



## wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 02:08 AM UTC

PDB ID : 5AHV / pdb\_00005ahv  
EMDB ID : EMD-2896  
Title : Cryo-EM structure of helical ANTH and ENTH tubules on PI(4,5)P2-containing membranes  
Authors : Skruzny, M.; Desfosses, A.; Prinz, S.; Dodonova, S.O.; Gieras, A.; Uetrecht, C.; Jakobi, A.J.; Abella, M.; Hagen, W.J.H.; Schulz, J.; Meijers, R.; Rybin, V.; Briggs, J.A.G.; Sachse, C.; Kaksonen, M.  
Deposited on : 2015-02-10  
Resolution : 13.60 Å(reported)  
Based on initial model : 1H0A

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/EMValidationReportHelp>

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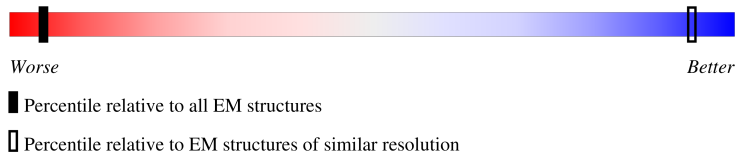
The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132  
MolProbity : **FAILED**  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.8.1  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

i

ELECTRON MICROSCOPY

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



| Metric  | EM structures<br>(#Entries) | Similar EM resolution<br>(#Entries, resolution range(Å)) |
|---------|-----------------------------|----------------------------------------------------------|
| Q-score | 25397                       | 66 ( 13.10 - 14.10 )                                     |

SEQUENCE-PLOTS INFOmissingINFO

## 2 Experimental information

| Property                             | Value                                                                     | Source    |
|--------------------------------------|---------------------------------------------------------------------------|-----------|
| EM reconstruction method             | SINGLE PARTICLE                                                           | Depositor |
| Imposed symmetry                     | HELICAL, twist=Not provided°, rise=Not provided Å, axial sym=Not provided | Depositor |
| Number of particles used             | 457344                                                                    | Depositor |
| Resolution determination method      | Not provided                                                              |           |
| CTF correction method                | EACH PARTICLE                                                             | Depositor |
| Microscope                           | FEI TITAN KRIOS                                                           | Depositor |
| Voltage (kV)                         | 120                                                                       | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 10                                                                        | Depositor |
| Minimum defocus (nm)                 | 500                                                                       | Depositor |
| Maximum defocus (nm)                 | 5000                                                                      | Depositor |
| Magnification                        | 59000                                                                     | Depositor |
| Image detector                       | GATAN ULTRASCAN 4000 (4k x 4k)                                            | Depositor |
| Maximum map value                    | 2.250                                                                     | Depositor |
| Minimum map value                    | -1.469                                                                    | Depositor |
| Average map value                    | 0.043                                                                     | Depositor |
| Map value standard deviation         | 0.551                                                                     | Depositor |
| Recommended contour level            | 0.35                                                                      | Depositor |
| Map size (Å)                         | 427.19998, 427.19998, 605.2                                               | wwPDB     |
| Map dimensions                       | 240, 240, 340                                                             | wwPDB     |
| Map angles (°)                       | 90.0, 90.0, 90.0                                                          | wwPDB     |
| Pixel spacing (Å)                    | 1.78, 1.78, 1.7800001                                                     | Depositor |

## 3 Model quality [i](#)

### 3.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

### 3.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

### 3.3 Torsion angles [i](#)

#### 3.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

#### 3.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

#### 3.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

### 3.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 3.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 3.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 3.7 Other polymers [i](#)

There are no such residues in this entry.

### 3.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

## 4 Map visualisation

This section contains visualisations of the EMDB entry EMD-2896. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 4.1 Orthogonal projections

This section was not generated.

### 4.2 Central slices

This section was not generated.

### 4.3 Largest variance slices

This section was not generated.

### 4.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

### 4.5 Orthogonal surface views

This section was not generated.

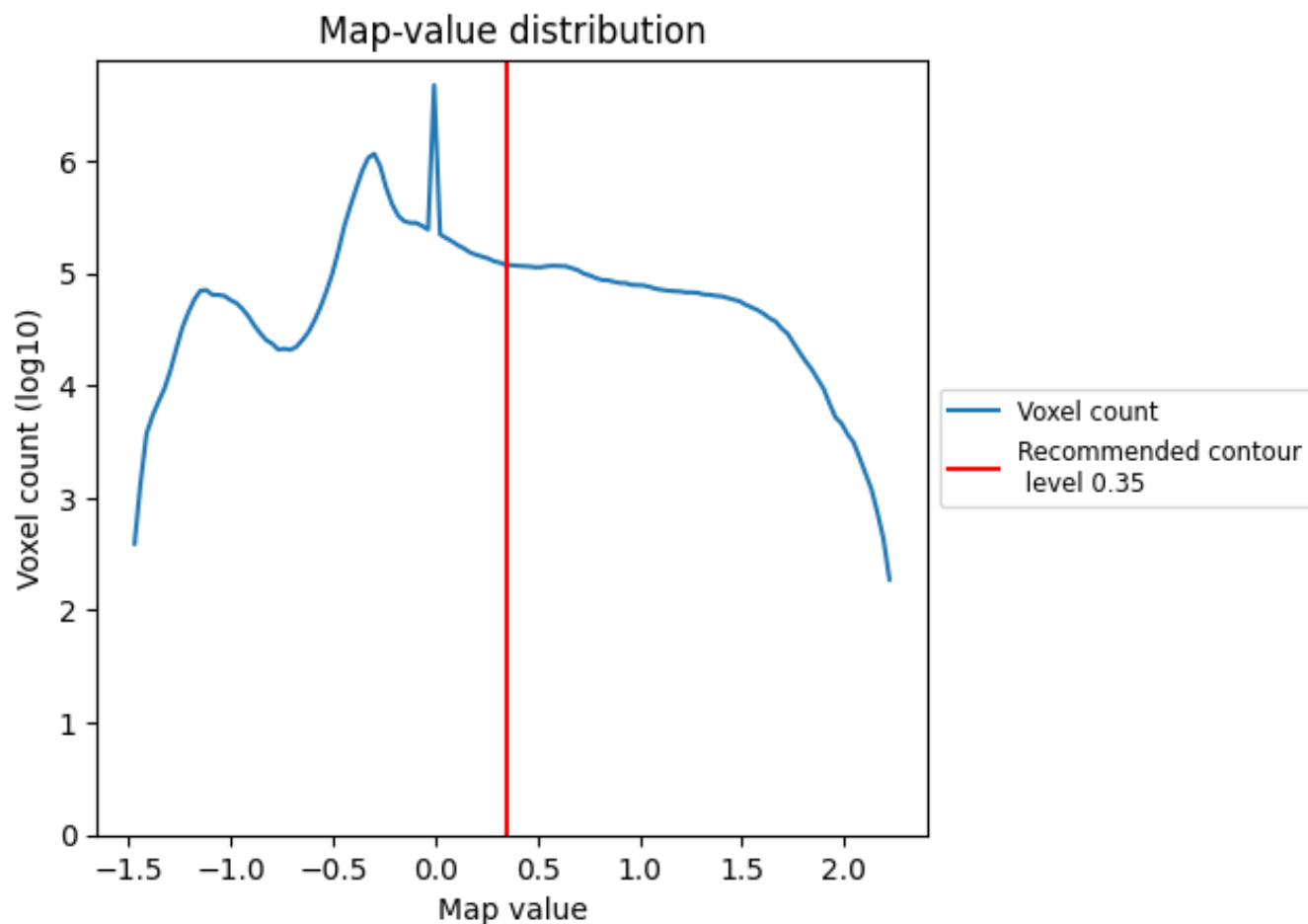
### 4.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

## 5 Map analysis [i](#)

This section contains the results of statistical analysis of the map.

### 5.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

### 5.2 Volume estimate versus contour level [i](#)

This section was not generated.

### 5.3 Rotationally averaged power spectrum [i](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

## 6 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

## 7 Map-model fit

This section contains information regarding the fit between EMDB map EMD-2896 and PDB model 5AHV. Per-residue inclusion information can be found in section ?? on page ??.

### 7.1 Map-model overlay

This section was not generated.

### 7.2 Q-score mapped to coordinate model

This section was not generated.

### 7.3 Atom inclusion mapped to coordinate model

This section was not generated.

### 7.4 Atom inclusion versus contour level

This section was not generated.

### 7.5 Map-model fit summary

This section was not generated.