



Full wwPDB EM Validation Report ⓘ

Aug 11, 2025 – 03:25 PM EDT

EMDB ID : EMD-46136
Title : A non-averaged 3D density map of an individual particle, with a 2D lattice formed by octahedral DNA origami and ferritin, was revealed by individual particle cryo-electron tomography (Particle #067).
Authors : Liu, J.; Ren, G.
Deposited on : 2024-08-05
Resolution : 63.00 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

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.dev126
Validation Pipeline (wwPDB-VP) : 2.45.1

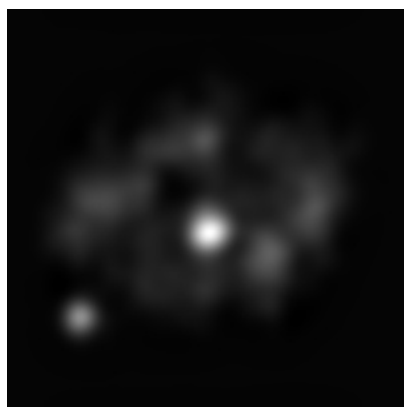
1 Experimental information

Property	Value	Source
EM reconstruction method	TOMOGRAPHY	Depositor
Imposed symmetry	Not Provided	
Number of tilted images used	1	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	The Contrast Transfer Function (CTF) was determined by Gctf and then corrected by TOMOCTF.	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	6.0	Depositor
Minimum defocus (nm)	2.0	Depositor
Maximum defocus (nm)	2.0	Depositor
Magnification	53000.0	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum voxel value	21.741	Depositor
Minimum voxel value	-0.819	Depositor
Average voxel value	0.099	Depositor
Voxel value standard deviation	0.519	Depositor
Recommended contour level	Not applicable	
Tomogram size (Å)	747.52, 747.52, 747.52	wwPDB
Tomogram dimensions	256, 256, 256	wwPDB
Tomogram angles (°)	90.0, 90.0, 90.0	wwPDB
Grid spacing (Å)	2.92, 2.92, 2.92	Depositor

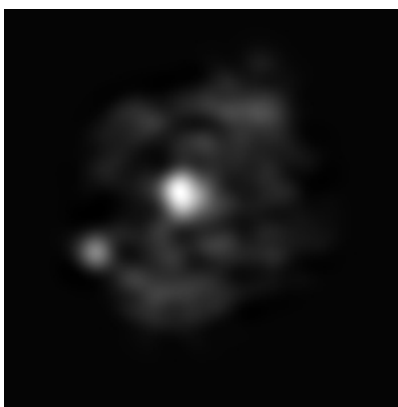
2 Tomogram visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-46136. These allow visual inspection of the internal detail of the tomogram and identification of artifacts.

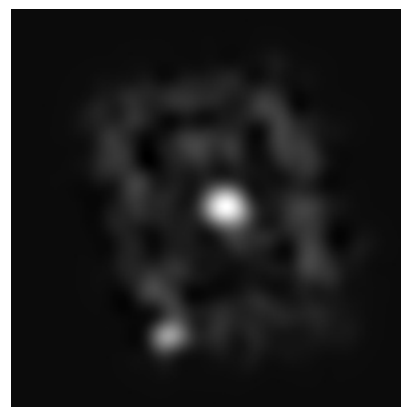
2.1 Orthogonal projections [i](#)



X



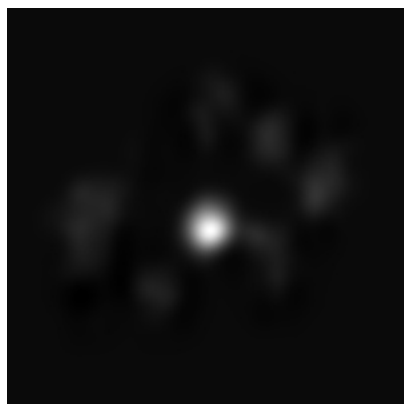
Y



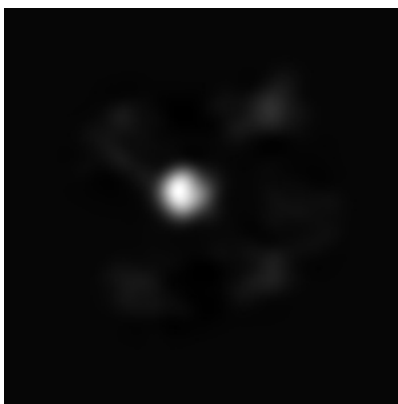
Z

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

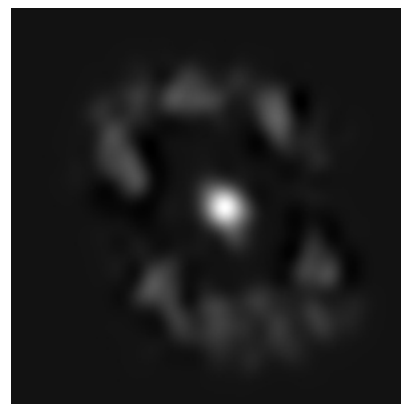
2.2 Central slices [i](#)



X Index: 128



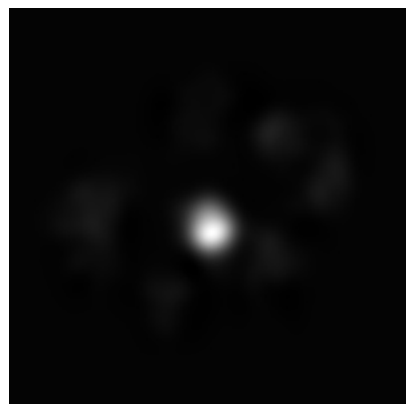
Y Index: 128



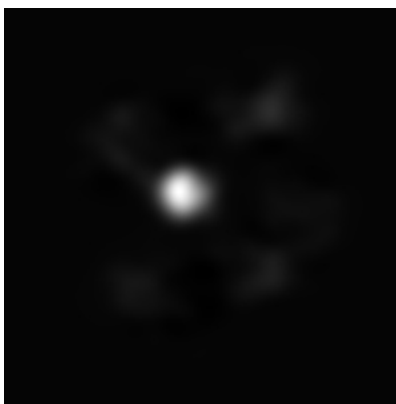
Z Index: 128

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

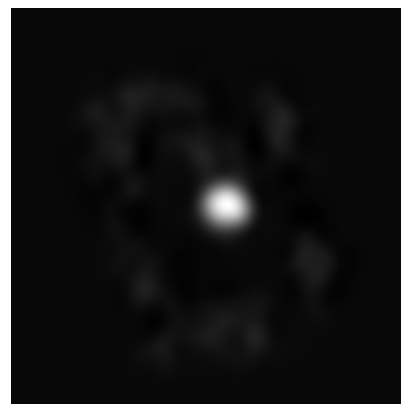
2.3 Largest variance slices [i](#)



X Index: 137



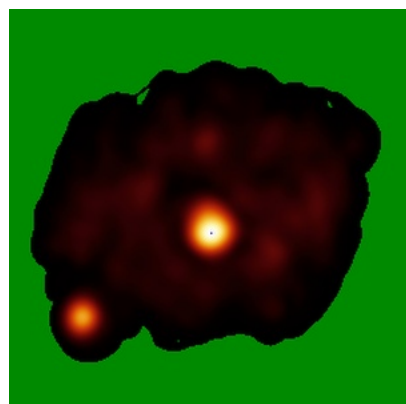
Y Index: 129



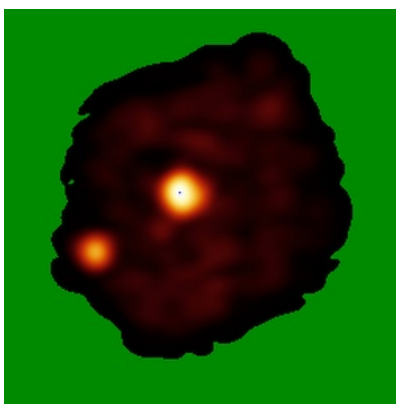
Z Index: 113

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

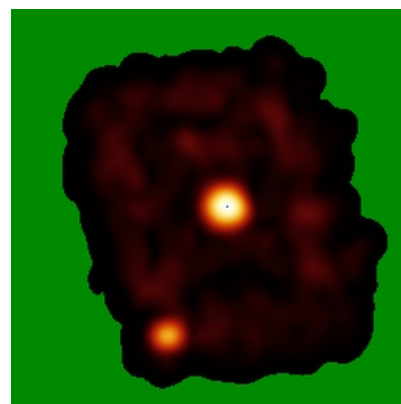
2.4 Orthogonal standard-deviation projections (False-color) [i](#)



X



Y



Z

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

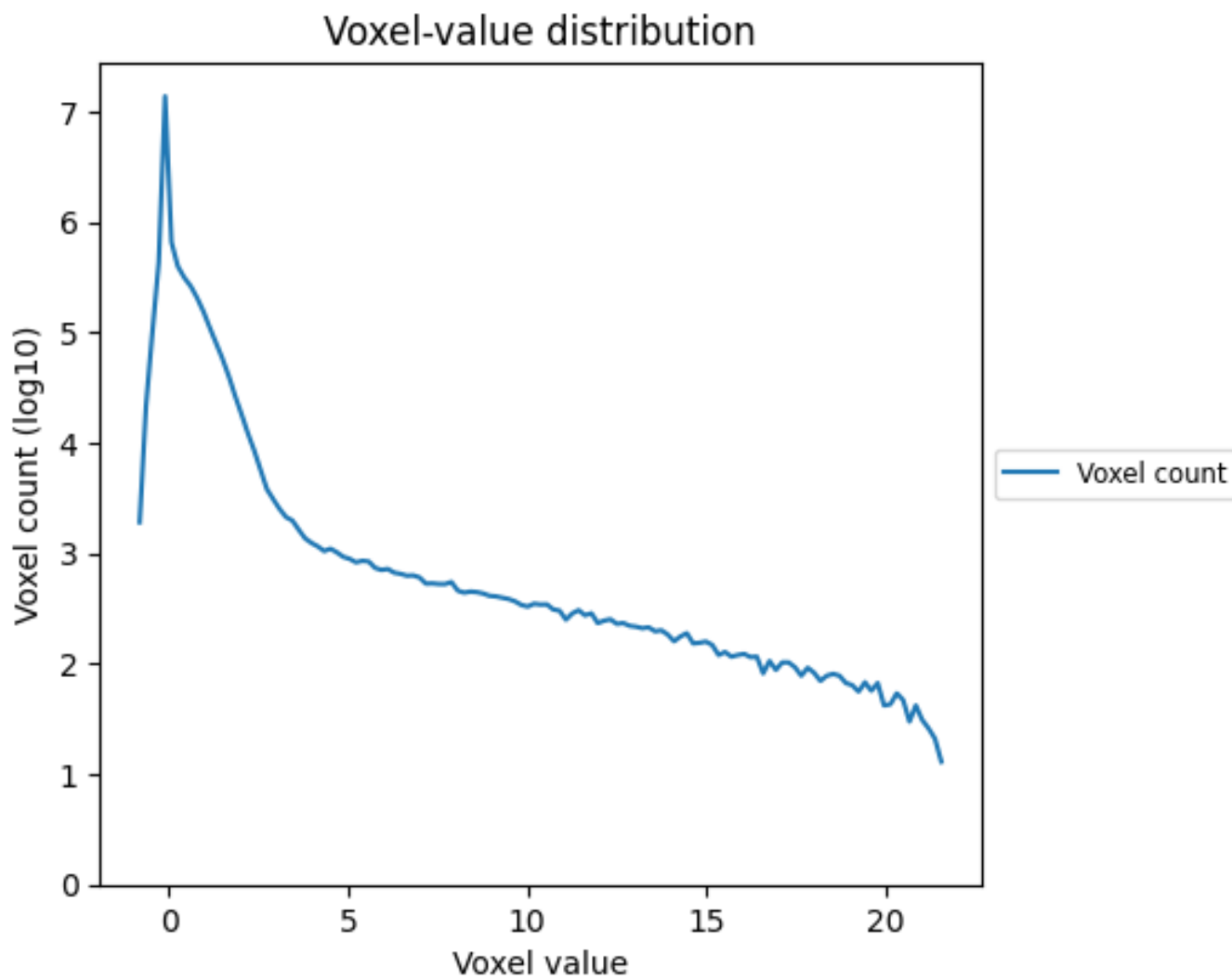
2.5 Mask visualisation [i](#)

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.