

Full wwPDB X-ray Structure Validation Report (i)

Oct 10, 2023 – 11:16 PM EDT

:	7JIP
:	Self-assembly of a 3D DNA crystal lattice (4x6 scramble junction version)
	containing the J22 immobile Holliday junction with R3 symmetry
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:	2020-07-23
:	3.16 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 (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:

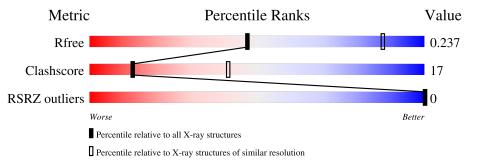
Refmac : 5.8.0158 CCP4 : 7.0.044 (Gargrove) Ideal geometry (proteins) : Engh & Huber (2001)	9)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996) Validation Pipeline (wwPDB-VP) : 2.35.1	

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.16 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	1665 (3.20-3.12)
Clashscore	141614	1804 (3.20-3.12)
RSRZ outliers	127900	1616 (3.20-3.12)

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% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length		Quality of chain	
1	А	12	25%	75%	
2	В	9	22%	78%	
3	С	6		67%	33%
4	D	15	20%	80%	



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2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 856 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(*GP*AP*CP*GP*AP*CP*AP*CP*TP* GP*A)-3').

Mol	Chain	Residues		Ate	\mathbf{oms}			ZeroOcc	AltConf	Trace
1	А	12	Total 245	C 117	N 51	O 66	Р 11	0	0	0

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

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
2	В	0	Total	С	Ν	0	Р	0	0	0
	D	9	183	86	34	54	9	0	0	0

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

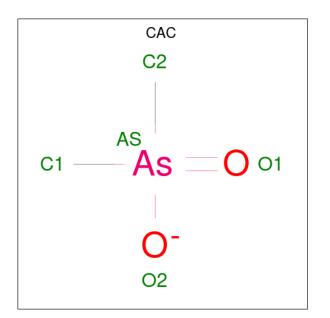
Mol	Chain	Residues		At	\mathbf{oms}			ZeroOcc	AltConf	Trace
3	С	6	Total 120	C 57	N 21	0 36	Р 6	0	0	0

• Molecule 4 is a DNA chain called DNA (5'-D(*TP*CP*GP*AP*GP*TP*CP*GP*GP*TP* GP*TP*CP*GP*T)-3').

Mol	Chain	Residues		Ate	oms			ZeroOcc	AltConf	Trace
4	п	15	Total	С	Ν	Ο	Р	0	Ο	0
-	D	15	307	147	54	92	14		0	0

• Molecule 5 is CACODYLATE ION (three-letter code: CAC) (formula: $C_2H_6AsO_2$).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	С	1	Total As 1 1	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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). 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(*GP*AP*AP*CP*GP*AP*CP*AP*CP*TP*GP*A)-3')

Chain A:	25%	75%		•
G1 A2 G5 G5 G1 C4 G1 C4 G1 C4 C4 C4 C4 C4 C4 C4 C4 C4 C4 C4 C4 C4	A12			
• Molecule 2:	DNA $(5'-D)$	O(P*CP*GP*GP*CP*GP*AP*	*CP*TP*C)-3')	
Chain B:	22%	78%		
C12 C13 C15 C15 C15 C18 T19 C18 C18 C20				
• Molecule 3:	DNA (5'-D	O(P*TP*CP*AP*CP*CP*G)-3	3')	
Chain C:		67%	33%	•
C1 A2 65 65				
• Molecule 4:	: DNA (5'-I	D(*TP*CP*GP*AP*GP*TP*	*CP*GP*GP*TP*(GP*TP*CP*GP*T)-3
Chain D:	20%	80%		
12 64 65 66 66 610 11	113 113 115 115 115 115 115 115 115 115			



4 Data and refinement statistics (i)

Property	Value	Source
Space group	Н 3	Depositor
Cell constants	113.02Å 113.02Å 49.34Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	44.06 - 3.16	Depositor
Resolution (A)	44.06 - 3.16	EDS
% Data completeness	88.9(44.06-3.16)	Depositor
(in resolution range)	88.9 (44.06-3.16)	EDS
R _{merge}	0.08	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$3.57 (at 3.19 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.11.1_2575	Depositor
R, R_{free}	0.214 , 0.236	Depositor
Λ, Λ_{free}	0.218 , 0.237	DCC
R_{free} test set	368 reflections $(10.28%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	96.2	Xtriage
Anisotropy	0.879	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.06 , -10.0	EDS
L-test for twinning ²	$< L > = 0.46, < L^2 > = 0.29$	Xtriage
Estimated twinning fraction	0.094 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	856	wwPDB-VP
Average B, all atoms $(Å^2)$	121.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.80% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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)

Bond lengths and bond angles in the following residue types are not validated in this section: CAC

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		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.58	0/276	0.79	0/424	
2	В	0.61	0/204	0.85	0/312	
3	С	0.56	0/133	0.86	0/202	
4	D	0.56	0/343	0.95	0/529	
All	All	0.57	0/956	0.88	0/1467	

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 (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	245	0	135	7	0
2	В	183	0	101	6	0
3	С	120	0	68	1	0
4	D	307	0	172	8	0
5	С	1	0	0	0	0
All	All	856	0	476	20	0

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.



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:12:DC:H2'	2:B:13:DG:C8	2.25	0.70
2:B:15:DC:H2'	2:B:16:DG:C8	2.26	0.70
2:B:18:DC:H2'	2:B:19:DT:C6	2.37	0.60
1:A:1:DG:H2'	1:A:2:DA:C8	2.40	0.57
2:B:15:DC:H2"	2:B:16:DG:H5'	1.87	0.55
1:A:8:DA:H2'	1:A:9:DC:C6	2.42	0.55
4:D:10:DG:H2'	4:D:11:DT:C6	2.43	0.53
4:D:12:DG:H2"	4:D:13:DT:H5"	1.91	0.53
4:D:6:DG:H2'	4:D:7:DT:C6	2.43	0.52
4:D:8:DC:H2"	4:D:9:DG:C8	2.50	0.47
4:D:3:DC:H2'	4:D:4:DG:C8	2.51	0.46
1:A:10:DT:H2"	1:A:11:DG:C8	2.51	0.45
2:B:18:DC:H2'	2:B:19:DT:C5	2.51	0.45
3:C:1:DC:H2"	3:C:2:DA:C8	2.54	0.43
1:A:5:DG:H1	4:D:14:DC:H42	1.69	0.41
1:A:4:DC:H2"	1:A:5:DG:C8	2.56	0.40
1:A:8:DA:C2	4:D:12:DG:C2	3.10	0.40
4:D:2:DT:H2'	4:D:3:DC:C6	2.57	0.40
1:A:2:DA:H2"	1:A:3:DA:H8	1.86	0.40
2:B:20:DC:H6	2:B:20:DC:H2'	1.76	0.40

All (20) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

There are no symmetry-related clashes.

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)

Of 1 ligands modelled in this entry, 1 is modelled with single atom - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	$\langle RSRZ \rangle$	#RSRZ>2		Z>2	$\mathbf{OWAB}(\mathbf{A}^2)$	Q < 0.9
1	А	12/12~(100%)	-1.35	0	100	100	115, 129, 138, 140	0
2	В	9/9~(100%)	-1.29	0	100	100	102, 108, 127, 131	0
3	С	6/6~(100%)	-1.19	0	100	100	103, 108, 112, 114	0
4	D	15/15~(100%)	-1.20	0	100	100	98, 119, 160, 160	0
All	All	42/42 (100%)	-1.26	0	100	100	98, 119, 140, 160	0

There are no RSRZ outliers to report.

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	\mathbf{Res}	Atoms	RSCC	RSR	$B-factors(Å^2)$	Q < 0.9
5	CAC	С	101	1/5	0.89	0.09	192,192,192,192	0



6.5 Other polymers (i)

There are no such residues in this entry.

