



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 07:50 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

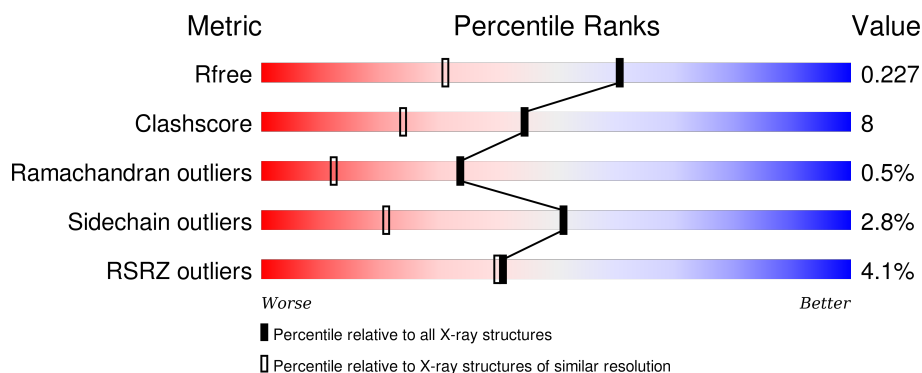
# 1 Overall quality at a glance ⓘ

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))
$R_{free}$	91344	1226 (1.66-1.66)
Clashscore	102246	1323 (1.66-1.66)
Ramachandran outliers	100387	1295 (1.66-1.66)
Sidechain outliers	100360	1295 (1.66-1.66)
RSRZ outliers	91569	1227 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	<div> <div>2%</div> <div>85%</div> <div>15%</div> </div>
1	B	113	<div> <div>6%</div> <div>75%</div> <div>23%</div> <div>•</div> </div>
1	C	113	<div> <div>%</div> <div>84%</div> <div>15%</div> <div>•</div> </div>
1	D	113	<div> <div>7%</div> <div>81%</div> <div>17%</div> <div>•</div> </div>
1	E	113	<div> <div>%</div> <div>81%</div> <div>19%</div> </div>

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

## 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
1	A	113	Total	C	N	O	S	0	0	0
			859	542	149	166	2			
1	B	113	Total	C	N	O	S	0	0	0
			850	535	149	164	2			
1	C	113	Total	C	N	O	S	0	0	0
			855	539	148	166	2			
1	D	113	Total	C	N	O	S	0	0	0
			856	540	148	166	2			
1	E	113	Total	C	N	O	S	0	0	0
			859	542	149	166	2			
1	F	113	Total	C	N	O	S	0	0	0
			855	539	148	166	2			

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

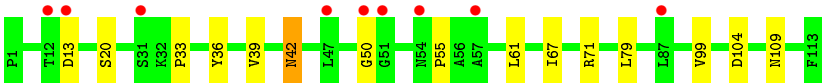
- Molecule 2 is water.

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



- Molecule 1: MIGRATION INHIBITORY FACTOR





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	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
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.10 (at 1.60Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.225 , 0.281 0.226 , 0.227	Depositor DCC
$R_{free}$ test set	3675 reflections (5.04%)	DCC
Wilson B-factor (Å <sup>2</sup> )	24.9	Xtriage
Anisotropy	0.067	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 49.8	EDS
Estimated twinning fraction	0.013 for h,-k,-h-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 79811 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	6166	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtriage'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.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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 ⓘ

### 5.3.1 Protein backbone ⓘ

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%)	21	4
1	C	111/113 (98%)	105 (95%)	4 (4%)	2 (2%)	11	1
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%)	34	12

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 ⓘ

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%)	82	68
1	B	94/96 (98%)	92 (98%)	2 (2%)	61	34
1	C	95/96 (99%)	91 (96%)	4 (4%)	36	10
1	D	95/96 (99%)	91 (96%)	4 (4%)	36	10
1	E	96/96 (100%)	94 (98%)	2 (2%)	61	34
1	F	95/96 (99%)	92 (97%)	3 (3%)	46	16
All	All	571/576 (99%)	555 (97%)	16 (3%)	51	21

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

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

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

Mol	Chain	Res	Type
1	C	109	ASN
1	D	28	ASN
1	F	6	ASN
1	C	42	ASN

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Mol	Chain	Res	Type
1	F	28	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 carbohydrates 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	113/113 (100%)	0.16	2 (1%) 71 75	13, 23, 37, 44	0
1	B	113/113 (100%)	0.68	7 (6%) 24 21	22, 35, 51, 62	0
1	C	113/113 (100%)	0.03	1 (0%) 85 87	14, 23, 42, 48	0
1	D	113/113 (100%)	0.71	8 (7%) 19 16	20, 33, 43, 46	0
1	E	113/113 (100%)	0.10	1 (0%) 85 87	15, 24, 36, 39	0
1	F	113/113 (100%)	0.52	9 (7%) 15 13	15, 27, 38, 52	0
All	All	678/678 (100%)	0.37	28 (4%) 41 40	13, 28, 43, 62	0

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	67	ILE	6.4
1	B	66	GLY	6.1
1	F	51	GLY	4.9
1	F	50	GLY	3.6
1	D	36	TYR	3.4

### 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 carbohydrates 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.