



## Full wwPDB EM Validation 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 Full wwPDB EM Validation 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 : 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.