



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 14, 2026 – 03:35 PM UTC

PDB ID : 5GVU / pdb_00005gvu
Title : crystal structure of BVDV NS3 helicase domain
Authors : Li, S.; Mao, X.
Deposited on : 2016-09-06
Resolution : 2.82 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

<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>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

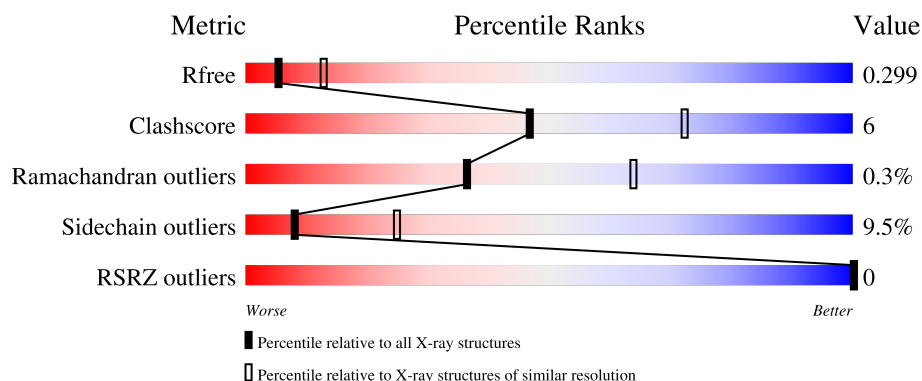
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.82 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}	180053	4591 (2.84-2.80)
Clashscore	190562	5010 (2.84-2.80)
Ramachandran outliers	187476	4916 (2.84-2.80)
Sidechain outliers	187428	4918 (2.84-2.80)
RSRZ outliers	180081	4594 (2.84-2.80)

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 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 $\leq 5\%$. 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	476	 77% 17% • 5%
1	B	476	 58% 14% • 25%
1	C	476	 64% 13% • 21%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9452 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 NS3 helicase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	454	Total	C	N	O	S	0	0	0
			3596	2289	609	680	18			
1	B	355	Total	C	N	O	S	0	0	0
			2824	1792	481	537	14			
1	C	377	Total	C	N	O	S	0	0	0
			2994	1902	512	565	15			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	15	Total	O	0	0
			15	15		
2	B	13	Total	O	0	0
			13	13		
2	C	10	Total	O	0	0
			10	10		

GLY	ARG	VAL	LYS	PRO	GLY	ARG	TYR	Y516	Q519	E520	T521	A522	D531	D542	L566	I567	T568	Q569	L570	D581	L582	P583	L601	E607	F614	P615	K616	E627	R635	E639	D640	V643	Y644	I645	Y646	A647	Q679	L683															
ASP	PRO	ALA	ASN	LEU	ARG	VAL	VAL	THR	THR	SER	GLN	SER	PRO	TYR	VAL	ILE	V449	A450	T451	R452	ALA	ILE	GLU	SER	GLY	VAL	THR	LEU	PRO	ASP	LEU	ASP	THR	VAL	ILE	D468	K472	C473	R476	V479	F485	I486	V487	K491	A494	V495	T496	V497	G498	E499	G505	R506	VAL
THR	THR	GLY	GLN	LYS	HIS	PRO	PRO	ILE	GLU	GLU	PHE	ILE	ALA	ALA	ASP	LEU	GLY	SER	GLY	GLN	PHE	LEU	ASP	ILE	ALA	GLY	LEU	LYS	ILE	PRO	VAL	LYS	ILE	PRO	PRO	VAL	ASP	ASP	ASP	VAL	ASP	GLU	MET	LYS	ASN	GLY	TYR	TYR	SER	GLY	GLU		
E208	I213	G219	T228	G231	K232	E235	L236	P237	I241	R246	H247	K248	R249	V250	R257	Y266	P267	R268	L269	K270	I274	T290	G291	I292	A310	A311	M312	V313	E314	L320	Q330	I334	I337	S341	A348	P353	ALA	GLY	SER	VAL													

4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	121.10Å 121.10Å 109.72Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.01 – 2.82 50.01 – 2.82	Depositor EDS
% Data completeness (in resolution range)	99.9 (50.01-2.82) 99.9 (50.01-2.82)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.90 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.8.0124, REFMAC 5.8.0124	Depositor
R, R_{free}	0.272 , 0.298 0.272 , 0.299	Depositor DCC
R_{free} test set	2121 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	48.6	Xtriage
Anisotropy	0.015	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 27.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.20$	Xtriage
Estimated twinning fraction	0.119 for -h,-k,l 0.119 for h,-h-k,-l 0.390 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9452	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.84% 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, 0.333 respectively for untwinned datasets, and 0.375, 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	0.58	0/3661	0.99	1/4949 (0.0%)
1	B	0.56	0/2875	1.03	3/3886 (0.1%)
1	C	0.59	0/3046	1.01	3/4115 (0.1%)
All	All	0.58	0/9582	1.01	7/12950 (0.1%)

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	634	ALA	N-CA-C	6.62	119.07	110.53
1	C	290	THR	N-CA-C	6.61	119.49	111.82
1	B	497	VAL	N-CA-C	6.01	116.80	110.72
1	A	634	ALA	N-CA-C	5.81	119.08	110.48
1	C	499	GLU	N-CA-C	5.39	119.57	113.15

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	3596	0	3626	41	0
1	B	2824	0	2833	40	0
1	C	2994	0	3025	29	0
2	A	15	0	0	0	0
2	B	13	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	10	0	0	0	0
All	All	9452	0	9484	108	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.

The worst 5 of 108 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:B:635:ARG:NH2	1:B:640:ASP:O	2.15	0.79
1:A:463:LEU:HG	1:A:507:VAL:HG12	1.64	0.78
1:B:312:MET:HE2	1:B:337:ILE:HG21	1.67	0.77
1:C:616:LYS:HE3	1:C:627:GLU:CD	2.13	0.73
1:C:476:ARG:HH11	1:C:476:ARG:HG3	1.53	0.72

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	442/476 (93%)	426 (96%)	14 (3%)	2 (0%)	24	53
1	B	347/476 (73%)	333 (96%)	14 (4%)	0	100	100
1	C	367/476 (77%)	353 (96%)	13 (4%)	1 (0%)	36	64
All	All	1156/1428 (81%)	1112 (96%)	41 (4%)	3 (0%)	36	64

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	505	GLY
1	A	231	GLY

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Mol	Chain	Res	Type
1	A	406	PRO

5.3.2 Protein sidechains ⓘ

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	391/407 (96%)	353 (90%)	38 (10%)	8	24
1	B	307/407 (75%)	279 (91%)	28 (9%)	9	27
1	C	325/407 (80%)	294 (90%)	31 (10%)	8	25
All	All	1023/1221 (84%)	926 (90%)	97 (10%)	8	25

5 of 97 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	582	LEU
1	C	268	ARG
1	B	592	ARG
1	B	683	LEU
1	C	468	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	265	GLN
1	C	569	GLN
1	A	669	GLN
1	B	223	GLN
1	B	265	GLN

5.3.3 RNA ⓘ

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 oligosaccharides 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 [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	454/476 (95%)	-1.26	0 100 100	31, 56, 122, 133	0
1	B	355/476 (74%)	-1.52	0 100 100	21, 38, 85, 116	0
1	C	377/476 (79%)	-1.29	0 100 100	29, 55, 103, 115	0
All	All	1186/1428 (83%)	-1.35	0 100 100	21, 48, 110, 133	0

There are no RSRZ outliers to report.

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 oligosaccharides 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.