



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 12:55 AM UTC

PDB ID : 4BKK / pdb_00004bkk
EMDB ID : EMD-2369
Title : The Respiratory Syncytial Virus nucleoprotein-RNA complex forms a left-handed helical nucleocapsid.
Authors : Bakker, S.E.; Duquerroy, S.; Galloux, M.; Loney, C.; Conner, E.; Eleouet, J.F.; Rey, F.A.; Bhella, D.
Deposited on : 2013-04-26
Resolution : Not provided
Based on initial model : 2WJ8

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 : 0.0.1.dev132
MolProbity : **FAILED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : 1.8.1
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 unknown.

There are no overall percentile quality scores available for this entry.

ENTRY-COMPOSITION INFOmissingINFO

SEQUENCE-PLOTS INFOmissingINFO

2 Experimental information

Property	Value	Source
EM reconstruction method	TOMOGRAPHY	Depositor
Imposed symmetry	HELICAL, twist=Not provided°, rise=Not provided Å, axial sym=Not provided	Depositor
Number of tilted images used	911	Depositor
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	JEOL 2200FSC	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	131	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	40000	Depositor
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor

3 Model quality [i](#)

3.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

3.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

3.3 Torsion angles [i](#)

3.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

3.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

3.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

3.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

3.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

3.6 Ligand geometry [i](#)

There are no ligands in this entry.

3.7 Other polymers [i](#)

There are no such residues in this entry.

3.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

4 Tomogram visualisation

This section contains visualisations of the EMDB entry EMD-2369. These allow visual inspection of the internal detail of the tomogram and identification of artifacts.

4.1 Orthogonal projections

This section was not generated.

4.2 Central slices

This section was not generated.

4.3 Largest variance slices

This section was not generated.

4.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

4.5 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

5 Tomogram analysis

This section contains the results of statistical analysis of the tomogram.

5.1 Map-value distribution

This section was not generated.

6 Map-model fit

This section was not generated.