



Public Data-based Report



# Validation Report Service

## Cryo-EM Map Validation Report

Report to assess Cryo-EM Volume Map at Level(s) 0

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This report has been generated based on data publicly available at [EMDB](#).

### Basic Entry Information:

**EMDB ID:** [EMD-5171](#)

**Title:** Structure of Fusarium poae virus 1 shows conserved and variable elements of partitivirus capsids and evolutionary links to picobirnaviruses

**Authors:** [See EMDB entry link](#)

**Deposited on:** 2010-03-09T00:00:00

**Reported Resolution:** (not reported)

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## Context

Cryo-electron microscopy is currently one of the most active techniques in Structural Biology. The number of maps deposited at the [Electron Microscopy Data Bank](#) is rapidly growing every year and keeping the quality of the submitted maps is essential to maintain the scientific quality of the field. The ultimate quality measure is the consistency of the map and an atomic model. However, this is only possible for high resolution maps. Over the years there have been many suggestions about validation measures of 3DEM maps. Unfortunately, most of these measures are not currently in use for their spread in multiple software tools and the associated difficulty to access them. To alleviate this problem, we made available a validation grading system that evaluate the information provided to assess the map.

This system grades a map from 0 to 5 depending on the amount of information available. In this way, a map could be validated at Level 0 (the deposited map), 1 (two half maps), 2 (2D classes), 3 (particles), 4 (... + angular assignment), 5 (... + micrographs and coordinates). In addition, we can have three optional qualifiers: A (... + atomic model), W (... + image processing workflow), and O (... + other techniques).

This Validation Report Service is explained in more detail in this [paper](#). For more information about the different methods and softwares used for this report, see the references [here](#).

### Summarized overall quality

The map seems to have some problem in its centering or extra space (see Sec. 2.1). There seems to be a problem with the suggested threshold (see Sec. 2.2). There seems to be a problem with the map's background (see Sec. 2.3).

**The overall score (passing tests) of this report is 0 out of 3 evaluable items.**

Some programs may not work properly since resolution parameter has not been reported.

0.a Mass analysis	Sec. 2.1	3 warnings
0.b Mask analysis	Sec. 2.2	1 warnings
0.c Background analysis	Sec. 2.3	2 warnings
0.d B-factor analysis	Sec. 2.4	Does not apply
0.e DeepRes	Sec. 2.5	Does not apply
0.e Local B-factor	Sec. 2.6	Does not apply
0.g Local Occupancy	Sec. 2.7	Does not apply
0.h Deep hand	Sec. 2.8	Does not apply

## Summary of the warnings across sections.

### Section 2.1 (0.a Mass analysis)

1. **The center of mass in  $\bar{X}$  may be significantly shifted. This is common when the refinement is applied exclusively to one protein region.**
2. **The center of mass in  $\bar{Y}$  may be significantly shifted. This is common when the refinement is applied exclusively to one protein region.**
3. **The center of mass in  $\bar{Z}$  may be significantly shifted. This is common when the refinement is applied exclusively to one protein region.**

### Section 2.2 (0.b Mask analysis)

1. **There might be a problem with noise and artifacts, because the average noise blob has a volume of 7.414875  $\text{\AA}^3$ .**

### Section 2.3 (0.c Background analysis)

1. **The null hypothesis that the background mean is 0 has been rejected because the p-value of the comparison is smaller than 0.001**
2. **There is a significant proportion of outlier values in the background (cdf5 ratio=8535.30)**

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# 1 Input data

Input map: emd\_5171.map

SHA256 hash: 7af3c261760597be303bf55461bfa0700a8da4ff0ce7748f8b0eec53a6aa9a54

Voxel size: 1.950000 (Å)

Visualization threshold: 2.100000

Resolution estimated by user: (not reported)

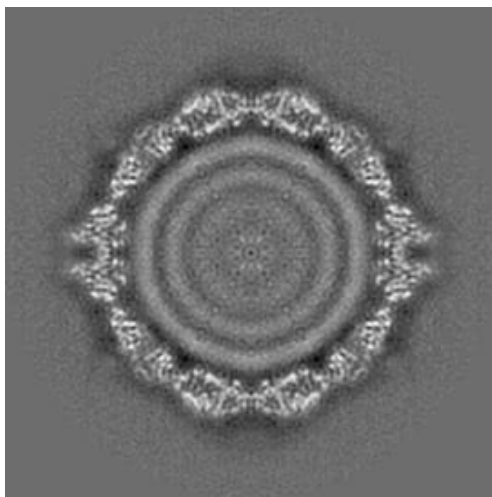
## Orthogonal slices of the input map

### **Explanation:**

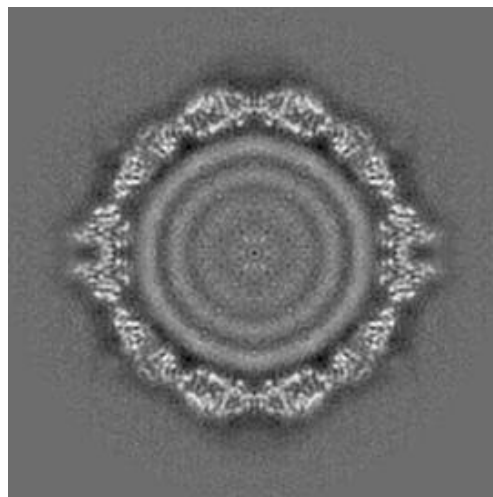
In the orthogonal slices of the map, the noise outside the protein should not have any structure (stripes going out, small blobs, particularly high or low densities, ...)

### **Results:**

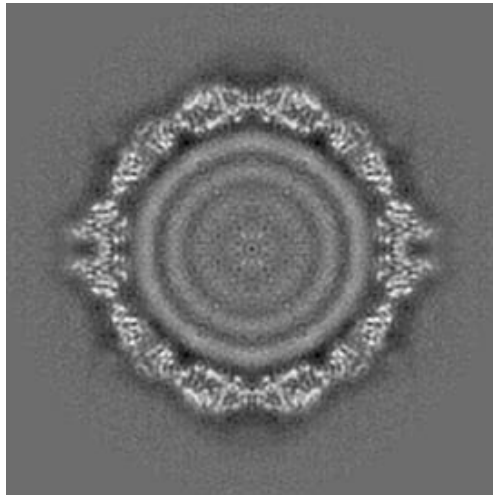
See Fig. 1.



(a) X Slice 135



(b) Y Slice 135



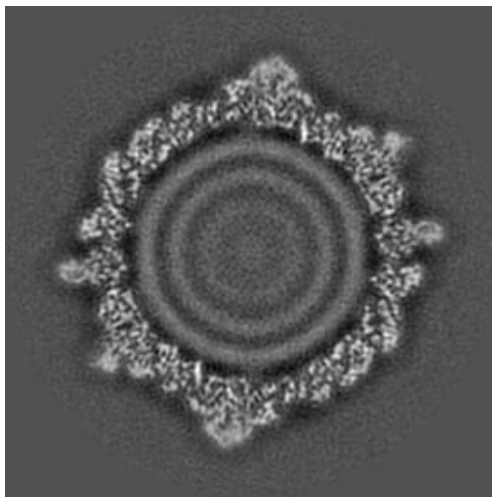
(c) Z Slice 135

Figure 1: Central slices of the input map in the three dimensions

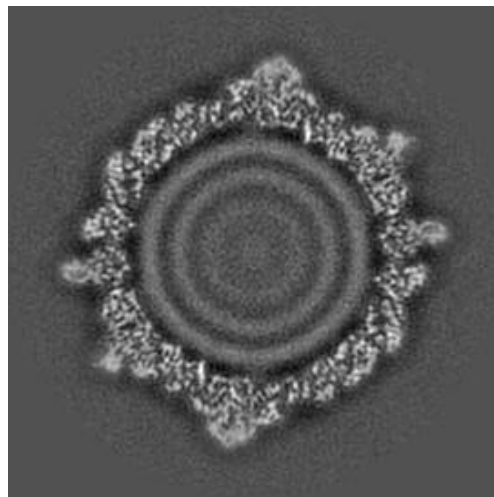
Orthogonal slices of maximum variance of the input map

**Results:**

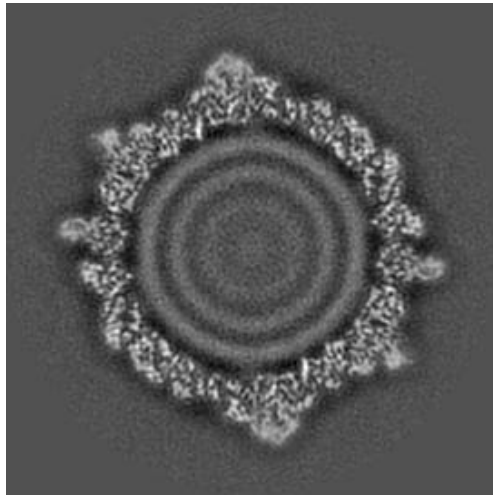
See Fig. 2.



(a) X Slice 145



(b) Y Slice 125



(c) Z Slice 125

Figure 2: Slices of maximum variation in the three dimensions

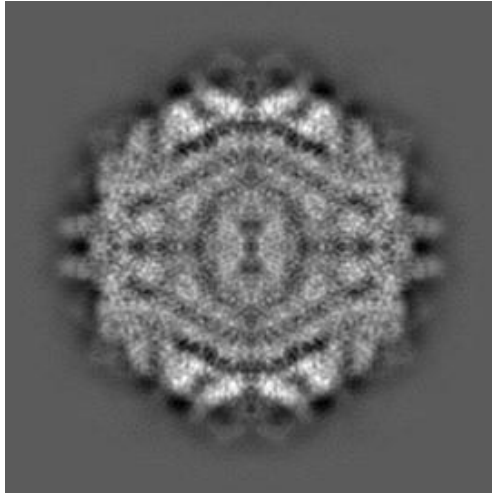
### Orthogonal projections of the input map

#### **Explanation:**

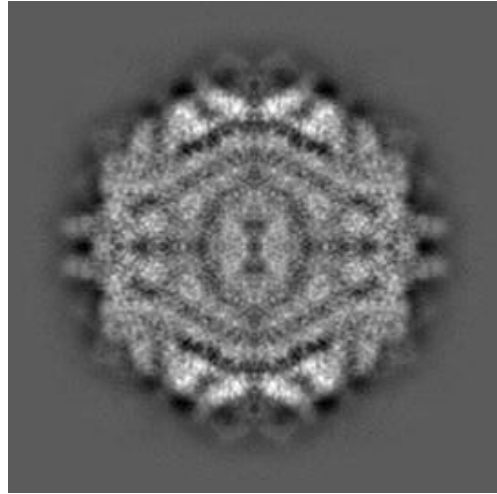
In the projections there should not be stripes (this is an indication of directional overweighting, or angular attraction), and there should not be a dark halo around or inside the structure (this is an indication of incorrect CTF correction or the reconstruction of a biased map).

#### **Results:**

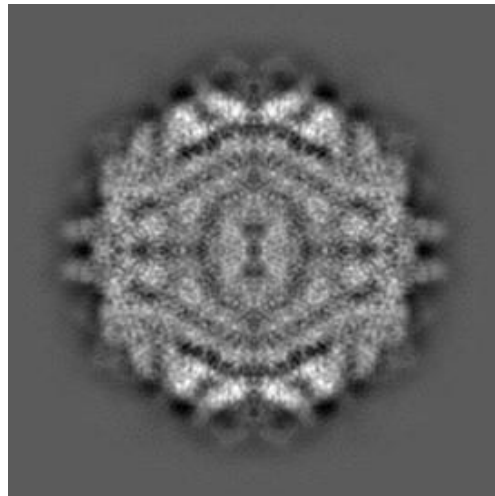
See Fig. 3.



(a) X Projection



(b) Y Projection



(c) Z Projection

Figure 3: Projections in the three dimensions

### Isosurface views of the input map

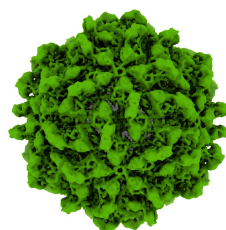
#### **Explanation:**

An isosurface is the surface of all points that have the same gray value. In these views there should not be many artifacts or noise blobs around the map.

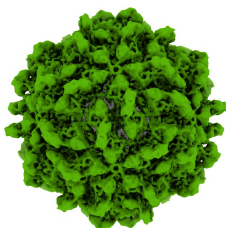
**Results:**  
See Fig. 4.



(a) View 1



(b) View 2



(c) View 3

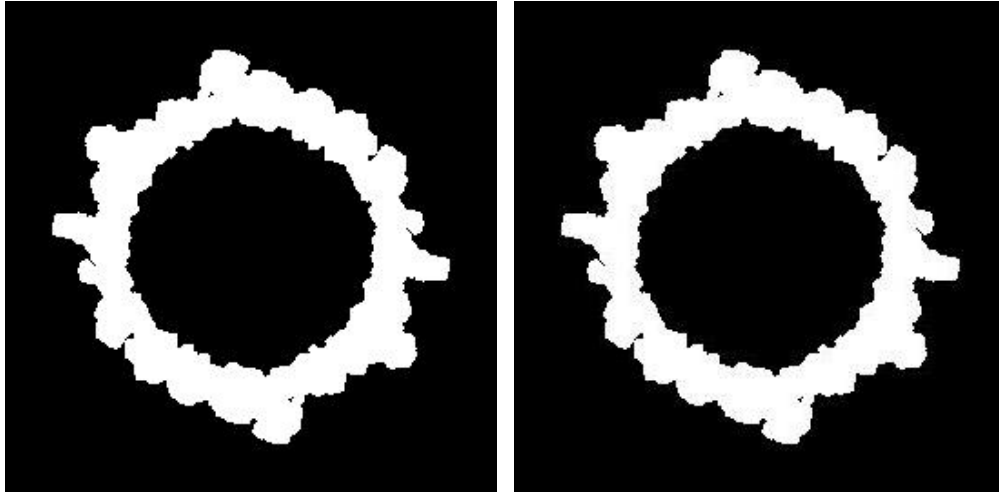
Figure 4: Isosurface at threshold=2.100000. Views generated by ChimeraX at a the following X, Y, Z angles: View 1 (0, -90, -90), View 2 (-90, 0, -90), View 3 (0, 0, 0).

### Orthogonal slices of maximum variance of the mask with hard borders

#### **Explanation:**

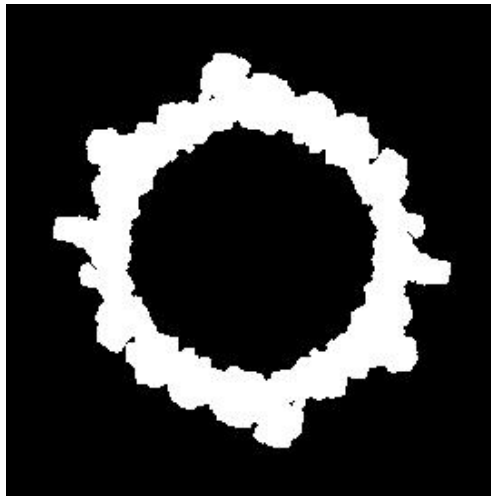
The mask with hard borders has been calculated at the suggested threshold 2.100000, the largest connected component was selected, and then dilated by 2Å.

**Results:**  
See Fig. 5.



(a) X Slice 120

(b) Y Slice 150



(c) Z Slice 120

Figure 5: Slices of maximum variation in the three dimensions of the mask with hard borders

Orthogonal slices of maximum variance of the mask with soft borders

**Explanation:**

The mask with soft borders has been calculated at the suggested threshold 2.100000, the largest connected component was selected, and then dilated by

2Å.

**Results:**  
See Fig. 6.



(a) X Slice 121



(b) Y Slice 149



(c) Z Slice 121

Figure 6: Slices of maximum variation in the three dimensions of the mask with soft borders

## 2 Level 0 analysis

### 2.1 Level 0.a Mass analysis

#### **Explanation:**

The reconstructed map must be relatively well centered in the box, and there should be at least  $30\text{\AA}$  (the exact size depends on the CTF) on each side to make sure that the CTF can be appropriately corrected.

#### **Results:**

The space from the left and right in X are 50.70 and 52.65  $\text{\AA}$ , respectively. There is a decentering ratio  $(\text{abs}(\text{Right-Left})/\text{Size})\%$  of 0.37%

The space from the left and right in Y are 50.70 and 52.65  $\text{\AA}$ , respectively. There is a decentering ratio  $(\text{abs}(\text{Right-Left})/\text{Size})\%$  of 0.37%

The space from the left and right in Z are 50.70 and 52.65  $\text{\AA}$ , respectively. There is a decentering ratio  $(\text{abs}(\text{Right-Left})/\text{Size})\%$  of 0.37%

The center of mass is at  $(x,y,z)=(31.27, 28.67, 26.79)$ . The decentering of the center of mass  $(\text{abs}(\text{Center})/\text{Size})\%$  is 38.46, 39.42, and 40.11, respectively.

**Automatic criteria:** The validation is OK if 1) the decentering and center of mass less than 20% of the map dimensions in all directions, and 2) the extra space on each direction is more than 20% of the map dimensions. For local and focused refinement, or similar, warnings are expected.

**WARNINGS:** 3 warnings

1. **The center of mass in X may be significantly shifted. This is common when the refinement is applied exclusively to one protein region.**
2. **The center of mass in Y may be significantly shifted. This is common when the refinement is applied exclusively to one protein region.**
3. **The center of mass in Z may be significantly shifted. This is common when the refinement is applied exclusively to one protein region.**

## 2.2 Level 0.b Mask analysis

### Explanation:

The map at the suggested threshold should have most of its mass concentrated in a single connected component. It is normal that after thresholding there are a few thousands of very small, disconnected noise blobs. However, their total mass should not exceed 10%. The raw mask (just thresholding) and the mask constructed for the analysis (thresholding + largest connected component + dilation) should significantly overlap. Overlap is defined by the overlapping coefficient  $(\text{size}(\text{Raw AND Constructed})/\text{size}(\text{Raw}))$  that is a number between 0 and 1, the closer to 1, the more they agree.

### Results:

Raw mask: At threshold 2.100000, there are 1711 connected components

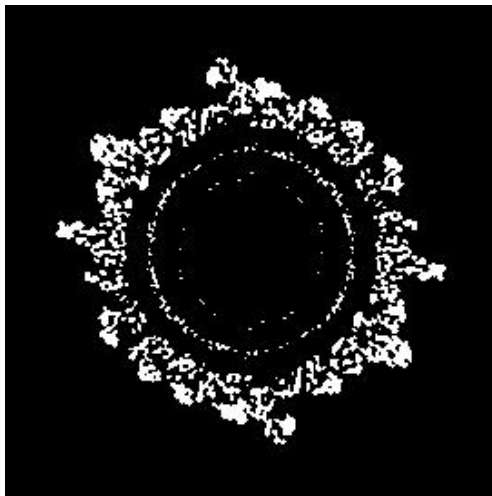
with a total number of voxels of 824648 and a volume of 6114661.84  $\text{\AA}^3$  (see Fig. 7). The size and percentage of the total number of voxels for the raw mask are listed below (up to 95% of the mass or the first 100 clusters, whatever happens first), the list contains (No. voxels (volume in  $\text{\AA}^3$ ), percentage, cumulated percentage):

(780420 (5786716.75), 94.64, 94.64)(5386 (39936.52), 0.65, 95.29)

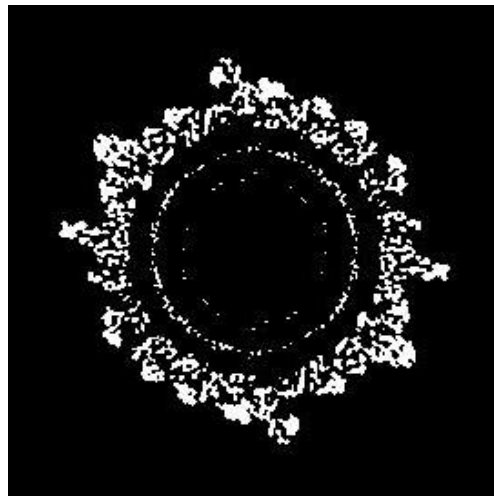
Number of components to reach 95% of the mass: 2

The average size of the remaining 1709 components is 22.73 voxels ( 7.41  $\text{\AA}^3$ ). Their size go from 5386 voxels (39936.52  $\text{\AA}^3$ ) to 1 voxels ( 7.41  $\text{\AA}^3$ ).

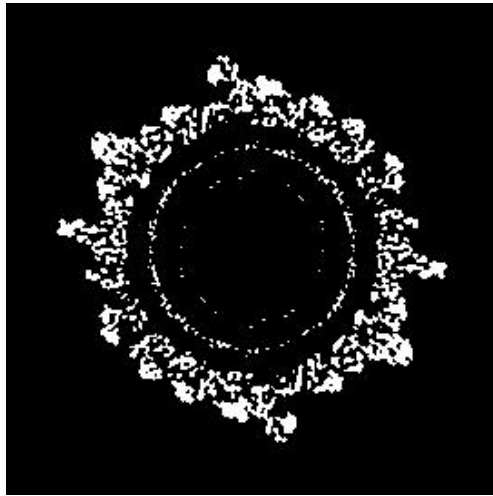
The slices of the raw mask can be seen in Fig. 7.



(a) X Slice 119



(b) Y Slice 151



(c) Z Slice 119

Figure 7: Maximum variance slices in the three dimensions of the raw mask

The following table shows the variation of the mass enclosed at different thresholds (see Fig. 8):

<b>Threshold</b>	<b>Voxel mass</b>	<b>Molecular mass(kDa)</b>	<b># Aminoacids</b>
0.4075	1980208.00	12164.87	110589.70
0.8150	1566939.00	9626.06	87509.65
1.2225	1286346.00	7902.32	71839.23
1.6300	1048156.00	6439.06	58536.91
2.0376	850908.00	5227.32	47521.10
2.4451	697584.00	4285.42	38958.34
2.8526	574992.00	3532.31	32111.88
3.2601	468144.00	2875.91	26144.68
3.6676	371784.00	2283.95	20763.21
4.0751	281112.00	1726.93	15699.41
4.4826	205104.00	1260.00	11454.55
4.8901	142128.00	873.12	7937.50
5.2977	95256.00	585.18	5319.81
5.7052	62280.00	382.60	3478.18
6.1127	39600.00	243.27	2211.56
6.5202	25200.00	154.81	1407.36
6.9277	14544.00	89.35	812.25
7.3352	8376.00	51.46	467.78
7.7427	4428.00	27.20	247.29
8.1502	1980.00	12.16	110.58
8.5578	888.00	5.46	49.59
8.9653	300.00	1.84	16.75
9.3728	156.00	0.96	8.71
9.7803	72.00	0.44	4.02

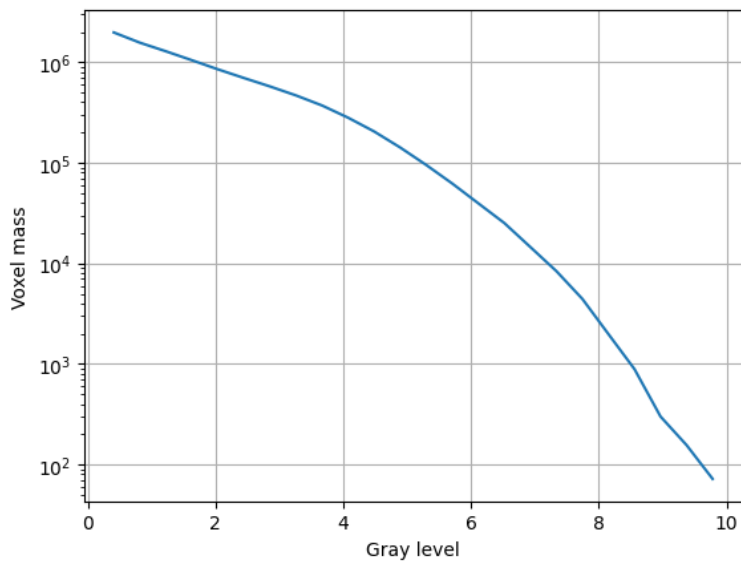


Figure 8: Voxel mass as a function of the gray level.

Constructed mask: After keeping the largest component of the previous mask and dilating it by  $2\text{\AA}$ , there is a total number of voxels of 2337934 and a volume of  $17335488.37 \text{\AA}^3$ . The overlap between the raw and constructed mask is 0.95.

**Automatic criteria:** The validation is OK if 1) to keep 95% of the mass we need to keep at most 5 connected components; and 2) the average volume of the blobs outside the given threshold has a size smaller than  $5\text{\AA}^3$ ; and 3) the overlap between the raw mask and the mask constructed for the analysis is larger than 75%.

**WARNINGS:** 1 warnings

1. **There might be a problem with noise and artifacts, because the average noise blob has a volume of  $7.414875 \text{\AA}^3$ .**

### 2.3 Level 0.c Background analysis

**Explanation:**

Background is defined as the region outside the macromolecule mask. The

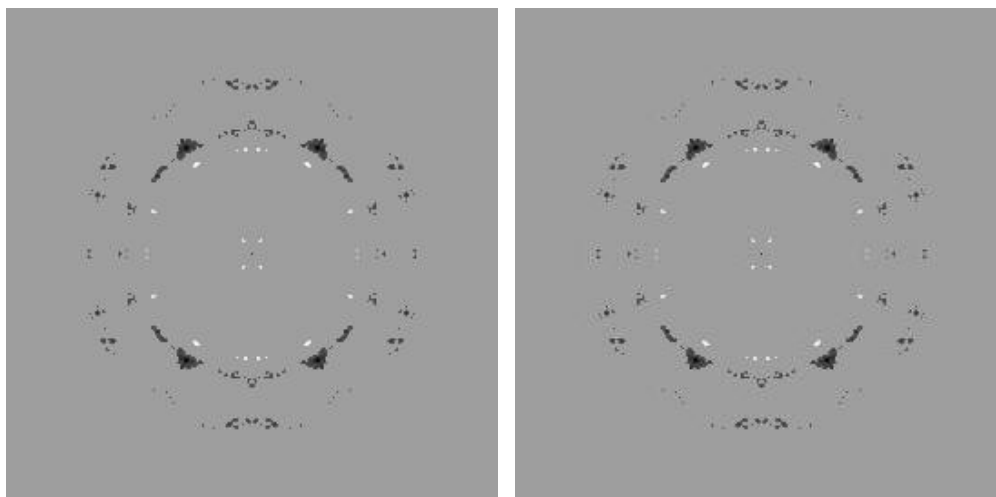
background mean should be zero, and the number of voxels with a very low or very high value (below 5 standard deviations of the noise) should be very small and they should be randomly distributed without any specific structure. Sometimes, you can see some structure due to the symmetry of the structure.

### Results:

The null hypothesis that the background mean is 0 was tested with a one-sample Student's t-test. The resulting t-statistic and p-value were -1307.92 and 0.000000, respectively.

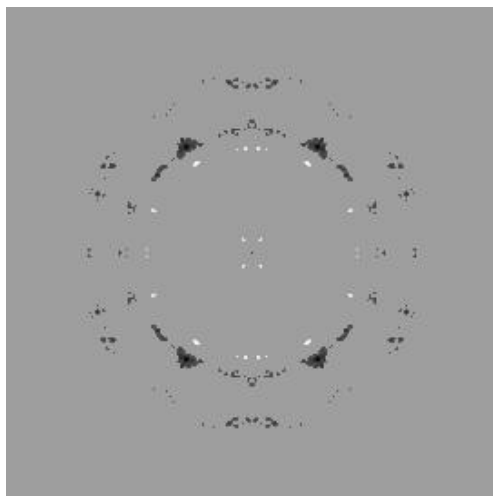
The mean and standard deviation ( $\sigma$ ) of the background were -0.166830 and 0.534579. The percentage of background voxels whose absolute value is larger than 5 times the standard deviation is 0.49 % (see Fig. 9). The same percentage from a Gaussian would be 0.000057% (ratio between the two percentages: 8535.300376).

Slices of the background beyond  $5\sigma$  can be seen in Fig. 9.



(a) X Slice 135

(b) Y Slice 135



(c) Z Slice 135

Figure 9: Maximum variance slices in the three dimensions of the parts of the background beyond  $5\sigma$

**Automatic criteria:** The validation is OK if 1) the p-value of the null hypothesis that the background has 0 mean is larger than 0.001; and 2) the number of voxels above or below 5 sigma is smaller than 20 times the amount expected for a Gaussian with the same standard deviation whose mean is 0.

**WARNINGS:** 2 warnings

1. **The null hypothesis that the background mean is 0 has been rejected because the p-value of the comparison is smaller than 0.001**
2. **There is a significant proportion of outlier values in the background (cdf5 ratio=8535.30)**

## 2.4 Level 0.d B-factor analysis

### **Explanation:**

The B-factor line (see this [link](#) for more details) fitted between  $15\text{\AA}$  and the resolution reported should have a slope that is between 0 and  $300\text{ \AA}^2$ .

### **Results:**

This method cannot be applied to maps with no resolution reported.

**STATUS:** Does not apply

## 2.5 Level 0.e Local resolution with DeepRes

### Explanation:

DeepRes (see this [link](#) for more details) measures the local resolution using a neural network that has been trained on the appearance of atomic structures at different resolutions. Then, by comparing the local appearance of the input map to the appearance of the atomic structures a local resolution label can be assigned.

### Results:

This method cannot be applied to maps with no resolution reported.

**STATUS:** Does not apply

## 2.6 Level 0.f Local B-factor

### Explanation:

LocBfactor (see this [link](#) for more details) estimates a local resolution B-factor by decomposing the input map into a local magnitude and phase term using the spiral transform.

### Results:

This method cannot be applied to maps with no resolution reported.

**STATUS:** Does not apply

## 2.7 Level 0.g Local Occupancy

### Explanation:

LocOccupancy (see this [link](#) for more details) estimates the occupancy of a voxel by the macromolecule.

### Results:

This method cannot be applied to maps with no resolution reported.

**STATUS:** Does not apply

## 2.8 Level 0.h Hand correction

### Explanation:

Deep Hand (see this [link](#) for more details) determines the correction of the hand for those maps with a resolution smaller than 5Å. The method calculates a value between 0 (correct hand) and 1 (incorrect hand) using a neural network to assign its hand.

### Results:

This method cannot be applied to maps with no resolution reported.

**STATUS:** Does not apply