



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 10:31 PM UTC

PDB ID : 2HPF / pdb\_00002hpf  
Title : COMPARISON OF THE STRUCTURES OF HIV-2 PROTEASE COMPLEXES IN THREE CRYSTAL SPACE GROUPS WITH AN HIV-1 PROTEASE COMPLEX STRUCTURE  
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Deposited on : 1994-09-21  
Resolution : 3.00 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0  
Xtrriage (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

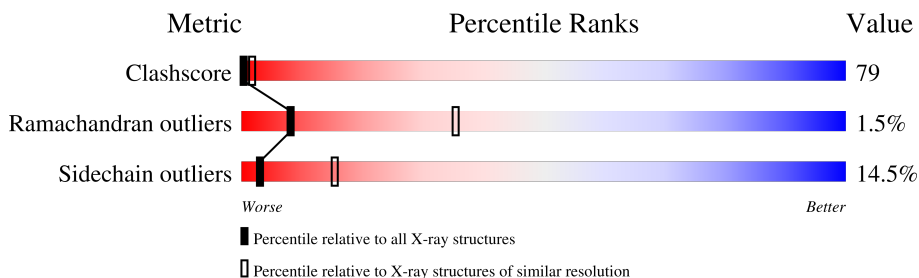
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)

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  $\geq 3$ , 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	99	
1	B	99	
2	S	8	

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 1622 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 HIV-2 PROTEASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	99	754	484	124	144	2	0	0	0
1	B	99	754	484	124	144	2	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	57	LEU	LYS	conflict	UNP P04584
B	57	LEU	LYS	conflict	UNP P04584

- Molecule 2 is a protein called UNIDENTIFIED PEPTIDE FRAGMENT.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	S	8	38	21	8	9	0	0	0

- Molecule 3 is water.

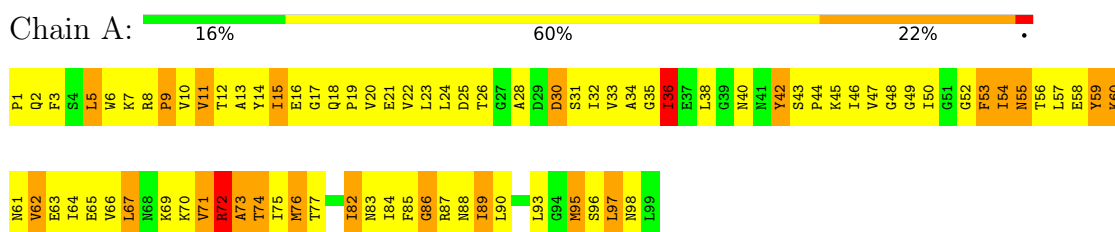
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	32	Total	O	0	0
			32	32		
3	B	42	Total	O	0	0
			42	42		
3	S	2	Total	O	0	0
			2	2		

### 3 Residue-property plots [i](#)

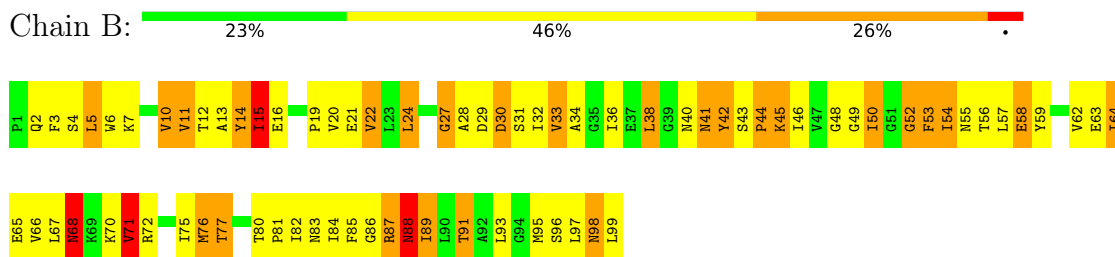
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

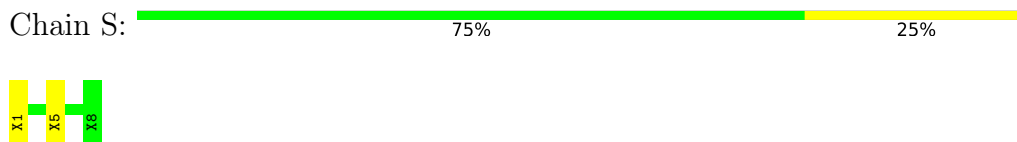
- Molecule 1: HIV-2 PROTEASE



- Molecule 1: HIV-2 PROTEASE



- Molecule 2: UNIDENTIFIED PEPTIDE FRAGMENT



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	80.17Å 80.17Å 71.14Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	10.00 – 3.00	Depositor
% Data completeness (in resolution range)	(Not available) (10.00-3.00)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, $R_{free}$	0.144 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	1622	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	21.0	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	1.49	5/766 (0.7%)	1.91	16/1039 (1.5%)
1	B	1.53	6/766 (0.8%)	1.95	20/1039 (1.9%)
All	All	1.51	11/1532 (0.7%)	1.93	36/2078 (1.7%)

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	1	2
1	B	0	4
All	All	1	6

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	45	LYS	CA-C	7.89	1.62	1.52
1	B	52	GLY	N-CA	6.64	1.53	1.44
1	B	15	ILE	CA-C	6.53	1.58	1.52
1	A	34	ALA	CA-C	6.52	1.60	1.52
1	A	6	TRP	NE1-CE2	-6.02	1.30	1.37

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	98	ASN	CA-CB-CG	-10.01	102.59	112.60
1	B	68	ASN	CA-CB-CG	8.93	121.53	112.60
1	B	52	GLY	N-CA-C	8.05	121.29	110.43
1	A	36	ILE	N-CA-C	8.02	120.03	107.28
1	A	9	PRO	N-CA-CB	8.00	108.03	102.35

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	36	ILE	CA

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	42	TYR	Sidechain
1	A	59	TYR	Sidechain
1	B	14	TYR	Sidechain
1	B	42	TYR	Sidechain
1	B	64	ILE	Mainchain

## 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	754	0	778	154	0
1	B	754	0	778	125	0
2	S	38	0	7	3	0
3	A	32	0	0	6	0
3	B	42	0	0	9	0
3	S	2	0	0	0	0
All	All	1622	0	1563	247	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 79.

The worst 5 of 247 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:2:GLN:NE2	3:A:110:HOH:O	1.64	1.29
1:A:10:VAL:HG11	1:A:21:GLU:OE2	1.36	1.24
1:A:13:ALA:CB	1:A:66:VAL:HG12	1.73	1.16
1:A:13:ALA:HB2	1:A:66:VAL:HG12	1.27	1.08
1:B:67:LEU:O	1:B:68:ASN:HB3	1.33	1.08

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	97/99 (98%)	82 (84%)	14 (14%)	1 (1%)	12	45
1	B	97/99 (98%)	88 (91%)	7 (7%)	2 (2%)	5	27
All	All	194/198 (98%)	170 (88%)	21 (11%)	3 (2%)	8	35

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	33	VAL
1	A	86	GLY
1	B	68	ASN

### 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	Percentiles	
1	A	83/83 (100%)	69 (83%)	14 (17%)	2	11
1	B	83/83 (100%)	73 (88%)	10 (12%)	5	22
All	All	166/166 (100%)	142 (86%)	24 (14%)	3	15

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	10	VAL
1	B	30	ASP
1	B	24	LEU

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Mol	Chain	Res	Type
1	B	41	ASN
1	A	55	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2	GLN
1	A	55	ASN
1	B	2	GLN
1	B	55	ASN
1	B	98	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](#)

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.