



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 01:48 AM UTC

PDB ID : 1AGF / pdb_00001agf
Title : ANTAGONIST HIV-1 GAG PEPTIDES INDUCE STRUCTURAL CHANGES IN HLA B8-HIV-1 GAG PEPTIDE (GGKKRYKL-5R MUTATION)
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Deposited on : 1997-03-24
Resolution : 2.20 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

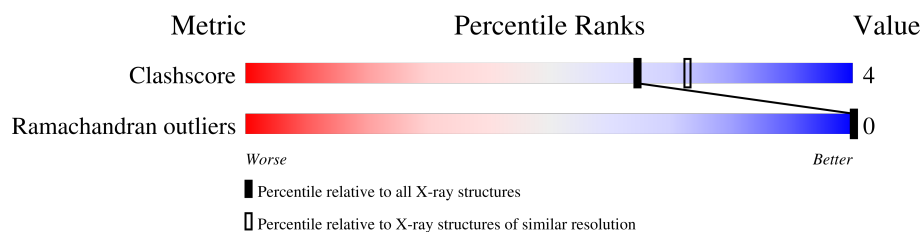
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 Å.

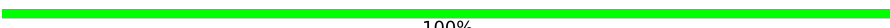
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)

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	276	 87% 12% .
2	B	99	 93% 7%
3	C	8	 100%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4805 atoms, of which 1355 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 B*0801.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	276	Total	C	H	N	O	S	5	0	0
			2787	1395	535	411	439	7			

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

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	99	Total	C	H	N	O	S	5	0	0
			1020	528	191	140	158	3			

- Molecule 3 is a protein called HIV-1 GAG PEPTIDE (GGKKRYKL - 5R MUTATION).

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	C	8	Total	C	H	N	O		0	0	0
			92	43	25	14	10				

- Molecule 4 is water.

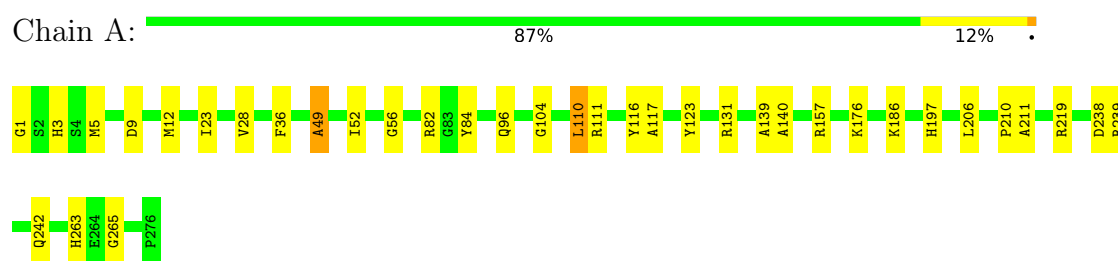
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	226	Total	H	O	0	0
			678	452	226		
4	B	67	Total	H	O	0	0
			201	134	67		
4	C	9	Total	H	O	0	0
			27	18	9		

3 Residue-property plots

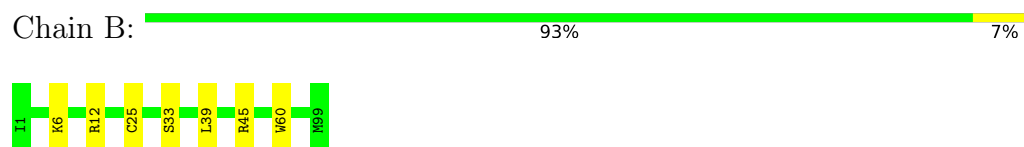
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: B*0801



- Molecule 2: BETA-2 MICROGLOBULIN



- Molecule 3: HIV-1 GAG PEPTIDE (GGKKRYKL - 5R MUTATION)



There are no outlier residues recorded for this chain.

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	50.60Å 81.30Å 110.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	14.00 – 2.20	Depositor
% Data completeness (in resolution range)	96.3 (14.00-2.20)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.181 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4805	wwPDB-VP
Average B, all atoms (Å ²)	12.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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	0.69	0/2314	1.04	13/3146 (0.4%)
2	B	0.63	0/852	1.01	2/1152 (0.2%)
3	C	0.59	0/67	0.89	0/83
All	All	0.67	0/3233	1.03	15/4381 (0.3%)

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.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	28	VAL	N-CA-C	-8.44	95.44	107.75
2	B	33	SER	N-CA-C	8.09	122.41	112.54
2	B	6	LYS	N-CA-C	-7.00	99.19	110.32
1	A	186	LYS	N-CA-C	-6.79	98.16	108.96
1	A	56	GLY	CA-C-N	6.19	126.38	119.32
1	A	56	GLY	C-N-CA	6.19	126.38	119.32
1	A	49	ALA	CA-C-N	5.97	125.45	119.24
1	A	49	ALA	C-N-CA	5.97	125.45	119.24
1	A	56	GLY	N-CA-C	5.72	118.86	112.00
1	A	176	LYS	N-CA-C	5.64	117.42	111.28
1	A	197	HIS	N-CA-C	5.62	120.20	113.23
1	A	110	LEU	N-CA-C	-5.34	105.03	112.45
1	A	5	MET	N-CA-C	-5.27	100.81	109.40
1	A	3	HIS	N-CA-C	5.23	117.34	109.23
1	A	211	ALA	N-CA-C	5.00	117.46	111.71

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	116	TYR	Sidechain

5.2 Too-close contacts ⓘ

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	2252	535	2095	20	0
2	B	829	191	794	3	1
3	C	67	25	80	0	0
4	A	226	452	0	2	2
4	B	67	134	0	1	0
4	C	9	18	0	0	0
All	All	3450	1355	2969	22	2

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 4.

All (22) 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:A:1:GLY:HA3	1:A:110:LEU:HD11	1.23	1.17
1:A:1:GLY:CA	1:A:110:LEU:HD11	2.14	0.68
1:A:1:GLY:HA2	1:A:104:GLY:HA2	1.77	0.65
1:A:49:ALA:O	1:A:52:ILE:HG22	1.99	0.62
1:A:263:HIS:CD2	1:A:265:GLY:H	2.21	0.58
1:A:12:MET:HB3	4:A:344:HOH:O	2.06	0.55
1:A:210:PRO:O	1:A:263:HIS:HE1	1.91	0.54
1:A:131:ARG:HH11	1:A:157:ARG:HH12	1.57	0.52
1:A:263:HIS:HD2	1:A:265:GLY:H	1.58	0.52
1:A:117:ALA:HB2	2:B:60:TRP:CE2	2.48	0.49
1:A:206:LEU:HD23	1:A:242:GLN:HB3	1.93	0.49
1:A:219:ARG:O	1:A:219:ARG:HG3	2.12	0.49
1:A:82:ARG:HD2	4:A:482:HOH:O	2.13	0.48
1:A:84:TYR:HB3	1:A:139:ALA:HB1	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:25:CYS:HB2	2:B:39:LEU:HD21	1.98	0.45
1:A:123:TYR:CZ	1:A:140:ALA:HA	2.51	0.45
1:A:23:ILE:HD12	1:A:36:PHE:O	2.19	0.42
1:A:110:LEU:O	1:A:111:ARG:HB3	2.21	0.41
1:A:238:ASP:O	1:A:239:ARG:HB3	2.20	0.41
1:A:36:PHE:CD1	1:A:36:PHE:C	2.98	0.41
2:B:45:ARG:HD2	4:B:144:HOH:O	2.21	0.41
1:A:9:ASP:O	1:A:96:GLN:HA	2.21	0.40

All (2) 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)
2:B:12:ARG:HH11	4:A:485:HOH:H2[1_655]	1.14	0.46
4:A:303:HOH:H2	4:A:491:HOH:O[2_344]	1.53	0.07

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	274/276 (99%)	267 (97%)	7 (3%)	0	100	100
2	B	97/99 (98%)	96 (99%)	1 (1%)	0	100	100
3	C	6/8 (75%)	6 (100%)	0	0	100	100
All	All	377/383 (98%)	369 (98%)	8 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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](#)

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.