



wwPDB EM Validation Summary Report ⓘ

May 5, 2026 – 06:18 PM JST

PDB ID : 9VY1 / pdb_00009vy1
EMDB ID : EMD-65448
Title : Cryo-EM structure of Peste Des Petits Ruminants Virus L Protein bound by Phosphoprotein Tetramer
Authors : Xue, L.; Gui, J.; Chang, T.; Pan, H.; Xiong, X.
Deposited on : 2025-07-20
Resolution : 2.40 Å(reported)

This is a wwPDB EM 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/EMValidationReportHelp>
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:

EMDB validation analysis : **FAILED**
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

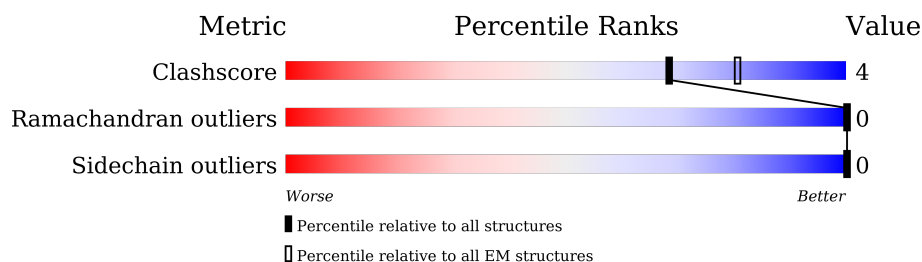
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.40 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)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	2183	
2	B	509	
2	C	509	
2	D	509	
2	E	509	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 11940 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 RNA-directed RNA polymerase L.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1146	Total	C	N	O	S	0	0
			9180	5891	1549	1688	52		

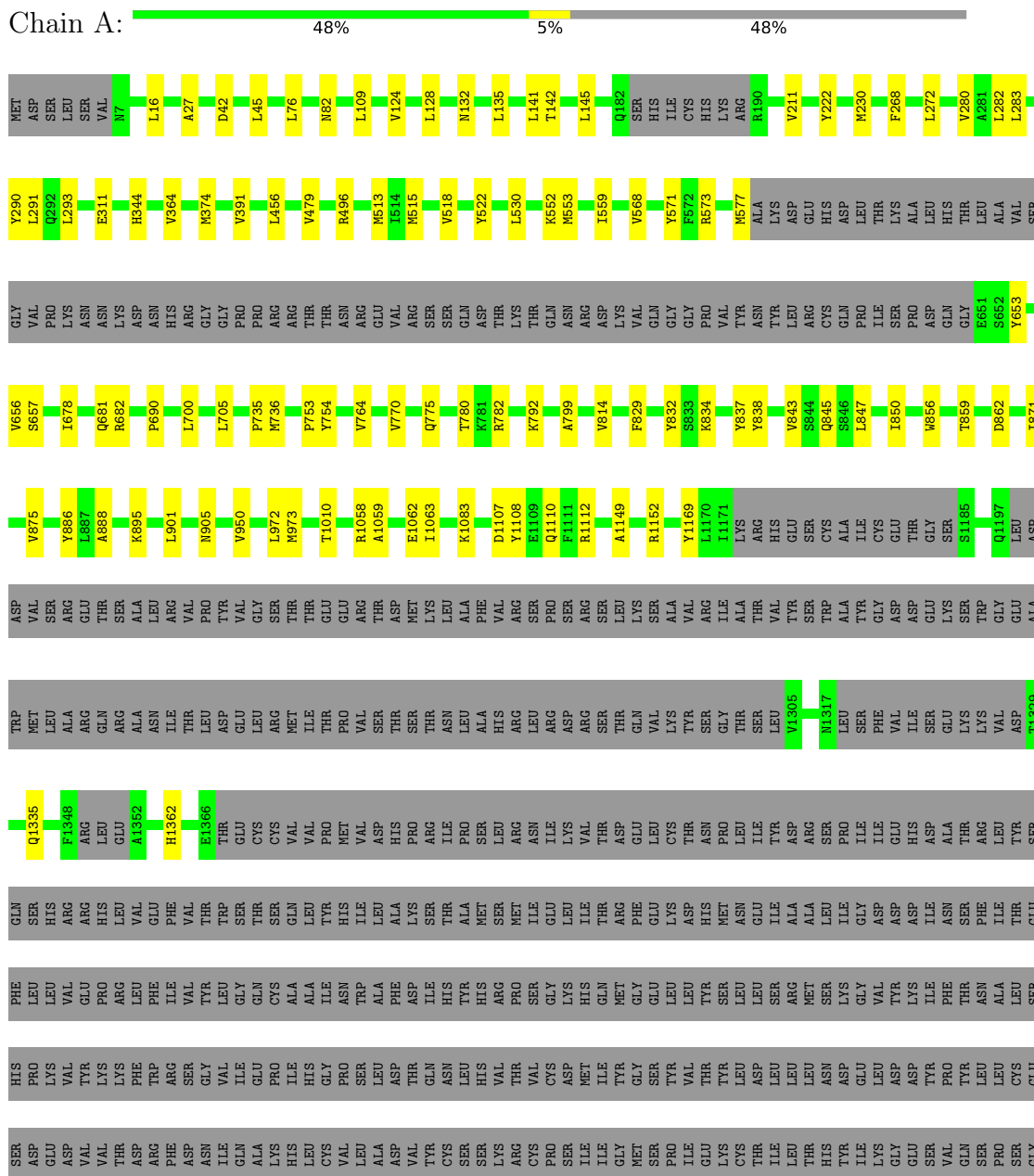
- Molecule 2 is a protein called Phosphoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	157	Total	C	N	O	S	1	0
			1221	771	216	232	2		
2	C	77	Total	C	N	O	S	0	0
			591	373	100	117	1		
2	D	59	Total	C	N	O	S	0	0
			452	286	77	88	1		
2	E	65	Total	C	N	O	S	0	0
			496	315	84	96	1		

3 Residue-property plots

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. 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. 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: RNA-directed RNA polymerase L



[illegible]

- Molecule 2: Phosphoprotein

Chain B: 27% 1% 69%

ALA	ASN	THR	ASP	GLU	ASN	MET
VAL	ASP	VAL	VAL	GLY	GLN	ALA
ASP	ASP	THR	GLU	LEU	SER	GLU
ARG	GLU	GLU	LYS	GLU	CYS	GLN
GLN	THR	CYS	LEU	ASP	SER	GLY
LYS	GLU	LEU	GLU	ASP	PRO	ALA
THR	THR	SER	GLY	ASP	ALA	TYR
ILE	GLU	ILE	ALA	SER	ILE	HIS
GLY	ASP	SER	ASP	LEU	GLY	VAL
THR	ASP	GLY	ILE	VAL	PRO	ASN
LYS	LEU	ALA	LYS	VAL	ASN	LYS
ALA	PHE	THR	GLU	GLN	LYS	GLY
ASN	LYS	GLN	VAL	ALA	VAL	LEU
SER	GLU	ALA	LEU	ASP	TYR	GLU
SER	ILE	VAL	ASN	PRO	LEU	CYS
SER	GLN	PRO	SER	GLN	SER	ILE
GLN	GLU	GLU	GLN	VAL	PRO	LYS
ASN	DS17	SER	LYS	ASP	GLY	SER
K430	A320	ARG	GLY	ASN	ASP	LEU
L434	S321	TRP	LYS	VAL	ASN	LYS
L437	I322	GLU	GLY	PHE	LEU	ALA
S459	A323	SER	GLY	GLY	GLY	ALA
V463	K324	SER	ARG	GLY	PHE	PRO
I464	I325	GLU	PHE	GLY	ARG	PRO
I468	H326	GLN	GLN	GLY	GLU	ASP
K478	S338	ASN	GLY	ASP	ILE	LEU
P509	I339	ALA	GLY	GLY	THR	SER
	P375	SER	THR	ASP	ASN	ILE
	GLY	GLY	LEU	ASP	ASP	ARG
	PHE	VAL	VAL	ARG	CYS	ASP
	GLY	LEU	PRO	VAL	GLU	THR
	ASP	LYS	LYS	VAL	ALA	ILE
	ILE	SER	ILE	GLU	GLY	GLU
	LYS	ALA	PRO	SER	LEU	SER
	ASP	SER	VAL	ASP	GLN	GLY
	PRO	ALA	LYS	ASP	GLN	GLY
	THR	GLU	HIS	PRO	LYS	LEU
	SER	THR	SER	SER	LYS	SER
	GLU	ILE	ARG	ARG	ARG	PRO
	VAL	GLN	PRO	ASP	SER	PRO
	GLU	GLY	SER	THR	ASN	GLY
	LEU	LEU	ALA	LEU	ASN	ARG
	ASN	THR	GLN	TYR	GLN	ALA
	PRO	GLN	SER	ASP	VAL	THR
	ASP	GLU	ILE	ARG	GLN	PRO
	L394	SER	LYS	GLY	ARG	ASN
	S399	GLY	GLY	SER	TYR	PRO
		THR	LYS	VAL	ASP	THR
		ILE	THR	ALA	VAL	THR
	G403	ALA	ASP	GLY	TYR	SER
	R404	SER	GLY	ASN	SER	GLU
	A405	LEU	ASN	VAL	HIS	GLY
		THR	SER	VAL	GLY	ASP
	L410	GLN	VAL	ALA	GLY	HIS
	LYS	PRO	SER	ARG	GLN	GLY
	PRO	GLY	SER	SER	GLY	THR
		THR	CYS	THR	THR	ILE

- Molecule 2: Phosphoprotein

Chain C:  13% 85%

MET	GLU	ALA	GLN	ALA	TYR	HIS	VAL	ASN	LYS	LEU	GLY	CYS	ILE	LYS	SER	LEU	LYS	ALA	PRO	ASP	ARG	ASP	THR	ILE	GLU	SER	TRP	ARG	GLU	GLY	LEU	PRO	SER	GLY	ALA	THR	PRO	ASP	THR	SER	GLU	GLY	HIS	GLN	SER	ILE
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	5435091	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor

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	0.16	0/9387	0.33	0/12715
2	B	0.16	0/1235	0.36	0/1655
2	C	0.18	0/595	0.39	0/799
2	D	0.22	0/454	0.55	0/609
2	E	0.19	0/499	0.40	0/668
All	All	0.17	0/12170	0.35	0/16446

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	9180	0	9151	60	0
2	B	1221	0	1308	12	0
2	C	591	0	627	11	0
2	D	452	0	493	9	0
2	E	496	0	536	9	0
All	All	11940	0	12115	89	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 4.

The worst 5 of 89 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:C:377:PHE:HA	2:D:370:ILE:HG13	1.64	0.79
2:B:399:SER:HB3	2:B:403:GLY:HA2	1.73	0.71
1:A:950:VAL:HG21	1:A:1335:GLN:HE21	1.58	0.67
1:A:530:LEU:HD13	1:A:700:LEU:HD21	1.78	0.64
1:A:770:VAL:HG22	1:A:775:GLN:HG3	1.79	0.64

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 PDB entries followed by that with respect to all EM entries.

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	1132/2183 (52%)	1104 (98%)	28 (2%)	0	100	100
2	B	152/509 (30%)	146 (96%)	6 (4%)	0	100	100
2	C	73/509 (14%)	70 (96%)	3 (4%)	0	100	100
2	D	57/509 (11%)	55 (96%)	2 (4%)	0	100	100
2	E	63/509 (12%)	62 (98%)	1 (2%)	0	100	100
All	All	1477/4219 (35%)	1437 (97%)	40 (3%)	0	100	100

There are no Ramachandran outliers to report.

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 PDB entries followed by that with respect to all EM entries.

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	1012/1937 (52%)	1012 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	143/436 (33%)	143 (100%)	0	100	100
2	C	70/436 (16%)	70 (100%)	0	100	100
2	D	54/436 (12%)	54 (100%)	0	100	100
2	E	58/436 (13%)	58 (100%)	0	100	100
All	All	1337/3681 (36%)	1337 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	326	HIS
2	E	329	ASN
1	A	1167	ASN
1	A	1335	GLN
1	A	1362	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 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 ⓘ

There are no chain breaks in this entry.