



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 03:26 AM UTC

PDB ID : 7UYG / pdb_00007uyg
Title : Structure of the first OTU domain from Legionella pneumophila effector protein LotA
Authors : Pruneda, J.N.
Deposited on : 2022-05-06
Resolution : 1.50 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
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

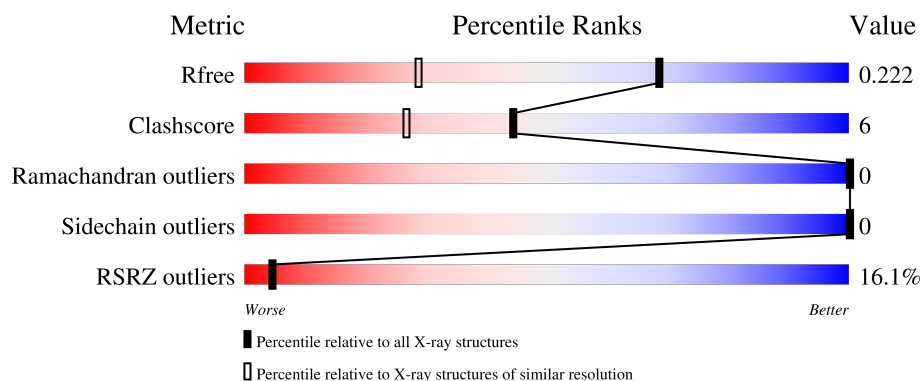
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 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	4037 (1.50-1.50)
Clashscore	190562	4235 (1.50-1.50)
Ramachandran outliers	187476	4153 (1.50-1.50)
Sidechain outliers	187428	4150 (1.50-1.50)
RSRZ outliers	180081	4039 (1.50-1.50)

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	296	15% 82% 10% 7%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2479 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.

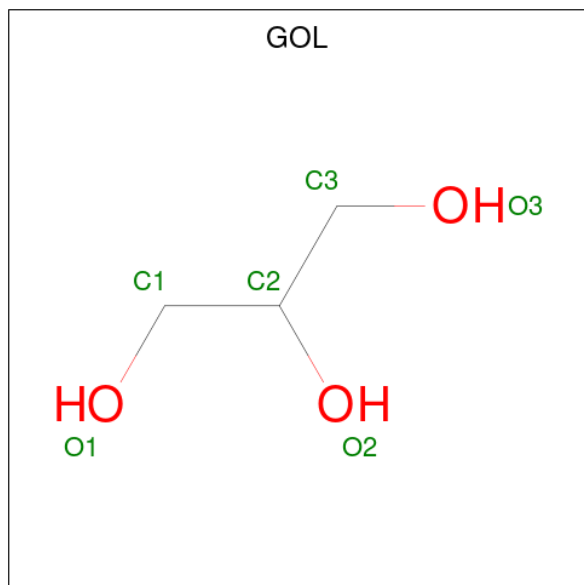
- Molecule 1 is a protein called LotA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	274	2174	1378	372	417	7	0	8	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP Q5ZTB4
A	0	PRO	-	expression tag	UNP Q5ZTB4

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is IODIDE ION (CCD ID: IOD) (formula: I).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	7	Total I 7 7	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	286	Total O 286 286	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	86.25Å 86.25Å 92.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.80 – 1.50 36.80 – 1.50	Depositor EDS
% Data completeness (in resolution range)	99.9 (36.80-1.50) 99.9 (36.80-1.50)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.41 (at 1.50Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.195 , 0.221 0.197 , 0.222	Depositor DCC
R_{free} test set	2895 reflections (5.14%)	wwPDB-VP
Wilson B-factor (Å ²)	21.5	Xtriage
Anisotropy	0.189	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 41.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2479	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.67% 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: GOL, IOD

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	0.26	0/2235	0.45	0/3028

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	2174	0	2145	26	0
2	A	12	0	16	4	0
3	A	7	0	0	0	0
4	A	286	0	0	11	1
All	All	2479	0	2161	26	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 (26) 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:232:GLU:HG3	1:A:241:LEU:HD21	1.68	0.76
1:A:13[B]:CYS:SG	4:A:598:HOH:O	2.44	0.74
1:A:97:GLU:OE2	4:A:401:HOH:O	2.05	0.74
1:A:13[A]:CYS:SG	4:A:474:HOH:O	2.46	0.71
1:A:242[B]:CYS:SG	4:A:634:HOH:O	2.49	0.71
1:A:153:ARG:NH1	4:A:405:HOH:O	2.25	0.69
1:A:53[A]:GLN:OE1	4:A:402:HOH:O	2.12	0.67
1:A:112:ASN:ND2	4:A:406:HOH:O	2.28	0.64
1:A:55:ASN:HB3	2:A:301:GOL:H32	1.82	0.61
1:A:91:GLN:NE2	4:A:407:HOH:O	2.36	0.57
1:A:198:TYR:O	4:A:403:HOH:O	2.18	0.56
1:A:171:PHE:CE1	1:A:175:LYS:HD3	2.44	0.52
1:A:243:ASN:ND2	1:A:246:ASP:OD2	2.43	0.52
1:A:12:ALA:HB1	1:A:15:PHE:HD2	1.78	0.49
1:A:185:LYS:NZ	4:A:404:HOH:O	2.24	0.48
1:A:228:LYS:NZ	4:A:408:HOH:O	2.37	0.47
1:A:135:LYS:HA	2:A:302:GOL:H12	1.96	0.47
1:A:232:GLU:HB2	1:A:239:ASN:HB2	1.97	0.46
1:A:55:ASN:ND2	1:A:56:PRO:HA	2.32	0.45
1:A:192:HIS:HE1	2:A:302:GOL:H31	1.81	0.44
1:A:134:PRO:HA	1:A:137:GLU:HG2	1.99	0.44
1:A:146:ALA:HB3	1:A:147:PRO:HD3	2.00	0.43
1:A:12:ALA:HB1	1:A:15:PHE:CD2	2.54	0.43
1:A:107:TRP:CZ3	1:A:108:LYS:HE2	2.56	0.41
1:A:192:HIS:CE1	2:A:302:GOL:H31	2.56	0.41
1:A:160:LYS:HD3	1:A:160:LYS:HA	1.84	0.40

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:A:667:HOH:O	4:A:675:HOH:O[3_545]	2.07	0.13

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	280/296 (95%)	271 (97%)	9 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	233/264 (88%)	233 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

Mol	Chain	Res	Type
1	A	55	ASN

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

Of 9 ligands modelled in this entry, 7 are monoatomic - leaving 2 for Mogul analysis.

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	$\# Z > 2$
2	GOL	A	301	-	5,5,5	0.99	0	5,5,5	1.07	0
2	GOL	A	302	-	5,5,5	0.89	0	5,5,5	0.97	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
2	GOL	A	301	-	-	0/4/4/4	-
2	GOL	A	302	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	302	GOL	O1-C1-C2-C3
2	A	302	GOL	C1-C2-C3-O3
2	A	302	GOL	O1-C1-C2-O2
2	A	302	GOL	O2-C2-C3-O3

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	GOL	1	0
2	A	302	GOL	3	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 ⓘ

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	274/296 (92%)	0.78	44 (16%) 4 4	11, 28, 64, 87	8 (2%)

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	194	PHE	8.9
1	A	2	ALA	5.3
1	A	237	HIS	5.1
1	A	266	TYR	4.7
1	A	220	GLU	4.6
1	A	93	HIS	4.4
1	A	190	ASP	4.0
1	A	191	PRO	4.0
1	A	269	ASP	3.7
1	A	222	ILE	3.7
1	A	11	GLY	3.7
1	A	234	GLN	3.6
1	A	192	HIS	3.3
1	A	236	GLU	3.2
1	A	262	SER	3.1
1	A	219	GLU	3.0
1	A	197	GLY	3.0
1	A	195	GLN	3.0
1	A	235	GLU	2.9
1	A	4	THR	2.9
1	A	263	LEU	2.8
1	A	268	GLY	2.7
1	A	5	ILE	2.7
1	A	198	TYR	2.7
1	A	193	ALA	2.7
1	A	8	THR	2.7
1	A	92	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	270	LYS	2.6
1	A	218	ARG	2.6
1	A	241	LEU	2.6
1	A	9	GLY	2.5
1	A	261	THR	2.5
1	A	275	PRO	2.5
1	A	10	ASP	2.5
1	A	217	ASN	2.5
1	A	267	ARG	2.4
1	A	265	ALA	2.3
1	A	91	GLN	2.3
1	A	243	ASN	2.3
1	A	215	VAL	2.3
1	A	240	VAL	2.2
1	A	223	THR	2.1
1	A	153	ARG	2.1
1	A	209	ALA	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](#)

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(Å ²)	Q<0.9
3	IOD	A	309	1/1	0.61	0.35	185,185,185,185	1
2	GOL	A	301	6/6	0.73	0.19	56,61,62,62	0
2	GOL	A	302	6/6	0.78	0.17	33,49,56,74	0
3	IOD	A	307	1/1	0.86	0.13	44,44,44,44	1
3	IOD	A	308	1/1	0.91	0.12	37,37,37,37	1
3	IOD	A	303	1/1	0.95	0.06	23,23,23,23	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	IOD	A	306	1/1	0.97	0.06	33,33,33,33	1
3	IOD	A	304	1/1	0.99	0.04	24,24,24,24	1
3	IOD	A	305	1/1	0.99	0.03	21,21,21,21	1

6.5 Other polymers [i](#)

There are no such residues in this entry.