

# Full wwPDB X-ray Structure Validation Report (i)

#### Dec 17, 2023 - 07:55 am GMT

PDB ID	:	3ZN6
Title	:	VP16-VP17 complex, a complex of the two major capsid proteins of bacterio-
		phage P23-77
Authors	:	Rissanen, I.; Grimes, J.M.; Pawlowski, A.; Mantynen, S.; Harlos, K.; Bamford,
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Deposited on	:	2013-02-13
Resolution	:	1.53  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 (i) 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 (1)) were used in the production of this report:

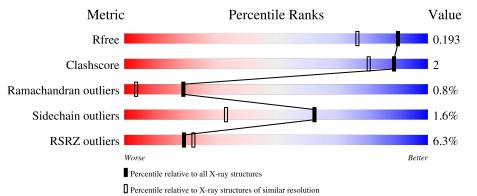
Refmac	: : :	<ul><li>1.13</li><li>2.36</li><li>20191225.v01 (using entries in the PDB archive December 25th 2019)</li><li>5.8.0158</li></ul>
CCP4 Ideal geometry (proteins) Ideal geometry (DNA, RNA) Validation Pipeline (wwPDB-VP)	:	Parkinson et al. (1996)

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY \, DIFFRACTION$ 

The reported resolution of this entry is 1.53 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
$R_{free}$	130704	2556 (1.56-1.52)
Clashscore	141614	2634(1.56-1.52)
Ramachandran outliers	138981	2580 (1.56-1.52)
Sidechain outliers	138945	2577 (1.56-1.52)
RSRZ outliers	127900	2524 (1.56-1.52)

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 <=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	А	291	4%	•	24%				
2	В	173	7%76%	6%	• 16%				



## 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 3334 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 VP17.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	А	221	Total 1757	C 1115	N 311	O 323	S 8	0	3	0

• Molecule 2 is a protein called VP16.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace		
2	В	145	Total 1180	С 764	N 200	O 216	0	5	0

• Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	1	Total Cl 1 1	0	0

• Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOc	c AltConf
4	В	1	Total Na 1 1	a 0	0

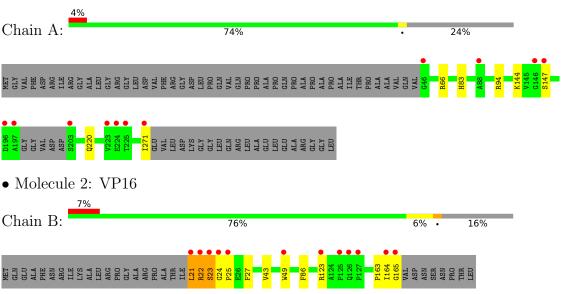
• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	244	Total O 244 244	0	0
5	В	151	Total O 151 151	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: VP17



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	76.78Å $69.61$ Å $81.62$ Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $104.99^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	22.40 - 1.53	Depositor
Resolution (A)	39.61 - 1.53	EDS
% Data completeness	98.1 (22.40-1.53)	Depositor
(in resolution range)	98.3(39.61-1.53)	EDS
R <sub>merge</sub>	0.06	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.85 (at 1.53 \text{\AA})$	Xtriage
Refinement program	BUSTER 2.11.4	Depositor
D D.	0.172 , $0.197$	Depositor
$R, R_{free}$	0.169 , $0.193$	DCC
$R_{free}$ test set	3111 reflections $(5.06%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	20.6	Xtriage
Anisotropy	0.239	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.35 , $45.1$	EDS
L-test for twinning <sup>2</sup>	$ \langle L  \rangle = 0.49, \langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	3334	wwPDB-VP
Average B, all atoms $(Å^2)$	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.44% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical 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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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, NA

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		
	Unain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.46	0/1813	0.61	0/2472	
2	В	0.56	0/1212	0.76	3/1658~(0.2%)	
All	All	0.50	0/3025	0.67	3/4130~(0.1%)	

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	В	163	PRO	C-N-CA	5.78	136.16	121.70
2	В	24[A]	GLY	N-CA-C	-5.40	99.60	113.10
2	В	24[B]	GLY	N-CA-C	-5.40	99.60	113.10

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	А	1757	0	1707	3	0
2	В	1180	0	1181	8	0
3	В	1	0	0	0	0
4	В	1	0	0	0	0
5	А	244	0	0	0	0
5	В	151	0	0	0	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	3334	0	2888	11	1

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 2.

All (11) 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)
2:B:22[B]:ARG:HB3	2:B:23[B]:SER:OG	1.73	0.88
2:B:49[A]:TRP:HE1	2:B:165:GLY:H	1.30	0.77
2:B:21[B]:LEU:HD23	2:B:22[B]:ARG:HG3	1.84	0.58
2:B:22[A]:ARG:HB3	2:B:27:PHE:HB3	1.85	0.58
2:B:23[B]:SER:HB3	2:B:27:PHE:CB	2.42	0.50
2:B:23[B]:SER:HB3	2:B:27:PHE:HB3	1.94	0.48
1:A:83:HIS:HB2	1:A:271:ILE:HD11	1.96	0.47
1:A:94:ARG:HA	1:A:220:GLN:OE1	2.19	0.42
2:B:22[A]:ARG:CB	2:B:27:PHE:HB3	2.48	0.42
2:B:43:VAL:HG22	2:B:49[B]:TRP:CE3	2.56	0.40
1:A:144:LYS:HE3	1:A:147:SER:HA	2.03	0.40

All (1) 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)
5:B:2016:HOH:O	5:B:2016:HOH:O[2_655]	1.95	0.25

#### 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	А	220/291~(76%)	219 (100%)	1 (0%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	В	147/173~(85%)	137~(93%)	6 (4%)	4 (3%)	5 0
All	All	367/464~(79%)	356~(97%)	7 (2%)	4 (1%)	19 2

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All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	В	164	ILE
2	В	25	PRO
2	В	23[A]	SER
2	В	23[B]	SER

#### 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	Analysed Rotameric Outliers		Percentiles		
1	А	187/234~(80%)	186 (100%)	1 (0%)	88 77		
2	В	128/147~(87%)	122~(95%)	6~(5%)	26 3		
All	All	315/381~(83%)	308~(98%)	7 (2%)	62 21		

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	66	ARG
2	В	21[A]	LEU
2	В	21[B]	LEU
2	В	22[A]	ARG
2	В	22[B]	ARG
2	В	86	PHE
2	В	123	ARG

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. There are no such side chains 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)

Of 2 ligands modelled in this entry, 2 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,  $95^{th}$  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	$\langle RSRZ \rangle$	#RSRZ>2		$OWAB(Å^2)$	Q<0.9	
1	А	221/291~(75%)	0.24	11 (4%)	28	32	16, 26, 46, 107	0
2	В	145/173~(83%)	0.27	12 (8%)	11	12	14, 22, 50, 71	0
All	All	366/464~(78%)	0.25	23~(6%)	20	23	14, 24, 49, 107	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	46	GLY	11.6
2	В	23[A]	SER	10.9
1	А	223	VAL	9.1
2	В	164	ILE	8.2
2	В	21[A]	LEU	7.4
2	В	25	PRO	7.3
1	А	196	ASP	6.7
1	А	197	ALA	6.3
2	В	24[A]	GLY	5.4
2	В	165	GLY	5.1
2	В	22[A]	ARG	4.8
1	А	271	ILE	4.4
2	В	125	PRO	4.1
1	А	203	SER	4.1
1	А	147	SER	3.9
1	А	224	GLU	3.6
1	А	146	GLY	3.1
2	В	127	PRO	3.1
2	В	49[A]	TRP	2.3
2	В	126	GLN	2.2
1	А	225	THR	2.2
2	В	123	ARG	2.0
1	А	88	ALA	2.0



#### 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,  $95^{th}$  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	${f B} ext{-factors}({ m \AA}^2)$	Q<0.9
3	CL	В	1166	1/1	0.99	0.06	28,28,28,28	1
4	NA	В	1167	1/1	0.99	0.05	27,27,27,27	1

#### 6.5 Other polymers (i)

There are no such residues in this entry.

