# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2025 – 04:05 AM EDT

| | | |
|---|---|---|
| PDB ID | : | 9ND4 |
| Title | : | [0,8,11-2] Shifted tensegrity triangle with an (arm,center,arm) distribution of (0,8,11) base pairs and 2 nt sticky ends |
| Authors | : | Horvath, A.; Vecchioni, S.; Woloszyn, K.; Ohayon, Y.P.; Sha, R. |
| Deposited on | : | 2025-02-17 |
| Resolution | : | 5.30 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.

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The following versions of software and data (see references ⓘ) were used in the production of this report:

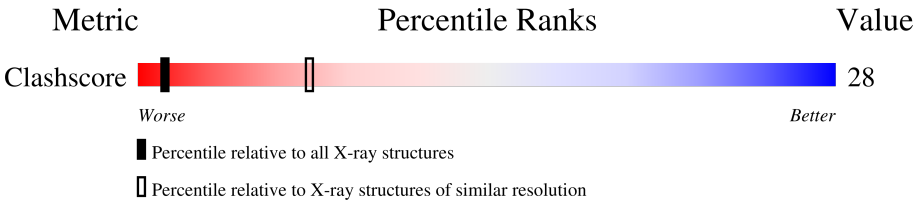
| | | |
|---|---|---|
| MolProbity | : | 4.02b-467 |
| Xtriage (Phenix) | : | 1.21 |
| EDS | : | FAILED |
| Percentile statistics | : | 20231227.v01 (using entries in the PDB archive December 27th 2023) |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.41.4 |

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
*X-RAY DIFFRACTION*

The reported resolution of this entry is 5.30 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 | 180529 | 1024 (6.60-4.00) |

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 <=5%

Note EDS failed to run properly.

| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 1 | A | 8 | 12% 88% |
| 2 | B | 6 | 17% 67% 17% |
| 3 | C | 15 | 40% 60% |
| 4 | D | 13 | 31% 69% |

## 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 855 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*AP*CP*AP*CP*CP*GP*T)-3').

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | | |
| 1 | A | 8 | 160 | 76 | 29 | 47 | 8 | 0 | 0 | 0 |

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

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | | |
| 2 | B | 6 | 120 | 59 | 19 | 37 | 5 | 0 | 0 | 0 |

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

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | | |
| 3 | C | 15 | 311 | 146 | 64 | 86 | 15 | 0 | 0 | 0 |

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

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | | |
| 4 | D | 13 | 264 | 127 | 47 | 78 | 12 | 0 | 0 | 0 |

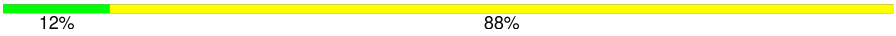
# 3 Residue-property plots (i)

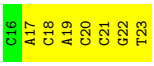
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

Note EDS failed to run properly.

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

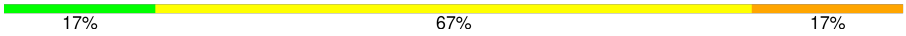
Chain A:




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

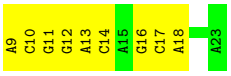
Chain B:





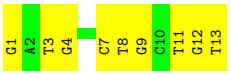
• Molecule 3: DNA (5'-D(P*AP*CP*GP*GP*AP*CP*AP*GP*CP*AP*GP*TP*GP*CP*A)-3')

Chain C:


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

Chain D:

# 4 Data and refinement statistics (i)

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

| Property | Value | Source |
|---|---|---|
| Space group | H 3 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 98.10Å 98.10Å 116.39Å<br>90.00° 90.00° 120.00° | Depositor |
| Resolution (Å) | 39.90 – 5.30 | Depositor |
| % Data completeness<br>(in resolution range) | 92.2 (39.90-5.30) | Depositor |
| $R_{merge}$ | (Not available) | Depositor |
| $R_{sym}$ | (Not available) | Depositor |
| $< I/\sigma(I) >$ [1] | 0.34 (at 5.41Å) | Xtriage |
| Refinement program | PHENIX 1.21.1_5286 | Depositor |
| R, $R_{free}$ | 0.124 , 0.145 | Depositor |
| Wilson B-factor (Å$^2$) | 393.5 | Xtriage |
| Anisotropy | 0.173 | Xtriage |
| L-test for twinning[2] | $< \|L\| > = 0.47$, $< L^2 > = 0.30$ | Xtriage |
| Estimated twinning fraction | 0.106 for -2/3*h-1/3*k+2/3*l,-1/3*h-2/3*k-2/3*l,2/3*h-2/3*k+1/3*l<br>0.066 for -h,1/3*h-1/3*k+2/3*l,2/3*h+4/3*k+1/3*l<br>0.069 for -1/3*h+1/3*k-2/3*l,-k,-4/3*h-2/3*k+1/3*l<br>0.069 for -h,2/3*h+1/3*k-2/3*l,-2/3*h-4/3*k-1/3*l<br>0.054 for 1/3*h+2/3*k+2/3*l,-k,4/3*h+2/3*k-1/3*l<br>0.097 for -1/3*h-2/3*k-2/3*l,-2/3*h-1/3*k+2/3*l,-2/3*h+2/3*k-1/3*l<br>0.141 for h,-h-k,-l | Xtriage |
| Total number of atoms | 855 | wwPDB-VP |
| Average B, all atoms (Å$^2$) | 523.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.13% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

# 5 Model quality

## 5.1 Standard geometry

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 | 0.82 | 0/178 | 1.18 | 0/271 |
| 2 | B | 0.58 | 0/133 | 1.28 | 1/204 (0.5%) |
| 3 | C | 0.61 | 0/350 | 0.89 | 0/538 |
| 4 | D | 0.56 | 0/295 | 1.04 | 0/454 |
| All | All | 0.64 | 0/956 | 1.05 | 1/1467 (0.1%) |

There are no bond length outliers.

All (1) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 2 | B | 6 | DG | O4'-C1'-N9 | 6.90 | 112.83 | 108.00 |

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

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 | 160 | 0 | 90 | 15 | 0 |
| 2 | B | 120 | 0 | 71 | 6 | 0 |
| 3 | C | 311 | 0 | 167 | 9 | 0 |
| 4 | D | 264 | 0 | 149 | 8 | 0 |
| All | All | 855 | 0 | 477 | 36 | 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 28.

All (36) 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:A:21:DC:H2' | 1:A:22:DG:C8 | 2.14 | 0.81 |
| 1:A:17:DA:H2" | 1:A:18:DC:H5" | 1.77 | 0.67 |
| 4:D:8:DT:H2' | 4:D:9:DG:C8 | 2.28 | 0.67 |
| 1:A:18:DC:H2" | 1:A:19:DA:N7 | 2.09 | 0.66 |
| 3:C:17:DC:H2' | 3:C:18:DA:C8 | 2.31 | 0.65 |
| 1:A:22:DG:H2" | 1:A:23:DT:H5" | 1.77 | 0.65 |
| 4:D:11:DT:H2" | 4:D:12:DG:C8 | 2.37 | 0.60 |
| 3:C:9:DA:H4' | 3:C:10:DC:OP1 | 2.05 | 0.56 |
| 4:D:3:DT:H2" | 4:D:4:DG:N7 | 2.22 | 0.54 |
| 1:A:18:DC:H2" | 1:A:19:DA:C8 | 2.45 | 0.52 |
| 1:A:22:DG:H2" | 1:A:23:DT:H6 | 1.74 | 0.52 |
| 1:A:21:DC:OP1 | 1:A:21:DC:H6 | 1.93 | 0.52 |
| 3:C:13:DA:H2" | 3:C:14:DC:H5' | 1.93 | 0.51 |
| 4:D:8:DT:H5" | 4:D:8:DT:H6 | 1.77 | 0.50 |
| 2:B:4:DC:H2" | 2:B:5:DT:H5" | 1.93 | 0.50 |
| 4:D:1:DG:H2' | 4:D:1:DG:N3 | 2.27 | 0.50 |
| 1:A:20:DC:H2" | 1:A:21:DC:C5 | 2.48 | 0.48 |
| 1:A:23:DT:OP1 | 1:A:23:DT:H4' | 2.13 | 0.48 |
| 3:C:12:DG:H2" | 3:C:13:DA:C8 | 2.48 | 0.48 |
| 1:A:21:DC:H2' | 1:A:22:DG:H8 | 1.76 | 0.48 |
| 1:A:20:DC:H1' | 1:A:21:DC:OP2 | 2.15 | 0.47 |
| 4:D:7:DC:H2' | 4:D:8:DT:H71 | 1.96 | 0.47 |
| 3:C:10:DC:H2" | 3:C:11:DG:C8 | 2.49 | 0.47 |
| 2:B:5:DT:H2" | 2:B:6:DG:O4' | 2.15 | 0.46 |
| 1:A:20:DC:H5" | 1:A:20:DC:H6 | 1.80 | 0.45 |
| 1:A:20:DC:H5" | 4:D:13:DT:H2" | 1.97 | 0.45 |
| 3:C:12:DG:H2" | 3:C:13:DA:N7 | 2.32 | 0.44 |
| 2:B:7:DT:H3' | 2:B:8:DG:H5" | 2.00 | 0.44 |
| 1:A:17:DA:H2 | 2:B:7:DT:H3 | 1.67 | 0.43 |
| 3:C:16:DG:H2' | 3:C:17:DC:H6 | 1.83 | 0.43 |
| 4:D:12:DG:H2' | 4:D:13:DT:H71 | 1.99 | 0.43 |
| 2:B:6:DG:H1' | 2:B:7:DT:C6 | 2.54 | 0.43 |
| 1:A:21:DC:H2" | 1:A:22:DG:O5' | 2.20 | 0.41 |
| 2:B:4:DC:C4 | 2:B:5:DT:C4 | 3.08 | 0.41 |
| 3:C:11:DG:H2" | 3:C:12:DG:H5" | 2.03 | 0.40 |
| 3:C:9:DA:H2" | 3:C:10:DC:H5" | 2.03 | 0.40 |

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

There are no protein molecules in this entry.

### 5.3.2 Protein sidechains

There are no protein molecules in this entry.

### 5.3.3 RNA

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry

There are no ligands in this entry.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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.