



## Full wwPDB EM Validation Report ⓘ

Dec 8, 2023 – 04:13 am GMT

EMDB ID : EMD-14525  
Title : AP2 adaptor protein recruited on the membrane in the presence of FCHO2 linker  
Authors : Kovtun, O.; Kaufman, J.G.G.; Owen, D.J.; Briggs, J.A.G.  
Deposited on : 2022-03-10  
Resolution : 9.90 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.dev70  
Validation Pipeline (wwPDB-VP) : 2.36

# 1 Experimental information

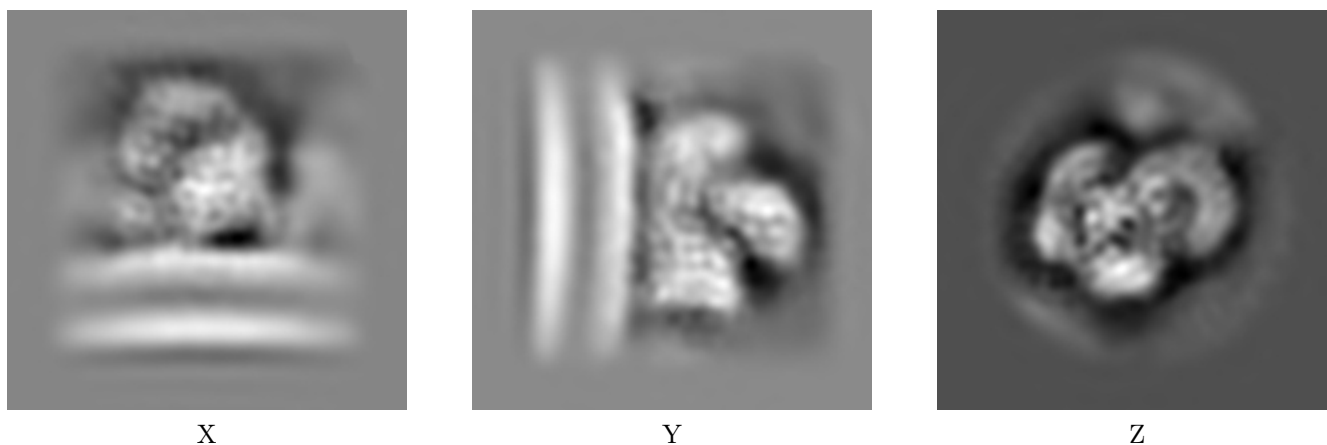
Property	Value	Source
EM reconstruction method	TOMOGRAPHY	Depositor
Imposed symmetry	Not Provided	
Number of tilted images used	51868	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	3.17	Depositor
Minimum defocus (nm)	1.0	Depositor
Maximum defocus (nm)	3.5	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum voxel value	0.400	Depositor
Minimum voxel value	-0.356	Depositor
Average voxel value	0.002	Depositor
Voxel value standard deviation	0.037	Depositor
Recommended contour level	Not applicable	
Tomogram size (Å)	217.728, 217.728, 217.728	wwPDB
Tomogram dimensions	128, 128, 128	wwPDB
Tomogram angles (°)	90.0, 90.0, 90.0	wwPDB
Grid spacing (Å)	1.701, 1.701, 1.701	Depositor

## 2 Tomogram visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14525. These allow visual inspection of the internal detail of the tomogram and identification of artifacts.

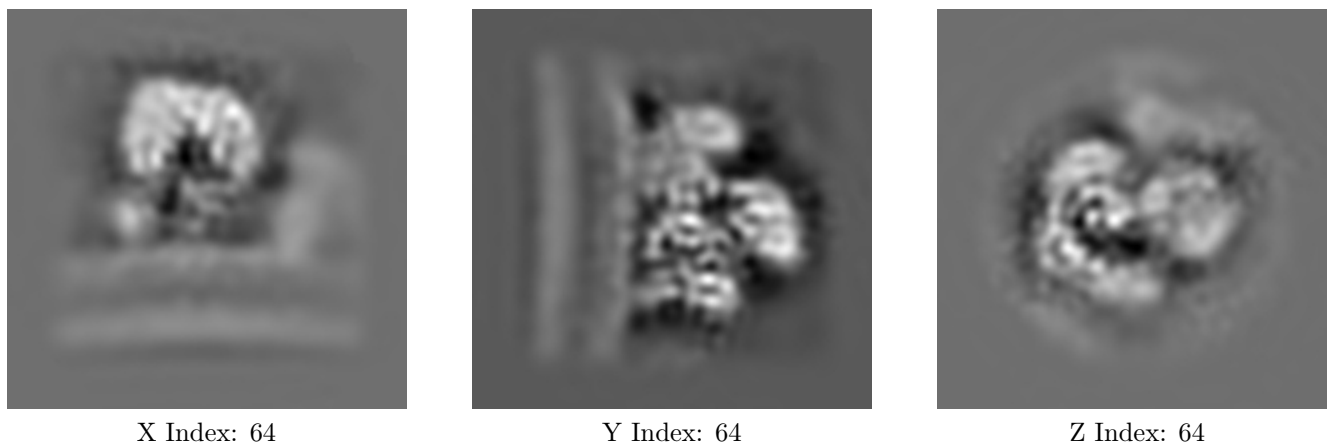
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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



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

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

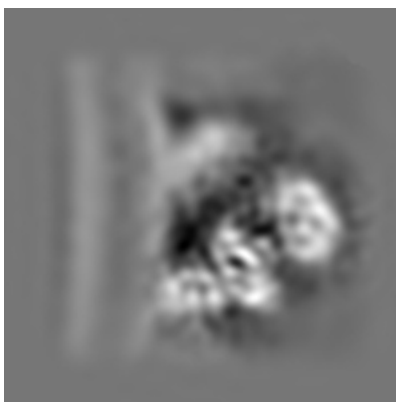


The images above show central slices of the tomogram in three orthogonal directions.

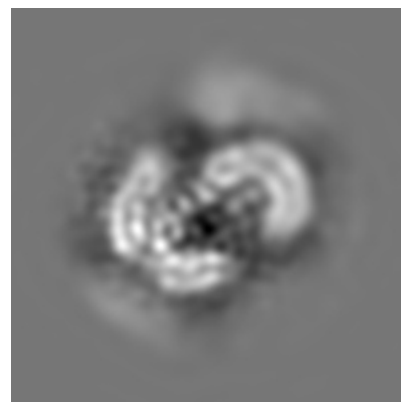
## 2.3 Largest variance slices [i](#)



X Index: 64



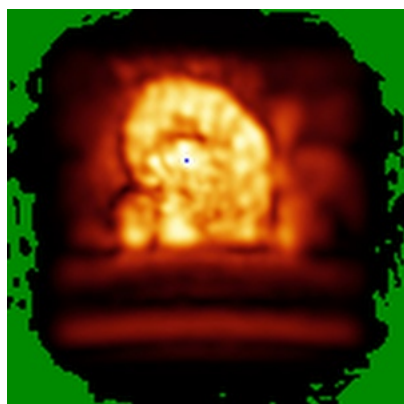
Y Index: 53



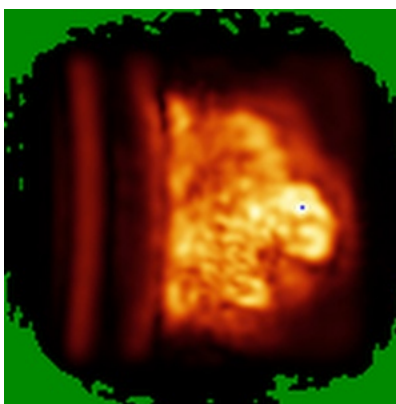
Z Index: 79

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

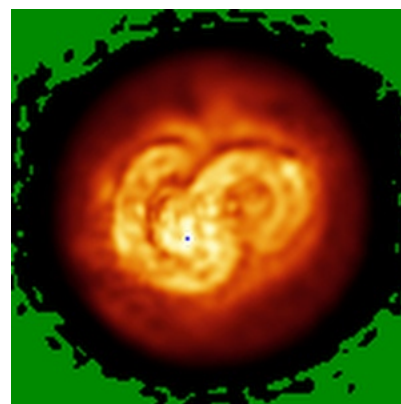
## 2.4 Orthogonal standard-deviation projections (False-color) [i](#)



X



Y



Z

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

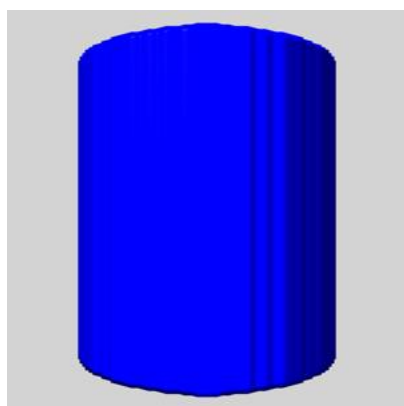
## 2.5 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

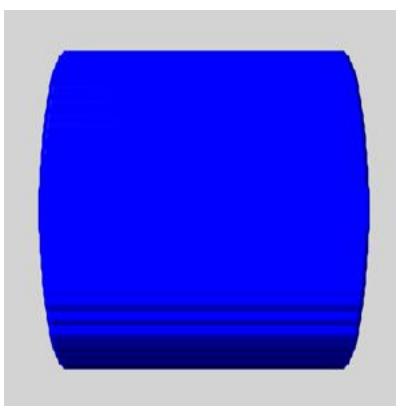
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

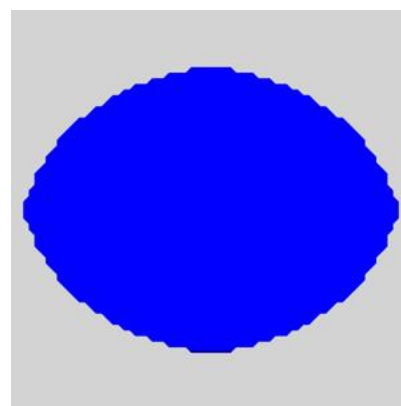
### 2.5.1 emd\_14525\_msk\_1.map [i](#)



X



Y

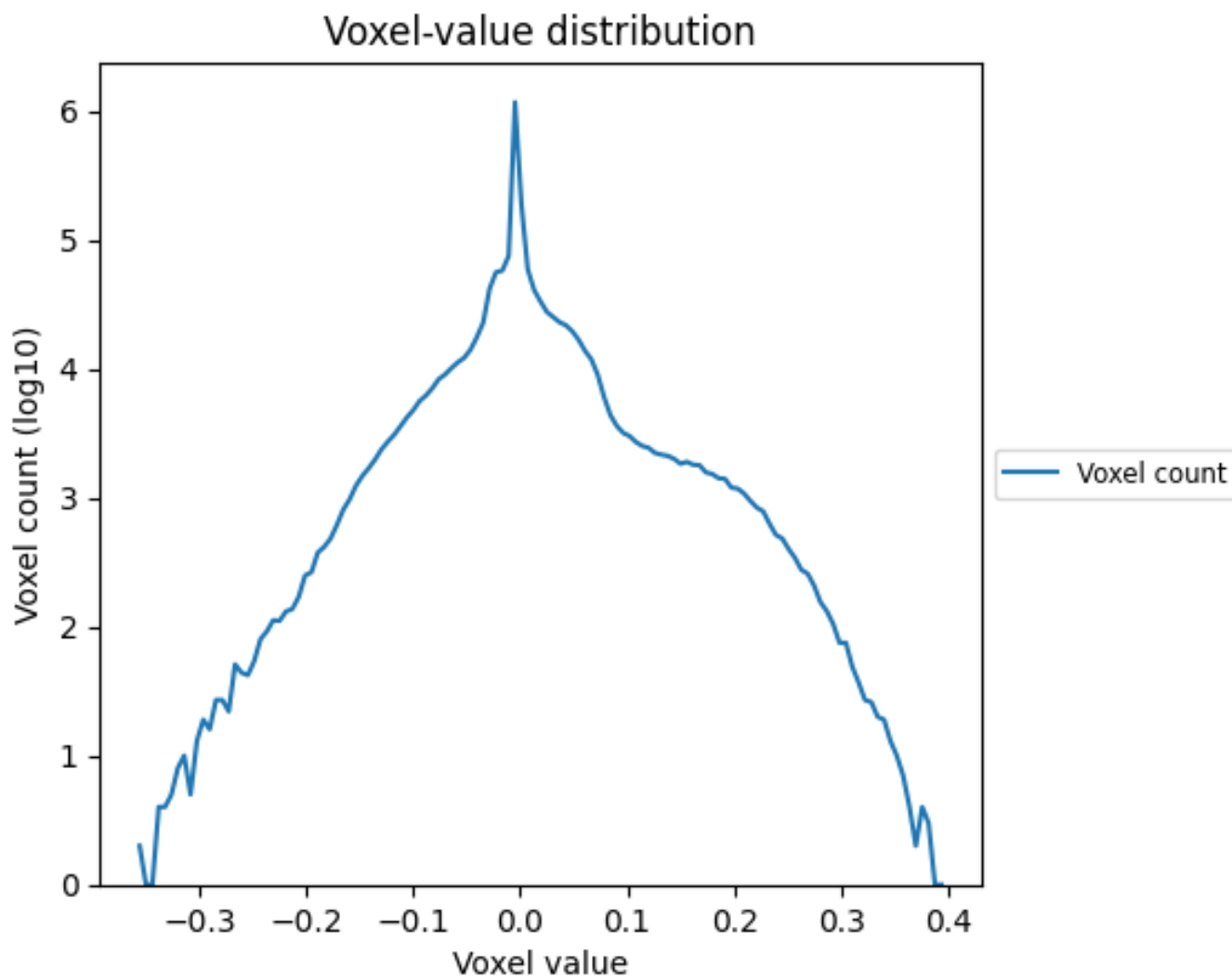


Z

### 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.