



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:50 AM UTC

PDB ID : 1HDM / pdb_00001hdm
Title : HISTOCOMPATIBILITY ANTIGEN HLA-DM
Authors : Wiley, D.C.; Mosyak, L.
Deposited on : 1998-09-09
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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

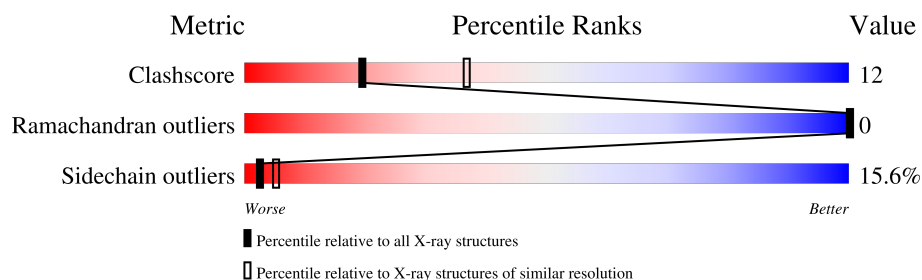
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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))
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (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 ≥ 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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	201	 63% 25% • 8%
2	B	193	 64% 25% 6% 5%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 2927 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 PROTEIN (CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	184	Total	C	N	O	S	0	0	0
			1482	968	234	274	6			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ALA	SEE REMARK 999	UNP P28067
A	?	-	PRO	SEE REMARK 999	UNP P28067
A	?	-	GLY	SEE REMARK 999	UNP P28067
A	179	PRO	ILE	conflict	UNP P28067

- Molecule 2 is a protein called PROTEIN (CLASS II HISTOCOMPATIBILITY ANTIGEN, M BETA CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	183	Total	C	N	O	S	0	0	0
			1445	915	248	271	11			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	GLU	SEE REMARK 999	UNP P28068
B	?	-	PHE	SEE REMARK 999	UNP P28068
B	?	-	GLY	SEE REMARK 999	UNP P28068
B	?	-	VAL	SEE REMARK 999	UNP P28068
B	?	-	LEU	SEE REMARK 999	UNP P28068
B	?	-	ARG	SEE REMARK 999	UNP P28068
B	?	-	PRO	SEE REMARK 999	UNP P28068

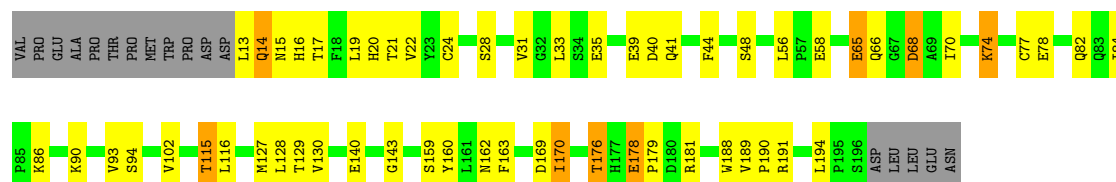
3 Residue-property plots [i](#)

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. 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. 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.

Note EDS was not executed.

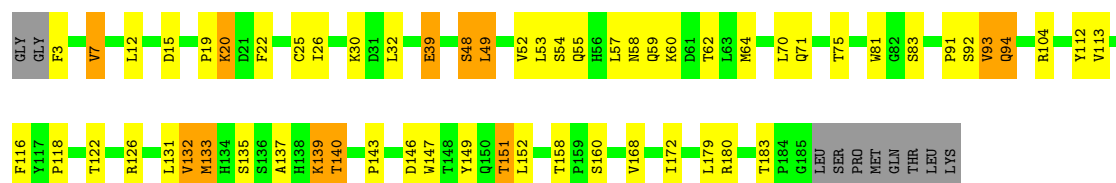
- Molecule 1: PROTEIN (CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN)

Chain A: 



- Molecule 2: PROTEIN (CLASS II HISTOCOMPATIBILITY ANTIGEN, M BETA CHAIN)

Chain B: 



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	95.39Å 109.93Å 105.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.00 – 2.50	Depositor
% Data completeness (in resolution range)	96.2 (34.00-2.50)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.55	Depositor
Refinement program	X-PLOR 3.8	Depositor
R, R_{free}	0.197 , 0.257	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2927	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

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	0.49	0/1533	0.91	3/2093 (0.1%)
2	B	0.47	0/1486	0.88	1/2031 (0.0%)
All	All	0.48	0/3019	0.90	4/4124 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	169	ASP	N-CA-C	7.59	120.67	110.35
1	A	178	GLU	N-CA-C	7.04	118.58	109.64
1	A	21	THR	N-CA-C	6.07	118.74	107.99
2	B	7	VAL	N-CA-C	-5.74	97.41	109.34

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	1482	0	1391	38	0
2	B	1445	0	1380	36	0
All	All	2927	0	2771	66	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 12.

All (66) 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:132:VAL:HG23	2:B:133:MET:HG3	1.55	0.88
1:A:22:VAL:HG22	1:A:33:LEU:HD13	1.71	0.72
2:B:58:ASN:HA	2:B:64:MET:HE3	1.72	0.71
1:A:20:HIS:HD2	1:A:35:GLU:OE2	1.74	0.70
2:B:19:PRO:HB2	2:B:70:LEU:HD22	1.75	0.68
1:A:68:ASP:HB3	1:A:70:ILE:HD12	1.78	0.65
1:A:41:GLN:NE2	1:A:44:PHE:HB3	2.12	0.65
2:B:91:PRO:HB3	2:B:116:PHE:HB3	1.80	0.64
1:A:127:MET:CE	1:A:181:ARG:HH21	2.12	0.62
1:A:129:THR:HB	1:A:176:THR:HG23	1.80	0.62
2:B:93:VAL:HA	2:B:112:TYR:O	2.01	0.61
1:A:129:THR:HB	1:A:176:THR:CG2	2.31	0.60
1:A:22:VAL:CG2	1:A:33:LEU:HD13	2.32	0.59
1:A:20:HIS:CD2	1:A:35:GLU:OE2	2.56	0.58
1:A:19:LEU:O	1:A:35:GLU:HA	2.05	0.57
2:B:131:LEU:HG	2:B:132:VAL:N	2.20	0.56
1:A:170:ILE:HG22	1:A:170:ILE:O	2.05	0.56
1:A:74:LYS:O	1:A:78:GLU:HG3	2.06	0.56
2:B:25:CYS:HB3	2:B:32:LEU:HD11	1.89	0.55
2:B:118:PRO:CD	2:B:172:ILE:HD11	2.38	0.54
1:A:170:ILE:HG12	1:A:189:VAL:HG12	1.90	0.54
2:B:143:PRO:HB3	2:B:149:TYR:CE2	2.43	0.53
1:A:127:MET:HE3	1:A:181:ARG:HH21	1.74	0.52
2:B:57:LEU:O	2:B:64:MET:HE3	2.09	0.52
1:A:178:GLU:OE1	1:A:179:PRO:HA	2.10	0.52
1:A:66:GLN:C	1:A:68:ASP:H	2.18	0.51
2:B:168:VAL:HG13	2:B:179:LEU:HD23	1.92	0.51
2:B:7:VAL:HG22	2:B:26:ILE:HD12	1.93	0.50
2:B:94:GLN:HA	2:B:94:GLN:OE1	2.11	0.50
2:B:48:SER:O	2:B:52:VAL:HG23	2.11	0.50
2:B:140:THR:O	2:B:151:THR:HG23	2.11	0.50
2:B:49:LEU:O	2:B:53:LEU:HG	2.12	0.49
2:B:146:ASP:O	2:B:147:TRP:HB2	2.11	0.49
1:A:65:GLU:OE2	1:A:66:GLN:N	2.46	0.49
2:B:140:THR:O	2:B:151:THR:CG2	2.62	0.48
1:A:127:MET:HE1	1:A:181:ARG:HH21	1.79	0.48
1:A:40:ASP:HB3	2:B:147:TRP:CE2	2.48	0.48
2:B:92:SER:O	2:B:113:VAL:HA	2.14	0.48
1:A:14:GLN:H	1:A:14:GLN:HG3	1.50	0.47
1:A:15:ASN:HD21	2:B:20:LYS:HG2	1.79	0.47
2:B:122:THR:HA	2:B:137:ALA:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:39:GLU:H	2:B:39:GLU:HG2	1.46	0.47
1:A:190:PRO:O	1:A:191:ARG:NH1	2.47	0.47
1:A:31:VAL:HG21	1:A:74:LYS:HG2	1.96	0.46
2:B:168:VAL:HG13	2:B:179:LEU:CD2	2.45	0.46
2:B:58:ASN:HA	2:B:64:MET:CE	2.43	0.45
1:A:17:THR:HG22	2:B:12:LEU:HD13	1.98	0.45
1:A:102:VAL:CG1	1:A:188:TRP:HB2	2.47	0.44
2:B:91:PRO:CB	2:B:116:PHE:HB3	2.47	0.44
1:A:16:HIS:HB2	2:B:81:TRP:HZ2	1.83	0.44
1:A:93:VAL:HG22	2:B:3:PHE:CE1	2.53	0.44
2:B:71:GLN:O	2:B:75:THR:HG23	2.18	0.44
1:A:40:ASP:HB3	2:B:147:TRP:NE1	2.33	0.43
1:A:68:ASP:HB3	1:A:70:ILE:CD1	2.47	0.43
1:A:16:HIS:HE1	2:B:15:ASP:OD2	2.01	0.43
2:B:91:PRO:HB2	2:B:113:VAL:HG13	1.99	0.43
1:A:143:GLY:HA3	1:A:160:TYR:O	2.19	0.42
1:A:170:ILE:O	1:A:170:ILE:CG2	2.64	0.42
2:B:132:VAL:O	2:B:133:MET:C	2.62	0.42
1:A:41:GLN:HE22	1:A:44:PHE:HB3	1.84	0.42
1:A:84:ILE:N	1:A:84:ILE:HD13	2.34	0.42
1:A:17:THR:HG22	2:B:12:LEU:CD1	2.50	0.41
1:A:65:GLU:OE2	1:A:65:GLU:HA	2.21	0.40
1:A:24:CYS:SG	1:A:77:CYS:C	3.05	0.40
1:A:115:THR:HB	1:A:162:ASN:OD1	2.21	0.40
2:B:137:ALA:O	2:B:139:LYS:HD2	2.20	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	178/201 (89%)	173 (97%)	5 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	175/193 (91%)	170 (97%)	5 (3%)	0	100	100
All	All	353/394 (90%)	343 (97%)	10 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	165/181 (91%)	141 (86%)	24 (14%)	3	6
2	B	162/170 (95%)	135 (83%)	27 (17%)	2	4
All	All	327/351 (93%)	276 (84%)	51 (16%)	2	5

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	LEU
1	A	14	GLN
1	A	28	SER
1	A	39	GLU
1	A	48	SER
1	A	56	LEU
1	A	58	GLU
1	A	65	GLU
1	A	68	ASP
1	A	74	LYS
1	A	82	GLN
1	A	86	LYS
1	A	90	LYS
1	A	94	SER
1	A	115	THR
1	A	116	LEU
1	A	128	LEU
1	A	130	VAL

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Mol	Chain	Res	Type
1	A	140	GLU
1	A	159	SER
1	A	163	PHE
1	A	170	ILE
1	A	176	THR
1	A	194	LEU
2	B	20	LYS
2	B	22	PHE
2	B	30	LYS
2	B	39	GLU
2	B	48	SER
2	B	49	LEU
2	B	54	SER
2	B	55	GLN
2	B	59	GLN
2	B	60	LYS
2	B	62	THR
2	B	83	SER
2	B	93	VAL
2	B	94	GLN
2	B	104	ARG
2	B	126	ARG
2	B	132	VAL
2	B	133	MET
2	B	135	SER
2	B	139	LYS
2	B	140	THR
2	B	151	THR
2	B	152	LEU
2	B	158	THR
2	B	160	SER
2	B	180	ARG
2	B	183	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	16	HIS
1	A	20	HIS
1	A	122	ASN
1	A	133	HIS
2	B	41	ASN

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Mol	Chain	Res	Type
2	B	72	ASN
2	B	86	ASN
2	B	102	ASN
2	B	142	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 oligosaccharides 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	B	3
1	A	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	46:CYS	C	47:ASN	N	7.75
1	A	68:ASP	C	69:ALA	N	3.80

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	84:ILE	C	85:PRO	N	3.22
1	B	133:MET	C	134:HIS	N	3.04
1	B	67:LEU	C	68:ASN	N	2.91

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.