



# wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 21, 2022 – 06:04 PM EDT

PDB ID : 7U43  
Title : [L334] Self-assembling tensegrity triangle with three turns, three turns and four turns of DNA per axis by extension and linker addition with P1 symmetry  
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Deposited on : 2022-02-28  
Resolution : 7.55 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](mailto: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>.

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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 : 2.29  
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) : 2.29

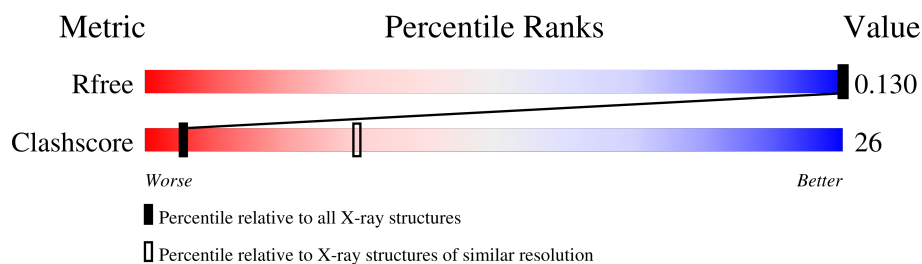
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

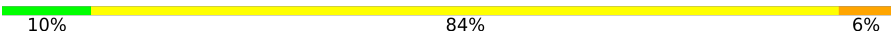



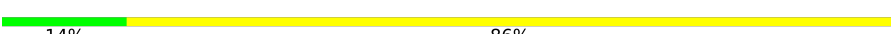




The reported resolution of this entry is 7.55 Å.

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	1004 (10.00-3.90)
Clashscore	141614	1069 (10.00-3.90)

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  $\geq 3$ , 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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	31	 10% 84% 6%
2	E	24	 8% 92%
3	D	24	 38% 63%
4	B	21	 38% 57% 5%
5	F	14	 14% 86%
6	C	31	 26% 71% .
7	M	21	 67% 33%
8	X	21	 29% 71%
9	Y	21	 43% 57%

## 2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 4258 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 (31-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	31	Total	C	N	O	P	0	0	0
			640	301	131	177	31			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	24	Total	C	N	O	P	0	0	0
			494	236	85	149	24			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	24	Total	C	N	O	P	0	0	0
			492	234	81	153	24			

- Molecule 4 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
4	B	21	Total	C	N	O	P	0	0	0
			432	204	84	123	21			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	14	Total	C	N	O	P	0	0	0
			294	139	56	85	14			

- Molecule 6 is a DNA chain called DNA (31-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	C	31	Total	C	N	O	P	0	0	0
			628	300	117	181	30			

- Molecule 7 is a DNA chain called DNA (5'-D(\*TP\*AP\*CP\*AP\*CP\*CP\*GP\*AP\*TP\*CP\*AP\*CP\*CP\*TP\*GP\*CP\*CP\*AP\*CP\*CP\*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	M	21	Total	C	N	O	P	0	0	0
			418	200	76	122	20			

- Molecule 8 is a DNA chain called DNA (5'-D(P\*GP\*TP\*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
8	X	21	Total	C	N	O	P	0	0	0
			425	203	73	128	21			

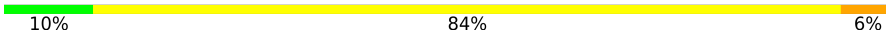
- Molecule 9 is a DNA chain called DNA (5'-D(P\*TP\*CP\*TP\*GP\*CP\*TP\*GP\*AP\*CP\*GP\*TP\*AP\*GP\*TP\*AP\*GP\*CP\*AP\*GP\*AP\*G)-3').

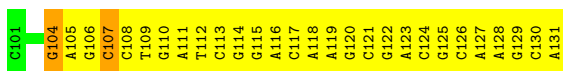
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	Y	21	Total	C	N	O	P	0	0	0
			435	206	82	126	21			

### 3 Residue-property plots [i](#)

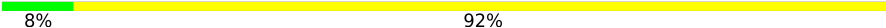
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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.

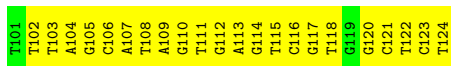
- Molecule 1: DNA (31-MER)

Chain A: 



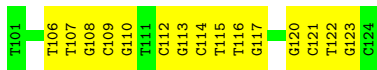
- Molecule 2: DNA (5'-D(P\*TP\*TP\*TP\*AP\*GP\*CP\*AP\*TP\*AP\*GP\*TP\*GP\*AP\*GP\*TP\*C P\*GP\*TP\*GP\*GP\*CP\*TP\*CP\*T)-3')

Chain E: 



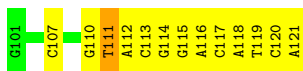
- Molecule 3: DNA (5'-D(P\*TP\*GP\*TP\*GP\*CP\*TP\*TP\*GP\*CP\*GP\*TP\*CP\*GP\*CP\*TP\*T P\*GP\*TP\*GP\*GP\*CP\*TP\*GP\*C)-3')

Chain D: 




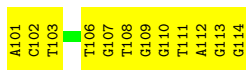
- Molecule 4: DNA (5'-D(P\*GP\*AP\*GP\*CP\*AP\*GP\*CP\*CP\*TP\*GP\*TP\*AP\*CP\*GP\*GP\*A P\*CP\*AP\*TP\*CP\*A)-3')

Chain B: 



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

Chain F: 



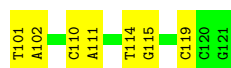
- Molecule 6: DNA (31-MER)

Chain C:  26% 71% .



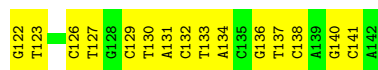
- Molecule 7: DNA (5'-D(\*TP\*AP\*CP\*AP\*CP\*CP\*GP\*AP\*TP\*CP\*AP\*CP\*CP\*TP\*GP\*CP\*CP\*AP\*CP\*CP\*G)-3')

Chain M:  67% 33%



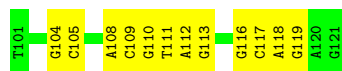
- Molecule 8: DNA (5'-D(P\*GP\*TP\*CP\*TP\*CP\*TP\*GP\*CP\*TP\*AP\*CP\*TP\*AP\*CP\*GP\*TP\*CP\*AP\*GP\*CP\*A)-3')

Chain X:  29% 71%



- Molecule 9: DNA (5'-D(P\*TP\*CP\*TP\*GP\*CP\*TP\*GP\*AP\*CP\*GP\*TP\*AP\*GP\*TP\*AP\*GP\*CP\*AP\*GP\*AP\*G)-3')

Chain Y:  43% 57%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	99.59Å 101.71Å 134.34Å 98.64° 109.49° 101.44°	Depositor
Resolution (Å)	42.78 – 7.55 96.92 – 7.55	Depositor EDS
% Data completeness (in resolution range)	60.5 (42.78-7.55) 53.8 (96.92-7.55)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.30 (at 7.43Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, $R_{free}$	0.115 , 0.124 0.115 , 0.130	Depositor DCC
$R_{free}$ test set	185 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	292.2	Xtriage
Anisotropy	0.538	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	1.00 , 2.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.65	EDS
Total number of atoms	4258	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	738.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 19.74% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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	A	0.77	0/721	1.02	2/1110 (0.2%)
2	E	0.83	0/552	1.21	0/851
3	D	0.74	0/548	1.14	0/845
4	B	0.75	0/485	1.10	3/746 (0.4%)
5	F	0.68	0/330	1.03	0/509
6	C	0.82	0/704	1.09	1/1083 (0.1%)
7	M	0.72	0/467	1.04	0/716
8	X	0.66	0/474	1.09	0/728
9	Y	0.62	0/488	1.02	0/752
All	All	0.74	0/4769	1.09	6/7340 (0.1%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	107	DC	O4'-C1'-N1	6.55	112.58	108.00
1	A	104	DG	O4'-C4'-C3'	-6.37	101.95	104.50
1	A	107	DC	O4'-C1'-N1	5.91	112.14	108.00
4	B	107	DC	C1'-O4'-C4'	-5.36	104.74	110.10
6	C	102	DA	O4'-C1'-N9	5.34	111.74	108.00

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	A	640	0	344	47	0
2	E	494	0	274	35	0
3	D	492	0	274	14	0
4	B	432	0	235	14	0
5	F	294	0	159	12	0
6	C	628	0	349	23	0
7	M	418	0	236	5	0
8	X	425	0	238	14	0
9	Y	435	0	237	14	0
All	All	4258	0	2346	171	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 26.

The worst 5 of 171 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)
2:E:102:DT:H2''	2:E:103:DT:H5''	1.56	0.87
1:A:113:DC:H1'	1:A:114:DG:C6	2.17	0.79
2:E:122:DT:H2'	2:E:123:DC:C6	2.18	0.79
2:E:106:DC:O2	6:C:128:DG:N2	2.16	0.78
1:A:127:DA:H2''	1:A:128:DA:H5''	1.67	0.76

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](#)

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.