



## wwPDB EM Validation Summary 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 wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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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

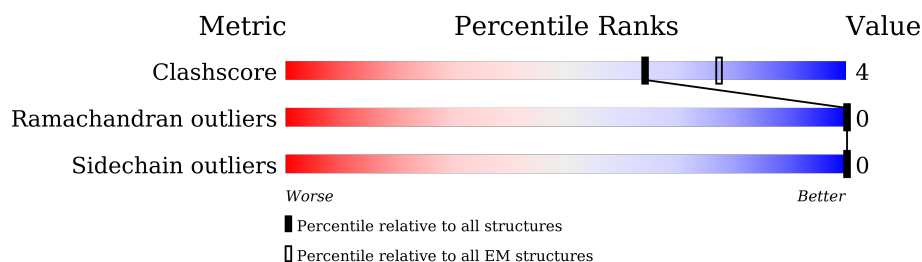
# 1 Overall quality at a glance

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  $\geq 3$ , 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	



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

- Molecule 2: Phosphoprotein

Chain B:  24% 5% 71%

ALA	ASP	VAL	GLU	GLY	THR	ASP	LYS	SER	MET
ASP	VAL	GLU	GLY	ILE	GLU	VAL	GLY	LYS	ALA
GLU	GLY	ALA	THR	ALA	THR	THR	GLN	CYS	GLN
LEU	ASP	SER	ALA	SER	LEU	GLU	ALA	SER	GLN
ASN	THR	LEU	LEU	LEU	GLY	GLY	ASP	ALA	ARG
PRO	THR	ASP	THR	THR	THR	GLY	SER	ILE	HIS
ASP	ASP	GLU	GLY	GLY	GLY	GLY	ILE	GLY	VAL
L394	L395	K396	ASP	GLY	GLY	ILE	MET	SER	LYS
P396	K395	P396	LEU	ALA	ALA	HIS	VAL	THR	ASN
A405	A405	A405	PHE	THR	THR	GLU	GLN	GLY	GLY
K411	K411	K411	SER	GLN	GLN	LEU	SER	GLY	LEU
LYS	LYS	LYS	ASP	CYS	CYS	LEU	GLY	GLY	GLU
PRO	PRO	PRO	VAL	ALA	ALA	LYS	LEU	ALA	CYS
VAL	VAL	VAL	GLN	ARG	ARG	LEU	ASP	PRO	ILE
ALA	ALA	ALA	LYS	SER	SER	SER	ASP	ILE	ARG
SER	SER	SER	THR	THR	THR	GLY	SER	ARG	LEU
ARG	ARG	ARG	ALA	GLU	GLU	ASN	LEU	GLN	LYS
GLN	GLN	GLN	LEU	PRO	PRO	ASN	SER	GLY	ALA
LEU	LEU	LEU	ALA	SER	SER	PHE	GLY	SER	PRO
GLN	GLN	GLN	LYS	PRO	PRO	LYS	ASP	GLY	ILE
GLY	GLY	GLY	I325	GLY	GLY	LEU	ASP	GLY	GLY
THR	THR	THR	I332	ALA	ALA	GLY	ASP	SER	SER
MET	MET	MET	I333	PRO	PRO	LYS	SER	ASP	LEU
ASN	ASN	ASN	I336	ALA	ALA	THR	GLU	ASP	ALA
GLY	GLY	GLY	L339	GLY	GLY	LEU	ASN	ALA	VAL
ARG	ARG	ARG	L342	ASN	ASN	LEU	ASN	ALA	GLU
THR	THR	THR	L345	VAL	VAL	VAL	SER	GLU	GLU
SER	SER	SER	E345	PRO	PRO	PRO	VAL	THR	ALA
E429	L433	L434	E349	GLU	GLU	PRO	ASP	ILE	ALA
L433	L434	L434	E345	CYS	VAL	PRO	ILE	PRO	ALA
K435	K435	K435	E349	VAL	VAL	ASN	GLY	SER	TRP
F437	F437	F437	E349	ASN	ASN	PRO	PRO	ARG	GLU
Q438	Q438	Q438	Q356	ALA	ALA	SER	ASP	ASN	ILE
K450	V450	V450	K371	LEU	LEU	ARG	THR	LEU	SER
V450	V450	V450	K371	ALA	ALA	ALA	GLY	GLN	ASP
S462	S462	S462	P375	ILE	ILE	SER	GLY	ALA	ASN
I498	I498	I498	E364	GLN	GLN	THR	TYR	SER	PRO
I498	I498	I498	L367	GLU	GLU	THR	ALA	SER	GLY
D493	D493	D493	K371	THR	THR	GLU	ILE	THR	CYS
L494	L494	L494	P375	SER	SER	LYS	ARG	GLN	ALA
K507	K507	K507	GLY	GLY	GLY	GLY	GLY	CYS	THR
			LEU	THR	THR	GLY	SER	HIS	LYS
			GLY	THR	THR	ASP	PRO	VAL	GLU
			LYS	SER	SER	ALA	TYR	GLU	GLU
			ASP	PRO	PRO	ARG	SER	ASP	ALA
			ASN	ASN	ARG	LEU	MET	HIS	ALA
			ASN	ASN	SER	ALA	GLY	SER	GLY
			PRO	PRO	THR	PHE	ARG	GLY	SER
			THR	THR	ASN	CYS	ALA	VAL	THR

- Molecule 2: Phosphoprotein

Chain C:  8% 91%

[illegible]

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.

The worst 5 of 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

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
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 [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	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 [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](#)

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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.