



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 22, 2026 – 11:26 AM EDT

PDB ID : 7U3S / pdb_00007u3s
Title : [2T7+21] Self-assembling tensegrity triangle with two turns of DNA and the sticky end addition of a two-turn linker per axis with R3 symmetry
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Deposited on : 2022-02-28
Resolution : 9.50 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 ⓘ 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	:	FAILED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

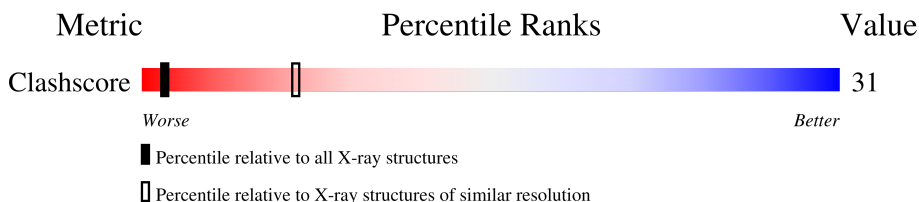
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 9.50 Å.

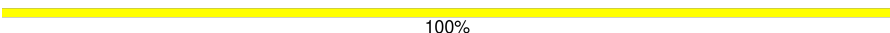
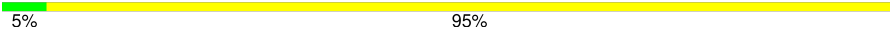
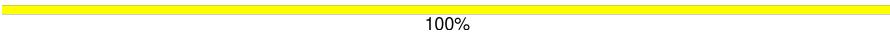
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	1001 (11.50-4.06)

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 $\leq 5\%$

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	B	7	 100%
2	C	8	 12% 88%
3	A	21	 5% 95%
4	D	6	 100%
5	X	21	 38% 62%
6	Y	21	 33% 67%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 1722 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*CP*GP*TP*AP*CP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	7	Total	C	N	O	P	0	0	0
			141	67	26	41	7			

- Molecule 2 is a DNA chain called DNA (5'-D(P*TP*CP*TP*GP*AP*TP*GP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	8	Total	C	N	O	P	0	0	0
			164	79	26	51	8			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	21	Total	C	N	O	P	0	0	0
			432	204	84	123	21			

- Molecule 4 is a DNA chain called DNA (5'-D(P*GP*GP*CP*TP*GP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	6	Total	C	N	O	P	0	0	0
			124	58	23	37	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	X	21	Total	C	N	O	P	0	0	0
			439	207	87	124	21			

- Molecule 6 is a DNA chain called DNA (5'-D(P*TP*CP*CP*TP*CP*TP*GP*CP*TP*AP*CP*TP*AP*CP*GP*TP*CP*AP*GP*CP*A)-3').

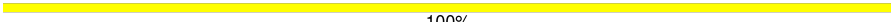
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	Y	21	Total 422	C 202	N 71	O 128	P 21	0	0	0

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. 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 failed to run properly.

- Molecule 1: DNA (5'-D(P*CP*CP*GP*TP*AP*CP*A)-3')

Chain B:  100%

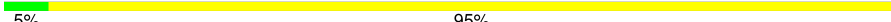
C130
C131
G132
T133
A134
C135
A136

- Molecule 2: DNA (5'-D(P*TP*CP*TP*GP*AP*TP*GP*T)-3')

Chain C:  12% 88%

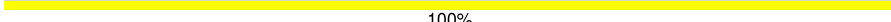
T122
G123
T124
G125
A126
T127
G128
T129

- Molecule 3: DNA (5'-D(P*GP*AP*GP*CP*AP*GP*CP*CP*TP*GP*TP*AP*CP*GP*GP*AP*CP*AP*TP*CP*A)-3')

Chain A:  5% 95%

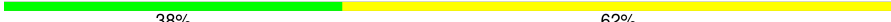
G101
A102
G103
C104
A105
G106
C107
C108
T109
G110
T111
A112
G113
G114
G115
A116
C117
A118
T119
C120
A121

- Molecule 4: DNA (5'-D(P*GP*GP*CP*TP*GP*C)-3')

Chain D:  100%

G137
G138
C139
T140
G141
C142

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

Chain X:  38% 62%

G122
A123
T124
T127
G128
A129
A133
G134
T135
A139
G140
A141
G142

- Molecule 6: DNA (5'-D(P*TP*CP*CP*TP*CP*TP*GP*CP*TP*AP*CP*TP*AP*CP*GP*TP*CP*AP*GP*CP*A)-3')

Chain Y:

33%

67%

T101	G102	C103	G107	C108	T109	T112	A113	C114	G115	T116	C117	A118	G119	C120	A121
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4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	212.73Å 212.73Å 174.80Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	37.01 – 9.50	Depositor
% Data completeness (in resolution range)	73.3 (37.01-9.50)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.186 , 0.190	Depositor
Wilson B-factor (Å ²)	(Not available)	Xtriage
Anisotropy	(Not available)	Xtriage
L-test for twinning ¹	$\langle L \rangle =$ (Not available), $\langle L^2 \rangle =$ (Not available)	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1722	wwPDB-VP
Average B, all atoms (Å ²)	798.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *(Not available)*

¹Theoretical 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](#)

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	0.62	0/157	1.01	0/239
2	C	0.47	0/182	0.80	0/279
3	A	0.53	0/485	0.73	0/746
4	D	0.48	0/138	0.64	0/211
5	X	0.38	0/494	0.51	0/762
6	Y	0.38	0/470	0.55	0/721
All	All	0.46	0/1926	0.67	0/2958

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	141	0	79	14	0
2	C	164	0	93	15	0
3	A	432	0	235	28	0
4	D	124	0	68	11	0
5	X	439	0	236	13	0
6	Y	422	0	238	12	0
All	All	1722	0	949	82	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 31.

The worst 5 of 82 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:130:DC:H1'	2:C:129:DT:H2''	1.47	0.97
5:X:127:DT:O2	6:Y:119:DG:N2	2.17	0.77
3:A:103:DG:H2''	3:A:104:DC:H5''	1.67	0.76
3:A:104:DC:H2''	3:A:105:DA:H8	1.51	0.75
4:D:140:DT:H2'	4:D:141:DG:C8	2.26	0.70

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](#)

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

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

6.4 Ligands

EDS failed to run properly - this section is therefore empty.

6.5 Other polymers

EDS failed to run properly - this section is therefore empty.