	0
2	D	6	0	0	0	0
2	E	4	0	0	0	0
2	F	6	0	0	0	0
2	G	4	0	0	0	0
2	H	5	0	0	0	0
All	All	1001	0	544	29	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 21.

All (29) 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:210:DG:H4'	1:G:704:DG:H5'	1.41	1.02
1:H:810:DG:H2'	1:H:811:DC:C5	2.18	0.78
1:F:610:DG:H2'	1:F:611:DC:C5	2.18	0.78
1:F:608:DG:N3	1:F:608:DG:H2'	2.03	0.72
1:H:810:DG:H2'	1:H:811:DC:H5	1.54	0.71
1:F:610:DG:H2'	1:F:611:DC:H5	1.56	0.70
1:B:210:DG:H4'	1:G:704:DG:C5'	2.24	0.66
1:B:210:DG:H1'	1:G:703:DC:OP1	1.99	0.63
1:H:808:DG:H2'	1:H:808:DG:N3	2.14	0.63
1:F:608:DG:H2"	1:F:609:DC:OP1	2.01	0.61
1:H:808:DG:H2"	1:H:809:DC:OP1	2.04	0.56
1:C:303:DC:H5"	1:F:610:DG:H1'	1.88	0.55
1:G:703:DC:H4'	1:G:704:DG:O5'	2.10	0.51
1:B:208:DG:O5'	1:C:306:DG:H1'	2.14	0.48
1:B:208:DG:H1'	1:C:305:DC:OP2	2.14	0.46
1:F:609:DC:H4'	1:F:610:DG:O5'	2.17	0.45
1:C:303:DC:OP1	1:F:610:DG:H1'	2.16	0.45
1:C:303:DC:H4'	1:C:304:DG:O5'	2.17	0.45
1:B:210:DG:C5'	1:G:704:DG:H4'	2.47	0.45
1:A:103:DC:H4'	1:A:104:DG:O5'	2.18	0.44
1:E:503:DC:H4'	1:E:504:DG:O5'	2.18	0.43
1:C:304:DG:H2'	1:C:305:DC:C5	2.54	0.43
1:C:305:DC:O4'	1:C:306:DG:C2	2.73	0.42
1:A:104:DG:H2'	1:A:105:DC:C5	2.55	0.42
1:H:808:DG:N3	1:H:808:DG:C2'	2.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:105:DC:O4'	1:A:106:DG:C2	2.74	0.41
1:H:809:DC:H4'	1:H:810:DG:O5'	2.21	0.41
1:A:102:DG:H2'	1:A:103:DC:C6	2.56	0.40
1:B:210:DG:C1'	1:G:703:DC:OP1	2.68	0.40

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)
1:H:807:DC:O5'	1:H:812:DG:O3'[2_556]	2.09	0.11
1:F:607:DC:O5'	1:F:612:DG:O3'[2_655]	2.10	0.10

5.3 Torsion angles

5.3.1 Protein backbone

There are no protein molecules in this entry.

5.3.2 Protein sidechains

There are no protein molecules in this entry.

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

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

6.1 Protein, DNA and RNA chains

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

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

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

6.4 Ligands

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

6.5 Other polymers

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