



## Full wwPDB EM Validation Report ⓘ

Mar 31, 2021 – 09:58 am BST

EMDB ID : EMD-1605  
Title : Solution structure of the KdpFABC P-type ATPase from Escherichia coli by electron microscopic single particle analysis  
Authors : Heitkamp, T.; Bottcher, B.; Greie, J.-C.  
Deposited on : 2009-03-17  
Resolution : 19.00 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/EMMapValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

---

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

EMDB validation analysis : 0.0.0.dev75  
Validation Pipeline (wwPDB-VP) : 2.18

# 1 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	Not Provided	
Number of particles used	10040	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI/PHILIPS CM120T	Depositor
Voltage (kV)	100	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	Not provided	
Minimum defocus (nm)	0.432	Depositor
Maximum defocus (nm)	0.864	Depositor
Magnification	48000.0	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	1448.240	Depositor
Minimum map value	-374.723	Depositor
Average map value	15.969	Depositor
Map value standard deviation	95.570	Depositor
Recommended contour level	150.0	Depositor
Map size (Å)	196, 196, 196	wwPDB
Map dimensions	70, 70, 70	wwPDB
Map angles (°)	90, 90, 90	wwPDB
Pixel spacing (Å)	2.8, 2.8, 2.8	Depositor

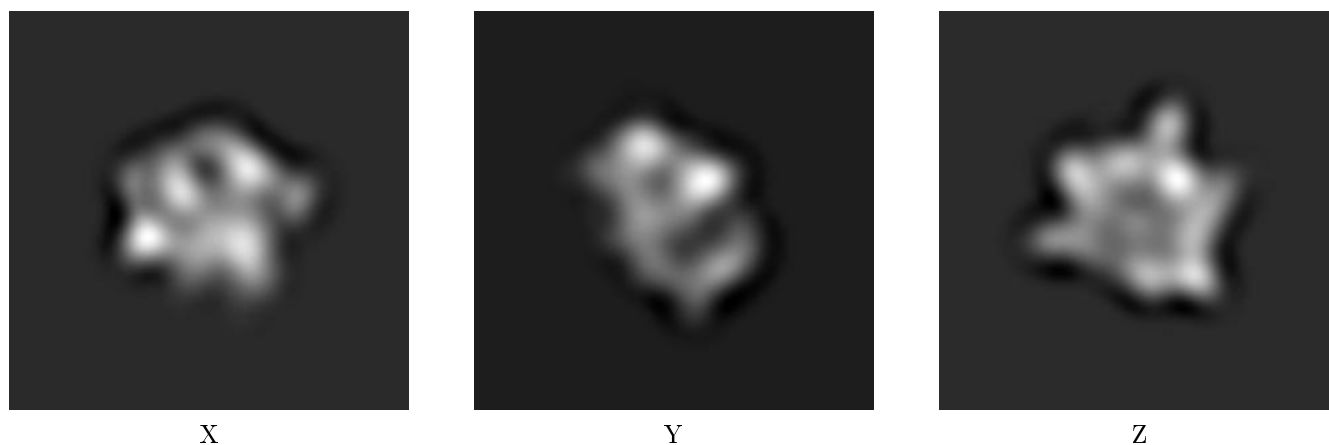
## 2 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1605. 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.

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

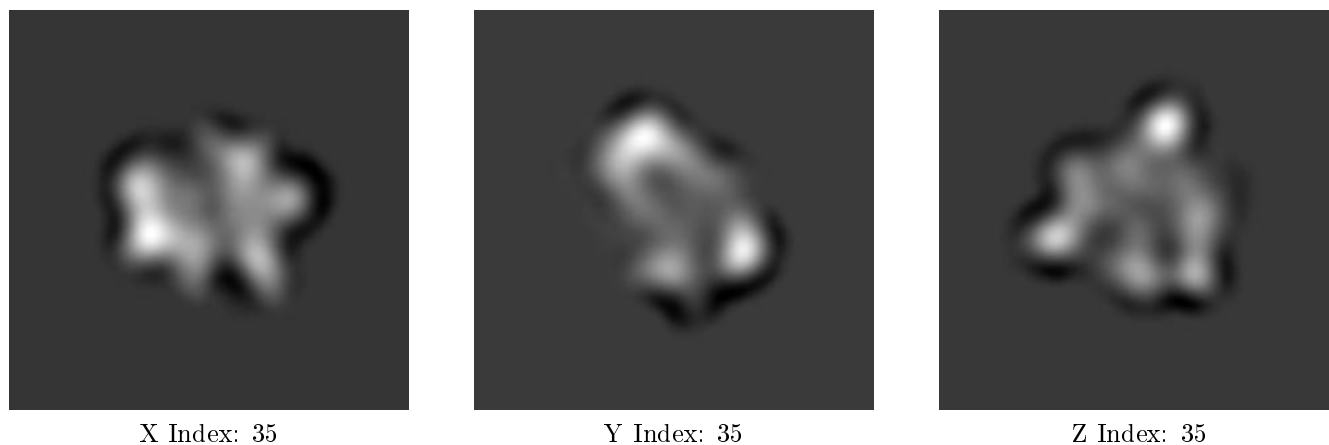
#### 2.1.1 Primary map



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

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

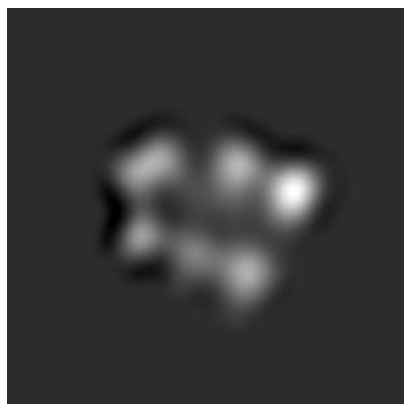
#### 2.2.1 Primary map



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

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

### 2.3.1 Primary map



X Index: 40



Y Index: 41

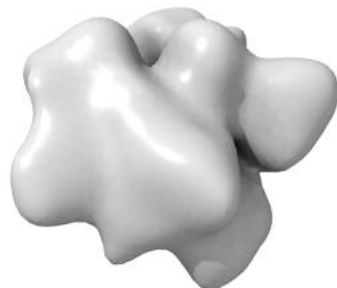


Z Index: 29

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

## 2.4 Orthogonal surface views [i](#)

### 2.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 150.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

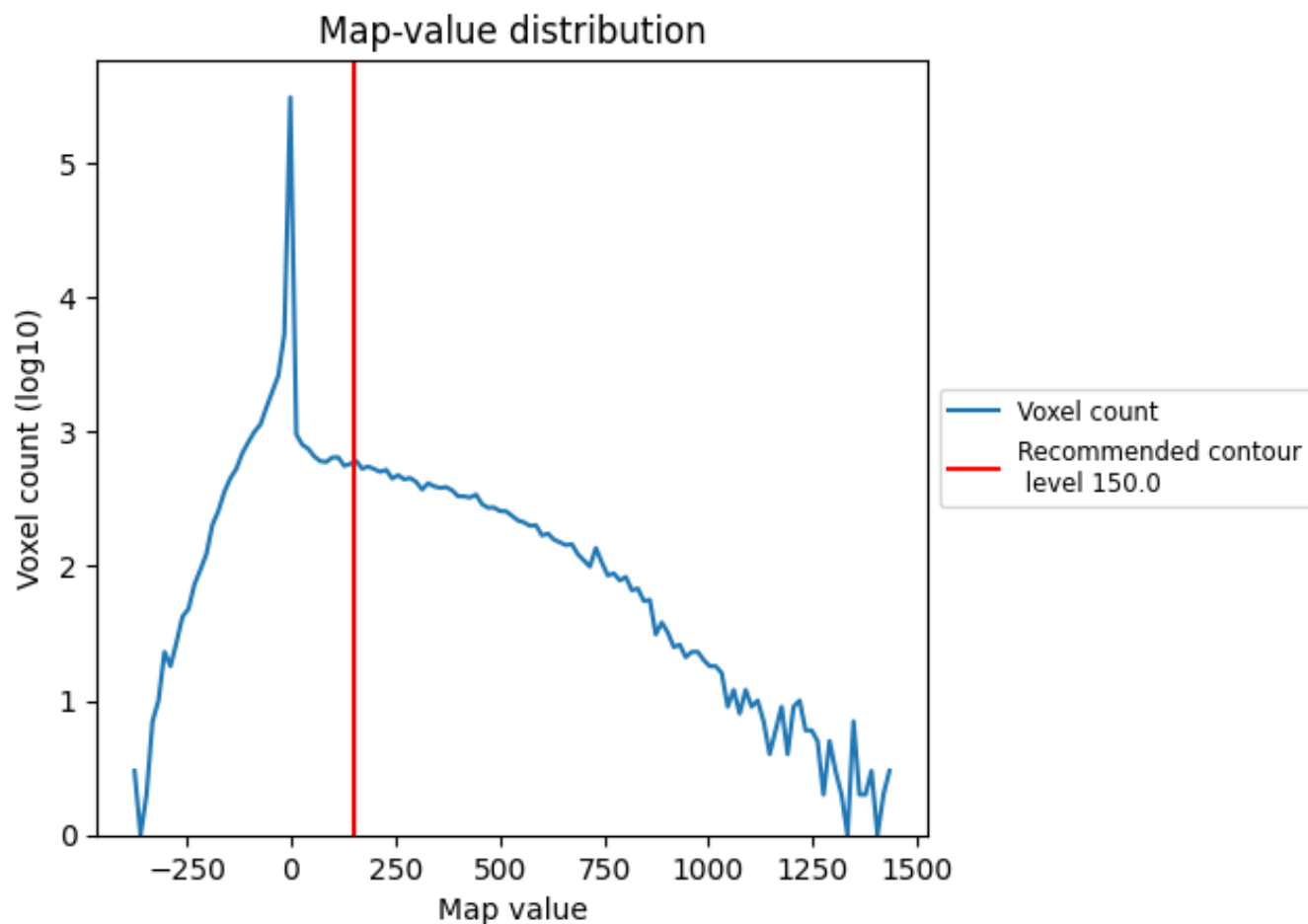
## 2.5 Mask visualisation

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

### 3 Map analysis [i](#)

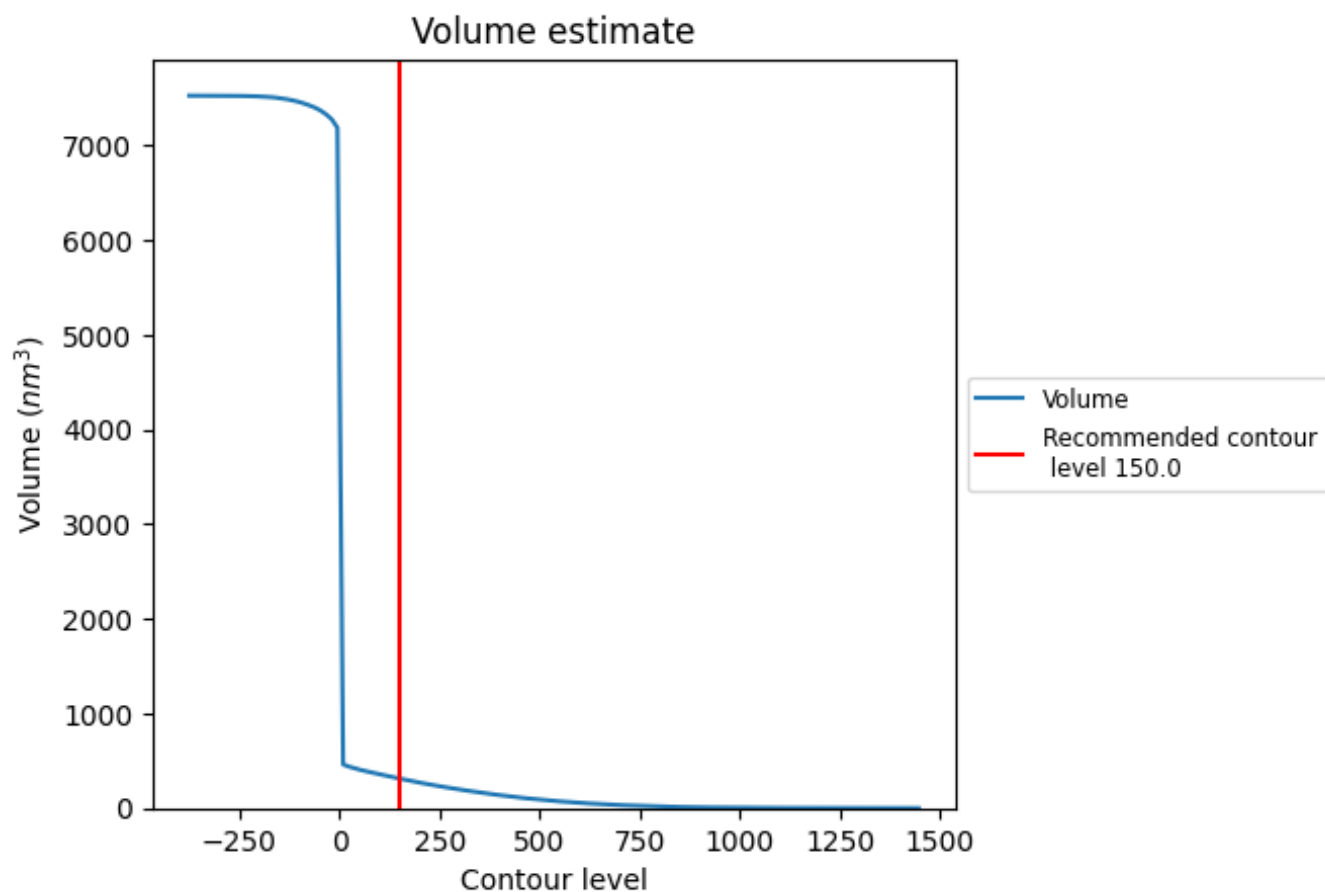
This section contains the results of statistical analysis of the map.

#### 3.1 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.

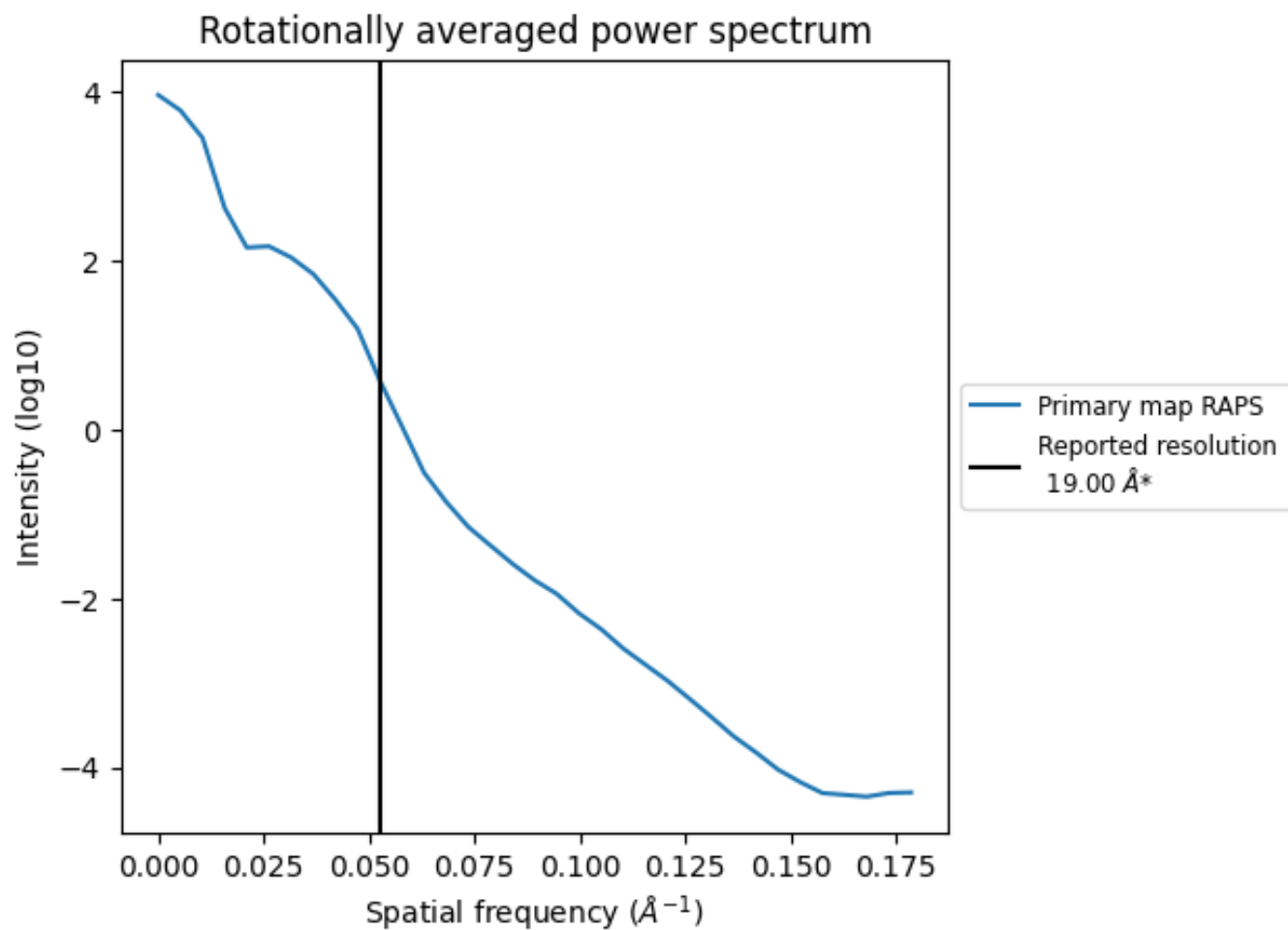
### 3.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is  $313 \text{ nm}^3$ ; this corresponds to an approximate mass of 283 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

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



\*Reported resolution corresponds to spatial frequency of 0.053 Å<sup>-1</sup>



## 4 Fourier-Shell correlation

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