



Full wwPDB EM Validation Report ⓘ

Jun 29, 2023 – 06:04 PM EDT

EMDB ID : EMD-25357
Title : Tertiary structure of an individual particle of self-folding RNA polymer (particle #046)
Authors : Liu, J.; Ren, G.
Deposited on : 2021-10-30
Resolution : 25.50 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

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>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev50
Validation Pipeline (wwPDB-VP) : 2.33

1 Experimental information

| Property | Value | Source |
|--------------------------------------|-------------------------------|-----------|
| EM reconstruction method | TOMOGRAPHY | Depositor |
| Imposed symmetry | Not Provided | |
| Number of tilted images used | 21 | Depositor |
| Resolution determination method | FSC 0.143 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) | Not provided | |
| Maximum defocus (nm) | Not provided | |
| Magnification | 81000.0 | Depositor |
| Image detector | GATAN K3 BIOQUANTUM (6k x 4k) | Depositor |
| Maximum voxel value | 5.395 | Depositor |
| Minimum voxel value | -1.532 | Depositor |
| Average voxel value | 0.032 | Depositor |
| Voxel value standard deviation | 0.301 | Depositor |
| Recommended contour level | Not applicable | |
| Tomogram size (\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 (\AA) | 1.88, 1.88, 1.88 | Depositor |

2 Tomogram visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25357. These allow visual inspection of the internal detail of the tomogram and identification of artifacts.

2.1 Orthogonal projections [i](#)



X



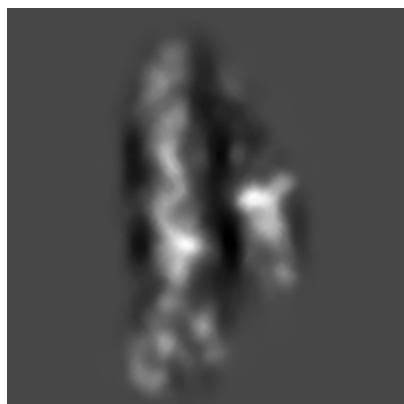
Y



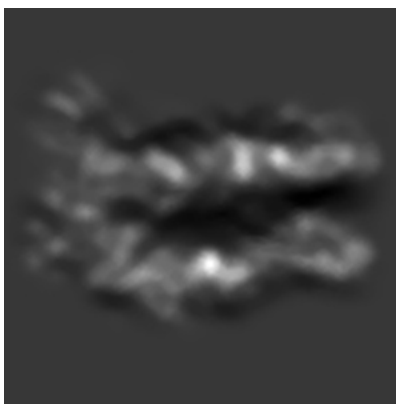
Z

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

2.2 Central slices [i](#)



X Index: 64



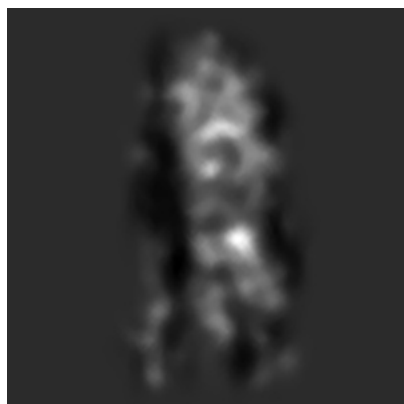
Y Index: 64



Z Index: 64

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

2.3 Largest variance slices [i](#)



X Index: 79



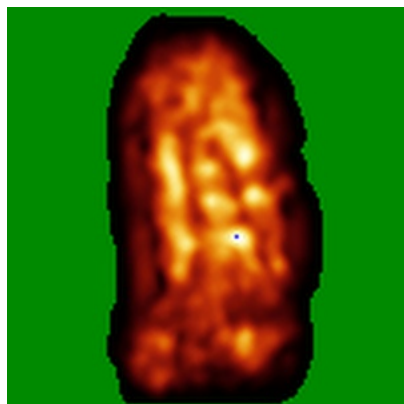
Y Index: 75



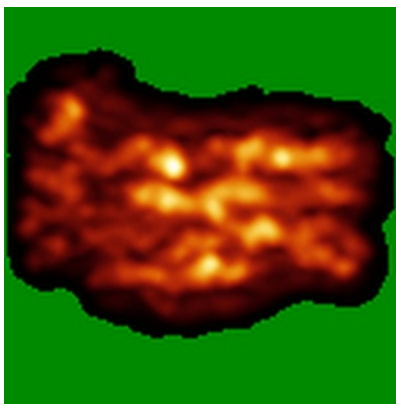
Z Index: 53

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

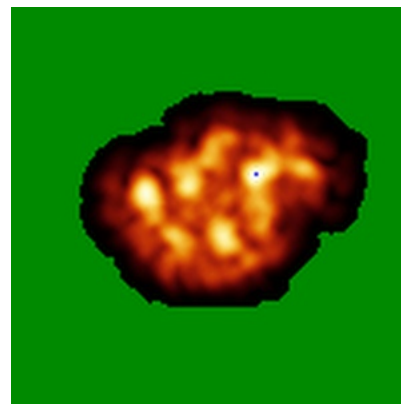
2.4 Orthogonal standard-deviation projections (False-color) [i](#)



X



Y



Z

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

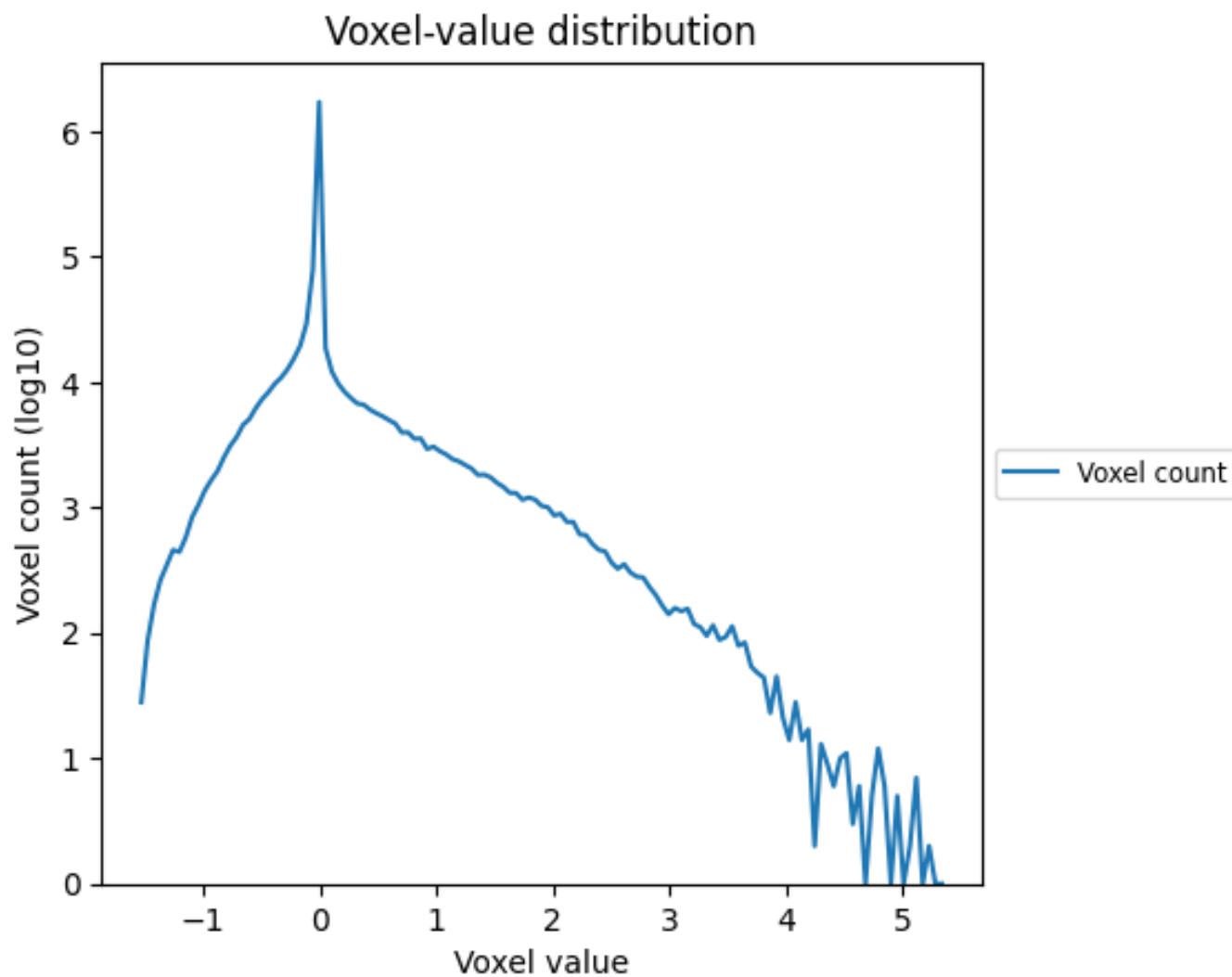
2.5 Mask visualisation [i](#)

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.