



wwPDB X-ray Structure Validation Summary Report

Feb 27, 2014 – 02:14 PM GMT

PDB ID : 4B8D
Title : TENSEGRITY TRIANGLE FROM ENZYMATICALLY MANUFACTURED DNA
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Deposited on : 2012-08-26
Resolution : 4.79 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

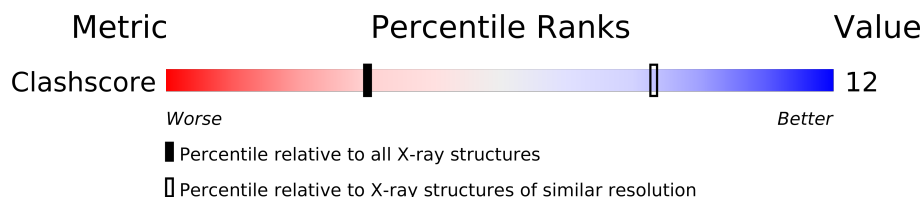
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	FAILED
Percentile statistics	:	21963
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 4.79 Å.

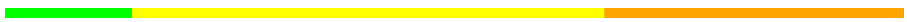



Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	79885	1320 (6.00-3.50)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	21	
2	B	7	
3	C	6	
4	D	8	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 863 atoms, of which 0 are hydrogen and 0 are deuterium.

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 5'-D(*GP*AP*GP*CP*AP*GP*CP*CP*TP*GP*TP*AP*CP*DGP*GP*AP*CP*AP*TP*CP*A)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	21	Total	C	N	O	P	0	0	0
			433	204	84	124	21			

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	8	Total	C	N	O	P	0	0	0
			165	79	26	52	8			

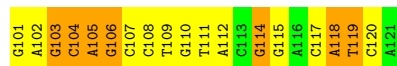
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

Note EDS failed to run properly.

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

Chain A: 



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

Chain B: 



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

Chain C: 



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

Chain D: 



4 Data and refinement statistics i

EDS failed to run properly - this section will therefore be incomplete.

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	106.44Å 106.44Å 95.15Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	42.28 – 4.79	Depositor
% Data completeness (in resolution range)	99.6 (42.28-4.79)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.40 (at 4.85Å)	Xtriage
Refinement program	BUSTER 2.11.2	Depositor
R, R_{free}	0.185 , 0.205	Depositor
Wilson B-factor (Å ²)	231.8	Xtriage
Anisotropy	0.689	Xtriage
Estimated twinning fraction	0.125 for h,-h-k,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Outliers	0 of 1980 reflections	Xtriage
Total number of atoms	863	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.06% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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	1.18	1/486 (0.2%)	2.47	32/746 (4.3%)
2	B	1.03	0/157	2.23	10/239 (4.2%)
3	C	1.27	0/138	2.67	7/211 (3.3%)
4	D	1.25	1/183 (0.5%)	2.67	14/279 (5.0%)
All	All	1.18	2/964 (0.2%)	2.50	63/1475 (4.3%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	101	DG	OP3-P	-10.30	1.48	1.61
4	D	101	DT	OP3-P	-9.77	1.49	1.61

The worst 5 of 63 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	102	DC	O4'-C1'-N1	19.82	121.88	108.00
1	A	111	DT	O4'-C1'-N1	17.24	120.07	108.00
3	C	213	DG	O4'-C1'-N9	16.18	119.33	108.00
1	A	102	DA	O4'-C1'-N9	13.82	117.67	108.00
4	D	106	DT	O4'-C1'-N1	12.43	116.70	108.00

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	433	0	235	8	0
2	B	141	0	79	3	0
3	C	124	0	68	2	0
4	D	165	0	93	3	0
All	All	863	0	475	13	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 12.

The worst 5 of 13 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:104:DC:H2''	1:A:105:DA:H5''	1.39	1.04
4:D:104:DG:H1'	4:D:105:DA:H5'	1.79	0.64
1:A:114:DG:H21	2:B:121:DG:H22	1.60	0.48
4:D:104:DG:H4'	4:D:105:DA:OP1	2.16	0.46
4:D:105:DA:H1'	4:D:106:DT:O4'	2.16	0.46

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

There are no protein chains in this entry.

5.3.2 Protein sidechains ⓘ

There are no protein chains in this entry.

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates 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 will therefore be empty.

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

EDS failed to run properly - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS failed to run properly - this section will therefore be empty.

6.4 Ligands ⓘ

EDS failed to run properly - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS failed to run properly - this section will therefore be empty.