



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 02:46 AM UTC

PDB ID : 8V0E / pdb_00008v0e
Title : ANK repeat of MIB1
Authors : Cao, R.; Blacklow, S.C.
Deposited on : 2023-11-17
Resolution : 2.39 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

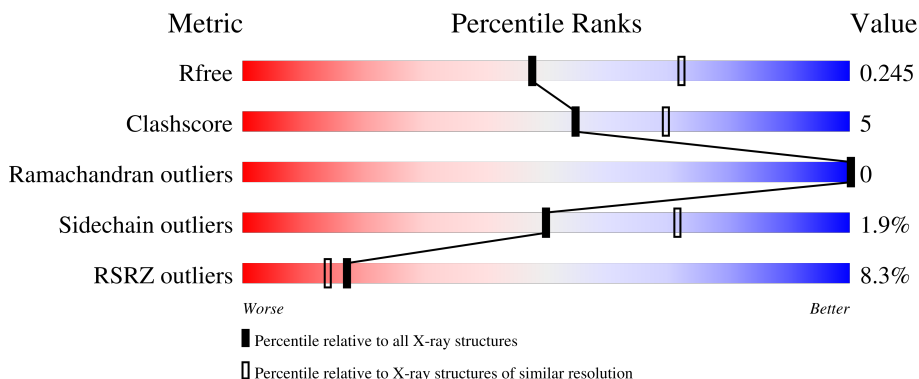
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.39 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	386	3% 80% 9% 11%
1	B	386	12% 76% 11% • 11%
2	D	5	100%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5341 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 MIB1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	344	Total	C	N	O	S	0	0	0
			2623	1613	497	504	9			
1	B	342	Total	C	N	O	S	0	0	0
			2542	1555	487	491	9			

- Molecule 2 is a protein called Unidentified MIB1 peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	5	Total	C	N	O	0	0	0
			25	15	5	5			

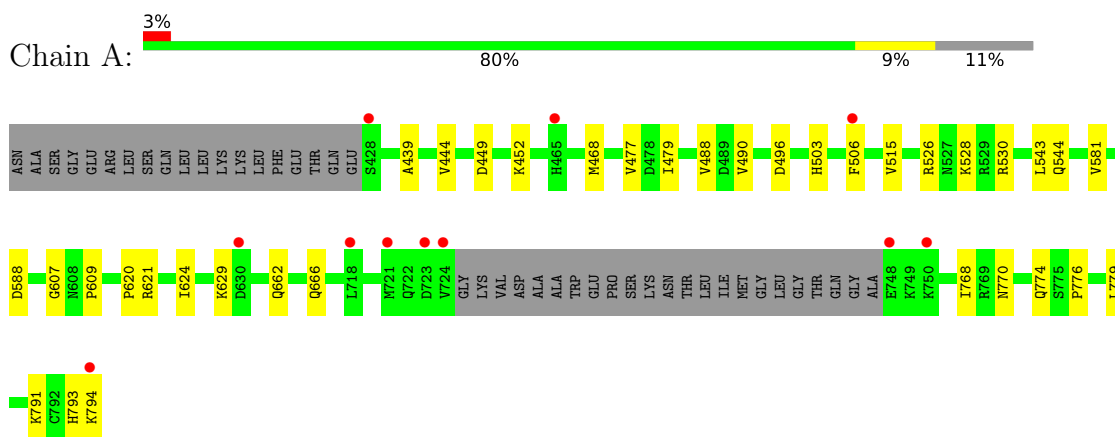
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	98	Total	O	0	0
			98	98		
3	B	53	Total	O	0	0
			53	53		

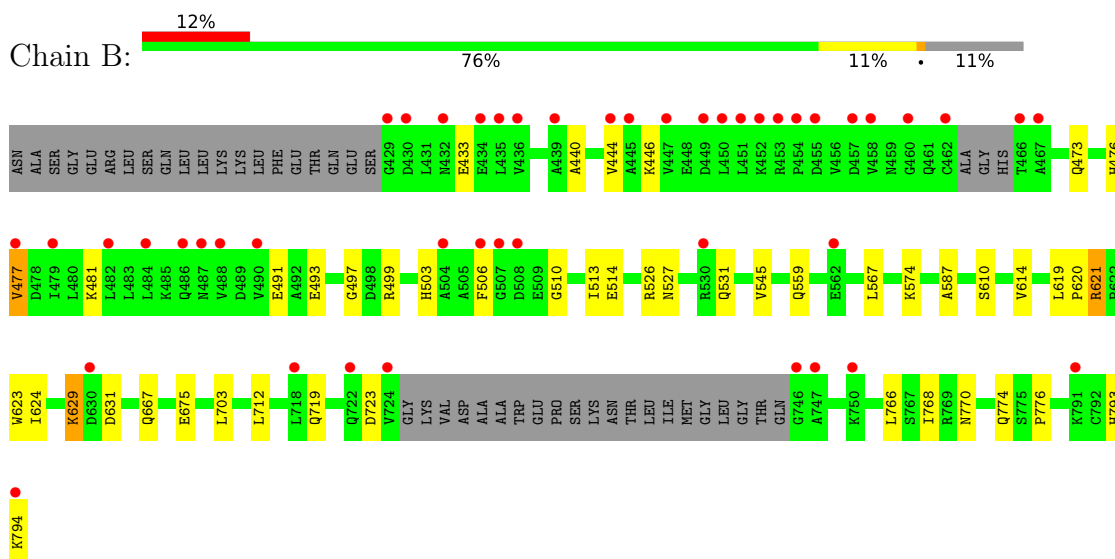
3 Residue-property plots [i](#)

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: E3 ubiquitin-protein ligase MIB1



- Molecule 1: E3 ubiquitin-protein ligase MIB1



- Molecule 2: Unidentified MIB1 peptide



There are no outlier residues recorded for this chain.

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	79.00Å 137.47Å 96.25Å 90.00° 108.14° 90.00°	Depositor
Resolution (Å)	47.64 – 2.39 47.64 – 2.39	Depositor EDS
% Data completeness (in resolution range)	97.7 (47.64-2.39) 98.4 (47.64-2.39)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.207 , 0.244 0.208 , 0.245	Depositor DCC
R_{free} test set	1856 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å ²)	44.8	Xtriage
Anisotropy	0.347	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 58.8	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	0.94	EDS
Total number of atoms	5341	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.39% 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	0.37	0/2659	0.58	0/3599
1	B	0.30	0/2576	0.52	0/3489
All	All	0.34	0/5235	0.55	0/7088

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	2623	0	2623	26	0
1	B	2542	0	2458	23	0
2	D	25	0	8	0	0
3	A	98	0	0	5	0
3	B	53	0	0	1	0
All	All	5341	0	5089	49	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 (49) 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:B:513:ILE:HD11	1:B:545:VAL:HG13	1.61	0.81
1:A:620:PRO:HD2	1:A:624:ILE:HD12	1.69	0.75
1:A:588:ASP:OD2	3:A:801:HOH:O	2.10	0.69
1:B:620:PRO:HD2	1:B:624:ILE:HD12	1.74	0.69
1:B:667:GLN:NE2	1:B:675:GLU:OE2	2.28	0.66
1:A:477:VAL:HG13	1:A:515:VAL:HG21	1.78	0.65
1:A:793:HIS:ND1	1:A:794:LYS:HG2	2.14	0.63
1:A:496:ASP:HA	1:A:528:LYS:HD3	1.80	0.62
1:B:493:GLU:HB3	1:B:497:GLY:HA2	1.81	0.62
1:B:526:ARG:NH2	1:B:559:GLN:O	2.33	0.62
1:B:768:ILE:O	1:B:776:PRO:HD3	2.01	0.61
1:B:621:ARG:HG2	1:B:623:TRP:CH2	2.36	0.61
1:A:439:ALA:HA	1:A:479:ILE:HD13	1.84	0.60
1:A:793:HIS:HE1	1:A:794:LYS:HE3	1.66	0.59
1:B:574:LYS:NZ	3:B:805:HOH:O	2.36	0.57
1:A:768:ILE:O	1:A:776:PRO:HD3	2.06	0.55
1:A:503:HIS:HA	1:A:506:PHE:CD2	2.42	0.54
1:B:510:GLY:O	1:B:514:GLU:HG3	2.07	0.54
1:B:510:GLY:HA2	1:B:513:ILE:HD12	1.88	0.53
1:B:703:LEU:HD21	1:B:766:LEU:HD23	1.91	0.51
1:B:491:GLU:HA	1:B:499:ARG:HD3	1.91	0.51
1:B:503:HIS:HA	1:B:506:PHE:CD2	2.45	0.50
1:B:477:VAL:HG22	1:B:481:LYS:HE2	1.94	0.50
1:A:543:LEU:HD11	1:A:581:VAL:HG21	1.93	0.50
1:B:719:GLN:O	1:B:723:ASP:HB2	2.12	0.50
1:A:544:GLN:NE2	3:A:809:HOH:O	2.44	0.49
1:A:468:MET:HG3	1:A:488:VAL:HG21	1.94	0.49
1:A:791:LYS:HD2	3:A:857:HOH:O	2.12	0.49
1:A:662:GLN:HB3	1:A:666:GLN:HA	1.95	0.49
1:A:793:HIS:CE1	1:A:794:LYS:HE3	2.45	0.49
1:A:526:ARG:HB3	1:A:530:ARG:HA	1.95	0.47
1:A:449:ASP:HA	1:A:452:LYS:HE3	1.96	0.47
1:B:793:HIS:ND1	1:B:794:LYS:HG2	2.30	0.46
1:B:610:SER:O	1:B:614:VAL:HG23	2.16	0.46
1:A:770:ASN:OD1	1:A:774:GLN:HG2	2.16	0.46
1:A:526:ARG:HG3	1:A:530:ARG:HH21	1.80	0.46
1:A:444:VAL:HG22	1:A:479:ILE:HG13	1.97	0.45
1:A:609:PRO:HD2	3:A:829:HOH:O	2.18	0.44
1:A:468:MET:HE3	1:A:468:MET:HB3	1.88	0.43
1:A:607:GLY:O	1:A:609:PRO:HD3	2.19	0.42
1:B:440:ALA:O	1:B:476:HIS:NE2	2.52	0.42
1:B:629:LYS:NZ	1:B:631:ASP:OD2	2.53	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:774:GLN:NE2	1:A:779:LEU:HD21	2.35	0.41
1:A:530:ARG:NE	3:A:812:HOH:O	2.45	0.41
1:B:473:GLN:HG3	1:B:506:PHE:HB2	2.03	0.41
1:B:527:ASN:OD1	1:B:531:GLN:N	2.51	0.41
1:B:770:ASN:OD1	1:B:774:GLN:HG2	2.21	0.41
1:B:567:LEU:HG	1:B:587:ALA:HB1	2.04	0.40
1:A:620:PRO:O	1:A:621:ARG:HG3	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	340/386 (88%)	333 (98%)	7 (2%)	0	100	100
1	B	336/386 (87%)	324 (96%)	12 (4%)	0	100	100
All	All	676/772 (88%)	657 (97%)	19 (3%)	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	281/314 (90%)	279 (99%)	2 (1%)	76	88

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	B	258/314 (82%)	250 (97%)	8 (3%)	35 57
All	All	539/628 (86%)	529 (98%)	10 (2%)	50 71

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	490	VAL
1	A	629	LYS
1	B	433	GLU
1	B	444	VAL
1	B	446	LYS
1	B	477	VAL
1	B	619	LEU
1	B	621	ARG
1	B	629	LYS
1	B	712	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	474	ASN
1	A	517	HIS
1	A	544	GLN
1	A	710	HIS
1	B	474	ASN
1	B	517	HIS
1	B	653	HIS

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	344/386 (89%)	0.17	11 (3%) 50 46	29, 50, 88, 122	0
1	B	342/386 (88%)	0.86	46 (13%) 7 5	35, 70, 142, 160	0
2	D	0/5	-	-	-	-
All	All	686/777 (88%)	0.51	57 (8%) 17 14	29, 59, 129, 160	0

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	724	VAL	5.5
1	B	747	ALA	5.0
1	B	724	VAL	4.6
1	B	432	ASN	4.6
1	B	746	GLY	4.5
1	B	507	GLY	4.5
1	B	462	CYS	4.2
1	B	722	GLN	3.8
1	B	451	LEU	3.8
1	B	447	VAL	3.7
1	B	449	ASP	3.7
1	B	457	ASP	3.6
1	B	506	PHE	3.5
1	B	486	GLN	3.5
1	B	453	ARG	3.5
1	B	458	VAL	3.4
1	B	454	PRO	3.4
1	B	430	ASP	3.3
1	B	436	VAL	3.3
1	B	467	ALA	3.2
1	B	630	ASP	3.2
1	B	435	LEU	3.2
1	B	444	VAL	3.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	450	LEU	3.1
1	B	429	GLY	3.0
1	B	477	VAL	3.0
1	B	452	LYS	2.9
1	B	508	ASP	2.8
1	B	466	THR	2.7
1	B	490	VAL	2.6
1	A	506	PHE	2.6
1	A	428	SER	2.6
1	A	718	LEU	2.6
1	B	445	ALA	2.6
1	B	482	LEU	2.5
1	B	460	GLY	2.5
1	B	562	GLU	2.5
1	B	718	LEU	2.5
1	A	721	MET	2.4
1	B	504	ALA	2.4
1	B	750	LYS	2.4
1	B	488	VAL	2.4
1	B	434	GLU	2.3
1	A	750	LYS	2.3
1	B	487	ASN	2.3
1	B	791	LYS	2.3
1	B	455	ASP	2.2
1	B	794	LYS	2.2
1	A	630	ASP	2.2
1	B	530	ARG	2.2
1	B	479	ILE	2.2
1	A	465	HIS	2.1
1	A	794	LYS	2.1
1	B	484	LEU	2.1
1	A	748	GLU	2.0
1	B	439	ALA	2.0
1	A	723	ASP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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.