



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 09:46 PM UTC

PDB ID : 1MHE / pdb_00001mhe
Title : THE HUMAN NON-CLASSICAL MAJOR HISTOCOMPATIBILITY COMPLEX MOLECULE HLA-E
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Deposited on : 1998-08-24
Resolution : 2.85 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 ⓘ 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

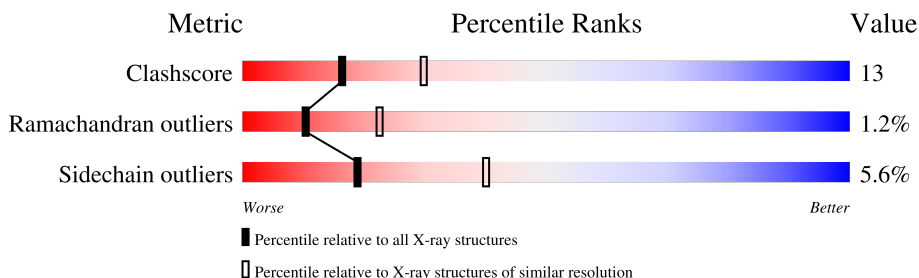
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	1446 (2.88-2.84)
Ramachandran outliers	187476	1406 (2.88-2.84)
Sidechain outliers	187428	1407 (2.88-2.84)

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	274	65% 28% 5% •
1	C	274	68% 27% •
2	B	100	81% 17% •
2	D	100	75% 23% •
3	P	9	22% 78%
3	Q	9	56% 44%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7752 atoms, of which 1459 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 HLA-E.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	273	Total	C	H	N	O	S	44	0	0
			2748	1396	514	401	430	7			
1	C	273	Total	C	H	N	O	S	0	0	0
			2748	1396	514	401	430	7			

- Molecule 2 is a protein called BETA-2-MICROGLOBULIN.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	100	Total	C	H	N	O	S	0	0	0
			1029	533	192	141	159	4			
2	D	100	Total	C	H	N	O	S	0	0	0
			1029	533	192	141	159	4			

- Molecule 3 is a protein called PEPTIDE (VMAPRTVLL).

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	P	9	Total	C	H	N	O	S	0	0	0
			85	45	16	12	11	1			
3	Q	9	Total	C	H	N	O	S	0	0	0
			85	45	16	12	11	1			

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	3	Total	H	O	0	0
			9	6	3		
5	C	5	Total	H	O	0	0
			14	9	5		

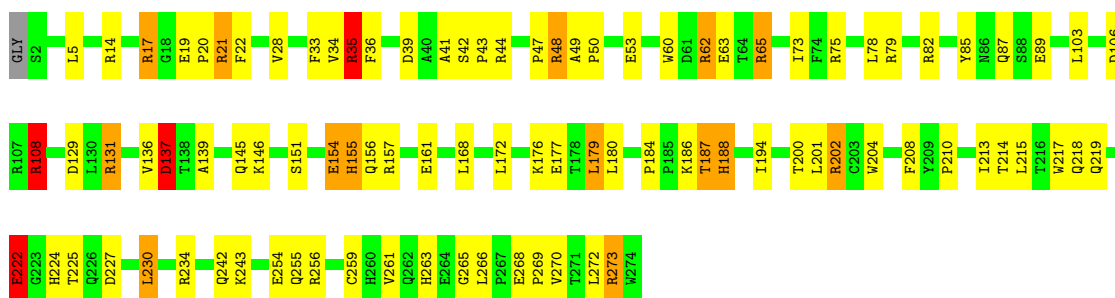
3 Residue-property plots

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.

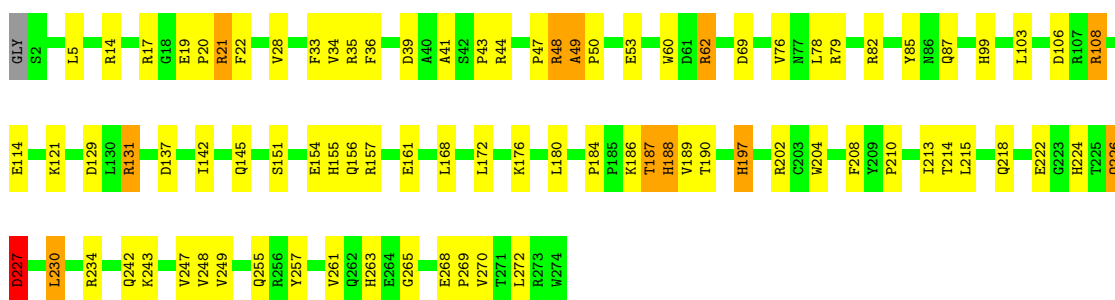
- Molecule 1: HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E

Chain A: 



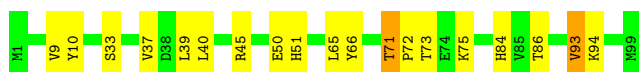
- Molecule 1: HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E

Chain C: 



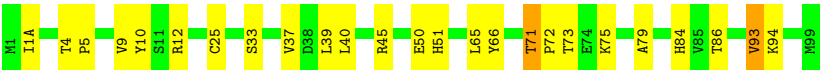
- Molecule 2: BETA-2-MICROGLOBULIN

Chain B: 

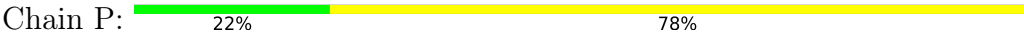


- Molecule 2: BETA-2-MICROGLOBULIN

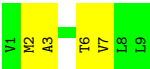
Chain D: 



● Molecule 3: PEPTIDE (VMAPRTVLL)



● Molecule 3: PEPTIDE (VMAPRTVLL)



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	182.20 Å 182.20 Å 88.40 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	25.00 – 2.85	Depositor
% Data completeness (in resolution range)	91.0 (25.00-2.85)	Depositor
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.202 , 0.235	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7752	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	0.65	0/2300	1.12	19/3127 (0.6%)
1	C	0.67	0/2300	1.12	18/3127 (0.6%)
2	B	0.69	0/860	0.98	3/1162 (0.3%)
2	D	0.58	0/860	1.02	6/1162 (0.5%)
3	P	0.73	0/69	1.60	3/92 (3.3%)
3	Q	0.73	0/69	1.18	1/92 (1.1%)
All	All	0.66	0/6458	1.10	50/8762 (0.6%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	35	ARG	CG-CD-NE	-8.27	93.81	112.00
3	P	3	ALA	CA-C-N	7.69	127.86	119.87
3	P	3	ALA	C-N-CA	7.69	127.86	119.87
1	A	35	ARG	NE-CZ-NH2	-7.52	112.43	119.20
1	C	249	VAL	N-CA-C	7.34	115.21	109.19

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	35	ARG	Sidechain

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	2234	514	2072	73	0
1	C	2234	514	2072	61	0
2	B	837	192	803	17	0
2	D	837	192	803	17	0
3	P	69	16	83	7	0
3	Q	69	16	83	1	0
4	A	5	0	0	0	0
5	A	3	6	0	0	0
5	C	5	9	0	0	0
All	All	6293	1459	5916	158	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 13.

The worst 5 of 158 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:C:226:GLN:O	1:C:227:ASP:HB2	1.77	0.83
1:A:202:ARG:HG2	1:A:204:TRP:NE1	1.98	0.79
1:A:35:ARG:HH11	1:A:48:ARG:HH11	1.32	0.76
1:A:17:ARG:N	1:A:17:ARG:HD3	2.05	0.71
1:C:218:GLN:HB2	1:C:222:GLU:O	1.90	0.71

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	271/274 (99%)	234 (86%)	32 (12%)	5 (2%)	6	15
1	C	271/274 (99%)	236 (87%)	31 (11%)	4 (2%)	8	18
2	B	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
2	D	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
3	P	7/9 (78%)	7 (100%)	0	0	100	100
3	Q	7/9 (78%)	4 (57%)	3 (43%)	0	100	100
All	All	752/766 (98%)	667 (89%)	76 (10%)	9 (1%)	10	22

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	225	THR
1	A	227	ASP
1	C	227	ASP
1	A	137	ASP
1	A	188	HIS

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	236/236 (100%)	217 (92%)	19 (8%)	11	23
1	C	236/236 (100%)	224 (95%)	12 (5%)	21	43
2	B	95/95 (100%)	93 (98%)	2 (2%)	47	70
2	D	95/95 (100%)	92 (97%)	3 (3%)	34	59
3	P	8/8 (100%)	7 (88%)	1 (12%)	4	8
3	Q	8/8 (100%)	7 (88%)	1 (12%)	4	8
All	All	678/678 (100%)	640 (94%)	38 (6%)	19	40

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	187	THR
2	D	93	VAL
1	C	197	HIS
1	C	270	VAL
3	Q	2	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	115	GLN
1	C	260	HIS
1	C	145	GLN
1	C	263	HIS
1	C	219	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](#)

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	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	SO4	A	1002	-	4,4,4	0.87	0	6,6,6	0.46	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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

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.