



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:34 AM UTC

PDB ID : 5O63 / pdb_00005o63
Title : Crystal structure of UbaLAI restriction endonuclease B3 domain domain (mutant L24M L53M L95M) with cognate DNA
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Deposited on : 2017-06-05
Resolution : 1.60 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

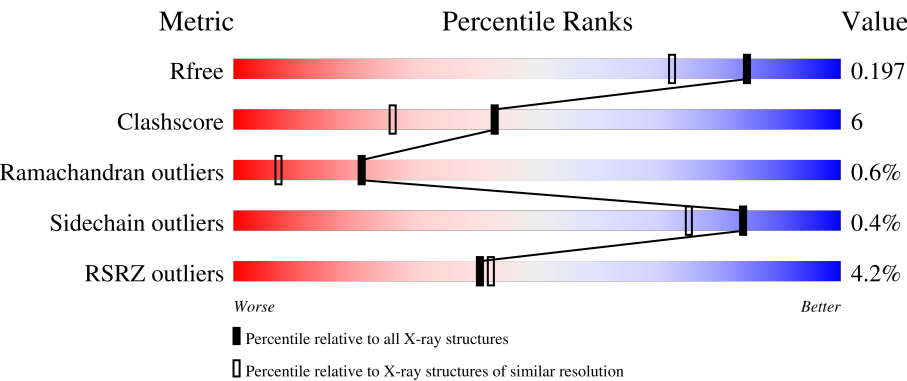
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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	4673 (1.60-1.60)
Clashscore	190562	4931 (1.60-1.60)
Ramachandran outliers	187476	4831 (1.60-1.60)
Sidechain outliers	187428	4830 (1.60-1.60)
RSRZ outliers	180081	4672 (1.60-1.60)

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	186	3% 77% 8% 15%
1	B	186	5% 76% 10% 13%
2	C	9	78% 22%
2	E	9	44% 56%
3	D	9	89% 11%

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Mol	Chain	Length	Quality of chain
3	F	9	67% 33%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3922 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 Restriction endonuclease UbaLAI.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	159	Total	C	N	O	S	0	11	0
			1333	853	229	246	5			
1	B	161	Total	C	N	O	S	0	13	0
			1365	871	233	254	7			

- Molecule 2 is a DNA chain called DNA (5'-D(*C*G*C*C*A*G*G*G*C*)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	9	Total	C	N	O	P	0	0	0
			181	86	34	53	8			
2	E	9	Total	C	N	O	P	0	2	0
			219	105	42	63	9			

- Molecule 3 is a DNA chain called DNA (5'-D(*G*C*C*C*T*G*G*C*G*)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	9	Total	C	N	O	P	0	0	0
			182	86	37	51	8			
3	F	9	Total	C	N	O	P	0	2	0
			223	105	45	63	10			

- Molecule 4 is water.

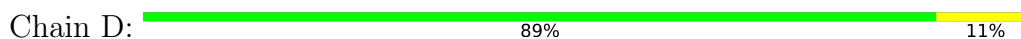
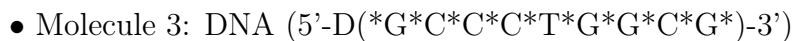
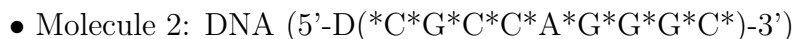
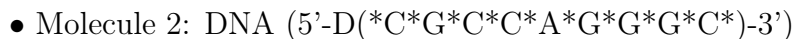
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	133	Total	O	0	0
			133	133		
4	B	137	Total	O	0	0
			137	137		
4	C	33	Total	O	0	0
			33	33		
4	D	40	Total	O	0	0
			40	40		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	41	Total	O	0	0
			41	41		
4	F	35	Total	O	0	0
			35	35		

- Molecule 1: Restriction endonuclease UbaLAI





- Molecule 3: DNA (5'-D(*G*C*C*C*T*G*G*C*G*)-3')

Chain F:  67% 33%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	40.77Å 94.58Å 123.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	51.68 – 1.60 51.68 – 1.60	Depositor EDS
% Data completeness (in resolution range)	99.2 (51.68-1.60) 99.5 (51.68-1.60)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.28 (at 1.60Å)	Xtriage
Refinement program	PHENIX 1.8.3	Depositor
R, R_{free}	0.159 , 0.191 0.169 , 0.197	Depositor DCC
R_{free} test set	6377 reflections (9.97%)	wwPDB-VP
Wilson B-factor (Å ²)	21.3	Xtriage
Anisotropy	0.570	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 47.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3922	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.66% 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](#)

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	1.03	1/1367 (0.1%)	0.99	0/1849
1	B	1.03	0/1399	0.99	0/1890
2	C	0.89	0/202	0.97	0/310
2	E	0.77	0/245	0.69	0/377
3	D	1.01	0/204	1.01	1/313 (0.3%)
3	F	0.77	0/249	0.89	0/380
All	All	0.99	1/3666 (0.0%)	0.96	1/5119 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	102	ARG	CZ-NH1	5.11	1.40	1.32

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	-2	DC	C1'-O4'-C4'	-5.55	101.37	109.70

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	1333	0	1295	17	0
1	B	1365	0	1333	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	181	0	102	1	0
2	E	219	0	125	6	0
3	D	182	0	101	0	0
3	F	223	0	124	11	0
4	A	133	0	0	2	0
4	B	137	0	0	2	1
4	C	33	0	0	0	1
4	D	40	0	0	0	0
4	E	41	0	0	0	0
4	F	35	0	0	2	0
All	All	3922	0	3080	41	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 6.

All (41) 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:76:HIS:CG	3:F:4[B]:DC:H2'	2.21	0.75
3:F:2:DG:H2''	3:F:3[B]:DG:C8	2.24	0.73
1:B:148:ILE:O	4:B:201:HOH:O	2.10	0.69
1:A:40:VAL:HG23	1:A:95:MET:HE1	1.77	0.67
1:A:101[B]:GLU:HG3	1:A:104:TYR:HD1	1.61	0.66
2:E:-2:DC:O2	3:F:3[B]:DG:N2	2.28	0.66
1:B:40:VAL:HG23	1:B:95:MET:HE1	1.81	0.63
1:A:101[B]:GLU:HG3	1:A:104:TYR:CD1	2.36	0.61
1:B:148:ILE:HG12	4:B:260:HOH:O	2.05	0.57
3:F:2:DG:C2	3:F:3[B]:DG:C2	2.93	0.57
1:A:76:HIS:CD2	3:F:4[B]:DC:H2'	2.39	0.57
1:B:11:LEU:HD11	1:B:71[B]:SER:HB3	1.90	0.54
1:A:63[B]:THR:HG21	1:A:82:LYS:NZ	2.24	0.53
3:F:2:DG:H4'	3:F:3[B]:DG:OP1	2.09	0.52
2:E:-2:DC:C2	3:F:3[B]:DG:N2	2.80	0.50
1:A:11:LEU:HD11	1:A:71:SER:HB2	1.94	0.49
1:A:18:THR:HG23	4:A:307:HOH:O	2.13	0.48
1:B:9[B]:LYS:HG3	1:B:19[B]:LEU:HD23	1.96	0.48
1:A:40:VAL:CG2	1:A:95:MET:HE1	2.43	0.47
3:F:2:DG:H2''	3:F:3[B]:DG:H8	1.73	0.47
1:B:22:ALA:HB3	1:B:160:ILE:HG13	1.97	0.46
1:B:18[B]:THR:HB	1:B:117:THR:HG1	1.81	0.46
2:E:3:DC:H2'	2:E:4:DG:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:HIS:CD2	4:F:126:HOH:O	2.70	0.45
3:F:2:DG:C2	3:F:3[B]:DG:N3	2.84	0.45
1:A:87:TYR:HB2	1:A:88:PRO:C	2.42	0.45
1:A:76:HIS:ND1	3:F:4[B]:DC:C2	2.85	0.45
1:B:87:TYR:HB2	1:B:88:PRO:C	2.42	0.44
1:A:76:HIS:HB2	3:F:4[B]:DC:C2	2.52	0.44
1:B:38:HIS:O	1:B:91:ARG:HD3	2.18	0.44
1:A:76:HIS:HD2	4:F:126:HOH:O	2.01	0.43
2:E:-3[B]:DC:O2	2:E:-2:DC:C2	2.71	0.43
1:A:63[B]:THR:HG21	1:A:82:LYS:HZ1	1.83	0.43
2:E:-4[B]:DG:H2''	2:E:-3[B]:DC:C6	2.54	0.42
2:E:-3[B]:DC:H1'	2:E:-2:DC:C6	2.53	0.42
1:B:72:LEU:HD23	1:B:72:LEU:HA	1.92	0.42
1:A:158[A]:ARG:NE	4:A:201:HOH:O	2.29	0.42
2:C:3:DC:H2'	2:C:4:DG:C8	2.55	0.41
1:B:109[B]:THR:HG23	1:B:125:PHE:CE2	2.56	0.41
1:A:63[B]:THR:CG2	1:A:82:LYS:NZ	2.83	0.41
1:B:11:LEU:CD1	1:B:71[B]:SER:HB3	2.51	0.41

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)
4:B:309:HOH:O	4:C:126:HOH:O[4_455]	2.14	0.06

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	168/186 (90%)	165 (98%)	2 (1%)	1 (1%)	21 7
1	B	171/186 (92%)	166 (97%)	4 (2%)	1 (1%)	21 7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	339/372 (91%)	331 (98%)	6 (2%)	2 (1%)	21	7

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	36	GLY
1	B	36	GLY

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	141/157 (90%)	141 (100%)	0	100	100
1	B	147/157 (94%)	146 (99%)	1 (1%)	76	63
All	All	288/314 (92%)	287 (100%)	1 (0%)	84	78

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

Mol	Chain	Res	Type
1	B	11	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	60	GLN

5.3.3 RNA ⓘ

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](#)

There are no ligands in this entry.

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	159/186 (85%)	0.08	6 (3%)	44	46	8, 26, 46, 57	11 (6%)
1	B	161/186 (86%)	0.15	9 (5%)	30	31	10, 25, 49, 75	13 (8%)
2	C	9/9 (100%)	-0.55	0	100	100	19, 25, 37, 47	0
2	E	9/9 (100%)	-0.42	0	100	100	12, 27, 32, 41	2 (22%)
3	D	9/9 (100%)	-0.68	0	100	100	20, 24, 27, 36	0
3	F	9/9 (100%)	-0.25	0	100	100	17, 24, 34, 35	2 (22%)
All	All	356/408 (87%)	0.05	15 (4%)	40	42	8, 26, 47, 75	28 (7%)

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	56	SER	5.0
1	B	161	ASP	4.5
1	A	148[A]	ILE	4.2
1	B	101[A]	GLU	3.1
1	A	160	ILE	2.8
1	B	148	ILE	2.5
1	A	2	ASN	2.5
1	B	160	ILE	2.5
1	B	1[A]	MET	2.5
1	B	54	PRO	2.4
1	B	55	ILE	2.4
1	B	133	GLY	2.3
1	A	5	ILE	2.2
1	A	54	PRO	2.1
1	A	55	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.