



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 11:56 AM UTC

PDB ID : 1M05 / pdb_00001m05
Title : HLA B8 in complex with an Epstein Barr Virus determinant
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Deposited on : 2002-06-11
Resolution : 1.90 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
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

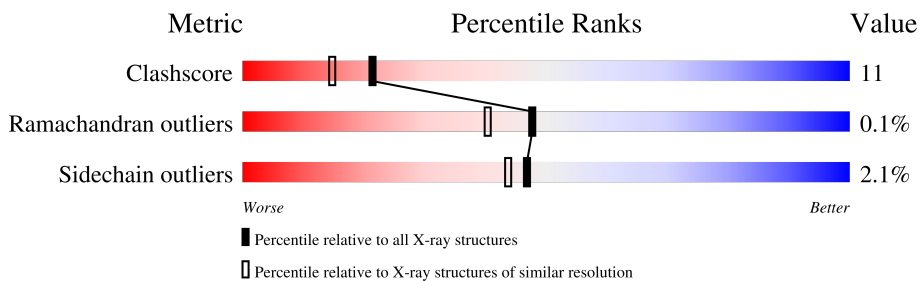
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	277	
1	C	277	
2	B	99	
2	D	99	
3	E	9	
3	F	9	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6986 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, B-8 B*0801 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	269	Total	C	N	O	S	0	0	0
			2193	1360	398	428	7			
1	C	269	Total	C	N	O	S	0	0	0
			2189	1357	397	428	7			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	99	Total	C	N	O	S	0	0	0
			829	528	140	158	3			
2	D	99	Total	C	N	O	S	0	0	0
			829	528	140	158	3			

- Molecule 3 is a protein called EBNA-3 nuclear protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	9	Total	C	N	O	0	0	0
			75	49	15	11			
3	F	9	Total	C	N	O	0	0	0
			75	49	15	11			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	9	LEU	ILE	SEE REMARK 999	UNP P12977
F	9	LEU	ILE	SEE REMARK 999	UNP P12977

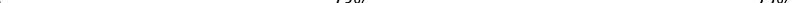
- Molecule 4 is CADMIUM ION (CCD ID: CD) (formula: Cd).

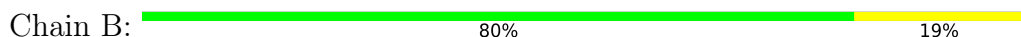
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total 1	Cd 1	0	0
4	D	1	Total 1	Cd 1	0	0

- Molecule 5 is water.

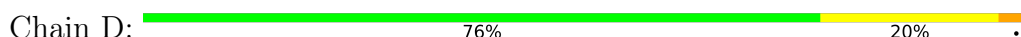
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	268	Total 268	O 268	0	0
5	B	117	Total 117	O 117	0	0
5	C	261	Total 261	O 261	0	0
5	D	123	Total 123	O 123	0	0
5	E	14	Total 14	O 14	0	0
5	F	11	Total 11	O 11	0	0

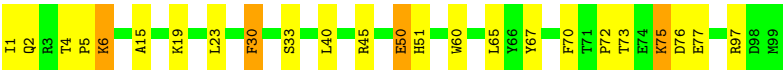
Note EDS was not executed.

- Chain A:  73% 22% . .



- Molecule 2: Beta-2-microglobulin



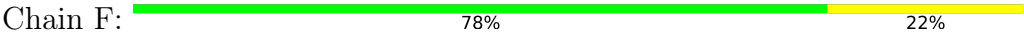


- Molecule 3: EBNA-3 nuclear protein



There are no outlier residues recorded for this chain.

- Molecule 3: EBNA-3 nuclear protein



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	85.40Å 90.10Å 125.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.90	Depositor
% Data completeness (in resolution range)	95.2 (50.00-1.90)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.242 , 0.283	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6986	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

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: CD

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	0.46	0/2252	1.02	13/3060 (0.4%)
1	C	0.43	0/2248	0.94	10/3056 (0.3%)
2	B	0.43	0/852	0.88	2/1152 (0.2%)
2	D	0.42	0/852	0.86	3/1152 (0.3%)
3	E	0.50	0/76	0.96	0/98
3	F	0.49	0/76	0.82	0/98
All	All	0.44	0/6356	0.95	28/8616 (0.3%)

There are no bond length outliers.

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	275	GLU	CA-C-N	15.33	139.00	119.84
1	A	275	GLU	C-N-CA	15.33	139.00	119.84
1	C	275	GLU	CA-C-N	-8.75	111.40	120.85
1	C	275	GLU	C-N-CA	-8.75	111.40	120.85
2	B	33	SER	N-CA-C	8.05	121.16	111.82

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	2193	0	2035	46	0
1	C	2189	0	2024	56	0
2	B	829	0	794	18	0
2	D	829	0	794	18	0
3	E	75	0	79	0	0
3	F	75	0	79	3	0
4	B	1	0	0	0	0
4	D	1	0	0	0	0
5	A	268	0	0	4	1
5	B	117	0	0	2	0
5	C	261	0	0	12	1
5	D	123	0	0	4	0
5	E	14	0	0	0	0
5	F	11	0	0	0	0
All	All	6986	0	5805	131	1

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 11.

The worst 5 of 131 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:D:75:LYS:HD3	2:D:75:LYS:H	1.39	0.88
2:B:75:LYS:HB3	5:B:199:HOH:O	1.78	0.83
1:A:49:ALA:O	1:A:52:ILE:HG22	1.83	0.78
1:C:49:ALA:O	1:C:52:ILE:HG22	1.83	0.77
1:C:201:LEU:HD12	1:C:249:VAL:HG11	1.67	0.77

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:425:HOH:O	5:C:477:HOH:O[1_545]	2.16	0.04

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	265/277 (96%)	247 (93%)	17 (6%)	1 (0%)	30	22
1	C	265/277 (96%)	253 (96%)	12 (4%)	0	100	100
2	B	97/99 (98%)	94 (97%)	3 (3%)	0	100	100
2	D	97/99 (98%)	94 (97%)	3 (3%)	0	100	100
3	E	7/9 (78%)	7 (100%)	0	0	100	100
3	F	7/9 (78%)	7 (100%)	0	0	100	100
All	All	738/770 (96%)	702 (95%)	35 (5%)	1 (0%)	48	40

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	276	PRO

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	229/236 (97%)	222 (97%)	7 (3%)	35	29
1	C	228/236 (97%)	226 (99%)	2 (1%)	70	73
2	B	94/94 (100%)	92 (98%)	2 (2%)	47	44
2	D	94/94 (100%)	91 (97%)	3 (3%)	34	27
3	E	6/6 (100%)	6 (100%)	0	100	100
3	F	6/6 (100%)	6 (100%)	0	100	100
All	All	657/672 (98%)	643 (98%)	14 (2%)	47	44

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	50	GLU
2	B	75	LYS
2	D	75	LYS
2	D	19	LYS
2	D	50	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	114	ASN
1	C	155	GLN
2	D	13	HIS
1	C	144	GLN
1	C	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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.