



## Full wwPDB EM Validation Report ⓘ

Oct 24, 2024 – 04:13 PM EDT

EMDB ID : EMD-25231  
Title : Tertiary structure of an individual particle of self-folding RNA polymer (particle #122)  
Authors : Liu, J.; Ren, G.  
Deposited on : 2021-10-28  
Resolution : 25.00 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMTomogramValidationReportHelp>  
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.dev113  
Validation Pipeline (wwPDB-VP) : 2.39

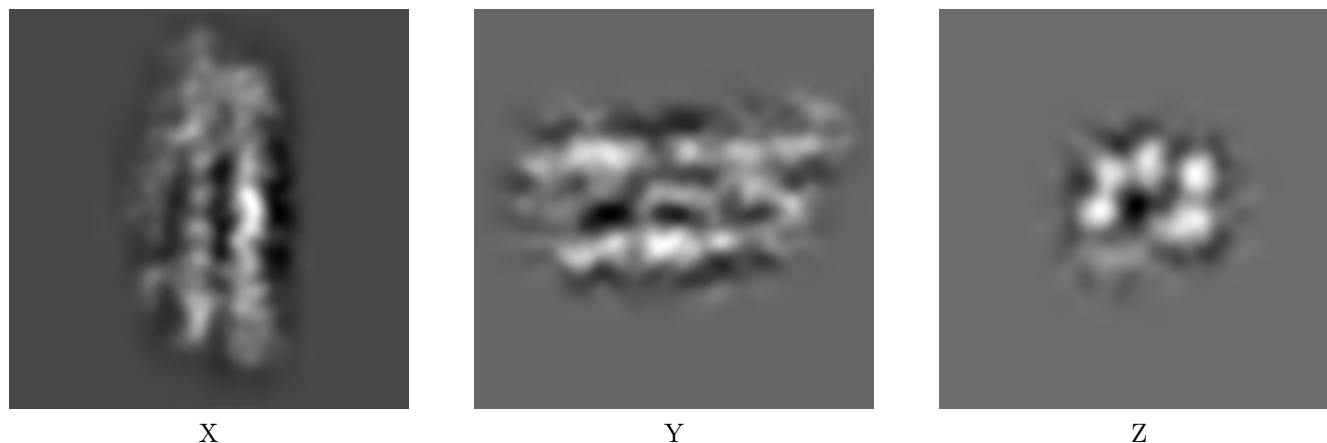
# 1 Experimental information

| Property                             | Value                         | Source    |
|--------------------------------------|-------------------------------|-----------|
| EM reconstruction method             | TOMOGRAPHY                    | Depositor |
| Imposed symmetry                     | Not Provided                  |           |
| Number of tilted images used         | 25                            | Depositor |
| Resolution determination method      | FSC 0.5 CUT-OFF               | Depositor |
| CTF correction method                | Not provided                  |           |
| Microscope                           | FEI TITAN KRIOS               | Depositor |
| Voltage (kV)                         | 300                           | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 8.0                           | Depositor |
| Minimum defocus (nm)                 | 2.0                           | Depositor |
| Maximum defocus (nm)                 | 3.0                           | Depositor |
| Magnification                        | 81000.0                       | Depositor |
| Image detector                       | GATAN K3 BIOQUANTUM (6k x 4k) | Depositor |
| Maximum voxel value                  | 5.055                         | Depositor |
| Minimum voxel value                  | -2.828                        | Depositor |
| Average voxel value                  | 0.017                         | Depositor |
| Voxel value standard deviation       | 0.323                         | Depositor |
| Recommended contour level            | Not applicable                |           |
| Tomogram size ( $\text{\AA}$ )       | 240.64, 240.64, 240.64        | wwPDB     |
| Tomogram dimensions                  | 128, 128, 128                 | wwPDB     |
| Tomogram angles ( $^\circ$ )         | 90.0, 90.0, 90.0              | wwPDB     |
| Grid spacing ( $\text{\AA}$ )        | 1.88, 1.88, 1.88              | Depositor |

## 2 Tomogram visualisation [i](#)

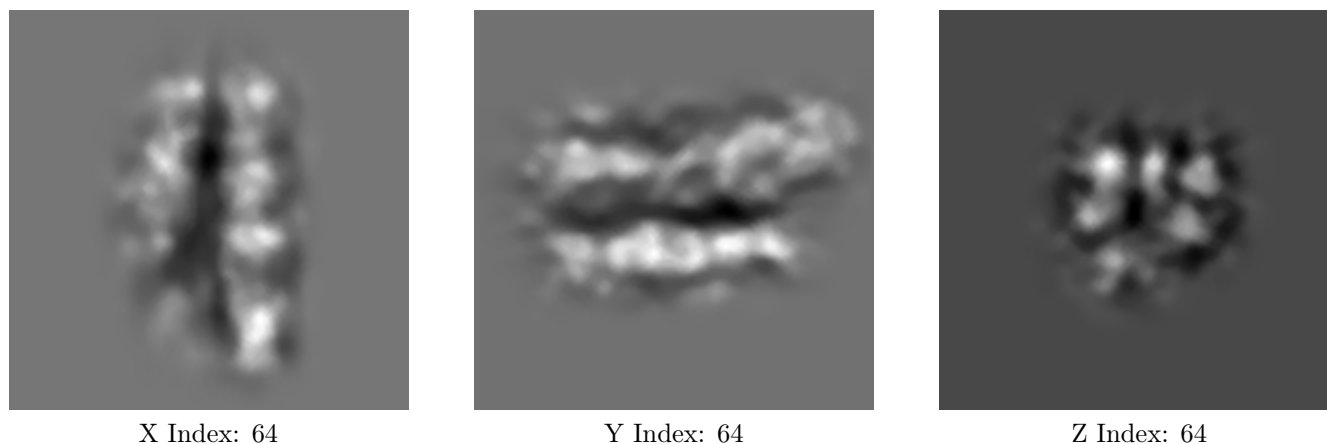
This section contains visualisations of the EMDB entry EMD-25231. These allow visual inspection of the internal detail of the tomogram and identification of artifacts.

### 2.1 Orthogonal projections [i](#)



The images above show the tomogram projected in three orthogonal directions.

### 2.2 Central slices [i](#)



The images above show central slices of the tomogram in three orthogonal directions.

## 2.3 Largest variance slices [i](#)



X Index: 53



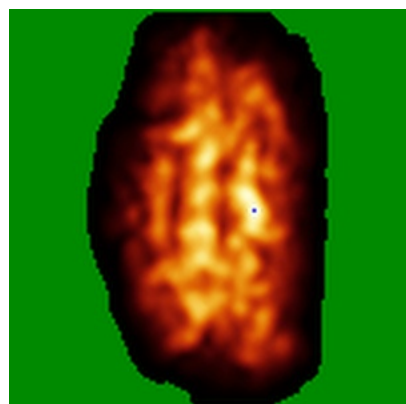
Y Index: 61



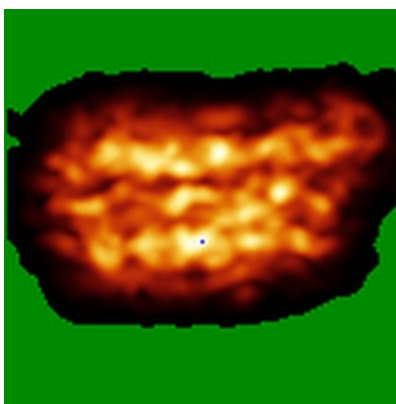
Z Index: 57

The images above show the largest variance slices of the tomogram in three orthogonal directions.

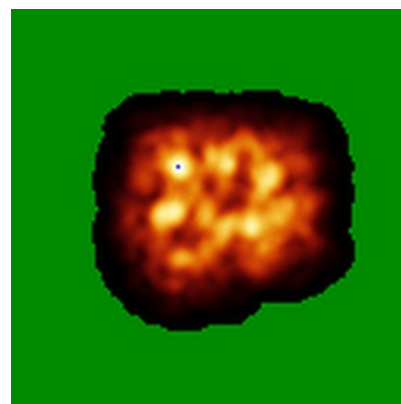
## 2.4 Orthogonal standard-deviation projections (False-color) [i](#)



X



Y



Z

The images above show the tomogram projected in three orthogonal directions.

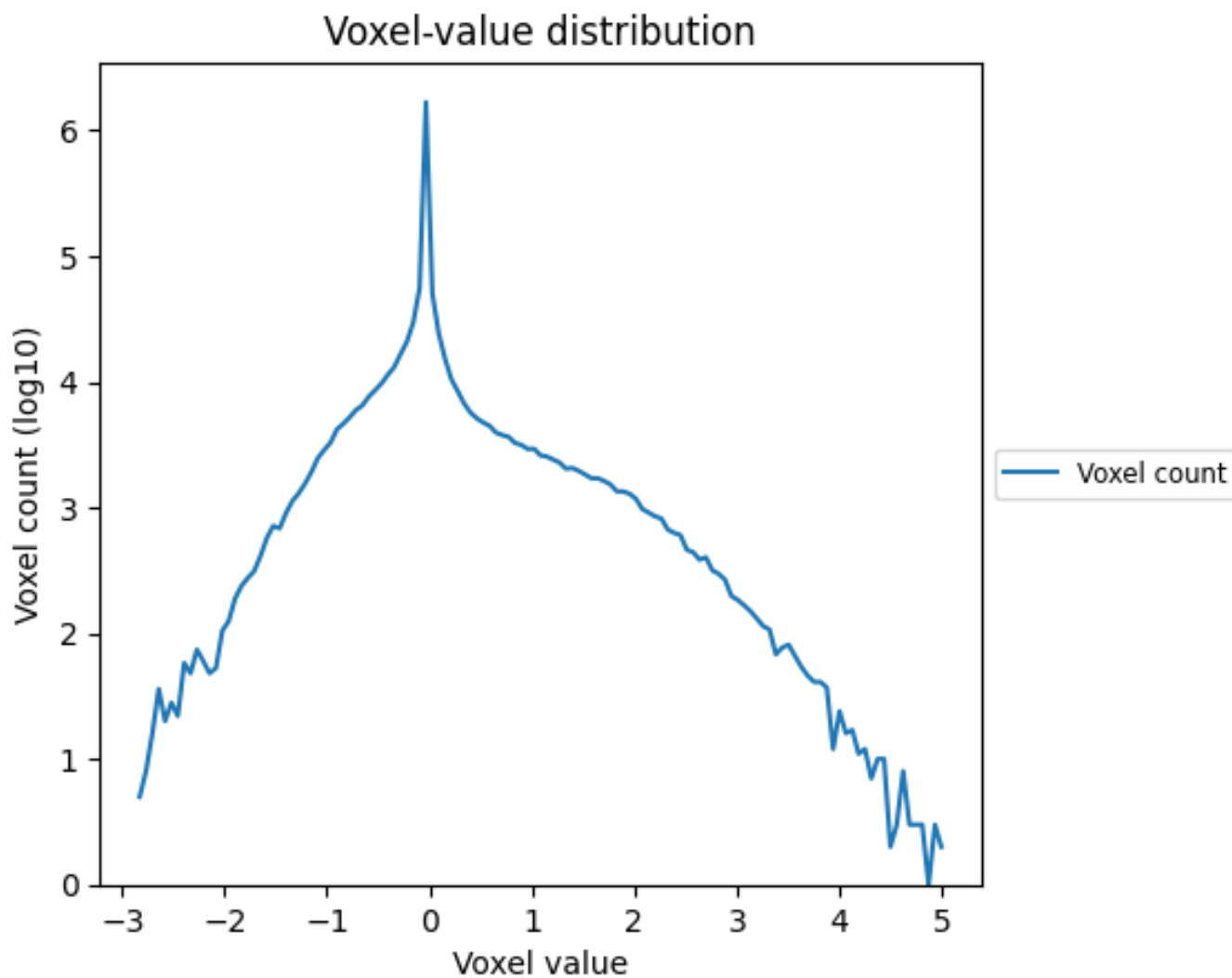
## 2.5 Mask visualisation [i](#)

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

### 3 Tomogram analysis [i](#)

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

#### 3.1 Voxel-value distribution [i](#)



The voxel-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic.