



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 12:44 AM UTC

PDB ID : 6ZQH / pdb_00006zqh
Title : Yeast Uba1 in complex with ubiquitin
Authors : Misra, M.; Schindelin, H.
Deposited on : 2020-07-09
Resolution : 2.03 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

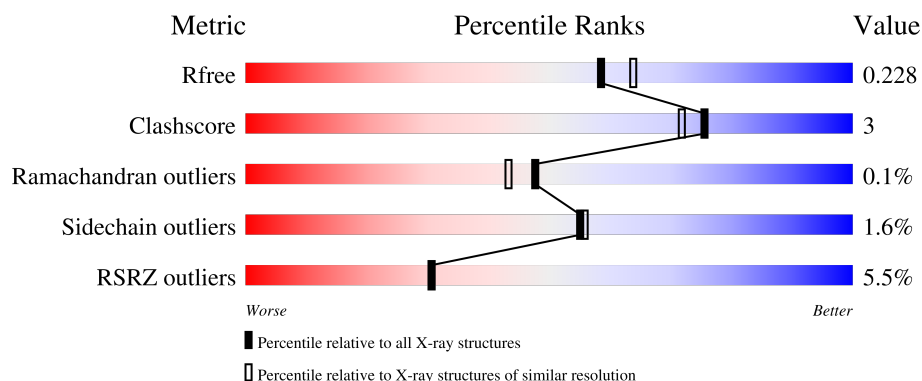
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.03 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	2260 (2.04-2.04)
Clashscore	190562	2333 (2.04-2.04)
Ramachandran outliers	187476	2318 (2.04-2.04)
Sidechain outliers	187428	2318 (2.04-2.04)
RSRZ outliers	180081	2260 (2.04-2.04)

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	1024	4% 91% 7%
1	C	1024	7% 91% 7%
2	B	76	84% 14%
2	D	76	% 84% 14%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 36105 atoms, of which 17238 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.

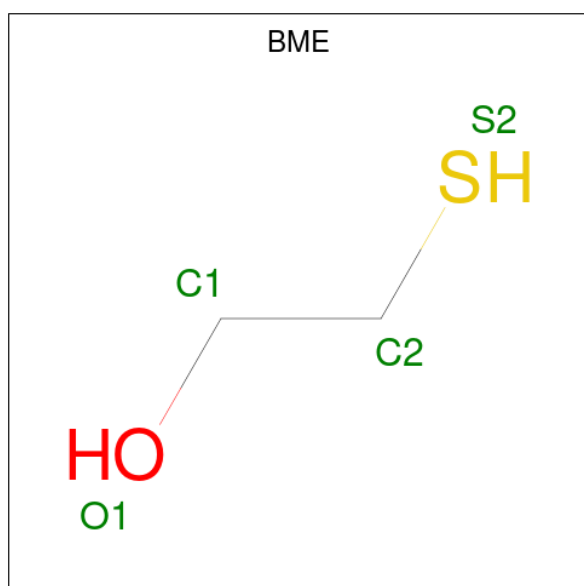
- Molecule 1 is a protein called Ubiquitin-activating enzyme E1 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	1005	Total	C	H	N	O	S	0	17	0
			15983	5122	7959	1317	1561	24			
1	C	1006	Total	C	H	N	O	S	0	14	0
			15948	5105	7937	1324	1558	24			

- Molecule 2 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	76	Total	C	H	N	O	S	0	1	0
			1247	380	638	108	120	1			
2	D	76	Total	C	H	N	O	S	0	2	0
			1239	379	630	106	123	1			

- Molecule 3 is BETA-MERCAPTOETHANOL (CCD ID: BME) (formula: C₂H₆OS).



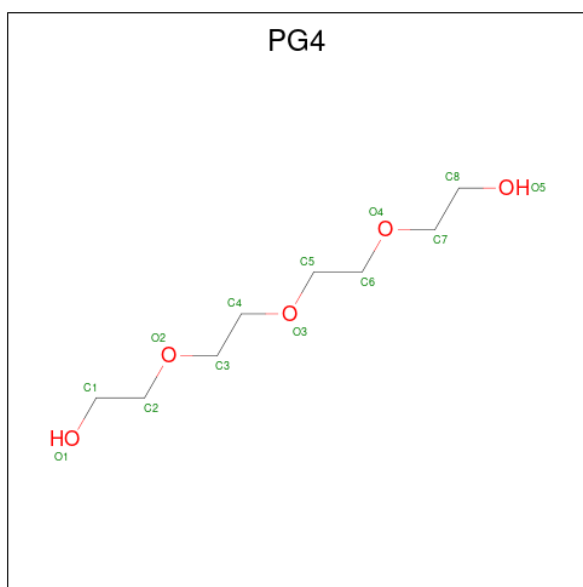
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	H	O	S	0	0
			10	2	6	1	1		
3	B	1	Total	C	H	O	S	0	0
			10	2	6	1	1		
3	C	1	Total	C	H	O	S	0	0
			10	2	6	1	1		
3	D	1	Total	C	H	O	S	0	0
			10	2	6	1	1		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			14	3	8	3		
4	A	1	Total	C	H	O	0	0
			14	3	8	3		
4	A	1	Total	C	H	O	0	0
			14	3	8	3		
4	C	1	Total	C	H	O	0	0
			14	3	8	3		

- Molecule 5 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: $C_8H_{18}O_5$).

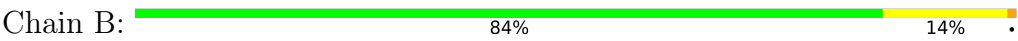


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	C	1	Total	C	H	O	0	0
			31	8	18	5		

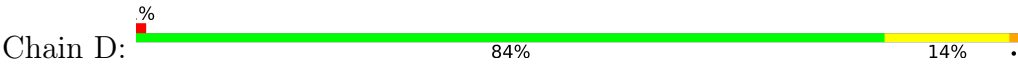
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	750	Total O 759 759	0	9
6	B	72	Total O 74 74	0	2
6	C	660	Total O 674 674	0	14
6	D	54	Total O 54 54	0	0

● Molecule 2: Ubiquitin-40S ribosomal protein S31



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4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2 ₁	Depositor
Cell constants a, b, c, α , β , γ	76.87Å 173.17Å 214.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.16 – 2.03 46.16 – 2.03	Depositor EDS
% Data completeness (in resolution range)	70.3 (46.16-2.03) 70.2 (46.16-2.03)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.13 (at 2.03Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.195 , 0.227 0.196 , 0.228	Depositor DCC
R_{free} test set	3251 reflections (1.68%)	wwPDB-VP
Wilson B-factor (Å ²)	27.6	Xtriage
Anisotropy	0.050	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 43.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	36105	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.66% 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: PG4, GOL, BME

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	0.14	0/8246	0.36	0/11157
1	C	0.16	0/8220	0.38	0/11117
2	B	0.14	0/617	0.38	0/826
2	D	0.13	0/623	0.35	0/835
All	All	0.15	0/17706	0.37	0/23935

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	811	LEU	Peptide

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	8024	7959	7930	52	1
1	C	8011	7937	7903	44	0
2	B	609	638	638	7	0
2	D	609	630	621	7	0
3	A	4	6	6	0	0
3	B	4	6	6	0	0
3	C	4	6	6	0	0
3	D	4	6	6	0	0
4	A	18	24	24	0	0
4	C	6	8	8	1	0
5	C	13	18	18	1	0
6	A	759	0	0	6	0
6	B	74	0	0	2	0
6	C	674	0	0	14	0
6	D	54	0	0	2	0
All	All	18867	17238	17166	105	1

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 3.

The worst 5 of 105 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:933[B]:ILE:HD11	1:A:1022:ILE:CD1	1.88	1.03
1:C:852[B]:ARG:NH2	6:C:1202:HOH:O	2.05	0.89
1:C:936:ASP:OD2	1:C:983:THR:OG1	1.90	0.88
1:A:933[B]:ILE:HD11	1:A:1022:ILE:HD11	1.58	0.83
2:B:25:ASN:OD1	6:B:201:HOH:O	1.97	0.81

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:LYS:NZ	1:A:500[B]:GLU:OE2[1_455]	2.13	0.07

5.3 Torsion angles

5.3.1 Protein backbone

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	1018/1024 (99%)	990 (97%)	27 (3%)	1 (0%)	48	43
1	C	1016/1024 (99%)	988 (97%)	27 (3%)	1 (0%)	48	43
2	B	75/76 (99%)	75 (100%)	0	0	100	100
2	D	76/76 (100%)	75 (99%)	1 (1%)	0	100	100
All	All	2185/2200 (99%)	2128 (97%)	55 (2%)	2 (0%)	48	43

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	220	ASP
1	C	220	ASP

5.3.2 Protein sidechains

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	905/900 (101%)	893 (99%)	12 (1%)	61	63
1	C	900/900 (100%)	887 (99%)	13 (1%)	59	60
2	B	70/69 (101%)	67 (96%)	3 (4%)	26	20
2	D	71/69 (103%)	67 (94%)	4 (6%)	19	12
All	All	1946/1938 (100%)	1914 (98%)	32 (2%)	55	56

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	24	ASP
2	D	33	LYS
2	B	24	ASP
1	A	1017	VAL
2	D	64	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	38	ASN
1	C	297	GLN
1	C	844	ASN
1	C	429	GLN
1	C	667	HIS

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](#)

9 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	GOL	A	1102	-	5,5,5	0.79	0	5,5,5	0.93	0
4	GOL	C	1103	-	5,5,5	0.90	0	5,5,5	1.01	0
3	BME	D	101	-	3,3,3	0.30	0	2,2,2	0.20	0
4	GOL	A	1103	-	5,5,5	0.80	0	5,5,5	0.96	0
3	BME	C	1102	-	3,3,3	0.25	0	2,2,2	0.11	0
4	GOL	A	1104	-	5,5,5	0.80	0	5,5,5	0.94	0
3	BME	B	101	-	3,3,3	0.32	0	2,2,2	0.12	0
3	BME	A	1101	-	3,3,3	0.28	0	2,2,2	0.18	0
5	PG4	C	1101	-	12,12,12	0.54	0	11,11,11	0.32	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	A	1102	-	-	4/4/4/4	-
4	GOL	C	1103	-	-	2/4/4/4	-
3	BME	D	101	-	-	0/1/1/1	-
4	GOL	A	1103	-	-	0/4/4/4	-
3	BME	C	1102	-	-	1/1/1/1	-
4	GOL	A	1104	-	-	1/4/4/4	-
3	BME	B	101	-	-	1/1/1/1	-
3	BME	A	1101	-	-	0/1/1/1	-
5	PG4	C	1101	-	-	7/10/10/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	101	BME	O1-C1-C2-S2
4	A	1102	GOL	C1-C2-C3-O3
4	C	1103	GOL	O1-C1-C2-C3
5	C	1101	PG4	O1-C1-C2-O2
5	C	1101	PG4	O2-C3-C4-O3

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	1103	GOL	1	0
5	C	1101	PG4	1	0

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 [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	1005/1024 (98%)	0.02	46 (4%)	37	37	10, 35, 80, 146	14 (1%)
1	C	1006/1024 (98%)	0.20	73 (7%)	21	21	12, 37, 93, 135	11 (1%)
2	B	76/76 (100%)	-0.14	0	100	100	16, 33, 48, 53	1 (1%)
2	D	76/76 (100%)	0.23	1 (1%)	75	76	25, 46, 62, 72	1 (1%)
All	All	2163/2200 (98%)	0.10	120 (5%)	30	30	10, 36, 88, 146	27 (1%)

The worst 5 of 120 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	814	PHE	6.5
1	C	811	LEU	6.1
1	A	12	GLY	5.8
1	C	801	LEU	5.1
1	A	644	THR	4.5

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
5	PG4	C	1101	13/13	0.73	0.19	48,58,59,59	0
4	GOL	A	1104	6/6	0.77	0.17	45,54,56,56	0
4	GOL	A	1102	6/6	0.83	0.11	54,65,66,66	0
4	GOL	A	1103	6/6	0.85	0.18	41,49,51,52	0
4	GOL	C	1103	6/6	0.86	0.23	34,41,44,44	0
3	BME	B	101	4/4	0.87	0.15	56,67,68,69	0
3	BME	D	101	4/4	0.88	0.14	59,71,71,71	0
3	BME	A	1101	4/4	0.93	0.11	45,54,55,57	0
3	BME	C	1102	4/4	0.93	0.10	42,50,52,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.