



## Full wwPDB EM Validation Report ⓘ

Jan 6, 2022 – 04:34 pm GMT

EMDB ID : EMD-13835  
Title : Subtomogram average of 80S ribosomes a cryo-FIB-lamella of Sum159 human cell line prepared after cryo-FIB-SEM volume imaging  
Authors : Klumpe, S.; Fung, H.K.H.; Goetz, S.K.; Plitzko, J.M.; Mahamid, J.  
Deposited on : 2021-11-03  
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.

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

EMDB validation analysis : 0.0.0.dev97  
Validation Pipeline (wwPDB-VP) : 2.24

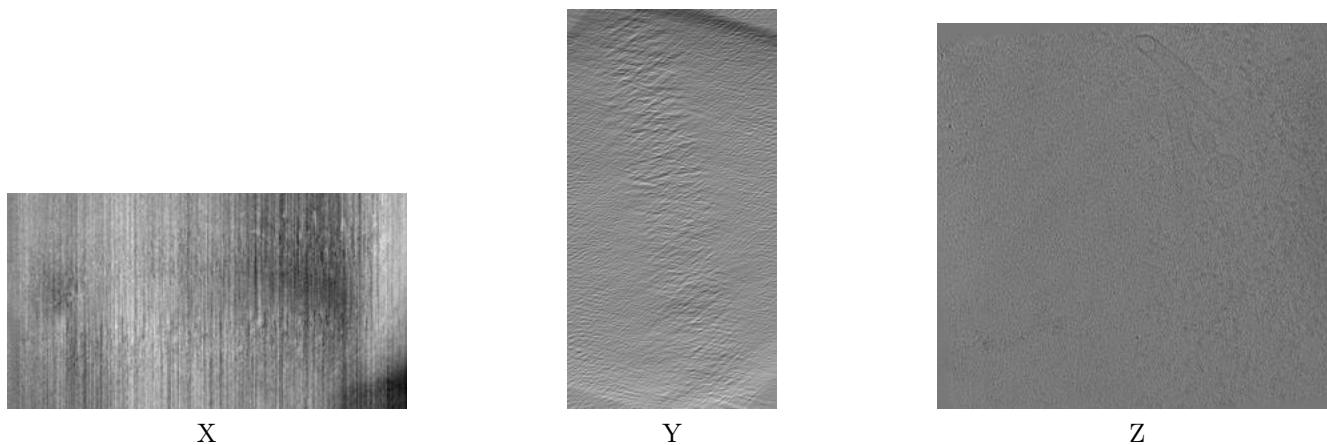
# 1 Experimental information

Property	Value	Source
EM reconstruction method	TOMOGRAPHY	Depositor
Imposed symmetry	Not Provided	
Number of tilted images used	57	Depositor
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	2.27915	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum voxel value	114.085	Depositor
Minimum voxel value	-152.923	Depositor
Average voxel value	0.628	Depositor
Voxel value standard deviation	5.579	Depositor
Recommended contour level	Not applicable	
Tomogram size ( $\text{\AA}$ )	12941.567, 12510.182, 6740.4	wwPDB
Tomogram dimensions	960, 928, 500	wwPDB
Tomogram angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Grid spacing ( $\text{\AA}$ )	13.4808, 13.480799, 13.4808	Depositor

## 2 Tomogram visualisation [i](#)

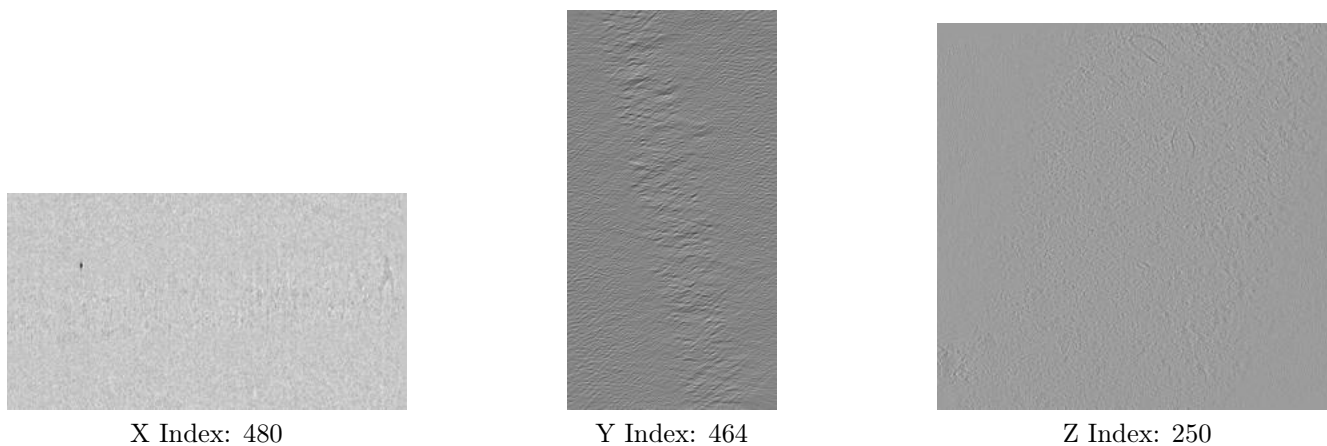
This section contains visualisations of the EMDB entry EMD-13835. These allow visual inspection of the internal detail of the tomogram and identification of artifacts.

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



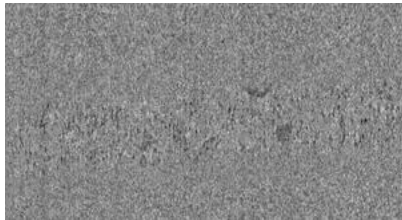
The images above show the tomogram projected in three orthogonal directions.

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



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

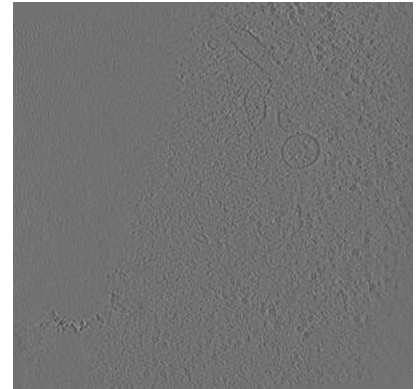
## 2.3 Largest variance slices [i](#)



X Index: 637



Y Index: 172



Z Index: 216

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

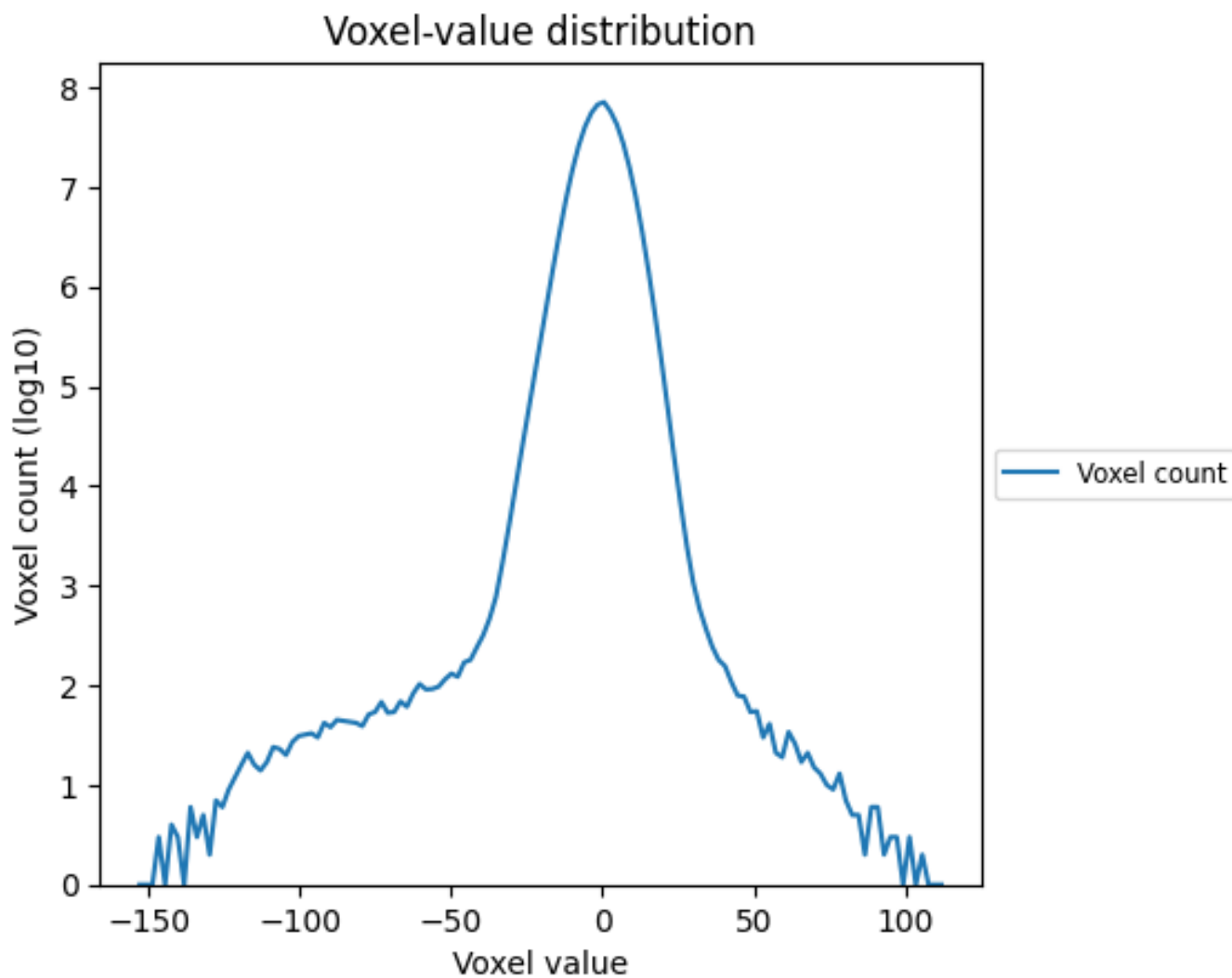
## 2.4 Mask visualisation [i](#)

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.