



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 7, 2023 – 03:47 PM EDT

PDB ID : 7U3W
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 : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.35
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) : 2.35

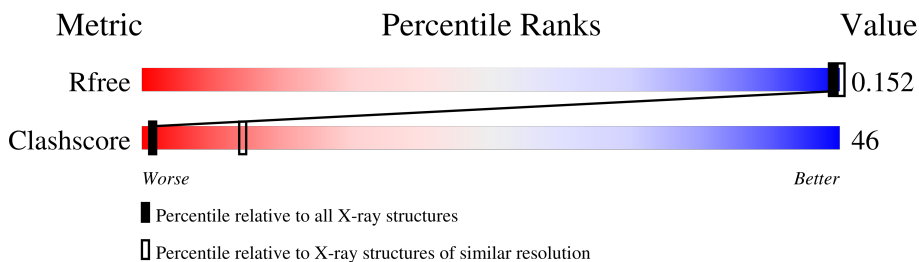
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


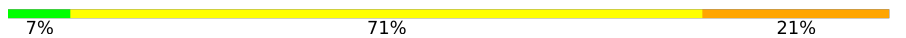







The reported resolution of this entry is 6.33 Å.

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}	130704	1009 (8.70-3.88)
Clashscore	141614	1058 (8.70-3.90)

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 ≥ 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	21	
2	E	14	
3	D	14	
4	B	21	
5	F	14	
6	C	21	
7	M	21	
8	X	21	
9	Y	21	

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
			Total	C	N	O	P			
1	A	21	426	203	82	121	20	0	0	0

- 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
			Total	C	N	O	P			
2	E	14	290	139	53	85	13	0	0	0

- 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
			Total	C	N	O	P			
3	D	14	288	137	55	83	13	0	0	0

- 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
			Total	C	N	O	P			
4	B	21	430	204	87	119	20	0	0	0

- 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
			Total	C	N	O	P			
5	F	14	284	137	46	88	13	0	0	0

- 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
			Total	C	N	O	P			
6	C	21	429	204	84	121	20	0	0	0

- 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
			Total	C	N	O	P			
7	M	21	418	200	76	122	20	0	0	0

- 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
			Total	C	N	O	P			
8	X	21	420	202	74	124	20	0	0	0

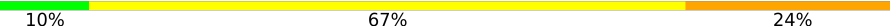
- Molecule 9 is a DNA chain called DNA (5'-D(P*TP*TP*TP*GP*CP*TP*GP*AP*CP*GP*TP*AP*GP*TP*AP*GP*TP*GP*CP*AP*G)-3').

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

- 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')

Chain A: 




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

Chain E: 




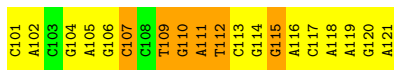
- Molecule 3: DNA (5'-D(*AP*GP*AP*GP*TP*CP*GP*TP*GP*GP*CP*TP*CP*G)-3')

Chain D: 



- 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')

Chain B: 



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

Chain F: 

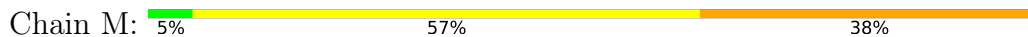


- Molecule 6: DNA (5'-D(*GP*AP*GP*CP*GP*AP*CP*CP*TP*GP*TP*AP*CP*GP*GP*AP*CP*AP*TP*CP*A)-3')

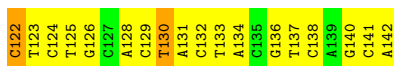
Chain C: 



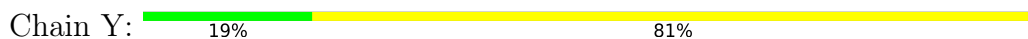
- Molecule 7: DNA (5'-D(*TP*AP*CP*AP*CP*CP*GP*AP*TP*CP*AP*CP*CP*TP*GP*CP*CP*AP*CP*CP*G)-3')



- 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')



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



4 Data and refinement statistics i

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 66.83 – 6.33	Depositor EDS
% Data completeness (in resolution range)	62.8 (36.49-6.33) 54.3 (66.83-6.33)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.83 (at 6.18Å)	Xtrriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.137 , 0.152 0.137 , 0.152	Depositor DCC
R_{free} test set	191 reflections (6.32%)	wwPDB-VP
Wilson B-factor (Å ²)	128.7	Xtrriage
Anisotropy	0.804	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.04 , 78.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtrriage
Estimated twinning fraction	0.089 for -k,-h,-l	Xtrriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	3420	wwPDB-VP
Average B, all atoms (Å ²)	572.0	wwPDB-VP

Xtrriage'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	1.41	3/478 (0.6%)	1.26	2/735 (0.3%)
2	E	1.30	2/325 (0.6%)	1.46	3/502 (0.6%)
3	D	1.54	2/323 (0.6%)	1.55	7/498 (1.4%)
4	B	1.56	5/484 (1.0%)	1.45	9/745 (1.2%)
5	F	1.45	2/316 (0.6%)	1.58	6/487 (1.2%)
6	C	1.96	10/482 (2.1%)	1.57	10/742 (1.3%)
7	M	1.97	15/467 (3.2%)	1.43	4/716 (0.6%)
8	X	1.06	0/469	1.17	2/720 (0.3%)
9	Y	1.05	1/487 (0.2%)	1.11	0/751
All	All	1.52	40/3831 (1.0%)	1.39	43/5896 (0.7%)

The worst 5 of 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	112	DA	N9-C4	13.06	1.45	1.37
6	C	111	DT	C1'-N1	11.55	1.64	1.49
7	M	120	DC	C1'-N1	11.54	1.64	1.49
4	B	111	DA	C3'-O3'	9.18	1.55	1.44
4	B	107	DC	C1'-N1	8.61	1.60	1.49

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	107	DC	O4'-C1'-N1	13.27	117.29	108.00
3	D	132	DC	O5'-P-OP1	-9.56	97.10	105.70
2	E	103	DT	O4'-C1'-N1	8.73	114.11	108.00
1	A	109	DT	O4'-C4'-C3'	-7.68	101.39	106.00
6	C	116	DA	O4'-C1'-N9	7.33	113.13	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	426	0	236	26	0
2	E	290	0	161	20	0
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 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.