



# Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 08:45 am BST

PDB ID : 5WZ3  
Title : Crystal structure of Zika virus NS5 RNA-dependent RNA polymerase(RdRP)  
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Deposited on : 2017-01-16  
Resolution : 1.80 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.

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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  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

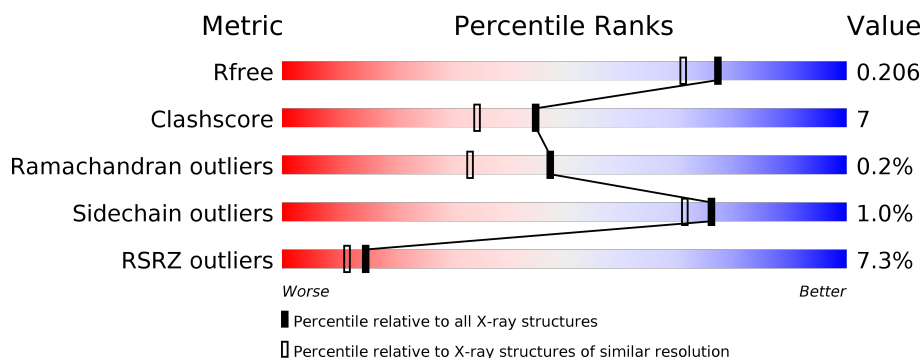
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.80 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))
$R_{free}$	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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 on 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  $\leq 5\%$ . 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	619	<div> <div>7%</div> <div>82%</div> <div>9%</div> <div>9%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5146 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 NS5 RdRp.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	565	Total	C	N	O	S	0	1	0
			4641	2929	845	837	30			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	269	HIS	-	expression tag	UNP A0A1B2ZC85
A	270	HIS	-	expression tag	UNP A0A1B2ZC85
A	271	HIS	-	expression tag	UNP A0A1B2ZC85
A	272	HIS	-	expression tag	UNP A0A1B2ZC85
A	273	HIS	-	expression tag	UNP A0A1B2ZC85
A	274	HIS	-	expression tag	UNP A0A1B2ZC85

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

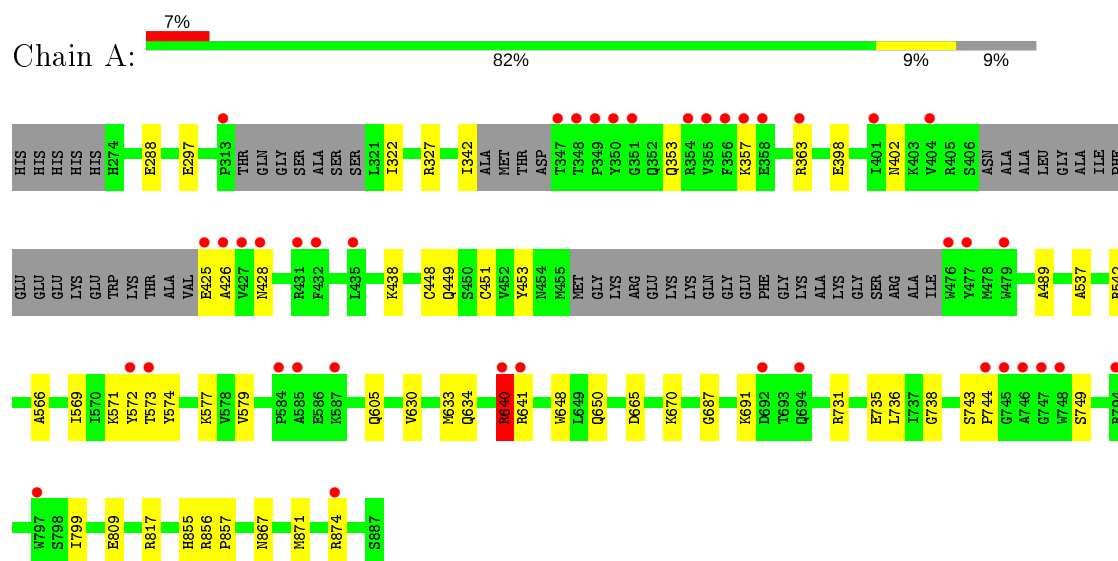
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Zn	0	0
			2	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	503	Total	O	0	0
			503	503		



- Molecule 1: NS5 RdRp



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	63.53Å 84.85Å 69.20Å 90.00° 113.37° 90.00°	Depositor
Resolution (Å)	34.16 – 1.80 34.16 – 1.80	Depositor EDS
% Data completeness (in resolution range)	98.5 (34.16-1.80) 98.5 (34.16-1.80)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.70 (at 1.81Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.178 , 0.206 0.180 , 0.206	Depositor DCC
$R_{free}$ test set	2953 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	18.4	Xtriage
Anisotropy	0.026	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 51.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5146	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.78% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<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.

## 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: ZN

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	0.31	0/4755	0.50	0/6429

There are no bond length outliers.

There are no bond angle outliers.

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	4641	0	4526	60	0
2	A	2	0	0	0	0
3	A	503	0	0	13	1
All	All	5146	0	4526	60	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 7.

All (60) 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:634:GLN:HE21	1:A:640:ARG:CD	1.13	1.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:634:GLN:NE2	1:A:640:ARG:HD3	1.26	1.40
1:A:633:MET:SD	3:A:1466:HOH:O	2.06	1.12
1:A:634:GLN:NE2	1:A:640:ARG:CD	1.97	1.02
1:A:634:GLN:HG2	1:A:640:ARG:NE	1.78	0.99
1:A:634:GLN:HE21	1:A:640:ARG:NE	1.62	0.98
1:A:438:LYS:NZ	3:A:1002:HOH:O	2.01	0.92
1:A:634:GLN:CG	1:A:640:ARG:NE	2.33	0.92
1:A:634:GLN:HG3	1:A:640:ARG:NH2	1.88	0.88
1:A:749:SER:HB2	3:A:1285:HOH:O	1.73	0.87
1:A:634:GLN:HG3	1:A:640:ARG:CZ	2.04	0.86
1:A:634:GLN:CG	1:A:640:ARG:CZ	2.53	0.86
1:A:634:GLN:HE21	1:A:640:ARG:HD3	0.69	0.85
1:A:634:GLN:HG2	1:A:640:ARG:HE	1.38	0.85
1:A:449:GLN:NE2	3:A:1002:HOH:O	2.11	0.84
1:A:855:HIS:CD2	1:A:857:PRO:HD2	2.15	0.82
1:A:867:ASN:OD1	3:A:1001:HOH:O	1.97	0.80
1:A:633:MET:HE2	3:A:1016:HOH:O	1.85	0.77
1:A:855:HIS:HD2	1:A:857:PRO:HD2	1.50	0.76
1:A:650:GLN:OE1	3:A:1003:HOH:O	2.05	0.75
1:A:453:TYR:OH	1:A:605:GLN:NE2	2.21	0.72
1:A:871:MET:HA	1:A:874:ARG:HE	1.54	0.72
1:A:322:ILE:HG21	1:A:327:ARG:HD3	1.72	0.70
1:A:537:ALA:HA	1:A:691:LYS:HE3	1.75	0.68
1:A:634:GLN:NE2	1:A:640:ARG:NE	2.32	0.66
1:A:871:MET:O	1:A:874:ARG:HG2	1.97	0.65
1:A:297:GLU:OE1	3:A:1004:HOH:O	2.15	0.63
1:A:342:ILE:HD13	1:A:735:GLU:OE1	1.99	0.62
1:A:634:GLN:HE22	1:A:640:ARG:HD3	1.50	0.62
1:A:426:ALA:N	3:A:1011:HOH:O	2.32	0.61
1:A:428:ASN:O	1:A:428:ASN:OD1	2.19	0.61
1:A:363:ARG:HG3	1:A:363:ARG:HH11	1.66	0.60
1:A:874:ARG:NH2	3:A:1010:HOH:O	2.31	0.59
1:A:398:GLU:O	1:A:402:ASN:ND2	2.38	0.55
1:A:363:ARG:HD2	3:A:1369:HOH:O	2.06	0.54
1:A:670:LYS:NZ	3:A:1018:HOH:O	2.41	0.54
1:A:353:GLN:O	1:A:357:LYS:HD2	2.09	0.53
1:A:630:VAL:HG21	1:A:648:TRP:CD1	2.45	0.52
1:A:448:CYS:SG	1:A:451:CYS:HB2	2.50	0.51
1:A:855:HIS:HD2	1:A:856:ARG:N	2.08	0.51
1:A:342:ILE:HD12	1:A:738:GLY:HA3	1.94	0.50
1:A:569:ILE:O	1:A:573:THR:HB	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:856:ARG:HB3	1:A:857:PRO:HD3	1.94	0.48
1:A:634:GLN:CG	1:A:640:ARG:NH2	2.67	0.48
1:A:871:MET:HA	1:A:874:ARG:NE	2.27	0.46
1:A:634:GLN:NE2	1:A:640:ARG:CZ	2.80	0.45
1:A:542:ARG:HD3	1:A:687:GLY:O	2.16	0.44
1:A:363:ARG:CG	1:A:363:ARG:HH11	2.30	0.44
1:A:731:ARG:HD3	1:A:736:LEU:HD21	1.99	0.44
1:A:398:GLU:HG2	1:A:398:GLU:H	1.66	0.43
1:A:453:TYR:HB2	1:A:579:VAL:HG22	1.99	0.43
1:A:634:GLN:CD	1:A:640:ARG:NE	2.71	0.43
1:A:855:HIS:C	1:A:855:HIS:CD2	2.93	0.42
1:A:855:HIS:CD2	1:A:856:ARG:N	2.86	0.42
1:A:489:ALA:HB1	1:A:566:ALA:HA	2.02	0.42
1:A:809:GLU:CD	1:A:817:ARG:HH22	2.23	0.42
1:A:665:ASP:OD1	3:A:1005:HOH:O	2.20	0.41
1:A:743:SER:HA	1:A:744:PRO:HD3	1.82	0.41
1:A:574:TYR:O	1:A:577:LYS:NZ	2.53	0.41
1:A:571:LYS:HZ3	1:A:572:TYR:HE1	1.68	0.41

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)
3:A:1212:HOH:O	3:A:1445:HOH:O[2_858]	2.12	0.08

## 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	556/619 (90%)	541 (97%)	14 (2%)	1 (0%)	47 33

All (1) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	A	640	ARG

### 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	497/538 (92%)	492 (99%)	5 (1%)	76 71

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	288	GLU
1	A	425	GLU
1	A	640	ARG
1	A	641	ARG
1	A	799	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	605	GLN
1	A	634	GLN
1	A	855	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 carbohydrates 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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	565/619 (91%)	0.03	41 (7%) 15 11	6, 23, 63, 107	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	350	TYR	9.2
1	A	477	TYR	7.1
1	A	640	ARG	6.9
1	A	351	GLY	6.7
1	A	347	THR	6.2
1	A	746	ALA	5.9
1	A	348	THR	5.6
1	A	476	TRP	4.8
1	A	354	ARG	4.6
1	A	431	ARG	4.5
1	A	425	GLU	4.3
1	A	355	VAL	4.3
1	A	641	ARG	4.1
1	A	428	ASN	3.8
1	A	748	TRP	3.7
1	A	349	PRO	3.7
1	A	357	LYS	3.7
1	A	404	VAL	3.6
1	A	363	ARG	3.5
1	A	747	GLY	3.5
1	A	745	GLY	3.2
1	A	479	TRP	3.0
1	A	692	ASP	3.0
1	A	313	PRO	3.0
1	A	572	TYR	2.9
1	A	797	TRP	2.9
1	A	744	PRO	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	694	GLN	2.6
1	A	358	GLU	2.6
1	A	427	VAL	2.6
1	A	401	ILE	2.4
1	A	874	ARG	2.3
1	A	356	PHE	2.2
1	A	585	ALA	2.2
1	A	587	LYS	2.2
1	A	426	ALA	2.2
1	A	432	PHE	2.1
1	A	584	PRO	2.1
1	A	435	LEU	2.1
1	A	573	THR	2.0
1	A	794	ARG	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 carbohydrates 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<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
2	ZN	A	902	1/1	0.97	0.06	22,22,22,22	0
2	ZN	A	901	1/1	1.00	0.04	14,14,14,14	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.