



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:53 PM UTC

PDB ID : 7ATH / pdb_00007ath
Title : Crystal structure of UipA
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Deposited on : 2020-10-30
Resolution : 2.34 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

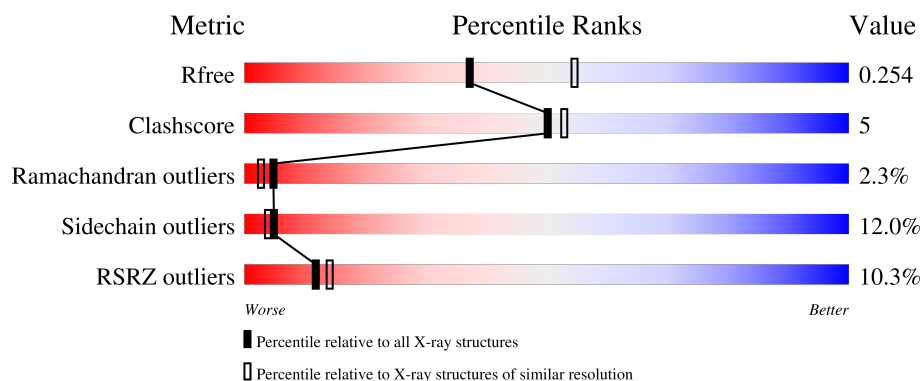
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.34 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	3031 (2.36-2.32)
Clashscore	190562	3127 (2.36-2.32)
Ramachandran outliers	187476	3095 (2.36-2.32)
Sidechain outliers	187428	3095 (2.36-2.32)
RSRZ outliers	180081	3033 (2.36-2.32)

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	AAA	206	7% 53% 10% • 34%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 975 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 UipA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	136	Total	C	N	O	S	0	0	0
			962	582	155	224	1			

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	76	MET	-	initiating methionine	UNP A0A3Q9JIL7
AAA	77	GLY	-	expression tag	UNP A0A3Q9JIL7
AAA	78	SER	-	expression tag	UNP A0A3Q9JIL7
AAA	79	SER	-	expression tag	UNP A0A3Q9JIL7
AAA	80	HIS	-	expression tag	UNP A0A3Q9JIL7
AAA	81	HIS	-	expression tag	UNP A0A3Q9JIL7
AAA	82	HIS	-	expression tag	UNP A0A3Q9JIL7
AAA	83	HIS	-	expression tag	UNP A0A3Q9JIL7
AAA	84	HIS	-	expression tag	UNP A0A3Q9JIL7
AAA	85	HIS	-	expression tag	UNP A0A3Q9JIL7
AAA	86	SER	-	expression tag	UNP A0A3Q9JIL7
AAA	87	SER	-	expression tag	UNP A0A3Q9JIL7
AAA	88	GLY	-	expression tag	UNP A0A3Q9JIL7
AAA	89	GLU	-	expression tag	UNP A0A3Q9JIL7
AAA	90	ASN	-	expression tag	UNP A0A3Q9JIL7
AAA	91	LEU	-	expression tag	UNP A0A3Q9JIL7
AAA	92	TYR	-	expression tag	UNP A0A3Q9JIL7
AAA	93	PHE	-	expression tag	UNP A0A3Q9JIL7
AAA	94	GLN	-	expression tag	UNP A0A3Q9JIL7

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	AAA	5	Total	Zn	0	0
			5	5		

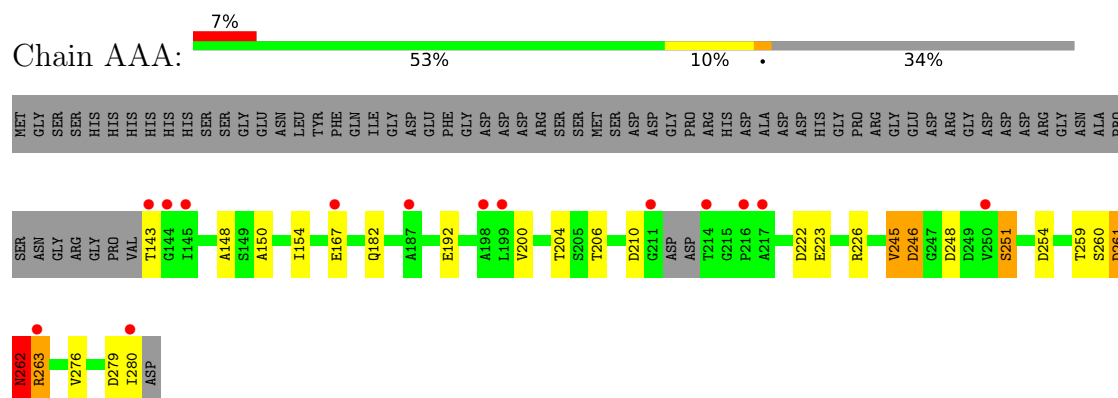
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	AAA	8	Total	O	0	0
			8	8		

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: UipA



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	96.13Å 96.13Å 52.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.99 – 2.34 42.99 – 2.34	Depositor EDS
% Data completeness (in resolution range)	99.7 (42.99-2.34) 99.8 (42.99-2.34)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.91 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.8.0257	Depositor
R, R_{free}	0.218 , 0.247 0.224 , 0.254	Depositor DCC
R_{free} test set	540 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	69.7	Xtriage
Anisotropy	0.078	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 38.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	975	wwPDB-VP
Average B, all atoms (Å ²)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.08% 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	AAA	1.14	0/967	1.55	5/1322 (0.4%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AAA	148	ALA	N-CA-C	-5.71	105.97	113.17
1	AAA	167	GLU	CB-CA-C	5.62	119.00	109.50
1	AAA	223	GLU	N-CA-C	-5.42	105.27	111.07
1	AAA	254	ASP	CB-CA-C	-5.39	98.67	109.35
1	AAA	245	VAL	N-CA-C	-5.14	108.28	113.47

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	AAA	962	0	907	10	0
2	AAA	5	0	0	0	0
3	AAA	8	0	0	0	0
All	All	975	0	907	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 5.

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:AAA:263:ARG:NH2	1:AAA:280:ILE:O	2.16	0.78
1:AAA:259:THR:HG22	1:AAA:263:ARG:O	1.99	0.63
1:AAA:260:SER:C	1:AAA:262:ASN:H	2.06	0.62
1:AAA:222:ASP:O	1:AAA:226:ARG:HG3	2.10	0.51
1:AAA:260:SER:C	1:AAA:262:ASN:N	2.72	0.48
1:AAA:251:SER:O	1:AAA:251:SER:OG	2.33	0.47
1:AAA:182:GLN:HB2	1:AAA:192:GLU:OE2	2.16	0.46
1:AAA:150:ALA:O	1:AAA:154:ILE:HG13	2.19	0.42
1:AAA:263:ARG:HD2	1:AAA:263:ARG:HA	1.83	0.42
1:AAA:245:VAL:O	1:AAA:246:ASP:C	2.64	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	AAA	132/206 (64%)	125 (95%)	4 (3%)	3 (2%)	5 3

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AAA	261	ASP
1	AAA	262	ASN
1	AAA	246	ASP

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	AAA	100/157 (64%)	88 (88%)	12 (12%)	5 4

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	143	THR
1	AAA	200	VAL
1	AAA	204	THR
1	AAA	206	THR
1	AAA	210	ASP
1	AAA	248	ASP
1	AAA	251	SER
1	AAA	261	ASP
1	AAA	262	ASN
1	AAA	263	ARG
1	AAA	276	VAL
1	AAA	279	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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

Of 5 ligands modelled in this entry, 5 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 [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	AAA	136/206 (66%)	0.71	14 (10%) 12 14	51, 71, 130, 154	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	145	ILE	4.9
1	AAA	280	ILE	4.5
1	AAA	214	THR	4.1
1	AAA	143	THR	3.9
1	AAA	217	ALA	3.4
1	AAA	211	GLY	3.4
1	AAA	199	LEU	3.3
1	AAA	144	GLY	3.2
1	AAA	263	ARG	2.9
1	AAA	198	ALA	2.6
1	AAA	167	GLU	2.6
1	AAA	250	VAL	2.5
1	AAA	216	PRO	2.1
1	AAA	187	ALA	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
2	ZN	AAA	304	1/1	0.94	0.11	71,71,71,71	1
2	ZN	AAA	303	1/1	0.95	0.07	138,138,138,138	0
2	ZN	AAA	305	1/1	0.97	0.07	146,146,146,146	0
2	ZN	AAA	302	1/1	0.98	0.07	118,118,118,118	0
2	ZN	AAA	301	1/1	0.98	0.05	114,114,114,114	0

6.5 Other polymers [i](#)

There are no such residues in this entry.