



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 01:04 am GMT

PDB ID : 3RWH  
Title : Rhesus macaque MHC class I molecule Mamu-B\*17-MF8  
Authors : Wu, Y.; Gao, F.; Liu, J.; Qi, J.X.; Price, D.A.; Gao, G.F.  
Deposited on : 2011-05-09  
Resolution : 2.60 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.

---

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

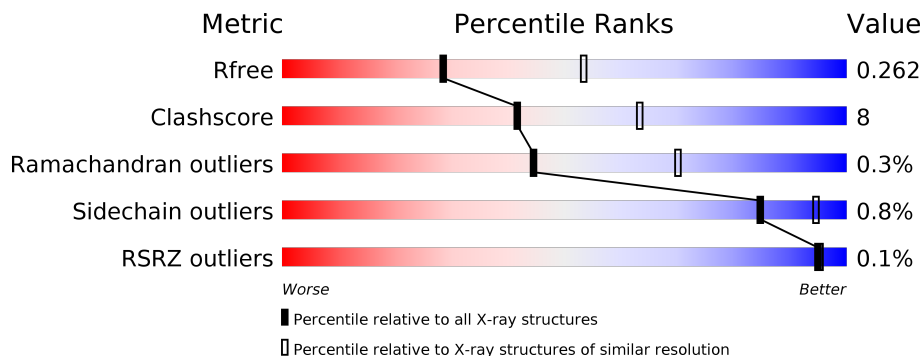
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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))
$R_{free}$	100719	2542 (2.60-2.60)
Clashscore	112137	2895 (2.60-2.60)
Ramachandran outliers	110173	2848 (2.60-2.60)
Sidechain outliers	110143	2848 (2.60-2.60)
RSRZ outliers	101464	2550 (2.60-2.60)

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 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	276	<div> <div style="width: 82%;"></div> <div style="width: 17%;"></div> </div> <div>82% 17%</div>
1	D	276	<div> <div style="width: 80%;"></div> <div style="width: 19%;"></div> </div> <div>80% 19%</div>
2	B	99	<div> <div style="width: 75%;"></div> <div style="width: 23%;"></div> <div style="width: 2%;"></div> </div> <div>75% 23% ..</div>
2	E	99	<div> <div style="width: 79%;"></div> <div style="width: 19%;"></div> <div style="width: 2%;"></div> </div> <div>79% 19% ..</div>
3	C	8	<div> <div style="width: 63%;"></div> <div style="width: 38%;"></div> </div> <div>63% 38%</div>
3	F	8	<div> <div style="width: 38%;"></div> <div style="width: 63%;"></div> </div> <div>38% 63%</div>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6850 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 Major histocompatibility complex class I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	276	Total	C	N	O	S	0	1	0
			2267	1410	412	438	7			
1	D	276	Total	C	N	O	S	0	1	0
			2267	1410	413	437	7			

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	98	Total	C	N	O	S	0	1	0
			822	522	142	154	4			
2	E	98	Total	C	N	O	S	0	0	0
			814	517	139	154	4			

- Molecule 3 is a protein called Pol MF8 peptide from Pol protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	8	Total	C	N	O	S	0	0	0
			72	47	13	11	1			
3	F	8	Total	C	N	O	S	0	0	0
			72	47	13	11	1			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	184	Total	O	0	0
			184	184		
4	B	80	Total	O	0	0
			80	80		
4	C	5	Total	O	0	0
			5	5		
4	D	172	Total	O	0	0
			172	172		

*Continued on next page...*

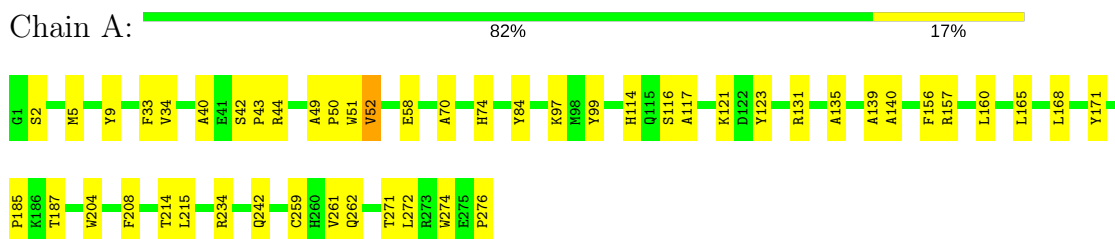
*Continued from previous page...*

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	93	Total 93	O 93	0	0
4	F	2	Total 2	O 2	0	0

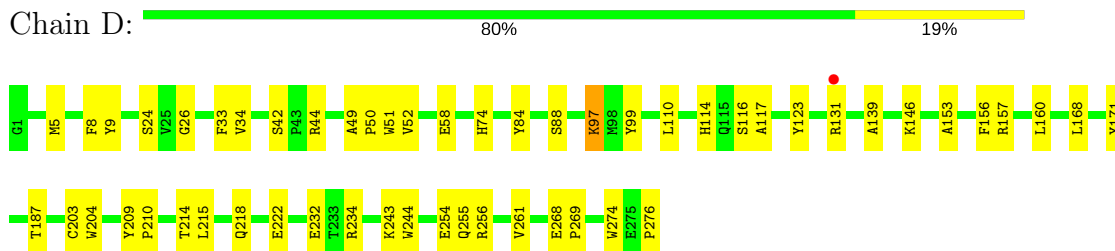
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

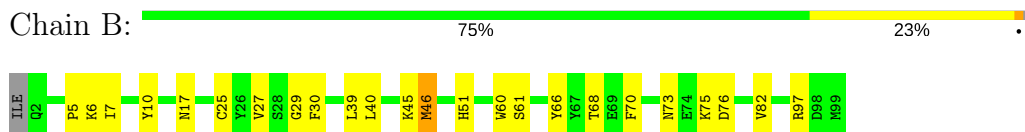
- Molecule 1: Major histocompatibility complex class I



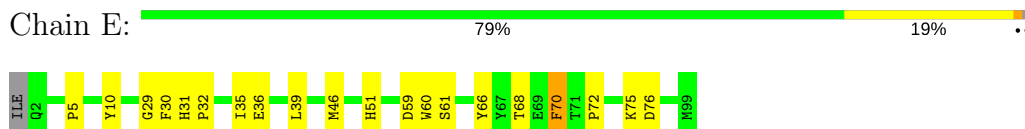
- Molecule 1: Major histocompatibility complex class I



- Molecule 2: Beta-2-microglobulin



- Molecule 2: Beta-2-microglobulin



- Molecule 3: Pol MF8 peptide from Pol protein





- Molecule 3: Pol MF8 peptide from Pol protein

Chain F: 38% 63%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	45.33Å 68.64Å 81.42Å 83.97° 88.86° 90.07°	Depositor
Resolution (Å)	26.98 – 2.60 45.32 – 2.49	Depositor EDS
% Data completeness (in resolution range)	97.1 (26.98-2.60) 88.9 (45.32-2.49)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.00 (at 2.48Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, $R_{free}$	0.227 , 0.272 0.217 , 0.262	Depositor DCC
$R_{free}$ test set	1477 reflections (5.07%)	DCC
Wilson B-factor (Å <sup>2</sup> )	24.7	Xtriage
Anisotropy	0.395	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 15.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.267 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	6850	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.45% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

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	0.20	0/2336	0.37	0/3169
1	D	0.21	0/2336	0.37	0/3169
2	B	0.21	0/850	0.36	0/1149
2	E	0.20	0/839	0.35	0/1135
3	C	0.21	0/74	0.42	0/97
3	F	0.21	0/74	0.40	0/97
All	All	0.21	0/6509	0.37	0/8816

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

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	2267	0	2097	33	0
1	D	2267	0	2099	41	0
2	B	822	0	782	14	0
2	E	814	0	769	13	0
3	C	72	0	73	2	0
3	F	72	0	73	4	0
4	A	184	0	0	2	0
4	B	80	0	0	0	0
4	C	5	0	0	0	0
4	D	172	0	0	2	0

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	E	93	0	0	1	0
4	F	2	0	0	0	0
All	All	6850	0	5893	98	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 98 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:A:5:MET:HB2	1:A:168:LEU:HD13	1.68	0.76
1:D:5:MET:HB2	1:D:168:LEU:HD13	1.71	0.72
1:D:215:LEU:HG	1:D:261:VAL:HG22	1.71	0.71
1:D:187:THR:HA	1:D:204:TRP:O	1.93	0.69
1:A:131:ARG:HG2	1:A:157:ARG:HH12	1.60	0.66

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	275/276 (100%)	265 (96%)	10 (4%)	0	100	100
1	D	275/276 (100%)	262 (95%)	11 (4%)	2 (1%)	25	49
2	B	97/99 (98%)	96 (99%)	1 (1%)	0	100	100
2	E	96/99 (97%)	95 (99%)	1 (1%)	0	100	100
3	C	6/8 (75%)	5 (83%)	1 (17%)	0	100	100
3	F	6/8 (75%)	5 (83%)	1 (17%)	0	100	100
All	All	755/766 (99%)	728 (96%)	25 (3%)	2 (0%)	44	70

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	255	GLN
1	D	243	LYS

### 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	233/232 (100%)	232 (100%)	1 (0%)	93	98
1	D	233/232 (100%)	232 (100%)	1 (0%)	93	98
2	B	93/93 (100%)	91 (98%)	2 (2%)	57	81
2	E	92/93 (99%)	91 (99%)	1 (1%)	78	92
3	C	8/8 (100%)	8 (100%)	0	100	100
3	F	8/8 (100%)	8 (100%)	0	100	100
All	All	667/666 (100%)	662 (99%)	5 (1%)	85	96

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	VAL
2	B	46	MET
2	B	70	PHE
1	D	97	LYS
2	E	70	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	17	ASN
2	E	17	ASN
1	D	180	GLN
1	A	197	HIS
1	D	218	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 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	276/276 (100%)	-0.33	0 100 100	8, 22, 42, 57	0
1	D	276/276 (100%)	-0.22	1 (0%) 92 91	11, 23, 50, 72	0
2	B	98/99 (98%)	-0.40	0 100 100	12, 20, 37, 58	0
2	E	98/99 (98%)	-0.33	0 100 100	13, 23, 40, 54	0
3	C	8/8 (100%)	-0.41	0 100 100	13, 17, 19, 20	0
3	F	8/8 (100%)	-0.10	0 100 100	14, 20, 22, 24	0
All	All	764/766 (99%)	-0.30	1 (0%) 95 95	8, 22, 46, 72	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	131	ARG	2.3

### 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 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.