

Full wwPDB X-ray Structure Validation Report (i)

Aug 30, 2023 - 05.55 AM EDT

PDB ID : 3MYJ

Title: Human Class I MHC HLA-A2 in complex with the WT-1 (126-134) (R1Y)

peptide variant.

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Deposited on : 2010-05-10

Resolution : 1.89 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
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:

 $Mol Probity \quad : \quad 4.02b\text{--}467$

Mogul: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.35

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)

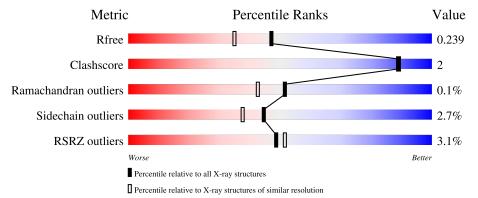
Validation Pipeline (wwPDB-VP) : 2.35

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 1.89 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},{\rm resolution\ range}(\mathring{\rm A})) \end{array}$
R_{free}	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	275	95%	5%
1			3%	
1	D	275	91%	7% •
2	В	100	90%	10%
2	Е	100	92%	7% •
3	С	9	78%	22%



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Mol	Chain	Length	Quality of chain
3	F	9	100%



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 6895 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 I histocompatibility antigen, A-2 alpha chain.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	275	Total 2274	C 1421	11	O 434	S 9	0	5	0
1	D	275	Total 2272			O 429	S 9	0	4	0

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

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	D	100	Total	С	N	О	S	0	2	0
2	Б	100	846	540	141	161	4	U		0
9	E	100	Total	С	N	О	S	0	1	0
2	E	100	841	537	141	159	4			U

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
В	0	MET	-	initiating methionine	UNP P61769
Е	0	MET	-	initiating methionine	UNP P61769

• Molecule 3 is a protein called Wilms tumor protein.

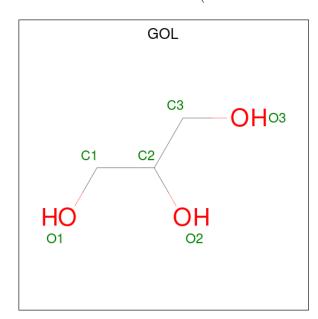
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	C	0	Total	С	N	О	S	0	0	0
3	C	9	79	55	10	13	1	U		U
2	r.	0	Total	С	N	О	S	0	0	0
3	ľ	9	79	55	10	13	1	U		U

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
С	1	TYR	ARG	engineered mutation	UNP P19544
F	1	TYR	ARG	engineered mutation	UNP P19544



• Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0

• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	146	Total O 146 146	0	0
5	В	75	Total O 75 75	0	0
5	D	192	Total O 192 192	0	0
5	Е	83	Total O 83 83	0	0
5	F	2	Total O 2 2	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 I histocompatibility antigen, A-2 alpha chain





	•	Molecule	3:	Wilms	tumor	protein
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Chain F: 100%

There are no outlier residues recorded for this chain.



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants	50.20Å 62.83Å 74.75Å	D
a, b, c, α , β , γ	81.91° 75.90° 77.94°	Depositor
Resolution (Å)	20.00 - 1.89	Depositor
rtesolution (A)	19.63 - 1.89	EDS
% Data completeness	96.2 (20.00-1.89)	Depositor
(in resolution range)	96.2 (19.63-1.89)	EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.16 (at 1.89Å)	Xtriage
Refinement program	REFMAC	Depositor
P. P.	0.185 , 0.230	Depositor
R, R_{free}	0.196 , 0.239	DCC
R_{free} test set	3333 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	25.4	Xtriage
Anisotropy	0.108	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.36, 37.0	EDS
L-test for twinning ²	$ < L >=0.50, < L^2>=0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6895	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.65% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities 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: GOL

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	Boı	nd lengths	Во	ond angles
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	A	0.95	0/2354	0.93	3/3193 (0.1%)
1	D	1.01	$2/2350 \ (0.1\%)$	1.08	$15/3188 \; (0.5\%)$
2	В	0.96	1/875 (0.1%)	0.91	1/1183 (0.1%)
2	Е	1.07	$2/867 \ (0.2\%)$	0.88	0/1172
3	С	0.99	0/83	1.04	0/112
3	F	0.89	0/83	1.01	0/112
All	All	0.99	5/6612 (0.1%)	0.98	19/8960 (0.2%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(A)
1	D	259	CYS	CB-SG	6.45	1.93	1.82
2	Е	80	CYS	CB-SG	-6.08	1.72	1.82
2	В	80	CYS	CB-SG	-5.63	1.72	1.81
1	D	99	TYR	CD1-CE1	-5.49	1.31	1.39
2	Е	89	GLN	CG-CD	-5.32	1.38	1.51

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	D	169	ARG	NE-CZ-NH1	14.86	127.73	120.30
1	D	169	ARG	NE-CZ-NH2	-13.25	113.68	120.30
1	D	108	ARG	NE-CZ-NH2	8.95	124.77	120.30
1	D	108	ARG	NE-CZ-NH1	-8.17	116.21	120.30
1	D	111	ARG	NE-CZ-NH2	-7.30	116.65	120.30
1	A	111	ARG	NE-CZ-NH2	-6.75	116.93	120.30
1	D	35	ARG	NE-CZ-NH1	6.73	123.66	120.30
1	D	110	LEU	CB-CG-CD1	6.35	121.80	111.00
1	D	35	ARG	NE-CZ-NH2	-6.02	117.29	120.30
1	D	111	ARG	NE-CZ-NH1	5.95	123.27	120.30



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Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
2	В	80	CYS	CA-CB-SG	-5.71	103.73	114.00
1	A	111	ARG	NE-CZ-NH1	5.54	123.07	120.30
1	D	61	ASP	CB-CG-OD1	5.52	123.26	118.30
1	A	129	ASP	CB-CG-OD1	5.48	123.24	118.30
1	D	37	ASP	CB-CG-OD1	5.44	123.20	118.30
1	D	129	ASP	CB-CG-OD1	5.35	123.11	118.30
1	D	29	ASP	CB-CG-OD1	-5.29	113.54	118.30
1	D	169	ARG	CB-CG-CD	5.21	125.16	111.60
1	D	157	ARG	NE-CZ-NH2	-5.17	117.71	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	2274	0	2127	6	0
1	D	2272	0	2130	12	0
2	В	846	0	816	6	0
2	Е	841	0	812	2	0
3	С	79	0	74	1	0
3	F	79	0	74	0	0
4	A	6	0	8	0	0
5	A	146	0	0	2	0
5	В	75	0	0	1	0
5	D	192	0	0	4	0
5	Е	83	0	0	0	0
5	F	2	0	0	0	0
All	All	6895	0	6041	23	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 2.

All (23) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



A + 1	A 4 0	Interatomic	Clash
Atom-1	Atom-2	${\rm distance}(\mathring{\rm A})$	overlap (Å)
1:D:70:HIS:NE2	5:D:303:HOH:O	2.22	0.65
2:B:85[B]:VAL:HG23	5:B:100:HOH:O	1.98	0.62
2:E:25:CYS:HB2	2:E:39:LEU:HD21	1.83	0.60
1:D:48:ARG:HD3	5:D:475:HOH:O	2.03	0.58
1:A:22:PHE:HE1	1:A:74:HIS:HD1	1.50	0.58
5:A:282:HOH:O	1:D:108:ARG:HD2	2.05	0.56
1:D:65:ARG:NH1	5:D:447:HOH:O	2.42	0.53
1:A:70:HIS:NE2	5:A:326:HOH:O	2.15	0.52
1:A:67:VAL:HB	3:C:2:MET:HE1	1.92	0.50
2:B:0:MET:HE2	2:B:0:MET:HB2	1.84	0.46
1:D:165:VAL:O	1:D:169:ARG:HG3	2.16	0.45
1:D:108:ARG:NH1	5:D:375:HOH:O	2.49	0.44
1:D:201:LEU:HD12	1:D:249:VAL:HG21	1.99	0.44
1:A:268:LYS:HB3	1:A:268:LYS:HE3	1.78	0.44
1:A:182:THR:O	1:D:108:ARG:NH1	2.50	0.44
1:A:117:ALA:HB2	2:B:60:TRP:CE2	2.53	0.43
1:D:133:TRP:HB2	1:D:144:LYS:HD2	2.00	0.43
2:B:39:LEU:HD23	2:B:39:LEU:HA	1.80	0.42
1:D:137:ASP:HB3	1:D:140:ALA:H	1.84	0.42
2:B:96:ASP:C	2:B:98[B]:ASP:H	2.23	0.41
2:B:25:CYS:HB2	2:B:39:LEU:HD21	2.03	0.41
1:D:117:ALA:HB2	2:E:60:TRP:CE2	2.56	0.40
1:D:48:ARG:HA	1:D:48:ARG:HD2	1.93	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	Perce	ntiles
1	A	$278/275 \ (101\%)$	270 (97%)	8 (3%)	0	100	100
1	D	277/275 (101%)	272 (98%)	5 (2%)	0	100	100
2	В	100/100 (100%)	97 (97%)	2(2%)	1 (1%)	15	6



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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	ntiles
2	E	99/100 (99%)	98 (99%)	1 (1%)	0	100	100
3	С	7/9 (78%)	7 (100%)	0	0	100	100
3	F	7/9 (78%)	7 (100%)	0	0	100	100
All	All	768/768 (100%)	751 (98%)	16 (2%)	1 (0%)	51	42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	В	97	ARG

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	Perce	ntiles
1	A	$236/231 \ (102\%)$	231 (98%)	5 (2%)	53	48
1	D	$235/231 \ (102\%)$	227 (97%)	8 (3%)	37	28
2	В	$97/95\ (102\%)$	96 (99%)	1 (1%)	76	76
2	E	96/95 (101%)	92 (96%)	4 (4%)	30	20
3	С	8/8 (100%)	7 (88%)	1 (12%)	4	1
3	F	8/8 (100%)	8 (100%)	0	100	100
All	All	$680/668 \; (102\%)$	661 (97%)	19 (3%)	44	36

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	35	ARG
1	A	128	GLU
1	A	138	MET
1	A	196	ASP
1	A	225	THR
2	В	70	PHE
3	С	5	ASN



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Mol	Chain	Res	Type
1	D	35	ARG
1	D	73	THR
1	D	110	LEU
1	D	137	ASP
1	D	157	ARG
1	D	207	SER
1	D	255[A]	GLN
1	D	255[B]	GLN
2	Е	58	LYS
2	Е	70	PHE
2	Е	83	ASN
2	Е	89	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	174	ASN
1	D	151	HIS
1	D	174	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)

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	Link	B	ond leng	$_{ m gths}$	В	ond ang	gles
	MIOI	туре	Chain	rtes	Lilik	Counts	RMSZ	# Z > 2	Counts	ounts RMSZ $\# Z > 2$	# Z >2
Ī	4	GOL	A	276	-	5,5,5	0.38	0	5,5,5	0.70	0

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
4	GOL	A	276	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	276	GOL	O1-C1-C2-C3
4	A	276	GOL	O1-C1-C2-O2

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	$\langle { m RSRZ} \rangle$	$\# \mathrm{RSRZ}{>}2$	$OWAB(Å^2)$	Q<0.9
1	A	$275/275\ (100\%)$	0.15	12 (4%) 34 37	11, 20, 29, 36	0
1	D	275/275 (100%)	0.14	9 (3%) 46 49	12, 19, 29, 39	0
2	В	100/100 (100%)	0.05	3 (3%) 50 53	13, 18, 28, 32	0
2	E	100/100 (100%)	-0.06	0 100 100	13, 19, 27, 31	0
3	С	9/9 (100%)	-0.08	0 100 100	20, 25, 28, 33	0
3	F	9/9 (100%)	0.12	0 100 100	19, 22, 27, 32	0
All	All	768/768 (100%)	0.10	24 (3%) 49 51	11, 19, 29, 39	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	16	GLY	4.8
1	D	18	GLY	3.8
1	A	18	GLY	3.7
1	A	194	VAL	3.6
1	A	17	ARG	3.4
1	D	194	VAL	3.2
1	A	196	ASP	3.2
1	A	16	GLY	3.2
2	В	48	LYS	2.9
1	D	90	ALA	2.7
1	A	113	TYR	2.6
1	A	195	SER	2.6
1	A	41	ALA	2.5
2	В	98[A]	ASP	2.5
1	A	225	THR	2.4
1	D	41	ALA	2.3
1	D	19	GLU	2.3
1	D	75	ARG	2.2
1	D	54	GLN	2.2



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Mol	Chain	Res	Type	RSRZ
2	В	58	LYS	2.2
1	A	222	GLU	2.1
1	D	17	ARG	2.1
1	A	75	ARG	2.0
1	A	192	HIS	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)

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.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
4	GOL	A	276	6/6	0.87	0.15	42,46,49,51	0

6.5 Other polymers (i)

There are no such residues in this entry.

