Public Data-based Report

Validation Report Service

Cryo-EM Map Validation Report

Report to assess Cryo-EM Volume Map at Level(s) 1, 0

This report has been generated based on data publicly available at EMDB.

Basic Entry Information:

EMDB ID: EMD-76984
Title: Consensus reconstruction of ATR-ATRIP-ETAA1 AAD(S95D/S111D)
Authors: See EMDB entry link
Deposited on: 2026-04-30T00:00:00
Reported Resolution: 2.9 Å

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Last update: **September 4, 2026, 7:19pm**

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). To know more about this service read this paper

This Validation Report Service uses Scipion (see this link for more detail) as workflow engine and ChimeraX (see this link for more detail) to generate the 3D views. For more information about the different methods and softwares used for this report, see the references here.

Summarized overall quality

The map seems to be well centered. 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 2 out of 4 evaluable items.

0.a Mass analysis	Sec.	2.1	OK
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	OK

Summary of the warnings across sections.

Section 2.2 (0.b Mask analysis)

1. **There might be a problem of connectivity at this threshold because more than 5 connected components are needed to reach 95% of the total mask. Probably a smaller threshold will not cause this issue.**

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=19980.26)**

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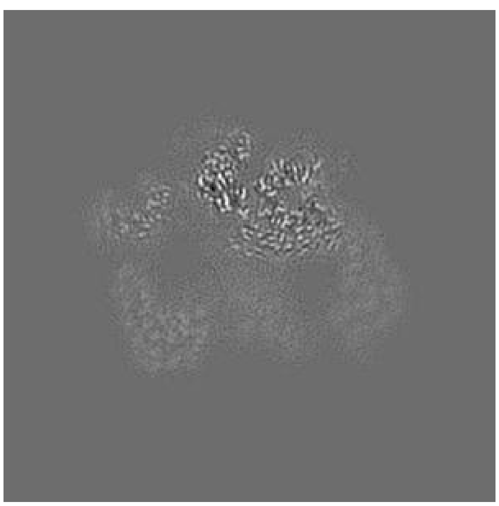
1 Input data

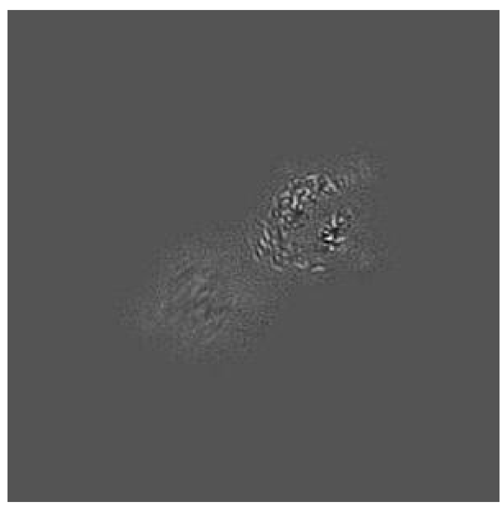
Input map: emd_76984.map
SHA256 hash: e0ccffc466ba37088d6ba4b9dc9a5492c23002131a2c6f520088d3665e76e46b
Voxel size: 1.064000 (Å)
Visualization threshold: 0.012000
Resolution estimated by user: 2.9

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 150

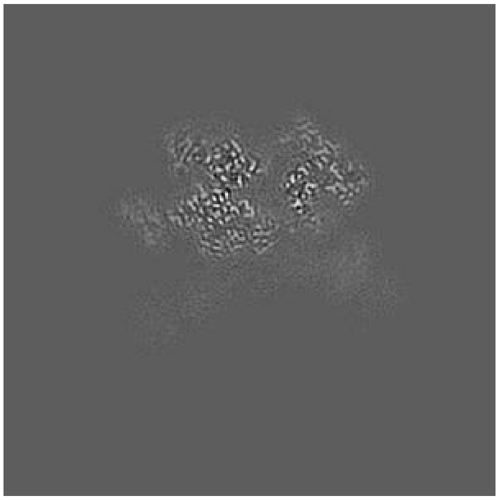

(b) Y Slice 150

(c) Z Slice 150

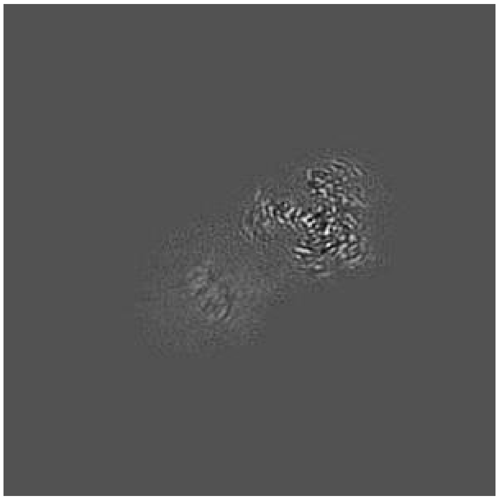
Figure 1: Central slices of the input map in the three dimensions

Orthogonal slices of maximum variance of the input map

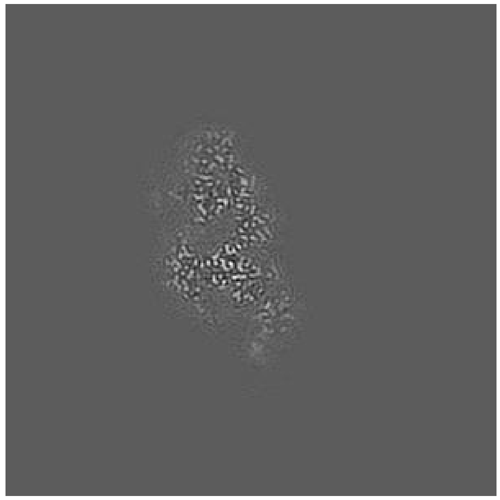
Results:
See Fig. 2.



(a) X Slice 131



(b) Y Slice 136



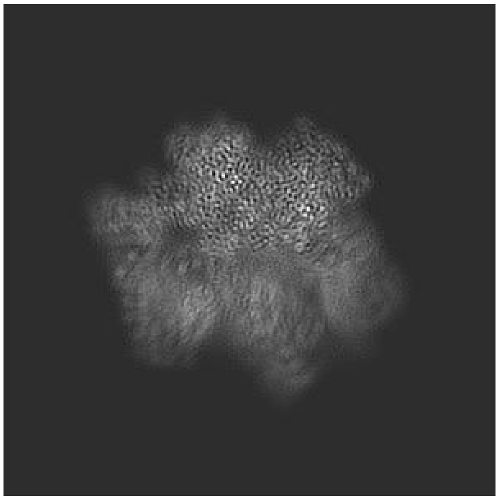
(c) Z Slice 194

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

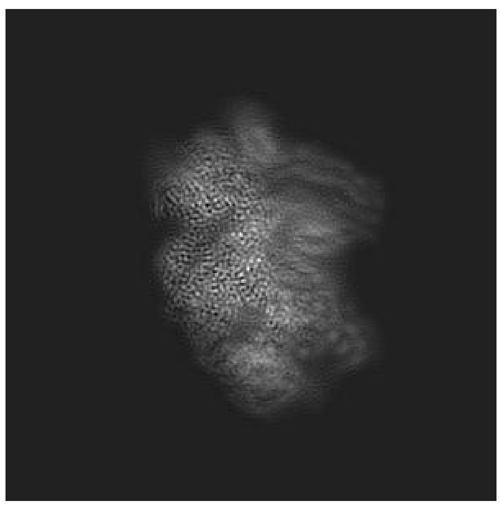

(c) Z Projection

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

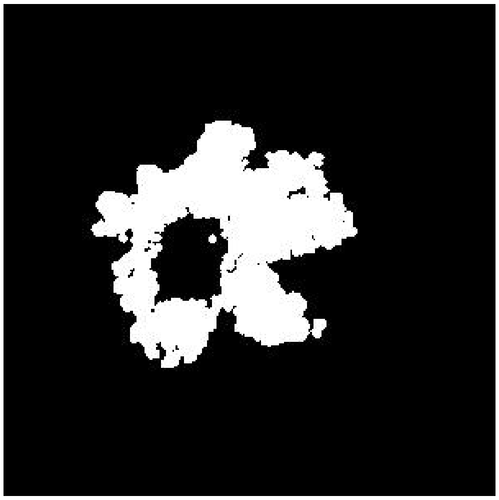
(c) View 3

Figure 4: Isosurface at threshold=0.012000. 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).

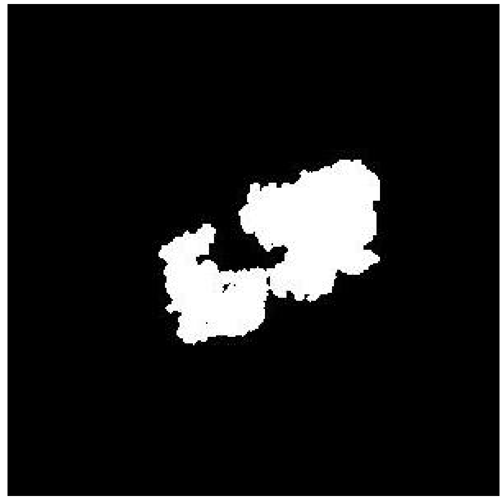
Orthogonal slices of maximum variance of the mask with hard borders

Explanation:
The mask with hard borders has been calculated at the suggested threshold 0.012000, the largest connected component was selected, and then dilated by 2Å.

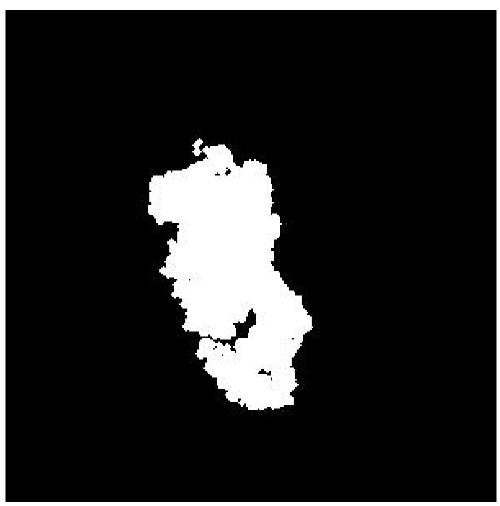
Results:
See Fig. 5.



(a) X Slice 155



(b) Y Slice 124



(c) Z Slice 178

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 0.012000, the largest connected component was selected, and then dilated by

2Å.

Results:
See Fig. 6.

(a) X Slice 155

(b) Y Slice 123

(c) Z Slice 173

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 30Å (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 91.50 and 81.93 Å, respectively. There is a decentering ratio (abs(Right-Left)/Size)% of 3.00%

The space from the left and right in Y are 55.33 and 77.67 Å, respectively. There is a decentering ratio (abs(Right-Left)/Size)% of 7.00%

The space from the left and right in Z are 76.61 and 71.29 Å, respectively. There is a decentering ratio (abs(Right-Left)/Size)% of 1.67%

The center of mass is at (x,y,z)=(154.20,148.04,151.01). The decentering of the center of mass (abs(Center)/Size)% is 1.40, 0.65, and 0.34, 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 reconstruction, focused refinement, or similar, warnings are expected.

STATUS: OK

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, there 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 (size(Raw AND Constructed)/size(Raw)) that is a number between 0 and 1, the closer to 1, the more they agree.

Results:

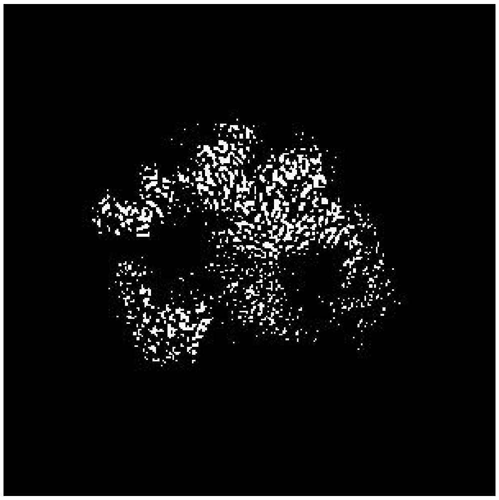
Raw mask: At threshold 0.012000, there are 8753 connected components with a total number of voxels of 232770 and a volume of 280383.14 Å^3 (see Fig. 7). The size and percentage of the total number of voxels for the raw mask are listed below (up to 95% of the mass or the first 100 clusters, whatever happens first), the list contains (No. voxels (volume in Å^3), percentage, cumulated percentage):

(202624 (244070.77), 87.05, 87.05)(3638 (4382.15), 1.56, 88.61)(1763 (2123.62), 0.76, 89.37)(913 (1099.75), 0.39, 89.76)(260 (313.18), 0.11, 89.87)(248 (298.73), 0.11, 89.98)(216 (260.18), 0.09, 90.07)(189 (227.66), 0.08, 90.15)(181 (218.02), 0.08, 90.23)(181 (218.02), 0.08, 90.31)(175 (210.80), 0.08, 90.38)(168 (202.36), 0.07, 90.46)(140 (168.64), 0.06, 90.52)(137 (165.02), 0.06, 90.58)(104 (125.27), 0.04, 90.62)(96 (115.64), 0.04, 90.66)(87 (104.80), 0.04, 90.70)(84 (101.18), 0.04, 90.74)(76 (91.55), 0.03, 90.77)(74 (89.14), 0.03, 90.80)(68 (81.91), 0.03, 90.83)(66 (79.50), 0.03, 90.86)(66 (79.50), 0.03, 90.89)(63 (75.89), 0.03, 90.91)(63 (75.89), 0.03, 90.94)(62 (74.68), 0.03, 90.97)(55 (66.25), 0.02, 90.99)(55 (66.25), 0.02, 91.01)(53 (63.84), 0.02, 91.04)(51 (61.43), 0.02, 91.06)(48 (57.82), 0.02, 91.08)(46 (55.41), 0.02, 91.10)(44 (53.00), 0.02, 91.12)(44 (53.00), 0.02, 91.14)(42 (50.59), 0.02, 91.15)(42 (50.59), 0.02, 91.17)(36 (43.36), 0.02, 91.19)(35 (42.16), 0.02, 91.20)(33 (39.75), 0.01, 91.22)(33 (39.75), 0.01, 91.23)(30 (36.14), 0.01, 91.24)(29 (34.93), 0.01, 91.26)(28 (33.73), 0.01, 91.27)(28 (33.73), 0.01, 91.28)(27 (32.52), 0.01, 91.29)(26 (31.32), 0.01, 91.30)(26 (31.32), 0.01, 91.31)(26 (31.32), 0.01, 91.33)(25 (30.11), 0.01, 91.34)(25 (30.11), 0.01, 91.35)(25 (30.11), 0.01, 91.36)(24 (28.91), 0.01, 91.37)(24 (28.91), 0.01, 91.38)(24 (28.91), 0.01, 91.39)(24 (28.91), 0.01, 91.40)(23 (27.70), 0.01, 91.41)(23 (27.70), 0.01, 91.42)(22 (26.50), 0.01, 91.43)(21 (25.30), 0.01, 91.44)(21 (25.30), 0.01, 91.45)(21 (25.30), 0.01, 91.46)(20 (24.09), 0.01, 91.46)(20 (24.09), 0.01, 91.47)(20 (24.09), 0.01, 91.48)(19 (22.89), 0.01, 91.49)(19 (22.89), 0.01, 91.50)(19 (22.89), 0.01, 91.51)(19 (22.89), 0.01, 91.51)(19 (22.89), 0.01, 91.52)(19 (22.89), 0.01, 91.53)(19 (22.89), 0.01, 91.54)(18 (21.68), 0.01, 91.55)(18 (21.68), 0.01, 91.55)(18 (21.68), 0.01, 91.56)(18 (21.68), 0.01, 91.57)(18 (21.68), 0.01, 91.58)(18 (21.68), 0.01, 91.58)(17 (20.48), 0.01, 91.59)(17 (20.48), 0.01, 91.60)(17 (20.48), 0.01, 91.61)(17 (20.48), 0.01, 91.61)(17 (20.48), 0.01, 91.62)(17 (20.48), 0.01, 91.63)(17 (20.48), 0.01, 91.64)(16 (19.27), 0.01, 91.64)(16 (19.27), 0.01, 91.65)(16 (19.27), 0.01, 91.66)(16 (19.27), 0.01, 91.66)(16 (19.27), 0.01, 91.67)(16 (19.27), 0.01, 91.68)(16 (19.27), 0.01, 91.68)(16 (19.27), 0.01, 91.69)(16 (19.27), 0.01, 91.70)(16 (19.27), 0.01, 91.70)(16 (19.27), 0.01, 91.71)(15 (18.07), 0.01, 91.72)(15 (18.07), 0.01, 91.72)(15 (18.07), 0.01, 91.73)(15 (18.07), 0.01, 91.74)

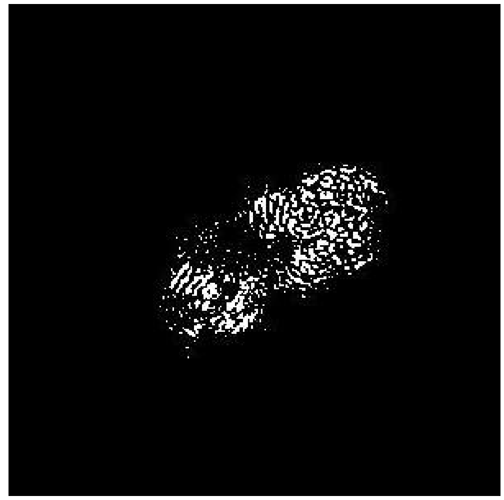
Number of components to reach 95% of the mass: 1383

The average size of the remaining 7370 components is 1.58 voxels (1.20 Å^3). Their size go from 4 voxels (4.82 Å^3) to 1 voxels (1.20 Å^3).

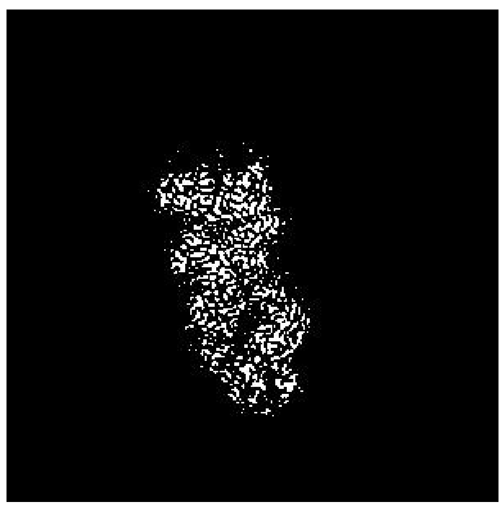
The slices of the raw mask can be seen in Fig. 7.



(a) X Slice 151



(b) Y Slice 126



(c) Z Slice 175

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):

Threshold	Voxel mass	Molecular mass(kDa)	# Aminoacids
0.0064	568814.00	567.66	5160.54
0.0127	209580.00	209.15	1901.41
0.0191	102553.00	102.34	930.41
0.0255	63881.00	63.75	579.56
0.0318	43761.00	43.67	397.02
0.0382	31265.00	31.20	283.65
0.0446	22640.00	22.59	205.40
0.0510	16476.00	16.44	149.48
0.0573	11888.00	11.86	107.85
0.0637	8386.00	8.37	76.08
0.0701	5841.00	5.83	52.99
0.0764	3967.00	3.96	35.99
0.0828	2591.00	2.59	23.51
0.0892	1643.00	1.64	14.91
0.0955	1045.00	1.04	9.48
0.1019	633.00	0.63	5.74
0.1083	361.00	0.36	3.28
0.1146	210.00	0.21	1.91
0.1210	119.00	0.12	1.08
0.1274	57.00	0.06	0.52
0.1338	28.00	0.03	0.25
0.1401	13.00	0.01	0.12
0.1465	5.00	0.00	0.05
0.1529	4.00	0.00	0.04

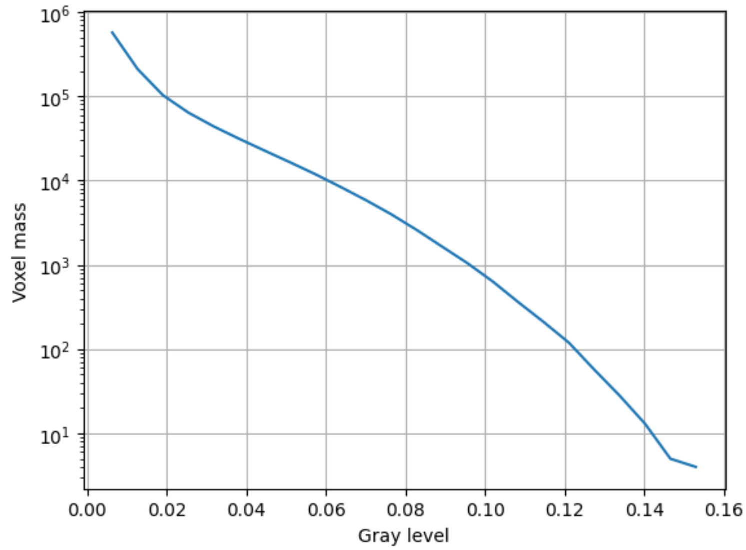


Figure 8: Voxel mass as a function of the gray level.

Constructed mask: After keeping the largest component of the previous mask and dilating it by 2Å, there is a total number of voxels of 874765 and a volume of 1053698.31 Å^3. The overlap between the raw and constructed mask is 0.90.

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 5Å^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 of connectivity at this threshold because more than 5 connected components are needed to reach 95% of the total mask. Probably a smaller threshold will not cause this issue.**

2.3 Level 0.c Background analysis

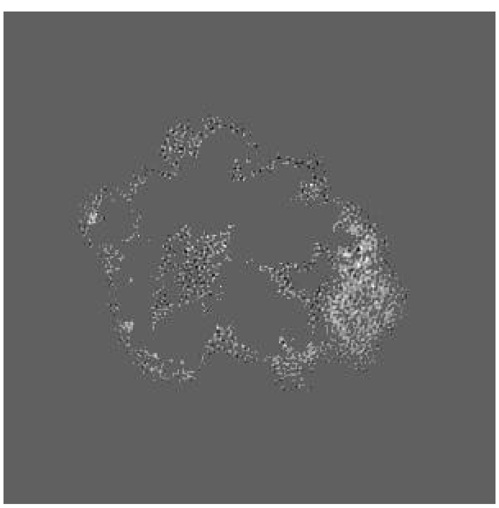
Explanation:
Background is defined as the region outside the macromolecule mask. The background mean should be zero, and the number of voxels with a very low or very high value (below 5 standard deviations of the noise) should be very small and they should be randomly distributed without any specific structure. Sometimes, you can see some structure due to the symmetry of the structure.

Results:

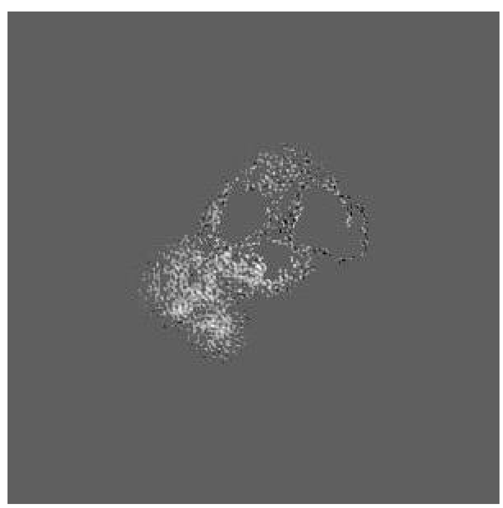
The null hypothesis that the background mean is 0 was tested with a one-sample Student's t-test. The resulting t-statistic and p-value were 435.20 and 0.000000, respectively.

The mean and standard deviation (sigma) of the background were 0.000084 and 0.000985. The percentage of background voxels whose absolute value is larger than 5 times the standard deviation is 1.15 % (see Fig. 9). The same percentage from a Gaussian would be 0.000057% (ratio between the two percentages: 19980.264824).

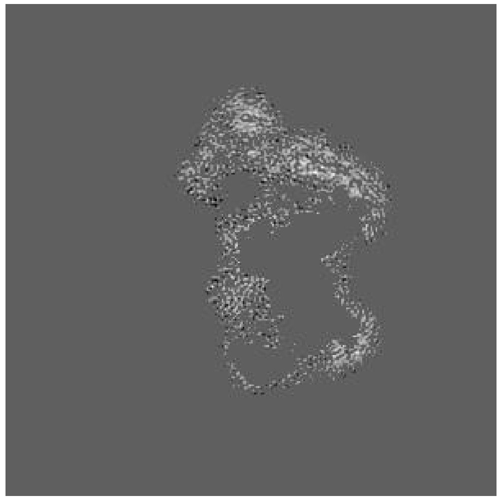
Slices of the background beyond 5*sigma can be seen in Fig. 9.



(a) X Slice 158



(b) Y Slice 209



(c) Z Slice 127

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=19980.26)**

2.4 Level 0.d B-factor analysis

Explanation:
The B-factor line (see this link for more details) fitted between 15Åand the resolution reported should have a slope that is between 0 and 300 Å^2.
Results:

Fig. 10 shows the logarithm (in natural units) of the structure factor (the module squared of the Fourier transform) of the experimental map, its fitted line, and the corrected map. The estimated B-factor was -4.2. The fitted line was $\log(|F|^2) = -1.0/R^2 + (-13.8)$.

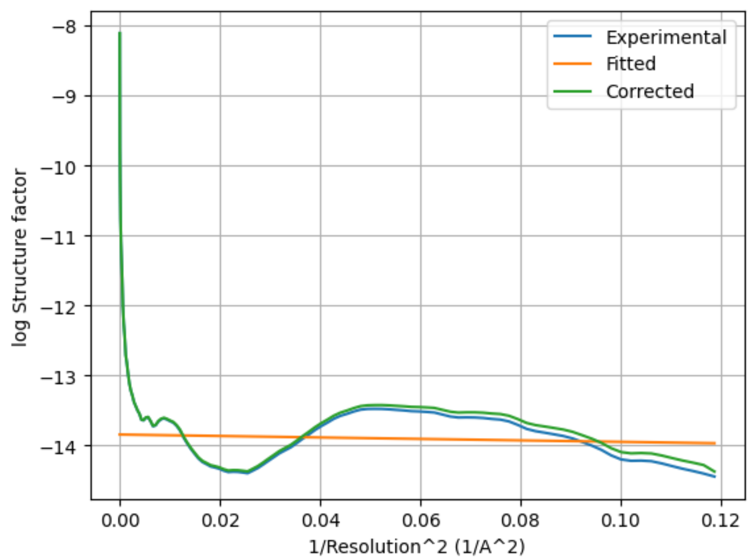
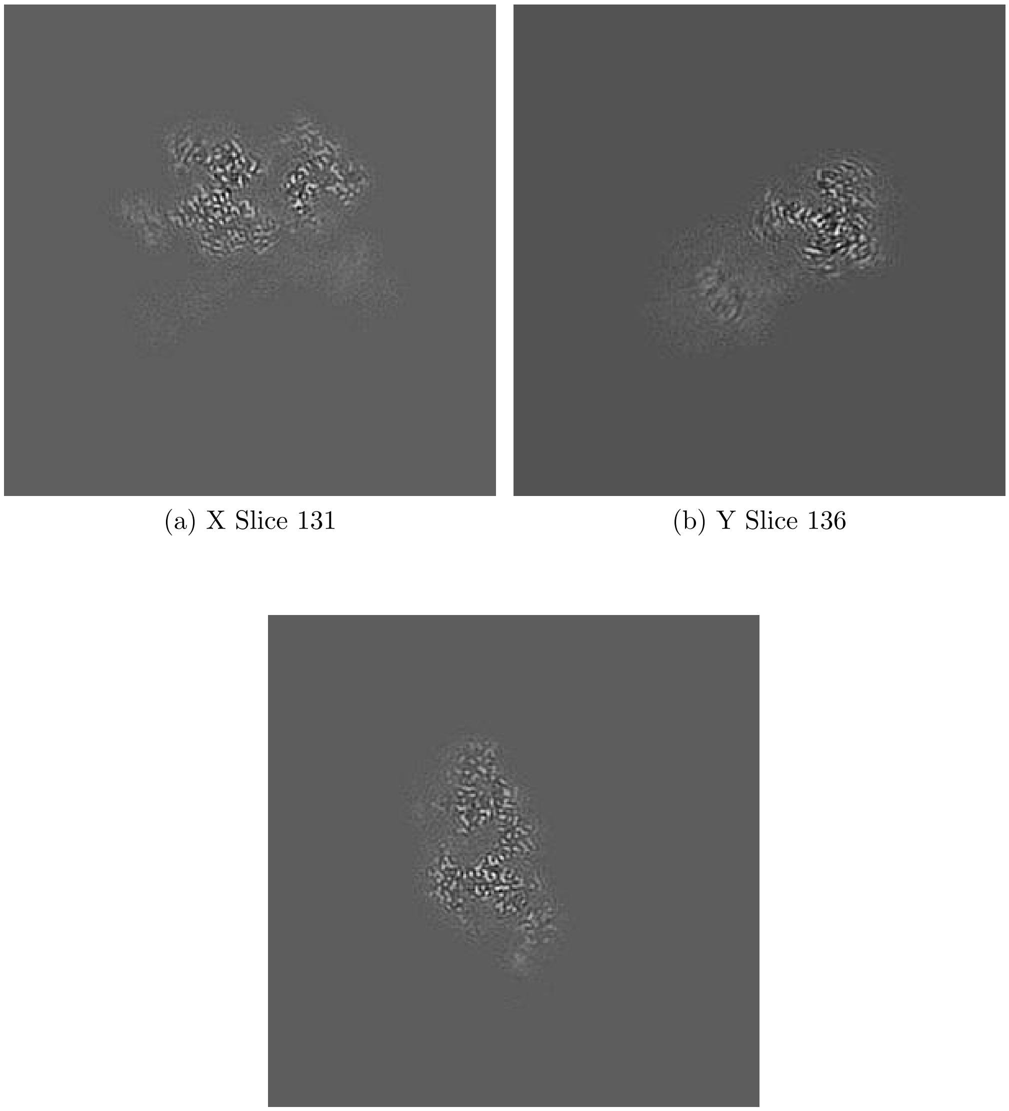


Figure 10: Guinier plot. The X-axis is the square of the inverse of the resolution in Å.



(a) X Slice 131

(b) Y Slice 136

(c) Z Slice 194

Figure 11: Slices of maximum variation in the three dimensions of the B-factor corrected map

Automatic criteria: The validation is OK if the B-factor is in the range [-300,0].

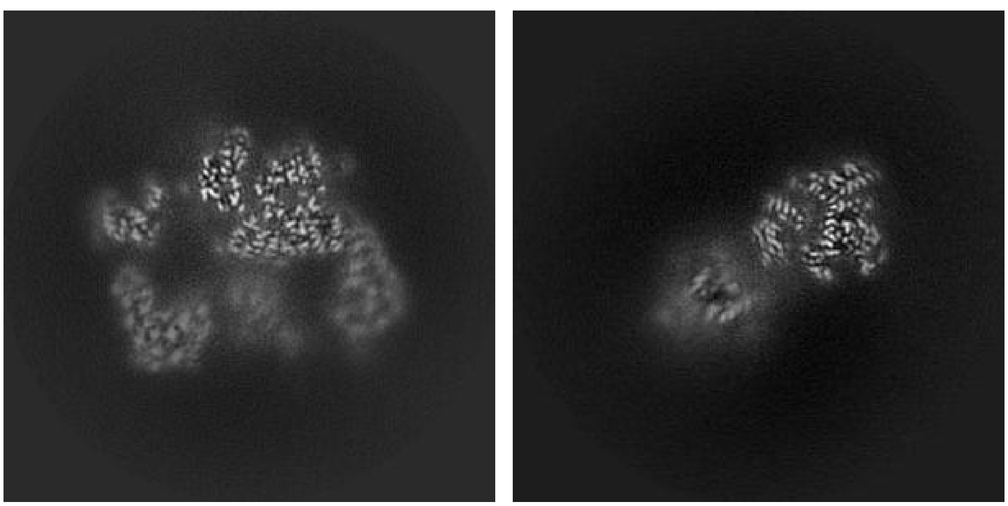
STATUS: OK

3 Half maps

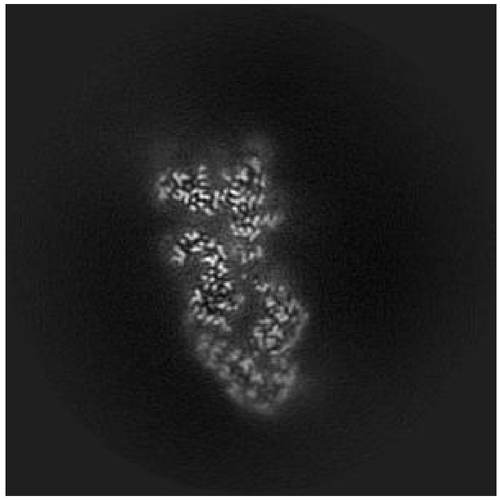
Half map 1: emd_76984_half_map_1.map
SHA256 hash: 2b5b9b15d70ef7073cab1cb06256cc4746ee12ca11848e2a11fb42c243a9ef1d

Half map 2: emd_76984_half_map_2.map
SHA256 hash: c58f9ad8c7b2f8b27ad6b47cc1628634635e69663e6705fb0cfc6cfbc8445c74

Slices of the first half map can be seen in Fig. 12.
Slices of the second half map can be seen in Fig. 13.
Slices of the difference between both maps can be seen in Fig. 14. There should not be any structure in this difference. Sometimes some patterns are seen if the map is symmetric.

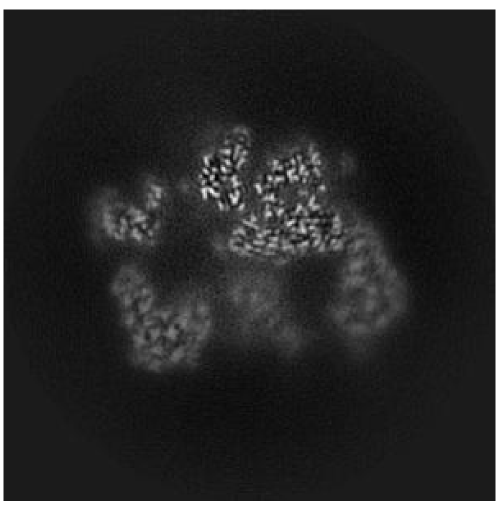


(a) X Slice 148 (b) Y Slice 141

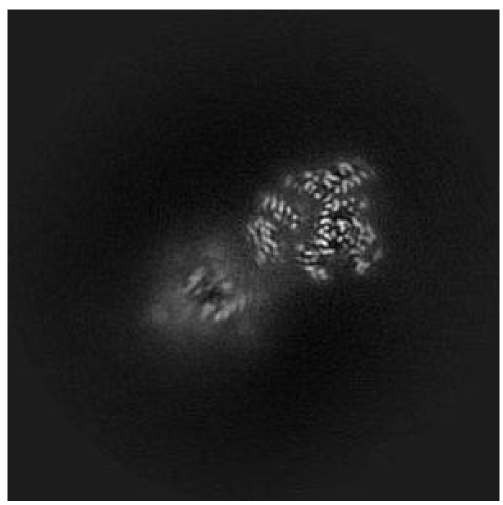


(c) Z Slice 175

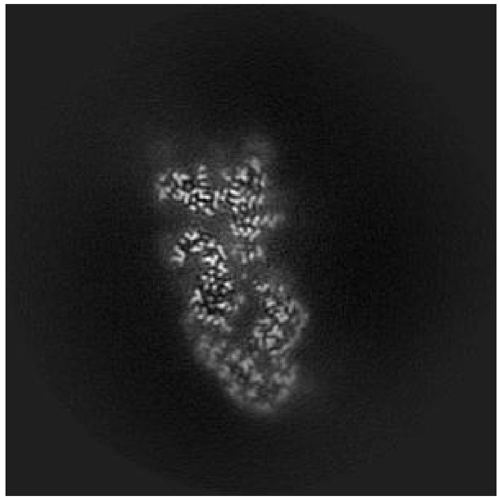
Figure 12: Slices of maximum variation in the three dimensions of Half 1



(a) X Slice 148

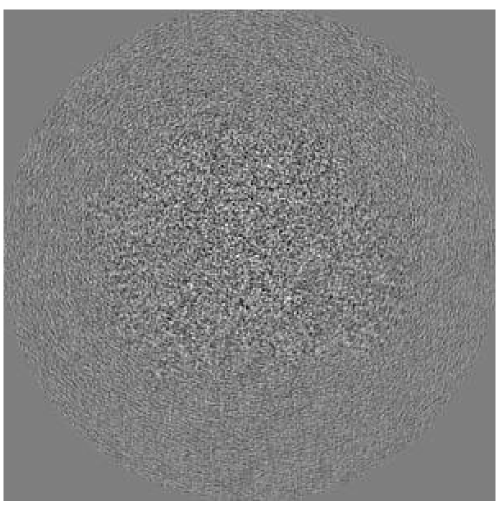


(b) Y Slice 141

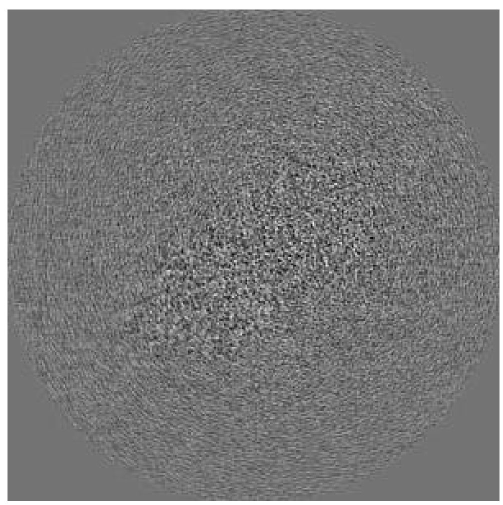


(c) Z Slice 175

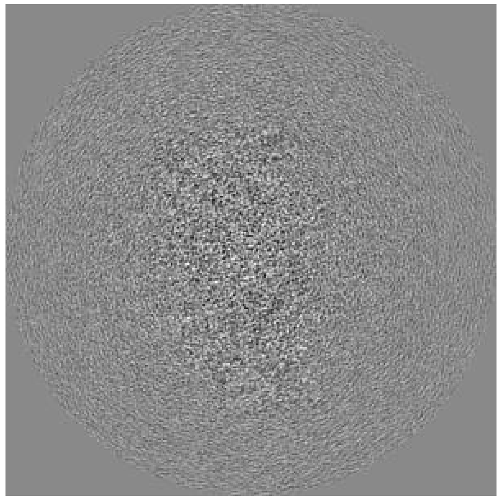
Figure 13: Slices of maximum variation in the three dimensions of Half 2



(a) X Slice 151



(b) Y Slice 149



(c) Z Slice 166

Figure 14: Slices of maximum variation in the three dimensions of the difference Half1-Half2.