



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 5, 2024 – 09:51 AM EST

PDB ID : 1VZV  
Title : STRUCTURE OF VARICELLA-ZOSTER VIRUS PROTEASE  
Authors : Qiu, X.; Jason, C.A.; Culp, J.S.; Richardson, S.B.; Debouck, C.; Smith, W.W.;  
Abdel-Meguid, S.S.  
Deposited on : 1997-02-10  
Resolution : 3.00 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](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 : 4.02b-467  
Xtrriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

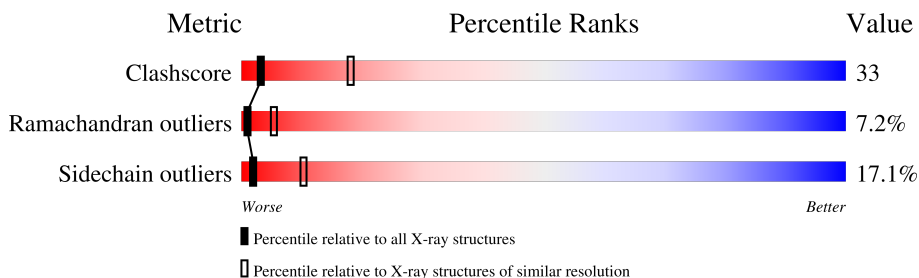
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 Å.

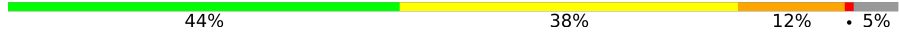
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (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	221	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1623 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 VARICELLA-ZOSTER VIRUS PROTEASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	211	1623	1039	282	295	7	0	0	0

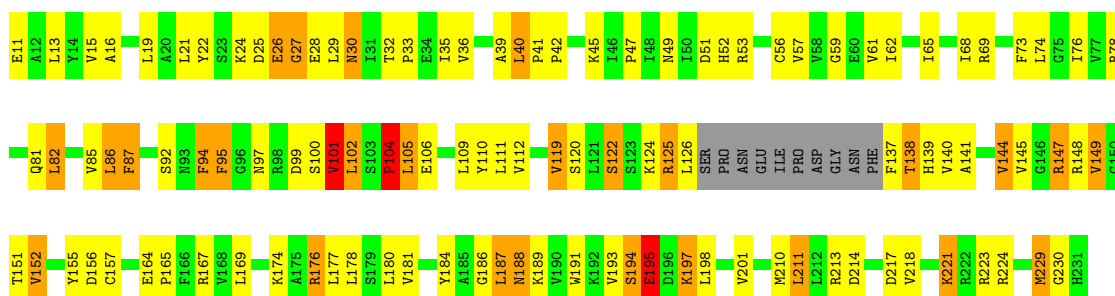
### 3 Residue-property plots [i](#)

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. 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: VARICELLA-ZOSTER VIRUS PROTEASE

Chain A: 



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 64 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00Å 90.00Å 117.40Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	7.00 – 3.00	Depositor
% Data completeness (in resolution range)	(Not available) (7.00-3.00)	Depositor
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, $R_{free}$	0.223 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	1623	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	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	0.69	0/1653	0.96	3/2245 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	94	PHE	N-CA-C	-5.92	95.02	111.00
1	A	125	ARG	N-CA-C	-5.88	95.13	111.00
1	A	149	VAL	N-CA-C	5.65	126.25	111.00

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	1623	0	1639	109	0
All	All	1623	0	1639	109	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 33.

All (109) 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:167:ARG:NE	1:A:229:MET:HB3	1.76	0.98
1:A:144:VAL:HG12	1:A:145:VAL:HG13	1.46	0.95
1:A:176:ARG:NH2	1:A:180:LEU:HD21	1.90	0.86
1:A:210:MET:HG3	1:A:211:LEU:HD13	1.56	0.86
1:A:85:VAL:HG12	1:A:195:GLU:HG3	1.59	0.84
1:A:25:ASP:HB2	1:A:148:ARG:HG2	1.63	0.79
1:A:109:LEU:HD21	1:A:156:ASP:HA	1.69	0.75
1:A:176:ARG:HH21	1:A:180:LEU:HD21	1.51	0.73
1:A:49:ASN:HB2	1:A:56:CYS:O	1.90	0.72
1:A:138:THR:HG22	1:A:139:HIS:HD2	1.56	0.70
1:A:11:GLU:HB3	1:A:105:LEU:HD13	1.73	0.69
1:A:221:LYS:HB3	1:A:221:LYS:NZ	2.13	0.63
1:A:78:ARG:HD2	1:A:189:LYS:O	1.99	0.62
1:A:221:LYS:HB3	1:A:221:LYS:HZ2	1.63	0.61
1:A:193:VAL:HG12	1:A:194:SER:H	1.64	0.61
1:A:22:TYR:OH	1:A:36:VAL:HG21	2.02	0.59
1:A:119:VAL:HG13	1:A:140:VAL:HG13	1.85	0.59
1:A:101:VAL:O	1:A:102:LEU:HB2	2.02	0.59
1:A:176:ARG:HH11	1:A:176:ARG:HG2	1.68	0.59
1:A:25:ASP:HA	1:A:149:VAL:HG13	1.85	0.58
1:A:214:ASP:O	1:A:218:VAL:HG23	2.03	0.58
1:A:24:LYS:CB	1:A:149:VAL:HG21	2.34	0.58
1:A:197:LYS:O	1:A:201:VAL:HG23	2.04	0.58
1:A:167:ARG:CZ	1:A:229:MET:HB3	2.34	0.57
1:A:176:ARG:HH11	1:A:176:ARG:CG	2.17	0.57
1:A:193:VAL:HG12	1:A:194:SER:N	2.20	0.57
1:A:147:ARG:HG3	1:A:147:ARG:HH11	1.70	0.57
1:A:214:ASP:HB3	1:A:217:ASP:HB2	1.86	0.56
1:A:29:LEU:HD11	1:A:147:ARG:NH1	2.19	0.56
1:A:94:PHE:O	1:A:95:PHE:HB2	2.06	0.56
1:A:94:PHE:HE1	1:A:110:TYR:CE1	2.23	0.56
1:A:61:VAL:HG22	1:A:73:PHE:CD2	2.41	0.56
1:A:177:LEU:O	1:A:181:VAL:HG23	2.06	0.56
1:A:52:HIS:HA	1:A:139:HIS:HE1	1.71	0.55
1:A:94:PHE:CE1	1:A:110:TYR:HE1	2.26	0.54
1:A:138:THR:HG22	1:A:139:HIS:CD2	2.42	0.53
1:A:78:ARG:O	1:A:191:TRP:HE3	1.91	0.53
1:A:33:PRO:HA	1:A:36:VAL:HG23	1.91	0.53
1:A:85:VAL:CG1	1:A:195:GLU:HG3	2.35	0.52
1:A:169:LEU:HD23	1:A:174:LYS:HG2	1.90	0.52
1:A:27:GLY:O	1:A:29:LEU:N	2.43	0.52
1:A:94:PHE:CE1	1:A:110:TYR:CE1	2.98	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:PRO:HG2	1:A:105:LEU:H	1.74	0.52
1:A:119:VAL:HA	1:A:141:ALA:O	2.10	0.52
1:A:176:ARG:CZ	1:A:180:LEU:HD11	2.40	0.52
1:A:61:VAL:HG22	1:A:73:PHE:HD2	1.74	0.51
1:A:13:LEU:HG	1:A:109:LEU:HD13	1.93	0.51
1:A:40:LEU:HB3	1:A:42:PRO:HD3	1.92	0.51
1:A:29:LEU:O	1:A:148:ARG:NH2	2.45	0.50
1:A:65:ILE:HG12	1:A:177:LEU:HD21	1.92	0.50
1:A:40:LEU:HA	1:A:41:PRO:C	2.33	0.50
1:A:29:LEU:HA	1:A:148:ARG:HH21	1.76	0.50
1:A:29:LEU:HB3	1:A:148:ARG:HE	1.78	0.49
1:A:59:GLY:HA3	1:A:76:ILE:O	2.12	0.49
1:A:15:VAL:HG22	1:A:155:TYR:CD2	2.48	0.49
1:A:105:LEU:HG	1:A:105:LEU:O	2.12	0.49
1:A:164:GLU:N	1:A:165:PRO:HD2	2.27	0.48
1:A:11:GLU:HB3	1:A:105:LEU:CD1	2.43	0.48
1:A:186:GLY:C	1:A:188:ASN:H	2.16	0.48
1:A:167:ARG:NH2	1:A:229:MET:SD	2.87	0.47
1:A:29:LEU:H	1:A:29:LEU:HD22	1.80	0.47
1:A:62:ILE:HD12	1:A:181:VAL:HG13	1.95	0.47
1:A:104:PRO:HD2	1:A:106:GLU:CG	2.44	0.47
1:A:52:HIS:ND1	1:A:139:HIS:CE1	2.83	0.47
1:A:81:GLN:O	1:A:85:VAL:HG13	2.15	0.46
1:A:124:LYS:HB2	1:A:137:PHE:O	2.15	0.46
1:A:104:PRO:HD2	1:A:106:GLU:HG3	1.96	0.46
1:A:167:ARG:CD	1:A:229:MET:HB3	2.44	0.46
1:A:167:ARG:HE	1:A:229:MET:HB3	1.72	0.46
1:A:13:LEU:CD2	1:A:112:VAL:HG11	2.45	0.46
1:A:26:GLU:C	1:A:30:ASN:HD22	2.20	0.45
1:A:189:LYS:HD3	1:A:191:TRP:CZ2	2.51	0.45
1:A:49:ASN:HB3	1:A:57:VAL:HG22	1.98	0.45
1:A:122:SER:HG	1:A:139:HIS:CE1	2.35	0.44
1:A:21:LEU:HD13	1:A:69:ARG:HH21	1.83	0.44
1:A:32:THR:O	1:A:36:VAL:HG23	2.18	0.44
1:A:32:THR:H	1:A:35:ILE:HD12	1.82	0.44
1:A:97:ASN:O	1:A:101:VAL:HG23	2.17	0.44
1:A:94:PHE:O	1:A:95:PHE:CB	2.65	0.44
1:A:167:ARG:CZ	1:A:229:MET:SD	3.06	0.43
1:A:25:ASP:CB	1:A:148:ARG:HG2	2.42	0.43
1:A:109:LEU:HD11	1:A:155:TYR:HB3	2.00	0.43
1:A:147:ARG:HG3	1:A:147:ARG:NH1	2.31	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:197:LYS:HG3	1:A:198:LEU:N	2.33	0.43
1:A:53:ARG:HB2	1:A:56:CYS:HB3	2.01	0.43
1:A:176:ARG:CG	1:A:176:ARG:NH1	2.78	0.43
1:A:82:LEU:HA	1:A:198:LEU:HD21	2.01	0.42
1:A:99:ASP:O	1:A:100:SER:C	2.58	0.42
1:A:124:LYS:HE3	1:A:124:LYS:HB3	1.86	0.42
1:A:147:ARG:H	1:A:147:ARG:HG2	1.41	0.42
1:A:122:SER:O	1:A:138:THR:HB	2.20	0.42
1:A:164:GLU:O	1:A:164:GLU:HG2	2.20	0.42
1:A:197:LYS:HE3	1:A:197:LYS:HB2	1.86	0.42
1:A:51:ASP:O	1:A:52:HIS:HB2	2.20	0.41
1:A:74:LEU:HD23	1:A:181:VAL:CG2	2.51	0.41
1:A:39:ALA:C	1:A:40:LEU:HD23	2.41	0.41
1:A:47:PRO:HD2	1:A:138:THR:O	2.20	0.41
1:A:152:VAL:HG11	1:A:223:ARG:HG3	2.03	0.41
1:A:124:LYS:HB2	1:A:138:THR:OG1	2.21	0.41
1:A:39:ALA:HB2	1:A:126:LEU:CB	2.50	0.41
1:A:87:PHE:HD1	1:A:87:PHE:HA	1.78	0.41
1:A:101:VAL:O	1:A:102:LEU:CB	2.66	0.41
1:A:122:SER:OG	1:A:139:HIS:NE2	2.50	0.41
1:A:86:LEU:HD12	1:A:86:LEU:HA	1.92	0.41
1:A:124:LYS:N	1:A:137:PHE:O	2.54	0.40
1:A:29:LEU:H	1:A:29:LEU:CD2	2.35	0.40
1:A:78:ARG:NH2	1:A:187:LEU:O	2.54	0.40
1:A:16:ALA:HA	1:A:73:PHE:O	2.22	0.40
1:A:41:PRO:HA	1:A:42:PRO:HD3	1.90	0.40

There are no symmetry-related clashes.

## 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	207/221 (94%)	174 (84%)	18 (9%)	15 (7%)	<b>1</b> <b>5</b>

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	102	LEU
1	A	104	PRO
1	A	125	ARG
1	A	138	THR
1	A	230	GLY
1	A	28	GLU
1	A	195	GLU
1	A	26	GLU
1	A	184	TYR
1	A	95	PHE
1	A	45	LYS
1	A	101	VAL
1	A	151	THR
1	A	27	GLY
1	A	144	VAL

### 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	175/193 (91%)	145 (83%)	30 (17%)	<b>2</b> <b>10</b>

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	LEU
1	A	30	ASN
1	A	40	LEU
1	A	68	ILE
1	A	82	LEU
1	A	86	LEU

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Mol	Chain	Res	Type
1	A	87	PHE
1	A	92	SER
1	A	101	VAL
1	A	104	PRO
1	A	105	LEU
1	A	111	LEU
1	A	119	VAL
1	A	120	SER
1	A	122	SER
1	A	147	ARG
1	A	152	VAL
1	A	157	CYS
1	A	176	ARG
1	A	178	LEU
1	A	187	LEU
1	A	188	ASN
1	A	194	SER
1	A	195	GLU
1	A	197	LYS
1	A	211	LEU
1	A	213	ARG
1	A	221	LYS
1	A	224	ARG
1	A	229	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 monosaccharides 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.