



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 11, 2026 – 11:38 PM UTC

PDB ID : 9UO7 / pdb_00009uo7
Title : L. donovani Cell cycle associated protein MOB1
Authors : Saw, S.; Parihar, P.S.; Pratap, J.V.
Deposited on : 2025-04-25
Resolution : 1.30 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	:	FAILED
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

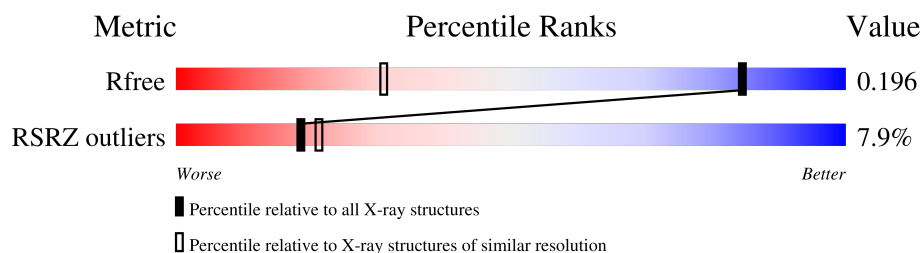
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.30 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	1553 (1.30-1.30)
RSRZ outliers	180081	1549 (1.30-1.30)

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 3704 atoms, of which 1718 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 Cell cycle associated protein MOB1, putative.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	214	Total	C	H	N	O	S	0	5	0
			3420	1135	1667	287	323	8			

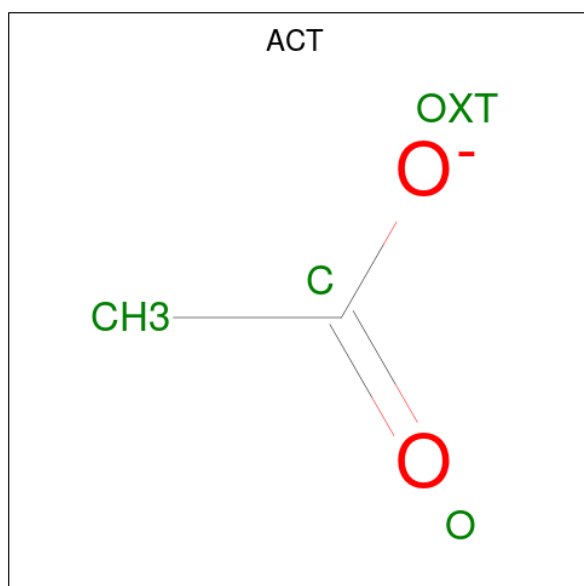
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	220	ASP	GLU	engineered mutation	UNP A0A3S5H5T5

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			7	2	3	2		

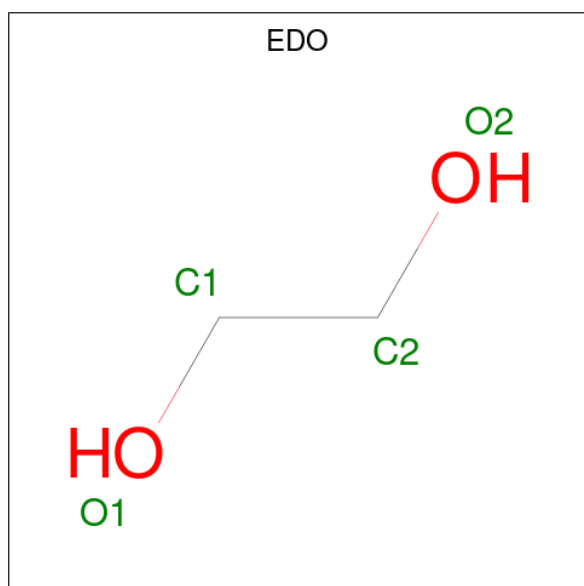
- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	13	Total	Na	0	0
			13	13		

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	5	Total	Cl	0	0
			5	5		

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	178	Total	O	0	0
			178	178		

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3 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	33.38Å 68.53Å 46.45Å 90.00° 110.07° 90.00°	Depositor
Resolution (Å)	36.80 – 1.30 36.80 – 1.30	Depositor EDS
% Data completeness (in resolution range)	99.7 (36.80-1.30) 99.7 (36.80-1.30)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.03 (at 1.31Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, R_{free}	0.179 , 0.197 0.179 , 0.196	Depositor DCC
R_{free} test set	4738 reflections (9.90%)	wwPDB-VP
Wilson B-factor (Å ²)	14.2	Xtriage
Anisotropy	0.666	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 37.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.034 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	3704	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.52% 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.

4 Model quality [i](#)

4.1 Standard geometry [i](#)

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4.2 Too-close contacts [i](#)

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4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

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4.3.2 Protein sidechains [i](#)

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4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

Of 28 ligands modelled in this entry, 19 are monoatomic - leaving 9 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	$\# Z > 2$
3	ACT	A	302	-	3,3,3	1.27	0	3,3,3	0.88	0
6	EDO	A	323	-	3,3,3	0.24	0	2,2,2	0.57	0
6	EDO	A	325	-	3,3,3	0.29	0	2,2,2	0.29	0
6	EDO	A	326	-	3,3,3	0.25	0	2,2,2	0.23	0
6	EDO	A	324	-	3,3,3	0.30	0	2,2,2	0.37	0
6	EDO	A	321	-	3,3,3	0.25	0	2,2,2	0.35	0
6	EDO	A	327	-	3,3,3	0.23	0	2,2,2	0.41	0
6	EDO	A	328	-	3,3,3	0.27	0	2,2,2	0.32	0
6	EDO	A	322	-	3,3,3	0.25	0	2,2,2	0.58	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
6	EDO	A	323	-	-	0/1/1/1	-
6	EDO	A	325	-	-	1/1/1/1	-
6	EDO	A	326	-	-	1/1/1/1	-
6	EDO	A	324	-	-	0/1/1/1	-
6	EDO	A	321	-	-	0/1/1/1	-
6	EDO	A	327	-	-	0/1/1/1	-
6	EDO	A	328	-	-	1/1/1/1	-
6	EDO	A	322	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	328	EDO	O1-C1-C2-O2
6	A	325	EDO	O1-C1-C2-O2
6	A	326	EDO	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

5 Fit of model and data [i](#)

5.1 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	214/223 (95%)	0.44	17 (7%) 18 21	8, 19, 36, 43	3 (1%)

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	191	PHE	5.5
1	A	9	PHE	5.1
1	A	190	TYR	4.1
1	A	192	ALA	3.9
1	A	24	GLY	3.8
1	A	95[A]	TYR	3.5
1	A	103	PRO	3.3
1	A	25	THR	3.2
1	A	28	TYR	2.9
1	A	139	TYR	2.9
1	A	102	PRO	2.6
1	A	33	PHE	2.6
1	A	159	ARG	2.5
1	A	138	ASP	2.5
1	A	94	ARG	2.2
1	A	93	PRO	2.1
1	A	80	TYR	2.0

5.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.4 Ligands ⓘ

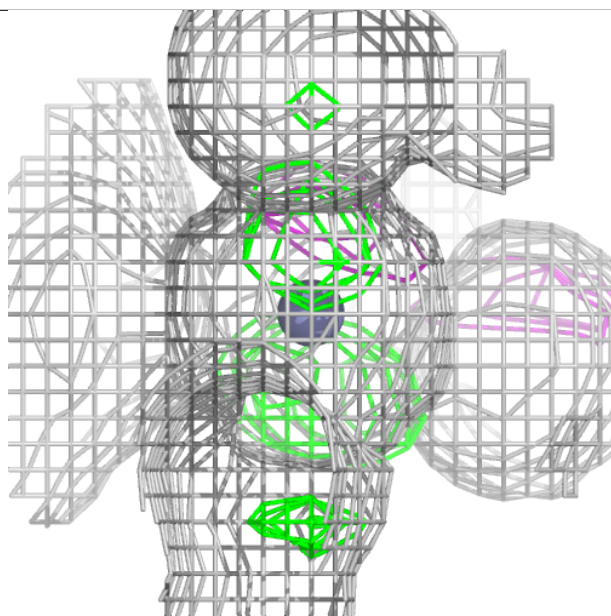
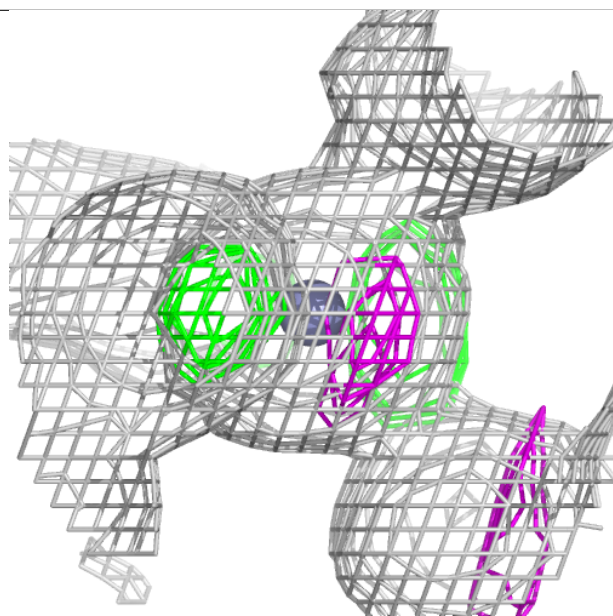
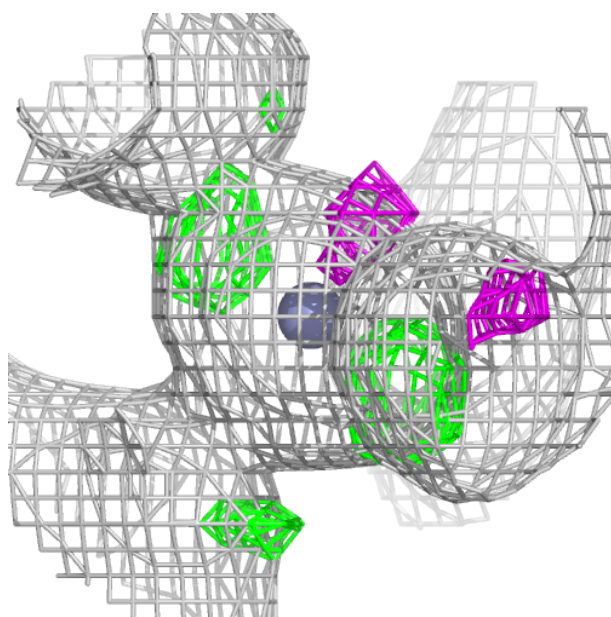
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	CL	A	320	1/1	0.61	0.19	62,62,62,62	0
6	EDO	A	323	4/4	0.65	0.15	35,43,48,49	0
6	EDO	A	322	4/4	0.70	0.16	35,42,49,49	0
6	EDO	A	327	4/4	0.71	0.14	21,31,45,53	0
3	ACT	A	302	4/4	0.75	0.14	28,35,37,44	0
6	EDO	A	321	4/4	0.76	0.14	36,43,48,52	0
5	CL	A	318	1/1	0.78	0.20	54,54,54,54	0
4	NA	A	305	1/1	0.78	0.19	44,44,44,44	0
4	NA	A	315	1/1	0.79	0.15	40,40,40,40	0
6	EDO	A	325	4/4	0.81	0.11	28,36,43,48	0
4	NA	A	314	1/1	0.82	0.17	36,36,36,36	0
6	EDO	A	328	4/4	0.83	0.11	22,33,42,49	0
6	EDO	A	326	4/4	0.85	0.11	31,40,43,51	0
5	CL	A	319	1/1	0.87	0.12	53,53,53,53	0
5	CL	A	316	1/1	0.88	0.11	57,57,57,57	0
4	NA	A	304	1/1	0.89	0.10	35,35,35,35	0
5	CL	A	317	1/1	0.89	0.13	57,57,57,57	0
4	NA	A	312	1/1	0.90	0.12	32,32,32,32	0
4	NA	A	313	1/1	0.90	0.12	35,35,35,35	0
4	NA	A	308	1/1	0.90	0.11	37,37,37,37	0
4	NA	A	310	1/1	0.90	0.11	38,38,38,38	0
4	NA	A	311	1/1	0.92	0.10	28,28,28,28	0
4	NA	A	303	1/1	0.93	0.11	32,32,32,32	0
6	EDO	A	324	4/4	0.93	0.08	21,26,32,32	0
4	NA	A	307	1/1	0.93	0.11	39,39,39,39	0
4	NA	A	309	1/1	0.95	0.16	33,33,33,33	0
4	NA	A	306	1/1	0.98	0.04	22,22,22,22	0
2	ZN	A	301	1/1	0.99	0.02	13,13,13,13	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around ZN A 301:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



5.5 Other polymers ⓘ

There are no such residues in this entry.