



wwPDB EM Validation Summary Report ⓘ

May 30, 2024 – 11:04 AM EDT

EMDB ID : EMD-28486
Title : Cryo-ET 3D reconstruction of an individual tetra-nucleosome-H1 particle in 5 mM NaCl and 20 mM HEPES buffer — Particle #194
Authors : Zhang, M.; Celis, C.D.; Liu, J.F.; Bustamante, C.; Ren, G.
Deposited on : 2022-10-04
Resolution : Not provided

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/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.dev92
Validation Pipeline (wwPDB-VP) : 2.36.2

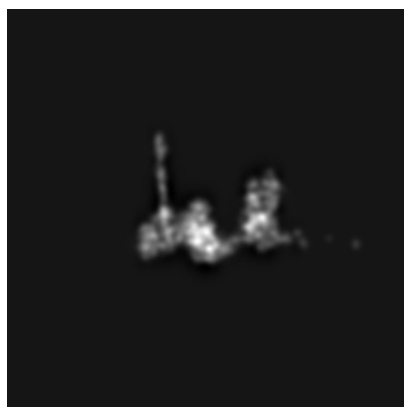
1 Experimental information

| Property | Value | Source |
|--------------------------------------|----------------------------|-----------|
| EM reconstruction method | TOMOGRAPHY | Depositor |
| Imposed symmetry | Not Provided | |
| Number of tilted images used | 35 | Depositor |
| Resolution determination method | Not provided | |
| CTF correction method | Not provided | |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 5.4 | Depositor |
| Minimum defocus (nm) | 2.5 | Depositor |
| Maximum defocus (nm) | 3.5 | Depositor |
| Magnification | Not provided | |
| Image detector | GATAN K2 QUANTUM (4k x 4k) | Depositor |
| Maximum voxel value | 1.221 | Depositor |
| Minimum voxel value | -0.254 | Depositor |
| Average voxel value | 0.001 | Depositor |
| Voxel value standard deviation | 0.015 | Depositor |
| Recommended contour level | Not applicable | |
| Tomogram size (\AA) | 1480.0, 1480.0, 1480.0 | wwPDB |
| Tomogram dimensions | 200, 200, 200 | wwPDB |
| Tomogram angles ($^\circ$) | 90.0, 90.0, 90.0 | wwPDB |
| Grid spacing (\AA) | 7.4, 7.4, 7.4 | Depositor |

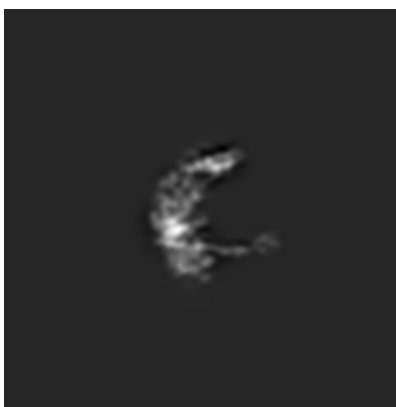
2 Tomogram visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-28486. 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: 100



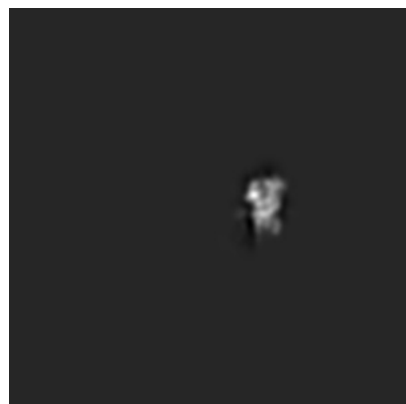
Y Index: 100



Z Index: 100

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

2.3 Largest variance slices [i](#)



X Index: 121



Y Index: 78



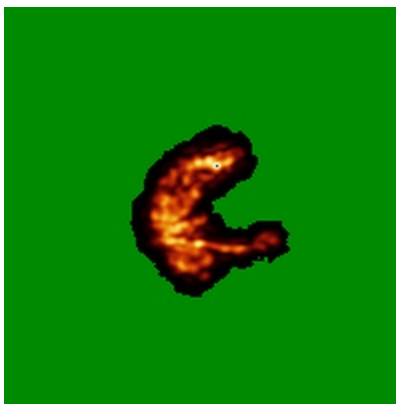
Z Index: 84

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

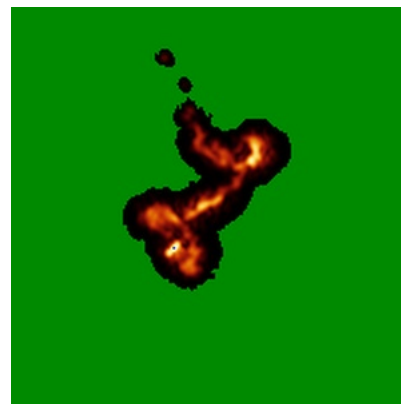
2.4 Orthogonal standard-deviation projections (False-color) [i](#)



X



Y



Z

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

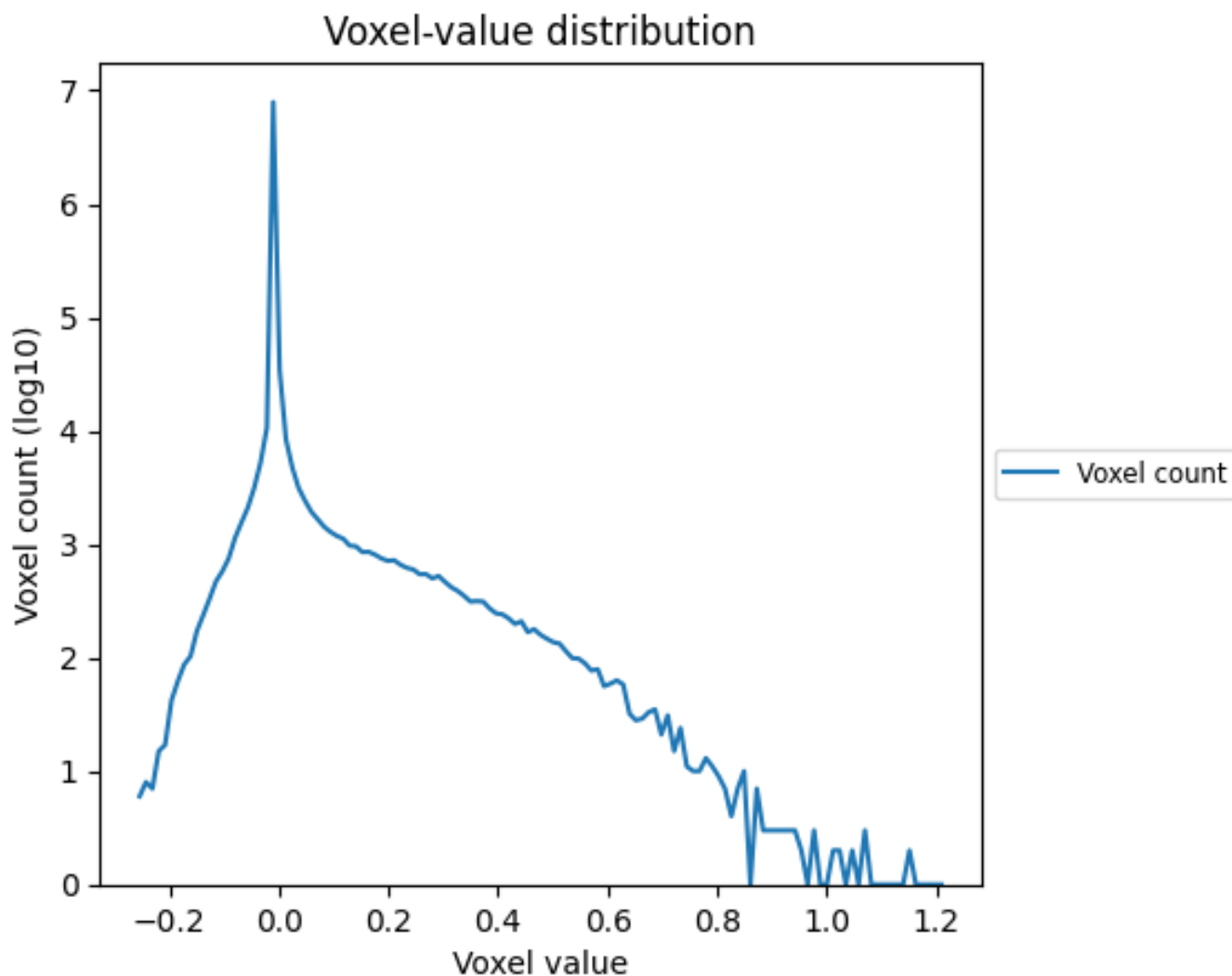
2.5 Mask visualisation [i](#)

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.