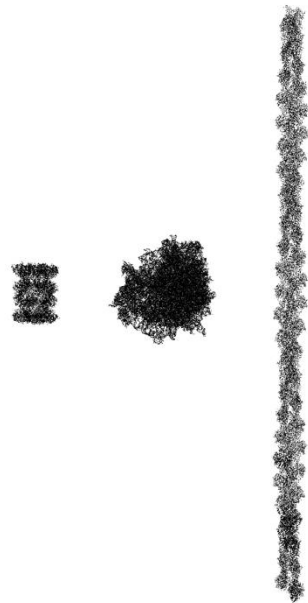
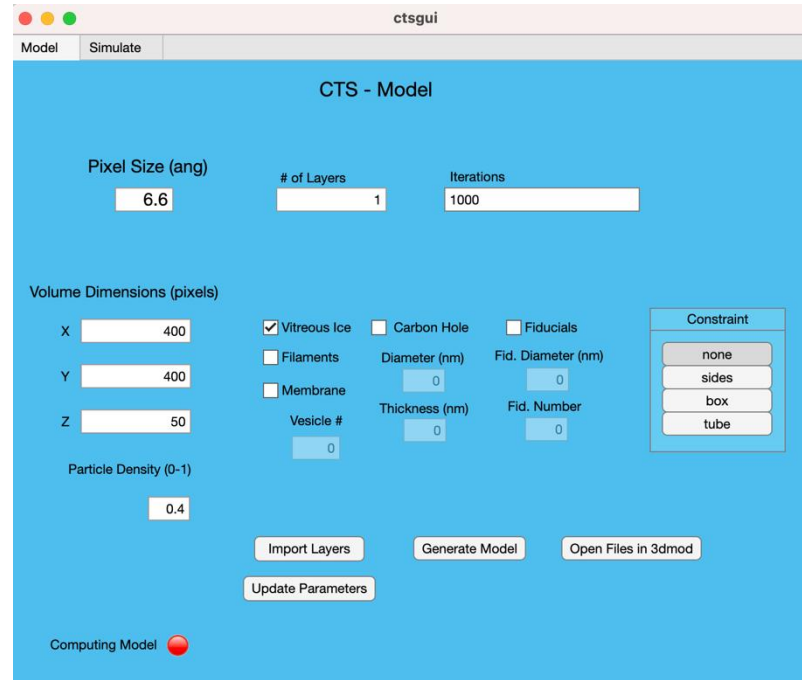
The background of the slide is a grayscale cryo-electron tomogram. It shows a dense field of biological structures. Large, roughly spherical or hexagonal objects with dark, well-defined borders are scattered throughout. These appear to be cross-sections of cells or large organelles. Between these larger structures, there are numerous smaller, more complex features, including parallel lines that could be microtubules or other cytoskeletal elements, and various smaller granular or vesicular structures. The overall texture is noisy and detailed, characteristic of cryo-ET data.

Training generalized networks using
real and synthetic cryo-ET data.

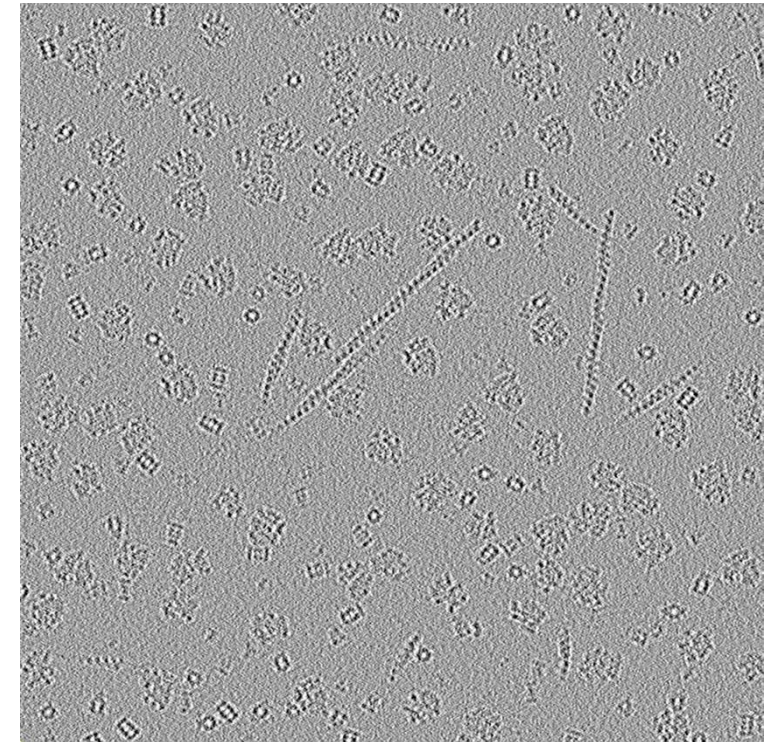
Atomic Models



CryoTomoSim



Synthetic Tomogram



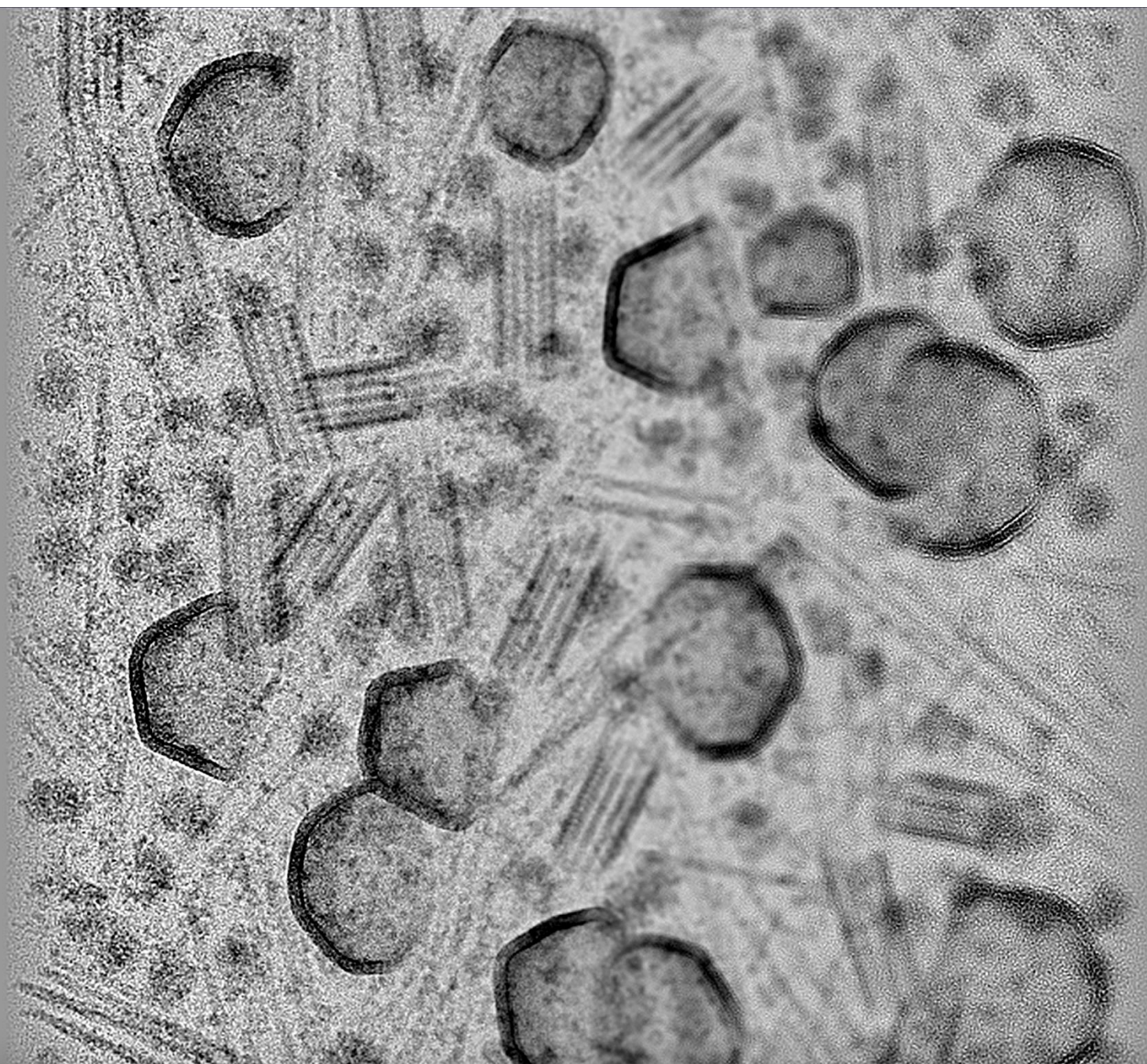
https://github.com/carsonpurnell/cryotomosim_CTS

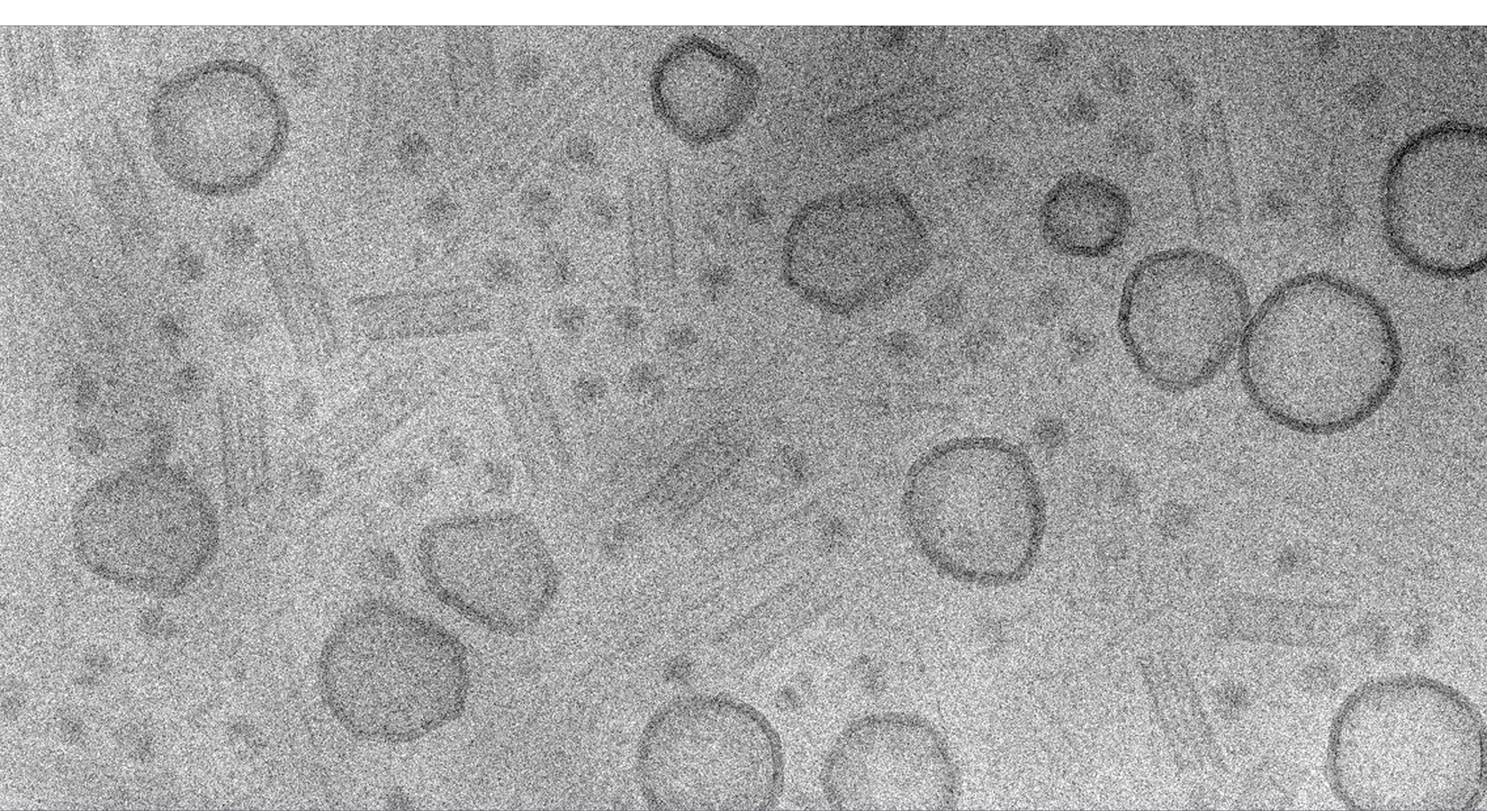
This is a black and white electron micrograph showing various cellular components. Large, roughly circular structures with dark, well-defined borders are scattered throughout the field of view. Interspersed among these are numerous smaller, dark, granular particles. Additionally, there are several elongated, parallel structures that appear as thin, dark lines or bundles. The overall texture is grainy, characteristic of electron microscopy.

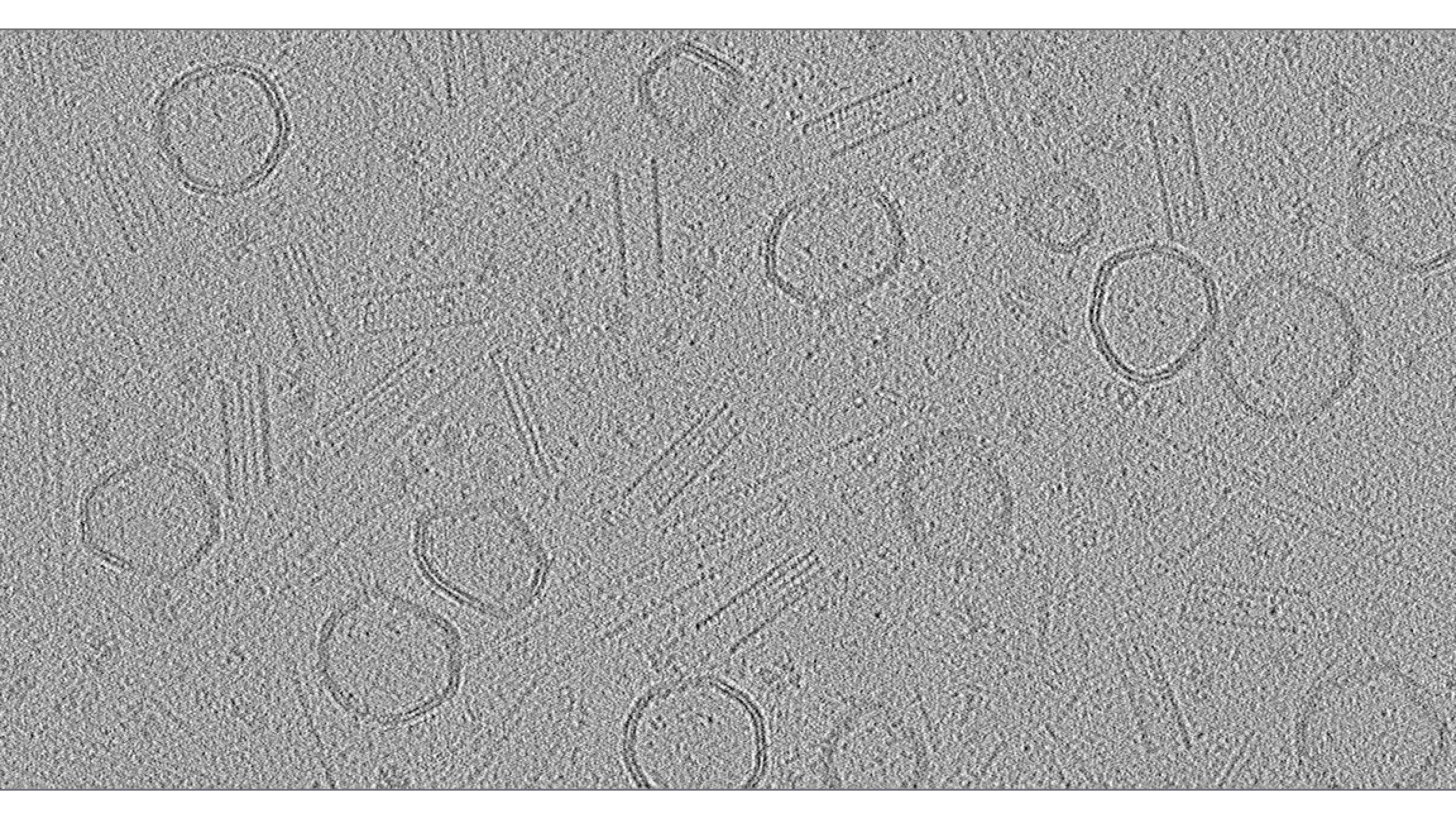
Macromolecular Assemblies

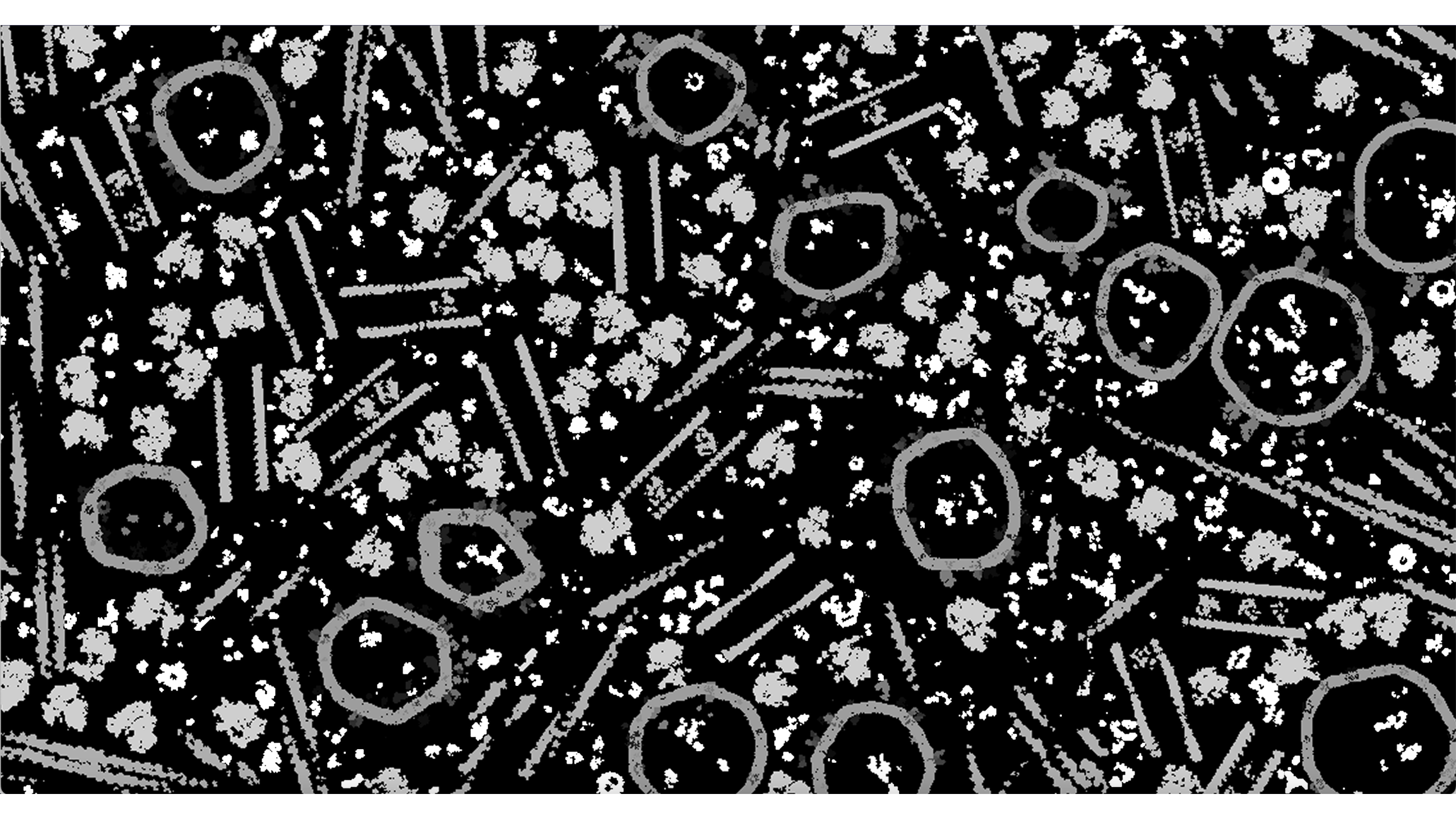
Linear Bundles

Membrane Complexes









Segmentation

Typical Deep Learning Parameters

All models were trained in Dragonfly as either semantic segmentation or regression U-Nets

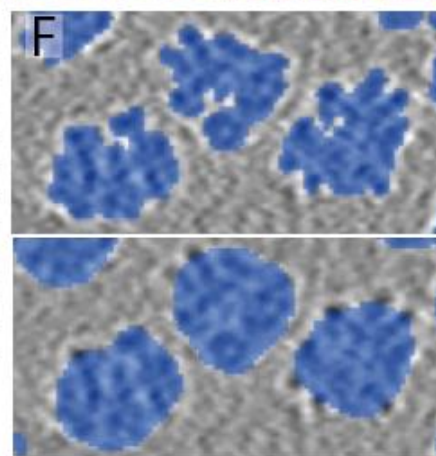
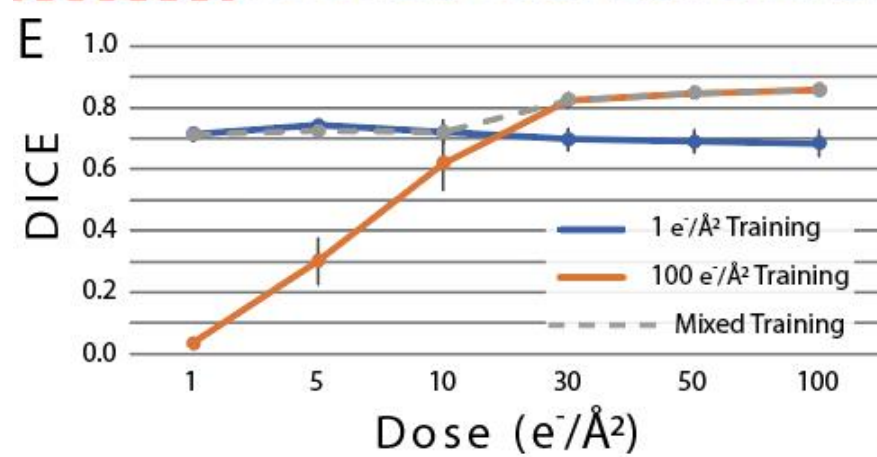
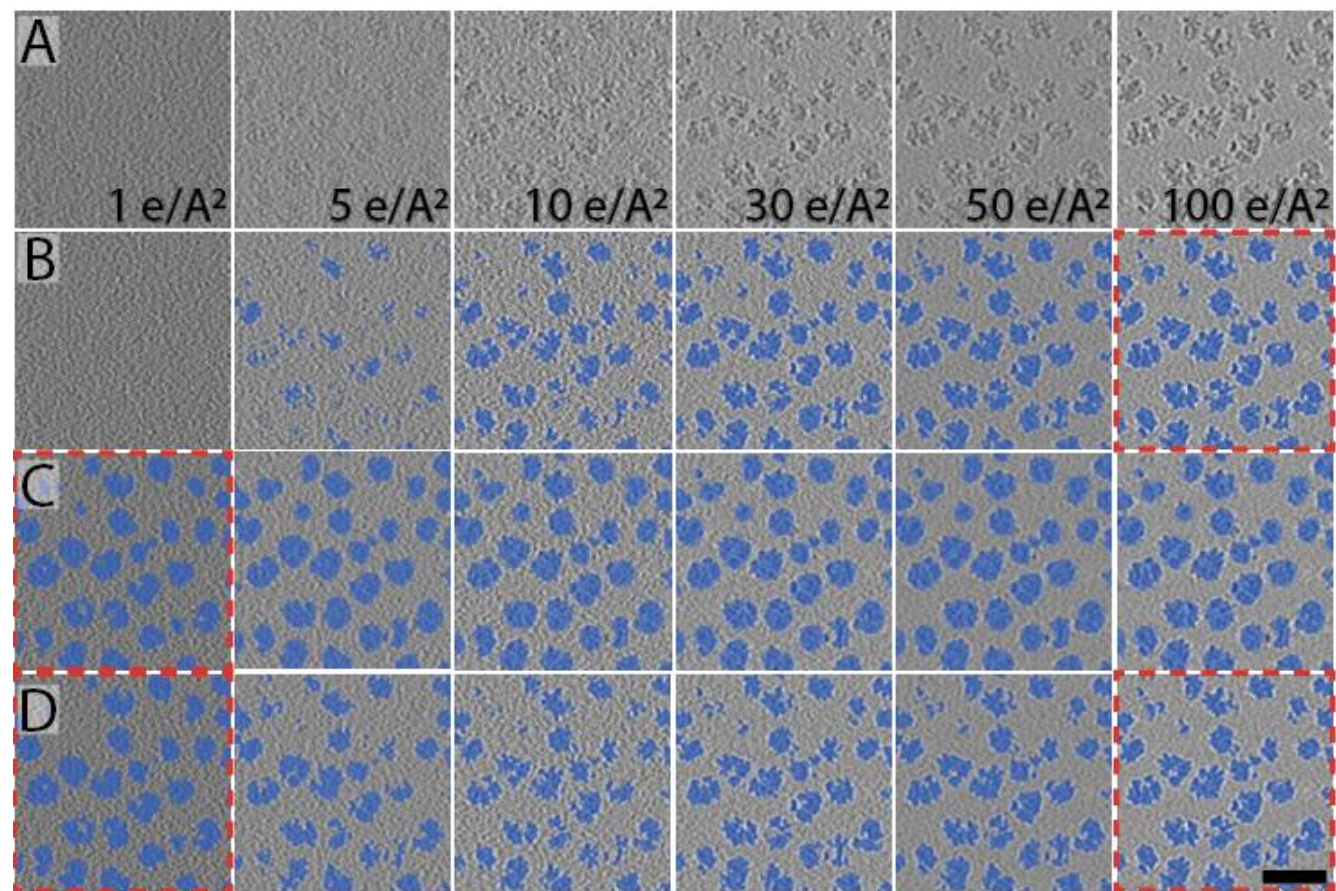
Patch Size: 128x128x11

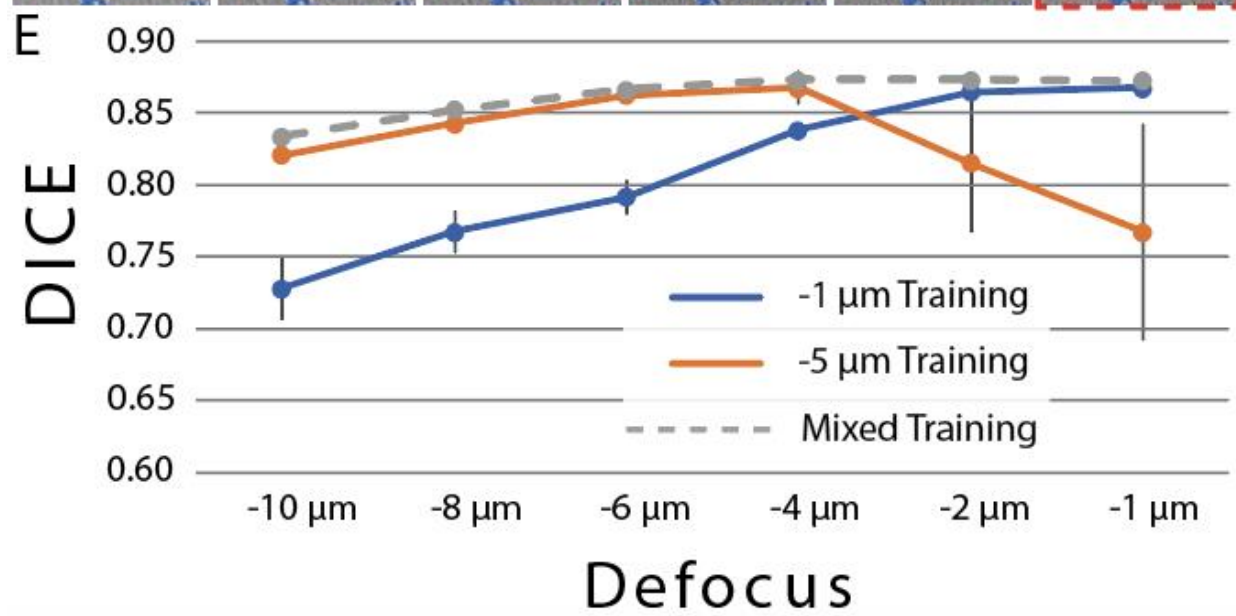
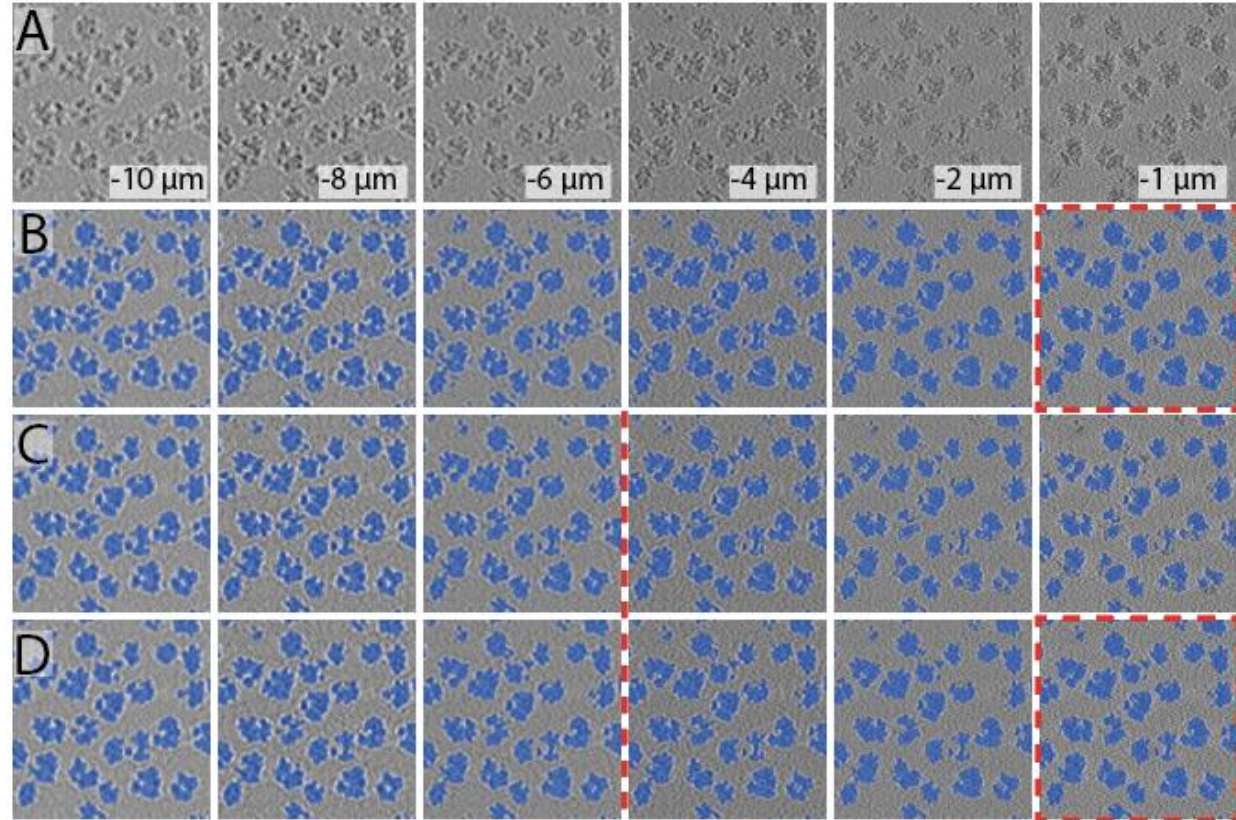
Batch Size: 8

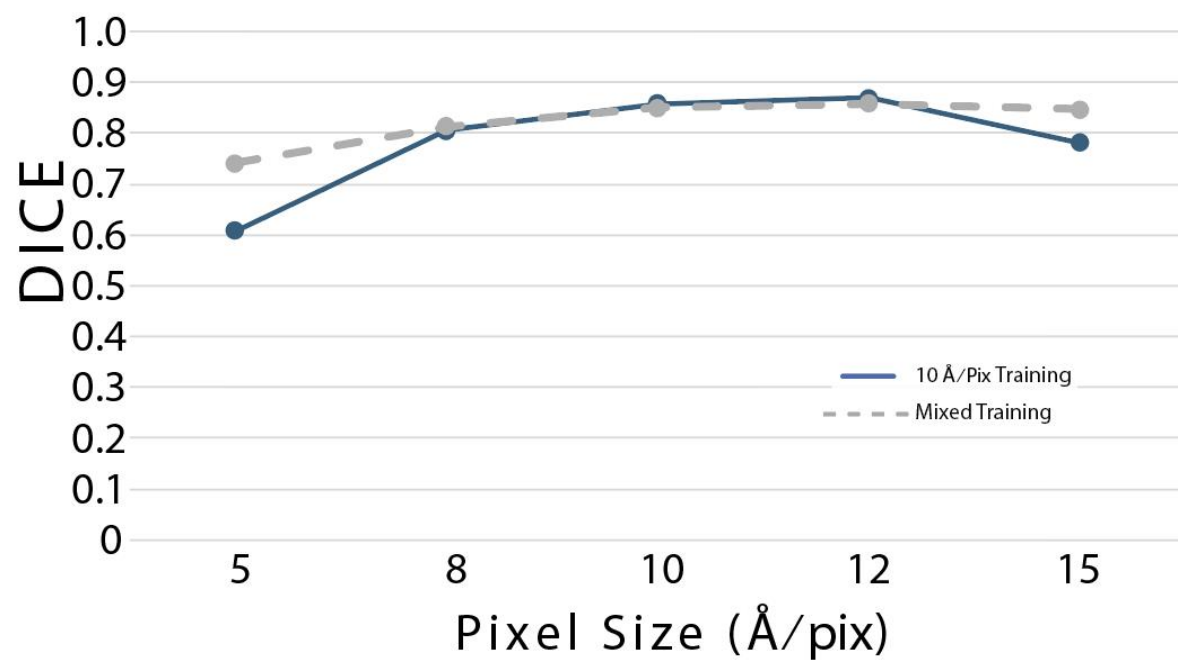
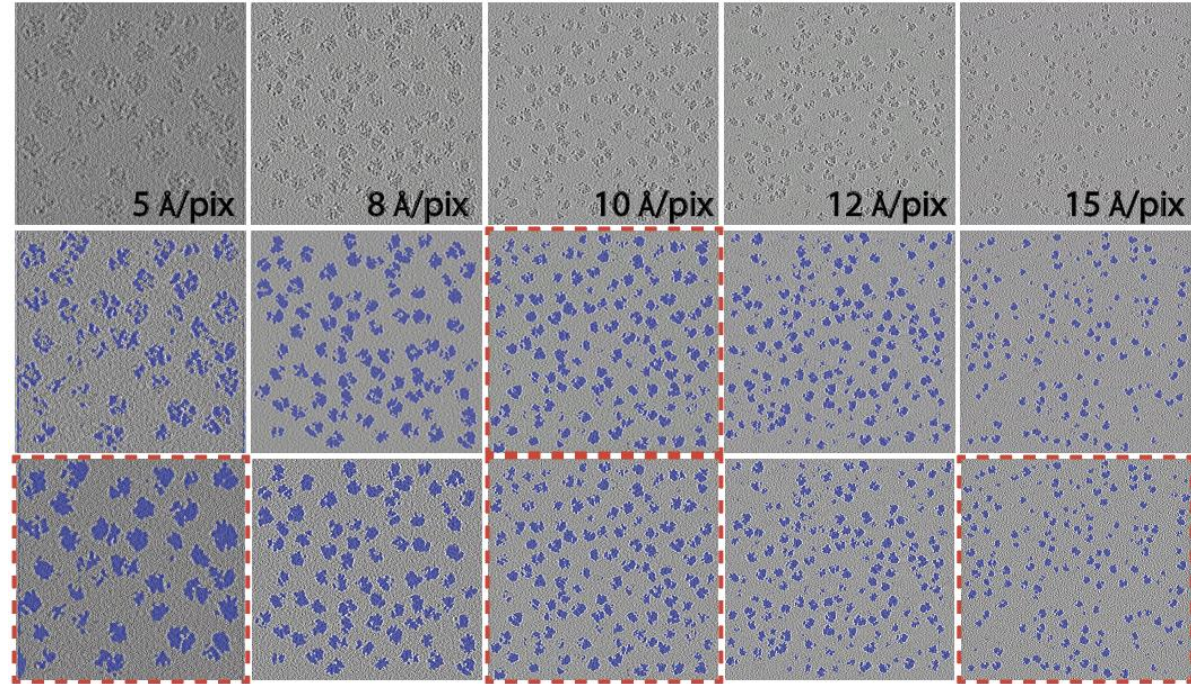
Loss: Categorical Cross Entropy (segmentation)
Mixed Gradient Loss (regression)

Optimization: Adadelata

Patience: 15 epochs







FileWorkflowsArtificial IntelligenceUtilitiesDeveloperHelp

MainSegment

Manipulate

Flip/Rotate

Window Leveling

5_recon_actin_cofilin_complex_actin_lo...

Log Y

Selected control point

Position (normalized):

Position (physical):

Value:

Lookup table (LUT)

Selected range

Plotted range/Data range

Color mapping

Opacity mapping

Gamma:

Annotate

Translate/Rotate

Probe

Scene's Views Properties

Show scale bar

Show legends

View mode:

Interactivity:

Background color:

Lighting

383.76 X 268.86 nm

Range Min: -732.13 Max: 652.48

Slice 24 / 50

Yaw: 0.0 °

Pitch: 180.0 °

Roll: -0.0 °

-X

Dragonfly Workstation (Version 2022.2 Build 12227) (/home/swulluslab/Downloads/nat_meth_reviewers.ORSsession)

Properties

Data Properties and Settings

cofilin_multicol

5_recon_actin_cofilin_complex...

atlas_actin_cofilin_actin_long_c...

Segmentation ...

mt_madness

Leading Edge DeepClean ...

Leading Edge Tomogram

1/7

Basic properties

Width: 400 px (264 nm)

Height: 400 px (264 nm)

Depth: 50 px (33 nm)

Time steps: 1

Total Voxels: 8,000,000

Volume: 2,299,968.00 nm³

Statistical properties

Labeled class count:

Labeled voxels count:

Volume of labeled voxels: 2,299,968 nm³ (100%)

Classes and scalar information

	Name	Count	Label
	atlas_acti...	47,907	1
	atlas_acti...	199,221	2
	atlas_acti...	115,916	3
	atlas_acti...	7,636,956	4

Background class:

Labeled voxels count:

Scalar information

Scalar type:

Measurement:

Min:

Max:

2D settings

Show only contour

Contour thickness:

Opacity and color

Dataset:

Use LUT

Smoothed

Highlight:

Clip

Grid size:

Keep box when object is hidden

Grid lines

Borders

Axes

Captions

Label:

Lock text

Visual effects

New Session

Preferences

File Workflows Artificial Intelligence Utilities Developer Help

Main Segment

Manipulate

Flip/Rotate

Window Leveling

5_recon_actin_cofilin_complex_actin_lo...

Log Y

Selected control point

Position (normalized): Color Alpha

Position (physical):

Value:

Lookup table (LUT)

grayscale More

Selected range

-732.13 652.48

Plotted range/Data range

-735.64 655.99

-732.13 652.48

Color mapping

Opacity mapping

Opacity:

Gamma: 1.00

Annotate

Translate/Rotate

Dynamic refresh 4 quadrants

Probe

Scene's Views Properties

Show scale bar Orthographic projection

Show legends Show text annotations

Anti-aliasing Edge detect

Edge detect only ROIs

View mode: Slice

Interactivity: Balanced

Background color:

Lighting

Light source position:

Use lighting

Shadow strength:

Shadow opacity:

383.76 X 268.86 nm

Range Min: -732.13 Max: 652.48

Slice 24 / 50

Yaw: 0.0 °

Pitch: 180.0 °

Roll: -0.0 °

Properties

Data Properties and Settings

1/7

Basic properties

Width: 400 px (264 nm)
Height: 400 px (264 nm)
Depth: 50 px (33 nm)
Time steps: 1
Total Voxels: 8,000,000
Volume: 2,299,968.00 nm³

Statistical properties

Labeled class count: 4

Labeled voxels count: 8,000,000

Volume of labeled voxels: 2,299,968 nm³ (100%)

Classes and scalar information

Name	Count	Label
atlas_actin... cls 1	47,907	1
atlas_actin... cls 2	199,221	2
atlas_actin... cls 3	115,916	3
atlas_actin... cls 4	7,636,956	4

Add Remove Merge

Background class: Drag class here None

Labeled voxels count: 0

Scalar Information

Scalar type:

Measurement:

Min: Max:

2D settings

Show only contour

Contour thickness:

Opacity and color

Dataset: Leading Edge Tomogram

Use LUT

Smoothed

Highlight:

Clip

Grid size: 30.00 nm

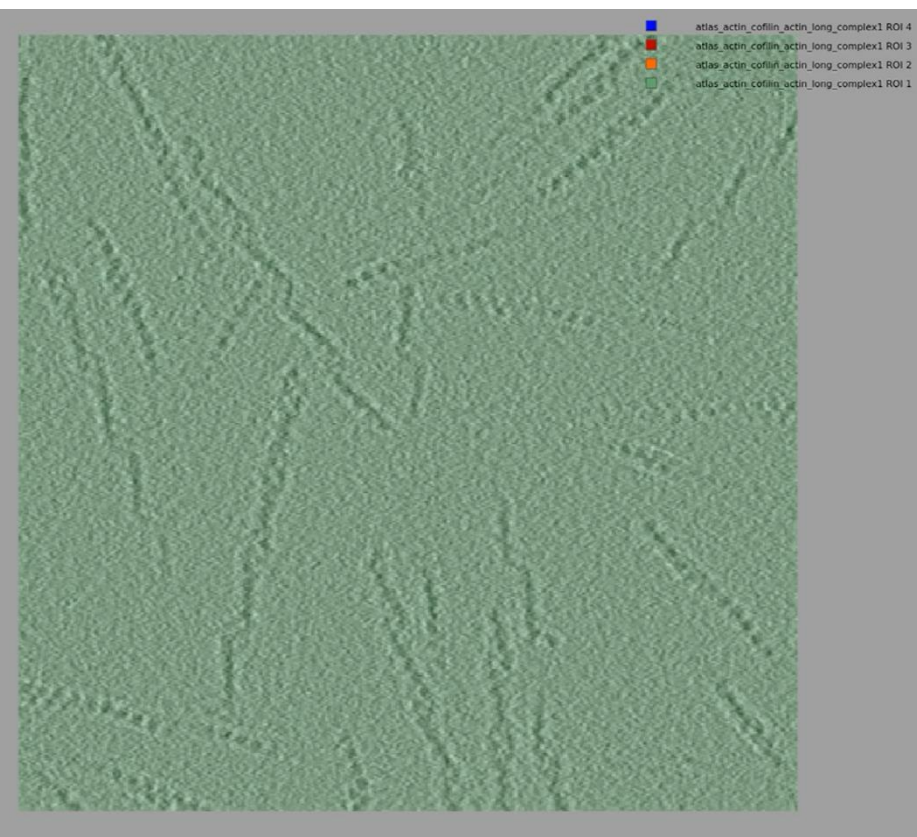
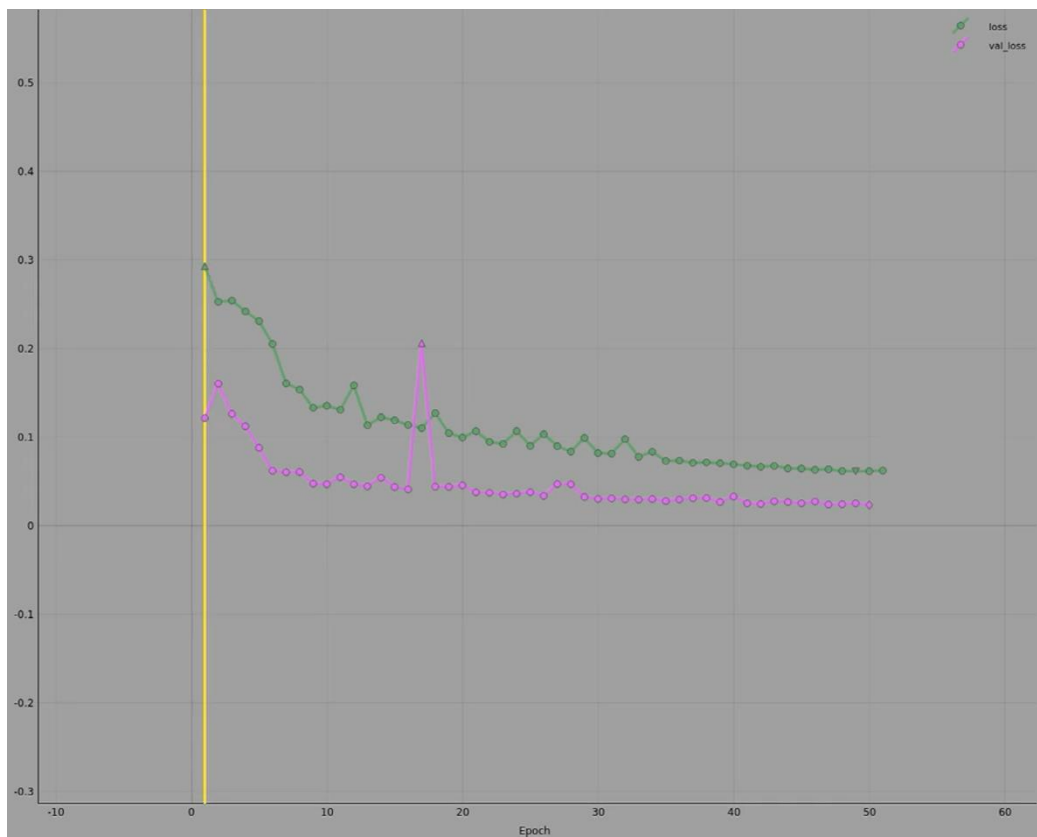
Keep box when object is hidden

Grid lines Borders Axes Captions

Label: Ticks (2 Axes) Lock text

Visual effects

New Session Preferences



Main Segment

Dilate Dimensionality: 3D
Erode Shape: Cube
Open Range: Range
Close Kernel size: 3
Smooth

Operations
Fill inner areas: 3D Apply
Clipped region: Add Remove
Interpolate: Z Apply

Image operations
Image: 5_recon_actin_cofilin_complex_actin
Overwrite... Split at Otsu Export

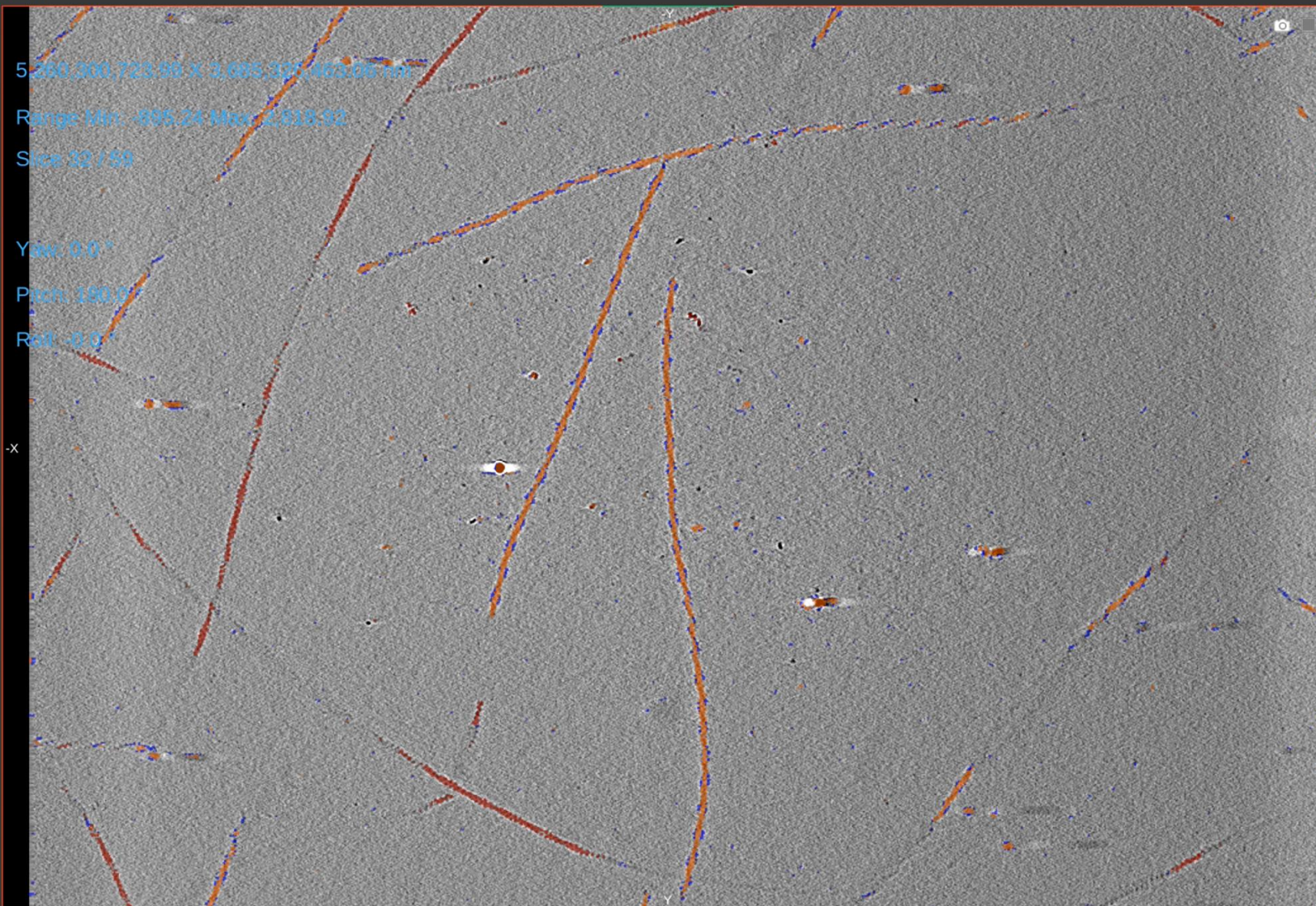
Export
To a Mesh To a Thickness Mesh

ROI Painter
Brush size Pixels nm
Diameter: 20 100,000,000

2D view tools
Single slice Multi-slice
Full
4-connected
Grid size: x: 32 y: 32
Sigma: 2.50
Radius: 1 Pixels

3D view tools
Full
6-connected

Segment with AI
Segmentation model:
Inputs
Classes
Segment on multiple axes
Vote type: Majority Soft vote
Preview Segment
Preview opacity:



Current state: Leveling using an area (Left mouse)

Properties

Data Properties and Settings

Segmentation cofilin_actin_split*
cofilactin_position_15
5_recon_actin_cofilin_complex_...
atlas_actin_cofilin_actin_long_c...
Leading Edge DeepClean ...
Leading Edge Tomogram
mt_madness
Segmentation ...
cofilin_multitool

1/9

Basic properties
Width: 1,023 px (5,115,000,000 nm)
Height: 1,440 px (7,200,000,000 nm)
Depth: 59 px (295,000,000 nm)
Time Steps: 1
Total Voxels: 86,914,080

Statistical properties
Labeled class count: 4
Labeled voxels count: 86,914,080
Volume of labeled voxels: 10,864,260,000,000.0

Classes and scalar information

Name
cofilin
cofilactin
actin
background

Add Remove Merge

Background class: Drag class here None

Labeled voxels count: 0

Scalar information
Scalar type:
Measurement:
Min:
Max:

2D settings
Show only contour
Contour thickness:

Opacity and color
Dataset:
Use LUT
Smoothed
Highlight:

Clip
Grid size: 1,000,000 nm
Keep box when object is hidden
Grid lines Borders Axes Captions
Label: Ticks (2 Axes) Lock text
Visual effects

New Session

Preferences

Main Segment

Dilate Dimensionality: 3D

Erode Shape: Cube

Open Range: Range

Close Kernel size: 3

Smooth

Operations

Fill inner areas: 3D Apply

Clipped region: Add Remove

Interpolate: Z Apply

Image operations

Image: 5_recon_actin_cofilin_complex_actin

Overwrite... Split at Otsu Export

Export

To a Mesh To a Thickness Mesh

ROI Painter

Brush size Pixels nm

Diameter: 20 100,000,000

2D view tools

Single slice Multi-slice

Full

4-connected

Grid size: x: 32 y: 32

Sigma: 2.50

Radius: 1 Pixels

3D view tools

Full

6-connected

Segment with AI

Segmentation model:

Inputs

Classes

Segment on multiple axes

Vote type: Majority Soft vote

Preview Segment

Preview opacity:

PD: 3,476,820,634.39 nm

Range Min: 0 Max: 255

Properties

Data Properties and Settings

Segmentation cofilin_actin_spli...

Segmentation cofilin_actin_spli...

cofilactin_position_15

5_recon_actin_cofilin_complex...

atlas_actin_cofilin_actin_long_c...

Leading Edge DeepClean ...

Leading Edge Tomogram

mt_madness

Segmentation ...

cofilin_multiroi

1/10

Basic properties

Width: 1,023 px (5,115,000,000 nm)

Height: 1,440 px (7,200,000,000 nm)

Depth: 59 px (295,000,000 nm)

Time Steps: 1

Total Voxels: 86,914,080

Statistical properties

Labeled class count: 4

Labeled voxels count: 86,600,740

Volume of labeled voxels: 10,825,092,500,000

Classes and scalar information

Name
cofilin
cofilactin
actin
background

Add Remove Merge

Background class: Drag class here Non

Labeled voxels count: 190,371

Scalar Information

Scalar type:

Measurement:

Min:

Max:

2D settings

Show only contour

Contour thickness:

Opacity and color

Use LUT

Smoothed

Diffuse:

Specular:

Highlight:

Labeled data:

Clip

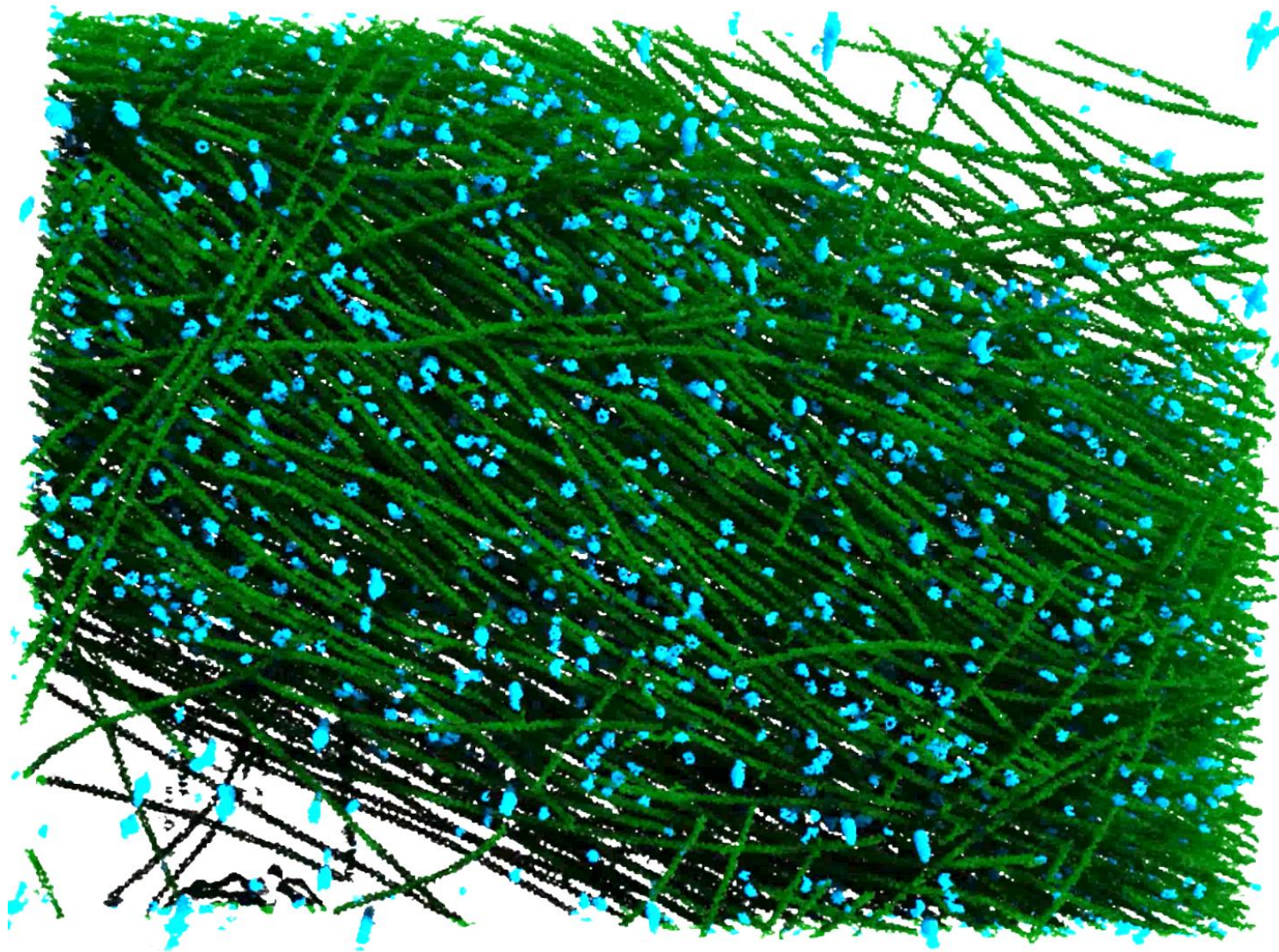
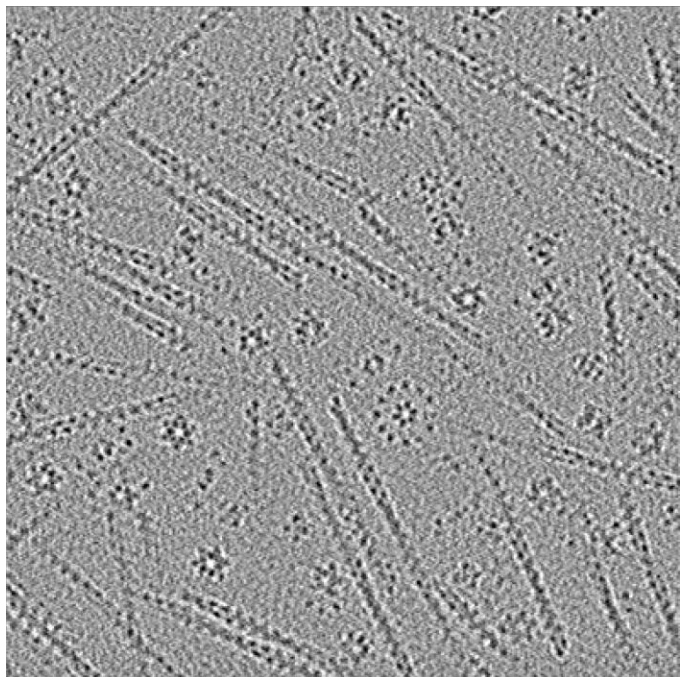
Grid size: 1,000,000 nm

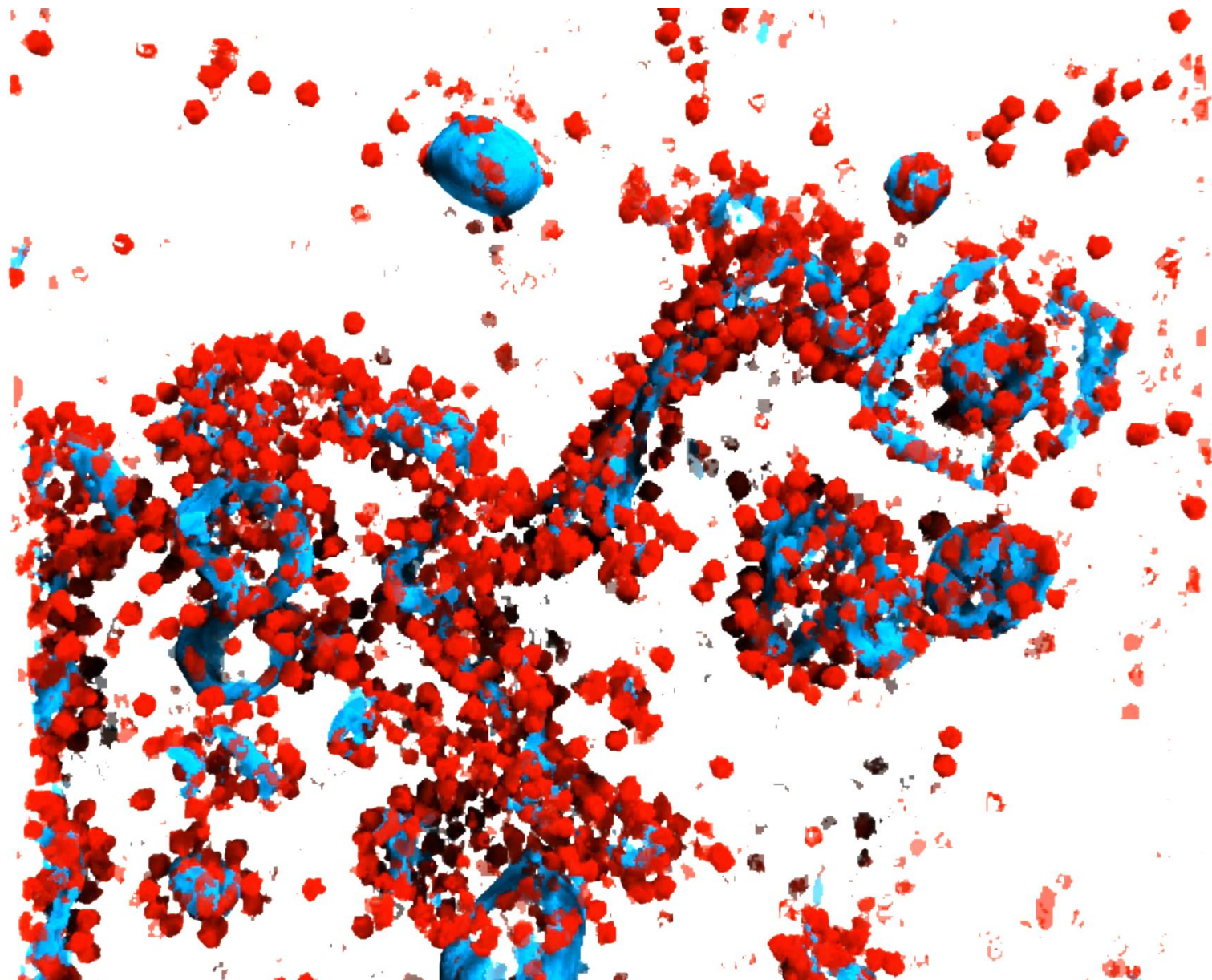
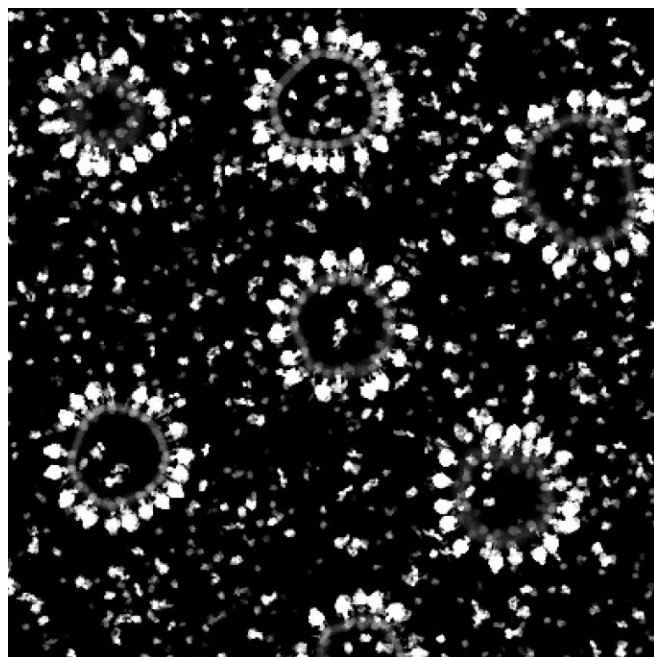
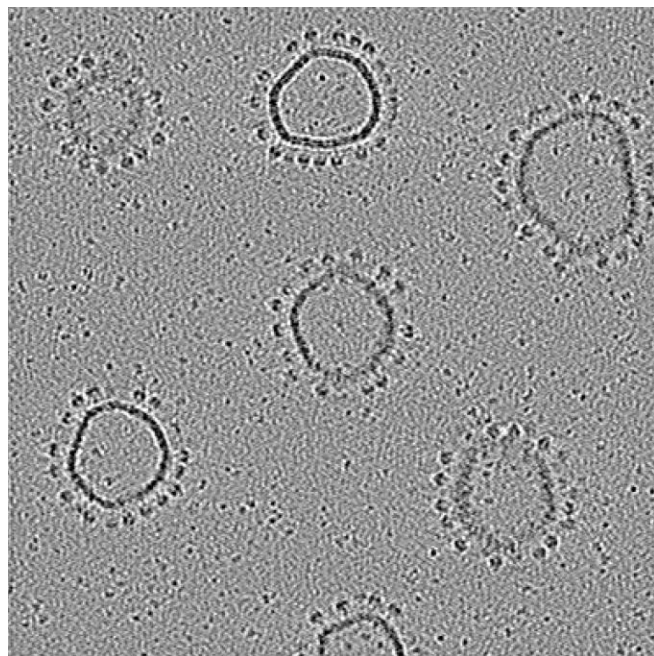
Keep box when object is hidden

Grid lines Borders Axes Captions

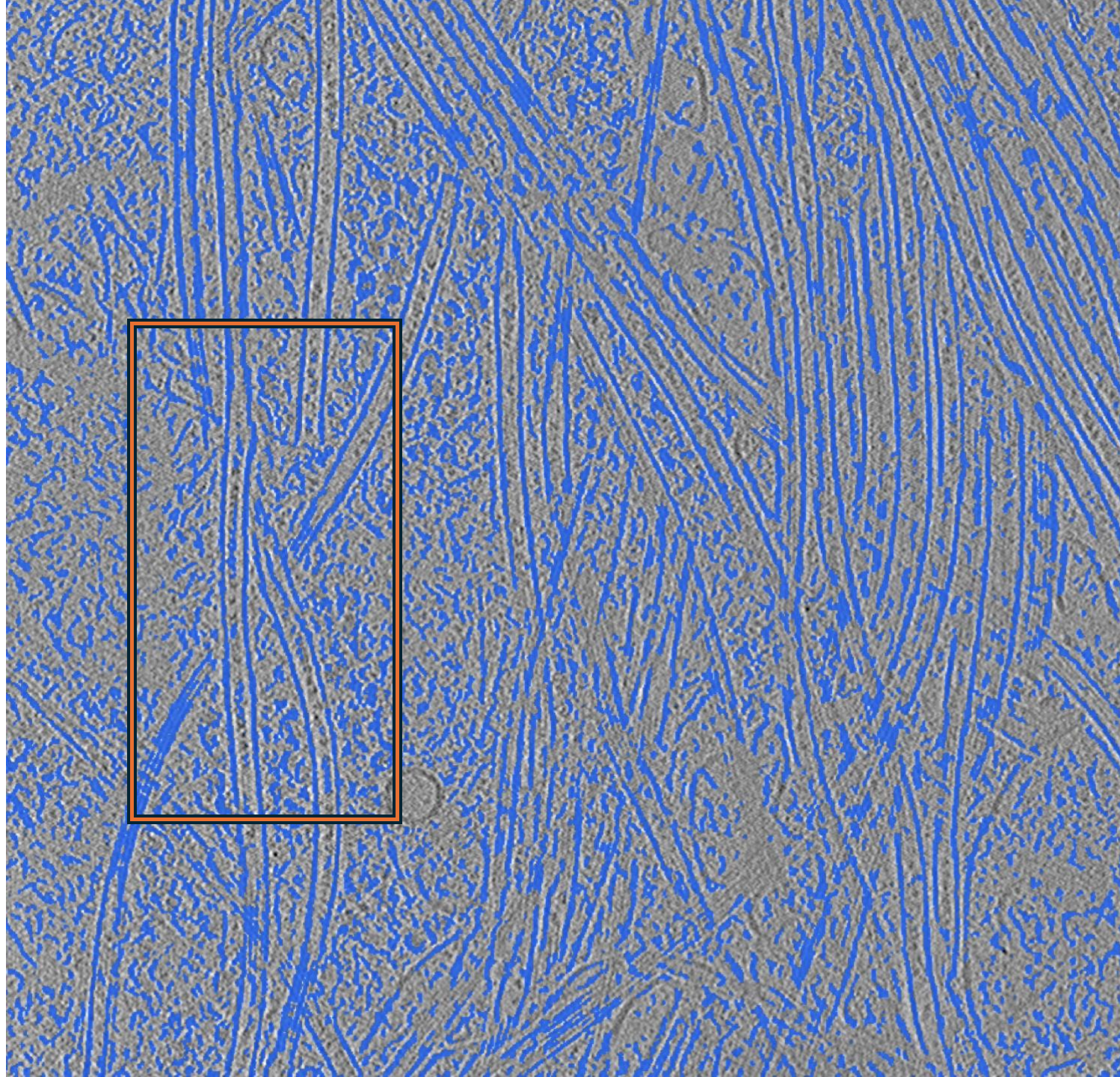
Label: Ticks (2 Axes) Lock text

Visual effects

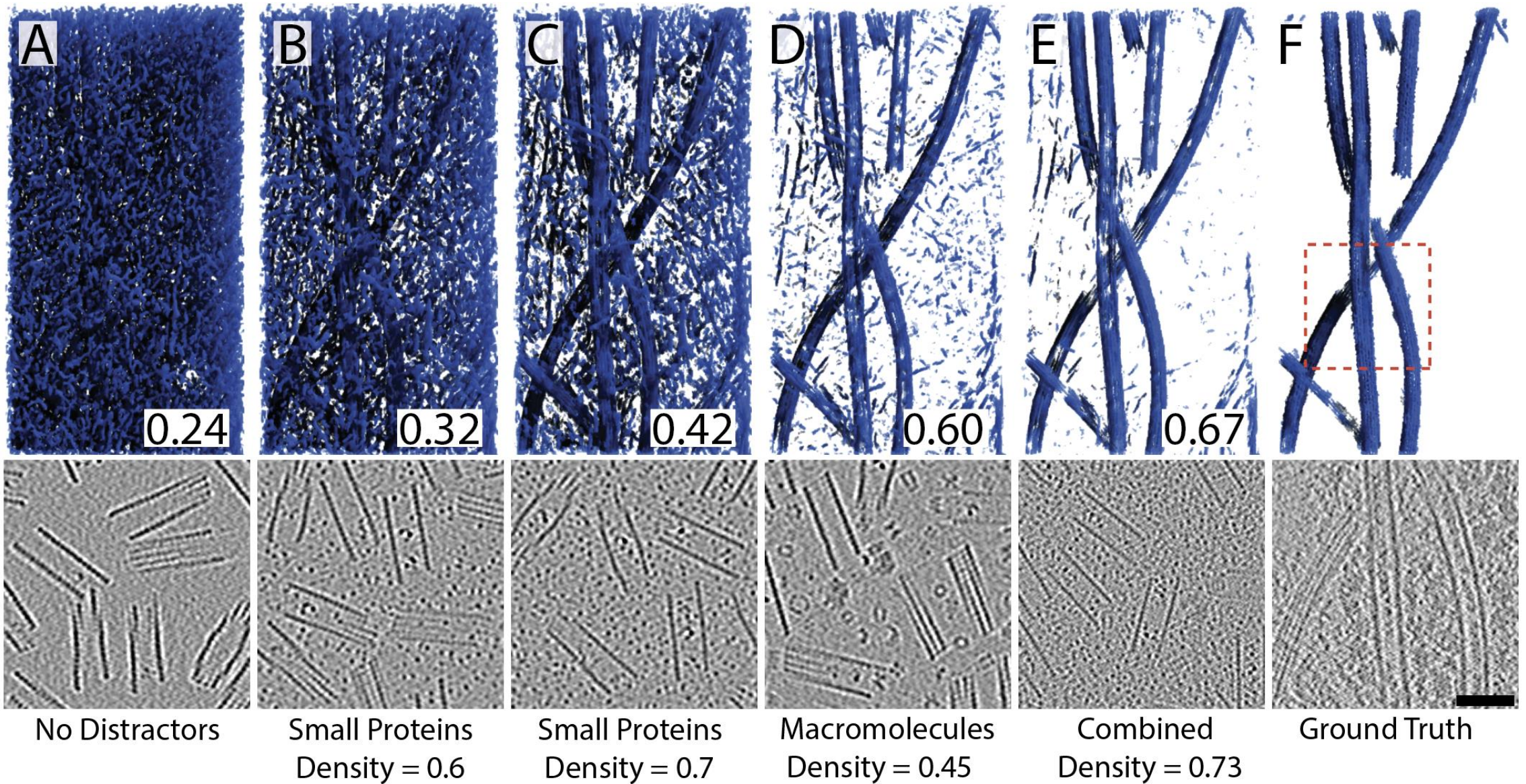


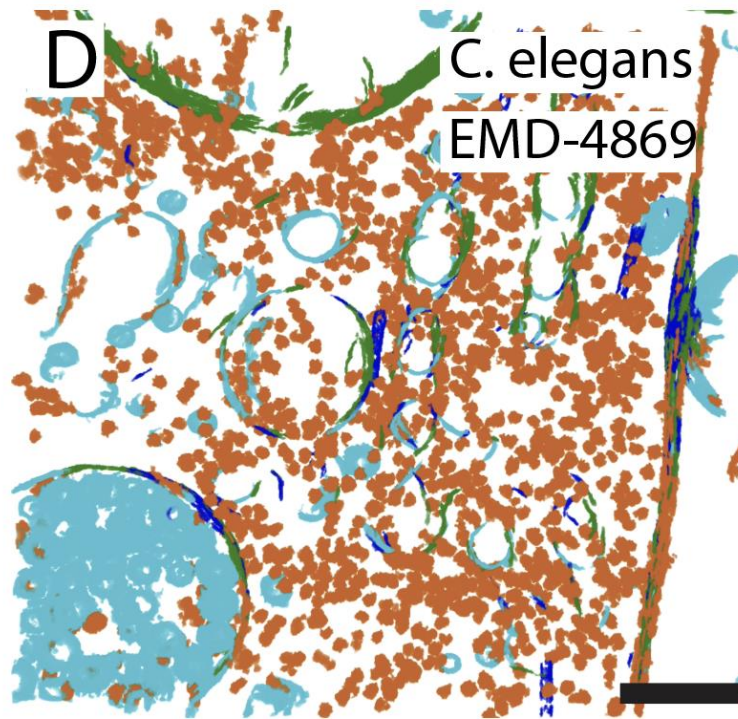
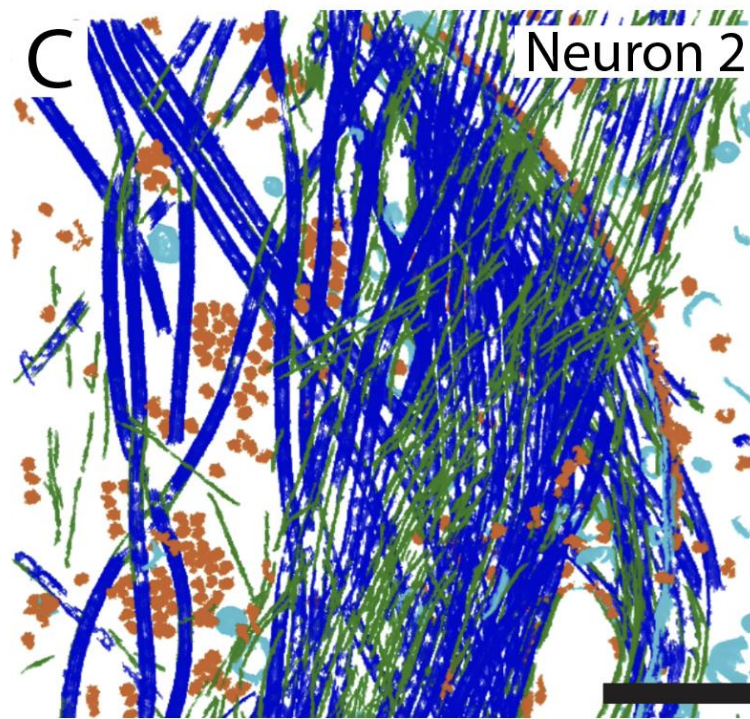
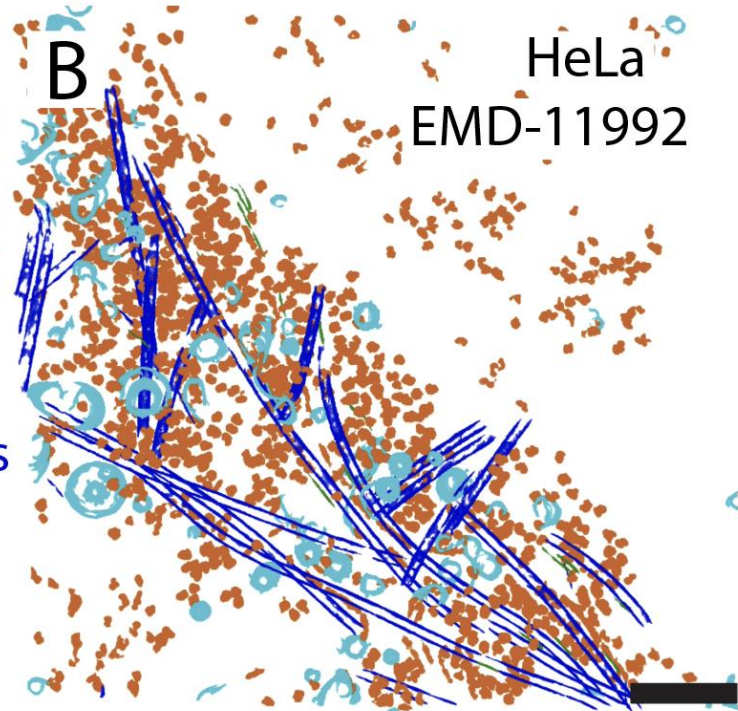
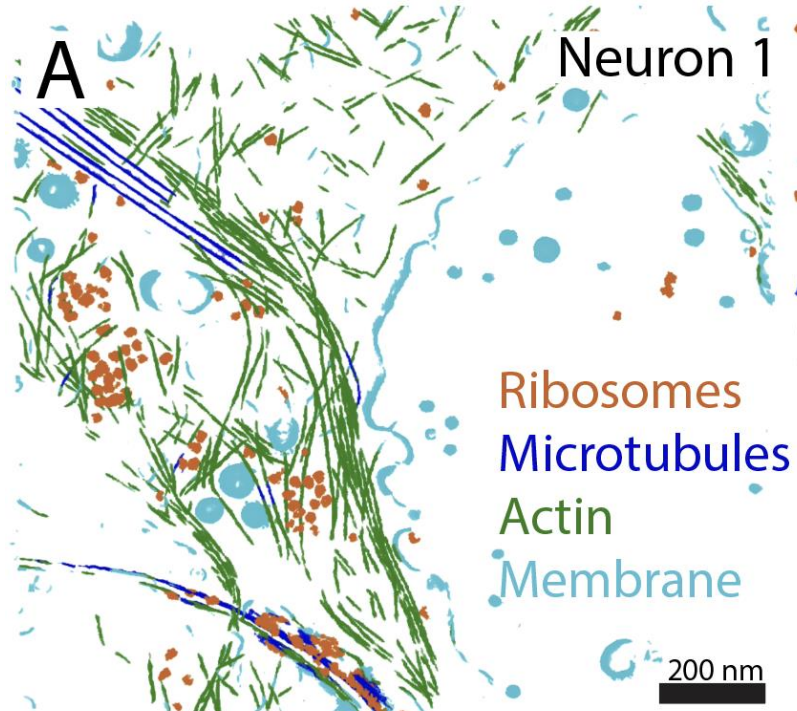


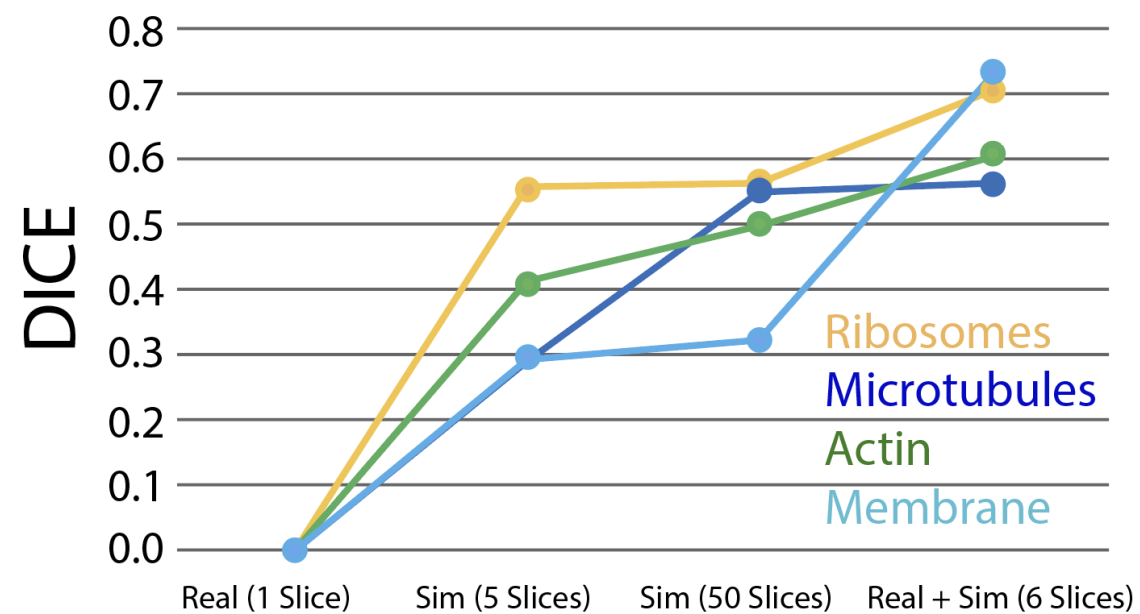
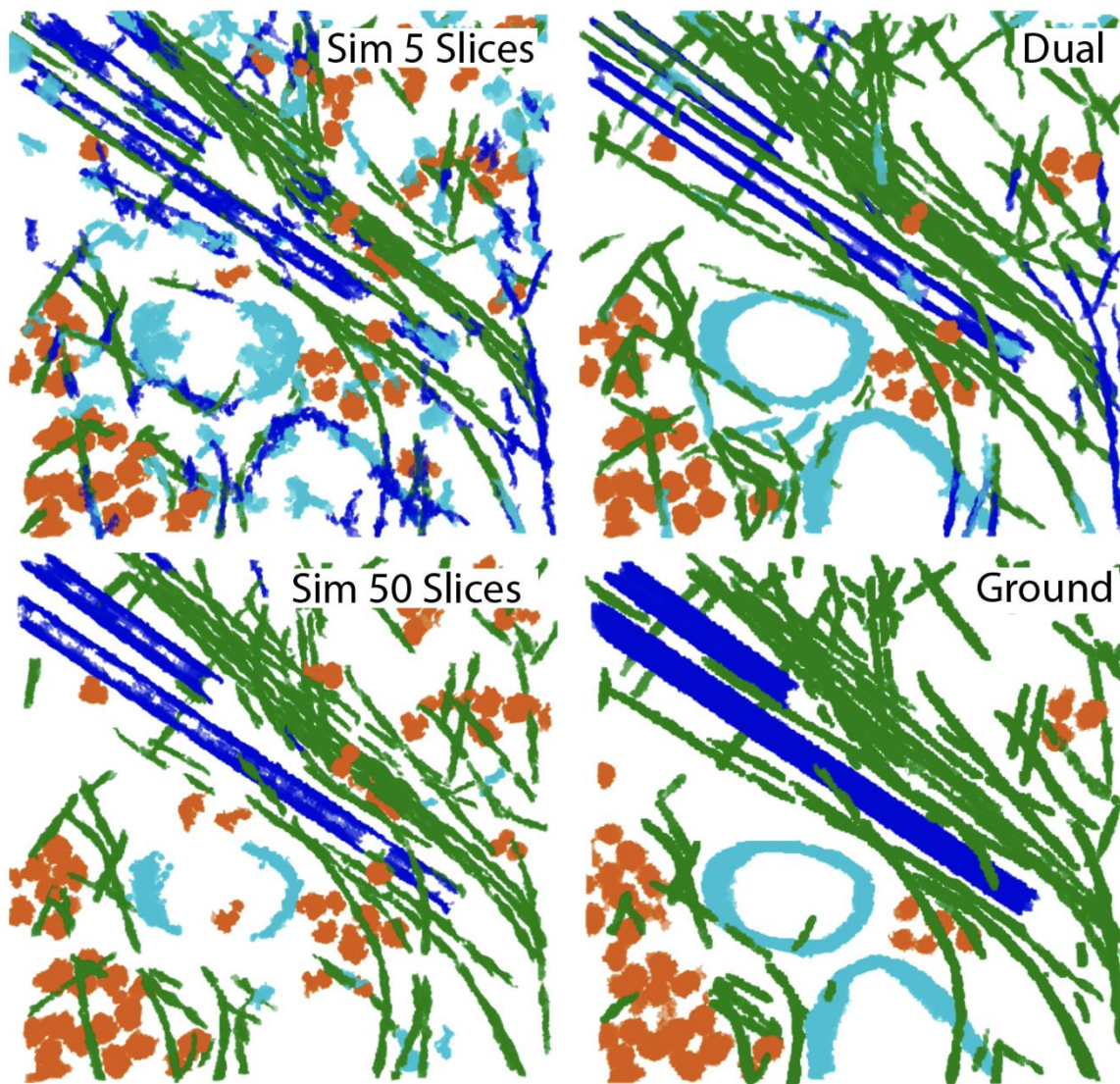


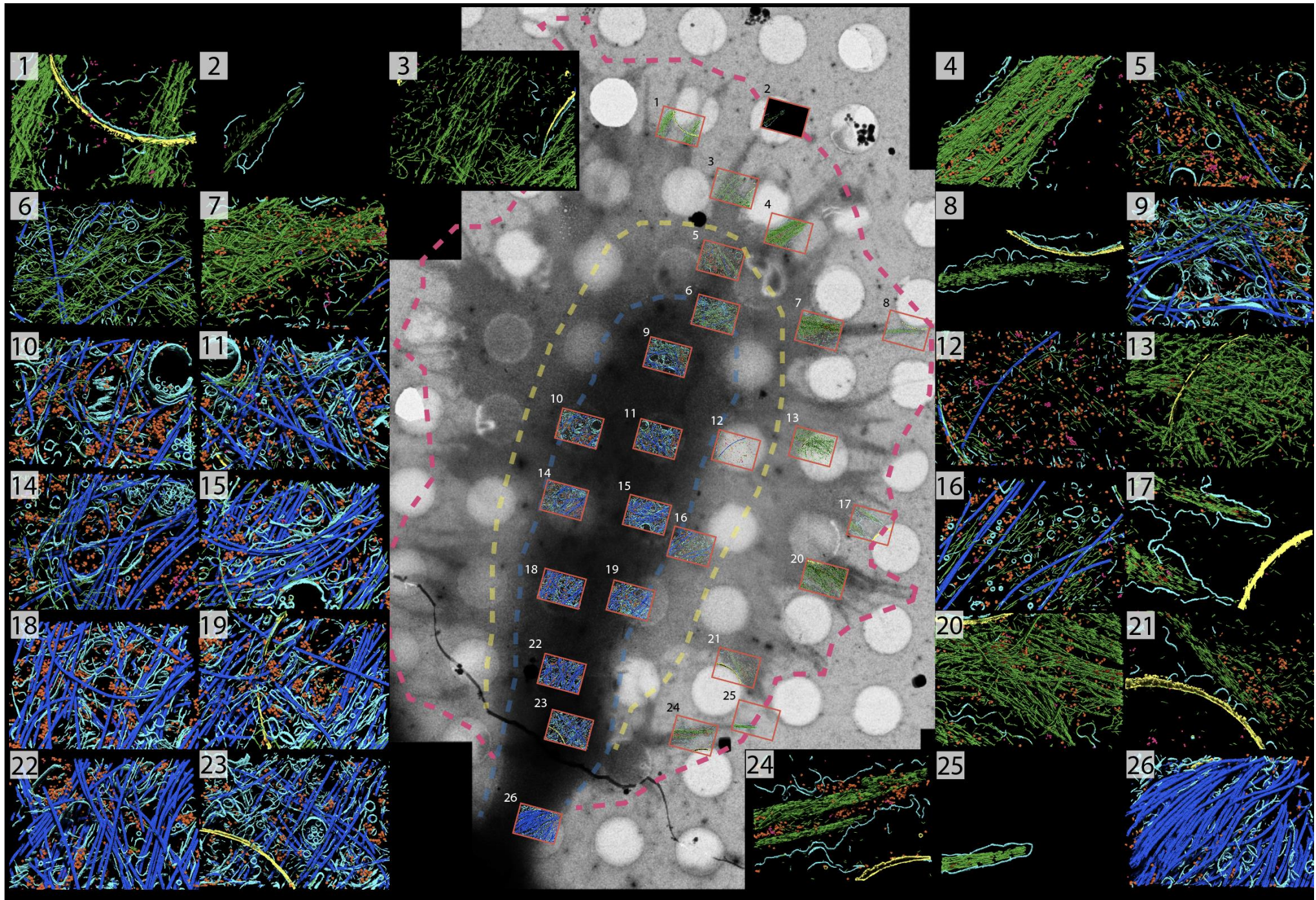


Diversify your crowding agents

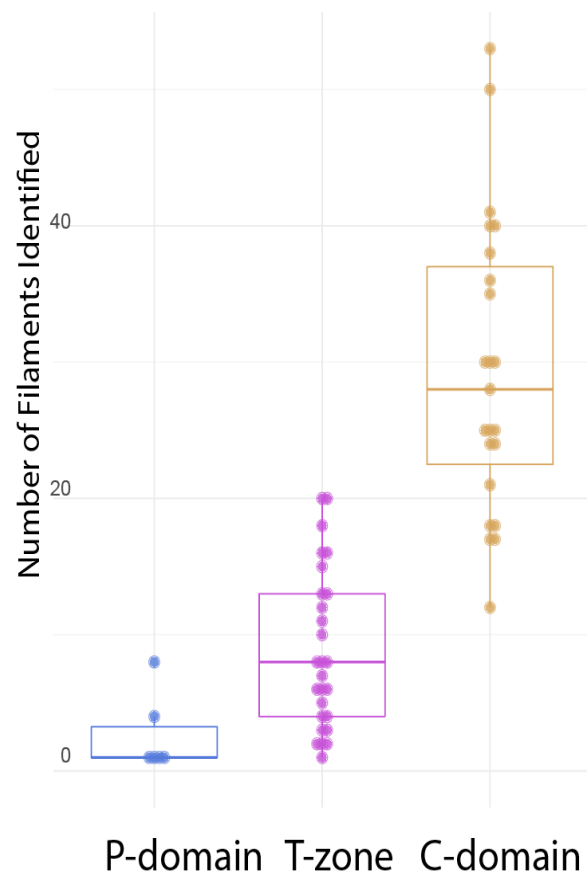




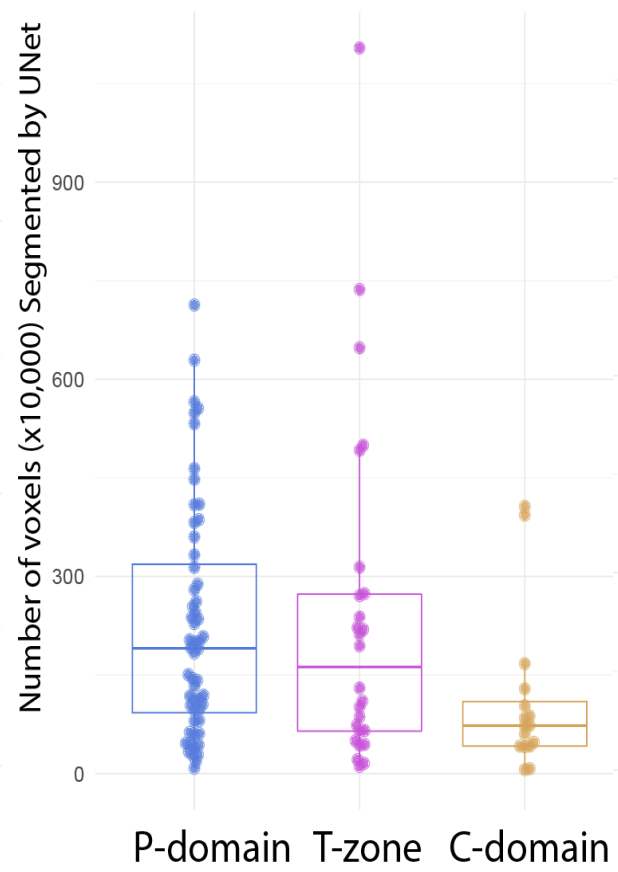




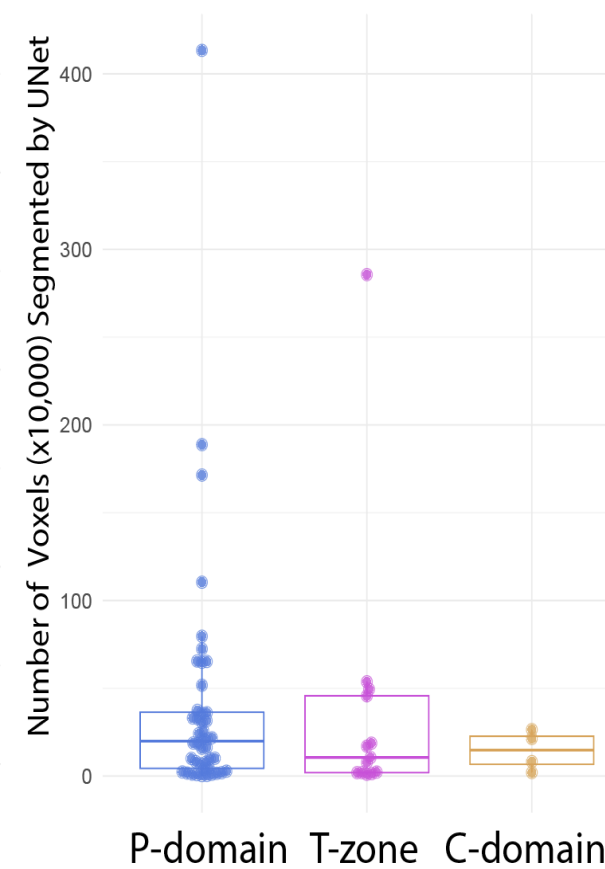
Microtubules



Total Actin

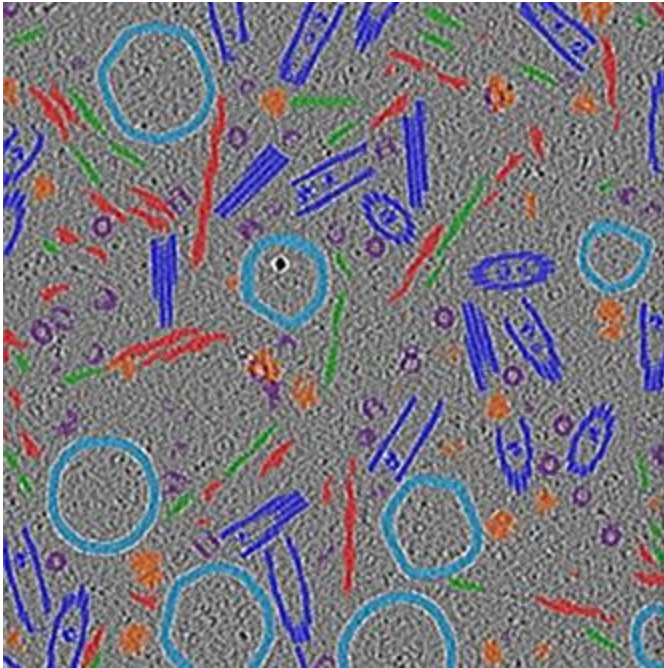


Total Cofilactin



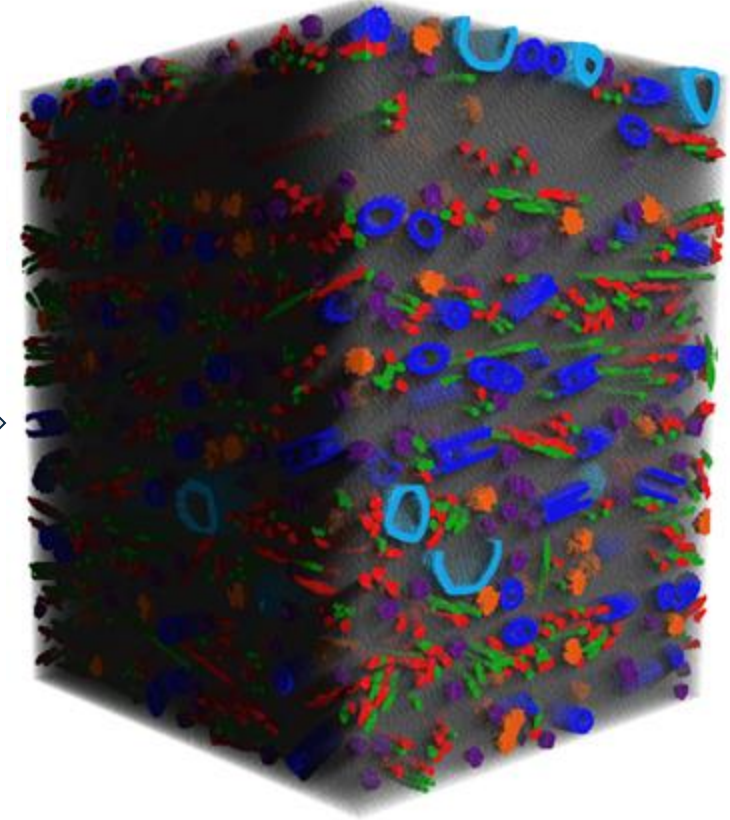
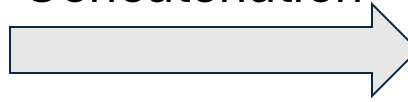
Training a generalized segmentation model

7 classes:
Membrane
TriC
Ribosome
Actin
Cofilactin
Microtubules
Background



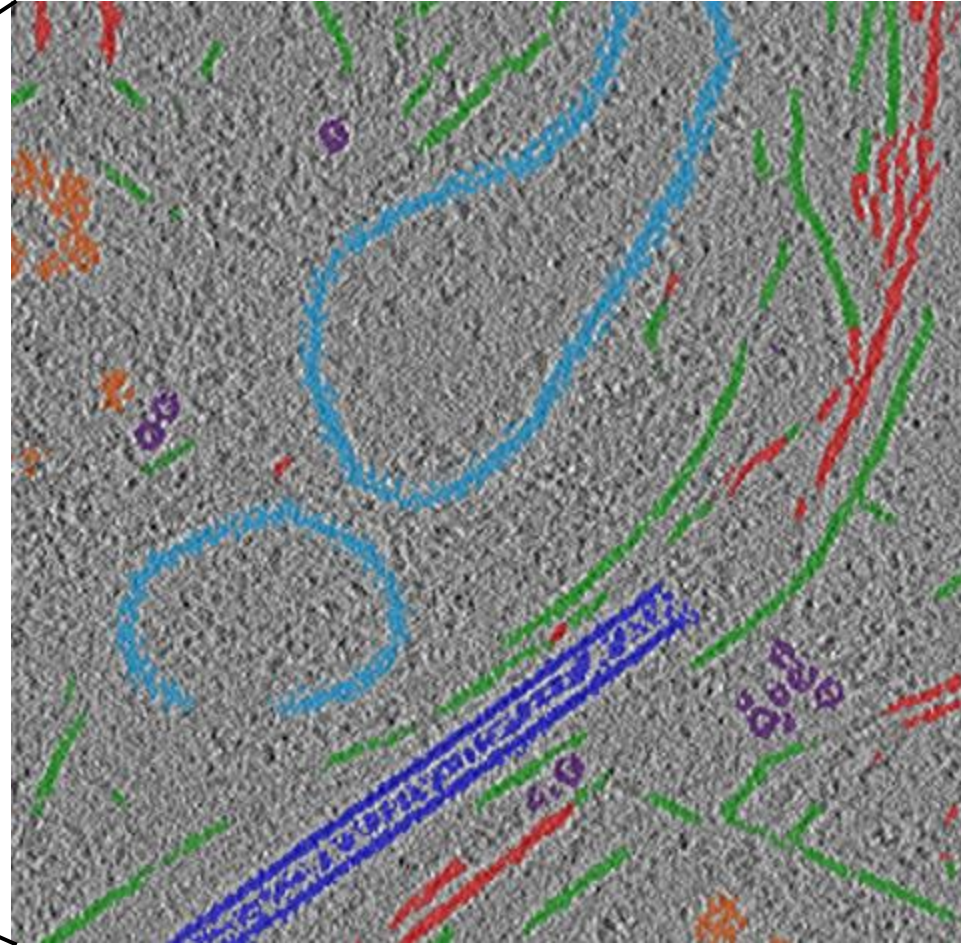
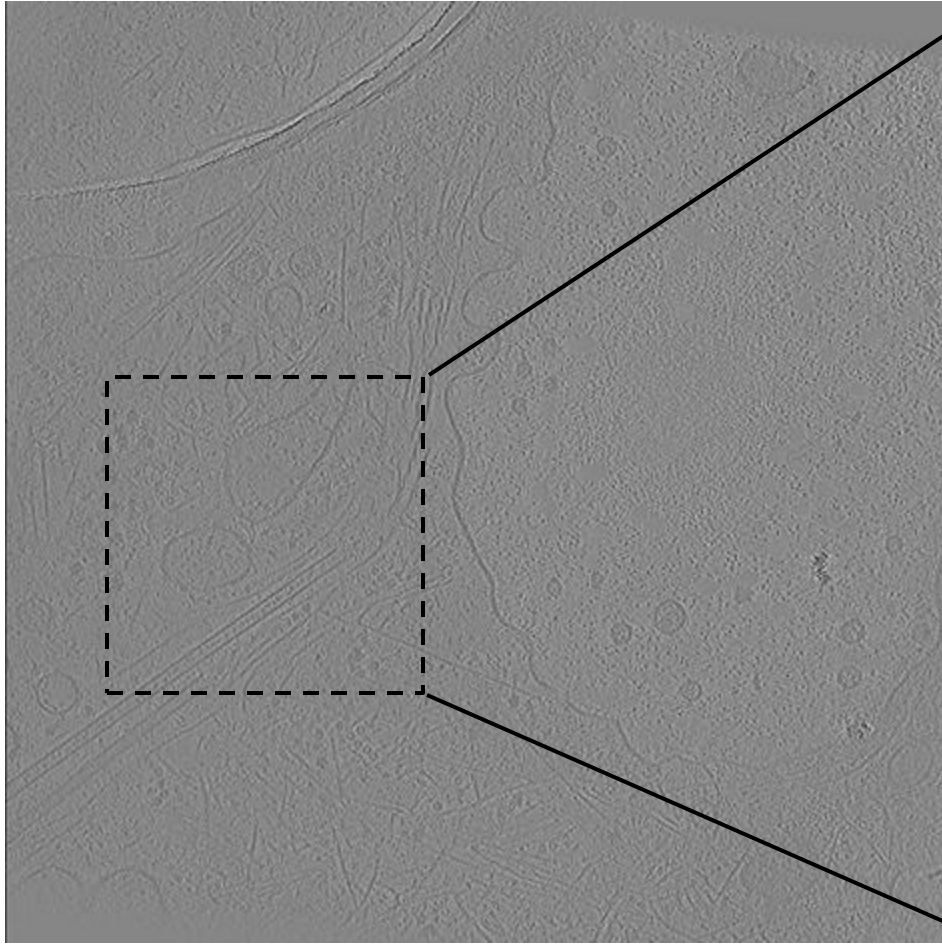
Slice through an example tomogram
of $400 \times 400 \times Z$ voxels,
where $Z=43-59$

Concatenation



$400 \times 400 \times 531$
voxels

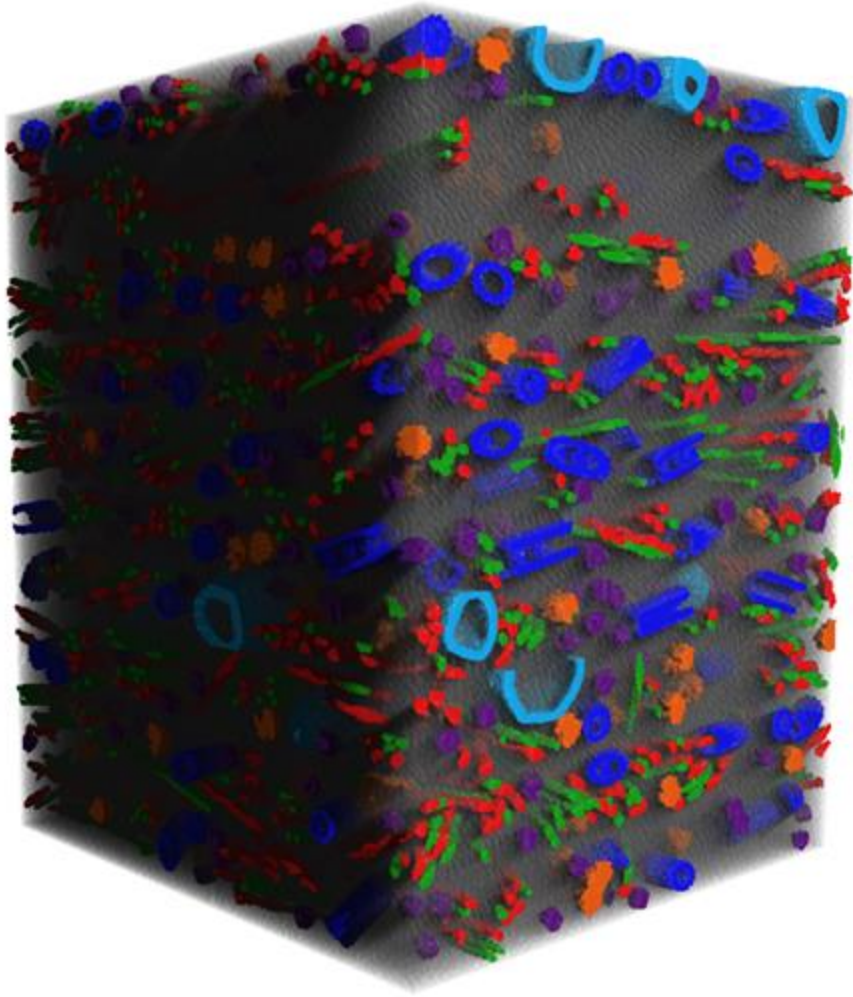
First iteration: Neuronal tomograms



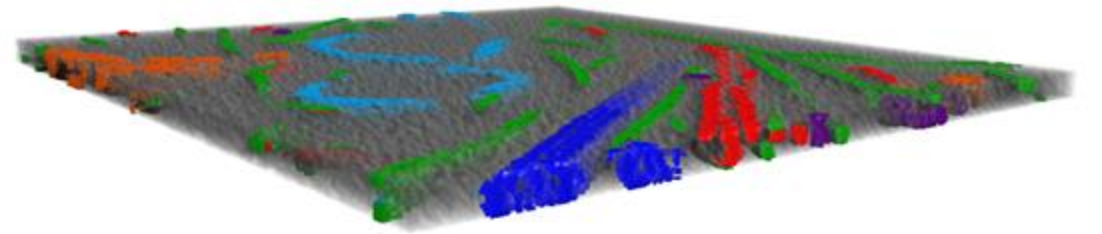
7 classes:
Membrane
TriC
Ribosome
Actin
Cofilactin
Microtubules
Background

400x400x19 voxels

Base network: Training data

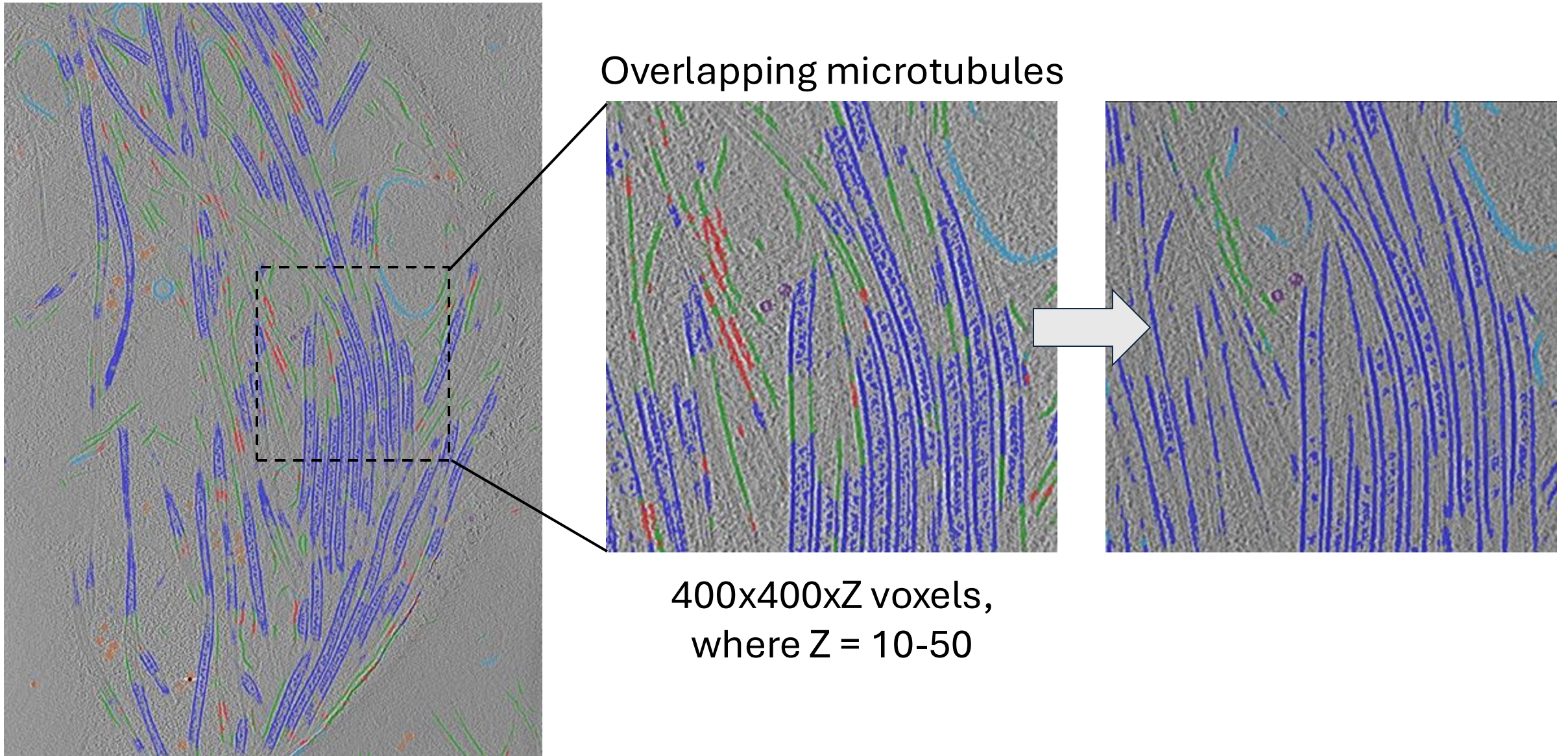


Synthetic block

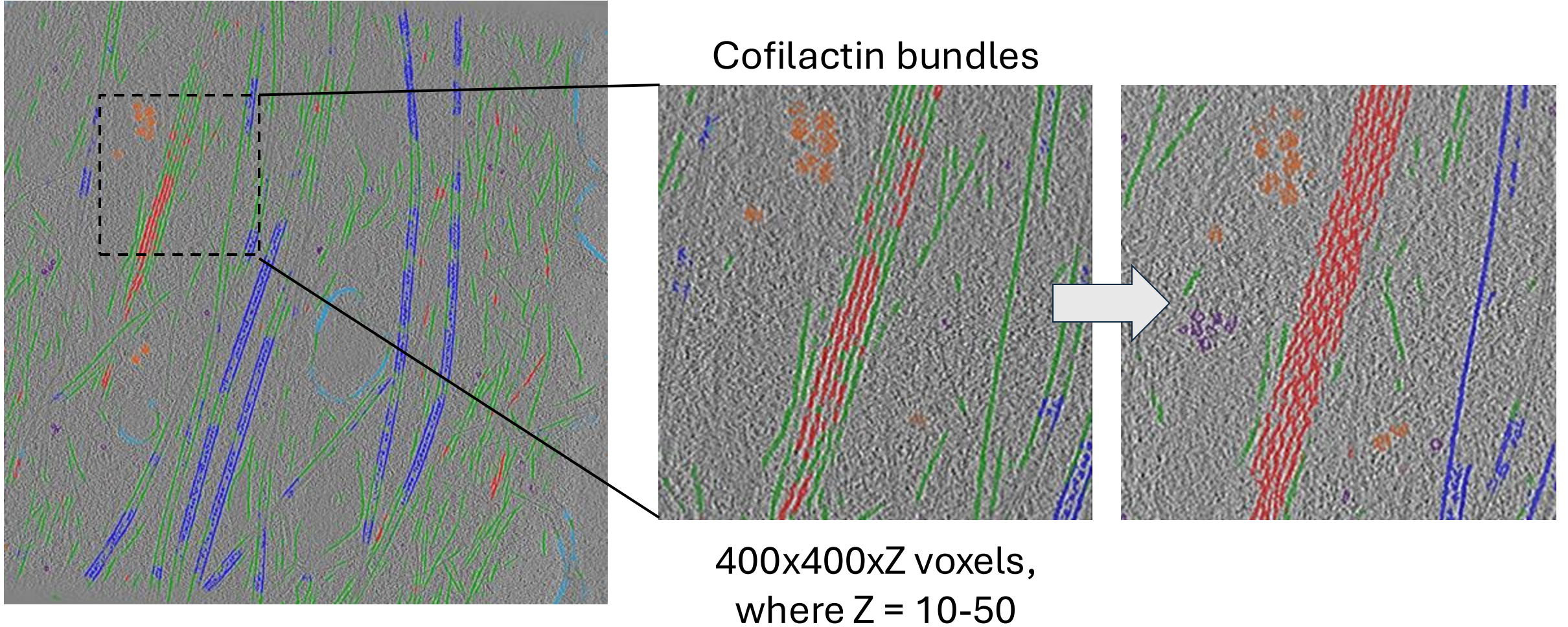


Real block

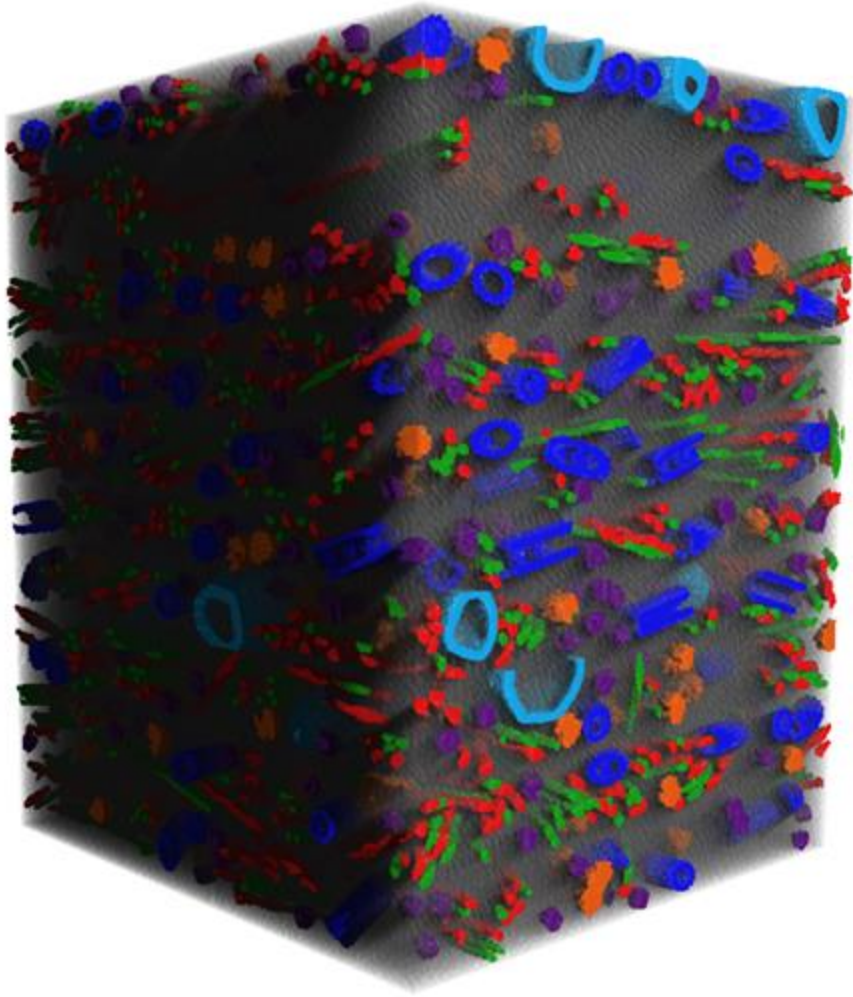
Result from first iteration & Hand-correction



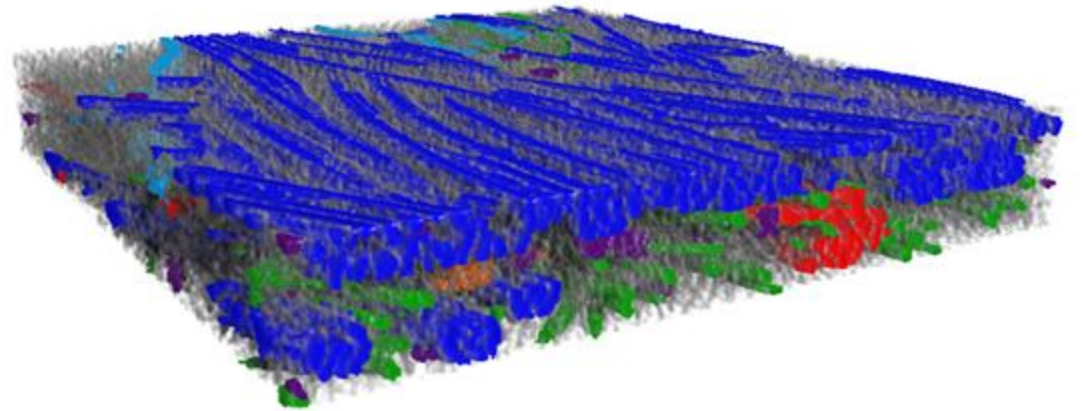
Result from first iteration & Hand-correction



Concatenation to update training data

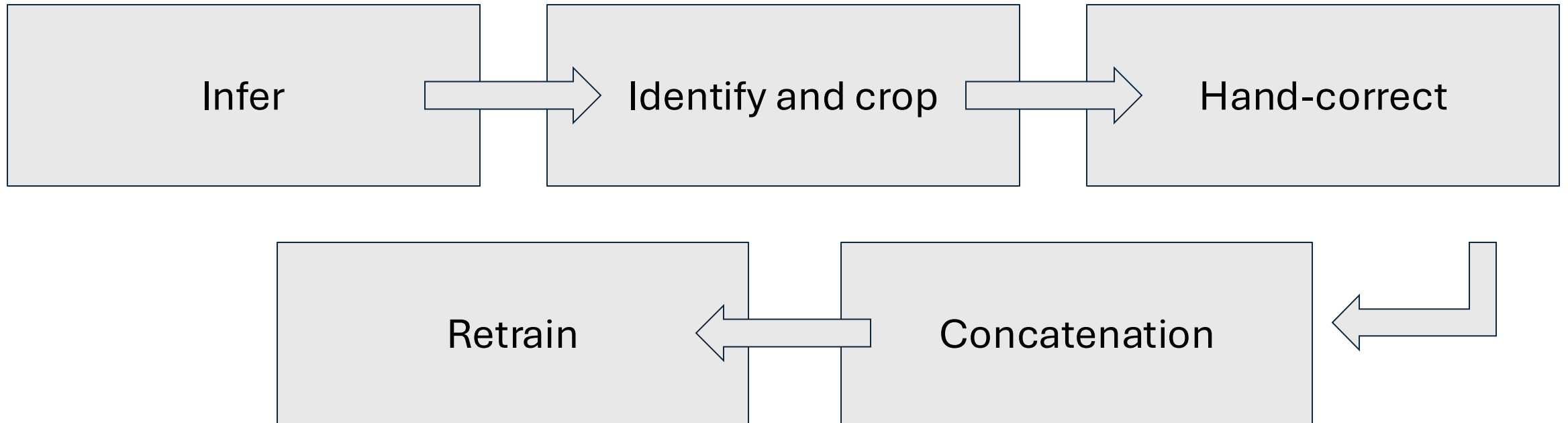


Synthetic block

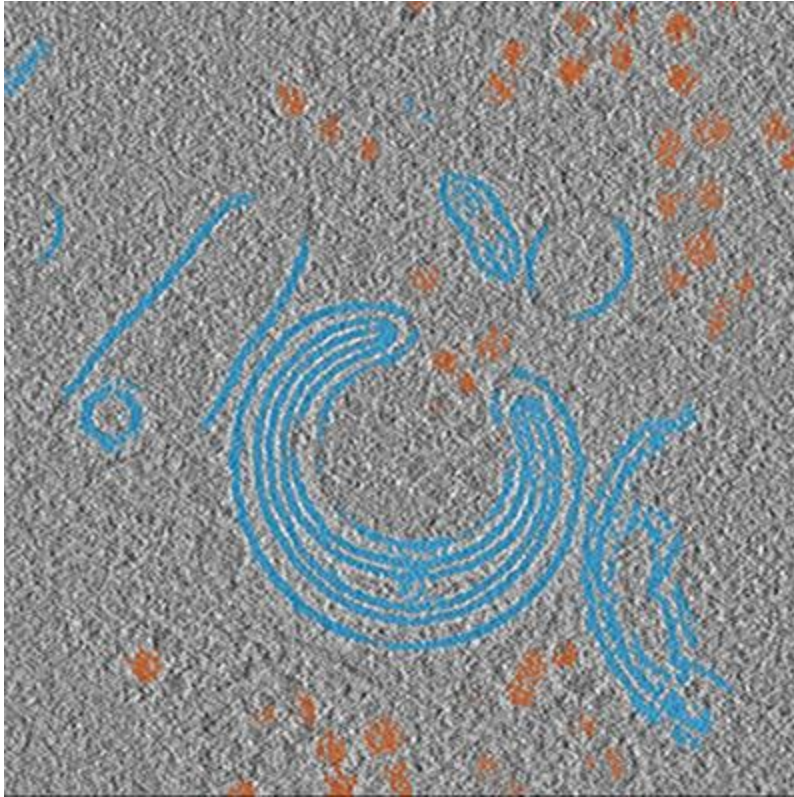


Real block

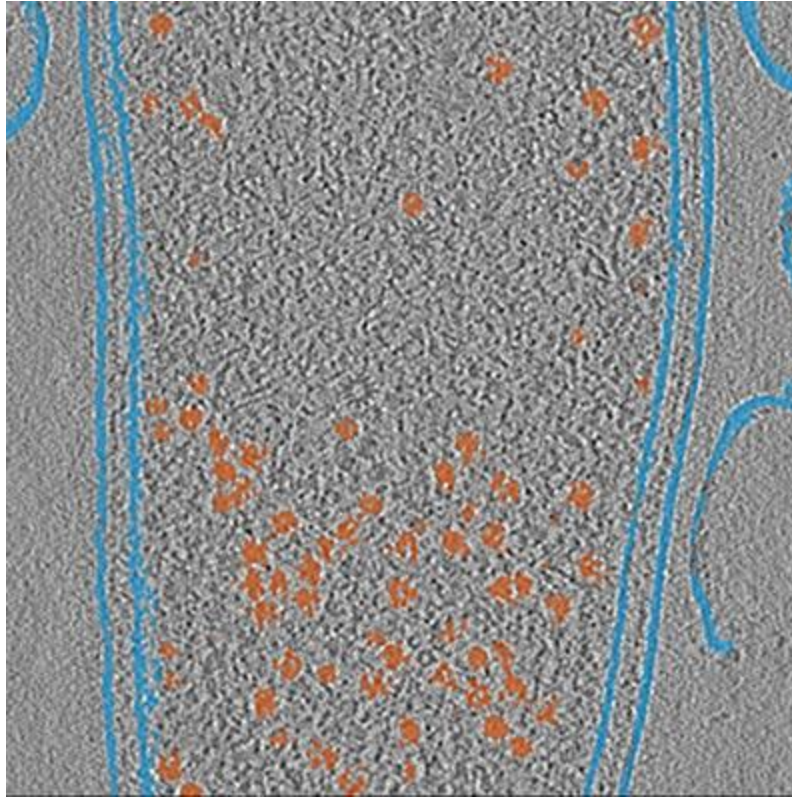
Basic workflow



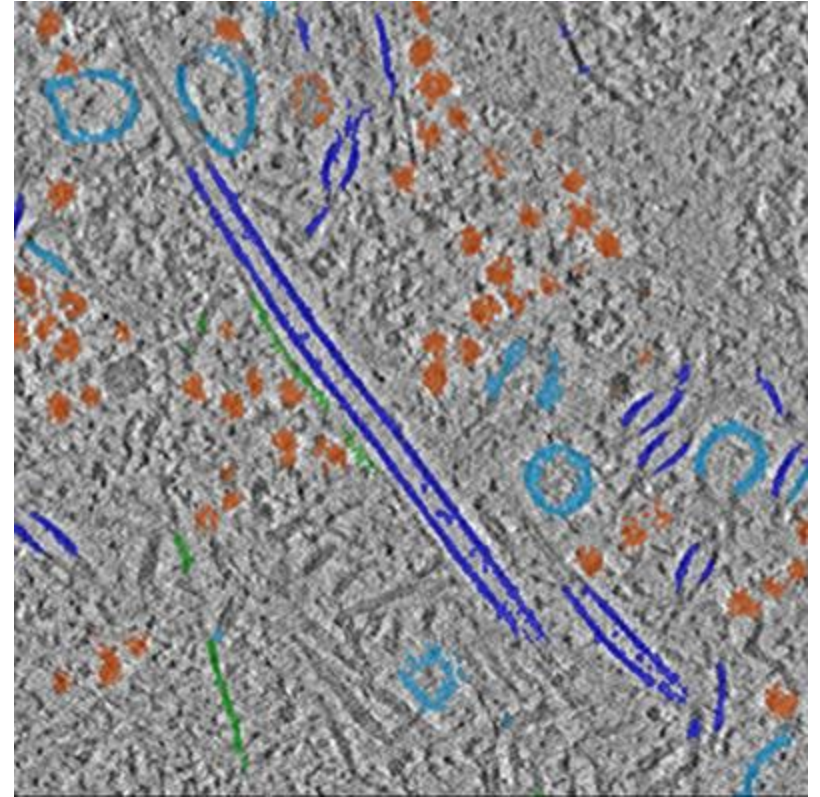
Second iteration: Non-neuronal tomograms



Eukaryotic multi-layer
membrane

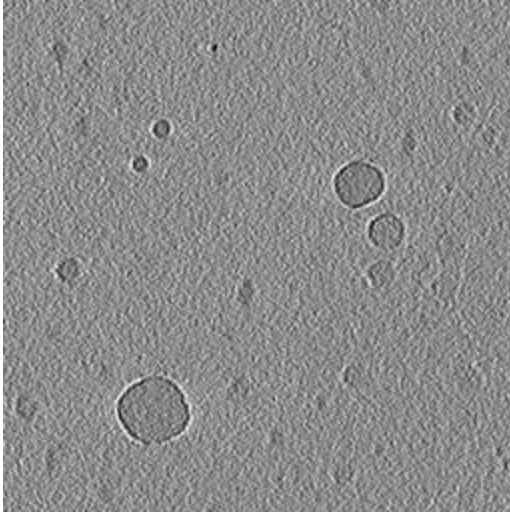


Bacterial double membrane

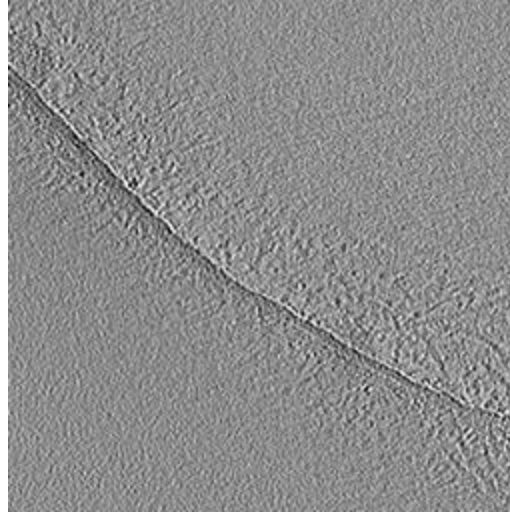


Eukaryotic Cytoplasm

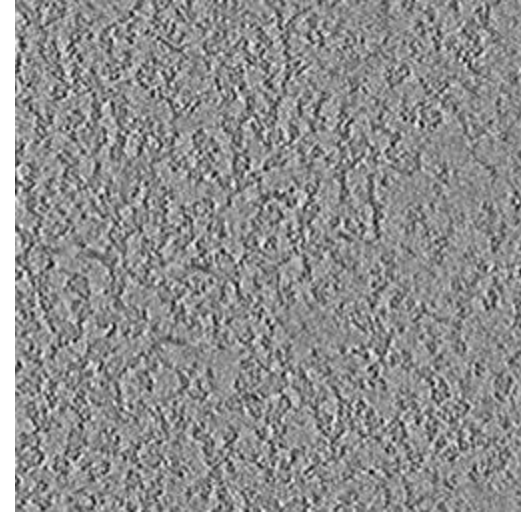
Third iteration: Tomographic artifacts



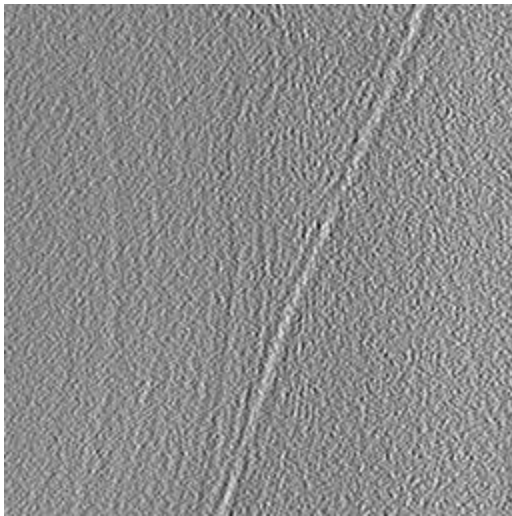
Ice



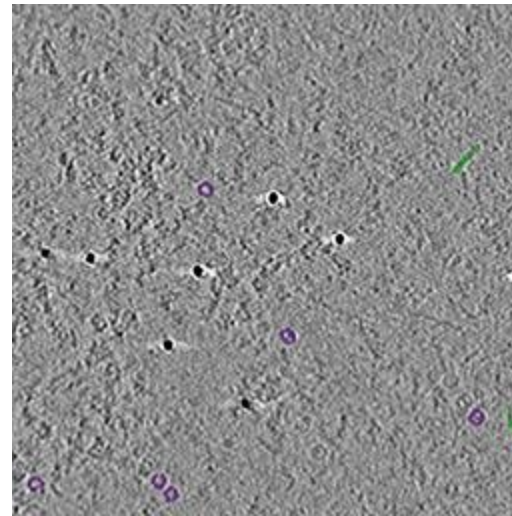
Carbon edge



Carbon surface

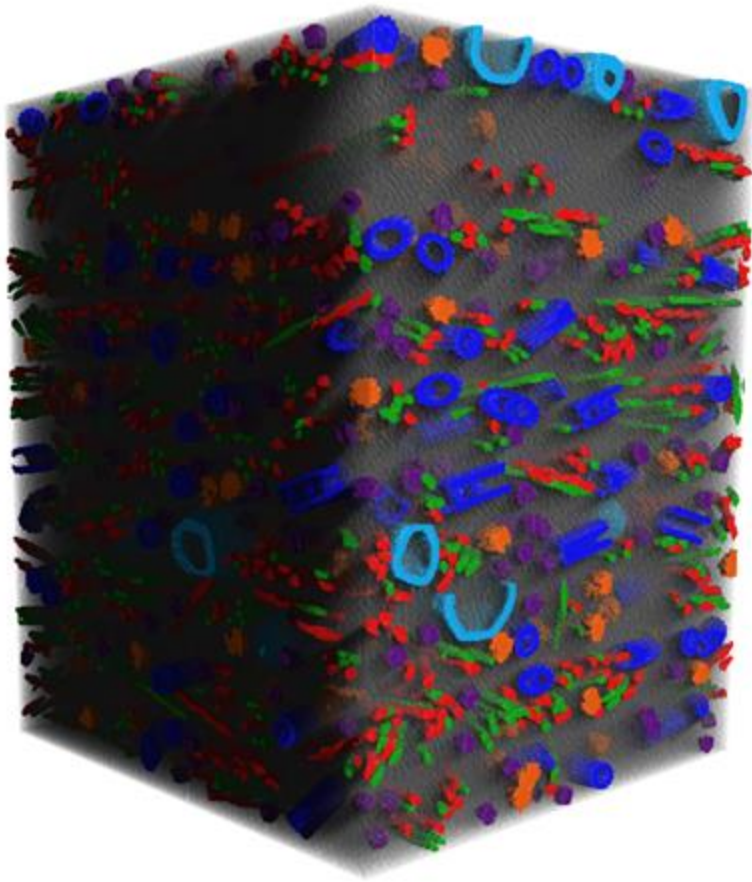


Tomographic fringing

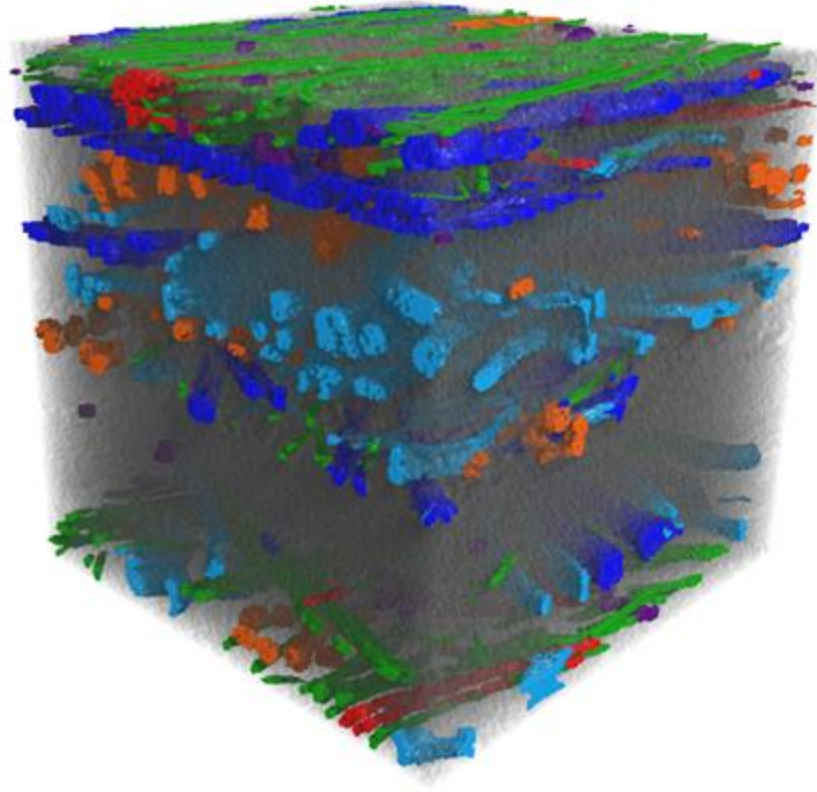


Gold fiducials

Final network: Training data



Synthetic data
(400x400x531)

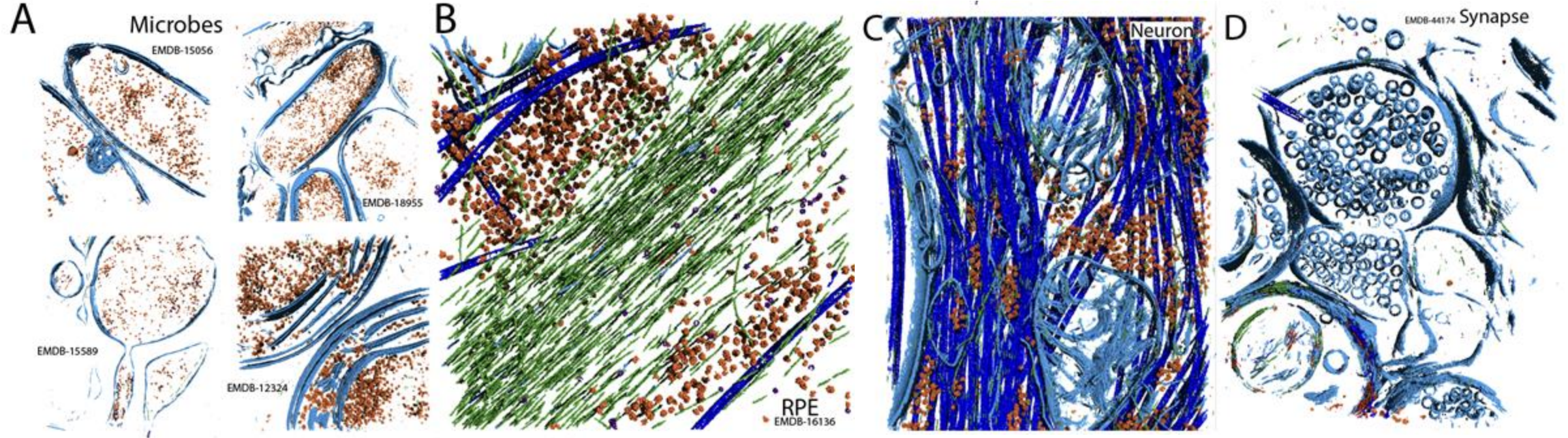


Real data (400x400x395)



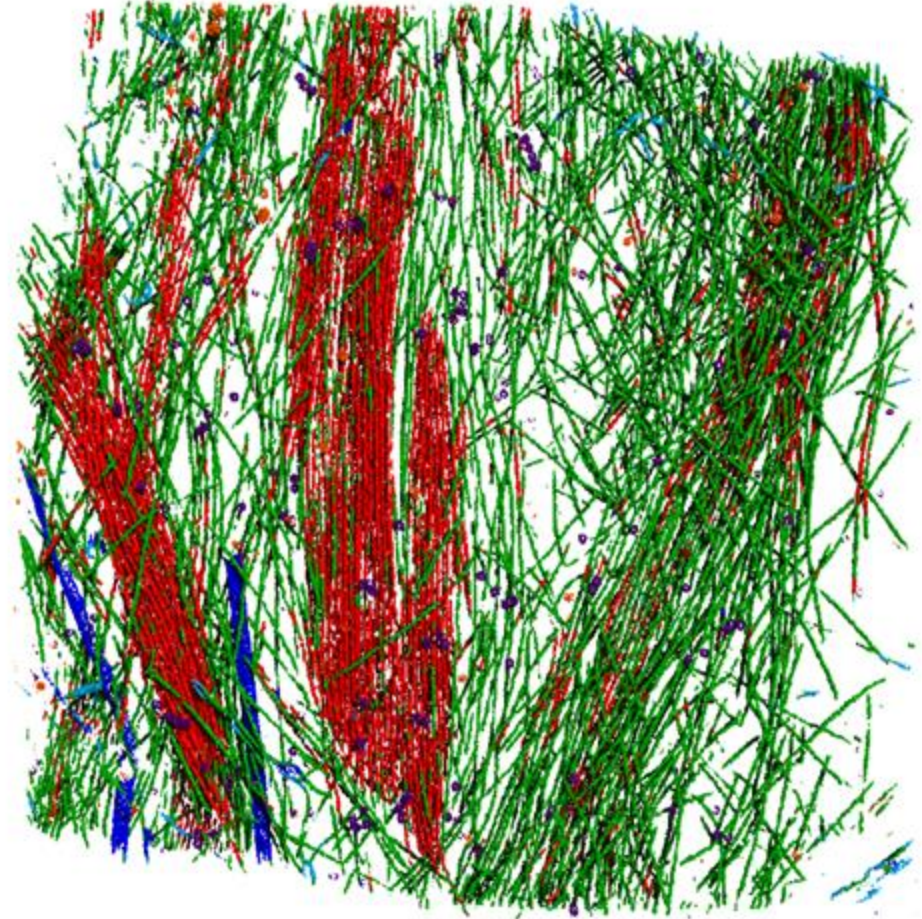
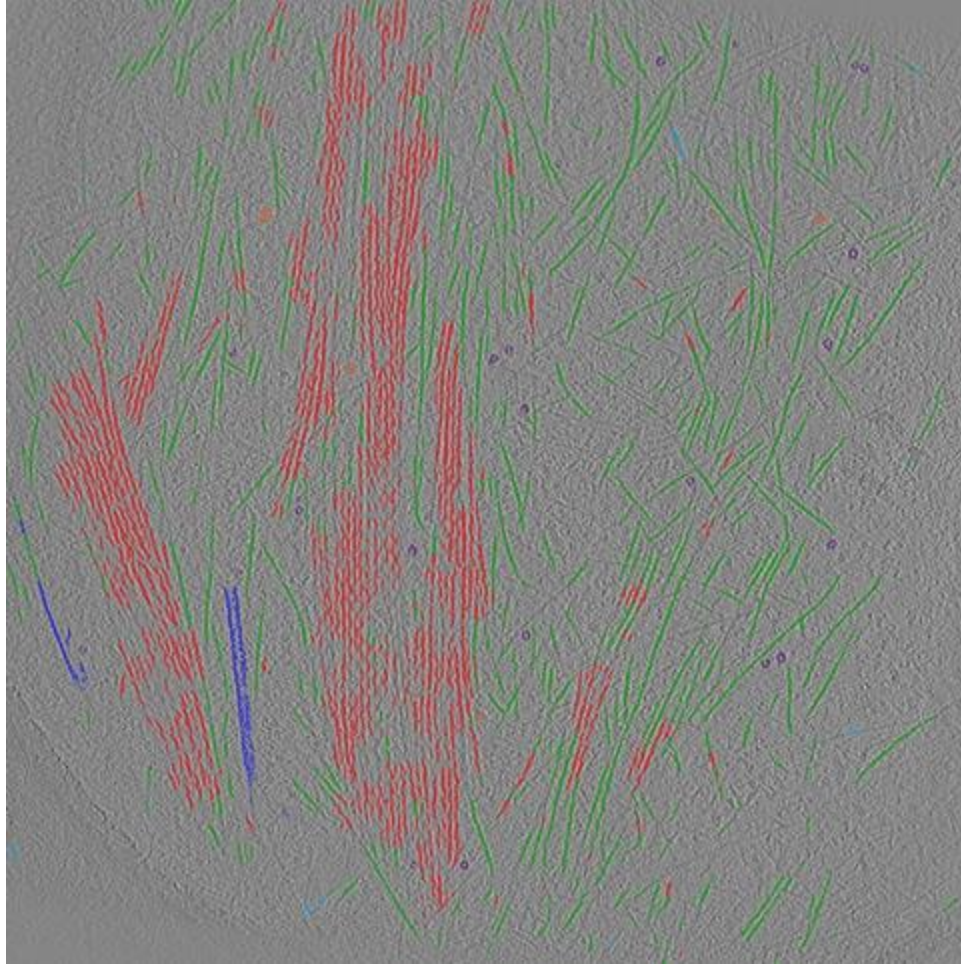
NeuralSeg

NeuralSeg can segment most cellular tomograms that meet its criteria



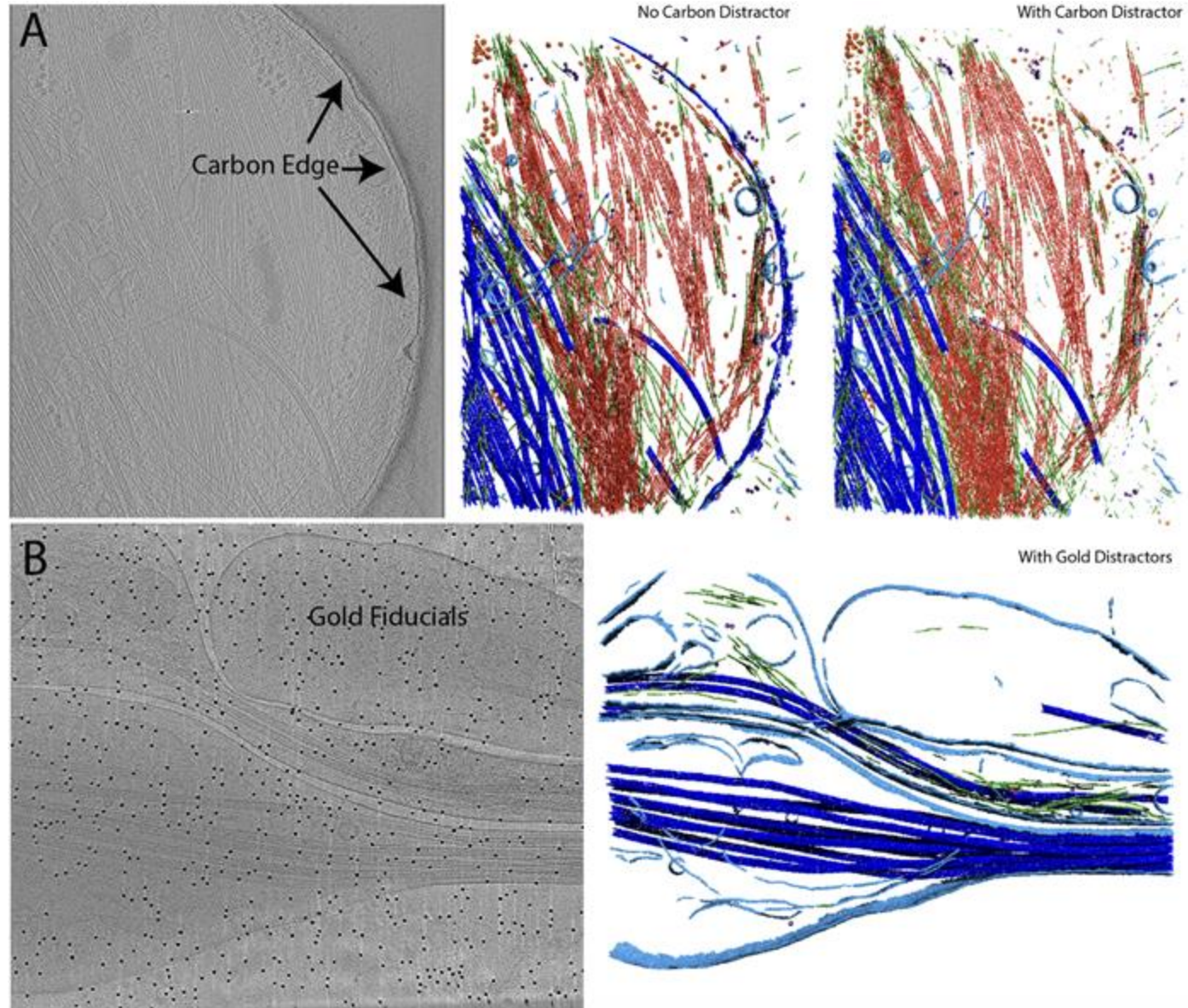
Ideal tomograms have 12-14 angstroms/pixel, -4 to -10 μ M defocus, and sufficient contrast.

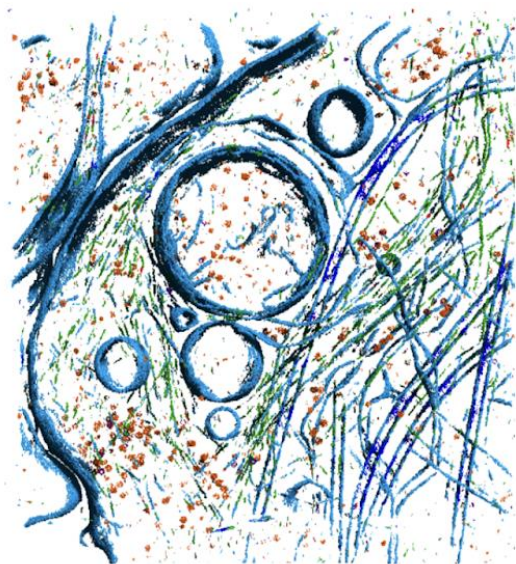
NeuralSeg can differentiate between actin and cofilactin



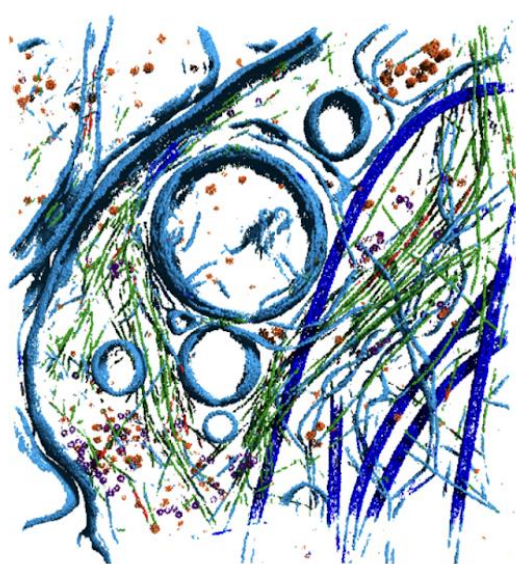
Bare actin and cofilin-decorated actin are distinguished as individual, bundles, or mixed bundles.

Typical tomographic artifacts are ignored

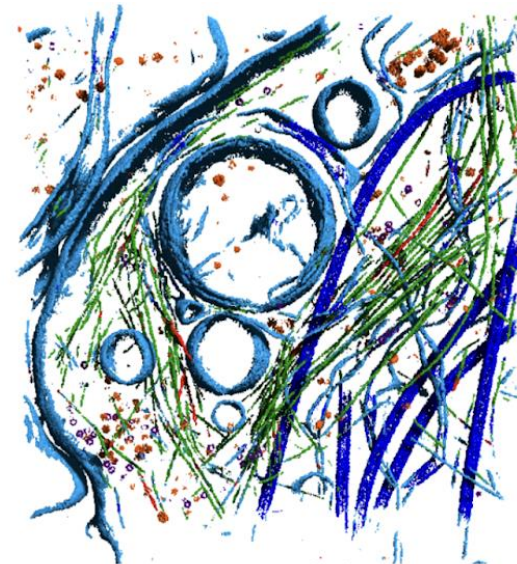




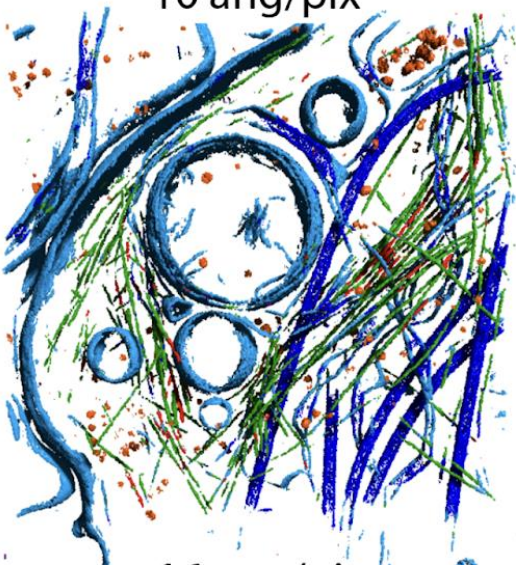
10 ang/pix



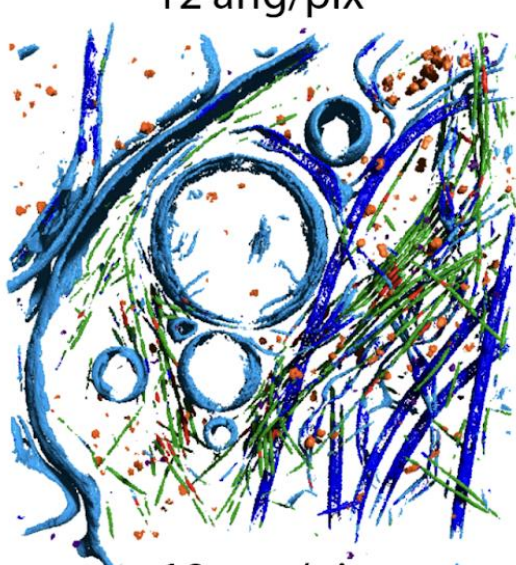
12 ang/pix



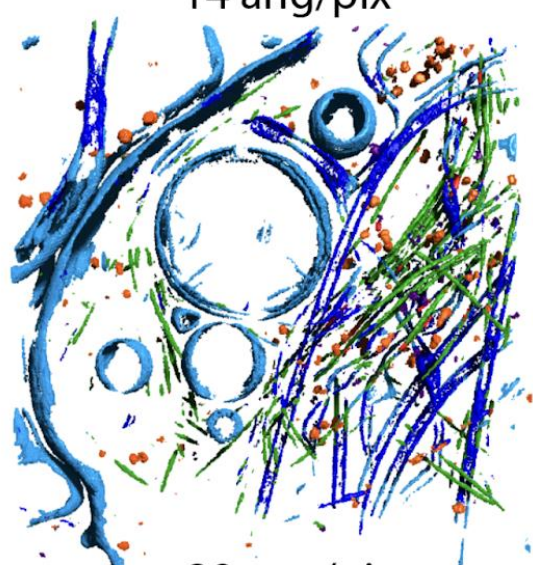
14 ang/pix



16 ang/pix



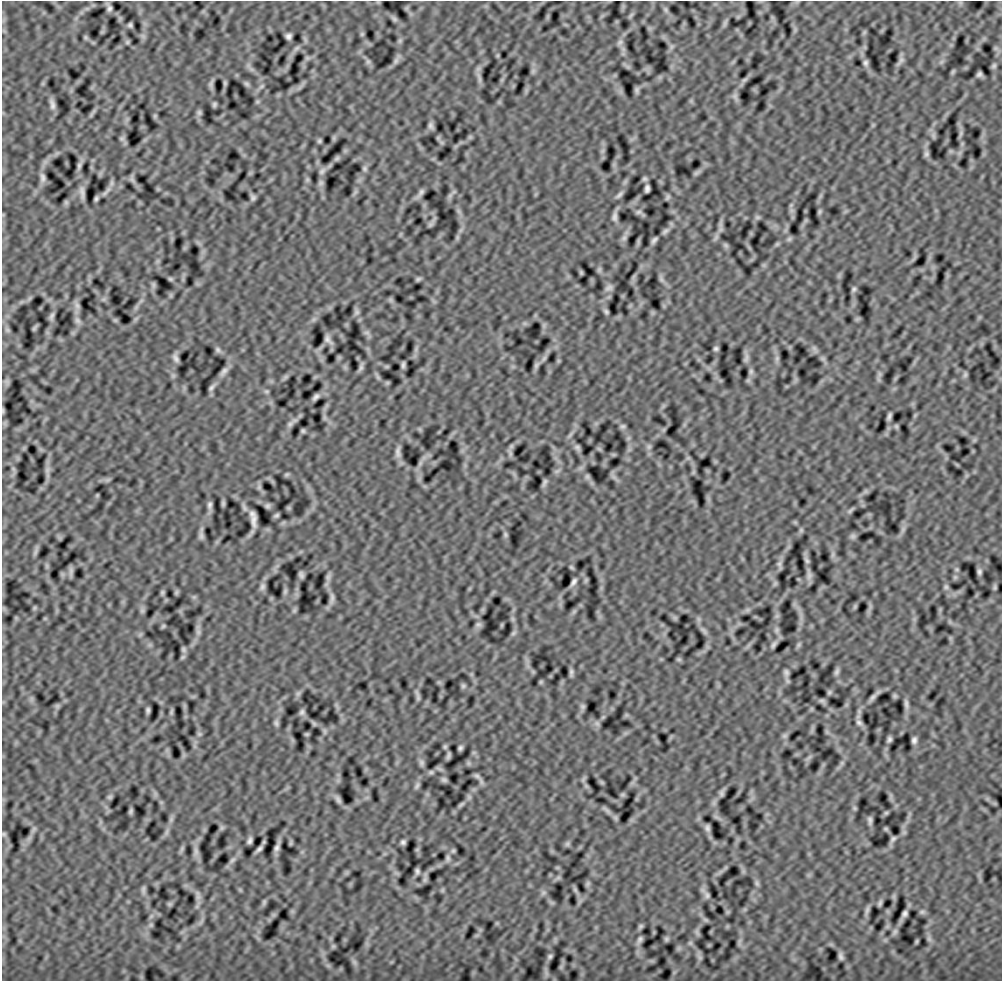
18 ang/pix



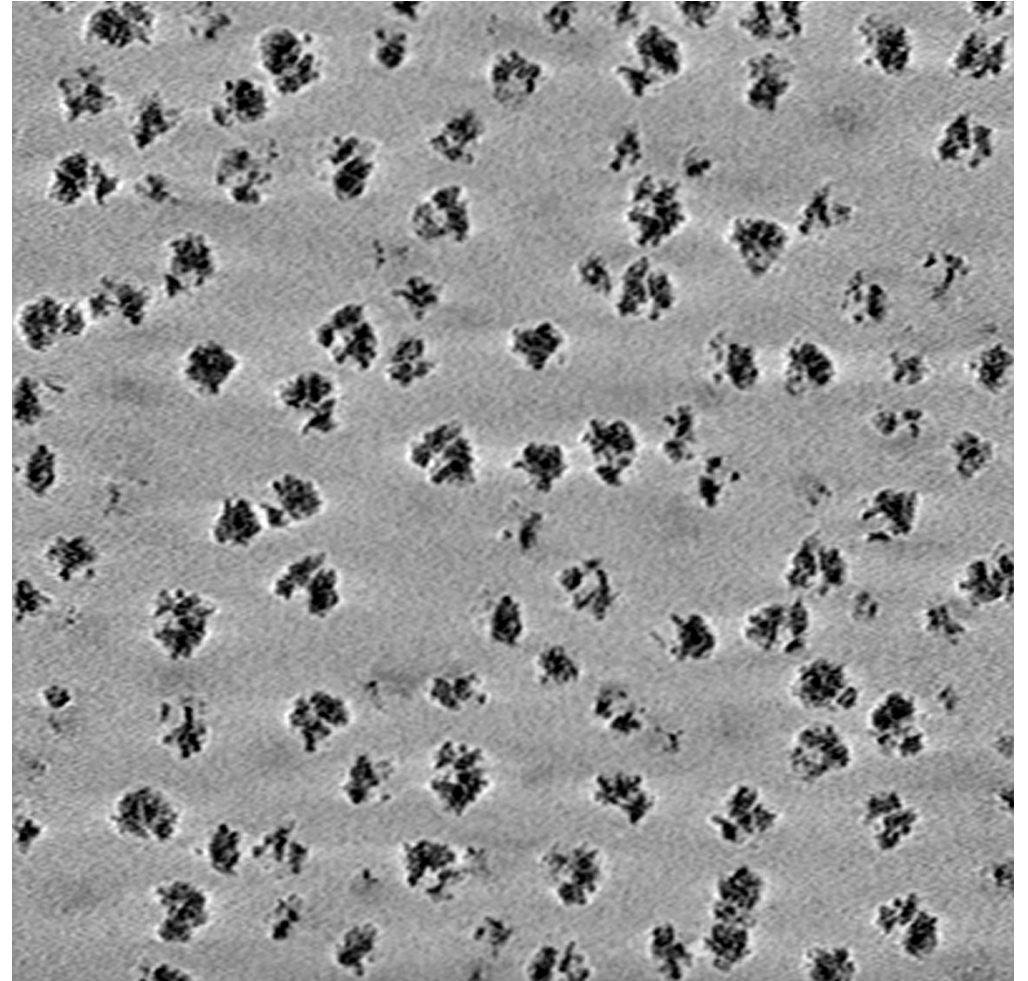
20 ang/pix

Denoising

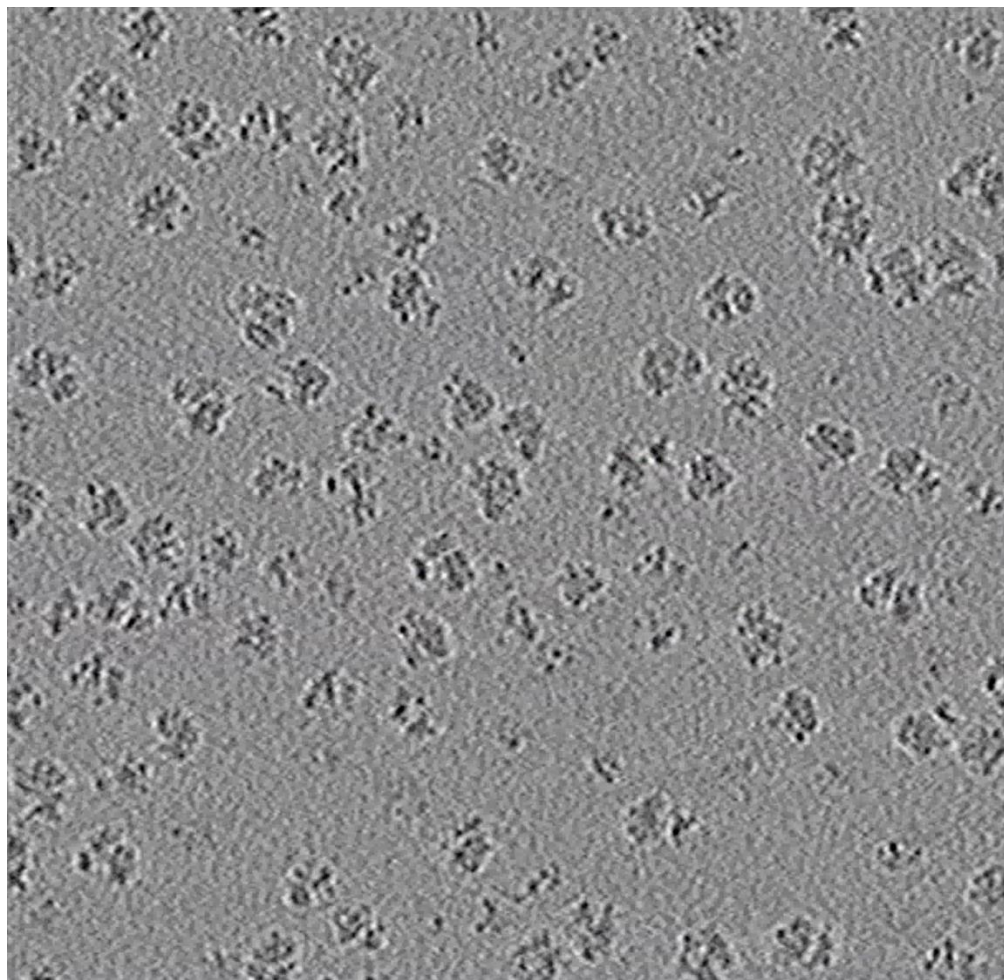
Tomo



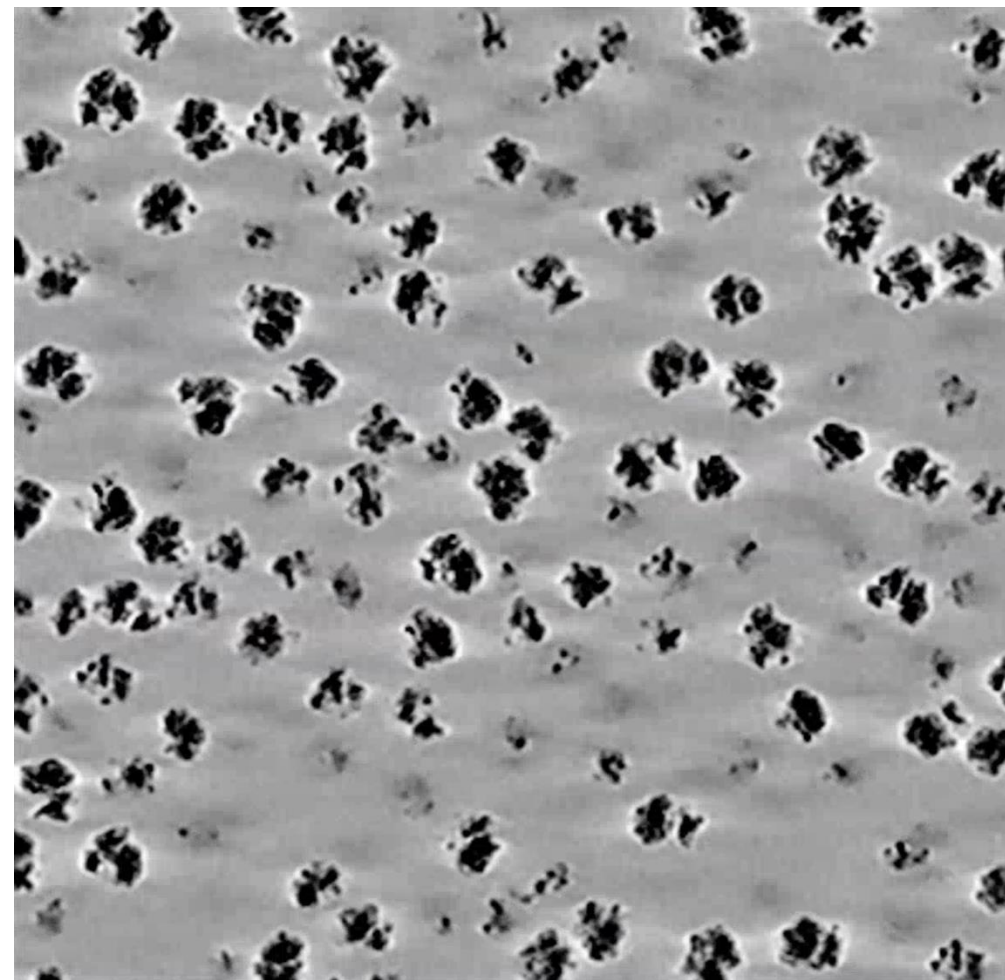
Ground Tomo



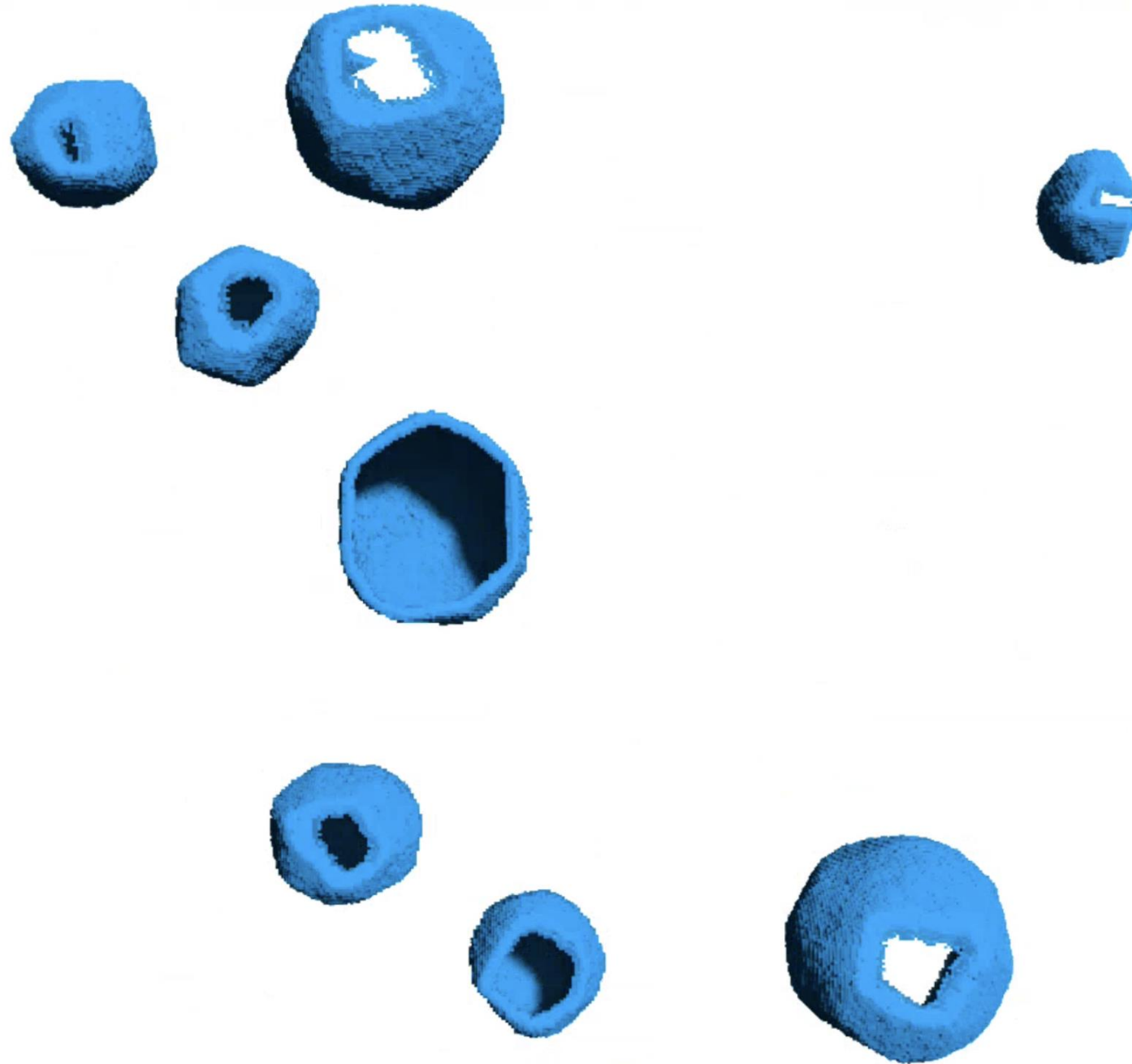
New Tomo



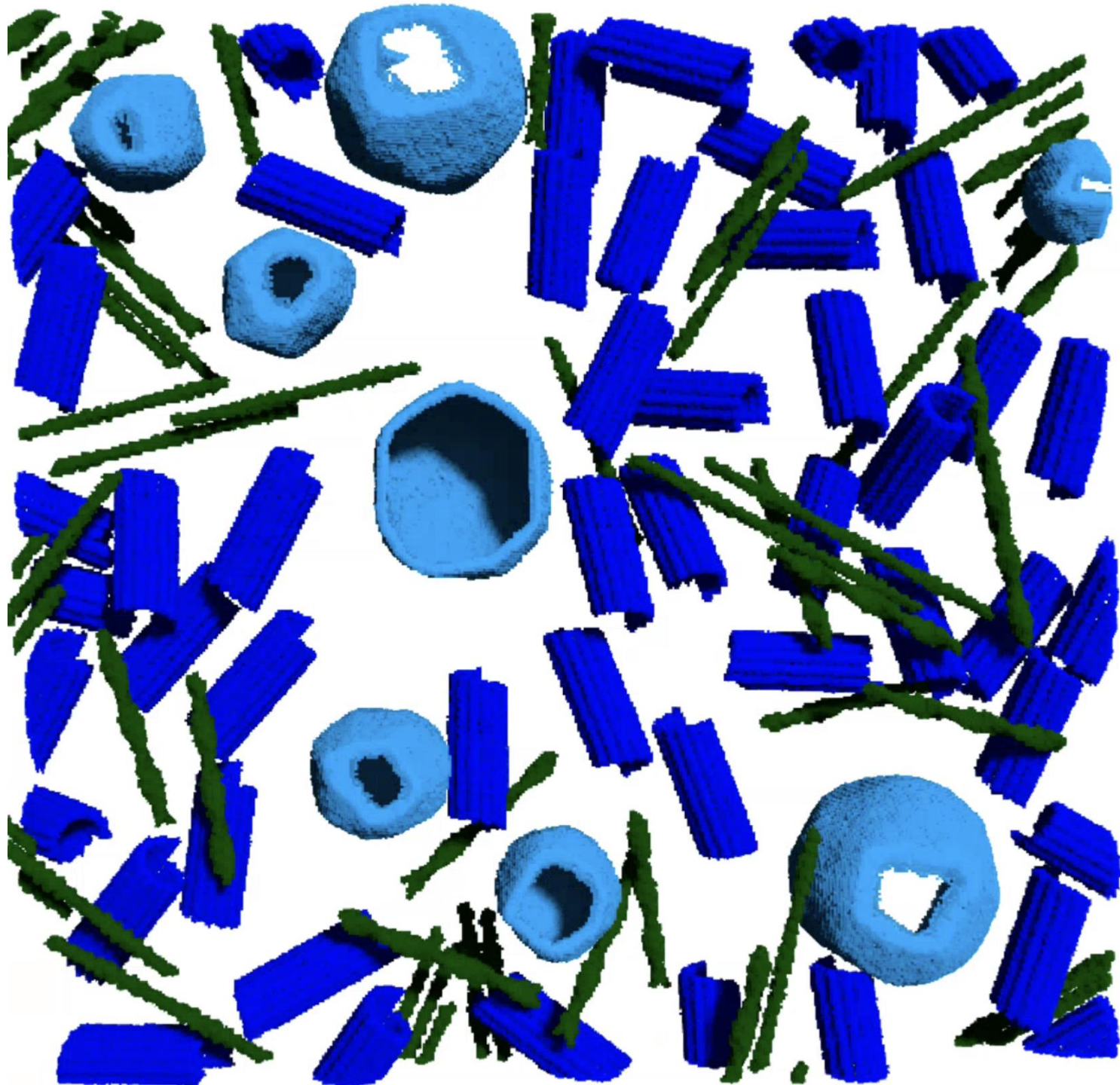
Denoised Tomo



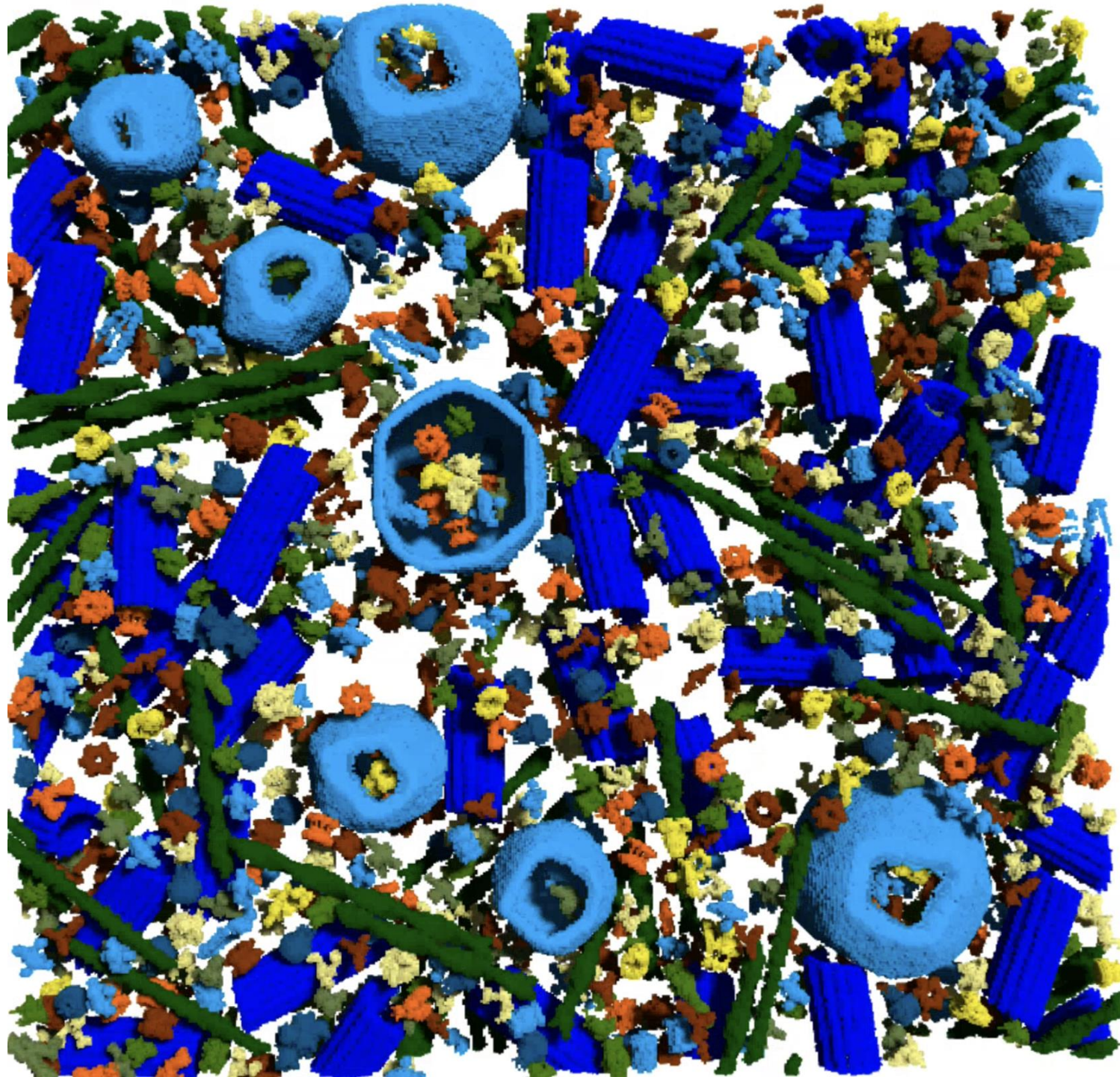
Membrane



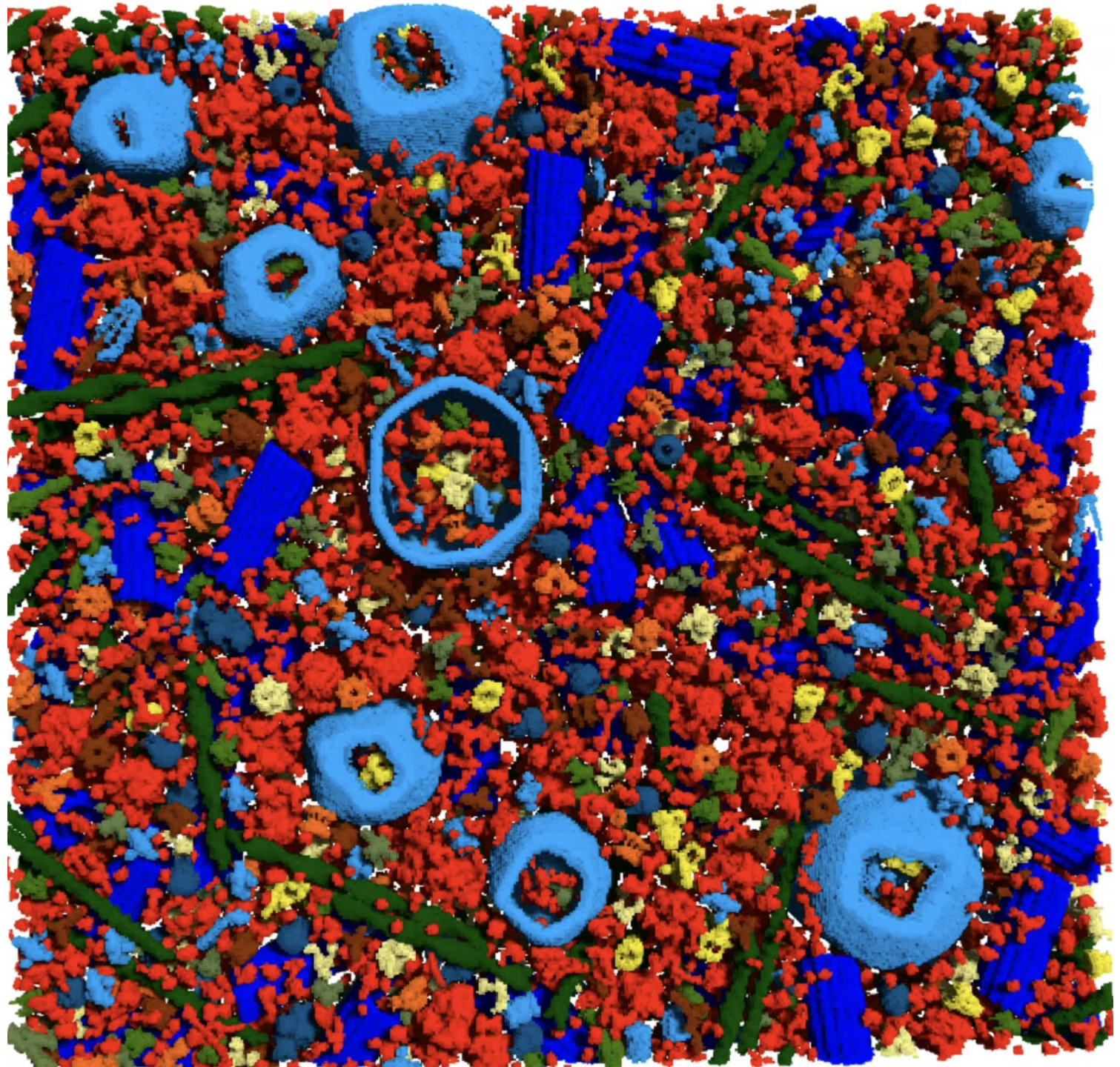
Cytoskeleton



Large Macromolecules
>200kDa



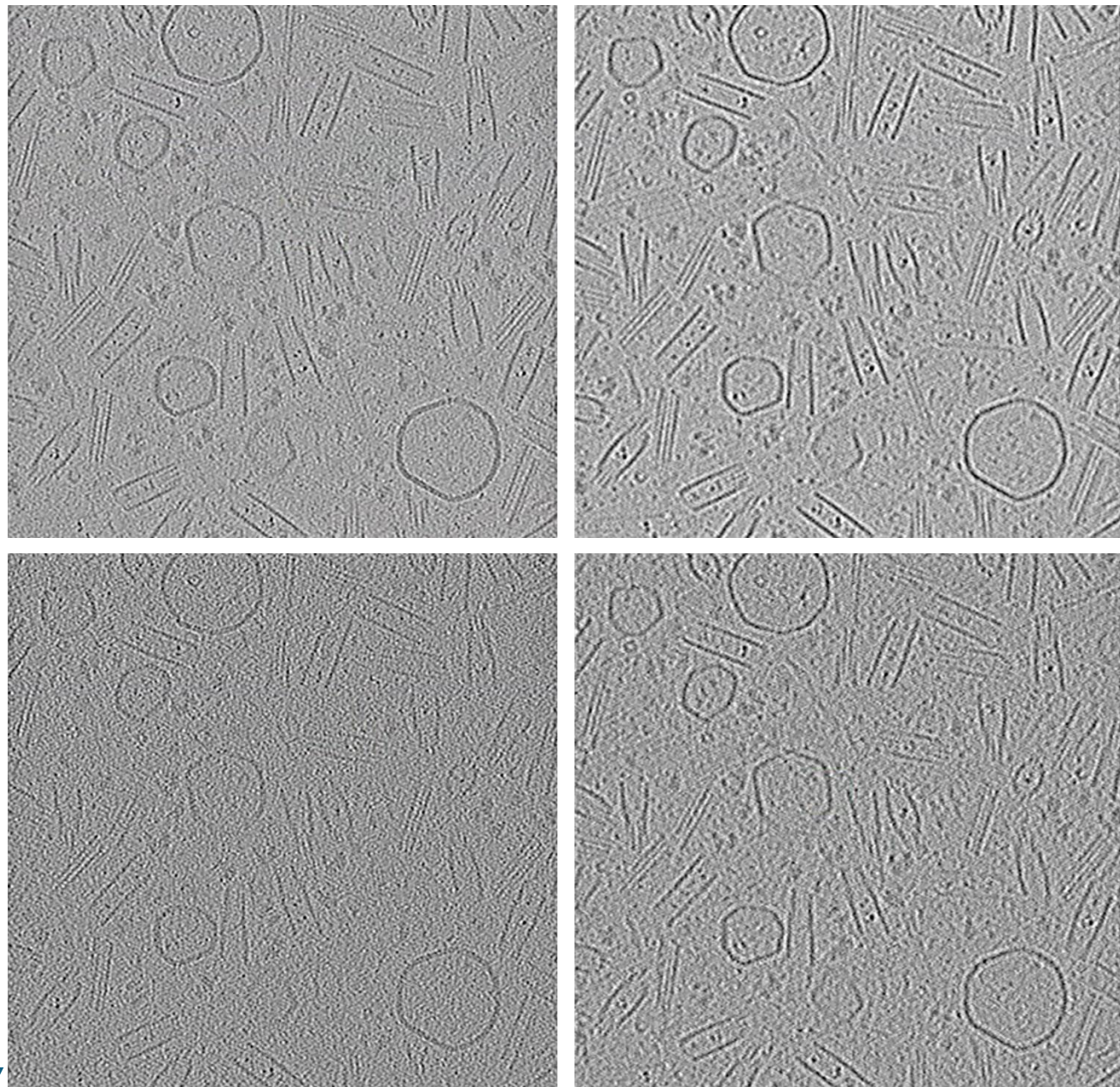
Small Macromolecules
<200kDa



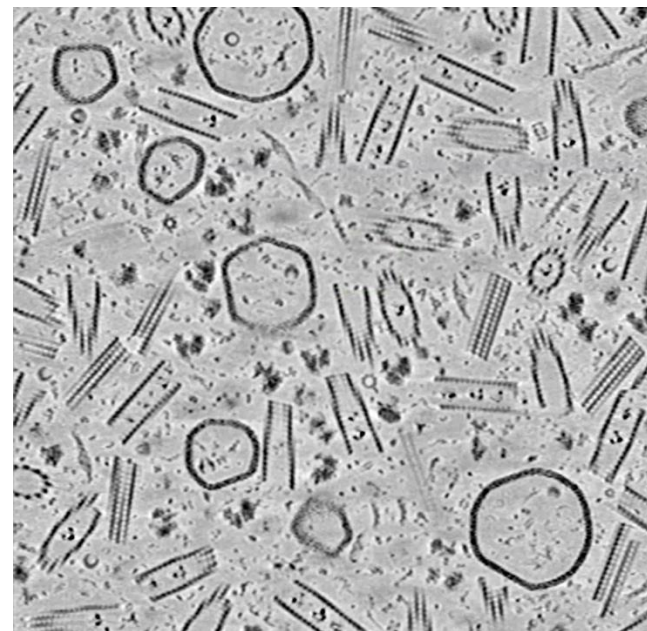
Defocus

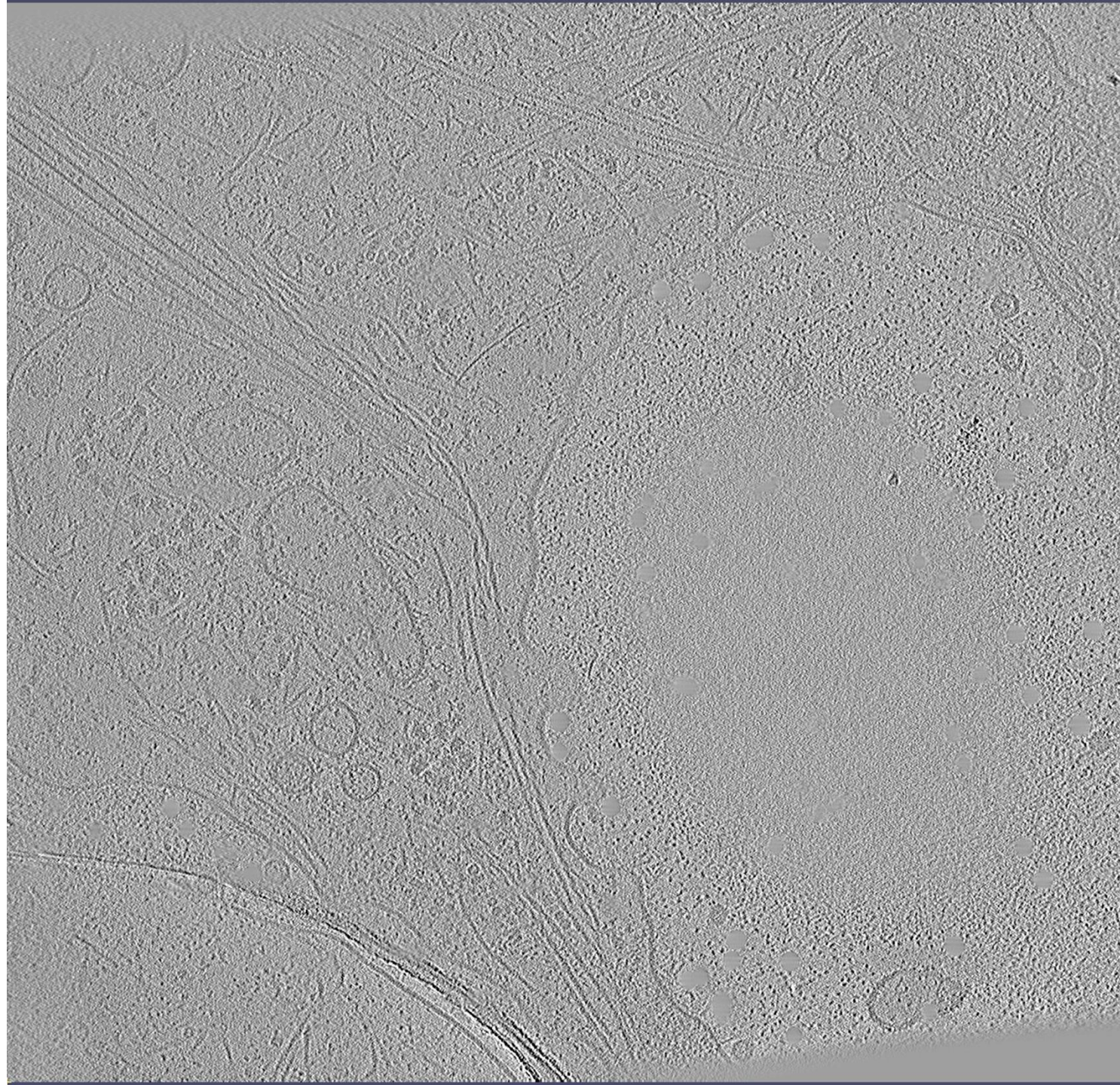


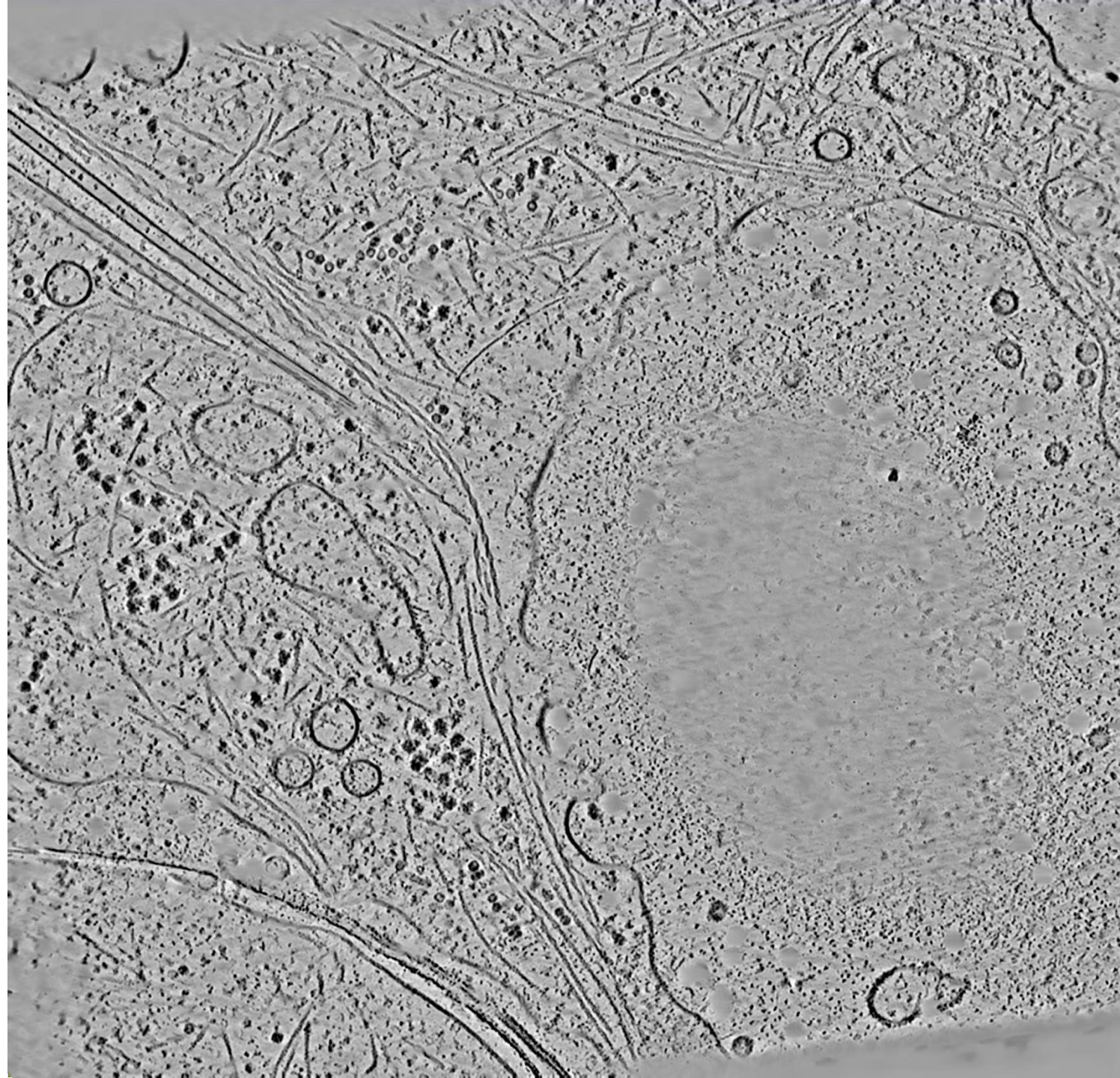
SNR



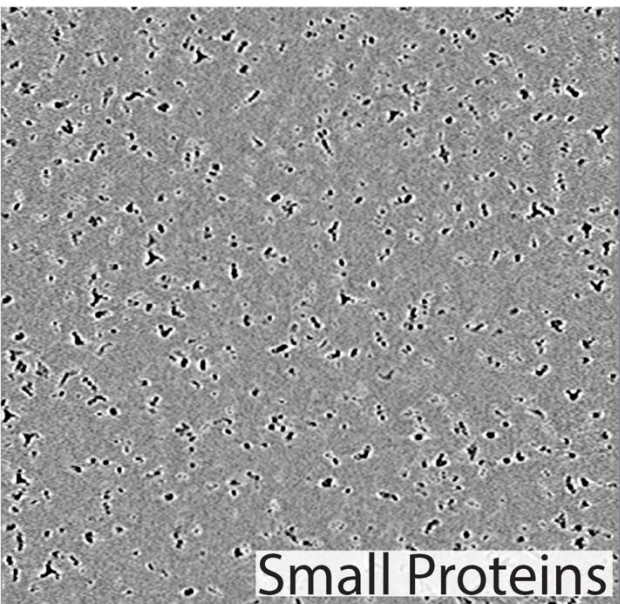
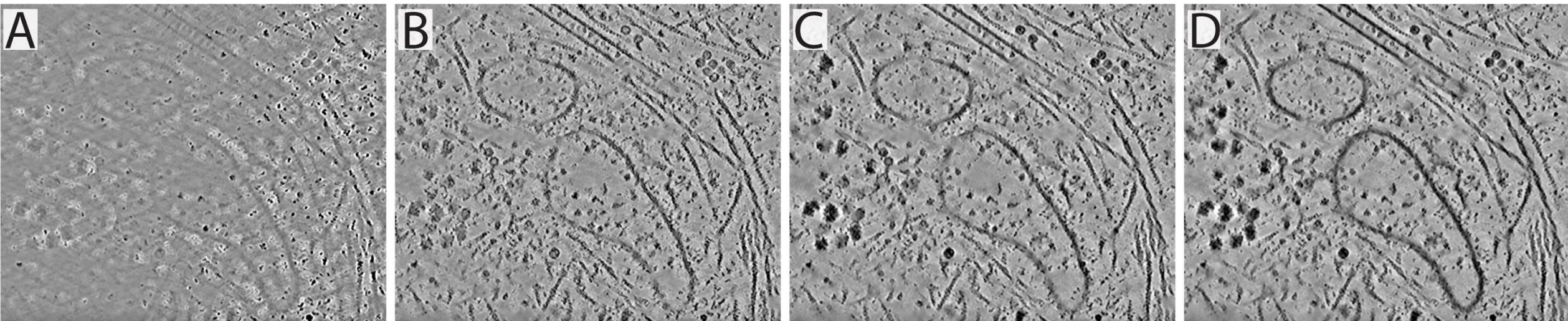
Ground





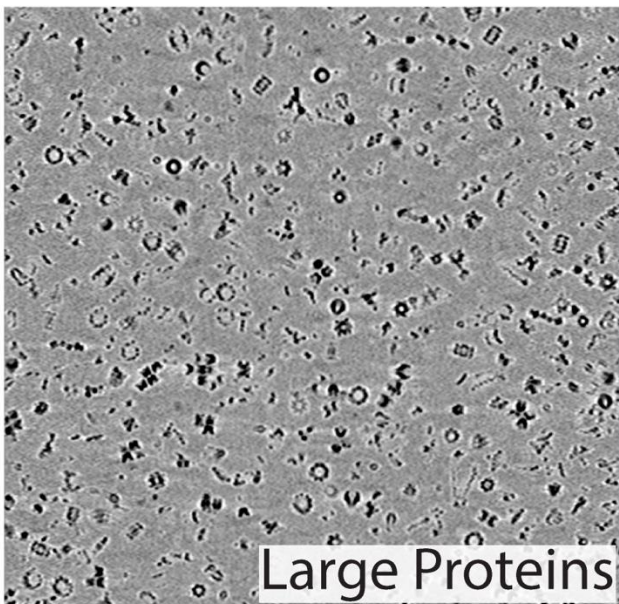


Diversify your inputs



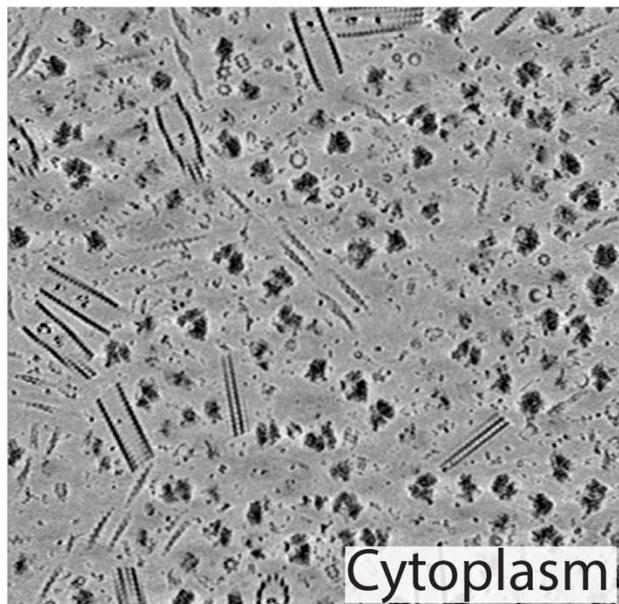
Small Proteins

<200 kDa



Large Proteins

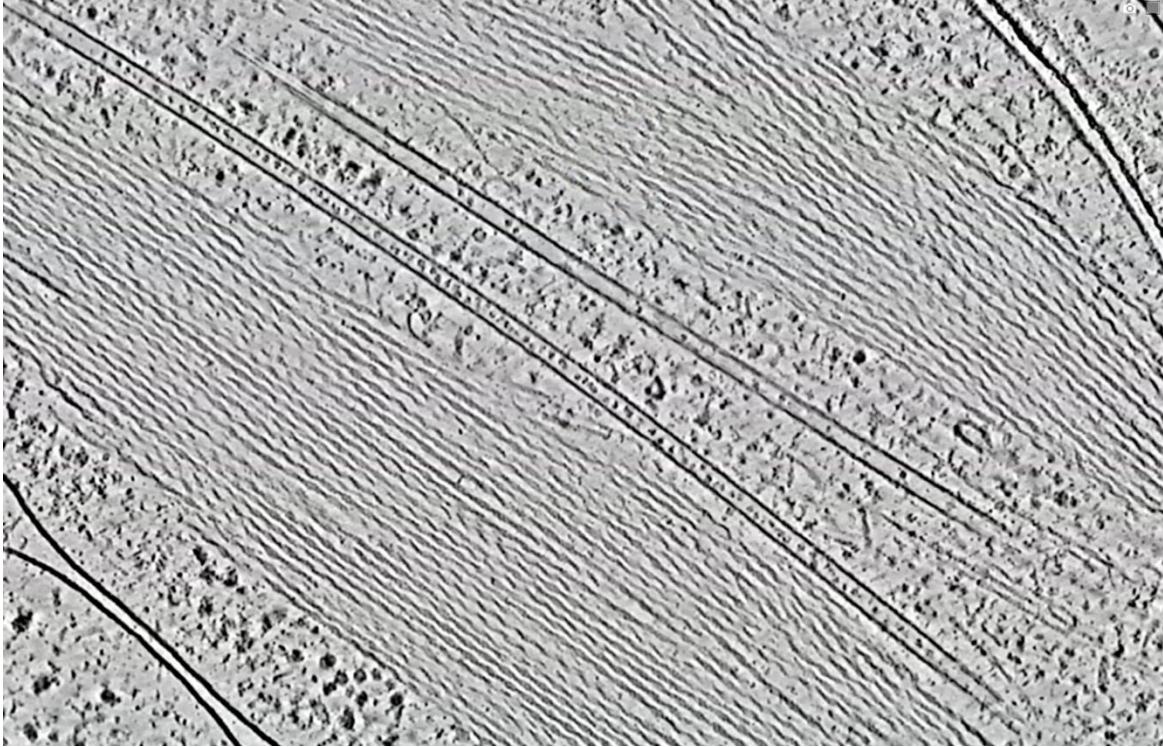
>200 kDa

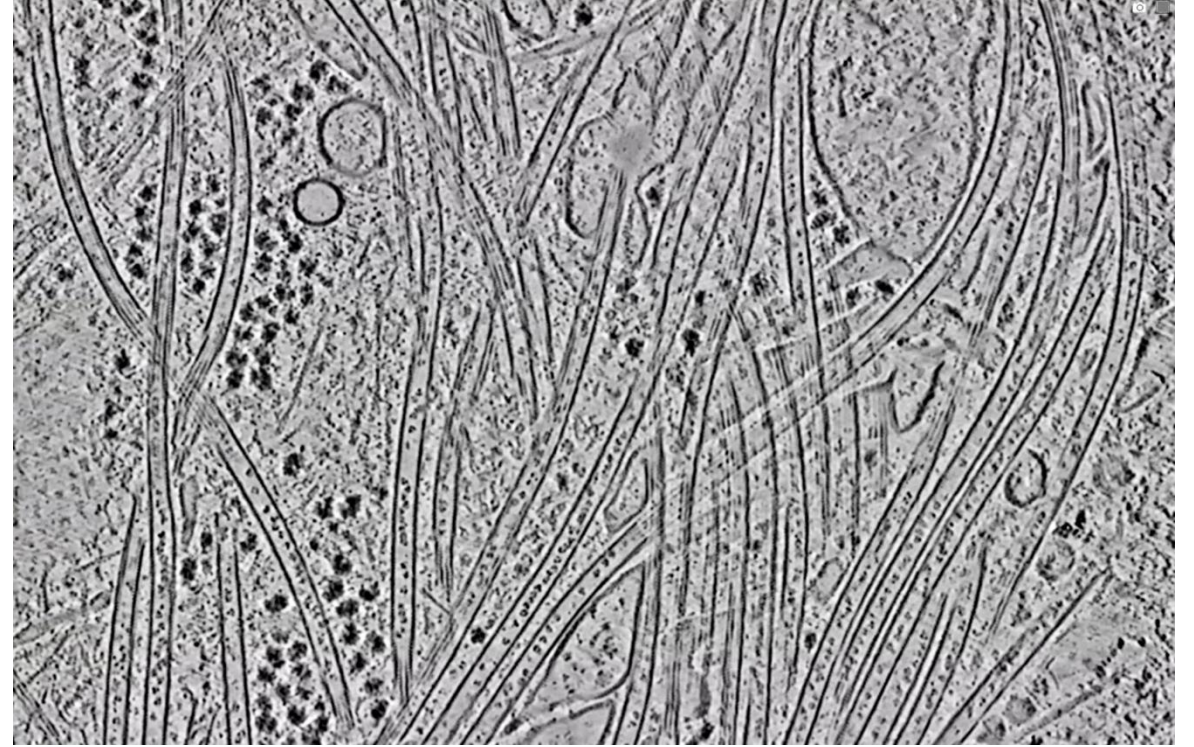
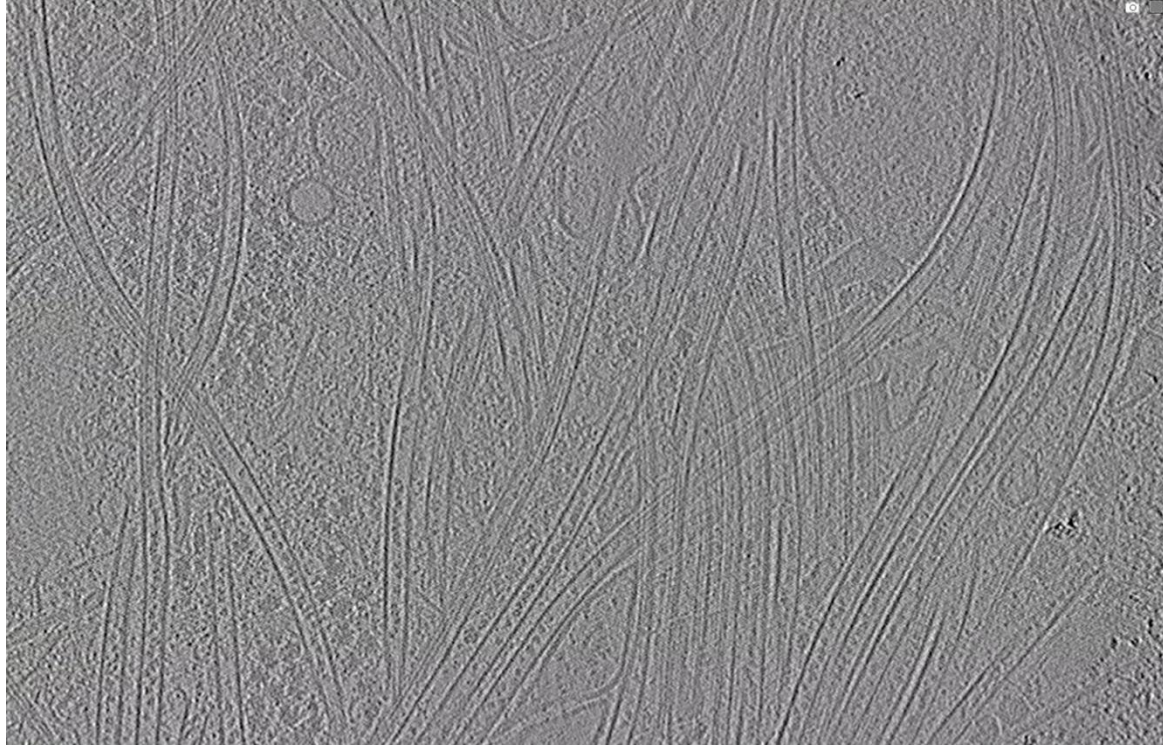


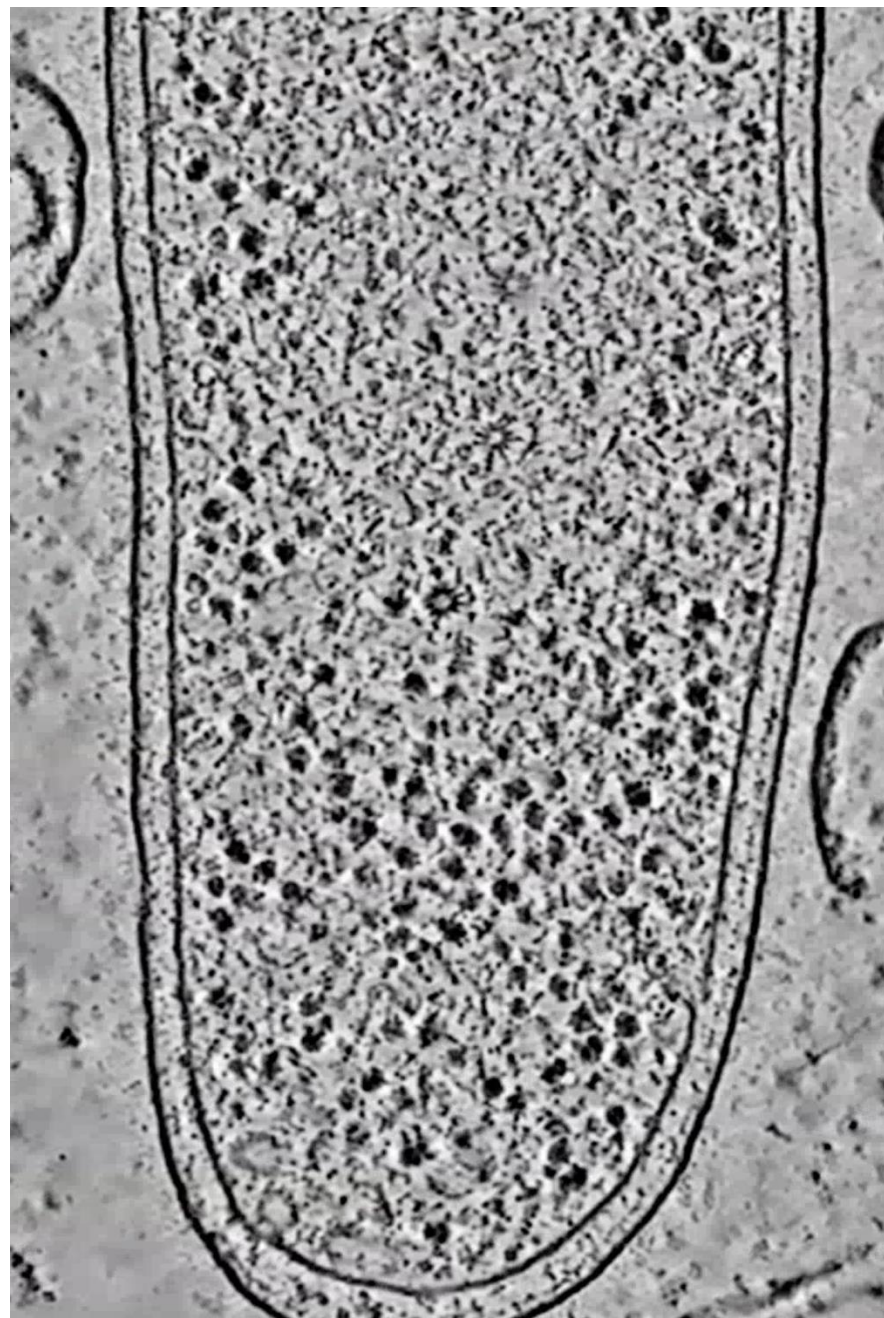
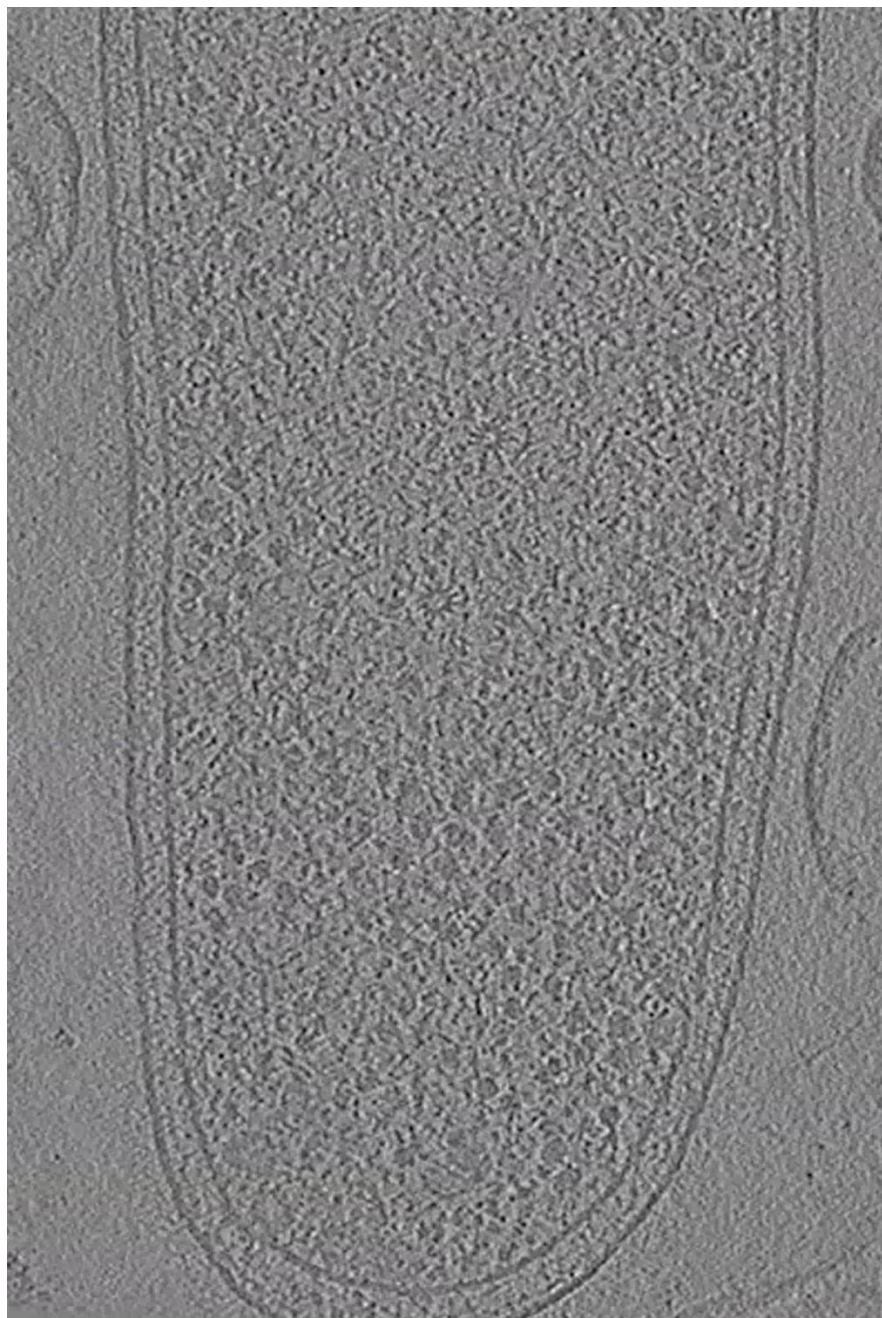
Cytoplasm

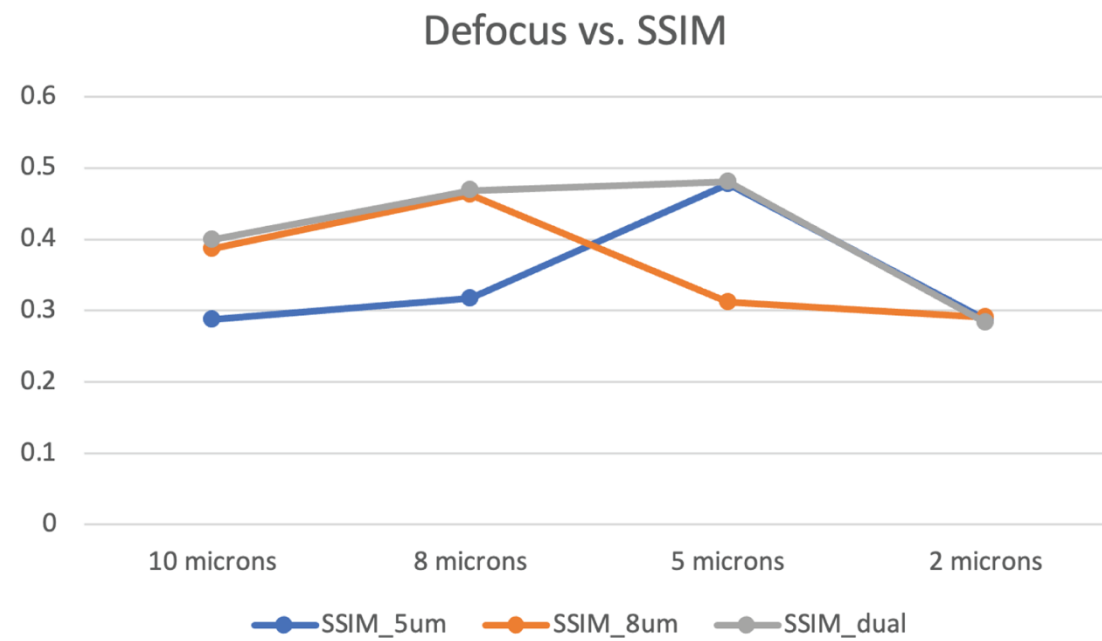
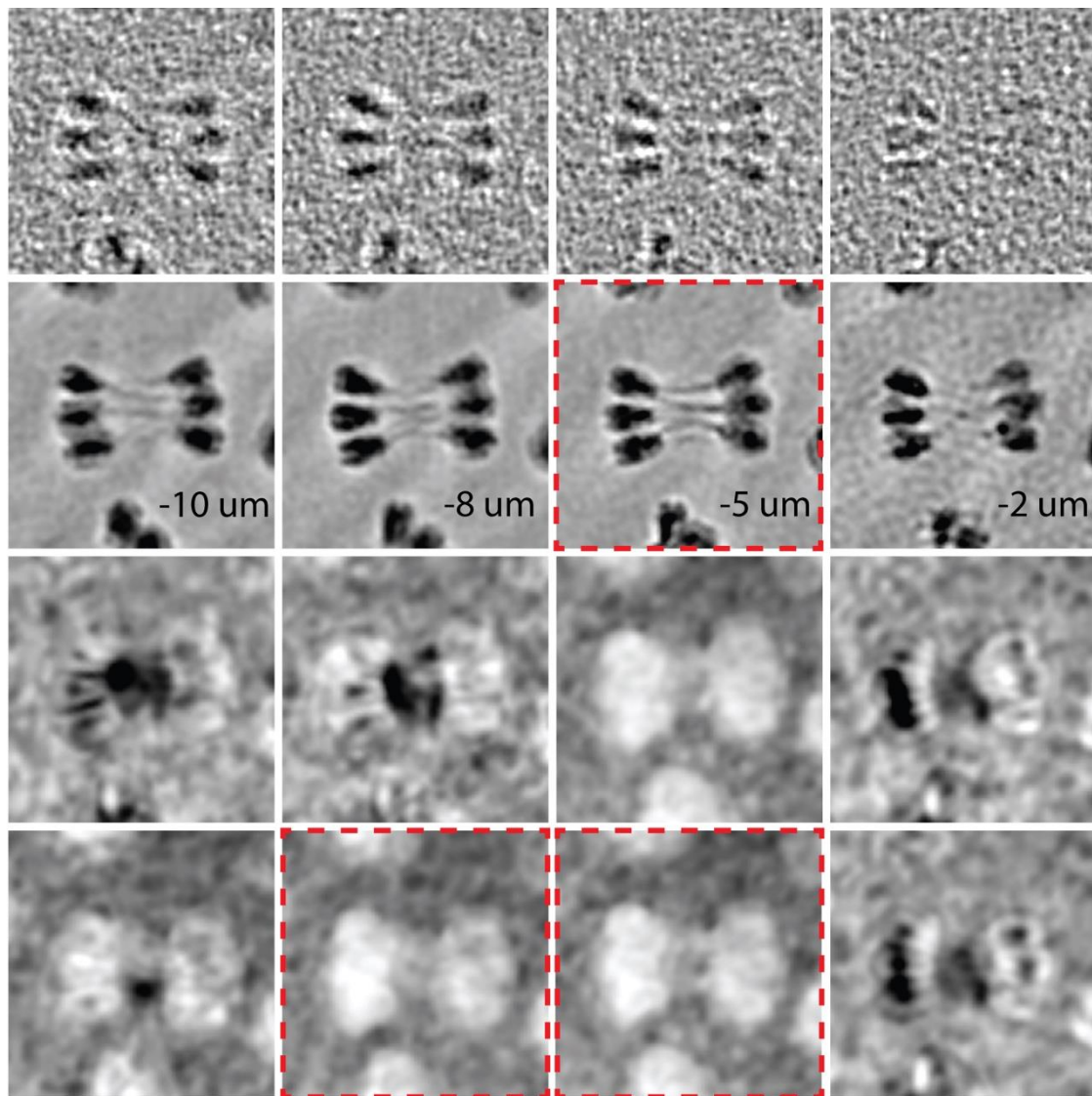


Everything











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Thanks for your attention!



DragonFly

Everyone

Funding/Support

NINDS, TSF, CryoEM

Core