



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 29, 2025 – 01:57 PM EDT

PDB ID : 2PWO / pdb_00002pwo
Title : Crystal Structure of HIV-1 CA146 A92E Psuedo Cell
Authors : Kelly, B.N.
Deposited on : 2007-05-11
Resolution : 1.45 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 Phenix2.0rc1
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

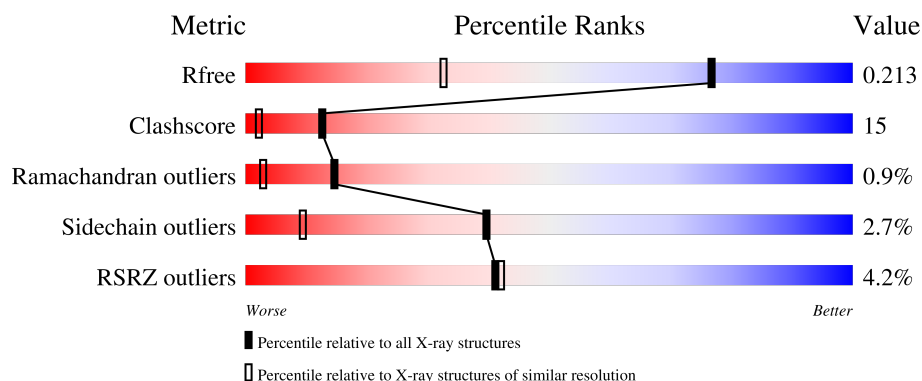
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.45 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))
R_{free}	164625	1556 (1.46-1.46)
Clashscore	180529	1653 (1.46-1.46)
Ramachandran outliers	177936	1635 (1.46-1.46)
Sidechain outliers	177891	1635 (1.46-1.46)
RSRZ outliers	164620	1556 (1.46-1.46)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	146	<div> <div>3%</div> <div>83%</div> <div>14%</div> <div>..</div> </div>
1	B	146	<div> <div>5%</div> <div>76%</div> <div>21%</div> <div>...</div> </div>
1	C	146	<div> <div>6%</div> <div>73%</div> <div>23%</div> <div>...</div> </div>
1	D	146	<div> <div>2%</div> <div>79%</div> <div>19%</div> <div>..</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5361 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 Gag-Pol polyprotein (Pr160Gag-Pol).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	144	Total	C	N	O	S	0	12	0
			1211	766	213	223	9			
1	B	143	Total	C	N	O	S	0	10	0
			1181	751	202	219	9			
1	C	145	Total	C	N	O	S	0	11	0
			1219	768	215	227	9			
1	D	145	Total	C	N	O	S	0	13	0
			1213	772	209	223	9			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	92	GLU	ALA	engineered mutation	UNP P12497
B	92	GLU	ALA	engineered mutation	UNP P12497
C	92	GLU	ALA	engineered mutation	UNP P12497
D	92	GLU	ALA	engineered mutation	UNP P12497

- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Cl	0	0
			1	1		
2	B	1	Total	Cl	0	0
			1	1		
2	C	1	Total	Cl	0	0
			1	1		
2	D	1	Total	Cl	0	0
			1	1		

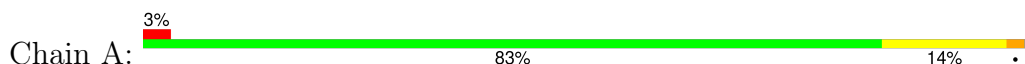
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	138	Total 138	O 138	0	0
3	B	123	Total 123	O 123	0	0
3	C	126	Total 126	O 126	0	0
3	D	146	Total 146	O 146	0	0

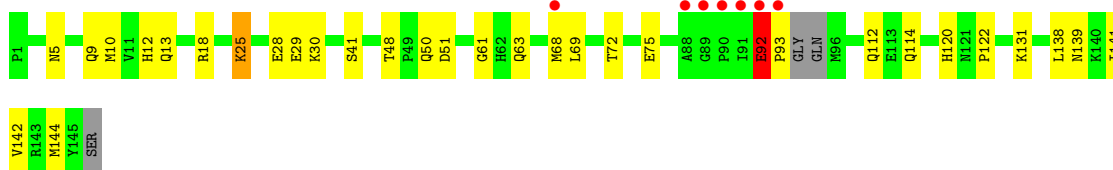
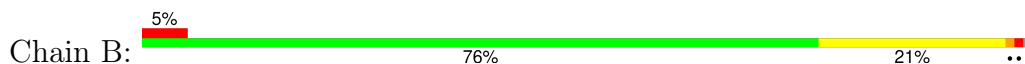
3 Residue-property plots [i](#)

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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

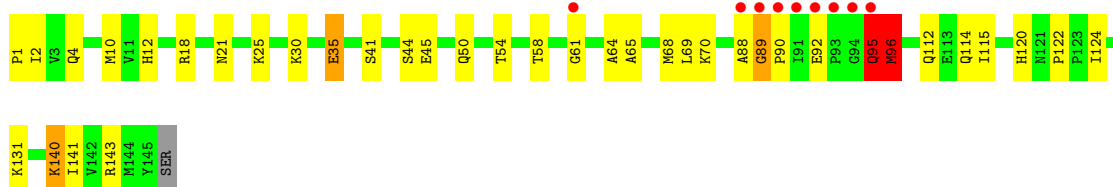
- Molecule 1: Gag-Pol polyprotein (Pr160Gag-Pol)



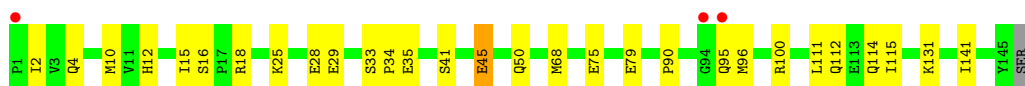
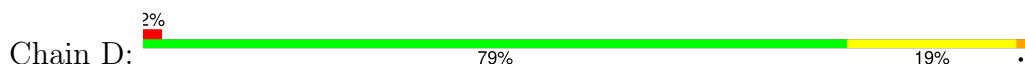
- Molecule 1: Gag-Pol polyprotein (Pr160Gag-Pol)



- Molecule 1: Gag-Pol polyprotein (Pr160Gag-Pol)



- Molecule 1: Gag-Pol polyprotein (Pr160Gag-Pol)



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	46.23Å 48.21Å 58.93Å 83.01° 71.28° 87.43°	Depositor
Resolution (Å)	30.03 – 1.45 30.03 – 1.45	Depositor EDS
% Data completeness (in resolution range)	90.7 (30.03-1.45) 91.0 (30.03-1.45)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.92 (at 1.45Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.170 , 0.216 0.168 , 0.213	Depositor DCC
R_{free} test set	3878 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	16.0	Xtriage
Anisotropy	0.077	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 41.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	5361	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 75.14 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.3372e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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: CL

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	0.96	0/1259	0.97	1/1708 (0.1%)
1	B	0.90	0/1235	0.91	0/1675
1	C	0.87	0/1259	0.95	2/1709 (0.1%)
1	D	0.92	1/1271 (0.1%)	0.90	0/1726
All	All	0.91	1/5024 (0.0%)	0.93	3/6818 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	15	ILE	CA-CB	7.68	1.63	1.54

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	96	MET	N-CA-C	-8.90	91.85	110.80
1	C	1	PRO	N-CD-CG	-6.58	93.33	103.20
1	A	6	LEU	N-CA-C	5.28	117.79	111.71

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	1211	0	1220	35	0
1	B	1181	0	1196	33	0
1	C	1219	0	1216	55	0
1	D	1213	0	1237	50	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	138	0	0	7	2
3	B	123	0	0	10	0
3	C	126	0	0	15	0
3	D	146	0	0	13	2
All	All	5361	0	4869	146	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 15.

The worst 5 of 146 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:45[B]:GLU:OE2	1:C:131[B]:LYS:NZ	1.67	1.27
1:C:18[A]:ARG:HD3	1:D:41[A]:SER:OG	1.32	1.23
1:B:92:GLU:HB3	1:B:93:PRO:HA	1.23	1.19
1:C:18[A]:ARG:CD	1:D:41[A]:SER:OG	1.98	1.11
1:B:92:GLU:HB3	1:B:93:PRO:CA	1.83	1.09

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)
3:A:960:HOH:O	3:D:1023:HOH:O[1_545]	1.84	0.36
3:A:972:HOH:O	3:D:999:HOH:O[1_545]	2.08	0.12

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	154/146 (106%)	152 (99%)	1 (1%)	1 (1%)	22	6
1	B	149/146 (102%)	146 (98%)	2 (1%)	1 (1%)	19	4
1	C	154/146 (106%)	150 (97%)	1 (1%)	3 (2%)	6	1
1	D	156/146 (107%)	155 (99%)	1 (1%)	0	100	100
All	All	613/584 (105%)	603 (98%)	5 (1%)	5 (1%)	14	3

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	92	GLU
1	C	89	GLY
1	C	95	GLN
1	C	96	MET
1	A	93	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	134/124 (108%)	129 (96%)	5 (4%)	29	4
1	B	132/124 (106%)	128 (97%)	4 (3%)	36	7
1	C	134/124 (108%)	129 (96%)	5 (4%)	29	4
1	D	136/124 (110%)	133 (98%)	3 (2%)	47	16
All	All	536/496 (108%)	519 (97%)	17 (3%)	40	6

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	10	MET
1	D	45[B]	GLU
1	B	63	GLN

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Mol	Chain	Res	Type
1	B	92	GLU
1	C	35[A]	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	4	GLN
1	D	139	ASN
1	C	50	GLN
1	D	53	ASN
1	C	12	HIS

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 4 ligands modelled in this entry, 4 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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	144/146 (98%)	0.05	5 (3%) 47 48	7, 16, 28, 38	12 (8%)
1	B	143/146 (97%)	0.04	7 (4%) 36 35	9, 17, 32, 62	10 (6%)
1	C	145/146 (99%)	0.11	9 (6%) 28 27	6, 18, 38, 56	11 (7%)
1	D	145/146 (99%)	-0.01	3 (2%) 63 64	7, 16, 28, 32	13 (8%)
All	All	577/584 (98%)	0.05	24 (4%) 41 42	6, 17, 29, 62	46 (7%)

The worst 5 of 24 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	89	GLY	5.3
1	A	2	ILE	4.5
1	D	1	PRO	3.8
1	B	93	PRO	3.6
1	C	88	ALA	3.6

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	CL	B	904	1/1	0.99	0.04	15,15,15,15	0
2	CL	A	902	1/1	1.00	0.04	17,17,17,17	0
2	CL	C	901	1/1	1.00	0.05	15,15,15,15	0
2	CL	D	903	1/1	1.00	0.04	17,17,17,17	0

6.5 Other polymers [i](#)

There are no such residues in this entry.