



## wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 01:23 PM UTC

EMDB ID : EMD-0529  
Title : Purified ribosome - A complete data processing workflow for CryoET and subtomogram averaging  
Authors : Chen, M.; Bell, J.M.; Ludtke, S.J.  
Deposited on : 2019-02-07  
Resolution : 8.40 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.

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.dev132  
Validation Pipeline (wwPDB-VP) : 2.49

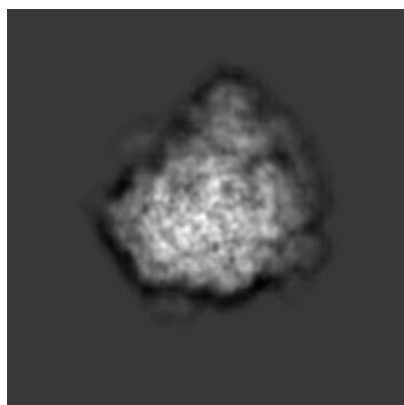
# 1 Experimental information

Property	Value	Source
EM reconstruction method	TOMOGRAPHY	Depositor
Imposed symmetry	Not Provided	
Number of tilted images used	3239	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	30.0	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum voxel value	6.825	Depositor
Minimum voxel value	-2.729	Depositor
Average voxel value	0.062	Depositor
Voxel value standard deviation	0.456	Depositor
Recommended contour level	Not applicable	
Tomogram size ( $\text{\AA}$ )	471.59998, 471.59998, 471.59998	wwPDB
Tomogram dimensions	180, 180, 180	wwPDB
Tomogram angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Grid spacing ( $\text{\AA}$ )	2.62, 2.62, 2.62	Depositor

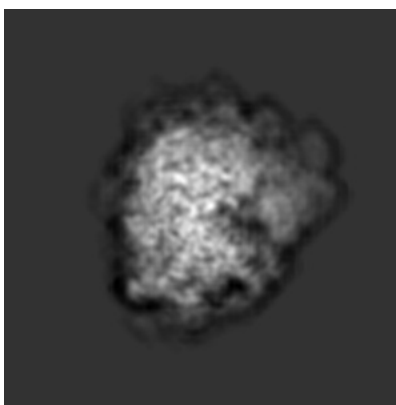
## 2 Tomogram visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0529. These allow visual inspection of the internal detail of the tomogram and identification of artifacts.

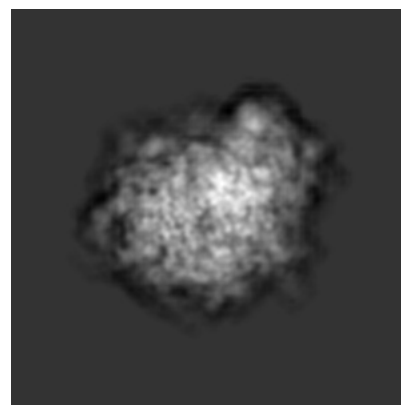
### 2.1 Orthogonal projections [i](#)



X



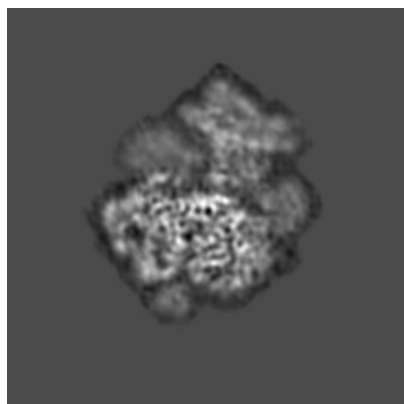
Y



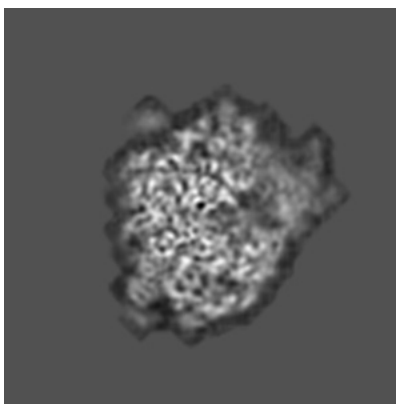
Z

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

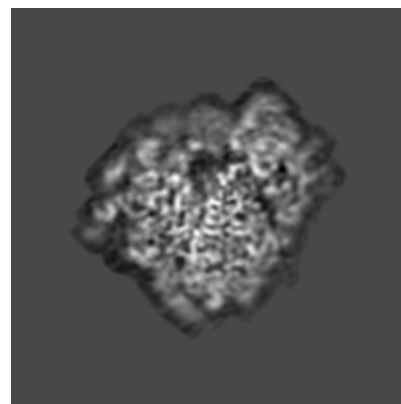
### 2.2 Central slices [i](#)



X Index: 90



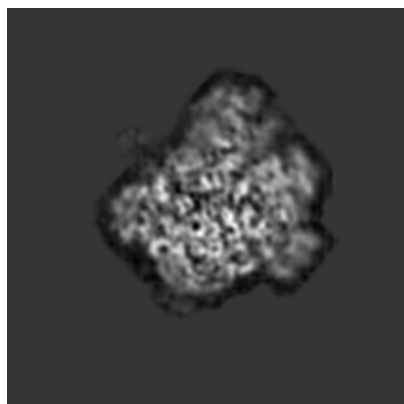
Y Index: 90



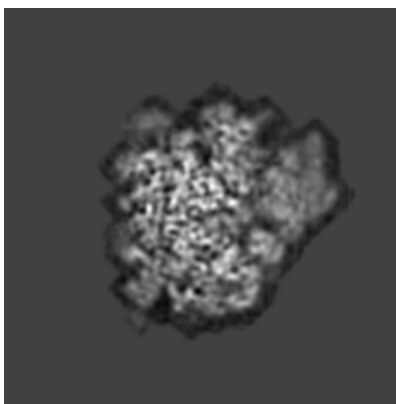
Z Index: 90

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

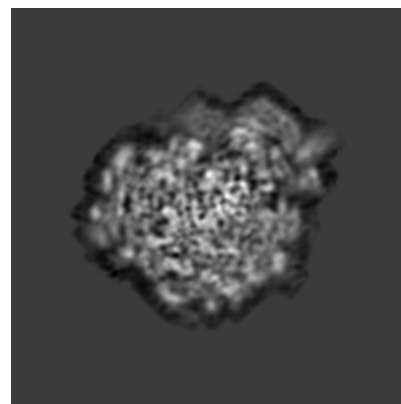
## 2.3 Largest variance slices [i](#)



X Index: 104



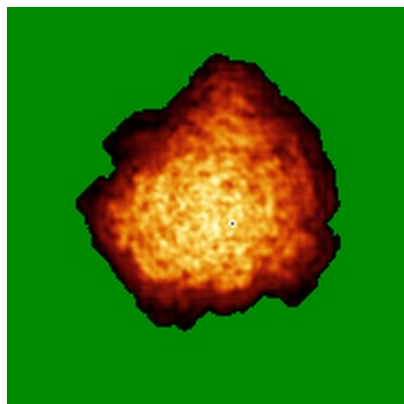
Y Index: 93



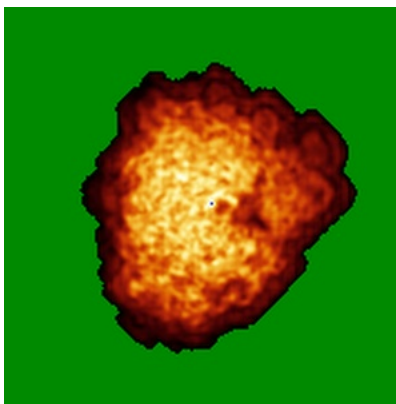
Z Index: 86

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

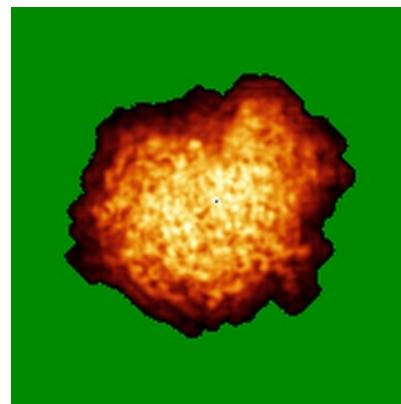
## 2.4 Orthogonal standard-deviation projections (False-color) [i](#)



X



Y



Z

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

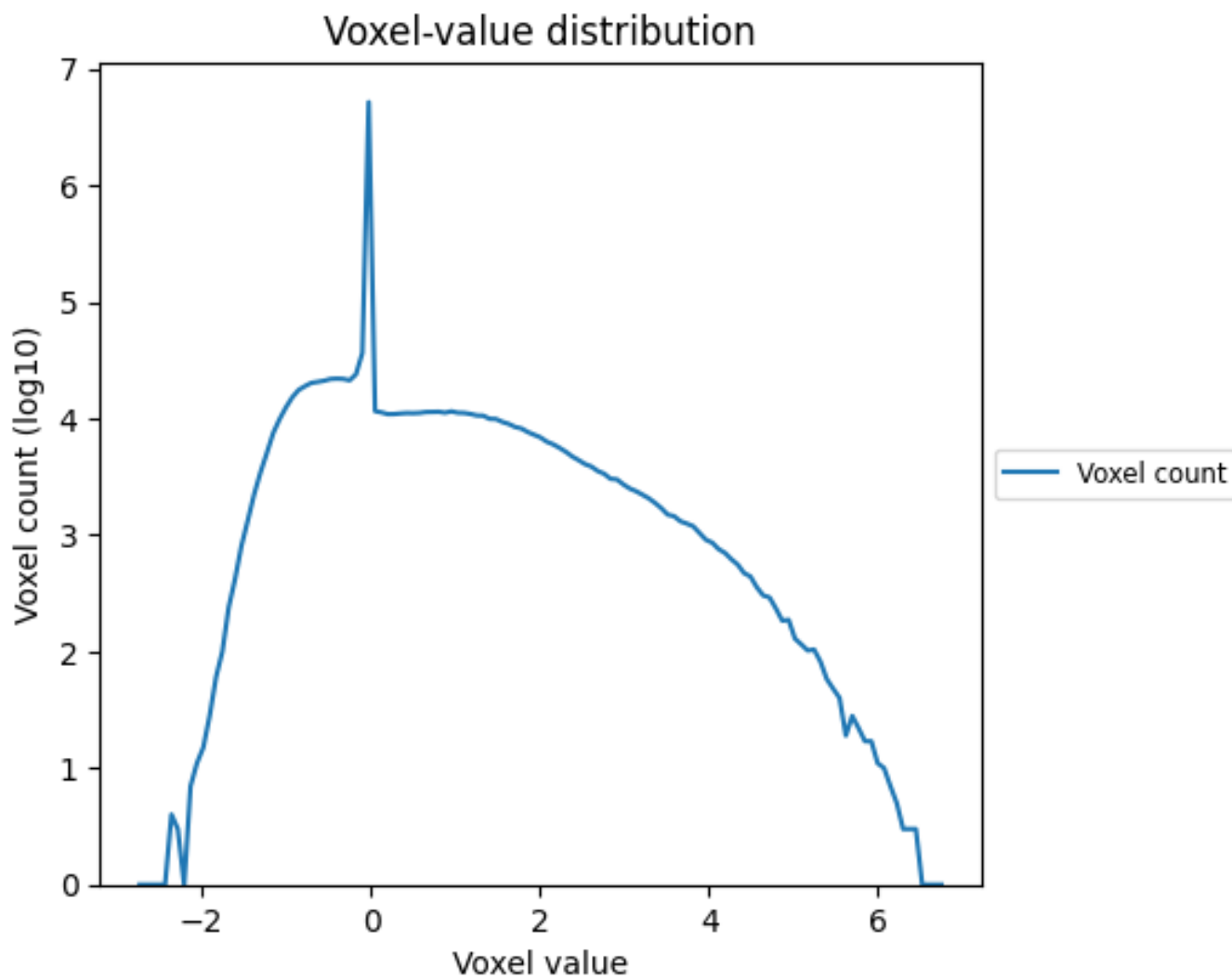
## 2.5 Mask visualisation [i](#)

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.