



wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 7, 2023 – 09:33 pm GMT

PDB ID : 1HFO
Title : The Structure of the Macrophage Migration Inhibitory Factor from *Trichinella Spiralis*.
Authors : Roe, S.M.; Meyer, D.J.
Deposited on : 2000-12-07
Resolution : 1.65 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 : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

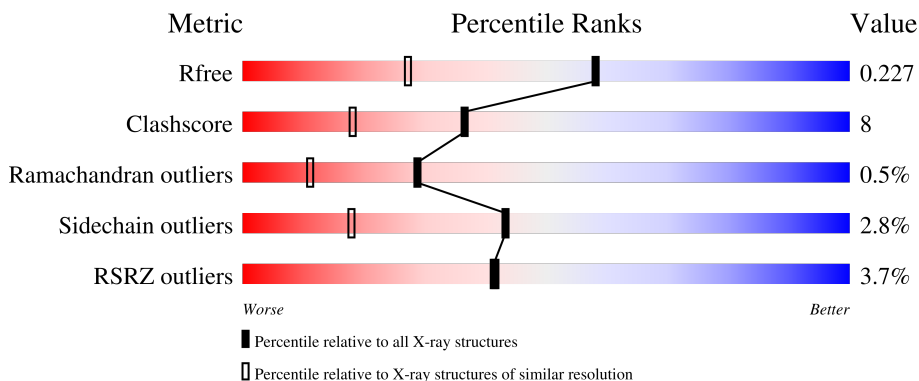
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.65 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}	130704	1827 (1.66-1.66)
Clashscore	141614	1931 (1.66-1.66)
Ramachandran outliers	138981	1891 (1.66-1.66)
Sidechain outliers	138945	1891 (1.66-1.66)
RSRZ outliers	127900	1791 (1.66-1.66)

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	113	 2% (poor fit), 85% (0-1 outliers), 15% (2-3 outliers)
1	B	113	 6% (poor fit), 75% (0-1 outliers), 23% (2-3 outliers), . (not modelled)
1	C	113	 84% (0-1 outliers), 15% (2-3 outliers), . (not modelled)
1	D	113	 5% (poor fit), 81% (0-1 outliers), 17% (2-3 outliers), . (not modelled)
1	E	113	 % (poor fit), 81% (0-1 outliers), 19% (2-3 outliers)

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Mol	Chain	Length	Quality of chain
1	F	113	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into three segments: a red segment on the left labeled '8%', a large green segment in the middle labeled '87%', and a yellow segment on the right labeled '12%'. A small black dot is located at the far right end of the bar.</p>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6166 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 MIGRATION INHIBITORY FACTOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	113	859	542	149	166	2	0	0	0
1	B	113	850	535	149	164	2	0	0	0
1	C	113	855	539	148	166	2	0	0	0
1	D	113	856	540	148	166	2	0	0	0
1	E	113	859	542	149	166	2	0	0	0
1	F	113	855	539	148	166	2	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	5	LEU	UNK	conflict	UNP Q9Y063
A	85	THR	LYS	conflict	UNP Q9Y063
B	5	LEU	UNK	conflict	UNP Q9Y063
B	85	THR	LYS	conflict	UNP Q9Y063
C	5	LEU	UNK	conflict	UNP Q9Y063
C	85	THR	LYS	conflict	UNP Q9Y063
D	5	LEU	UNK	conflict	UNP Q9Y063
D	85	THR	LYS	conflict	UNP Q9Y063
E	5	LEU	UNK	conflict	UNP Q9Y063
E	85	THR	LYS	conflict	UNP Q9Y063
F	5	LEU	UNK	conflict	UNP Q9Y063
F	85	THR	LYS	conflict	UNP Q9Y063

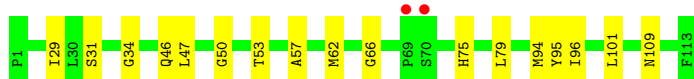
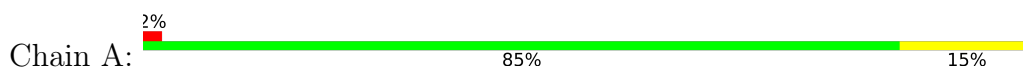
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	178	Total 178	O 178	0	0
2	B	162	Total 162	O 162	0	0
2	C	171	Total 171	O 171	0	0
2	D	156	Total 156	O 156	0	0
2	E	218	Total 218	O 218	0	0
2	F	147	Total 147	O 147	0	0

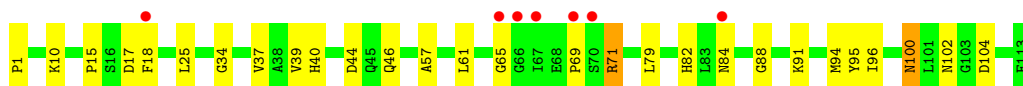
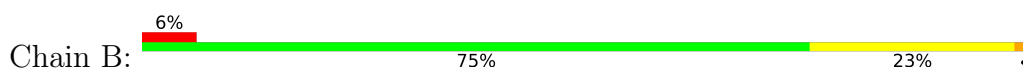
3 Residue-property plots [i](#)

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.

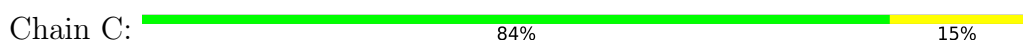
- Molecule 1: MIGRATION INHIBITORY FACTOR



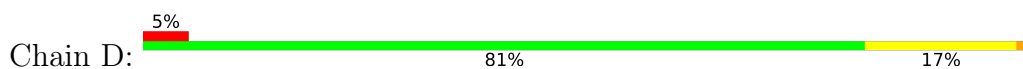
- Molecule 1: MIGRATION INHIBITORY FACTOR



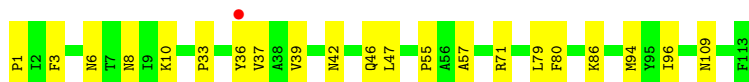
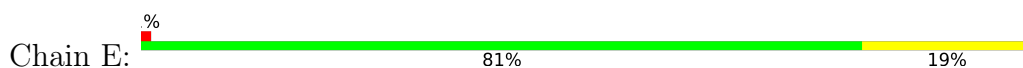
- Molecule 1: MIGRATION INHIBITORY FACTOR




- Molecule 1: MIGRATION INHIBITORY FACTOR

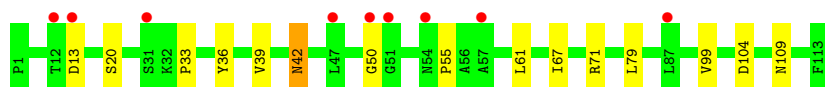


- Molecule 1: MIGRATION INHIBITORY FACTOR



- Molecule 1: MIGRATION INHIBITORY FACTOR

Chain F:  8% 87% 12%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	110.13Å 88.34Å 86.36Å 90.00° 131.13° 90.00°	Depositor
Resolution (Å)	28.33 – 1.65 28.33 – 1.60	Depositor EDS
% Data completeness (in resolution range)	97.4 (28.33-1.65) 97.2 (28.33-1.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.10 (at 1.60Å)	Xtrriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.225 , 0.281 0.226 , 0.227	Depositor DCC
R_{free} test set	4021 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	24.9	Xtrriage
Anisotropy	0.067	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 49.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.013 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6166	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.63% 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](#)

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	0.44	0/879	0.66	0/1193
1	B	0.36	0/870	0.58	0/1180
1	C	0.41	0/875	0.67	0/1189
1	D	0.40	0/876	0.63	0/1190
1	E	0.41	0/879	0.69	0/1193
1	F	0.39	0/875	0.66	0/1189
All	All	0.40	0/5254	0.65	0/7134

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	859	0	841	15	0
1	B	850	0	826	21	0
1	C	855	0	830	12	0
1	D	856	0	832	16	0
1	E	859	0	841	15	0
1	F	855	0	830	12	0
2	A	178	0	0	4	0
2	B	162	0	0	0	0
2	C	171	0	0	4	0
2	D	156	0	0	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	218	0	0	4	0
2	F	147	0	0	6	0
All	All	6166	0	5000	80	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 8.

The worst 5 of 80 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:D:101:LEU:HD22	2:F:2118:HOH:O	1.77	0.83
1:E:79:LEU:HD23	1:E:96:ILE:HD13	1.60	0.81
1:B:65:GLY:H	1:B:100:ASN:HD21	1.31	0.78
1:D:46:GLN:HG3	2:D:2039:HOH:O	1.86	0.76
1:B:91:LYS:HB3	1:C:109:ASN:O	1.85	0.75

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	Percentiles	
1	A	111/113 (98%)	107 (96%)	4 (4%)	0	100	100
1	B	111/113 (98%)	107 (96%)	3 (3%)	1 (1%)	17	4
1	C	111/113 (98%)	105 (95%)	4 (4%)	2 (2%)	8	0
1	D	111/113 (98%)	108 (97%)	3 (3%)	0	100	100
1	E	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	F	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
All	All	666/678 (98%)	645 (97%)	18 (3%)	3 (0%)	29	11

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	69	PRO
1	C	109	ASN
1	C	110	GLY

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	96/96 (100%)	95 (99%)	1 (1%)	76	62
1	B	94/96 (98%)	92 (98%)	2 (2%)	53	29
1	C	95/96 (99%)	91 (96%)	4 (4%)	30	8
1	D	95/96 (99%)	91 (96%)	4 (4%)	30	8
1	E	96/96 (100%)	94 (98%)	2 (2%)	53	29
1	F	95/96 (99%)	92 (97%)	3 (3%)	39	13
All	All	571/576 (99%)	555 (97%)	16 (3%)	43	18

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	104	ASP
1	F	42	ASN
1	D	42	ASN
1	E	109	ASN
1	D	4	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	109	ASN
1	F	6	ASN
1	F	109	ASN
1	F	28	ASN

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Mol	Chain	Res	Type
1	E	109	ASN

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, 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	113/113 (100%)	0.13	2 (1%) 68 71	13, 23, 37, 44	0
1	B	113/113 (100%)	0.64	7 (6%) 20 19	22, 35, 51, 62	0
1	C	113/113 (100%)	-0.00	0 100 100	14, 23, 42, 48	0
1	D	113/113 (100%)	0.65	6 (5%) 26 25	20, 33, 43, 46	0
1	E	113/113 (100%)	0.07	1 (0%) 84 86	15, 24, 36, 39	0
1	F	113/113 (100%)	0.49	9 (7%) 12 12	15, 27, 38, 52	0
All	All	678/678 (100%)	0.33	25 (3%) 41 41	13, 28, 43, 62	0

The worst 5 of 25 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	66	GLY	6.1
1	B	67	ILE	6.1
1	F	51	GLY	4.8
1	F	50	GLY	3.5
1	D	36	TYR	3.3

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.