



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 2MLL / pdb_00002mll
Title : MISTLETOE LECTIN I FROM VISCUM ALBUM
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Deposited on : 1999-03-16
Resolution : 2.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

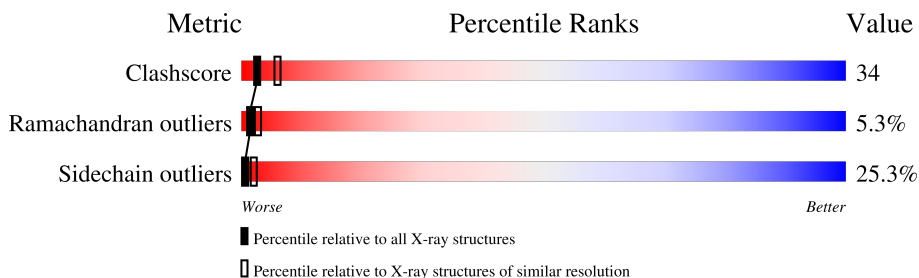
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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))
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)

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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	241	
2	B	255	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3963 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.

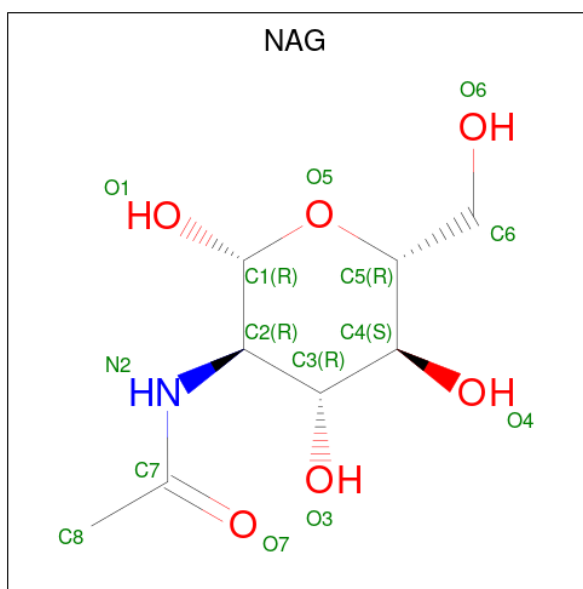
- Molecule 1 is a protein called PROTEIN (RIBOSOME-INACTIVATING PROTEIN TYPE II).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	241	Total 1809	C 1145	N 307	O 353	S 4	0	0	0

- Molecule 2 is a protein called PROTEIN (RIBOSOME-INACTIVATING PROTEIN TYPE II).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	255	Total 1897	C 1177	N 332	O 376	S 12	0	0	0

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	Total 14	C 8	N 1	O 5	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	108	Total	O	0	0
			108	108		
4	B	107	Total	O	0	0
			107	107		

4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	107.65Å 107.65Å 311.28Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	8.00 – 2.70	Depositor
% Data completeness (in resolution range)	99.1 (8.00-2.70)	Depositor
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.251 , 0.319	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	3963	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

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:
NAG

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	1.08	0/1845	3.57	298/2508 (11.9%)
2	B	1.18	2/1935 (0.1%)	3.54	351/2637 (13.3%)
All	All	1.14	2/3780 (0.1%)	3.55	649/5145 (12.6%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	29
2	B	0	50
All	All	0	79

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	94	THR	N-CA	-7.57	1.36	1.46
2	B	7	THR	N-CA	-6.18	1.39	1.46

The worst 5 of 649 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	172	ARG	CD-NE-CZ	36.24	175.13	124.40
2	B	196	GLY	CA-C-N	27.58	158.55	120.49
2	B	196	GLY	C-N-CA	27.58	158.55	120.49
2	B	231	ALA	O-C-N	-26.55	88.05	122.83
2	B	17	ASN	OD1-CG-ND2	24.88	147.47	122.60

There are no chirality outliers.

5 of 79 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	2	GLU	Mainchain
1	A	23	LEU	Mainchain
1	A	30	SER	Mainchain
1	A	44	GLY	Mainchain
1	A	50	GLY	Mainchain

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	1809	0	1777	118	0
2	B	1897	0	1821	137	1
3	A	14	0	13	4	0
3	B	28	0	26	0	0
4	A	108	0	0	9	2
4	B	107	0	0	9	3
All	All	3963	0	3637	252	5

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 34.

The worst 5 of 252 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)
2:B:29:ASN:ND2	2:B:30:GLN:H	1.52	1.05
2:B:121:ASP:H	2:B:126:GLN:NE2	1.56	1.01
1:A:108:ASN:HD21	3:A:303:NAG:C1	1.75	0.98
1:A:102:ARG:NH2	4:A:361:HOH:O	1.94	0.97
1:A:102:ARG:NE	4:A:361:HOH:O	1.82	0.97

All (5) 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:336:HOH:O	4:A:336:HOH:O[10_665]	0.98	1.22
4:B:409:HOH:O	4:B:409:HOH:O[12_554]	1.13	1.07
4:B:319:HOH:O	4:B:319:HOH:O[12_554]	1.27	0.93
4:A:358:HOH:O	4:A:358:HOH:O[10_665]	1.95	0.25
2:B:69:GLY:O	4:B:319:HOH:O[12_554]	2.11	0.09

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	239/241 (99%)	196 (82%)	29 (12%)	14 (6%)	1	2
2	B	253/255 (99%)	217 (86%)	24 (10%)	12 (5%)	2	3
All	All	492/496 (99%)	413 (84%)	53 (11%)	26 (5%)	1	3

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	89	SER
1	A	94	ARG
1	A	218	PRO
2	B	80	ALA
2	B	165	LYS

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	193/193 (100%)	135 (70%)	58 (30%)	0	1
2	B	203/203 (100%)	161 (79%)	42 (21%)	1	3
All	All	396/396 (100%)	296 (75%)	100 (25%)	0	2

5 of 100 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	238	LEU
2	B	96	ILE
2	B	240	ILE
2	B	4	SER
2	B	38	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	30	GLN
2	B	145	ASN
2	B	126	GLN
2	B	183	GLN
1	A	173	GLN

5.3.3 RNA [i](#)

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](#)

3 ligands are modelled in this entry.

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	NAG	B	302	2	14,14,15	1.29	2 (14%)	17,19,21	2.87	9 (52%)
3	NAG	A	303	-	14,14,15	1.13	1 (7%)	17,19,21	2.75	6 (35%)
3	NAG	B	301	2	14,14,15	1.49	2 (14%)	17,19,21	3.38	4 (23%)

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
3	NAG	B	302	2	-	2/6/23/26	0/1/1/1
3	NAG	A	303	-	-	5/6/23/26	0/1/1/1
3	NAG	B	301	2	-	2/6/23/26	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	301	NAG	O7-C7	-4.16	1.13	1.23
3	A	303	NAG	O7-C7	-3.30	1.15	1.23
3	B	302	NAG	O7-C7	-3.05	1.16	1.23
3	B	301	NAG	O5-C5	-2.19	1.39	1.43
3	B	302	NAG	C1-C2	-2.03	1.49	1.52

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	301	NAG	C1-O5-C5	12.73	129.25	112.19
3	A	303	NAG	C4-C3-C2	-7.73	99.69	111.02
3	B	302	NAG	C3-C4-C5	-5.37	100.50	110.23
3	B	302	NAG	O3-C3-C4	5.14	122.49	110.38
3	B	302	NAG	O4-C4-C3	4.92	121.96	110.38

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	303	NAG	C8-C7-N2-C2
3	A	303	NAG	O7-C7-N2-C2
3	A	303	NAG	O5-C5-C6-O6
3	B	301	NAG	O5-C5-C6-O6
3	B	302	NAG	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	303	NAG	4	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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.