



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:55 AM UTC

PDB ID : 7JNL / pdb_00007jnl
Title : Self-assembly of a 3D DNA crystal lattice (4x6 scramble duplex version) containing the J34 immobile Holliday junction with R3 symmetry
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Deposited on : 2020-08-04
Resolution : 3.00 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

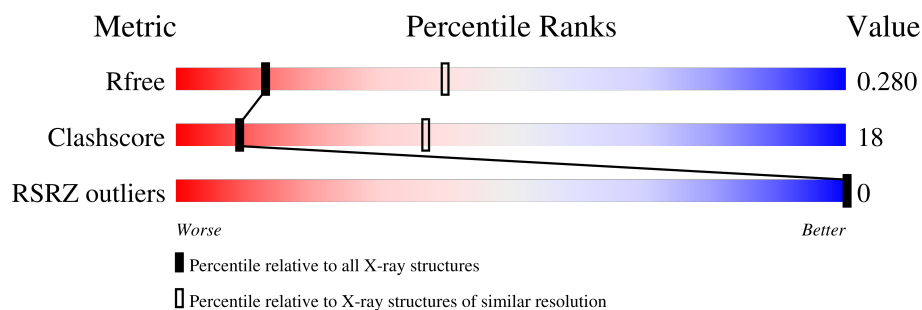
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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 $\leq 5\%$. 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	B	21	
2	C	8	
3	D	7	
4	A	6	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 862 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*AP*CP*GP*AP*CP*AP*AP*AP*GP*AP*CP*GP*TP*CP*GP*AP*GP*TP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	21	Total	C	N	O	P	0	0	0
			432	205	89	118	20			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	8	Total	C	N	O	P	0	0	0
			162	78	30	47	7			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	7	Total	C	N	O	P	0	0	0
			143	69	21	46	7			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	A	6	Total	C	N	O	P	0	0	0
			121	58	20	37	6			

- Molecule 5 is CACODYLATE ION (CCD ID: CAC) (formula: C₂H₆AsO₂).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	As	0	0
			1	1		
5	C	1	Total	As	0	0
			1	1		

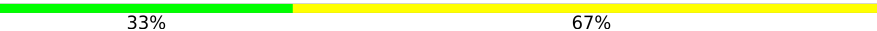
- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	2	Total	Mg	0	0
			2	2		

3 Residue-property plots

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*AP*AP*GP*AP*CP*GP*TP*CP*GP*AP*GP*TP*C)-3')

Chain B: 

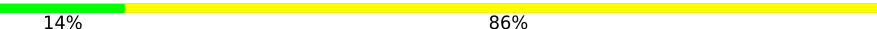


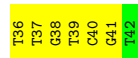
- Molecule 2: DNA (5'-D(*TP*CP*GP*AP*GP*TP*CP*G)-3')

Chain C: 



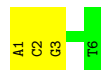
- Molecule 3: DNA (5'-D(P*TP*TP*GP*TP*CP*GP*T)-3')

Chain D: 



- Molecule 4: DNA (5'-D(P*AP*CP*GP*TP*CP*T)-3')

Chain A: 



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	111.80Å 111.80Å 51.30Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.33 – 3.00 45.33 – 3.00	Depositor EDS
% Data completeness (in resolution range)	93.8 (45.33-3.00) 93.8 (45.33-3.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.38 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.11.1_2575	Depositor
R, R_{free}	0.232 , 0.280 0.233 , 0.280	Depositor DCC
R_{free} test set	451 reflections (9.46%)	wwPDB-VP
Wilson B-factor (Å ²)	96.9	Xtriage
Anisotropy	0.160	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.09 , 0.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.065 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	862	wwPDB-VP
Average B, all atoms (Å ²)	89.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.32% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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.

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, MG

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	B	0.29	0/487	0.43	0/750
2	C	0.32	0/181	0.54	0/278
3	D	0.26	0/158	0.47	0/242
4	A	0.34	0/134	0.49	0/204
All	All	0.30	0/960	0.47	0/1474

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	B	432	0	235	17	0
2	C	162	0	92	8	0
3	D	143	0	82	7	0
4	A	121	0	69	2	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
6	B	2	0	0	0	0
All	All	862	0	478	23	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 18.

All (23) 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:10:DC:H2'	1:B:11:DG:C8	2.17	0.79
1:B:12:DA:H2''	1:B:13:DC:H5''	1.64	0.78
3:D:38:DG:H2''	3:D:39:DT:H5''	1.66	0.77
1:B:11:DG:H1	3:D:40:DC:H42	1.35	0.74
1:B:25:DG:N2	2:C:32:DG:H22	1.87	0.71
1:B:25:DG:H22	2:C:32:DG:H1	1.40	0.69
1:B:25:DG:H22	2:C:32:DG:H22	1.42	0.67
1:B:7:DG:H2''	1:B:8:DA:C8	2.32	0.64
3:D:36:DT:H2'	3:D:37:DT:C6	2.34	0.63
1:B:25:DG:H22	2:C:32:DG:N2	1.97	0.61
3:D:40:DC:H2'	3:D:41:DG:C8	2.35	0.61
1:B:25:DG:H1	2:C:32:DG:H1	1.50	0.58
1:B:25:DG:N2	2:C:32:DG:H1	2.01	0.57
1:B:21:DT:H2''	1:B:22:DC:H5'	1.87	0.56
1:B:9:DA:H2''	1:B:10:DC:O5'	2.08	0.52
1:B:17:DG:H2''	1:B:18:DA:H5''	1.94	0.50
1:B:10:DC:H42	3:D:41:DG:H1	1.63	0.46
1:B:23:DG:H2''	1:B:24:DA:H8	1.82	0.45
2:C:35:DG:H2''	4:A:1:DA:O4'	2.18	0.44
1:B:11:DG:H1	3:D:40:DC:N4	2.09	0.44
1:B:13:DC:H42	3:D:38:DG:H1	1.67	0.43
4:A:2:DC:H2''	4:A:3:DG:C8	2.54	0.43
2:C:31:DA:H2'	2:C:31:DA:OP2	2.18	0.43

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are modelled with single atom and 2 are monoatomic - 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, 95th 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	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	B	21/21 (100%)	0.19	0 100 100	77, 88, 103, 106	0
2	C	8/8 (100%)	0.70	0 100 100	68, 88, 98, 101	0
3	D	7/7 (100%)	0.45	0 100 100	76, 88, 111, 112	0
4	A	6/6 (100%)	0.13	0 100 100	70, 75, 82, 84	0
All	All	42/42 (100%)	0.32	0 100 100	68, 88, 106, 112	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 oligosaccharides 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, 95th 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	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	MG	B	103	1/1	0.83	0.44	89,89,89,89	0
6	MG	B	102	1/1	0.85	0.17	70,70,70,70	0
5	CAC	B	101	1/5	0.88	0.21	177,177,177,177	0
5	CAC	C	101	1/5	0.96	0.15	123,123,123,123	0

6.5 Other polymers [i](#)

There are no such residues in this entry.