



# Full wwPDB X-ray Structure Validation Report i

May 27, 2024 – 02:31 PM JST

PDB ID : 8JRJ  
Title : Crystal structure of the bat MHC II molecule at 2.8 Å resolution  
Authors : Wang, S.  
Deposited on : 2023-06-17  
Resolution : 2.50 Å (reported)

This is a Full wwPDB X-ray Structure Validation 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  
<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
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
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)	:	2.36.2

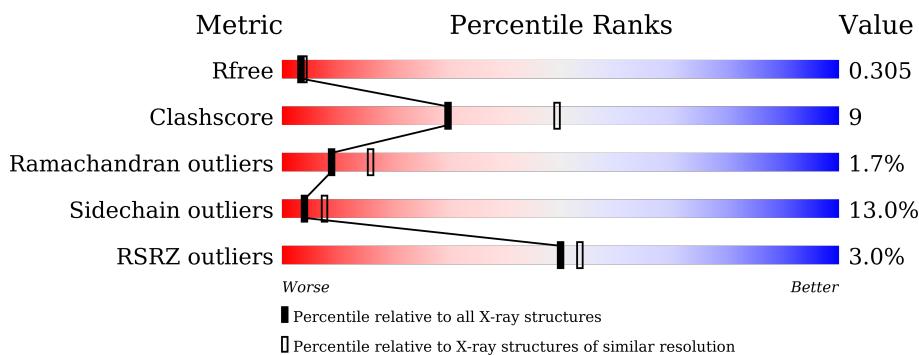
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

## X-RAY DIFFRACTION

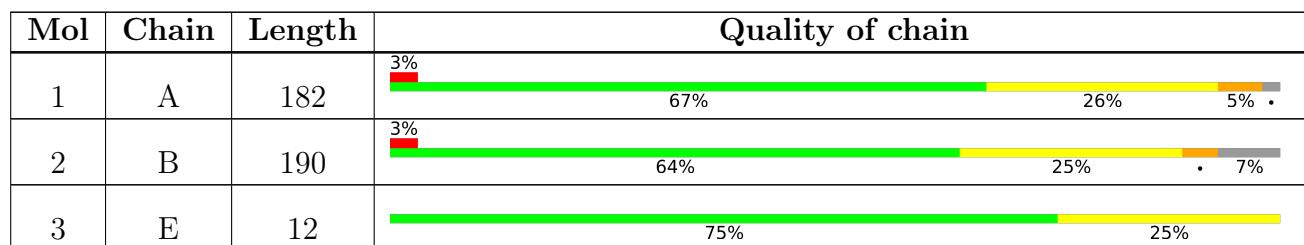
The reported resolution of this entry is 2.50 Å.

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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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  $\geq 3$ , 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.



## 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3017 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 HLA class II histocompatibility antigen, DR alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	178	1465	955	229	273	8	0	0	0

- Molecule 2 is a protein called MHC class II histocompatibility antigen, DR-1 beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	177	1440	910	256	268	6	0	0	0

- Molecule 3 is a protein called ALA-SER-PHE-ILE-ILE-ARG-SER-MET-PRO-GLN-GLU-T HR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	E	12	95	60	16	18	1	0	0	0

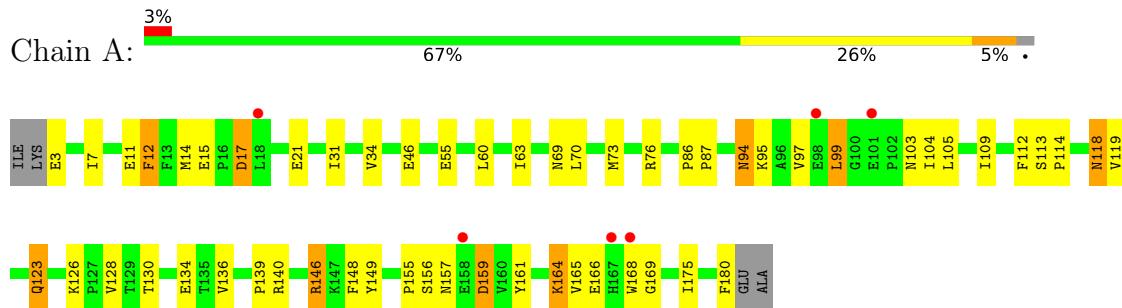
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	9	9	9	0	0
4	B	8	8	8	0	0

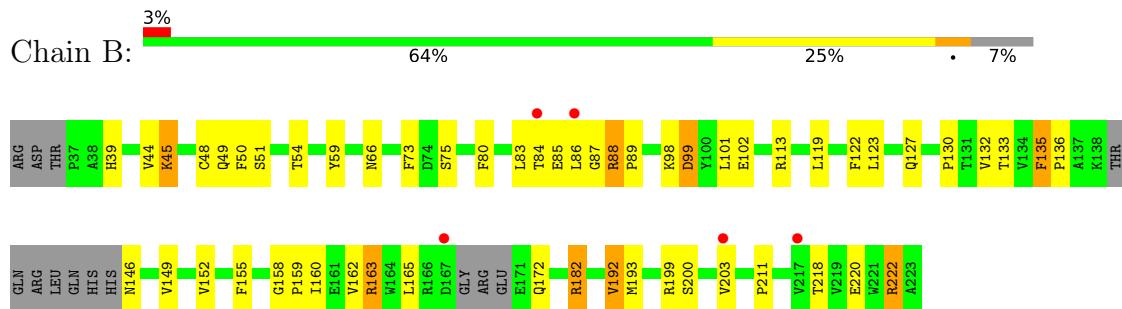
### 3 Residue-property plots [\(i\)](#)

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.

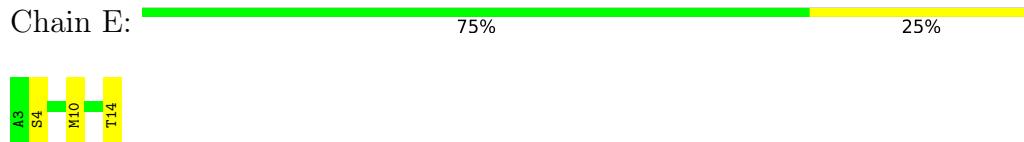
- Molecule 1: HLA class II histocompatibility antigen, DR alpha chain



- Molecule 2: MHC class II histocompatibility antigen, DR-1 beta chain



- Molecule 3: ALA-SER-PHE-ILE-ILE-ARG-SER-MET-PRO-GLN-GLU-THR



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	92.56Å 92.56Å 108.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	70.49 – 2.50 70.49 – 2.50	Depositor EDS
% Data completeness (in resolution range)	93.3 (70.49-2.50) 93.3 (70.49-2.50)	Depositor EDS
$R_{merge}$	0.18	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) >$ <sup>1</sup>	1.20 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
$R$ , $R_{free}$	0.246 , 0.291 0.258 , 0.305	Depositor DCC
$R_{free}$ test set	775 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	55.8	Xtriage
Anisotropy	0.158	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 37.5	EDS
L-test for twinning <sup>2</sup>	$<  L  > = 0.49$ , $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	3017	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.40% 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  $< |L| >$ ,  $< L^2 >$  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	0.70	0/1511	0.89	0/2054
2	B	0.72	0/1478	0.92	1/2007 (0.0%)
3	E	0.72	0/96	0.79	0/128
All	All	0.71	0/3085	0.90	1/4189 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
2	B	182	ARG	NE-CZ-NH2	5.76	123.18	120.30

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	1465	0	1394	34	0
2	B	1440	0	1362	30	0
3	E	95	0	95	2	0
4	A	9	0	0	0	0
4	B	8	0	0	0	0
All	All	3017	0	2851	55	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 9.

All (55) 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)
2:B:149:VAL:HG22	2:B:193:MET:HG2	1.61	0.82
1:A:17:ASP:OD1	1:A:17:ASP:N	2.16	0.79
2:B:162:VAL:HG11	2:B:192:VAL:HG21	1.72	0.71
1:A:164:LYS:HB2	1:A:175:ILE:HG12	1.77	0.67
2:B:73:PHE:HB2	2:B:80:PHE:CE1	2.32	0.65
1:A:15:GLU:HB2	1:A:70:LEU:HD21	1.83	0.61
2:B:203:VAL:HG22	2:B:222:ARG:NH2	2.17	0.59
1:A:99:LEU:HA	1:A:155:PRO:HB2	1.83	0.59
1:A:94:ASN:C	1:A:94:ASN:HD22	2.10	0.55
2:B:130:PRO:HB3	2:B:155:PHE:HB3	1.88	0.53
2:B:99:ASP:N	2:B:99:ASP:OD1	2.40	0.53
1:A:140:ARG:HG3	1:A:146:ARG:HD3	1.90	0.53
2:B:59:TYR:HB3	2:B:75:SER:HB3	1.92	0.51
1:A:109:ILE:O	1:A:146:ARG:HA	2.10	0.51
1:A:139:PRO:HB2	2:B:45:LYS:NZ	2.26	0.51
1:A:69:ASN:O	1:A:73:MET:HG2	2.10	0.50
1:A:156:SER:OG	1:A:159:ASP:HB2	2.12	0.50
2:B:85:GLU:O	2:B:87:GLY:N	2.44	0.50
1:A:76:ARG:NH2	2:B:89:PRO:HG3	2.28	0.49
2:B:54:THR:O	2:B:113:ARG:NH2	2.45	0.49
1:A:134:GLU:HA	1:A:148:PHE:O	2.14	0.48
2:B:87:GLY:O	2:B:88:ARG:C	2.52	0.47
2:B:155:PHE:CD2	2:B:160:ILE:HD12	2.50	0.47
2:B:73:PHE:HB2	2:B:80:PHE:CD1	2.49	0.47
1:A:86:PRO:HB3	1:A:169:GLY:O	2.14	0.47
2:B:162:VAL:CG1	2:B:192:VAL:HG21	2.42	0.46
1:A:76:ARG:HH22	2:B:89:PRO:HG3	1.79	0.46
1:A:139:PRO:HB2	2:B:45:LYS:HZ3	1.80	0.46
2:B:132:VAL:HG22	2:B:152:VAL:HG13	1.98	0.45
2:B:123:LEU:HD23	2:B:123:LEU:HA	1.84	0.45
1:A:69:ASN:ND2	3:E:10:MET:CE	2.80	0.45
1:A:11:GLU:HG3	2:B:44:VAL:HB	1.99	0.45
1:A:63:ILE:HD13	1:A:63:ILE:HA	1.85	0.44
1:A:12:PHE:C	1:A:12:PHE:CD1	2.90	0.44
1:A:69:ASN:HD22	3:E:10:MET:CE	2.30	0.44
2:B:135:PHE:HB2	2:B:136:PRO:HD2	1.99	0.44
2:B:162:VAL:HG11	2:B:192:VAL:CG2	2.45	0.44
1:A:15:GLU:HB2	1:A:70:LEU:CD2	2.47	0.43
1:A:119:VAL:HG21	1:A:149:TYR:CE1	2.53	0.43
1:A:14:MET:HE2	2:B:39:HIS:HB3	2.01	0.43

Continued on next page...

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:GLU:CD	2:B:49:GLN:HE21	2.19	0.42
1:A:123:GLN:HG2	1:A:161:TYR:CE2	2.54	0.42
2:B:162:VAL:O	2:B:163:ARG:HD3	2.19	0.42
1:A:97:VAL:HG12	1:A:180:PHE:CE2	2.55	0.42
1:A:103:ASN:OD1	1:A:104:ILE:N	2.51	0.42
1:A:113:SER:OG	1:A:114:PRO:HA	2.19	0.42
1:A:21:GLU:OE1	1:A:136:VAL:HB	2.20	0.41
1:A:31:ILE:HG12	2:B:123:LEU:HD11	2.01	0.41
1:A:87:PRO:HB3	1:A:112:PHE:HB3	2.01	0.41
2:B:88:ARG:CB	2:B:89:PRO:CD	2.98	0.41
2:B:48:CYS:HB3	2:B:50:PHE:CE2	2.56	0.41
1:A:7:ILE:HD11	2:B:119:LEU:HD12	2.03	0.41
1:A:118:ASN:HD22	1:A:118:ASN:HA	1.48	0.41
2:B:158:GLY:N	2:B:159:PRO:HD2	2.36	0.40
1:A:34:VAL:HG11	1:A:60:LEU:CD1	2.52	0.40

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	176/182 (97%)	162 (92%)	13 (7%)	1 (1%)	25 43
2	B	171/190 (90%)	155 (91%)	11 (6%)	5 (3%)	4 6
3	E	10/12 (83%)	9 (90%)	1 (10%)	0	100 100
All	All	357/384 (93%)	326 (91%)	25 (7%)	6 (2%)	9 16

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	86	LEU
1	A	159	ASP

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
2	B	66	ASN
2	B	88	ARG
2	B	122	PHE
2	B	211	PRO

### 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	162/165 (98%)	143 (88%)	19 (12%)	5   10
2	B	157/169 (93%)	135 (86%)	22 (14%)	3   6
3	E	11/11 (100%)	9 (82%)	2 (18%)	1   3
All	All	330/345 (96%)	287 (87%)	43 (13%)	4   7

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	PHE
1	A	17	ASP
1	A	46	GLU
1	A	55	GLU
1	A	94	ASN
1	A	95	LYS
1	A	99	LEU
1	A	105	LEU
1	A	118	ASN
1	A	123	GLN
1	A	126	LYS
1	A	128	VAL
1	A	130	THR
1	A	146	ARG
1	A	157	ASN
1	A	164	LYS
1	A	165	VAL
1	A	166	GLU

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	168	TRP
2	B	45	LYS
2	B	51	SER
2	B	83	LEU
2	B	84	THR
2	B	98	LYS
2	B	99	ASP
2	B	101	LEU
2	B	102	GLU
2	B	127	GLN
2	B	133	THR
2	B	135	PHE
2	B	146	ASN
2	B	163	ARG
2	B	165	LEU
2	B	172	GLN
2	B	182	ARG
2	B	192	VAL
2	B	199	ARG
2	B	200	SER
2	B	218	THR
2	B	220	GLU
2	B	222	ARG
3	E	4	SER
3	E	14	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	69	ASN
1	A	78	ASN
1	A	94	ASN
1	A	118	ASN
2	B	52	ASN
2	B	97	GLN
2	B	146	ASN
2	B	153	ASN
3	E	12	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 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<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	178/182 (97%)	0.19	6 (3%) 45 48	34, 60, 107, 153	0
2	B	177/190 (93%)	0.24	5 (2%) 53 56	44, 67, 122, 138	0
3	E	12/12 (100%)	0.90	0 100 100	57, 81, 117, 144	0
All	All	367/384 (95%)	0.24	11 (2%) 50 53	34, 64, 115, 153	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	168	TRP	4.2
2	B	86	LEU	2.6
1	A	18	LEU	2.5
1	A	101	GLU	2.5
2	B	167	ASP	2.5
1	A	98	GLU	2.4
2	B	217	VAL	2.4
1	A	158	GLU	2.3
1	A	167	HIS	2.3
2	B	203	VAL	2.2
2	B	84	THR	2.0

### 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.