



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:54 AM GMT

PDB ID : 2V8O
Title : STRUCTURE OF THE MURRAY VALLEY ENCEPHALITIS VIRUS RNA
HELICASE TO 1.9A RESOLUTION
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Deposited on : 2007-08-09
Resolution : 1.90 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
<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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

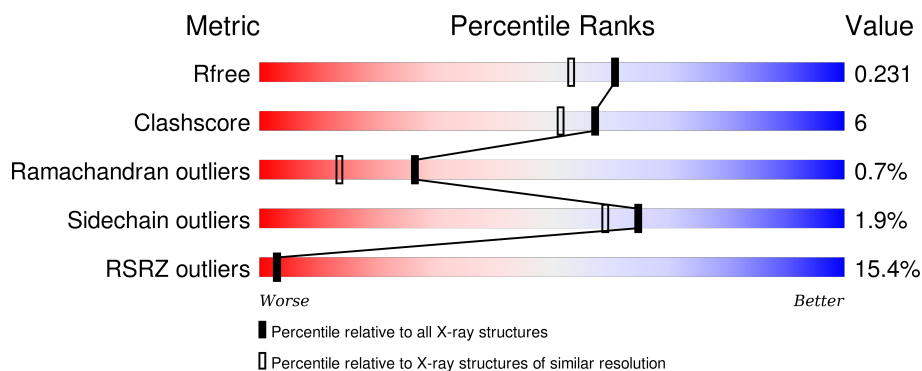
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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}	91344	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

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	444	<div> <div>15%</div> <div>84%</div> <div>11%</div> <div>••</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3667 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 FLAVIVIRIN PROTEASE NS3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	429	Total	C	N	O	S	0	0	0
			3383	2129	605	634	15			

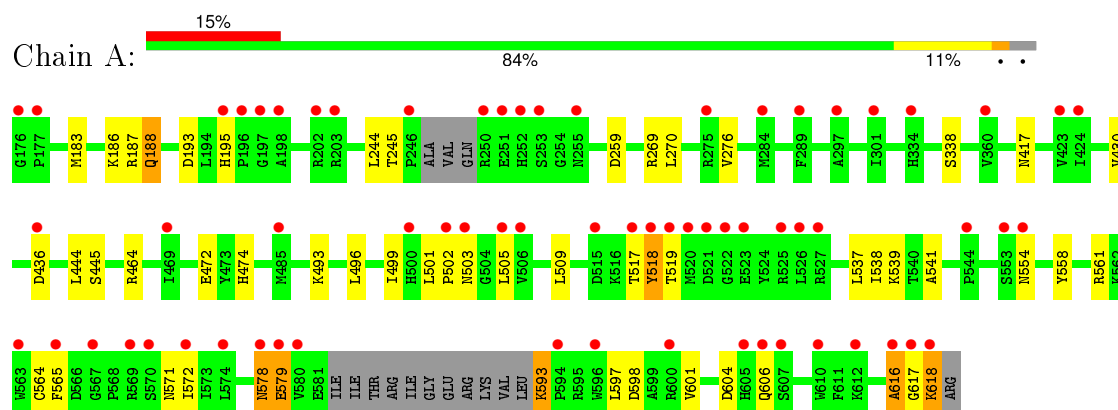
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	284	Total	O	0	0
			284	284		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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: FLAVIVIRIN PROTEASE NS3



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	42.52Å 76.41Å 70.61Å 90.00° 91.73° 90.00°	Depositor
Resolution (Å)	70.53 – 1.90 28.41 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.9 (70.53-1.90) 99.9 (28.41-1.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.35 (at 1.91Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.180 , 0.223 0.188 , 0.231	Depositor DCC
R_{free} test set	1789 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	31.5	Xtriage
Anisotropy	0.036	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 62.8	EDS
Estimated twinning fraction	0.029 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 35616 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3667	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.20% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

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	0.44	0/3460	0.61	0/4693

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	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	436	ASP	Peptide
1	A	593	LYS	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	3383	0	3338	40	0
2	A	284	0	0	1	0
All	All	3667	0	3338	40	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 6.

All (40) 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:616:ALA:HB3	1:A:617:GLY:HA3	1.42	1.02
1:A:417:ASN:HD22	1:A:464:ARG:HH12	1.05	0.96
1:A:616:ALA:CB	1:A:617:GLY:HA3	2.00	0.92
1:A:417:ASN:ND2	1:A:464:ARG:HH12	1.71	0.89
1:A:417:ASN:HD22	1:A:464:ARG:NH1	1.77	0.81
1:A:616:ALA:HB3	1:A:617:GLY:CA	2.21	0.69
1:A:564:CYS:O	1:A:593:LYS:CB	2.44	0.65
1:A:501:LEU:HD23	1:A:505:LEU:HB3	1.79	0.64
1:A:616:ALA:CB	1:A:617:GLY:CA	2.74	0.64
1:A:270:LEU:HD23	1:A:276:VAL:HG21	1.80	0.63
1:A:571:ASN:HA	1:A:597:LEU:HD11	1.80	0.63
1:A:517:THR:O	1:A:518:TYR:HB2	1.99	0.62
1:A:564:CYS:O	1:A:593:LYS:HB2	2.00	0.60
1:A:193:ASP:OD1	1:A:195:HIS:CE1	2.56	0.59
1:A:269:ARG:HG2	1:A:276:VAL:HG22	1.84	0.59
1:A:270:LEU:HB3	1:A:499:ILE:HG23	1.87	0.57
1:A:183:MET:HA	1:A:188:GLN:HG2	1.89	0.55
1:A:244:LEU:HD11	1:A:259:ASP:HB3	1.90	0.54
1:A:598:ASP:O	1:A:601:VAL:HG22	2.08	0.54
1:A:572:ILE:HG21	1:A:579:GLU:HG2	1.92	0.52
1:A:195:HIS:CE1	2:A:2021:HOH:O	2.63	0.52
1:A:564:CYS:O	1:A:593:LYS:HB3	2.09	0.52
1:A:244:LEU:CD1	1:A:259:ASP:HB3	2.41	0.52
1:A:472:GLU:OE1	1:A:474:HIS:HE1	1.93	0.51
1:A:430:VAL:HG13	1:A:445:SER:O	2.10	0.50
1:A:417:ASN:ND2	1:A:464:ARG:NH1	2.47	0.48
1:A:244:LEU:HD12	1:A:244:LEU:N	2.28	0.48
1:A:565:PHE:HA	1:A:593:LYS:HB3	1.95	0.47
1:A:578:ASN:HB3	1:A:579:GLU:O	2.16	0.46
1:A:338:SER:OG	1:A:474:HIS:HD2	1.98	0.46
1:A:617:GLY:CA	1:A:618:LYS:C	2.83	0.46
1:A:558:TYR:O	1:A:561:ARG:NH1	2.49	0.45
1:A:493:LYS:HZ1	1:A:519:THR:HG23	1.81	0.45
1:A:430:VAL:CG1	1:A:444:LEU:HB3	2.48	0.43
1:A:186:LYS:O	1:A:187:ARG:HB2	2.19	0.42
1:A:496:LEU:HD22	1:A:509:LEU:HD23	2.01	0.42
1:A:493:LYS:NZ	1:A:519:THR:HG23	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:537:LEU:O	1:A:541:ALA:HB3	2.20	0.41
1:A:538:ILE:HG13	1:A:539:LYS:N	2.36	0.41
1:A:604:ASP:OD1	1:A:606:GLN:HG2	2.22	0.40

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	423/444 (95%)	405 (96%)	15 (4%)	3 (1%)	26 14

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	502	PRO
1	A	616	ALA
1	A	518	TYR

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	360/373 (96%)	353 (98%)	7 (2%)	65 59

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

Mol	Chain	Res	Type
1	A	188	GLN
1	A	245	THR
1	A	503	ASN
1	A	554	ASN
1	A	578	ASN
1	A	579	GLU
1	A	618	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	188	GLN
1	A	195	HIS
1	A	370	ASN
1	A	417	ASN
1	A	474	HIS
1	A	554	ASN
1	A	578	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 carbohydrates 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 ⓘ

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, 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	429/444 (96%)	1.01	66 (15%) 3 3	31, 42, 78, 100	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	197	GLY	9.6
1	A	617	GLY	8.0
1	A	580	VAL	7.7
1	A	198	ALA	7.4
1	A	616	ALA	6.9
1	A	196	PRO	6.4
1	A	518	TYR	5.7
1	A	195	HIS	5.7
1	A	519	THR	5.6
1	A	578	ASN	5.4
1	A	520	MET	5.3
1	A	500	HIS	4.9
1	A	565	PHE	4.6
1	A	502	PRO	4.1
1	A	255	ASN	4.1
1	A	610	TRP	3.9
1	A	618	LYS	3.9
1	A	594	PRO	3.9
1	A	574	LEU	3.8
1	A	569	ARG	3.8
1	A	521	ASP	3.6
1	A	605	HIS	3.6
1	A	572	ILE	3.6
1	A	436	ASP	3.5
1	A	517	THR	3.5
1	A	250	ARG	3.4
1	A	469	ILE	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	554	ASN	3.4
1	A	570	SER	3.4
1	A	563	TRP	3.2
1	A	275	ARG	3.2
1	A	252	HIS	3.1
1	A	176	GLY	3.1
1	A	423	VAL	3.1
1	A	506	VAL	3.0
1	A	246	PRO	3.0
1	A	515	ASP	3.0
1	A	567	GLY	2.9
1	A	485	MET	2.9
1	A	553	SER	2.9
1	A	522	GLY	2.8
1	A	505	LEU	2.7
1	A	301	ILE	2.7
1	A	526	LEU	2.7
1	A	202	ARG	2.7
1	A	527	ARG	2.7
1	A	203	ARG	2.7
1	A	334	HIS	2.7
1	A	360	VAL	2.6
1	A	297	ALA	2.6
1	A	289	PHE	2.6
1	A	579	GLU	2.5
1	A	525	ARG	2.4
1	A	424	ILE	2.3
1	A	253	SER	2.3
1	A	544	PRO	2.2
1	A	284	MET	2.2
1	A	177	PRO	2.2
1	A	600	ARG	2.2
1	A	503	ASN	2.1
1	A	251	GLU	2.1
1	A	523	GLU	2.1
1	A	596	TRP	2.1
1	A	606	GLN	2.1
1	A	612	LYS	2.0
1	A	607	SER	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.