



Full wwPDB EM Validation Report ⓘ

May 5, 2026 – 06:20 PM JST

PDB ID : 9VXZ / pdb_00009vxz
EMDB ID : EMD-65446
Title : Cryo-EM structure of Measles Virus L Protein bound by Phosphoprotein Tetramer
Authors : Xue, L.; Gui, J.; Chang, T.; Pan, H.; Xiong, X.
Deposited on : 2025-07-20
Resolution : 2.68 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

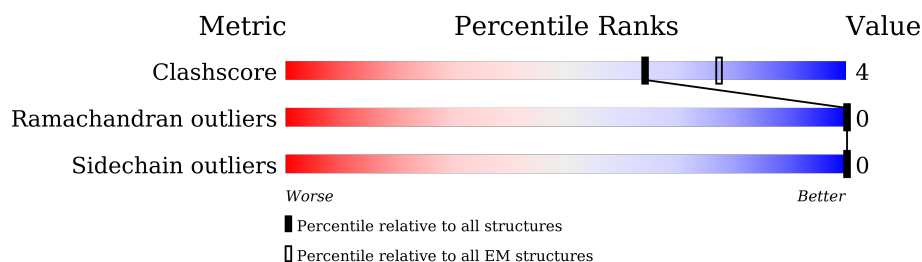
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.68 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	51% 6% 43%
2	B	507	24% 5% 71%
2	C	507	8% . 91%
2	D	507	11% . 87%
2	E	507	9% . 89%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12553 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	1255	Total	C	N	O	S	0	0
			10082	6445	1743	1839	55		

- Molecule 2 is a protein called Phosphoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	148	Total	C	N	O	S	0	0
			1159	736	208	210	5		
2	C	47	Total	C	N	O	S	0	0
			372	233	65	73	1		
2	D	67	Total	C	N	O	S	0	0
			514	322	87	104	1		
2	E	55	Total	C	N	O	S	0	0
			425	269	74	81	1		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total	Zn	0
			1	1	

[illegible]

- Molecule 2: Phosphoprotein

Chain B:  24% 5% 71%

ALA	GLU	THR	ASP	LYS	SER	MET
ASP	GLU	GLU	VAL	ILE	GLY	ALA
VAL	ILE	ILE	GLU	GLN	PRO	GLY
GLU	GLY	ALA	THR	ASP	CYS	GLN
LEU	ASP	SER	ALA	GLU	LEU	GLN
ASN	THR	LEU	GLY	ALA	SER	ALA
PRO	THR	LEU	GLY	ASP	ALA	ARG
ASP	THR	THR	GLY	SER	ILE	HIS
L394	ASP	GLY	GLY	ILE	GLY	VAL
K395	GLU	GLY	ILE	MET	SER	LYS
P396	LEU	ALA	HIS	VAL	THR	ASN
	PHE	THR	GLU	GLN	GLY	GLY
A405	SER	GLN	LEU	SER	GLY	LEU
	ASP	CYS	LEU	GLY	GLY	GLU
K411	VAL	ALA	LYS	LEU	ALA	CYS
PRO	GLN	ARG	LEU	ASP	PRO	ILE
LYS	ASP	LYS	GLN	GLY	ARG	ARG
VAL	ILE	SER	SER	ASP	ILE	ALA
ALA	LYS	PRO	ARG	SER	ARG	LEU
SER	THR	SER	GLY	THR	GLY	LYS
ARG	ALA	GLU	ASN	LEU	GLN	ALA
GLN	LEU	PRO	ASN	SER	GLY	GLU
LEU	LEU	SER	PHE	GLY	SER	PRO
LEU	ALA	GLY	PRO	GLY	ILE	ILE
GLN	LYS	PRO	LYS	ASP	GLY	GLY
GLY	I325	PRO	LYS	ASP	GLY	GLY
MET		GLY	LEU	ASP	SER	SER
THR	I332	ALA	GLY	GLU	GLU	LEU
ASN	I333	PRO	LYS	SER	ASP	ALA
GLY		ALA	THR	GLU	ASP	VAL
ARG	L336	GLY	LEU	ASN	ALA	GLU
THR		ASN	ASN	SER	GLY	GLU
SER	L339	VAL	VAL	ASP	THR	ALA
		PRO	PRO	VAL	LEU	MET
S429	L342	GLU	PRO	ASP	GLY	ALA
L433		CYS	PRO	ILE	ILE	ALA
L434	E245	VAL	PRO	GLY	PRO	THR
K435		SER	ASN	GLY	SER	GLU
E436	I349	ASN	PRO	PRO	ARG	SER
F437	Q356	ALA	SER	ASP	ASN	ILE
Q438		ALA	ARG	THR	ASN	GLY
	I360	LEU	ALA	GLN	LEU	ASP
V450		ILE	SER	GLY	ALA	ASN
	E364	GLN	THR	TYR	ALA	PRO
S462		GLU	SER	ILE	SER	GLY
	L367	THR	GLY	THR	THR	GLN
T488		THR	THR	GLY	GLY	ASP
	M371	PRO	PRO	ARG	ARG	GLU
D493		GLU	ILE	ASP	GLN	ALA
L494		SER	LYS	GLY	CYS	THR
	P375	GLY	LYS	SER	TYR	CYS
K507	GLY	THR	GLY	ALA	HIS	LYS
	LEU	THR	THR	PRO	VAL	GLU
	GLY	ILE	ASP	ILE	TYR	GLU
	LYS	SER	ALA	SER	ASP	GLU
	ASP	PRO	ARG	MET	HIS	ALA
	PRO	ARG	LEU	GLY	SER	GLY
	ASN	ARG	ALA	PHE	GLY	SER
	ASP	GLN	SER	ALA	GLU	SER
	PRO	ASN	PHE	ALA	VAL	GLY
	THR	ASN	GLY	SER	ALA	LEU

- Molecule 2: Phosphoprotein

Chain C: 8% . 91%

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

Chain E:  9% . 89%



[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	4035198	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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0.13	0/10307	0.32	0/13966
2	B	0.13	0/1168	0.34	0/1556
2	C	0.17	0/373	0.35	0/497
2	D	0.16	0/517	0.35	0/696
2	E	0.18	0/427	0.43	0/570
All	All	0.13	0/12792	0.32	0/17285

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	10082	0	10102	76	0
2	B	1159	0	1261	21	0
2	C	372	0	398	7	0
2	D	514	0	535	8	0
2	E	425	0	462	9	0
3	A	1	0	0	0	0
All	All	12553	0	12758	103	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 (103) 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:1180:CYS:SG	1:A:1364:HIS:HE1	2.11	0.71
2:B:356:GLN:HE21	2:E:356:GLN:HE22	1.37	0.69
2:B:434:LEU:HD23	2:B:436:GLU:H	1.60	0.67
2:B:342:LEU:HA	2:B:345:GLU:HG2	1.76	0.66
1:A:1397:LEU:HD12	1:A:1398:ILE:HG23	1.76	0.66
1:A:989:SER:H	1:A:1147:ARG:HH22	1.45	0.63
2:D:352:GLN:HG2	2:D:355:ARG:HH22	1.63	0.63
1:A:933:LEU:HD12	1:A:934:PRO:HD2	1.80	0.62
1:A:1081:THR:HG22	1:A:1085:LEU:HD23	1.81	0.62
1:A:1190:PHE:HB2	1:A:1361:LEU:HB3	1.83	0.60
2:C:363:LEU:HD23	2:D:363:LEU:HD22	1.86	0.58
1:A:1109:GLU:HG2	1:A:1112:ARG:HH21	1.68	0.57
1:A:530:LEU:HB3	1:A:705:LEU:HD22	1.86	0.57
1:A:457:ASP:HA	1:A:1029:MET:HE1	1.86	0.57
2:E:329:ASN:HA	2:E:332:ILE:HG12	1.86	0.57
1:A:197:THR:HA	1:A:202:GLU:HG2	1.87	0.56
1:A:1057:PRO:HG2	1:A:1157:LEU:HD11	1.88	0.56
2:B:339:LEU:HA	2:B:342:LEU:HD23	1.88	0.56
1:A:266:ASP:HA	1:A:269:PHE:HD2	1.71	0.54
1:A:1269:VAL:HG21	1:A:1274:LEU:HD13	1.88	0.53
1:A:1302:THR:HG22	1:A:1304:LEU:H	1.73	0.53
1:A:456:LEU:HD13	1:A:510:PRO:HB2	1.91	0.52
1:A:1009:ILE:HG23	1:A:1103:LEU:HD22	1.91	0.52
1:A:14:VAL:HG11	1:A:856:TRP:HB2	1.92	0.52
1:A:27:ALA:HB2	1:A:45:LEU:HD21	1.92	0.51
1:A:1392:LEU:HD23	1:A:1394:THR:H	1.75	0.51
1:A:656:VAL:HG21	1:A:792:LYS:HB3	1.93	0.51
1:A:929:ARG:HH12	1:A:1118:LEU:HB3	1.75	0.51
1:A:289:ALA:HB2	1:A:304:PHE:HD2	1.76	0.50
2:B:488:ILE:HG22	2:B:494:LEU:HD12	1.92	0.50
1:A:681:GLN:HG2	2:D:372:ILE:HD13	1.94	0.50
1:A:30:GLU:HB3	1:A:49:ILE:HG21	1.94	0.49
1:A:1166:MET:HG2	1:A:1365:VAL:HG22	1.93	0.49
1:A:16:LEU:HD22	1:A:230:MET:HB2	1.95	0.49
1:A:307:HIS:ND1	1:A:821:ASN:HB3	2.27	0.49
2:E:333:ILE:HA	2:E:336:LEU:HG	1.95	0.49
1:A:460:LEU:HD21	1:A:1029:MET:HG2	1.93	0.49
2:C:328:ASP:O	2:C:332:ILE:HG12	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:762:SER:HB3	1:A:806:ILE:HD12	1.95	0.49
1:A:853:CYS:HB2	1:A:874:THR:HG21	1.94	0.49
1:A:333:ALA:O	1:A:337:ILE:HG13	2.13	0.49
1:A:1062:GLU:HG2	1:A:1244:VAL:HG21	1.94	0.48
2:C:367:LEU:HD21	2:D:367:LEU:HD11	1.95	0.48
2:B:375:PRO:HD2	2:B:438:GLN:HE22	1.78	0.48
1:A:193:PRO:HB2	1:A:204:LEU:HD11	1.95	0.48
1:A:781:LYS:HD2	1:A:799:VAL:HG11	1.96	0.48
1:A:752:ILE:HA	1:A:755:LEU:HD12	1.95	0.47
1:A:832:TYR:HE1	1:A:837:TYR:HB2	1.80	0.47
2:B:345:GLU:O	2:B:349:ILE:HG12	2.15	0.47
1:A:371:ARG:HH12	1:A:728:ASP:HA	1.78	0.47
1:A:142:ARG:HB2	1:A:145:ILE:HG13	1.96	0.47
1:A:152:LEU:HD11	1:A:891:LEU:HD13	1.95	0.47
1:A:331:ILE:HG21	2:B:462:SER:HB3	1.96	0.47
2:B:396:PRO:HG2	2:E:370:ILE:HA	1.96	0.47
2:C:367:LEU:HG	2:D:367:LEU:HD21	1.95	0.47
2:B:333:ILE:HD13	2:B:336:LEU:HD12	1.98	0.46
1:A:1171:ILE:HG23	1:A:1175:GLU:HB3	1.97	0.46
1:A:291:LEU:HB2	1:A:346:THR:HG21	1.98	0.46
1:A:836:ILE:HB	1:A:843:VAL:HB	1.98	0.45
1:A:286:LEU:HD22	1:A:290:TYR:HE2	1.81	0.45
1:A:801:ARG:HD2	2:B:450:VAL:HG13	1.98	0.45
2:C:331:LYS:HG3	2:D:332:ILE:HD12	1.99	0.45
1:A:1099:VAL:O	1:A:1103:LEU:HG	2.17	0.45
1:A:497:ARG:HB3	1:A:500:ASP:HB2	1.99	0.45
1:A:920:LEU:HD23	1:A:926:LEU:HD23	1.99	0.45
1:A:1029:MET:HE3	1:A:1397:LEU:HD23	1.99	0.45
1:A:1013:LEU:HD12	1:A:1013:LEU:HA	1.80	0.44
1:A:916:VAL:HA	1:A:1115:MET:HE1	1.98	0.44
1:A:1171:ILE:HD11	1:A:1177:CYS:HB2	1.98	0.44
1:A:171:VAL:HG22	1:A:203:LEU:HD21	1.99	0.44
1:A:201:VAL:HG12	1:A:214:SER:HA	1.97	0.44
1:A:403:ARG:HD2	1:A:571:TYR:HE1	1.81	0.44
1:A:674:GLU:HB2	2:E:374:ILE:HD11	2.00	0.44
1:A:286:LEU:HD11	1:A:312:ILE:HD11	1.99	0.44
1:A:411:LEU:HD11	1:A:446:VAL:HG22	1.99	0.44
1:A:685:GLU:HA	2:D:388:VAL:HG13	2.00	0.44
1:A:462:MET:HA	1:A:465:LYS:HE3	1.99	0.43
1:A:400:TYR:HB3	1:A:409:PRO:HD3	1.99	0.43
1:A:94:LEU:HB3	1:A:168:TRP:HZ2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:347:GLU:HG2	2:D:351:LYS:HE3	2.00	0.43
1:A:379:VAL:HG21	2:B:433:LEU:HD11	2.01	0.43
1:A:109:LEU:HD23	1:A:109:LEU:HA	1.91	0.43
1:A:272:LEU:HB3	1:A:276:THR:OG1	2.19	0.43
2:B:332:ILE:O	2:B:336:LEU:HG	2.19	0.43
2:B:488:ILE:HG23	2:B:493:ASP:HB3	2.01	0.43
2:B:364:GLU:HA	2:E:363:LEU:HD21	2.01	0.42
1:A:810:ARG:HA	1:A:810:ARG:HD3	1.84	0.42
1:A:120:VAL:HG11	1:A:928:ILE:HG21	2.01	0.42
1:A:871:ILE:HD13	1:A:895:LYS:HB3	2.01	0.42
2:B:371:MET:HB3	2:B:394:LEU:HD12	2.03	0.41
2:B:332:ILE:HD11	2:C:332:ILE:HG23	2.02	0.41
1:A:1388:LEU:HD23	1:A:1388:LEU:HA	1.92	0.41
1:A:973:MET:HE2	1:A:973:MET:HB3	1.92	0.41
2:B:405:ALA:HB2	2:E:375:PRO:HD3	2.03	0.41
1:A:653:TYR:HD2	1:A:782:ARG:HG2	1.86	0.41
1:A:1304:LEU:HD12	1:A:1345:GLU:HG3	2.02	0.41
2:B:349:ILE:HG23	2:C:353:ILE:HD13	2.03	0.41
2:B:360:ILE:HD13	2:B:360:ILE:HA	1.94	0.41
2:B:367:LEU:HD13	2:E:363:LEU:HD22	2.03	0.41
1:A:291:LEU:HD12	1:A:346:THR:HB	2.03	0.40
1:A:657:SER:HB2	1:A:780:THR:HG22	2.03	0.40
1:A:672:ARG:HD2	2:E:374:ILE:HG21	2.03	0.40
1:A:42:ASP:HB2	1:A:364:VAL:HG21	2.03	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	1241/2183 (57%)	1199 (97%)	42 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	142/507 (28%)	136 (96%)	6 (4%)	0	100	100
2	C	45/507 (9%)	45 (100%)	0	0	100	100
2	D	63/507 (12%)	63 (100%)	0	0	100	100
2	E	53/507 (10%)	53 (100%)	0	0	100	100
All	All	1544/4211 (37%)	1496 (97%)	48 (3%)	0	100	100

There are no Ramachandran outliers to report.

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 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	1114/1945 (57%)	1114 (100%)	0	100	100
2	B	132/416 (32%)	132 (100%)	0	100	100
2	C	45/416 (11%)	45 (100%)	0	100	100
2	D	61/416 (15%)	61 (100%)	0	100	100
2	E	50/416 (12%)	50 (100%)	0	100	100
All	All	1402/3609 (39%)	1402 (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 (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	313	HIS
1	A	358	HIS
2	B	326	HIS
2	B	356	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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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](#)

There are no chain breaks in this entry.