

wwPDB X-ray Structure Validation Summary Report (i)

Aug 14, 2023 – 04:26 pm BST

PDB ID : 8AP3

Title : Structure of A. thaliana MIF/D-DT-like protein-2 (MDL2)

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Deposited on : 2022-08-09

Resolution : 1.40 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 (i) 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 (1)) were used in the production of this report:

 $\begin{array}{ccc} \text{MolProbity} & : & 4.02\text{b-}467 \\ \text{Xtriage (Phenix)} & : & 1.13 \end{array}$

EDS : 2.35

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Refmac : 5.8.0158

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

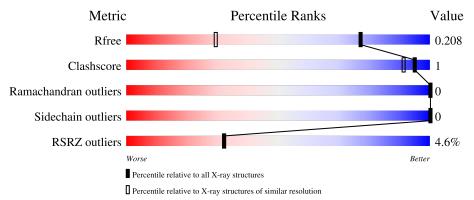
Validation Pipeline (wwPDB-VP) : 2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY\ DIFFRACTION$

The reported resolution of this entry is 1.40 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	1714 (1.40-1.40)
Clashscore	141614	1812 (1.40-1.40)
Ramachandran outliers	138981	1763 (1.40-1.40)
Sidechain outliers	138945	1762 (1.40-1.40)
RSRZ outliers	127900	1674 (1.40-1.40)

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 <=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	122	92%		7%
1	В	122	89%	6%	6%
1	С	122	99%		



2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 2823 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 MIF homologue.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	114	Total	С	N	О	S	0	0	0
1	A	114	837	537	132	165	3	0	0	0
1	D	115	Total	С	N	О	S	4	9	0
1	Ъ	110	856	550	134	169	3	4	2	U
1	С	122	Total	С	N	О	S	0	2	0
1		122	909	583	147	176	3	U	3	U

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	115	LEU	-	expression tag	UNP Q42335
A	116	GLU	-	expression tag	UNP Q42335
A	117	HIS	-	expression tag	UNP Q42335
A	118	HIS	-	expression tag	UNP Q42335
A	119	HIS	-	expression tag	UNP Q42335
A	120	HIS	_	expression tag	UNP Q42335
A	121	HIS	-	expression tag	UNP Q42335
A	122	HIS	_	expression tag	UNP Q42335
В	115	LEU	-	expression tag	UNP Q42335
В	116	GLU	-	expression tag	UNP Q42335
В	117	HIS	-	expression tag	UNP Q42335
В	118	HIS	-	expression tag	UNP Q42335
В	119	HIS	-	expression tag	UNP Q42335
В	120	HIS	_	expression tag	UNP Q42335
В	121	HIS	-	expression tag	UNP Q42335
В	122	HIS	_	expression tag	UNP Q42335
С	115	LEU	-	expression tag	UNP Q42335
С	116	GLU	-	expression tag	UNP Q42335
С	117	HIS	-	expression tag	UNP Q42335
С	118	HIS	-	expression tag	UNP Q42335
С	119	HIS	-	expression tag	UNP Q42335
С	120	HIS	-	expression tag	UNP Q42335
С	121	HIS	-	expression tag	UNP Q42335

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Chain	Residue	Modelled	Actual	Comment	Reference
С	122	HIS	-	expression tag	UNP Q42335

• Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	76	Total O 76 76	0	0
2	В	64	Total O 64 64	0	0
2	С	81	Total O 81 81	0	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: MIF homologue

Chain A:

92%

• Molecule 1: MIF homologue

9%

Chain B:

89%

6%

6%

Molecule 1: MIF homologue

Phain B:

99%

• Molecule 1: MIF homologue

• Molecule 1: MIF homologue



4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 21 21 21	Depositor	
Cell constants	46.22Å 79.24Å 84.60Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	37.32 - 1.40	Depositor	
resolution (A)	37.32 - 1.40	EDS	
% Data completeness	100.0 (37.32-1.40)	Depositor	
(in resolution range)	100.0 (37.32-1.40)	EDS	
R_{merge}	0.04	Depositor	
R_{sym}	(Not available)	Depositor	
$< I/\sigma(I) > 1$	2.82 (at 1.40Å)	Xtriage	
Refinement program	PHENIX (1.18_3845: ???)	Depositor	
R, R_{free}	0.184 , 0.208	Depositor	
it, it free	0.184 , 0.208	DCC	
R_{free} test set	3175 reflections $(5.13%)$	wwPDB-VP	
Wilson B-factor (Å ²)	19.2	Xtriage	
Anisotropy	0.389	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.37, 44.0	EDS	
L-test for twinning ²	$ < L > = 0.50, < L^2> = 0.33$	Xtriage	
Estimated twinning fraction	No twinning to report.	Xtriage	
F_o, F_c correlation	0.97	EDS	
Total number of atoms	2823	wwPDB-VP	
Average B, all atoms $(Å^2)$	21.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.57% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

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	Mol Chain		lengths	Bond	angles
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	A	0.51	0/852	0.71	0/1155
1	В	0.51	0/874	0.71	0/1184
1	С	0.48	0/937	0.68	0/1271
All	All	0.50	0/2663	0.70	0/3610

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	837	0	842	1	0
1	В	856	0	866	4	0
1	С	909	0	899	1	0
2	A	76	0	0	0	0
2	В	64	0	0	0	0
2	С	81	0	0	0	0
All	All	2823	0	2607	6	0

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 1.

The worst 5 of 6 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:B:105:SER:HB3	1:B:115:LEU:HD22	1.80	0.63
1:B:8:ASN:HB3	1:B:48:MET:HG2	1.85	0.58
1:B:65:ILE:HG12	1:B:102:THR:HG23	1.93	0.48
1:B:65:ILE:HD13	1:B:104:GLY:HA2	1.95	0.48
1:A:98:LYS:HG3	1:A:100:TYR:CE1	2.48	0.48

There are no symmetry-related clashes.

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	Perce	entiles
1	A	112/122 (92%)	111 (99%)	1 (1%)	0	100	100
1	В	115/122 (94%)	114 (99%)	1 (1%)	0	100	100
1	С	123/122 (101%)	118 (96%)	5 (4%)	0	100	100
All	All	350/366 (96%)	343 (98%)	7 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	92/102 (90%)	92 (100%)	0	100 100
1	В	95/102 (93%)	95 (100%)	0	100 100
1	С	99/102 (97%)	99 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric			
All	All	286/306 (94%)	286 (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. There are no such sidechains identified.

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 monosaccharides 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 (i)

6.1 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, 95^{th} 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 $>$	$\# \mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q < 0.9
1	A	114/122~(93%)	0.08	1 (0%) 84 82	13, 18, 26, 29	0
1	В	114/122 (93%)	0.54	11 (9%) 8 7	15, 22, 31, 36	0
1	С	122/122 (100%)	0.33	4 (3%) 46 46	13, 17, 25, 35	0
All	All	350/366 (95%)	0.32	16 (4%) 32 32	13, 19, 29, 36	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	114	LEU	4.6
1	В	115	LEU	4.6
1	С	118	HIS	4.4
1	С	117	HIS	4.4
1	С	122	HIS	4.2

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 monosaccharides 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.

