



wwPDB EM Validation Summary Report ⓘ

Sep 14, 2025 – 12:19 AM JST

PDB ID : 9KNQ / pdb_00009knq
EMDB ID : EMD-62459
Title : Measles virus L-P complex in apo state
Authors : Wang, Y.R.; Zhang, H.Q.
Deposited on : 2024-11-19
Resolution : 3.00 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 Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.45.1

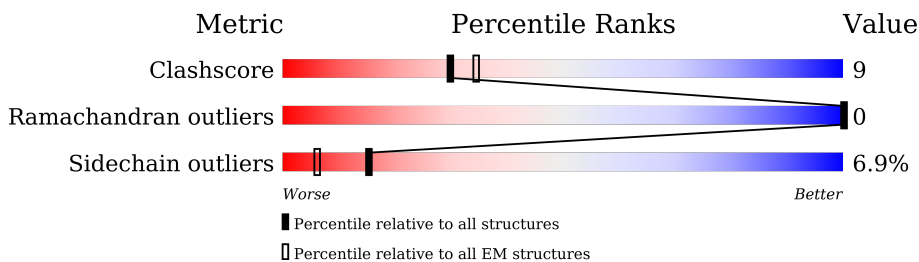
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	507	
2	C	507	
2	D	507	
2	E	507	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12606 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	1284	Total	C	N	O	S	0	0
			10307	6574	1784	1890	59		

- Molecule 2 is a protein called Phosphoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	52	Total	C	N	O	S	0	0
			398	252	69	76	1		
2	D	61	Total	C	N	O	S	0	0
			461	289	77	94	1		
2	E	42	Total	C	N	O	S	0	0
			328	209	56	62	1		
2	C	142	Total	C	N	O	S	0	0
			1110	708	196	201	5		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
3	A	2	Total	Zn	0
			2	2	

[illegible]

- Molecule 2: Phosphoprotein

Chain B: 6% 1% 93%

[illegible]

GLN	LEU	GLY	LYS	VAL	SER	ASP	THR	GLY	PRO	ALA	SER	ARG	SER	VAL	ILE	ILE	ARG	SER	SER	LYS	LYS	ARG	THR	LEU	MET	THR	LEU	LEU	ASP	ASP	ILE	LYS	GLY	ALA	ASN	ASP	LEU	ALA	LYS	PRO
HIS	GLN	MET	LEU	MET	LYS	ILE	ILE	MET	LYS																															

- Molecule 2: Phosphoprotein

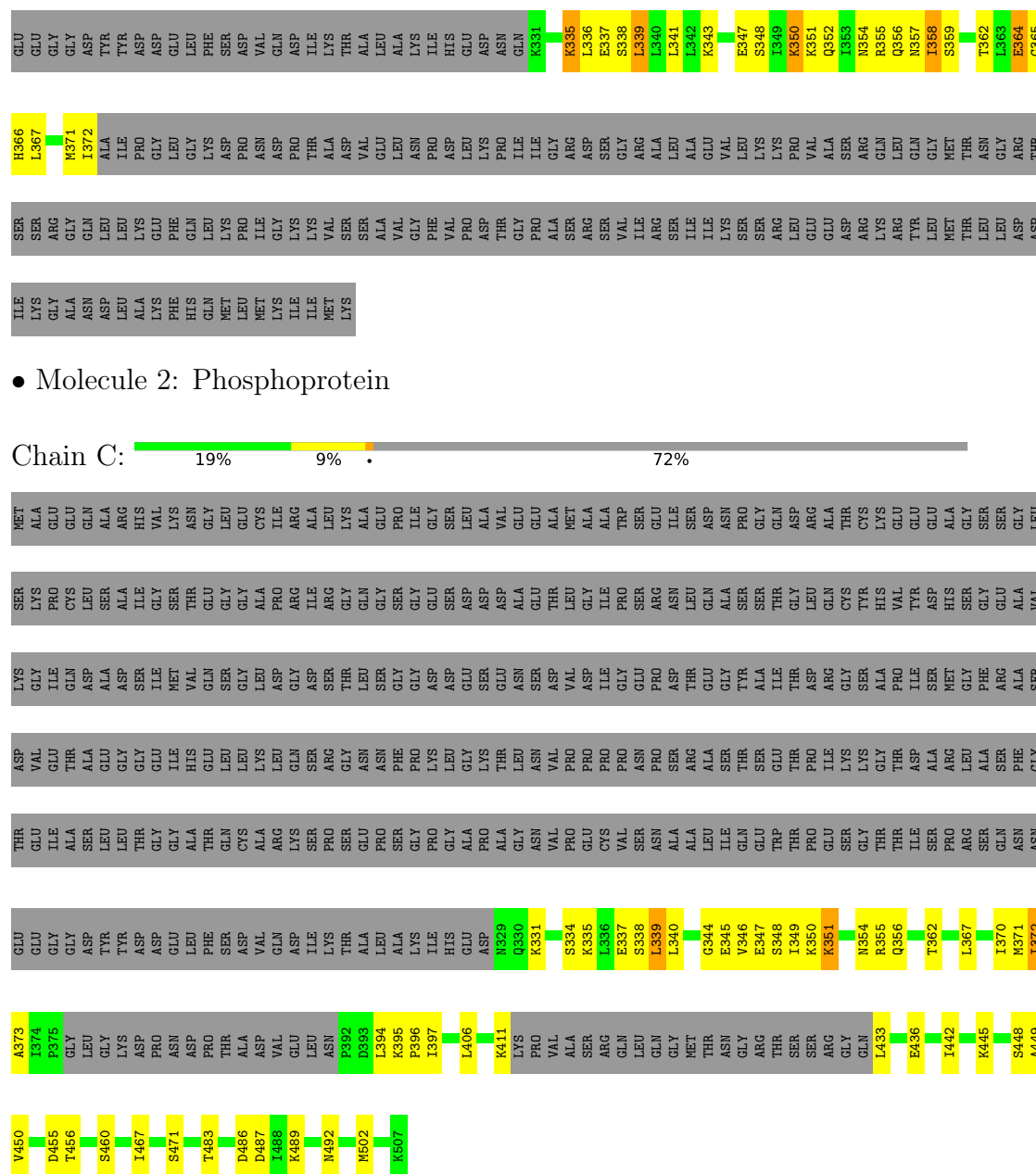
Chain D: 7% 2% 88%

Lys	Ile	Lys	Gly		Glu	Thr	Asp	Lys	Ser	
Ile		K379	Lys	Glu	Glu	Glu	Val	Gly	Lys	Met
Ile		D380	Lys	Glu	Ile	Ile	Glu	Ile	Pro	Ala
Lys		P381	Val	Gly	Ala	Ala	Thr	Thr	Cys	
	Ser	N382	Ser	Asp	Ser	Ser	Ala	Asp	Leu	Gln
	Ala	D383	Ser	Tyr	Tyr	Leu	Glu	Ala	Ser	Ala
	Val		Val	Tyr	Tyr	Leu	Gly	Asp	Arg	
	Val	Y388	Val	Asp	Asp	Thr	Gly	Ser	Ile	His
	Phe	E389	Phe	Asp	Glu	Gly	Ile	Ile	Gly	Val
	Val		Val	Leu	Leu	Ala	His	Val	Thr	Asn
	Pro	D393	Pro	Phe	Phe	Thr	Glu	Gln	Gly	Gly
	Asp		Asp	Ser	Ser	Gln	Leu	Ser	Gly	Leu
	Gly		Gly	Pro	Asp	Cys	Leu	Gly	Gly	Glu
	Pro		Pro	Val	Ala	Ala	Lys	Leu	Ala	Cys
	Ala		Ala	Gln	Gln	Arg	Asp	Asp	Pro	Ile
	Ser		Ser	Asp	Asp	Ser	Lys	Gly	Arg	Ala
	Arg		Arg	Ile	Ile	Pro	Ser	Asp	Ile	Leu
	Ser		Ser	Lys	Lys	Ser	Arg	Ser	Gly	Ala
	Val		Val	Thr	Thr	Gly	Gly	Thr	Arg	Leu
	Ile		Ile	Ala	Ala	Pro	Asn	Leu	Gln	Ala
	Arg		Arg	Ala	Ala	Ser	Phe	Gly	Ser	Pro
	Ser		Ser	Lys	Lys	Gly	Pro	Gly	Gly	Ile
	Ile		Ile	Ile	Ile	Pro	Lys	Asp	Glu	Gly
	Lys		Lys	His	His	Gly	Leu	Asp	Ser	Ser
	Lys		Lys	Glu	Glu	Ala	Gly	Asp	Leu	Ala
	Ser		Ser	Leu	Leu	Pro	Lys	Ser	Asp	Val
	Ser		Ser	Asn	Asn	Ala	Thr	Asp	Ala	Glu
	Arg		Arg	Lys	Lys	Gly	Leu	Asn	Ala	Glu
	Leu		Leu	Lys	Lys	Asn	Asn	Ser	Gly	Val
	Glu		Glu	Val	Ile	Val	Val	Asp	Thr	Ala
	Glu		Glu	Ala		Pro	Pro	Val	Leu	Ala
	Asp		Asp	Ser	S334	Glu	Pro	Asp	Gly	Met
	Arg		Arg	Arg	K335	Cys	Pro	Ile	Ile	Ala
	Lys		Lys	Gln	L336	Val	Pro	Gly	Pro	Trp
	Arg		Arg	Leu		Ser	Asn	Glu	Ser	Ser
	Tyr		Tyr	Gln	E345	Ala	Pro	Asp	Glu	Ile
	Leu		Leu	Gly	Y346	Asn	Ser	Pro	Asn	Ser
	Met		Met	Met	E347	Ala	Arg	Thr	Asp	Ala
	Thr		Thr	Thr	S348	Leu	Ala	Glu	Ser	Asp
	Leu		Leu	Asn	I349	Ile	Ser	Gly	Ala	Asn
	Asp		Asp	Gly		Gln	Thr	Ser	Pro	Gly
	Ile		Ile	Ser	Q352	Glu	Ser	Ala	Ser	Pro
	Lys		Lys	Ser	I353	Trp	Thr	Ile	Gln	Thr
	Gly		Gly	Arg		Pro	Pro	Asp	Arg	Arg
	Ala		Ala	Arg	N357	Glu	Ile	Arg	Gln	Ala
	Asn		Asn	Gln	S358	Ser	Lys	Gly	Cys	Thr
	Asp		Asp	Gln	S359	Gly	Lys	Ser	Thr	Ala
	Leu		Leu	Leu	I360	Thr	Gly	Ser	Cys	Ala
	Ala		Ala	Lys	S361	Thr	Thr	Pro	His	Lys
	Lys		Lys	Glu	T362	Ile	Asp	Ile	Val	Glu
	Phe		Phe	Phe	I363	Ser	Ala	Ser	Tyr	Glu
	His		His	Gln	E364	Pro	Arg	Met	His	Ala
	Lys		Lys	Leu	L367	Arg	Leu	Gly	Ser	Ala
	Met		Met	Lys		Ser	Ala	Phe	Gly	Ser
	Leu		Leu	Pro	I372	Gln	Ser	Arg	Glu	Ser
	Met		Met	Ile	K373	Asn	Phe	Ser	Ala	Val
				Thr	L374	Ser	Gly	Ser	Val	Met

- Molecule 2: Phosphoprotein

Chain E: 92%

[illegible]



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	185565	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)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (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	0.17	0/10537	0.36	0/14283
2	B	0.17	0/399	0.41	0/532
2	C	0.15	0/1119	0.41	0/1490
2	D	0.18	0/465	0.60	3/628 (0.5%)
2	E	0.18	0/328	0.48	0/436
All	All	0.17	0/12848	0.38	3/17369 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	D	374	ILE	CA-C-N	5.68	140.62	127.00
2	D	374	ILE	C-N-CA	5.68	140.62	127.00
2	D	374	ILE	C-N-CD	-5.12	109.34	120.60

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	10307	0	10315	149	0
2	B	398	0	438	16	0
2	C	1110	0	1216	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	461	0	483	21	0
2	E	328	0	367	22	0
3	A	2	0	0	0	0
All	All	12606	0	12819	226	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 9.

The worst 5 of 226 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:1177:CYS:O	1:A:1181:GLU:HB2	1.78	0.83
2:D:379:LYS:HD2	2:D:380:ASP:H	1.41	0.83
1:A:1186:ASN:HB2	1:A:1318:LEU:HD23	1.64	0.80
1:A:1266:ARG:HD3	1:A:1399:TYR:HB2	1.65	0.78
1:A:729:GLN:HG2	1:A:730:ILE:HG23	1.66	0.78

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	1276/2183 (58%)	1189 (93%)	87 (7%)	0	100	100
2	B	50/507 (10%)	48 (96%)	2 (4%)	0	100	100
2	C	136/507 (27%)	123 (90%)	13 (10%)	0	100	100
2	D	59/507 (12%)	47 (80%)	12 (20%)	0	100	100
2	E	40/507 (8%)	35 (88%)	5 (12%)	0	100	100
All	All	1561/4211 (37%)	1442 (92%)	119 (8%)	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	1144/1945 (59%)	1070 (94%)	74 (6%)	14	43
2	B	47/416 (11%)	45 (96%)	2 (4%)	25	58
2	C	127/416 (30%)	118 (93%)	9 (7%)	12	40
2	D	55/416 (13%)	48 (87%)	7 (13%)	3	17
2	E	40/416 (10%)	34 (85%)	6 (15%)	2	12
All	All	1413/3609 (39%)	1315 (93%)	98 (7%)	15	42

5 of 98 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1184	SER
1	A	1394	THR
1	A	1235	LEU
1	A	1321	VAL
2	B	368	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	809	GLN
2	C	356	GLN
1	A	1186	ASN
2	D	356	GLN
1	A	1061	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](#)

Of 2 ligands modelled in this entry, 2 are 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.