



## Full wwPDB EM Validation Report ⓘ

Mar 20, 2024 – 05:30 PM JST

EMDB ID : EMD-35401  
Title : Chromatin mass in frog erythrocyte nuclei in 110 mM PBS buffer (diluted by H<sub>2</sub>O)  
Authors : Ping, Z.; Yan, L.; Haonan, Z.  
Deposited on : 2023-02-17  
Resolution : Not provided

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.dev70  
Validation Pipeline (wwPDB-VP) : 2.36

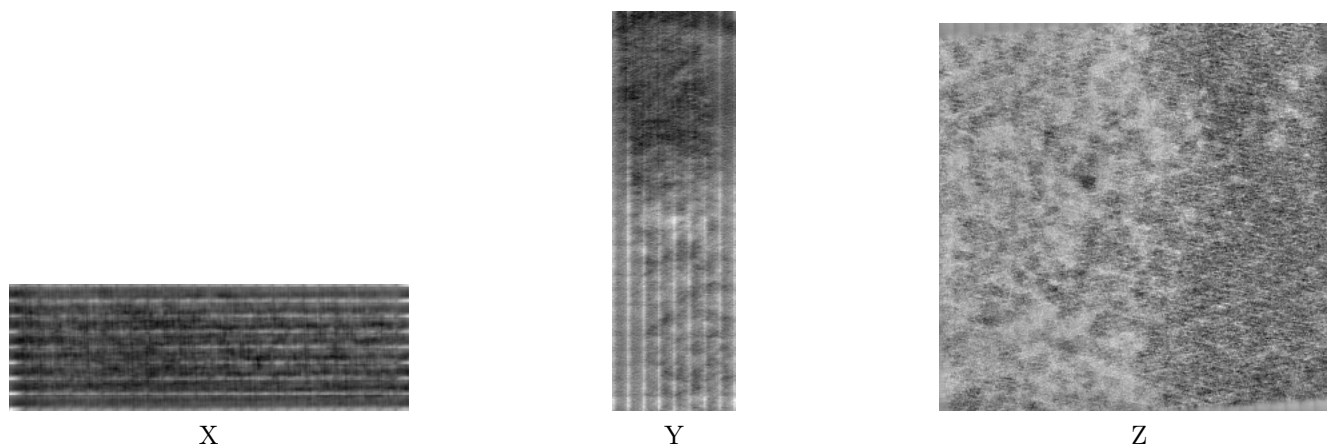
# 1 Experimental information

Property	Value	Source
EM reconstruction method	TOMOGRAPHY	Depositor
Imposed symmetry	Not Provided	
Number of tilted images used	50	Depositor
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	3.0	Depositor
Minimum defocus (nm)	4.0	Depositor
Maximum defocus (nm)	4.0	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum voxel value	1.313	Depositor
Minimum voxel value	-3.237	Depositor
Average voxel value	-0.468	Depositor
Voxel value standard deviation	0.283	Depositor
Recommended contour level	Not applicable	
Tomogram size ( $\text{\AA}$ )	10368.0, 10027.801, 3175.2002	wwPDB
Tomogram dimensions	1280, 1238, 392	wwPDB
Tomogram angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Grid spacing ( $\text{\AA}$ )	8.1, 8.1, 8.1	Depositor

## 2 Tomogram visualisation [i](#)

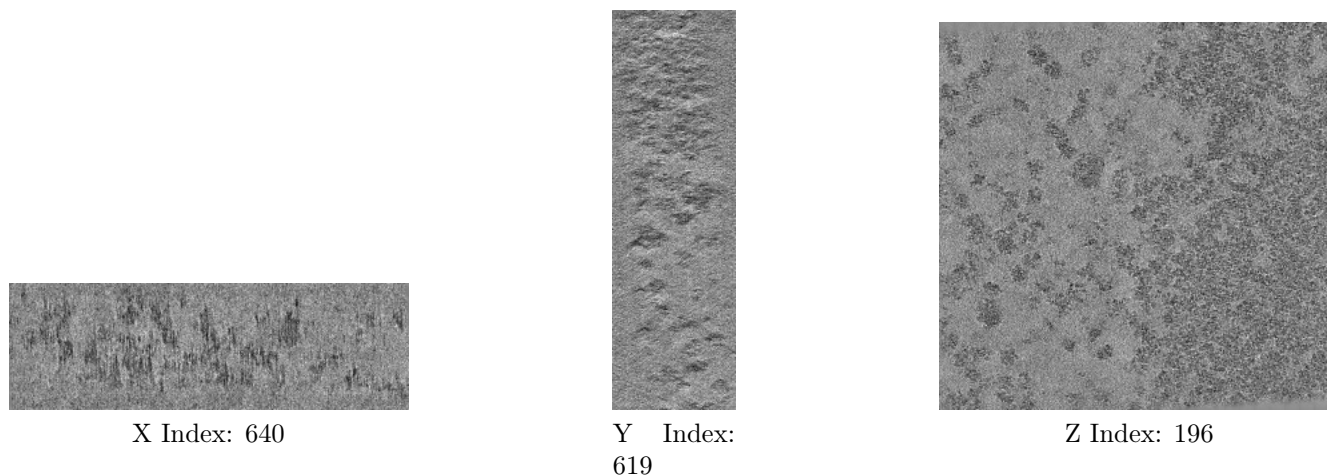
This section contains visualisations of the EMDB entry EMD-35401. These allow visual inspection of the internal detail of the tomogram and identification of artifacts.

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



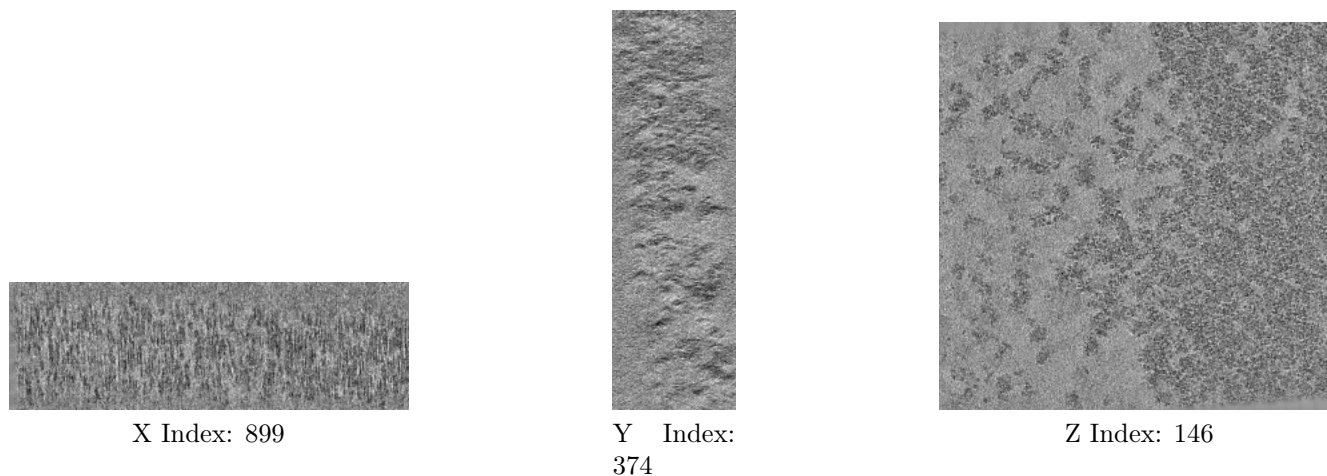
The images above show the tomogram projected in three orthogonal directions.

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



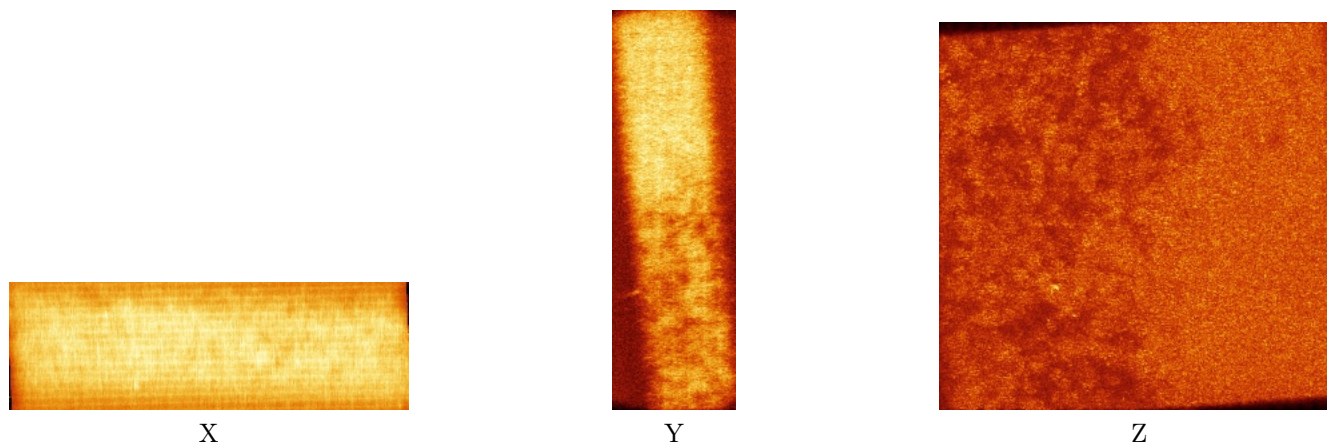
The images above show central slices of the tomogram in three orthogonal directions.

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



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

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



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

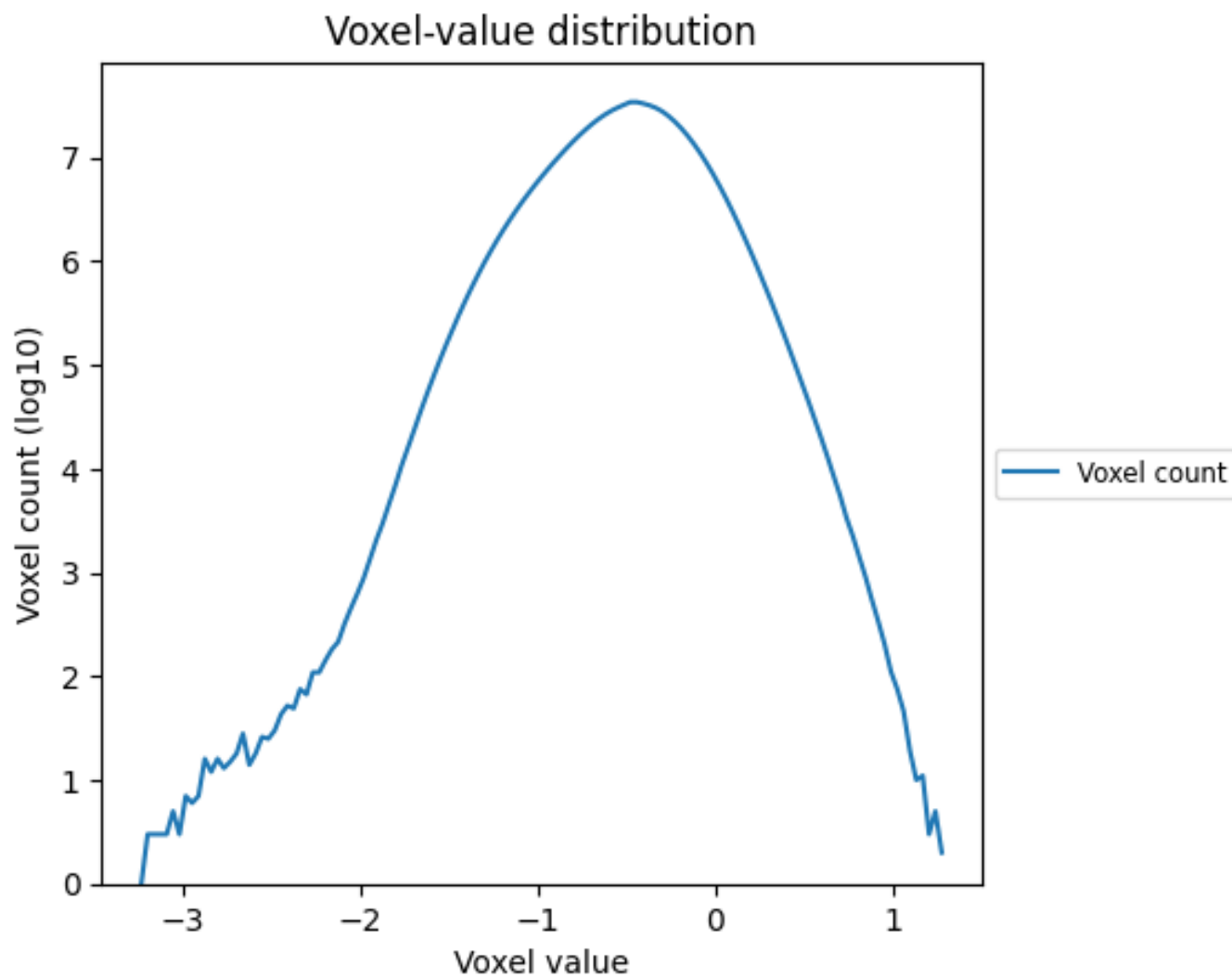
## 2.5 Mask visualisation [i](#)

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.