



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 4TVR / pdb_00004tvr
Title : Tandem Tudor and PHD domains of UHRF2
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Deposited on : 2014-06-27
Resolution : 2.29 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

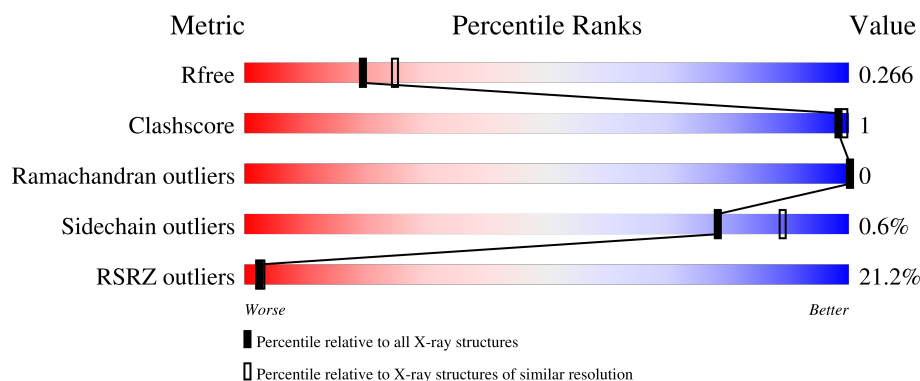
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.29 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	280	17% 78% • 21%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	UNX	A	410	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 1806 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 E3 ubiquitin-protein ligase UHRF2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	222	Total	C	N	O	S	0	4	0
			1741	1098	315	315	13			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	108	GLY	-	expression tag	UNP Q96PU4
A	?	-	ASN	deletion	UNP Q96PU4
A	?	-	GLY	deletion	UNP Q96PU4
A	?	-	SER	deletion	UNP Q96PU4
A	?	-	SER	deletion	UNP Q96PU4
A	?	-	CYS	deletion	UNP Q96PU4
A	?	-	LYS	deletion	UNP Q96PU4
A	?	-	ARG	deletion	UNP Q96PU4
A	?	-	THR	deletion	UNP Q96PU4
A	383	ALA	GLU	engineered mutation	UNP Q96PU4

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

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

- Molecule 3 is UNKNOWN ATOM OR ION (CCD ID: UNX) (formula: X).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	7	Total	X	0	0
			7	7		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	53	Total	O	0	2
			55	55		

- Molecule 1: E3 ubiquitin-protein ligase UHRF2



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	71.28Å 71.28Å 120.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.29 50.00 – 2.29	Depositor EDS
% Data completeness (in resolution range)	98.5 (50.00-2.29) 98.5 (50.00-2.29)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.75 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.8.0071	Depositor
R, R_{free}	0.229 , 0.260 0.238 , 0.266	Depositor DCC
R_{free} test set	721 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	62.7	Xtriage
Anisotropy	0.002	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 63.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	1806	wwPDB-VP
Average B, all atoms (Å ²)	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.49% 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, UNX

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	0.42	0/1779	0.62	0/2411

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	1741	0	1625	2	0
2	A	3	0	0	0	0
3	A	7	0	0	0	0
4	A	55	0	0	1	0
All	All	1806	0	1625	2	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 1.

All (2) 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:212:GLN:NE2	4:A:501:HOH:O	2.35	0.53
1:A:120:ILE:HB	1:A:129:VAL:HB	1.92	0.50

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	216/280 (77%)	208 (96%)	8 (4%)	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	178/245 (73%)	177 (99%)	1 (1%)	78	89

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	230	ARG

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 [i](#)

Of 10 ligands modelled in this entry, 3 are monoatomic and 7 are unknown - 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 [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 ⓘ

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	222/280 (79%)	1.09	47 (21%) 2 3	30, 67, 157, 170	4 (1%)

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	368	ALA	5.2
1	A	154	ALA	5.0
1	A	371	ILE	4.9
1	A	392	CYS	4.8
1	A	205	GLU	4.7
1	A	376	PRO	4.5
1	A	381	VAL	4.4
1	A	375	ASN	4.1
1	A	393	LYS	3.9
1	A	377	PRO	3.8
1	A	367	VAL	3.7
1	A	338	PRO	3.7
1	A	362	CYS	3.6
1	A	206	ASP	3.5
1	A	204	ASP	3.3
1	A	358	MET	3.1
1	A	343	HIS	3.1
1	A	341	LYS	3.0
1	A	339	GLU	3.0
1	A	360	LEU	3.0
1	A	287	LEU	2.9
1	A	379	ASP	2.9
1	A	390	PRO	2.9
1	A	319	ALA	2.8
1	A	373	CYS	2.8
1	A	356	PRO	2.8
1	A	294	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	331	CYS	2.7
1	A	337	ASP	2.7
1	A	274	ILE	2.7
1	A	117	ALA	2.6
1	A	387	TRP	2.6
1	A	292	GLY	2.6
1	A	333	LEU	2.5
1	A	113	THR	2.4
1	A	286	PHE	2.4
1	A	365	CYS	2.4
1	A	271	LEU	2.3
1	A	369	TYR	2.3
1	A	389	CYS	2.2
1	A	361	LEU	2.2
1	A	114	SER	2.2
1	A	353	LYS	2.1
1	A	391	SER	2.1
1	A	332	ASP	2.1
1	A	363	ASP	2.0
1	A	120	ILE	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(Å ²)	Q<0.9
3	UNX	A	409	1/1	0.59	0.32	62,62,62,62	0
3	UNX	A	410	1/1	0.70	0.42	47,47,47,47	1
2	ZN	A	403	1/1	0.79	0.16	118,118,118,118	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	UNX	A	405	1/1	0.82	0.16	68,68,68,68	0
3	UNX	A	404	1/1	0.83	0.25	76,76,76,76	0
3	UNX	A	408	1/1	0.84	0.34	65,65,65,65	0
3	UNX	A	406	1/1	0.90	0.28	63,63,63,63	0
3	UNX	A	407	1/1	0.91	0.14	59,59,59,59	0
2	ZN	A	402	1/1	0.93	0.12	94,94,94,94	0
2	ZN	A	401	1/1	0.97	0.09	87,87,87,87	0

6.5 Other polymers [i](#)

There are no such residues in this entry.