



# Full wwPDB EM Validation Report ⓘ

Oct 14, 2022 – 05:10 AM EDT

EMDB ID : EMD-28526  
Title : Cryo-ET 3D reconstruction of an individual tetra-nucleosome particle in 50 mM NaCl and 20 mM HEPES buffer — Particle #175  
Deposited on : 2022-10-05  
Resolution : Not provided

**This wwPDB validation report is for manuscript review**

This is a Full wwPDB EM Validation Report.

This report is produced by the wwPDB biocuration pipeline after annotation of the structure.

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.dev43  
Validation Pipeline (wwPDB-VP) : 2.31.2

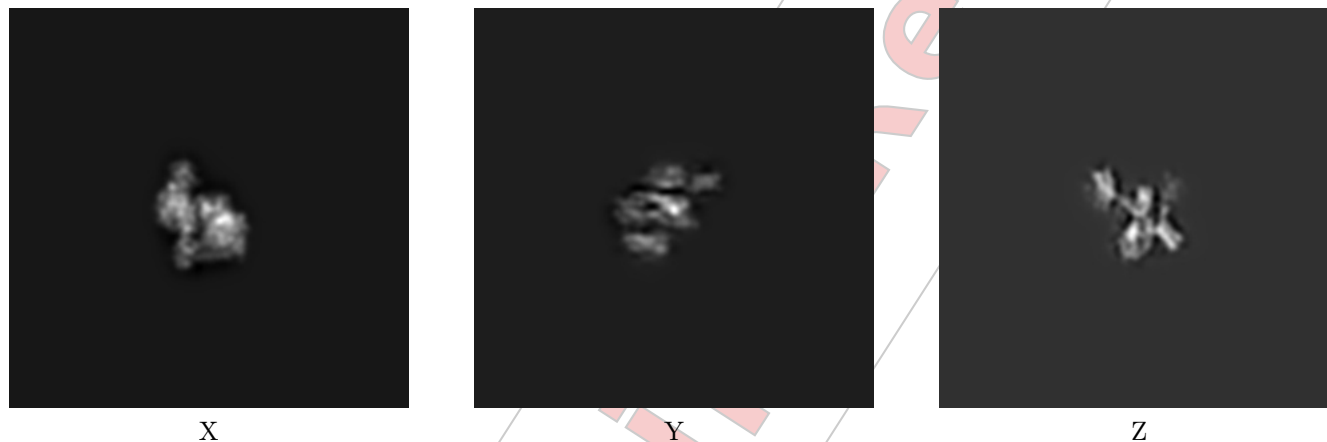
# 1 Experimental information ⓘ

Property	Value	Source
EM reconstruction method	TOMOGRAPHY	Depositor
Imposed symmetry	POINT, Not provided	
Number of tilted images used	35	Depositor
Resolution determination method	Not provided	
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	5.4	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum voxel value	1.070	Depositor
Minimum voxel value	-0.356	Depositor
Average voxel value	0.001	Depositor
Voxel value standard deviation	0.014	Depositor
Recommended contour level	0.07	Depositor
Tomogram size (Å)	1480.0, 1480.0, 1480.0	wwPDB
Tomogram dimensions	200, 200, 200	wwPDB
Tomogram angles (°)	90.0, 90.0, 90.0	wwPDB
Grid spacing (Å)	7.4, 7.4, 7.4	Depositor

## 2 Tomogram visualisation ⓘ

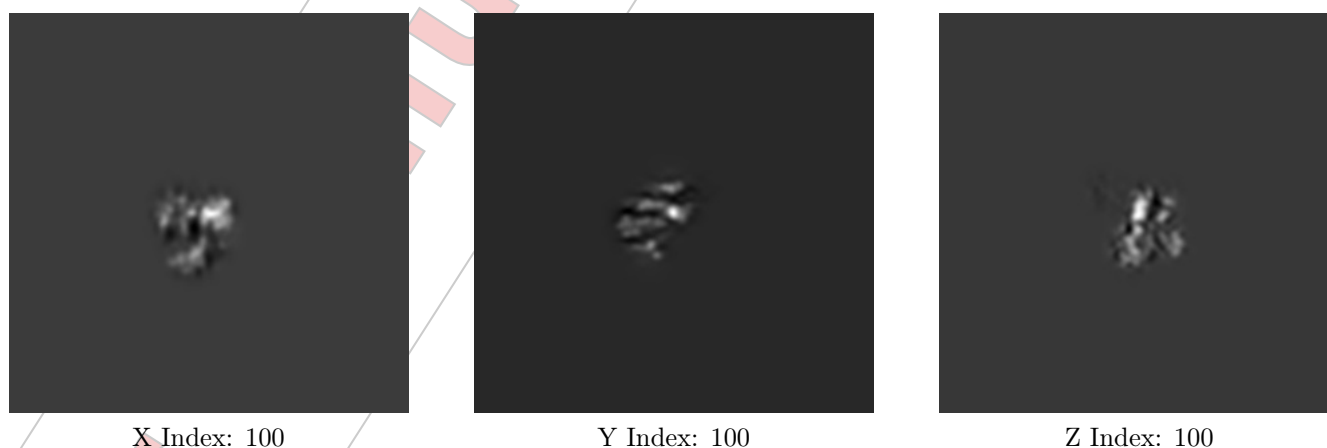
This section contains visualisations of the EMDB entry EMD-28526. These allow visual inspection of the internal detail of the tomogram and identification of artifacts.

### 2.1 Orthogonal projections ⓘ



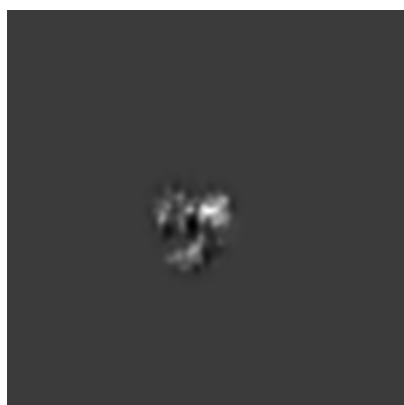
The images above show the tomogram projected in three orthogonal directions.

### 2.2 Central slices ⓘ



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

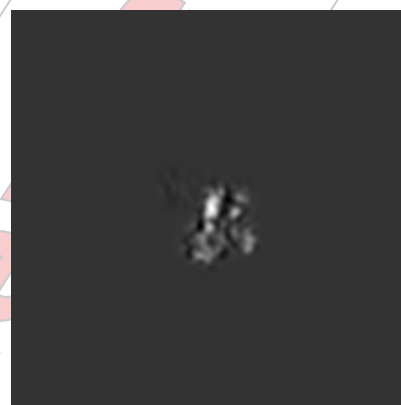
## 2.3 Largest variance slices [i](#)



X Index: 100



Y Index: 88



Z Index: 99

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

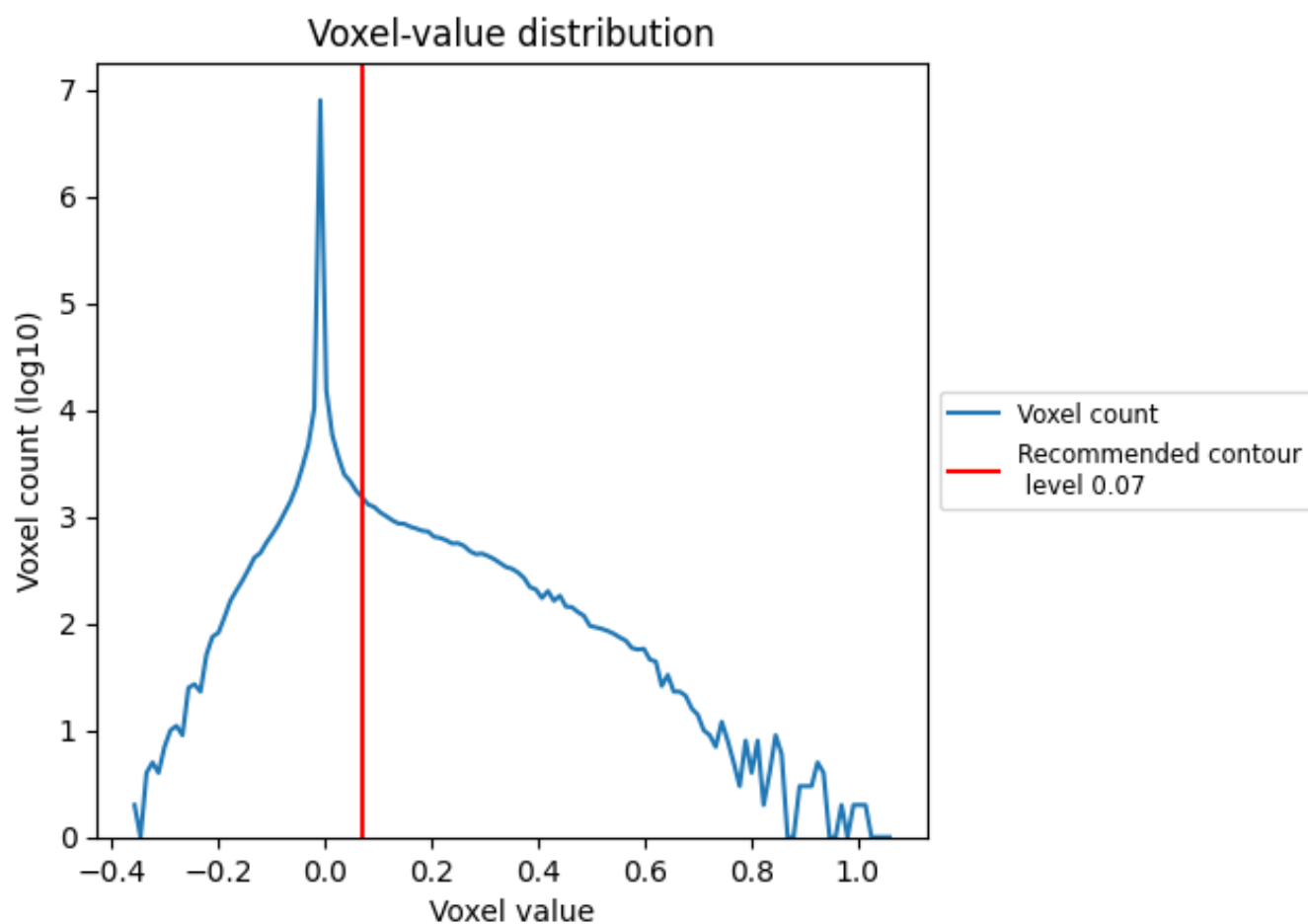
## 2.4 Mask visualisation [i](#)

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.