

# wwPDB X-ray Structure Validation Summary Report (i)

Jan 4, 2024 – 04:55 pm GMT

PDB ID : 5FMU

Title : MmIFT54 CH-domain Authors : Weber, K.; Lorentzen, E.

Deposited on : 2015-11-09

Resolution : 1.59 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:

MolProbity : 4.02b-467

Mogul : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.36

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

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

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

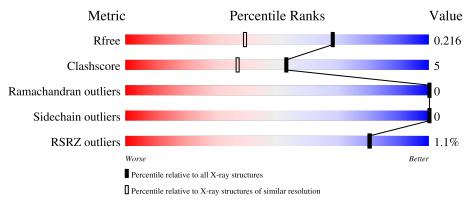
Validation Pipeline (wwPDB-VP) : 2.36

# 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.59 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\mathring{\rm A})}) \end{array}$
$R_{free}$	130704	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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	137	82%	13%	·
1	В	137	89%	7%	<del>-</del>
1	С	137	87%	9%	-
1	D	137	85%	12%	•



# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4524 atoms, of which 13 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 TRAF3-INTERACTING PROTEIN 1.

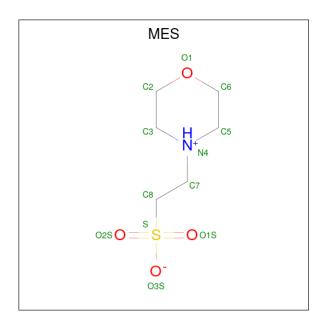
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	131	Total	С	N	О	S	0	4	0
1	A	191	1024	655	183	179	7	U	4	
1	В	132	Total	С	N	О	S	0	1	0
1	Б	132	1010	644	173	186	7			U
1	С	132	Total	С	N	О	S	0	1	0
1		132	995	635	173	180	7	U	1	U
1	D	199	Total	С	N	О	S	0	<u> </u>	0
	133	1037	661	185	184	7	0	5	U	

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP Q149C2
A	-2	ALA	-	expression tag	UNP Q149C2
A	-1	ALA	-	expression tag	UNP Q149C2
A	0	SER	-	expression tag	UNP Q149C2
В	-3	GLY	-	expression tag	UNP Q149C2
В	-2	ALA	-	expression tag	UNP Q149C2
В	-1	ALA	-	expression tag	UNP Q149C2
В	0	SER	-	expression tag	UNP Q149C2
С	-3	GLY	-	expression tag	UNP Q149C2
С	-2	ALA	-	expression tag	UNP Q149C2
С	-1	ALA	-	expression tag	UNP Q149C2
С	0	SER	-	expression tag	UNP Q149C2
D	-3	GLY	-	expression tag	UNP Q149C2
D	-2	ALA	-	expression tag	UNP Q149C2
D	-1	ALA	-	expression tag	UNP Q149C2
D	0	SER	-	expression tag	UNP Q149C2

• Molecule 2 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula:  $C_6H_{13}NO_4S$ ).





Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
2	С	1	Total 25	C 6	H 13	N 1	O 4	S 1	0	0

#### • Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	121	Total O 121 121	0	0
3	В	147	Total O 147 147	0	0
3	С	78	Total O 78 78	0	0
3	D	87	Total O 87 87	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: TRAF3-INTERACTING PROTEIN 1

Chain A:

82%

13%

• Molecule 1: TRAF3-INTERACTING PROTEIN 1

Chain B:

89%

7%

• Molecule 1: TRAF3-INTERACTING PROTEIN 1

Chain C:

87%

9%

• Molecule 1: TRAF3-INTERACTING PROTEIN 1

Chain C:

87%

9%

• Molecule 1: TRAF3-INTERACTING PROTEIN 1

Chain C:

87%

9%

• Molecule 1: TRAF3-INTERACTING PROTEIN 1

Chain D:

85%

12%

• Molecule 1: TRAF3-INTERACTING PROTEIN 1



# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants	37.93Å 59.39Å 61.18Å	Donogitor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$109.17^{\circ}  105.15^{\circ}  89.65^{\circ}$	Depositor
Resolution (Å)	36.47 - 1.59	Depositor
Resolution (A)	36.47 - 1.59	EDS
% Data completeness	94.1 (36.47-1.59)	Depositor
(in resolution range)	87.9 (36.47-1.59)	EDS
$R_{merge}$	0.15	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	0.77 (at 1.59Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.8.4_1496)	Depositor
D D.	0.183 , 0.214	Depositor
$R, R_{free}$	0.185 , $0.216$	DCC
$R_{free}$ test set	1227 reflections (2.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	17.7	Xtriage
Anisotropy	0.317	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.33, 46.4	EDS
L-test for twinning <sup>2</sup>	$< L > = 0.49, < L^2> = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4524	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 8.15% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical 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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: MES

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		
IVIOI		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.34	0/1048	0.49	0/1408	
1	В	0.38	0/1026	0.50	0/1382	
1	С	0.34	0/1011	0.49	0/1366	
1	D	0.31	0/1065	0.46	0/1435	
All	All	0.34	0/4150	0.48	0/5591	

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	1024	0	1104	14	0
1	В	1010	0	1060	7	0
1	С	995	0	1029	10	0
1	D	1037	0	1100	15	0
2	С	12	13	12	0	0
3	A	121	0	0	3	0
3	В	147	0	0	4	0
3	С	78	0	0	3	0
3	D	87	0	0	3	0
All	All	4511	13	4305	45	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 5.

The worst 5 of 45 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:1:MET:HG2	1:B:101:PRO:HG2	1.71	0.72
1:C:1:MET:HG2	1:C:101:PRO:HG2	1.74	0.69
1:A:66[B]:LYS:NZ	3:A:2082:HOH:O	2.31	0.64
1:B:65:ASP:OD1	3:B:2096:HOH:O	2.14	0.64
1:C:106:GLU:OE1	3:C:2058:HOH:O	2.15	0.62

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	ntiles
1	A	133/137 (97%)	131 (98%)	2 (2%)	0	100	100
1	В	131/137 (96%)	129 (98%)	2 (2%)	0	100	100
1	С	131/137 (96%)	129 (98%)	2 (2%)	0	100	100
1	D	136/137 (99%)	135 (99%)	1 (1%)	0	100	100
All	All	531/548 (97%)	524 (99%)	7 (1%)	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 Outlier		Percentile	
1	A	110/115~(96%)	110 (100%)	0	100	100
1	В	108/115~(94%)	108 (100%)	0	100	100
1	С	103/115 (90%)	103 (100%)	0	100	100
1	D	111/115 (96%)	111 (100%)	0	100	100
All	All	432/460 (94%)	432 (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)

1 ligand is 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	Dog I	Res Link	Bond lengths			Bond angles		
IVIOI				LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2	
2	MES	С	1133	-	12,12,12	1.88	1 (8%)	14,16,16	1.96	5 (35%)	

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
2	MES	С	1133	-	-	2/6/14/14	0/1/1/1

#### All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\text{\AA})$	Ideal(A)
2	С	1133	MES	C8-S	-6.09	1.68	1.77

#### All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
2	С	1133	MES	C5-N4-C3	4.40	118.73	108.83
2	С	1133	MES	O2S-S-C8	2.43	109.84	106.92
2	С	1133	MES	C7-N4-C5	2.37	117.31	111.23
2	С	1133	MES	O1-C6-C5	2.32	116.91	111.80
2	С	1133	MES	C2-C3-N4	2.18	113.41	110.10

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	С	1133	MES	C8-C7-N4-C5
2	С	1133	MES	C7-C8-S-O1S

There are no ring outliers.

No monomer is involved in short contacts.

#### 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></rsrz>	# RSRZ > 2	$OWAB(Å^2)$	Q < 0.9
1	A	131/137 (95%)	-0.21	1 (0%) 86 86	14, 23, 33, 36	0
1	В	132/137 (96%)	-0.29	1 (0%) 86 86	13, 19, 31, 49	0
1	С	132/137 (96%)	-0.04	2 (1%) 73 73	14, 23, 43, 49	0
1	D	133/137 (97%)	0.01	2 (1%) 73 73	15, 25, 42, 46	0
All	All	528/548 (96%)	-0.13	6 (1%) 80 80	13, 22, 38, 49	0

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	С	2	ASN	3.0
1	В	131	GLY	2.6
1	A	131	GLY	2.5
1	D	3	ALA	2.4
1	С	1	MET	2.1

#### 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)

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,  $95^{th}$  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.



$\mathbf{M}$	ol Type	Chain	Res	Atoms	RSCC	RSR	$ m B ext{-}factors(\AA^2)$	Q<0.9
2	MES	С	1133	12/12	0.96	0.10	20,27,34,38	0

# 6.5 Other polymers (i)

There are no such residues in this entry.

