



## wwPDB EM Validation Summary Report ⓘ

Dec 5, 2023 – 10:42 pm GMT

EMDB ID : EMD-16203  
Title : Cryo electron tomogram of Streptomyces coelicolor - Ghost cells  
Authors : Casu, B.; Sallmen, J.W.; Schlimpert, S.; Pilhofer, M.  
Deposited on : 2022-11-22  
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](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

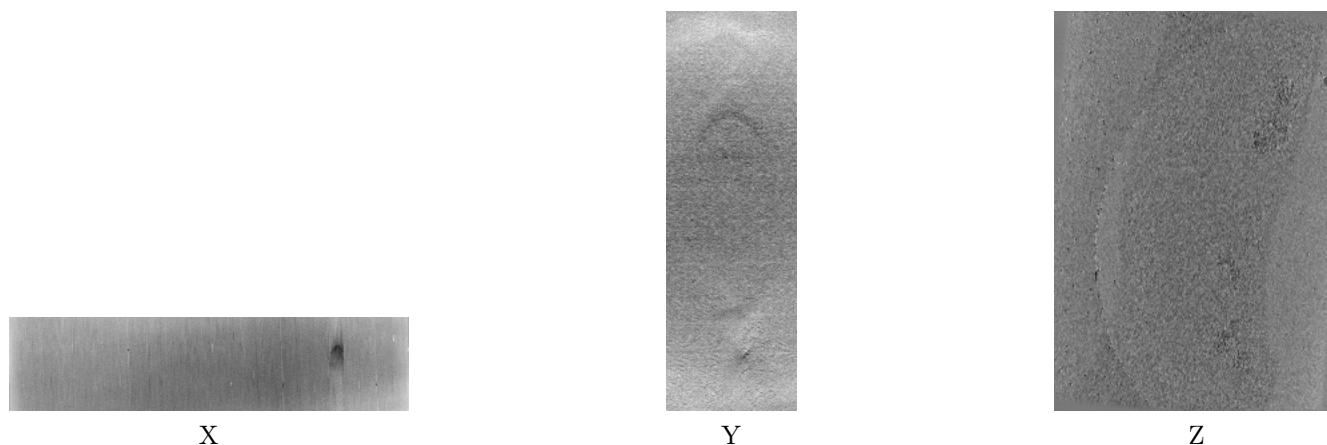
# 1 Experimental information

| Property                             | Value                     | Source    |
|--------------------------------------|---------------------------|-----------|
| EM reconstruction method             | TOMOGRAPHY                | Depositor |
| Imposed symmetry                     | Not Provided              |           |
| Number of tilted images used         | 61                        | Depositor |
| Resolution determination method      | Not provided              |           |
| CTF correction method                | Not provided              |           |
| Microscope                           | FEI TITAN KRIOS           | Depositor |
| Voltage (kV)                         | 300                       | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 2.1                       | Depositor |
| Minimum defocus (nm)                 | 8.0                       | Depositor |
| Maximum defocus (nm)                 | 8.0                       | Depositor |
| Magnification                        | Not provided              |           |
| Image detector                       | GATAN K2 SUMMIT (4k x 4k) | Depositor |
| Maximum voxel value                  | 272.000                   | Depositor |
| Minimum voxel value                  | -428.000                  | Depositor |
| Average voxel value                  | 1.806                     | Depositor |
| Voxel value standard deviation       | 11.768                    | Depositor |
| Recommended contour level            | Not applicable            |           |
| Tomogram size ( $\text{\AA}$ )       | 13926.4, 19584.0, 4515.2  | wwPDB     |
| Tomogram dimensions                  | 1024, 1440, 332           | wwPDB     |
| Tomogram angles ( $^\circ$ )         | 90.0, 90.0, 90.0          | wwPDB     |
| Grid spacing ( $\text{\AA}$ )        | 13.6, 13.6, 13.6          | Depositor |

## 2 Tomogram visualisation [i](#)

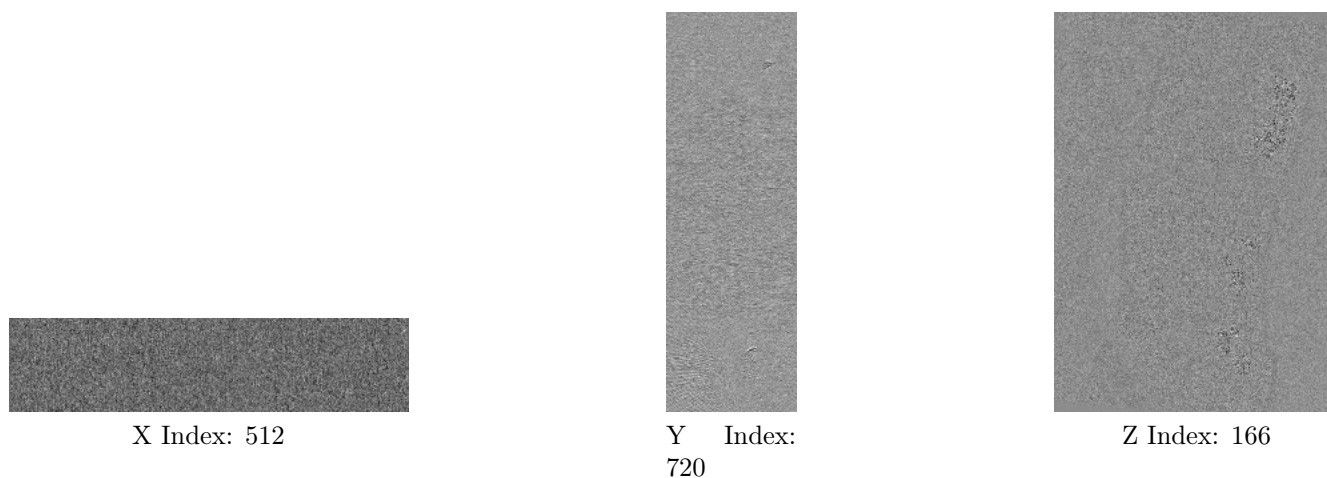
This section contains visualisations of the EMDB entry EMD-16203. These allow visual inspection of the internal detail of the tomogram and identification of artifacts.

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



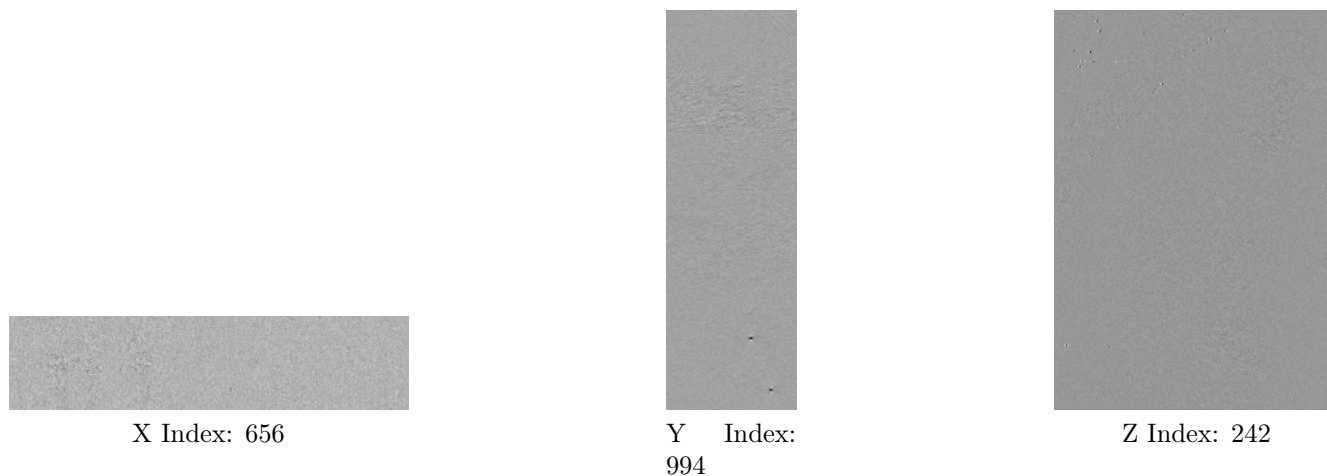
The images above show the tomogram projected in three orthogonal directions.

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



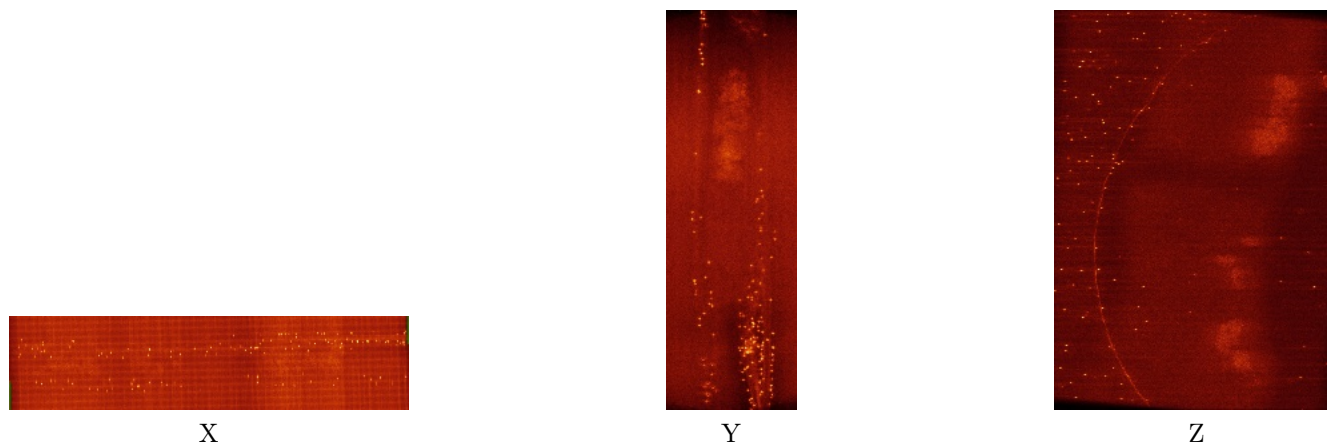
The images above show central slices of the tomogram in three orthogonal directions.

## 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.

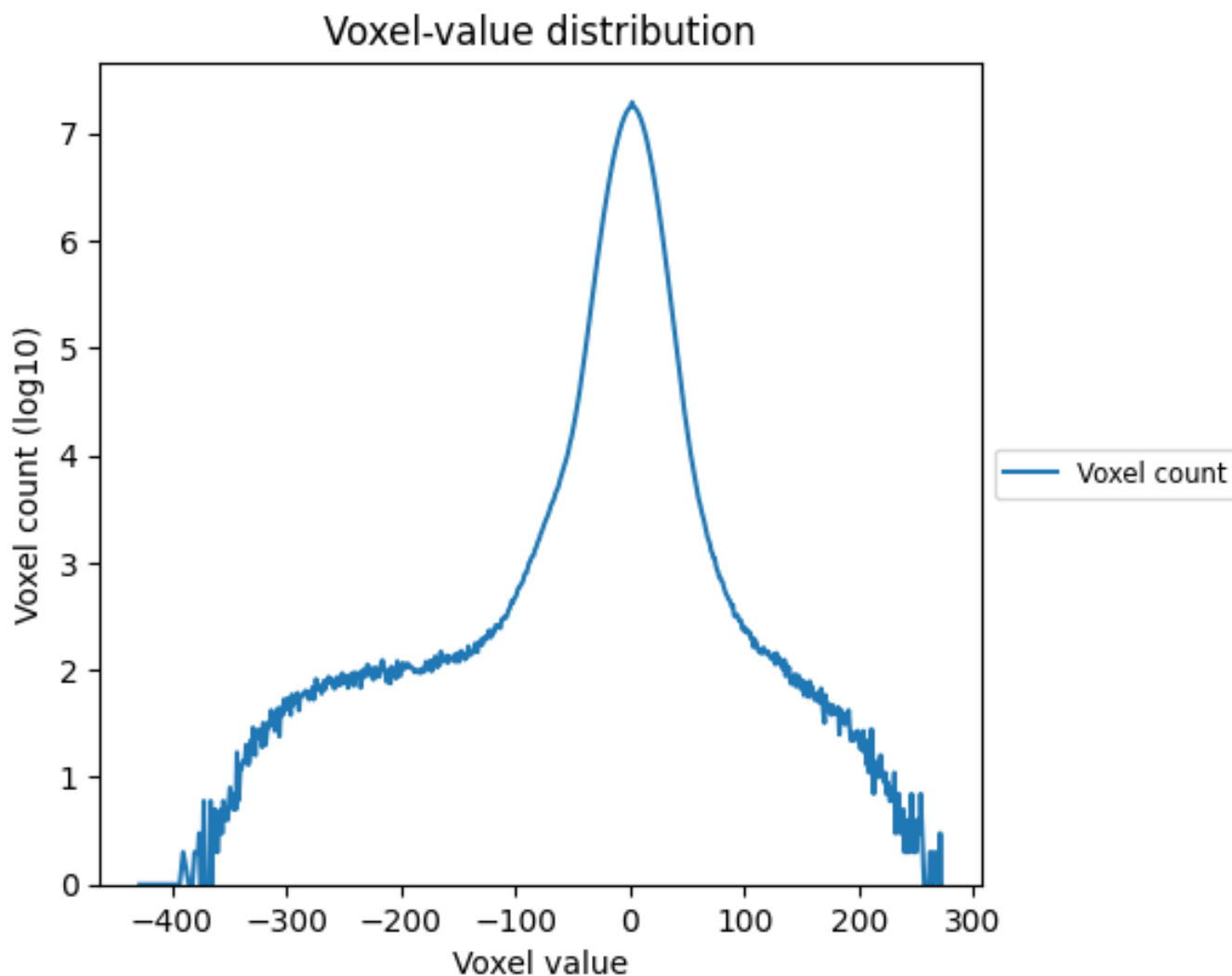
## 2.5 Mask visualisation [i](#)

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.