



## wwPDB EM Validation Summary Report ⓘ

Mar 31, 2021 – 10:28 am BST

EMDB ID : EMD-2884  
Title : Cryo-Molecular electron tomography of PfEMP1-IT4Var60)  
Authors : Akhouri, R.R.; Goel, S.; Furusho, H.; Skoglund, U.; Wahlgren, M.  
Deposited on : 2015-02-08  
Resolution : 20.00 Å(reported)

This is a wwPDB EM Validation Summary 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.dev75  
Validation Pipeline (wwPDB-VP) : 2.18

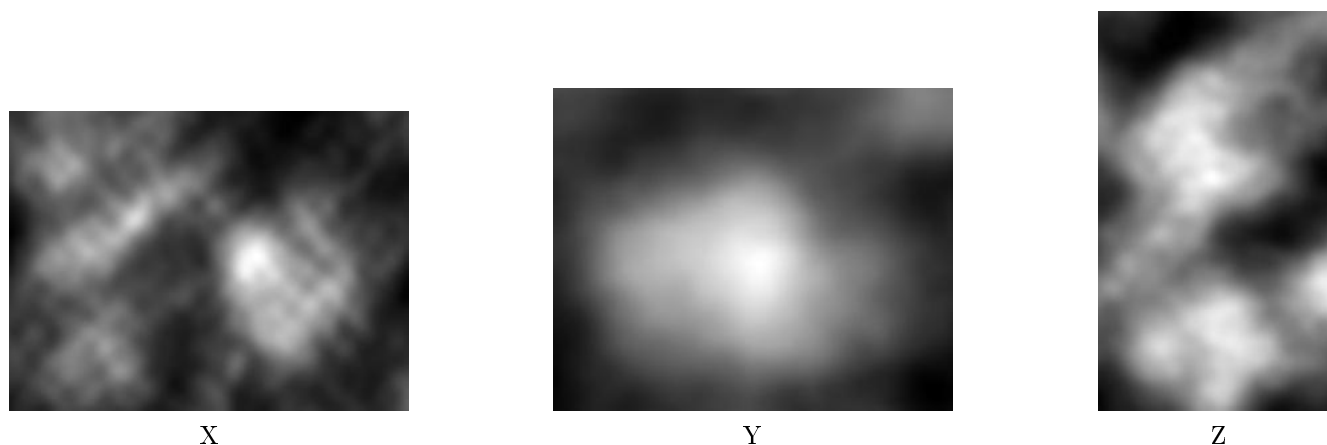
# 1 Experimental information ⓘ

| Property                             | Value                         | Source    |
|--------------------------------------|-------------------------------|-----------|
| EM reconstruction method             | TOMOGRAPHY                    | Depositor |
| Imposed symmetry                     | Not Provided                  |           |
| Number of tilted images used         | 281                           | Depositor |
| Resolution determination method      | Not provided                  |           |
| CTF correction method                | each frame                    | Depositor |
| Microscope                           | FEI TITAN KRIOS               | Depositor |
| Voltage (kV)                         | 300                           | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 40                            | Depositor |
| Minimum defocus (nm)                 | 0.0007                        | Depositor |
| Maximum defocus (nm)                 | 0.0015                        | Depositor |
| Magnification                        | 37000.0                       | Depositor |
| Image detector                       | FEI FALCON II (4k x 4k)       | Depositor |
| Maximum voxel value                  | 0.028                         | Depositor |
| Minimum voxel value                  | 0.000                         | Depositor |
| Average voxel value                  | 0.006                         | Depositor |
| Voxel value standard deviation       | 0.004                         | Depositor |
| Recommended contour level            | 0.013                         | Depositor |
| Tomogram size ( $\text{\AA}$ )       | 140.554, 233.50099, 174.55899 | wwPDB     |
| Tomogram dimensions                  | 62, 103, 77                   | wwPDB     |
| Tomogram angles ( $^\circ$ )         | 90.0, 90.0, 90.0              | wwPDB     |
| Grid spacing ( $\text{\AA}$ )        | 2.267, 2.267, 2.267           | Depositor |

## 2 Tomogram visualisation [i](#)

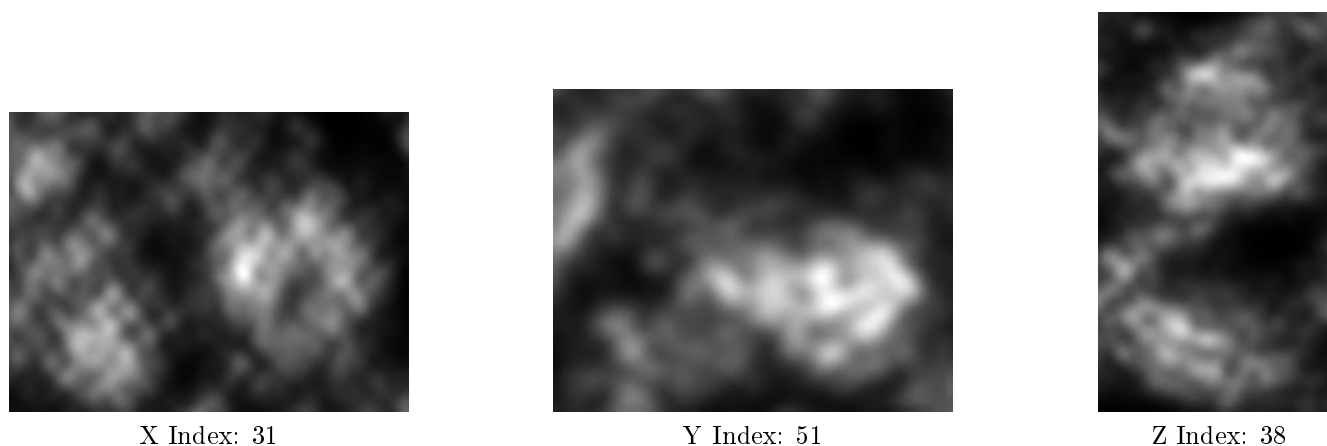
This section contains visualisations of the EMDB entry EMD-2884. These allow visual inspection of the internal detail of the tomogram and identification of artifacts.

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



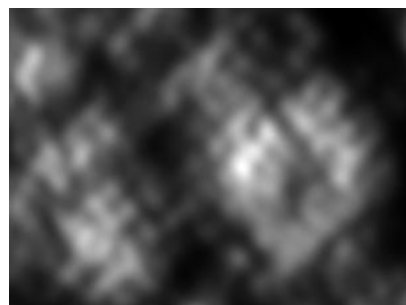
The images above show the tomogram projected in three orthogonal directions.

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

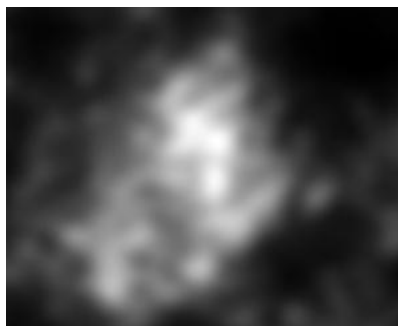


The images above show central slices of the tomogram in three orthogonal directions.

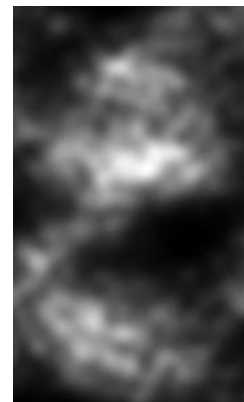
## 2.3 Largest variance slices [i](#)



X Index: 29



Y Index: 63



Z Index: 39

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

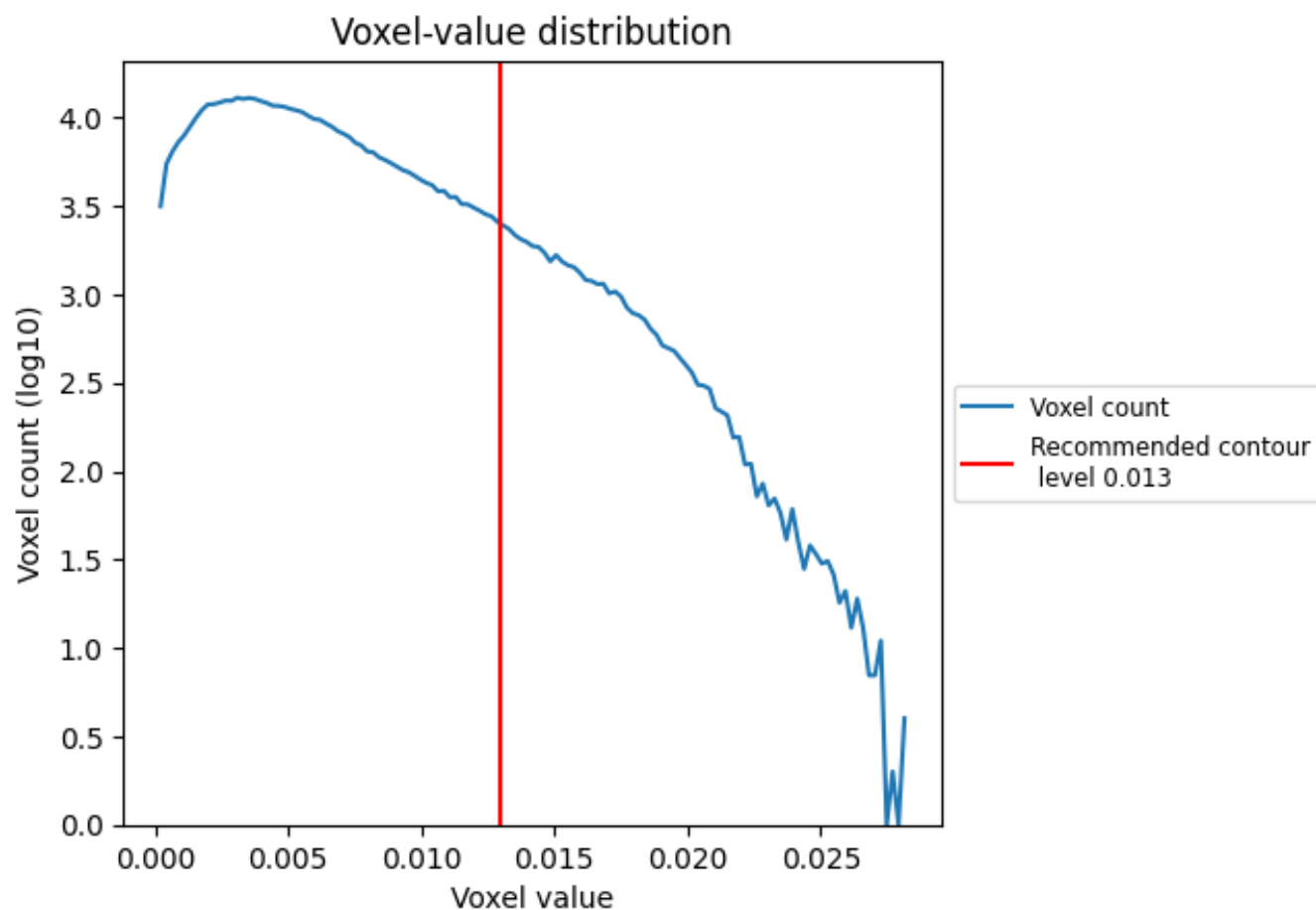
## 2.4 Mask visualisation [i](#)

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.