



Full wwPDB EM Validation 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 Full wwPDB EM Validation 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

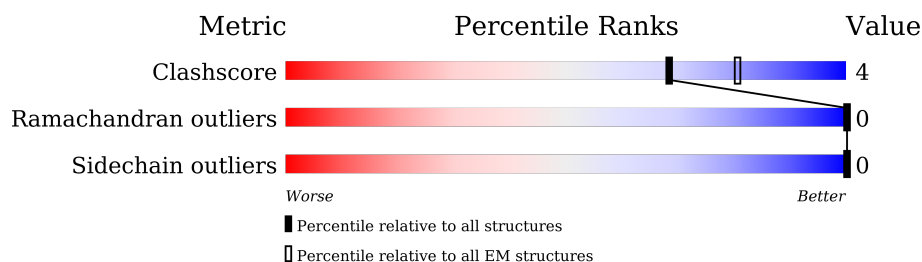
1 Overall quality at a glance

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		

[illegible]

- Molecule 2: Phosphoprotein

Chain B: 27% . 69%

ALA	ASP	ASN	THR	ASP	GLU	ASN	ASN	MET
VAL	ASP	ASP	VAL	VAL	GLY	GLN	GLN	ALA
ASP	ASP	ASP	THR	GLU	LEU	SER	SER	GLU
ARG	GLU	GLU	GLU	GLY	LYS	CYS	CYS	GLN
GLN	GLU	GLU	LEU	GLU	ASP	PRO	PRO	ALA
LYS	THR	THR	SER	GLY	ASP	ALA	ALA	TYR
ILE	ILE	ILE	ILE	ALA	SER	ILE	ILE	HIS
GLY	GLY	GLY	SER	ASP	LEU	GLY	GLY	VAL
THR	THR	THR	GLY	ILE	VAL	PRO	PRO	ASN
LYS	ASP	ASP	ALA	GLN	VAL	ASN	LYS	LYS
ALA	PHE	PHE	THR	GLU	GLN	LYS	GLY	GLY
ASN	LYS	LYS	GLN	VAL	ALA	VAL	VAL	LEU
SER	GLU	GLU	ALA	LEU	ASP	TYR	GLU	GLU
SER	ILE	ILE	VAL	ASN	PRO	LEU	CYS	GLY
S429	S429	D317	PRO	SER	PRO	SER	ILE	ILE
K430	K430	GLN	GLU	GLN	VAL	PRO	LYS	LYS
L434	L434	SER	ARG	GLY	ASN	GLY	ASP	SER
L437	L437	THR	THR	LYS	ASN	ASN	ASP	LEU
S459	S459	GLU	GLU	GLY	PHE	LEU	LYS	ALA
V463	V463	SER	SER	GLY	GLY	ASN	GLY	SER
I464	I464	GLU	GLU	PHE	GLY	PHE	ASP	PRO
I468	I468	GLN	GLN	GLN	GLY	GLU	GLU	PRO
K478	K478	ASN	ASN	GLN	ASP	ILE	ILE	ASP
P509	P509	GLY	ALA	GLY	GLY	THR	THR	THR
		S338	SER	VAL	ASP	ASN	ASN	ILE
		I339	SER	GLY	LEU	ASP	ASP	ARG
		P375	SER	ARG	SER	CYS	ASP	ASP
		GLY	THR	THR	THR	GLU	GLU	THR
		PHE	VAL	VAL	ASP	GLU	ALA	ILE
		GLY	LEU	PRO	VAL	VAL	ALA	ILE
		LYS	LYS	GLY	ASP	GLY	GLY	GLY
		ASP	SER	ILE	SER	LEU	LEU	SER
		ILE	ALA	PRO	GLY	GLY	GLY	THR
		LYS	ALA	ARG	PRO	GLY	LYS	SER
		THR	GLU	SER	ASP	ARG	ARG	PRO
		THR	THR	THR	SER	LYS	LYS	SER
		GLU	ILE	ARG	ARG	ARG	PRO	PRO
		VAL	GLN	PRO	ASP	ASN	SER	SER
		GLU	GLY	GLY	THR	ASN	GLY	GLY
		ASN	THR	ALA	LEU	SER	ARG	ALA
		LEU	LEU	GLN	TYR	GLN	GLN	ALA
		ASP	GLN	SER	ASP	VAL	THR	THR
		PRO	GLU	ILE	ARG	GLN	PRO	PRO
		L394	SER	LYS	GLY	ARG	ASN	ASN
		GLY	GLY	LYS	SER	TYR	PRO	PRO
		S399	THR	GLY	VAL	THR	ASP	ASP
		ILE	ILE	THR	ALA	VAL	THR	THR
		G403	ALA	ASP	GLY	TYR	SER	SER
		R404	SER	GLY	ASN	SER	GLU	GLY
		A405	LEU	SER	VAL	HIS	ASP	GLY
		L410	THR	SER	VAL	GLY	GLY	HIS
		LYS	GLN	VAL	ALA	GLY	GLY	GLY
		PRO	PRO	SER	ARG	GLU	GLY	HIS
		LYS	LYS	SER	SER	SER	GLY	GLY
		PRO	GLN	GLY	THR	THR	THR	THR

- Molecule 2: Phosphoprotein

Chain C:  13% 85%

[illegible]

WORLDWIDE
PDB
PROTEIN DATA BANK

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.

All (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
1:A:515:MET:HA	1:A:518:VAL:HG22	1.80	0.63
1:A:530:LEU:HB3	1:A:705:LEU:HD22	1.81	0.62
1:A:522:TYR:HB2	1:A:553:MET:HE1	1.82	0.61
1:A:875:VAL:HG13	1:A:888:ALA:HB1	1.85	0.59
2:B:405:ALA:HB2	2:E:375:PRO:HG3	1.86	0.58
2:C:335:LYS:HG3	2:E:336:LEU:HD13	1.85	0.57
1:A:109:LEU:HD11	1:A:905:ASN:HB3	1.86	0.57
1:A:16:LEU:HD22	1:A:230:MET:HB2	1.88	0.56
1:A:76:LEU:HD22	1:A:82:ASN:HD22	1.71	0.56
1:A:1149:ALA:HA	1:A:1152:ARG:HH21	1.71	0.55
2:C:351:LYS:HG2	2:C:355:LYS:HE3	1.88	0.55
2:B:434:LEU:HB2	2:B:437:LEU:HD13	1.90	0.54
1:A:859:THR:HB	1:A:1010:THR:HG21	1.89	0.54
1:A:268:PHE:HB3	1:A:272:LEU:HD12	1.89	0.53
1:A:27:ALA:HB2	1:A:45:LEU:HD21	1.90	0.53
2:B:339:ILE:HD13	2:E:339:ILE:HG22	1.92	0.52
2:B:322:ILE:HG22	2:B:326:HIS:CE1	2.47	0.50
1:A:142:THR:HB	1:A:145:LEU:HD13	1.93	0.50
1:A:764:VAL:HG11	1:A:799:ALA:HB1	1.94	0.50
2:E:336:LEU:HA	2:E:339:ILE:HG12	1.94	0.50
1:A:479:VAL:HG12	1:A:496:ARG:HH22	1.77	0.49
1:A:374:MET:HE2	1:A:735:PRO:HB2	1.94	0.49
2:E:331:THR:HG22	2:E:335:LYS:HZ3	1.78	0.49
1:A:132:ASN:HD22	1:A:141:LEU:HD23	1.77	0.48
1:A:513:MET:HE1	1:A:552:LYS:HG2	1.95	0.48
1:A:282:LEU:HD11	1:A:311:GLU:HB3	1.96	0.48
2:D:352:GLN:O	2:D:356:GLN:HG2	2.13	0.48
1:A:1058:ARG:O	1:A:1062:GLU:HG2	2.14	0.48
1:A:856:TRP:CZ3	1:A:862:ASP:HB3	2.50	0.47
1:A:290:TYR:O	1:A:293:LEU:HB2	2.14	0.47
1:A:280:VAL:O	1:A:283:LEU:HB2	2.15	0.47
1:A:128:LEU:HD13	1:A:886:TYR:HB3	1.96	0.46
1:A:847:LEU:HD23	1:A:850:ILE:HD12	1.97	0.46
1:A:1108:TYR:O	1:A:1112:ARG:HG3	2.16	0.46
2:B:410:LEU:HD23	2:B:434:LEU:HD23	1.98	0.46
1:A:344:HIS:HA	1:A:843:VAL:HG13	1.98	0.45
1:A:657:SER:HB2	1:A:780:THR:HG22	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:339:ILE:HD11	2:E:339:ILE:HD12	1.98	0.45
2:E:332:ILE:O	2:E:336:LEU:HG	2.17	0.45
1:A:515:MET:HE3	1:A:515:MET:HB3	1.87	0.44
1:A:291:LEU:HD21	1:A:838:TYR:CD2	2.53	0.44
1:A:568:VAL:O	1:A:571:TYR:HB2	2.18	0.44
2:E:352:GLN:O	2:E:356:GLN:HG3	2.18	0.44
1:A:109:LEU:HD22	1:A:901:LEU:HB3	2.00	0.43
1:A:754:TYR:CE1	1:A:814:VAL:HG11	2.53	0.43
1:A:1169:TYR:HB2	1:A:1362:HIS:CE1	2.53	0.43
1:A:653:TYR:HD2	1:A:782:ARG:HG2	1.83	0.43
1:A:656:VAL:HG21	1:A:792:LYS:HB3	1.99	0.43
2:B:320:ALA:O	2:B:324:LYS:HG2	2.18	0.43
1:A:690:PRO:HB3	2:C:386:SER:HA	1.98	0.43
2:B:430:LYS:HB3	2:D:374:ILE:HG21	2.01	0.43
1:A:682:ARG:HA	1:A:682:ARG:HD3	1.89	0.43
1:A:1107:ASP:O	1:A:1110:GLN:HG3	2.18	0.43
1:A:391:VAL:HB	1:A:753:PRO:HB3	2.00	0.43
2:C:329:ASN:HA	2:C:332:ILE:HG12	2.00	0.43
1:A:829:PHE:HA	1:A:837:TYR:O	2.19	0.43
1:A:832:TYR:HB3	1:A:837:TYR:HE1	1.84	0.43
2:C:325:ILE:HG23	2:D:324:LYS:NZ	2.33	0.43
2:C:332:ILE:HD12	2:D:335:LYS:HZ1	1.83	0.43
1:A:124:VAL:HG23	1:A:972:LEU:HD21	2.01	0.42
1:A:973:MET:HE2	1:A:973:MET:HB3	1.92	0.42
1:A:1059:ALA:O	1:A:1063:ILE:HG12	2.18	0.42
2:B:459:SER:O	2:B:463:VAL:HG23	2.20	0.42
2:C:326:HIS:CE1	2:D:324:LYS:HZ2	2.38	0.42
2:D:330:LYS:HA	2:D:330:LYS:HD3	1.84	0.42
2:C:355:LYS:O	2:C:358:ILE:HG22	2.20	0.42
1:A:834:LYS:HG2	1:A:845:GLN:HE22	1.85	0.41
1:A:135:LEU:HD23	1:A:135:LEU:HA	1.90	0.41
1:A:736:MET:HE3	1:A:736:MET:HB3	1.90	0.41
1:A:1083:LYS:HE3	1:A:1083:LYS:HB2	1.91	0.41
2:D:322:ILE:HG22	2:D:326:HIS:CE1	2.55	0.41
1:A:1108:TYR:CE2	1:A:1112:ARG:HD2	2.55	0.41
2:B:464:ILE:O	2:B:468:ILE:HG13	2.20	0.41
1:A:42:ASP:HB2	1:A:364:VAL:HG21	2.02	0.41
1:A:211:VAL:HG22	1:A:222:TYR:HD1	1.85	0.41
1:A:678:ILE:HD12	1:A:678:ILE:HA	1.96	0.41
1:A:871:ILE:HD13	1:A:895:LYS:HB3	2.02	0.41
1:A:1108:TYR:CZ	1:A:1112:ARG:HD2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:338:SER:HB2	2:D:339:ILE:HD12	2.03	0.41
2:E:342:LEU:O	2:E:346:VAL:HG23	2.20	0.41
1:A:573:ARG:HH11	1:A:577:MET:HB3	1.86	0.40
1:A:456:LEU:HD11	1:A:559:ILE:HG23	2.04	0.40
2:B:478:LYS:HE3	2:B:478:LYS:HB2	1.94	0.40
1:A:681:GLN:HG2	2:C:372:ILE:HD13	2.02	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 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
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. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	341	HIS
1	A	404	HIS
1	A	529	ASN
1	A	1167	ASN
1	A	1335	GLN
1	A	1362	HIS
2	B	438	GLN
2	C	326	HIS
2	E	329	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 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.