



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 14, 2026 – 10:52 AM UTC

PDB ID : 1IJS / pdb_00001ijs
Title : CPV (STRAIN D) mutant A300D, complex (VIRAL COAT/DNA), VP2,
PH=7.5, T=4 DEGREES C
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Deposited on : 1996-09-12
Resolution : 3.25 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)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

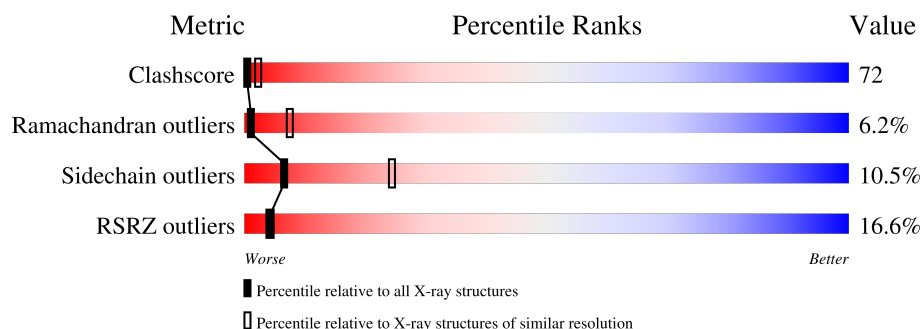
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.25 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	1660 (3.30-3.22)
Ramachandran outliers	187476	1630 (3.30-3.22)
Sidechain outliers	187428	1629 (3.30-3.22)
RSRZ outliers	180081	1605 (3.30-3.22)

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	N	9	33% 33% 67%
2	A	2	100%
3	P	584	15% 28% 48% 15% 6%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4571 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 DNA chain called DNA (5'-D(*CP*CP*AP*CP*CP*CP*CP*AP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	N	9	Total	C	N	O	P	0	0	0
			178	84	33	52	9			

- Molecule 2 is a DNA chain called DNA (5'-D(*AP*C)-3').

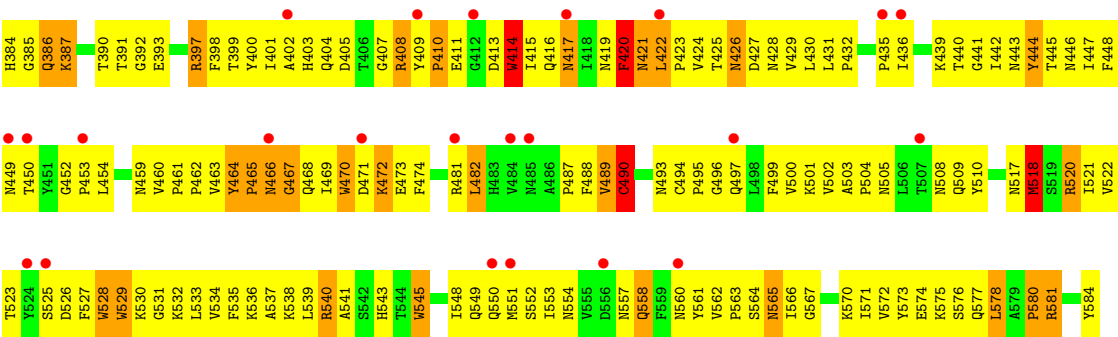
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	2	Total	C	N	O	P	0	0	0
			40	19	8	11	2			

- Molecule 3 is a protein called PROTEIN (PARVOVIRUS COAT PROTEIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	P	548	Total	C	N	O	S	0	0	0
			4353	2765	742	830	16			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	300	ASP	ALA	engineered mutation	UNP P30129
P	386	GLN	LYS	conflict	UNP P30129



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	267.60Å 268.50Å 274.30Å 61.90° 62.60° 60.20°	Depositor
Resolution (Å)	(Not available) – 3.25 200.00 – 3.25	Depositor EDS
% Data completeness (in resolution range)	(Not available) ((Not available)-3.25) 32.2 (200.00-3.25)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	11.97 (at 3.25Å)	Xtriage
Refinement program	NONE	Depositor
R, R_{free}	(Not available) , (Not available) 0.529 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	32.4	Xtriage
Anisotropy	0.329	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 48.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.014 for -h+k,-h,-h+l 0.014 for -k,h-k,-k+l 0.028 for h,h-k,h-l 0.035 for -h+k,k,k-l 0.018 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.06	EDS
Total number of atoms	4571	wwPDB-VP
Average B, all atoms (Å ²)	11.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.88% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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	N	0.81	1/198 (0.5%)	0.94	0/299
2	A	0.54	0/44	0.87	0/65
3	P	1.39	42/4483 (0.9%)	1.35	38/6133 (0.6%)
All	All	1.36	43/4725 (0.9%)	1.33	38/6497 (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
3	P	0	1

The worst 5 of 43 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	P	490	CYS	CA-C	19.62	1.77	1.52
3	P	490	CYS	N-CA	-16.10	1.26	1.46
3	P	81	ARG	CD-NE	15.01	1.67	1.46
3	P	239	ASP	C-N	-13.03	1.15	1.33
3	P	252	VAL	N-CA	-10.21	1.34	1.46

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	P	490	CYS	N-CA-CB	13.87	130.77	109.83
3	P	81	ARG	CG-CD-NE	11.47	137.24	112.00
3	P	81	ARG	CA-CB-CG	8.43	130.96	114.10
3	P	47	ASN	CA-C-N	6.06	131.72	122.93
3	P	47	ASN	C-N-CA	6.06	131.72	122.93

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	P	81	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	N	178	0	99	7	0
2	A	40	0	23	12	0
3	P	4353	0	4144	621	0
All	All	4571	0	4266	640	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 72.

The worst 5 of 640 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)
3:P:96:MET:CE	3:P:221:SER:H	1.02	1.57
3:P:490:CYS:C	3:P:490:CYS:CA	1.77	1.54
3:P:424:VAL:HG21	3:P:429:VAL:CG2	1.35	1.51
2:A:1:DA:C3'	2:A:2:DC:H5''	1.48	1.44
3:P:276:THR:CG2	3:P:581:ARG:HB2	1.48	1.44

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
3	P	546/584 (94%)	442 (81%)	70 (13%)	34 (6%)	1 7

5 of 34 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	P	38	VAL
3	P	159	GLN
3	P	369	ASN
3	P	370	GLN
3	P	386	GLN

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
3	P	477/496 (96%)	427 (90%)	50 (10%)	6 24

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	P	230	THR
3	P	357	ILE
3	P	578	LEU
3	P	231	ASN
3	P	349	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
3	P	292	ASN
3	P	543	HIS
3	P	384	HIS
3	P	557	ASN
3	P	492	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	P	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	P	239:ASP	C	240:ASP	N	1.15

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	N	9/9 (100%)	1.33	3 (33%) 1 1	12, 12, 12, 12	0
2	A	2/2 (100%)	0.54	0 100 100	12, 12, 12, 12	0
3	P	548/584 (93%)	1.07	90 (16%) 4 4	0, 12, 12, 15	0
All	All	559/595 (93%)	1.07	93 (16%) 4 4	0, 12, 12, 15	0

The worst 5 of 93 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	P	340	ALA	9.6
3	P	257	THR	5.7
3	P	223	THR	5.4
3	P	91	ALA	4.8
3	P	97	ALA	4.3

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.