



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 23, 2017 – 03:37 PM EDT

PDB ID : 5G52
Title : Crystallographic structure of full particle of Deformed Wing Virus
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Deposited on : 2016-05-18
Resolution : 3.80 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20029077
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029077

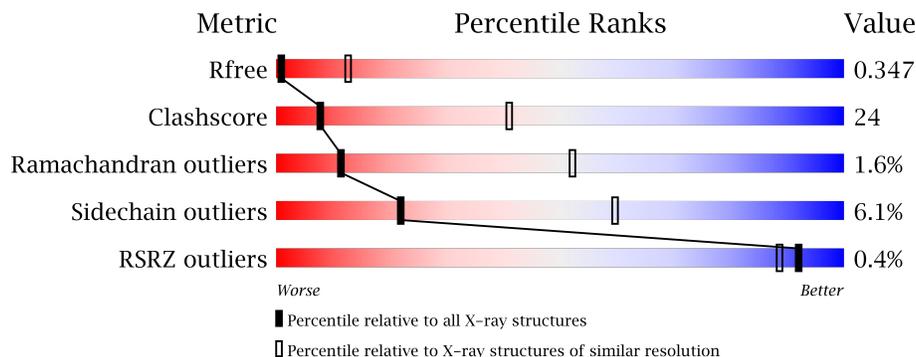
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.80 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}	100719	1019 (4.08-3.52)
Clashscore	112137	1030 (4.04-3.56)
Ramachandran outliers	110173	1011 (4.06-3.54)
Sidechain outliers	110143	1005 (4.06-3.54)
RSRZ outliers	101464	1032 (4.08-3.52)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	243	 .%
2	B	250	
3	C	397	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7045 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 VP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	243	1910	1217	326	357	10	0	0	0

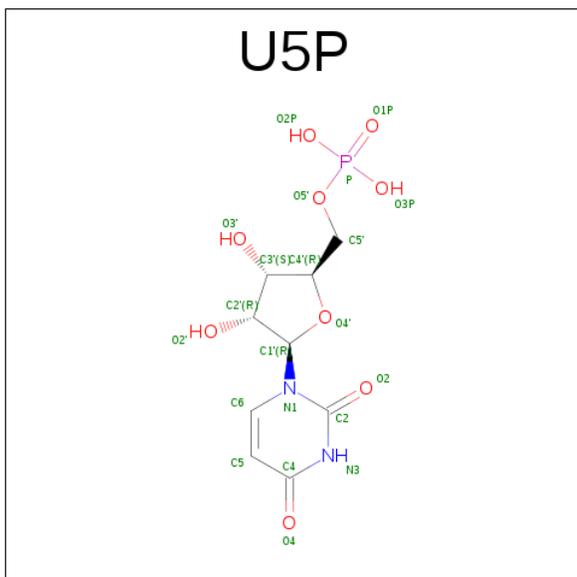
- Molecule 2 is a protein called VP2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	250	1973	1253	335	378	7	0	0	0

- Molecule 3 is a protein called VP3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	397	3142	2015	541	574	12	0	0	0

- Molecule 4 is URIDINE-5'-MONOPHOSPHATE (three-letter code: U5P) (formula: C₉H₁₃N₂O₉P).

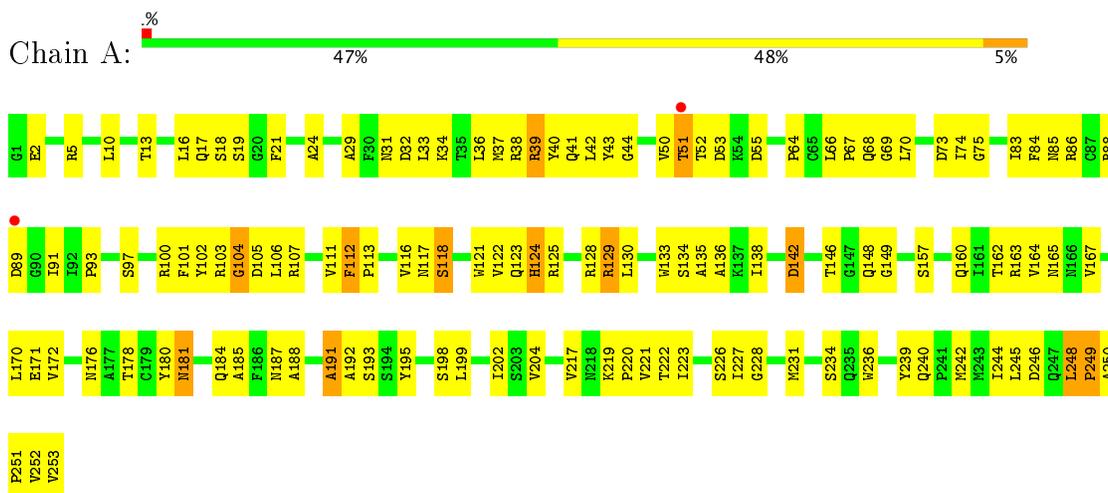


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
4	C	1	20	9	2	8	1	0	0

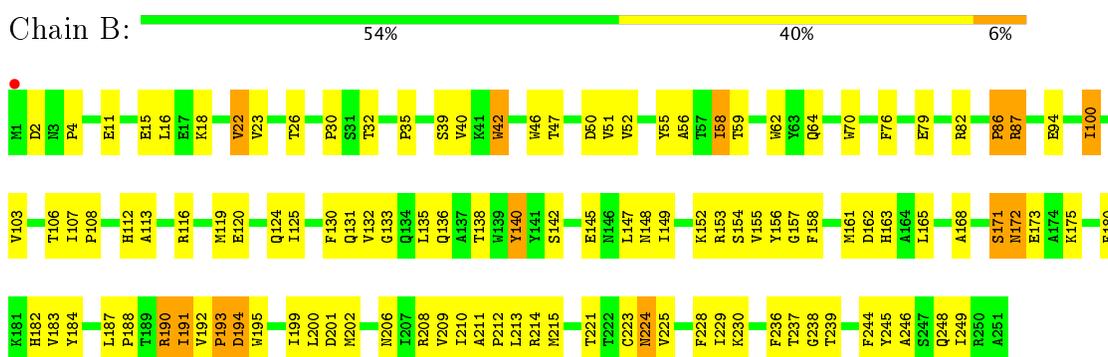
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

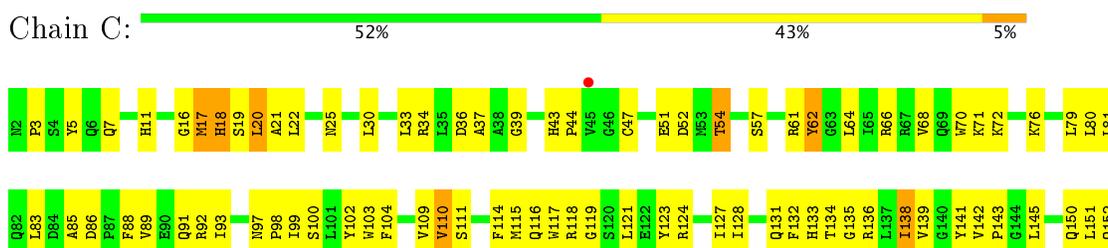
- Molecule 1: VP1



- Molecule 2: VP2



- Molecule 3: VP3



M153	M154	M155	M156	M157	M158	M159	M160	Y163	Y164	Y165	Y166	Y167	Y168	N172	N173	N174	Y178	Y179	Y180	Y183	R184	P185	W186	W187	Y188	R189	K190	Y191	G192	G193	N194	Y195	L196	P197	T200	P203	S204	T205	L206	F207	W208	Y209	W210	Q211	Y212	P213	L214	Y220	S221	D222	T223	I224
D225	I226	W227	W228	Y229	W230	R231	G232	G233	F236	E237	W238	C239	V240	Q243	P244	S245	L246	G247	W248	W249	W250	D253	F254	I255	L256	R257	W258	D259	E260	E261	Y262	R263	A264	A269	P270	Y271	Y272	A273	C274	Y275	W276	H277	S278	S284	L285	S303	E308	L309	L312	R313		
Y322	G323	T324	T329	N330	W333	P334	S335	Y339	N340	I341	A348	E349	R350	A355	Q356	H357	L364	A369	L372	F373	Q378	Q379	K383	N388	P389	V390	W391	E392	Y393	N394	R395	A396	F397	L398																		

4 Data and refinement statistics

Property	Value	Source
Space group	I 2 3	Depositor
Cell constants a, b, c, α , β , γ	360.13Å 360.13Å 360.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.80 – 3.80 29.80 – 3.80	Depositor EDS
% Data completeness (in resolution range)	75.0 (29.80-3.80) 75.0 (29.80-3.80)	Depositor EDS
R_{merge}	0.37	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.34 (at 3.75Å)	Xtrriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.283 , 0.322 0.331 , 0.347	Depositor DCC
R_{free} test set	2844 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	53.4	Xtrriage
Anisotropy	0.000	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	3.36 , 1.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.23$	Xtrriage
Estimated twinning fraction	0.048 for -l,-k,-h	Xtrriage
F_o, F_c correlation	0.66	EDS
Total number of atoms	7045	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.78% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² 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: U5P

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	0.32	0/1957	0.71	1/2660 (0.0%)
2	B	0.31	0/2024	0.64	3/2763 (0.1%)
3	C	0.28	0/3238	0.53	1/4418 (0.0%)
All	All	0.30	0/7219	0.61	5/9841 (0.1%)

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
1	A	0	1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	86	PRO	C-N-CA	5.97	136.62	121.70
2	B	86	PRO	CA-C-N	5.57	129.45	117.20
1	A	191	ALA	C-N-CA	5.38	135.15	121.70
2	B	171	SER	C-N-CA	5.35	135.08	121.70
3	C	168	LEU	CA-CB-CG	5.07	126.95	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	104	GLY	Peptide

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	1910	0	1851	126	0
2	B	1973	0	1928	95	0
3	C	3142	0	3051	162	0
4	C	20	0	11	0	0
All	All	7045	0	6841	336	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 24.

The worst 5 of 336 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:191:ALA:H	1:A:192:ALA:HB3	1.33	0.92
1:A:133:TRP:HB2	2:B:147:LEU:HD11	1.54	0.89
2:B:55:TYR:HH	2:B:112:HIS:HE2	1.19	0.88
1:A:192:ALA:HB2	2:B:194:ASP:HB3	1.55	0.88
1:A:38:ARG:HB3	1:A:39:ARG:HA	1.60	0.84

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
1	A	239/243 (98%)	183 (77%)	49 (20%)	7 (3%)	5 41
2	B	248/250 (99%)	204 (82%)	40 (16%)	4 (2%)	11 52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	395/397 (100%)	339 (86%)	53 (13%)	3 (1%)	22	65
All	All	882/890 (99%)	726 (82%)	142 (16%)	14 (2%)	11	52

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	29	ALA
1	A	118	SER
1	A	193	SER
2	B	87	ARG
2	B	172	ASN

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	207/207 (100%)	199 (96%)	8 (4%)	37	70
2	B	221/221 (100%)	204 (92%)	17 (8%)	15	52
3	C	338/338 (100%)	316 (94%)	22 (6%)	20	57
All	All	766/766 (100%)	719 (94%)	47 (6%)	22	60

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	194	ASP
3	C	17	MET
3	C	240	VAL
2	B	239	THR
3	C	18	HIS

Some 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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	U5P	C	1399	-	14,21,22	1.14	1 (7%)	15,30,33	4.34	2 (13%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	U5P	C	1399	-	-	0/3/25/26	0/2/2/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	1399	U5P	C4-N3	2.87	1.38	1.33

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	1399	U5P	C5-C4-N3	-3.80	114.05	123.12
4	C	1399	U5P	C4-N3-C2	16.15	128.00	114.13

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	206:PHE	C	217:VAL	N	14.19

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	243/243 (100%)	0.03	2 (0%) 86 79	23, 43, 77, 107	0
2	B	250/250 (100%)	-0.06	1 (0%) 92 88	22, 39, 58, 120	0
3	C	397/397 (100%)	0.03	1 (0%) 93 91	20, 43, 85, 98	0
All	All	890/890 (100%)	0.01	4 (0%) 92 88	20, 42, 80, 120	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	51	THR	2.7
2	B	1	MET	2.4
1	A	89	ASP	2.1
3	C	45	VAL	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
4	U5P	C	1399	20/21	0.89	0.29	-	41,98,100,101	0

6.5 Other polymers [i](#)

There are no such residues in this entry.