



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:26 AM UTC

PDB ID : 7VIJ / pdb_00007vij
Title : Crystal structure of USP7-HUBL domain
Authors : Feng, N.; Zeng, K.W.
Deposited on : 2021-09-27
Resolution : 2.30 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

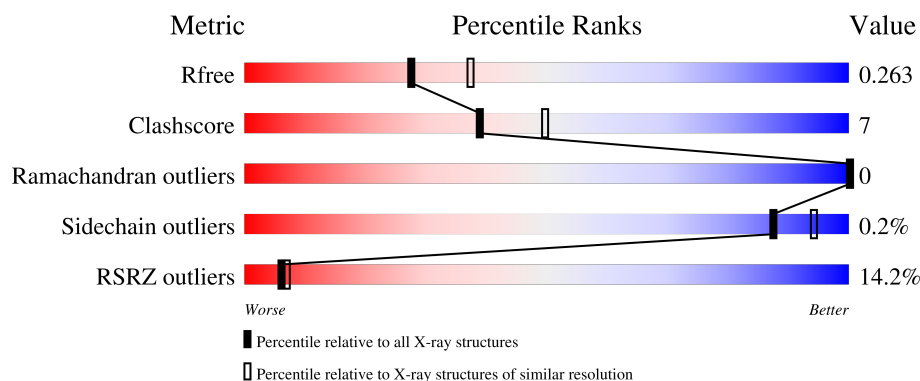
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	529	14% 87% 13%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4396 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
1	A	529	Total	C	N	O	S	0	0	0
			4340	2762	733	818	27			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	555	GLY	-	expression tag	UNP Q93009
A	556	PRO	-	expression tag	UNP Q93009
A	557	LEU	-	expression tag	UNP Q93009
A	558	GLY	-	expression tag	UNP Q93009
A	559	SER	-	expression tag	UNP Q93009

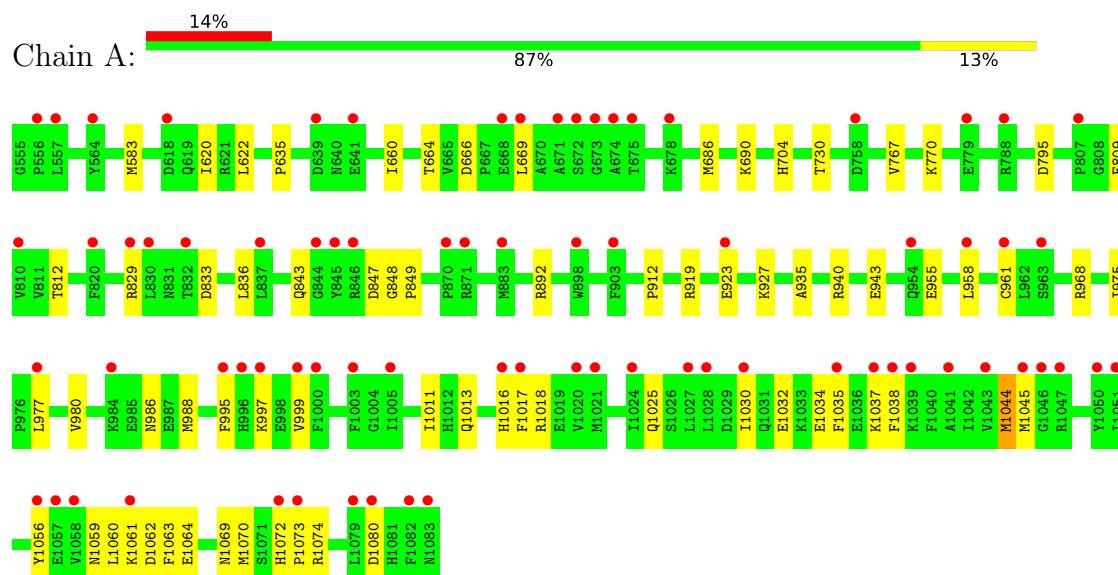
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	56	Total	O	0	0
			56	56		

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: Ubiquitin carboxyl-terminal hydrolase 7



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	80.14Å 81.43Å 149.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.39 – 2.30 45.39 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.3 (45.39-2.30) 99.3 (45.39-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.72 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.14 _3260	Depositor
R, R_{free}	0.218 , 0.263 0.222 , 0.263	Depositor DCC
R_{free} test set	1995 reflections (4.51%)	wwPDB-VP
Wilson B-factor (Å ²)	60.2	Xtriage
Anisotropy	0.603	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 38.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.017 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4396	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.36% 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](#)

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	0.36	0/4440	0.57	0/5995

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	4340	0	4252	58	0
2	A	56	0	0	1	0
All	All	4396	0	4252	58	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 7.

All (58) 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:1030:ILE:HD12	1:A:1034:GLU:OE1	1.57	1.04
1:A:1044:MET:HE3	1:A:1044:MET:HA	1.36	1.02
1:A:1032:GLU:OE2	1:A:1032:GLU:N	2.08	0.86
1:A:1025:GLN:HB2	1:A:1035:PHE:CE2	2.17	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:809:PHE:HB2	1:A:829:ARG:HH21	1.49	0.78
1:A:1044:MET:HE3	1:A:1044:MET:CA	2.14	0.77
1:A:1044:MET:HE2	1:A:1045:MET:N	2.02	0.73
1:A:1044:MET:CE	1:A:1045:MET:H	2.01	0.72
1:A:1030:ILE:HD12	1:A:1034:GLU:CD	2.17	0.69
1:A:1044:MET:CE	1:A:1045:MET:N	2.55	0.69
1:A:809:PHE:HB2	1:A:829:ARG:NH2	2.12	0.65
1:A:1044:MET:HE2	1:A:1045:MET:H	1.62	0.61
1:A:843:GLN:NE2	1:A:849:PRO:O	2.35	0.59
1:A:795:ASP:OD1	1:A:812:THR:HG22	2.03	0.59
1:A:935:ALA:HA	1:A:977:LEU:HD11	1.84	0.58
1:A:1045:MET:O	1:A:1045:MET:HG3	2.03	0.58
1:A:1018:ARG:HD3	1:A:1056:TYR:CE1	2.38	0.58
1:A:988:MET:HE2	1:A:1060:LEU:HD22	1.87	0.57
1:A:1044:MET:HA	1:A:1044:MET:CE	2.22	0.56
1:A:988:MET:HE3	1:A:1011:ILE:HD11	1.86	0.56
1:A:1038:PHE:HA	1:A:1080:ASP:O	2.08	0.54
1:A:1044:MET:HE3	1:A:1045:MET:H	1.72	0.53
1:A:1044:MET:HE1	1:A:1073:PRO:O	2.10	0.52
1:A:833:ASP:HB3	1:A:836:LEU:HD12	1.92	0.52
1:A:995:PHE:CD2	1:A:999:VAL:HA	2.46	0.51
1:A:940:ARG:HD3	1:A:975:ILE:HG12	1.92	0.51
1:A:1016:HIS:HA	1:A:1056:TYR:HB3	1.92	0.51
1:A:1044:MET:HE3	1:A:1045:MET:N	2.27	0.50
1:A:977:LEU:O	1:A:980:VAL:HG12	2.12	0.50
1:A:1069:ASN:ND2	1:A:1072:HIS:HB2	2.28	0.49
1:A:770:LYS:NZ	2:A:1104:HOH:O	2.45	0.49
1:A:1013:GLN:HB2	1:A:1060:LEU:HG	1.96	0.48
1:A:1044:MET:CA	1:A:1044:MET:CE	2.85	0.48
1:A:958:LEU:HB2	1:A:961:CYS:SG	2.54	0.48
1:A:1059:ASN:HB3	1:A:1062:ASP:OD2	2.14	0.48
1:A:943:GLU:OE2	1:A:968:ARG:HD2	2.15	0.47
1:A:988:MET:HE1	1:A:1063:PHE:HB2	1.97	0.46
1:A:686:MET:HE2	1:A:704:HIS:CD2	2.51	0.45
1:A:1017:PHE:H	1:A:1056:TYR:HA	1.82	0.45
1:A:1025:GLN:HB2	1:A:1035:PHE:CZ	2.53	0.44
1:A:622:LEU:HG	1:A:660:ILE:HG21	2.00	0.44
1:A:986:ASN:OD1	1:A:986:ASN:N	2.51	0.44
1:A:583:MET:HE3	1:A:635:PRO:CD	2.48	0.43
1:A:690:LYS:O	1:A:767:VAL:HA	2.18	0.43
1:A:1032:GLU:N	1:A:1032:GLU:CD	2.73	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:995:PHE:HE2	1:A:997:LYS:O	2.00	0.43
1:A:847:ASP:OD1	1:A:848:GLY:N	2.52	0.42
1:A:730:THR:HG21	1:A:770:LYS:HG2	2.01	0.42
1:A:1018:ARG:HD3	1:A:1056:TYR:CZ	2.54	0.42
1:A:620:ILE:HG22	1:A:664:THR:HG22	2.01	0.42
1:A:1017:PHE:CB	1:A:1056:TYR:HA	2.50	0.41
1:A:1070:MET:O	1:A:1074:ARG:NH2	2.53	0.41
1:A:1061:LYS:HA	1:A:1064:GLU:CD	2.45	0.41
1:A:666:ASP:HB3	1:A:669:LEU:HB3	2.02	0.41
1:A:919:ARG:HB2	1:A:955:GLU:HB3	2.01	0.41
1:A:923:GLU:O	1:A:927:LYS:HG3	2.20	0.41
1:A:1034:GLU:HA	1:A:1037:LYS:HD3	2.02	0.40
1:A:892:ARG:O	1:A:912:PRO:HD2	2.21	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	527/529 (100%)	516 (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	484/484 (100%)	483 (100%)	1 (0%)	87	94

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

Mol	Chain	Res	Type
1	A	1044	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	581	ASN
1	A	683	HIS
1	A	792	HIS
1	A	805	ASN
1	A	1025	GLN

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 ⓘ

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 ⓘ

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	529/529 (100%)	0.93	75 (14%) 6 7	42, 71, 115, 129	0

All (75) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	845	TYR	7.5
1	A	1082	PHE	5.5
1	A	1045	MET	4.7
1	A	674	ALA	4.6
1	A	1020	VAL	4.2
1	A	1035	PHE	3.9
1	A	1046	GLY	3.8
1	A	820	PHE	3.7
1	A	1073	PRO	3.7
1	A	1057	GLU	3.5
1	A	1050	TYR	3.4
1	A	1016	HIS	3.3
1	A	1058	VAL	3.3
1	A	673	GLY	3.2
1	A	669	LEU	3.2
1	A	1056	TYR	3.2
1	A	1024	ILE	3.2
1	A	810	VAL	3.1
1	A	1028	LEU	3.1
1	A	870	PRO	3.0
1	A	996	HIS	3.0
1	A	997	LYS	3.0
1	A	995	PHE	3.0
1	A	779	GLU	3.0
1	A	678	LYS	2.9
1	A	1027	LEU	2.9
1	A	829	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	1072	HIS	2.8
1	A	1083	ASN	2.8
1	A	1000	PHE	2.7
1	A	1017	PHE	2.7
1	A	758	ASP	2.7
1	A	671	ALA	2.7
1	A	844	GLY	2.6
1	A	903	PHE	2.6
1	A	1021	MET	2.6
1	A	1061	LYS	2.6
1	A	1079	LEU	2.6
1	A	675	THR	2.5
1	A	999	VAL	2.5
1	A	954	GLN	2.5
1	A	1047	ARG	2.5
1	A	1051	ILE	2.5
1	A	564	TYR	2.5
1	A	557	LEU	2.4
1	A	641	GLU	2.4
1	A	618	ASP	2.4
1	A	871	ARG	2.4
1	A	1030	ILE	2.4
1	A	977	LEU	2.4
1	A	898	TRP	2.4
1	A	846	ARG	2.3
1	A	883	MET	2.3
1	A	923	GLU	2.3
1	A	984	LYS	2.3
1	A	807	PRO	2.3
1	A	963	SER	2.3
1	A	668	GLU	2.3
1	A	830	LEU	2.2
1	A	1043	VAL	2.2
1	A	837	LEU	2.2
1	A	961	CYS	2.2
1	A	1038	PHE	2.2
1	A	832	THR	2.2
1	A	958	LEU	2.1
1	A	672	SER	2.1
1	A	1037	LYS	2.1
1	A	556	PRO	2.1
1	A	1003	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	1041	ALA	2.1
1	A	1039	LYS	2.0
1	A	1005	ILE	2.0
1	A	639	ASP	2.0
1	A	1080	ASP	2.0
1	A	788	ARG	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.