



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 25, 2026 – 09:57 PM UTC

PDB ID : 6MBD / pdb_00006mbd
Title : Human Mcl-1 in complex with the designed peptide dM1
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Deposited on : 2018-08-29
Resolution : 1.95 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
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

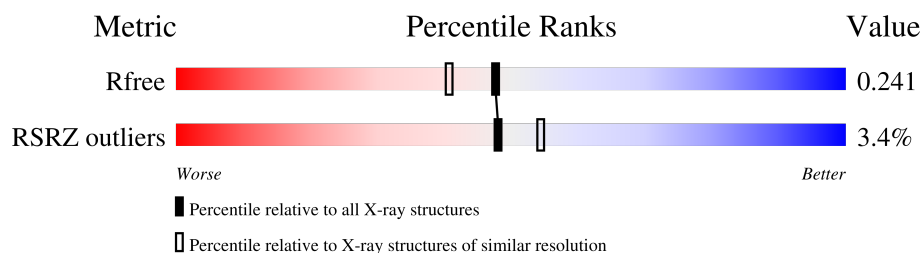
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	3494 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5923 atoms, of which 2876 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 Induced myeloid leukemia cell differentiation protein Mcl-1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	155	Total	C	H	N	O	S	0	1	0
			2504	782	1254	229	235	4			
1	B	154	Total	C	H	N	O	S	0	0	0
			2473	773	1238	227	231	4			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	170	GLY	-	expression tag	UNP Q07820
A	171	SER	-	expression tag	UNP Q07820
B	170	GLY	-	expression tag	UNP Q07820
B	171	SER	-	expression tag	UNP Q07820

- Molecule 2 is a protein called dM1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	23	Total	C	H	N	O	0	0	0
			373	113	192	31	37			
2	D	23	Total	C	H	N	O	0	0	0
			373	113	192	31	37			

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	4	Total	Zn	0	1
			5	5		
3	B	2	Total	Zn	0	0
			2	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	86	Total 86	O 86	0	0
4	B	80	Total 80	O 80	0	0
4	C	16	Total 16	O 16	0	0
4	D	11	Total 11	O 11	0	0

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3 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	64.79Å 69.73Å 84.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.30 – 1.95 24.30 – 1.95	Depositor EDS
% Data completeness (in resolution range)	95.9 (24.30-1.95) 96.2 (24.30-1.95)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.47 (at 1.95Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.196 , 0.240 0.197 , 0.241	Depositor DCC
R_{free} test set	1994 reflections (6.90%)	wwPDB-VP
Wilson B-factor (Å ²)	29.6	Xtriage
Anisotropy	0.513	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.45 , 42.2	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	0.96	EDS
Total number of atoms	5923	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.11% 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 7 ligands modelled in this entry, 7 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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 ⓘ

5.1 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	155/155 (100%)	-0.14	2 (1%) 75 81	14, 32, 59, 77	1 (0%)
1	B	154/155 (99%)	0.18	7 (4%) 38 44	25, 38, 74, 89	0
2	C	23/25 (92%)	0.11	2 (8%) 16 18	25, 38, 58, 68	0
2	D	23/25 (92%)	0.19	1 (4%) 40 46	27, 41, 67, 68	0
All	All	355/360 (98%)	0.03	12 (3%) 48 54	14, 35, 68, 89	1 (0%)

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	281	ILE	3.0
1	B	238	LYS	3.0
1	B	202	SER	2.8
2	D	-2	ALA	2.7
2	C	19	LYS	2.7
1	B	322	GLU	2.7
1	A	281	ILE	2.5
1	B	198	PRO	2.4
1	A	200	GLY	2.4
2	C	-3	ALA	2.4
1	B	321	VAL	2.3
1	B	196	THR	2.2

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

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

5.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.4 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	ZN	A	403	1/1	0.91	0.08	55,55,55,55	0
3	ZN	A	401	1/1	0.97	0.06	63,63,63,63	0
3	ZN	A	402[B]	1/1	0.98	0.04	39,39,39,39	1
3	ZN	A	402[A]	1/1	0.98	0.04	28,28,28,28	1
3	ZN	A	404	1/1	0.99	0.03	32,32,32,32	0
3	ZN	B	401	1/1	0.99	0.06	44,44,44,44	0
3	ZN	B	402	1/1	0.99	0.03	32,32,32,32	0

5.5 Other polymers [i](#)

There are no such residues in this entry.