



## Full wwPDB EM Validation Report ⓘ

Dec 5, 2022 – 02:10 PM JST

EMDB ID : EMD-30761  
Title : Liganded EGFR averaged cluster 21  
Authors : Purba, E.R.; Saita, E.I.; Akhouri, R.R.; Ofverstedt, L.G.; Wilken, G.; Skoglund, U.; Maruyama, I.N.  
Deposited on : 2020-12-04  
Resolution : 15.00 Å(reported)

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>.

---

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

EMDB validation analysis : 0.0.1.dev43  
Validation Pipeline (wwPDB-VP) : 2.31.3

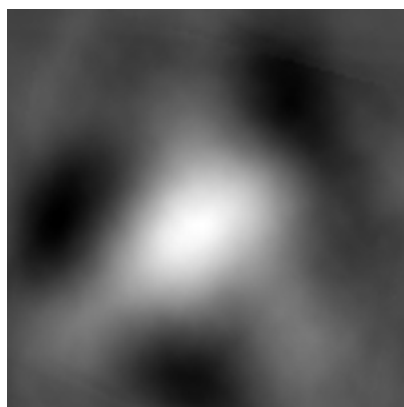
# 1 Experimental information

| Property                             | Value                           | Source    |
|--------------------------------------|---------------------------------|-----------|
| EM reconstruction method             | TOMOGRAPHY                      | Depositor |
| Imposed symmetry                     | Not Provided                    |           |
| Number of tilted images used         | 141                             | Depositor |
| Resolution determination method      | OTHER                           | Depositor |
| CTF correction method                | Not provided                    |           |
| Microscope                           | FEI TITAN KRIOS                 | Depositor |
| Voltage (kV)                         | 300                             | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 90.0                            | Depositor |
| Minimum defocus (nm)                 | 1.0                             | Depositor |
| Maximum defocus (nm)                 | 1.5                             | Depositor |
| Magnification                        | 37000.0                         | Depositor |
| Image detector                       | FEI FALCON II (4k x 4k)         | Depositor |
| Maximum voxel value                  | 0.704                           | Depositor |
| Minimum voxel value                  | 0.152                           | Depositor |
| Average voxel value                  | 0.399                           | Depositor |
| Voxel value standard deviation       | 0.066                           | Depositor |
| Recommended contour level            | Not applicable                  |           |
| Tomogram size ( $\text{\AA}$ )       | 248.38002, 248.38002, 248.38002 | wwPDB     |
| Tomogram dimensions                  | 110, 110, 110                   | wwPDB     |
| Tomogram angles ( $^\circ$ )         | 90.0, 90.0, 90.0                | wwPDB     |
| Grid spacing ( $\text{\AA}$ )        | 2.2580001, 2.2580001, 2.2580001 | Depositor |

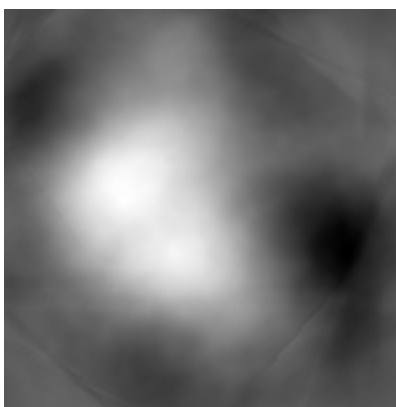
## 2 Tomogram visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30761. These allow visual inspection of the internal detail of the tomogram and identification of artifacts.

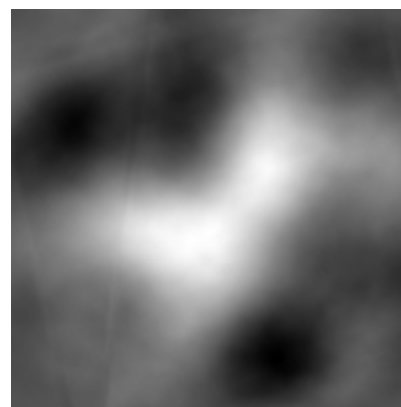
### 2.1 Orthogonal projections [i](#)



X



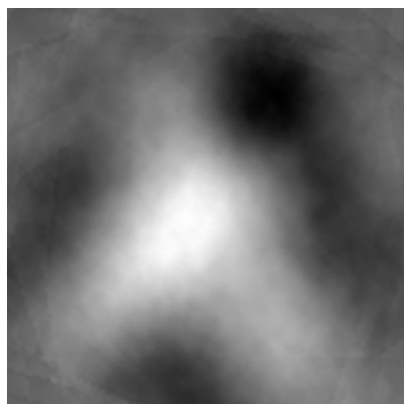
Y



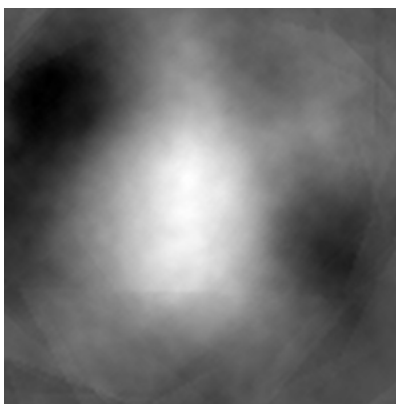
Z

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

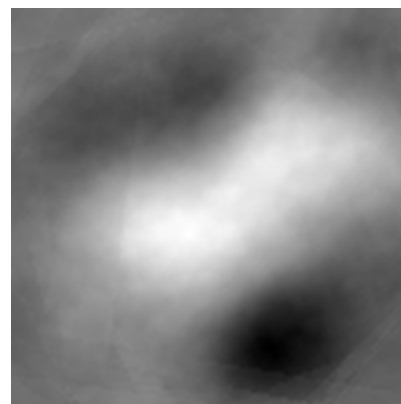
### 2.2 Central slices [i](#)



X Index: 55



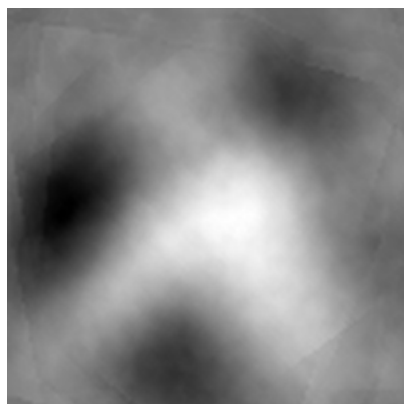
Y Index: 55



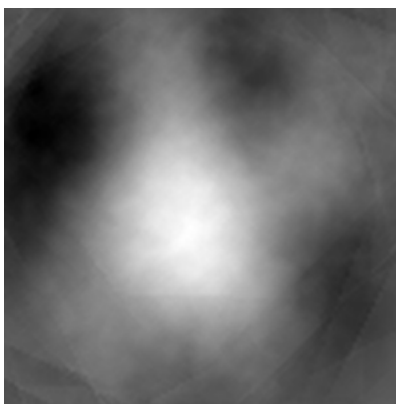
Z Index: 55

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

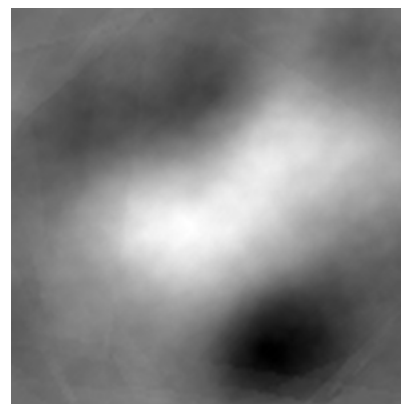
## 2.3 Largest variance slices [i](#)



X Index: 68



Y Index: 48



Z Index: 53

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

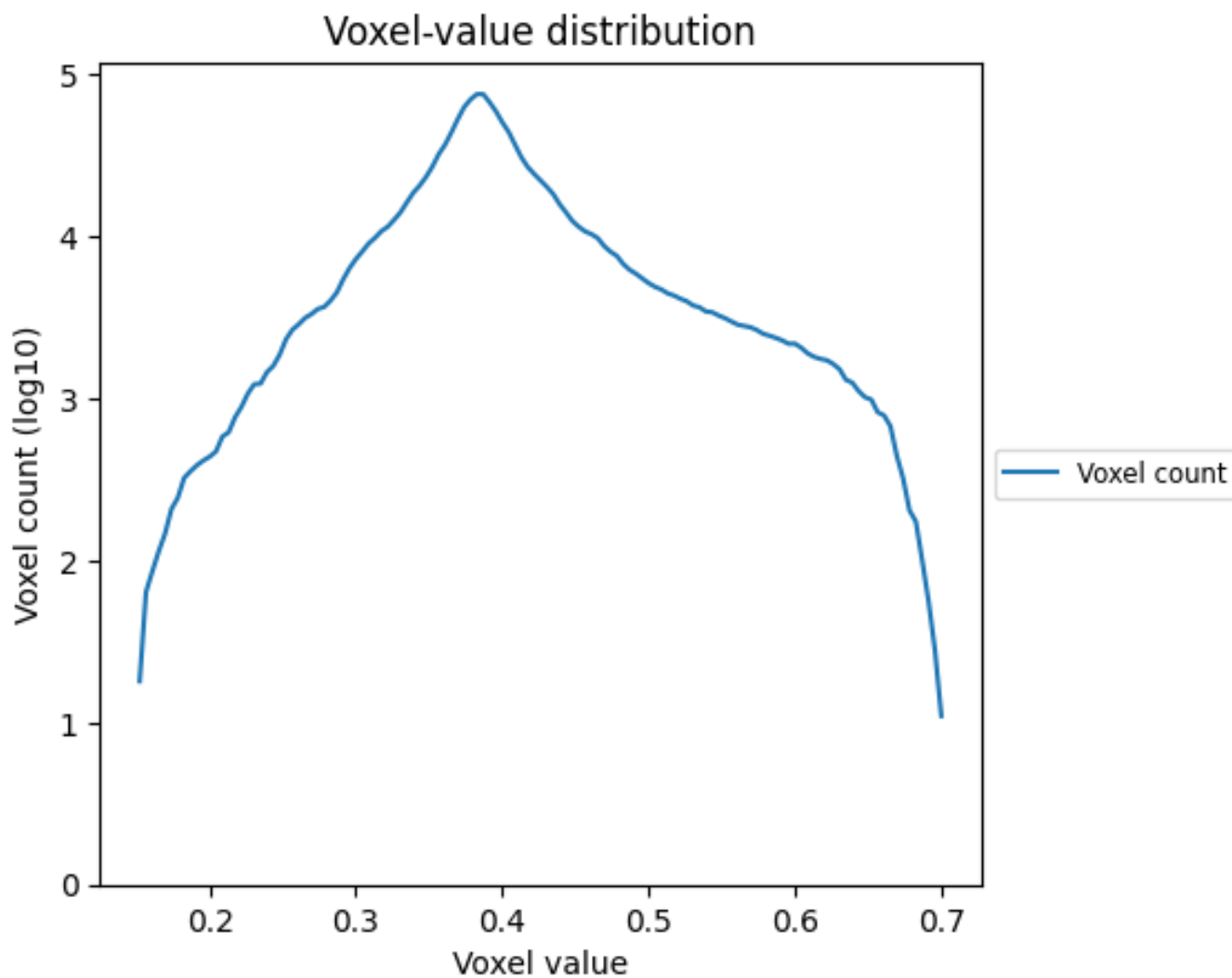
## 2.4 Mask visualisation [i](#)

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.