



## Full wwPDB EM Validation Report ⓘ

Dec 14, 2020 – 01:43 PM JST

EMDB ID : EMD-6322  
Title : Genome and RdRp structure within the capsid of no-transcribing cypovirus  
Authors : , Liu.H.; , Cheng.L.  
Deposited on : 2015-04-21  
Resolution : 12.00 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.

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

EMDB validation analysis : 0.0.0.dev61  
Validation Pipeline (wwPDB-VP) : 2.15.1

# 1 Experimental information

Property	Value	Source
EM reconstruction method	singleParticle	Depositor
Imposed symmetry	Not Provided	
Number of images used	28000	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	Not provided	
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	125390.0	Depositor
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor
Maximum map value	50.604	Depositor
Minimum map value	-34.171	Depositor
Average map value	3.756	Depositor
Map value standard deviation	13.521	Depositor
Recommended contour level	22.0	Depositor
Map size ( $\text{\AA}$ )	717.6, 717.6, 717.6	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	2.392, 2.392, 2.392	Depositor

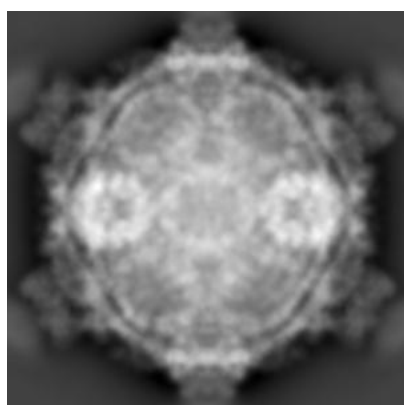
## 2 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6322. These allow visual inspection of the internal detail of the map and identification of artifacts.

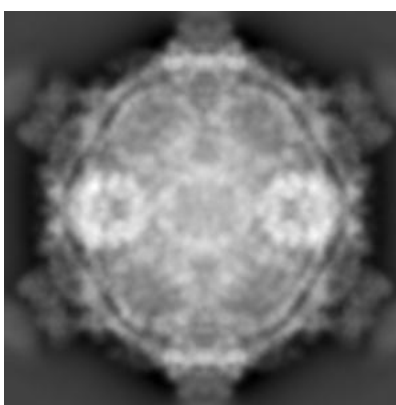
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

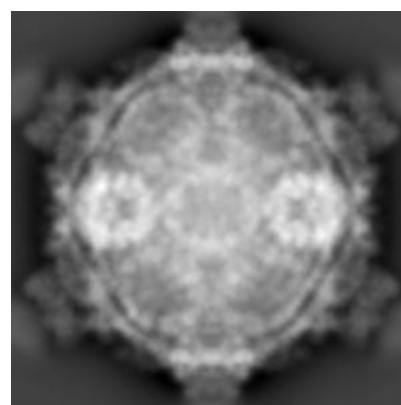
#### 2.1.1 Primary map



X



Y

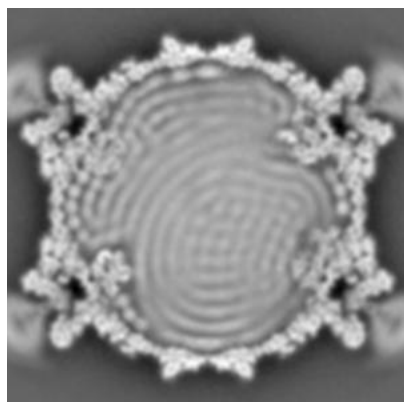


Z

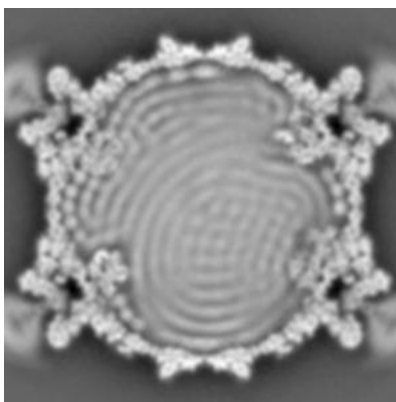
The images above show the map projected in three orthogonal directions.

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

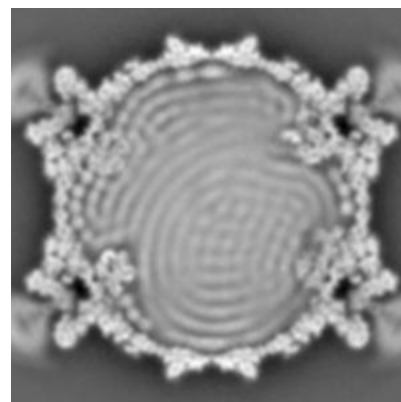
#### 2.2.1 Primary map



X Index: 150



Y Index: 150

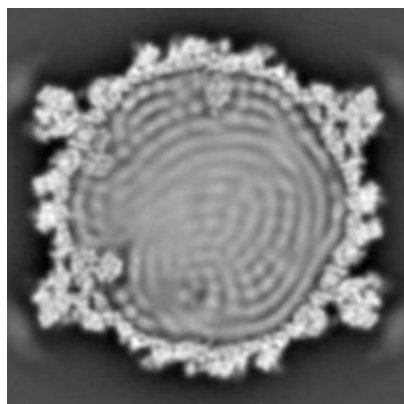


Z Index: 150

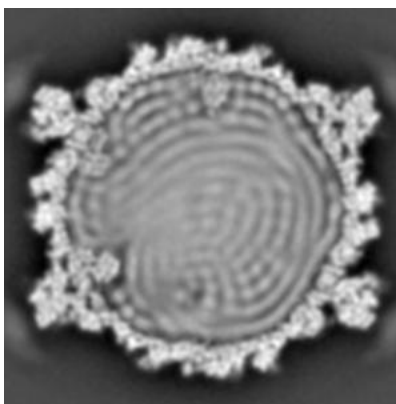
The images above show central slices of the map in three orthogonal directions.

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

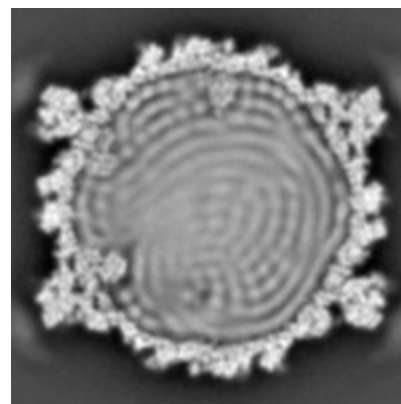
### 2.3.1 Primary map



X Index: 126



Y Index: 126

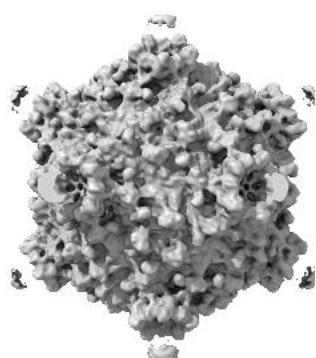


Z Index: 126

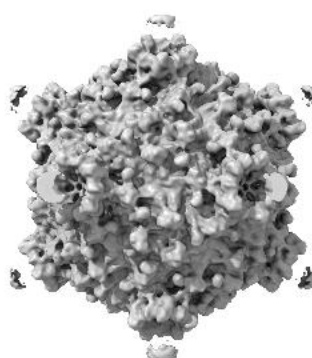
The images above show the largest variance slices of the map in three orthogonal directions.

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

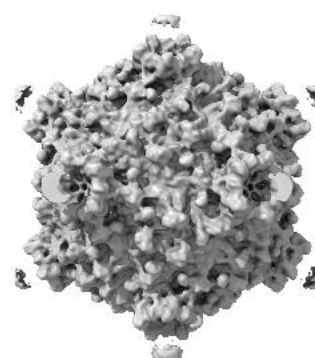
### 2.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 22.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

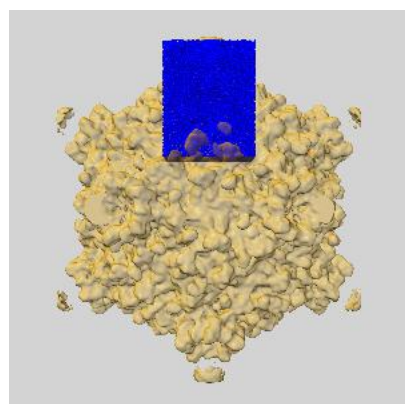
## 2.5 Mask visualisation [i](#)

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

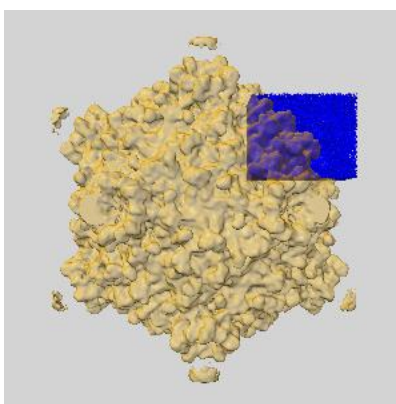
A mask typically either:

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

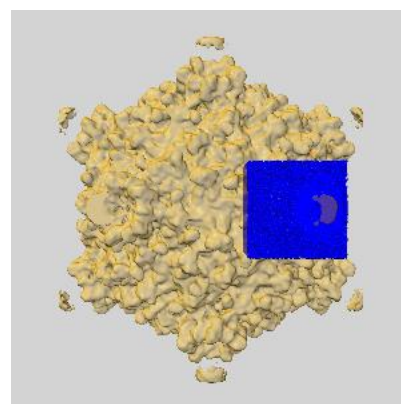
### 2.5.1 emd\_6322\_msk.map [i](#)



X

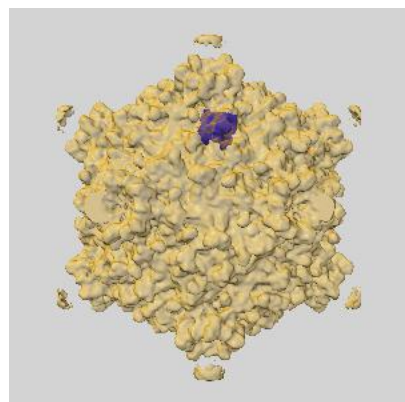


Y

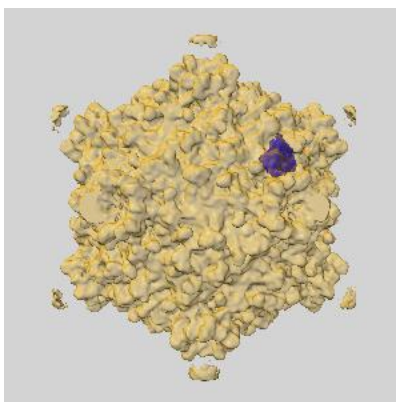


Z

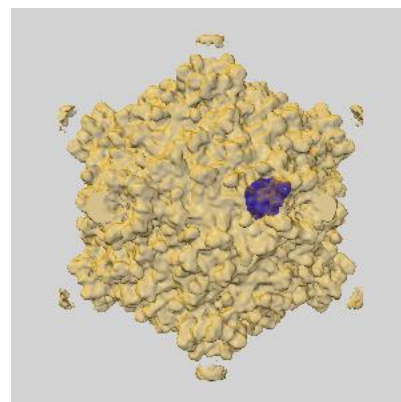
### 2.5.2 emd\_6322\_msk\_1.map [i](#)



X



Y

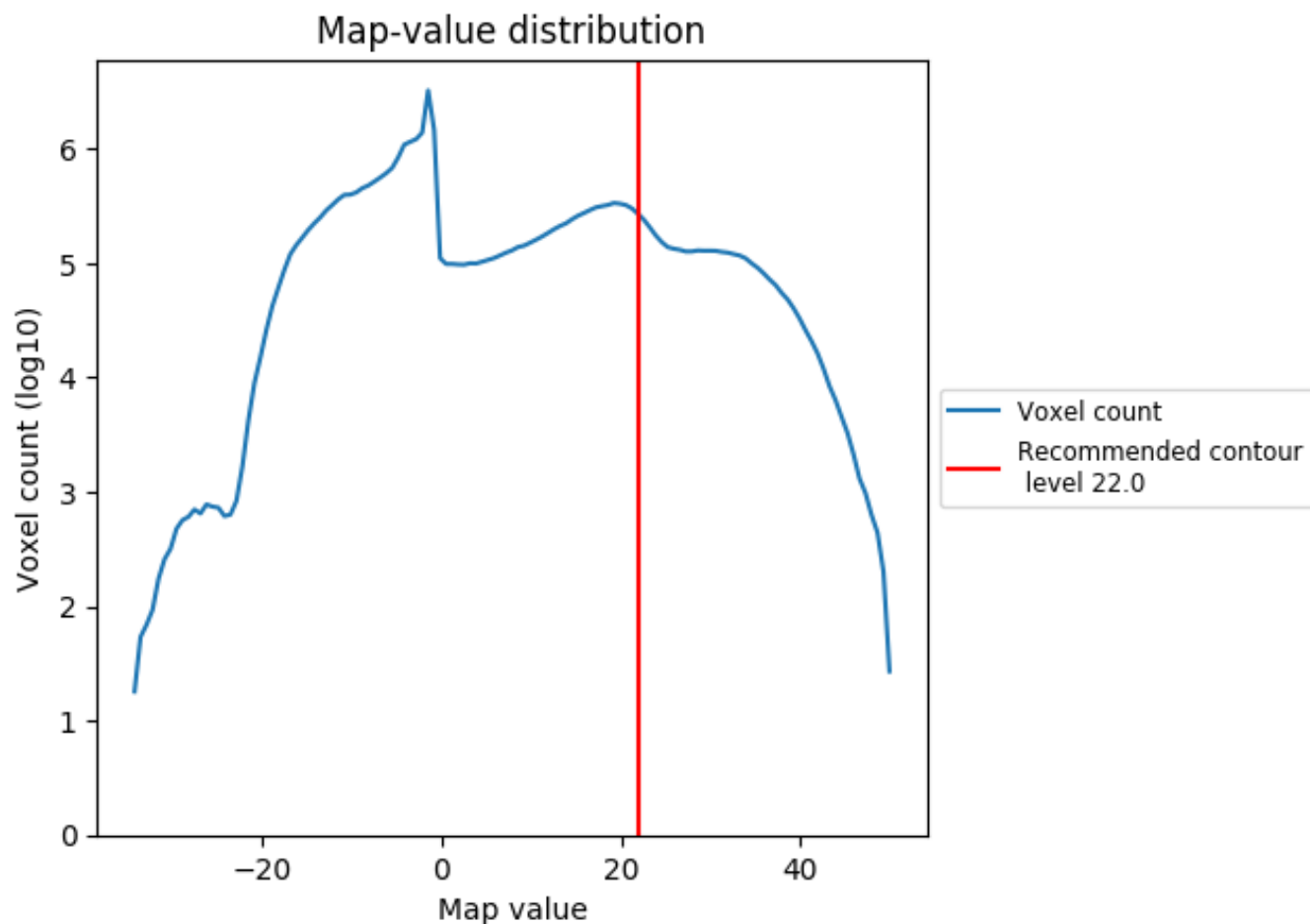


Z

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

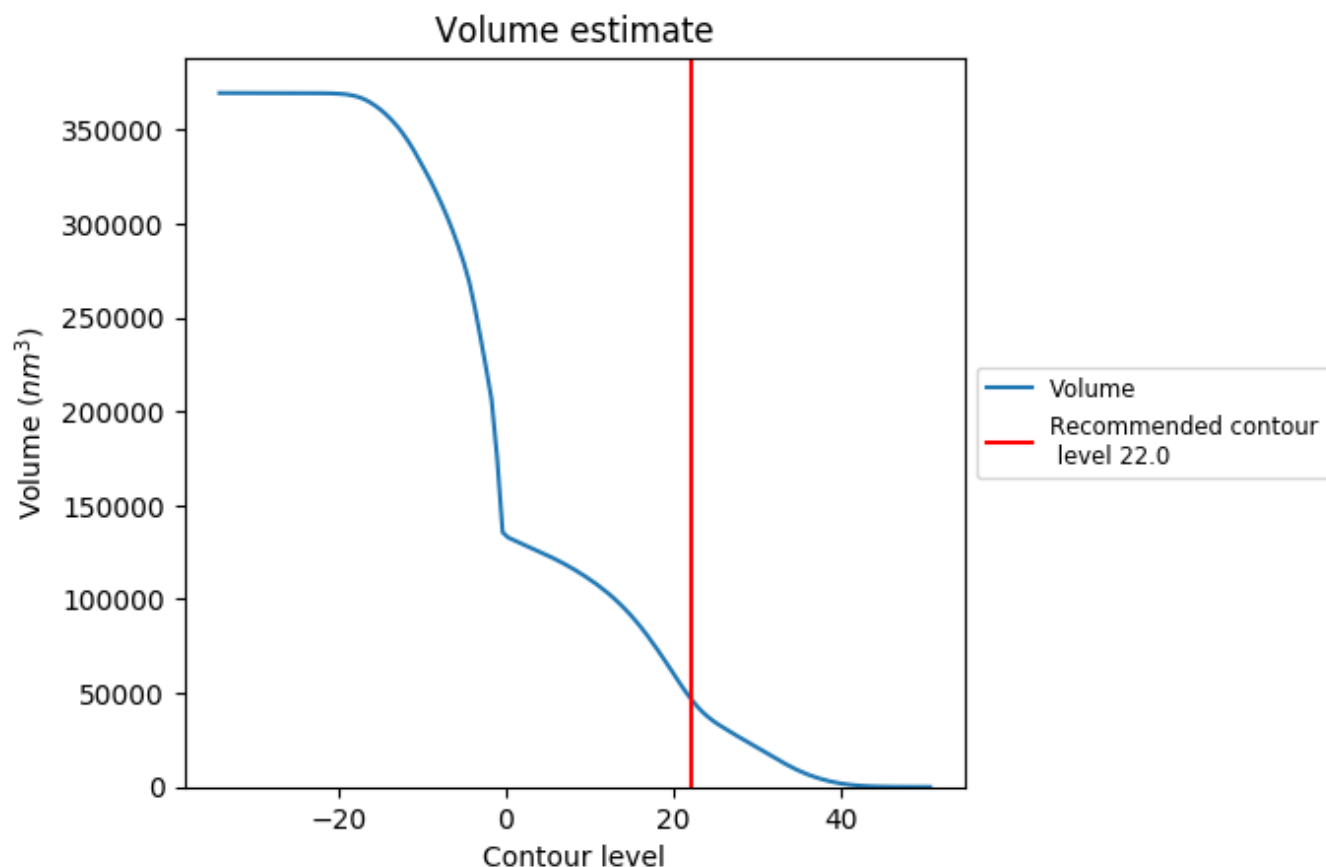
This section contains the results of statistical analysis of the map.

#### 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.

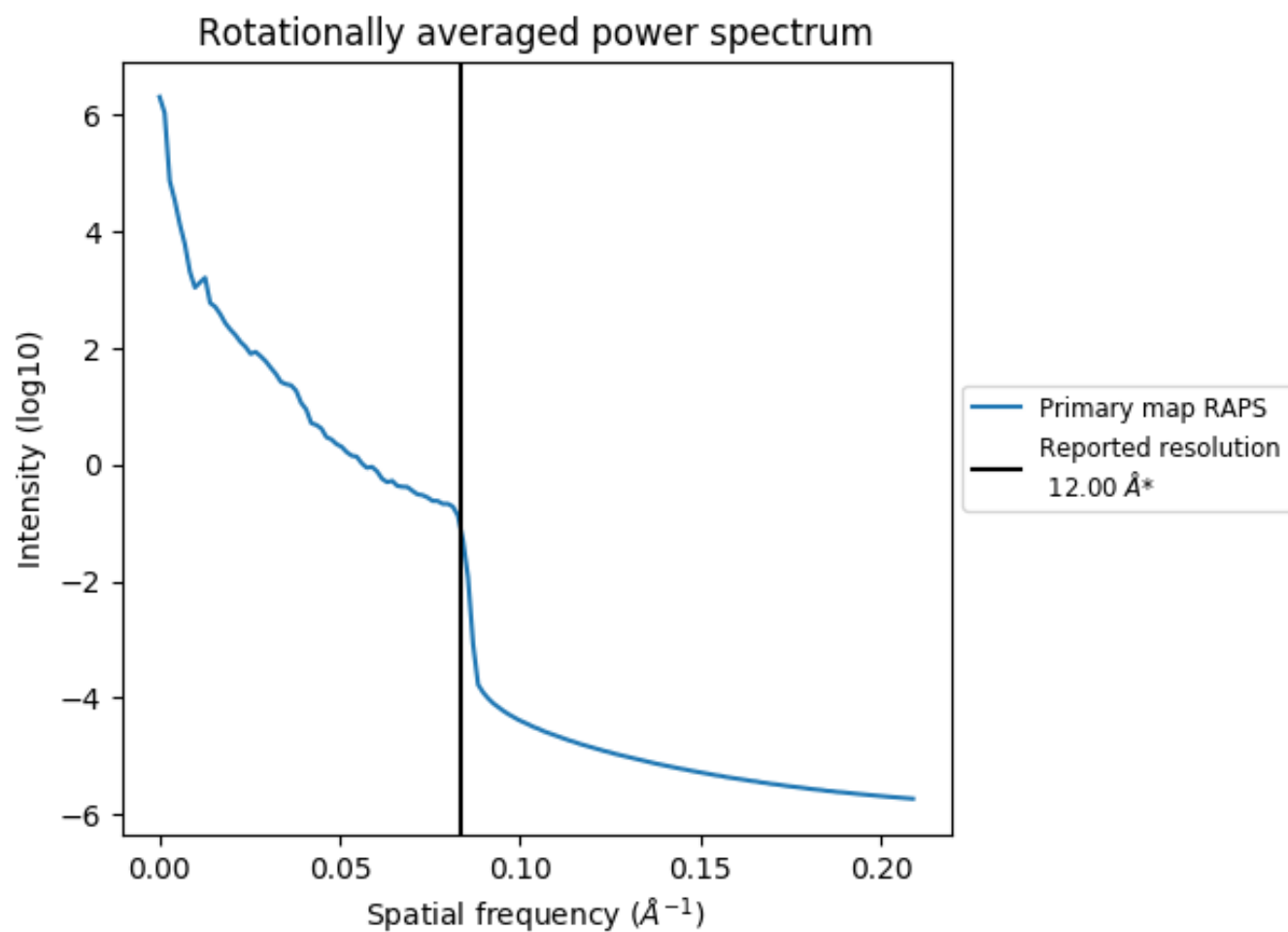
### 3.2 Volume estimate [i](#)



The volume at the recommended contour level is 47345  $\text{nm}^3$ ; this corresponds to an approximate mass of 42768 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 ⓘ



\*Reported resolution corresponds to spatial frequency of 0.083 Å<sup>-1</sup>



## 4 Fourier-Shell correlation ⓘ

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