



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 4PYZ / pdb_00004pyz
Title : Crystal structure of the first two Ubl domains of Deubiquitylase USP7
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(SGC)
Deposited on : 2014-03-28
Resolution : 2.84 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

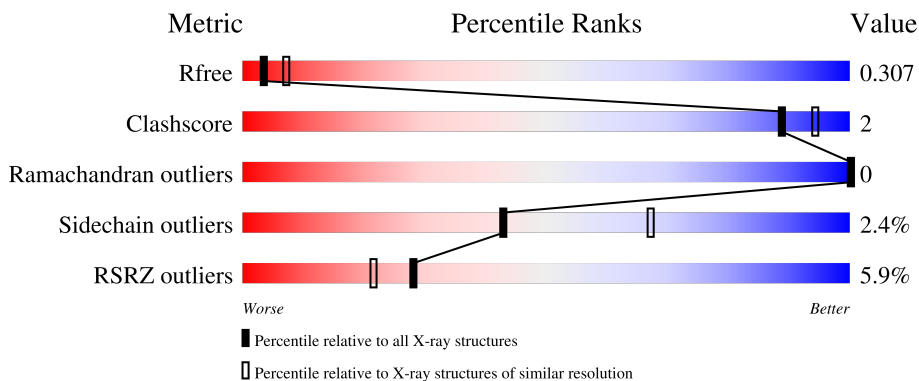
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


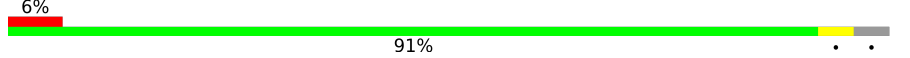
The reported resolution of this entry is 2.84 Å.

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	1520 (2.86-2.82)
Clashscore	190562	1559 (2.86-2.82)
Ramachandran outliers	187476	1517 (2.86-2.82)
Sidechain outliers	187428	1518 (2.86-2.82)
RSRZ outliers	180081	1521 (2.86-2.82)

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	273	 5% 87% 9% . .
1	B	273	 6% 91% . .

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4106 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 Ubiquitin carboxyl-terminal hydrolase 7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	263	2077	1308	352	404	13	0	2	0
1	B	261	2015	1271	335	395	14	0	1	0

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	521	SER	-	expression tag	UNP Q93009
A	522	HIS	-	expression tag	UNP Q93009
A	523	HIS	-	expression tag	UNP Q93009
A	524	HIS	-	expression tag	UNP Q93009
A	525	HIS	-	expression tag	UNP Q93009
A	526	HIS	-	expression tag	UNP Q93009
A	527	HIS	-	expression tag	UNP Q93009
A	528	SER	-	expression tag	UNP Q93009
A	529	SER	-	expression tag	UNP Q93009
A	530	GLY	-	expression tag	UNP Q93009
A	531	LEU	-	expression tag	UNP Q93009
A	532	VAL	-	expression tag	UNP Q93009
A	533	PRO	-	expression tag	UNP Q93009
A	534	ARG	-	expression tag	UNP Q93009
A	535	GLY	-	expression tag	UNP Q93009
A	536	SER	-	expression tag	UNP Q93009
B	521	SER	-	expression tag	UNP Q93009
B	522	HIS	-	expression tag	UNP Q93009
B	523	HIS	-	expression tag	UNP Q93009
B	524	HIS	-	expression tag	UNP Q93009
B	525	HIS	-	expression tag	UNP Q93009
B	526	HIS	-	expression tag	UNP Q93009
B	527	HIS	-	expression tag	UNP Q93009
B	528	SER	-	expression tag	UNP Q93009
B	529	SER	-	expression tag	UNP Q93009

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Chain	Residue	Modelled	Actual	Comment	Reference
B	530	GLY	-	expression tag	UNP Q93009
B	531	LEU	-	expression tag	UNP Q93009
B	532	VAL	-	expression tag	UNP Q93009
B	533	PRO	-	expression tag	UNP Q93009
B	534	ARG	-	expression tag	UNP Q93009
B	535	GLY	-	expression tag	UNP Q93009
B	536	SER	-	expression tag	UNP Q93009

- Molecule 2 is UNKNOWN ATOM OR ION (CCD ID: UNX) (formula: X).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	2	Total X 2 2	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	6	Total O 6 6	0	0
3	B	6	Total O 6 6	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	68.33Å 103.75Å 116.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.71 – 2.84 40.71 – 2.84	Depositor EDS
% Data completeness (in resolution range)	98.3 (40.71-2.84) 98.7 (40.71-2.84)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.70 (at 2.86Å)	Xtrriage
Refinement program	BUSTER-TNT BUSTER 2.10.0, BUSTER 2.10.0	Depositor
R, R_{free}	0.244 , 0.287 0.254 , 0.307	Depositor DCC
R_{free} test set	630 reflections (3.14%)	wwPDB-VP
Wilson B-factor (Å ²)	66.4	Xtrriage
Anisotropy	1.097	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 33.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4106	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.73% 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: 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	0.75	0/2119	1.21	1/2876 (0.0%)
1	B	0.73	0/2056	1.16	0/2795
All	All	0.74	0/4175	1.18	1/5671 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	726	PHE	CA-CB-CG	5.30	119.10	113.80

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	2077	0	1938	11	0
1	B	2015	0	1840	5	0
2	B	2	0	0	0	0
3	A	6	0	0	0	0
3	B	6	0	0	0	0
All	All	4106	0	3778	15	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 2.

The worst 5 of 15 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:620:ILE:HG22	1:A:664:THR:HG22	1.93	0.50
1:A:577:GLY:HA2	1:B:577:GLY:HA2	1.95	0.49
1:B:602:LEU:HB3	1:B:644:GLY:HA2	1.95	0.48
1:A:625:MET:HE1	1:A:661:PHE:HB2	1.96	0.47
1:A:772:ASP:HB3	1:A:774:GLU:HG2	1.98	0.46

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	263/273 (96%)	259 (98%)	4 (2%)	0	100	100
1	B	260/273 (95%)	253 (97%)	7 (3%)	0	100	100
All	All	523/546 (96%)	512 (98%)	11 (2%)	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	216/249 (87%)	209 (97%)	7 (3%)	34	59
1	B	203/249 (82%)	200 (98%)	3 (2%)	57	77
All	All	419/498 (84%)	409 (98%)	10 (2%)	43	67

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	534	ARG
1	B	544	LEU
1	B	743	THR
1	A	705	ILE
1	A	723	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	775	ASN
1	B	700	ASN
1	B	617	GLN
1	B	581	ASN
1	B	626	GLN

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 2 ligands modelled in this entry, 2 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

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	A	263/273 (96%)	0.69	15 (5%) 29 22	47, 79, 101, 113	2 (0%)
1	B	261/273 (95%)	0.70	16 (6%) 27 21	46, 81, 101, 114	1 (0%)
All	All	524/546 (95%)	0.70	31 (5%) 28 21	46, 80, 101, 114	3 (0%)

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	687	LEU	4.3
1	B	705	ILE	4.2
1	B	605	PHE	4.1
1	B	609	LEU	3.6
1	B	596	VAL	3.4

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(\AA^2)	Q<0.9
2	UNX	B	1000	1/1	0.74	0.29	30,30,30,30	0
2	UNX	B	1001	1/1	0.86	0.30	30,30,30,30	0

6.5 Other polymers [i](#)

There are no such residues in this entry.