



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 09:45 AM UTC

PDB ID : 7N5U / pdb_00007n5u
Title : ZBTB7A Zinc Finger Domain Bound to DNA Duplex Containing GGACCC
(Oligo 21)
Authors : Horton, J.R.; Ren, R.; Cheng, X.
Deposited on : 2021-06-06
Resolution : 2.86 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>.

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

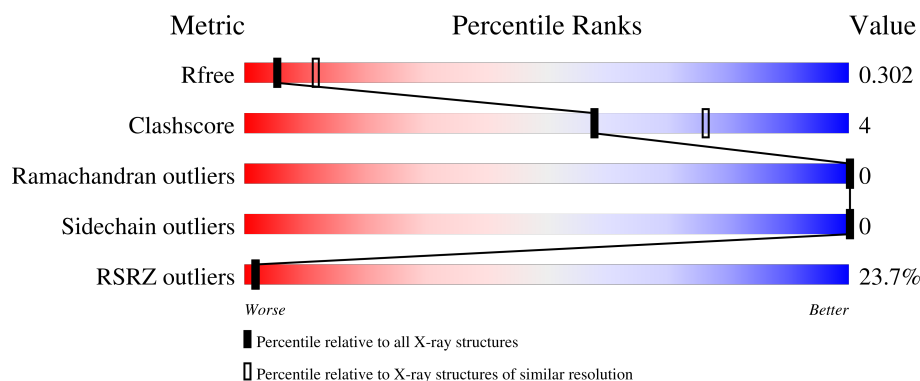
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.86 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	1407 (2.88-2.84)
Clashscore	190562	1446 (2.88-2.84)
Ramachandran outliers	187476	1406 (2.88-2.84)
Sidechain outliers	187428	1407 (2.88-2.84)
RSRZ outliers	180081	1408 (2.88-2.84)

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	143	15% 49% 8% 43%
2	X	16	12% 69% 31%
3	Y	16	25% 100%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 1290 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 protein called Zinc finger and BTB domain-containing protein 7A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	82	Total	C	N	O	S	0	0	0
			631	395	124	105	7			

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	365	GLY	-	expression tag	UNP O95365
A	366	PRO	-	expression tag	UNP O95365
A	367	LEU	-	expression tag	UNP O95365
A	368	GLY	-	expression tag	UNP O95365
A	501	LEU	-	expression tag	UNP O95365
A	502	GLU	-	expression tag	UNP O95365
A	503	ARG	-	expression tag	UNP O95365
A	504	PRO	-	expression tag	UNP O95365
A	505	HIS	-	expression tag	UNP O95365
A	506	ARG	-	expression tag	UNP O95365
A	507	ASP	-	expression tag	UNP O95365

- Molecule 2 is a DNA chain called DNA Strand I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	X	16	Total	C	N	O	P	0	0	0
			324	155	64	90	15			

- Molecule 3 is a DNA chain called DNA Strain II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	Y	16	Total	C	N	O	P	0	0	0
			325	157	56	97	15			

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	3	Total 3	Zn 3	0	0

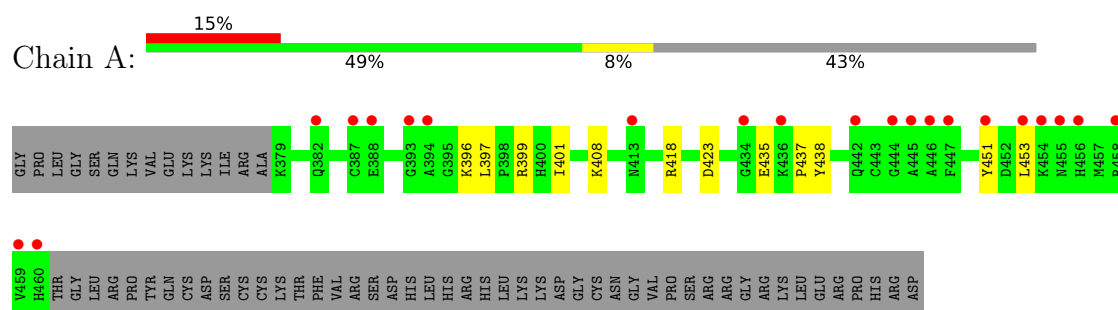
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	6	Total 6	O 6	0	0
5	Y	1	Total 1	O 1	0	0

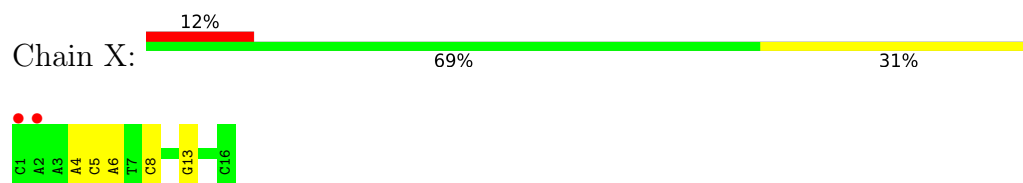
3 Residue-property plots [i](#)

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 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.

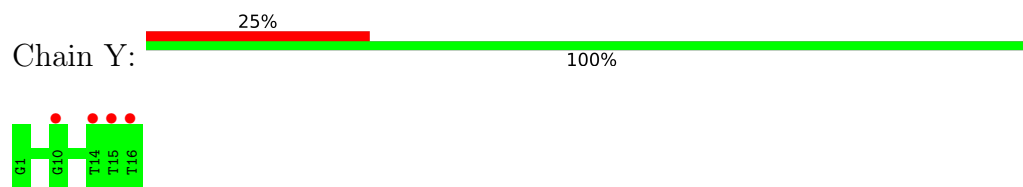
- Molecule 1: Zinc finger and BTB domain-containing protein 7A



- Molecule 2: DNA Strand I



- Molecule 3: DNA Strain II



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	63.38Å 103.61Å 37.07Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.11 – 2.86 40.11 – 2.86	Depositor EDS
% Data completeness (in resolution range)	73.6 (40.11-2.86) 73.7 (40.11-2.86)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.48 (at 2.86Å)	Xtriage
Refinement program	PHENIX 1.19.1_4122	Depositor
R, R_{free}	0.248 , 0.300 0.246 , 0.302	Depositor DCC
R_{free} test set	446 reflections (7.38%)	wwPDB-VP
Wilson B-factor (Å ²)	30.8	Xtriage
Anisotropy	0.095	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 55.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	1290	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.20% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0.11	0/647	0.25	0/870
2	X	0.18	0/364	0.35	0/559
3	Y	0.17	0/363	0.38	0/559
All	All	0.15	0/1374	0.32	0/1988

There are no bond length outliers.

There are no bond angle outliers.

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	631	0	587	8	0
2	X	324	0	180	4	0
3	Y	325	0	182	0	0
4	A	3	0	0	0	0
5	A	6	0	0	0	0
5	Y	1	0	0	0	0
All	All	1290	0	949	10	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 4.

All (10) 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:399:ARG:NH2	2:X:13:DG:N7	2.42	0.65
1:A:408:LYS:O	1:A:418:ARG:NH1	2.31	0.64
1:A:438:TYR:HB3	1:A:453:LEU:HD22	1.93	0.50
1:A:451:TYR:OH	2:X:8:DC:OP2	2.26	0.48
2:X:5:DC:H1'	2:X:6:DA:H5'	1.97	0.46
1:A:397:LEU:O	1:A:401:ILE:HG12	2.18	0.44
1:A:423:ASP:OD1	1:A:423:ASP:N	2.48	0.42
1:A:396:LYS:O	1:A:399:ARG:HG2	2.18	0.42
1:A:435:GLU:HG2	1:A:437:PRO:HD3	2.02	0.42
2:X:4:DA:H1'	2:X:5:DC:H5'	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	80/143 (56%)	76 (95%)	4 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	61/126 (48%)	61 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	449	HIS

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 ⓘ

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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

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	82/143 (57%)	1.35	21 (25%) 1 1	17, 45, 98, 121	0
2	X	16/16 (100%)	1.47	2 (12%) 8 6	42, 58, 94, 95	0
3	Y	16/16 (100%)	1.19	4 (25%) 2 1	32, 57, 89, 90	0
All	All	114/175 (65%)	1.35	27 (23%) 2 2	17, 52, 98, 121	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	434	GLY	4.0
1	A	458	ARG	4.0
2	X	1	DC	3.8
1	A	442	GLN	3.8
1	A	460	HIS	3.6
1	A	459	VAL	3.6
1	A	445	ALA	3.6
1	A	444	GLY	3.5
1	A	447	PHE	3.2
2	X	2	DA	2.7
1	A	382	GLN	2.7
1	A	394	ALA	2.7
1	A	387	CYS	2.7
3	Y	16	DT	2.5
3	Y	10	DG	2.5
1	A	446	ALA	2.5
1	A	388	GLU	2.4
1	A	456	HIS	2.4
1	A	436	LYS	2.4
1	A	454	LYS	2.3
1	A	393	GLY	2.3
1	A	451	TYR	2.2
3	Y	14	DT	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	413	ASN	2.0
1	A	455	ASN	2.0
3	Y	15	DT	2.0
1	A	453	LEU	2.0

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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	ZN	A	603	1/1	0.87	0.10	155,155,155,155	0
4	ZN	A	602	1/1	0.99	0.06	15,15,15,15	0
4	ZN	A	601	1/1	0.99	0.03	46,46,46,46	0

6.5 Other polymers [i](#)

There are no such residues in this entry.