



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 05:01 PM UTC

PDB ID : 7U3W / pdb_00007u3w
Title : [L224] Self-assembling tensegrity triangle with two turns, two turns and four turns of DNA per axis by linker addition with P1 symmetry
Authors : Woloszyn, K.; Vecchioni, S.; Seeman, N.C.; Sha, R.; Ohayon, Y.P.
Deposited on : 2022-02-28
Resolution : 6.33 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	:	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

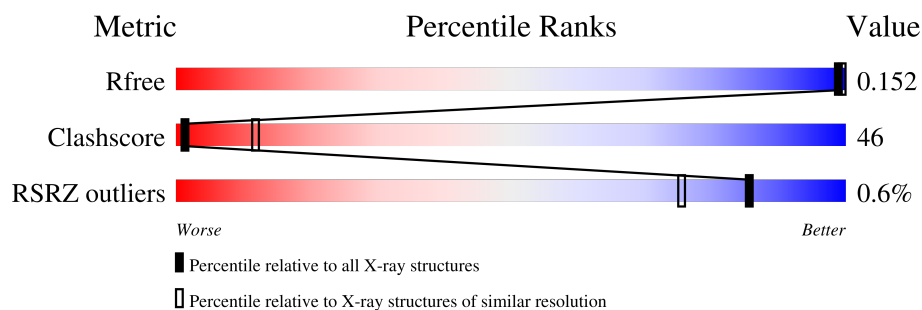
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 6.33 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	1154 (8.50-4.00)
Clashscore	190562	1016 (8.60-4.02)
RSRZ outliers	180081	1147 (8.50-4.00)

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	A	21	5% 10% 90%
2	E	14	14% 86%
3	D	14	100%
4	B	21	19% 76% 5%
5	F	14	100%
6	C	21	10% 86% 5%
7	M	21	10% 90%

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Mol	Chain	Length	Quality of chain
8	X	21	 14% 86%
9	Y	21	 24% 76%

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 3420 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(*AP*AP*CP*CP*TP*AP*CP*CP*TP*GP*GP*CP*AP*GP*GP*AP*CP*GP*AP*CP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	21	Total	C	N	O	P	0	0	0
			426	203	82	121	20			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	14	Total	C	N	O	P	0	0	0
			290	139	53	85	13			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	14	Total	C	N	O	P	0	0	0
			288	137	55	83	13			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	B	21	Total	C	N	O	P	0	0	0
			430	204	87	119	20			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	14	Total	C	N	O	P	0	0	0
			284	137	46	88	13			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	C	21	Total	C	N	O	P	0	0	0
			429	204	84	121	20			

- 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(*CP*TP*CP*TP*GP*CP*AP*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
			420	202	74	124	20			

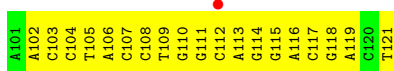
- Molecule 9 is a DNA chain called DNA (5'-D(P*TP*TP*TP*GP*CP*TP*GP*AP*CP*GP*TP*AP*GP*TP*AP*GP*TP*GP*CP*AP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	Y	21	Total	C	N	O	P	0	0	0
			435	207	78	129	21			

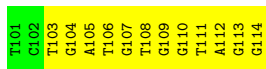
3 Residue-property plots

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.

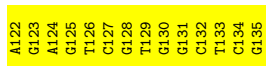
- Molecule 1: DNA (5'-D(*AP*AP*CP*CP*TP*AP*CP*CP*TP*GP*GP*CP*AP*GP*GP*AP*CP*GP*AP*CP*T)-3')



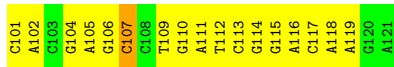
- Molecule 2: DNA (5'-D(*TP*CP*TP*GP*AP*TP*GP*TP*GP*GP*TP*AP*GP*G)-3')



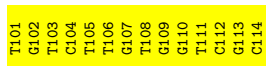
- Molecule 3: DNA (5'-D(*AP*GP*AP*GP*TP*CP*GP*TP*GP*GP*CP*TP*CP*G)-3')



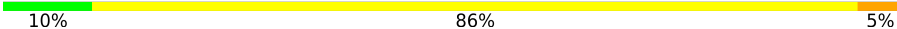
- Molecule 4: DNA (5'-D(*CP*AP*CP*GP*AP*GP*CP*CP*TP*GP*AP*TP*CP*GP*GP*AP*CP*AP*AP*GP*A)-3')



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



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

Chain C:  10% 86% 5%

G101	A102	G103	C104	G105	A106	C107	C108	T109	G110	T111	A112	C113	G114	G115	A116	C117	A118	T119	G120	A121
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- 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:  10% 90%

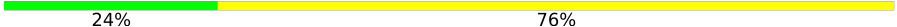
T101	A102	C103	A104	G105	C106	G107	A108	T109	C110	A111	C112	C113	T114	G115	C116	C117	A118	G119	C120	G121
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- Molecule 8: DNA (5'-D(*CP*TP*CP*TP*GP*CP*AP*CP*TP*AP*CP*TP*AP*CP*GP*TP*CP*AP*GP*CP*A)-3')

Chain X:  14% 86%

G122	T123	C124	T125	G126	C127	A128	C129	T130	A131	C132	T133	A134	C135	G136	T137	C138	A139	G140	C141	A142
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- Molecule 9: DNA (5'-D(P*TP*TP*TP*GP*CP*TP*GP*AP*CP*GP*TP*AP*GP*TP*AP*GP*TP*GP*CP*AP*G)-3')

Chain Y:  24% 76%

T101	T102	G107	A108	C109	G110	T111	A112	G113	T114	A115	G116	T117	G118	C119	A120	G121
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	67.47Å 68.56Å 131.42Å 77.89° 79.65° 83.53°	Depositor
Resolution (Å)	36.49 – 6.33 36.49 – 6.33	Depositor EDS
% Data completeness (in resolution range)	62.8 (36.49-6.33) 54.2 (36.49-6.33)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.83 (at 6.18Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.137 , 0.152 0.138 , 0.152	Depositor DCC
R_{free} test set	191 reflections (3.98%)	wwPDB-VP
Wilson B-factor (Å ²)	128.7	Xtriage
Anisotropy	0.804	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.05 , 121.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	0.089 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.99	EDS
Total number of atoms	3420	wwPDB-VP
Average B, all atoms (Å ²)	572.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.29% 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](#)

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	0.66	0/478	0.84	0/735
2	E	0.62	0/325	0.93	0/502
3	D	0.75	0/323	0.98	0/498
4	B	0.77	0/484	0.94	1/745 (0.1%)
5	F	0.73	0/316	0.95	0/487
6	C	0.89	0/482	1.05	1/742 (0.1%)
7	M	0.89	0/467	0.92	0/716
8	X	0.49	0/469	0.68	0/720
9	Y	0.47	0/487	0.63	0/751
All	All	0.71	0/3831	0.88	2/5896 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
4	B	107	DC	O4'-C1'-N1	5.93	117.29	108.40
6	C	112	DA	O5'-C5'-C4'	5.52	119.08	110.80

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	426	0	236	26	0
2	E	290	0	161	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	288	0	159	32	0
4	B	430	0	235	37	0
5	F	284	0	162	30	0
6	C	429	0	236	42	0
7	M	418	0	236	29	0
8	X	420	0	238	21	0
9	Y	435	0	239	23	0
All	All	3420	0	1902	243	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 46.

The worst 5 of 243 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)
7:M:117:DC:H2''	7:M:118:DA:H5'	1.45	0.96
4:B:115:DG:H2'	4:B:116:DA:H8	1.32	0.94
2:E:112:DA:H2'	2:E:113:DG:C8	2.03	0.94
2:E:107:DG:H2''	2:E:108:DT:H5''	1.49	0.92
4:B:110:DG:H2'	4:B:111:DA:C8	2.04	0.91

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 [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	A	21/21 (100%)	-0.04	1 (4%) 35 36	463, 513, 678, 691	0
2	E	14/14 (100%)	-0.47	0 100 100	481, 538, 657, 661	0
3	D	14/14 (100%)	-0.48	0 100 100	435, 495, 610, 679	0
4	B	21/21 (100%)	-0.26	0 100 100	376, 461, 490, 503	0
5	F	14/14 (100%)	-0.63	0 100 100	492, 508, 532, 541	0
6	C	21/21 (100%)	-0.33	0 100 100	344, 438, 523, 536	0
7	M	21/21 (100%)	-0.17	0 100 100	343, 429, 499, 510	0
8	X	21/21 (100%)	-0.26	0 100 100	673, 774, 1015, 1022	0
9	Y	21/21 (100%)	-0.35	0 100 100	664, 770, 957, 995	0
All	All	168/168 (100%)	-0.31	1 (0%) 85 75	343, 508, 943, 1022	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	112	DC	3.5

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.