

Amira Software for cryo-electron tomography

Complete your cryo-ET workflow from tomogram reconstruction to biological insight

Thermo Scientific™ Amira™ Software supports the cryo-ET workflow by transforming reconstructed tomograms into actionable biological insights through advanced visualization, image processing, AI-powered segmentation, and quantitative analysis.

Cryo-ET visualizes cellular structures and macromolecular assemblies in their native environment at nanometer-scale resolution. With Thermo Scientific™ instruments and software for cryo-ET acquisition and reconstruction, researchers can generate detailed tomograms that reveal cellular organization and molecular architecture *in situ*.

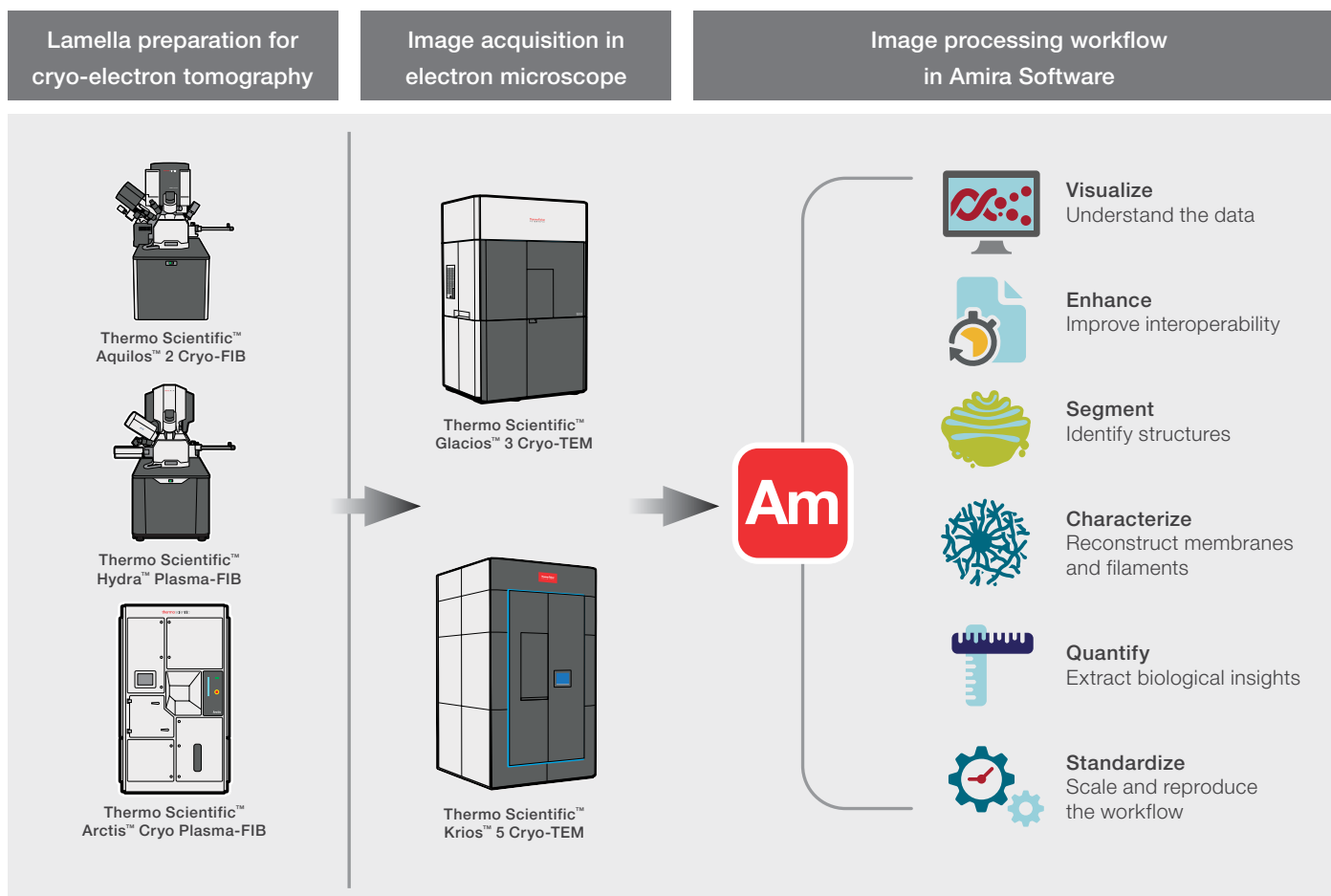
Amira Software provides an integrated environment for post-acquisition cryo-ET data analysis. It can help you visualize 3D tomograms, enhance image quality, identify cellular structures, and perform quantitative measurements within a single platform. Dedicated tools for membrane detection, filament tracing, AI-powered segmentation, and automated workflows help accelerate interpretation of cryo-ET images and support reproducible research.

Key features

- Visualize cellular structures in native 3D context
- Enhance cryo-ET data for downstream analysis
- Accelerate segmentation with AI-powered workflows
- Reveal membrane organization and morphology
- Quantify filament architecture and dynamics
- Standardize analysis with reproducible workflows



ED reconstruction of the nuclear pore complex (green), nuclear membrane (yellow), nucleosomes (purple), and ribosomes (blue) using 200 kV cryo-TEM from a sample that was prepared with the Thermo Scientific™ Arctis™ Cryo-Plasma-FIB. Data segmentation with Amira Software. 3D rendering created in Blender.



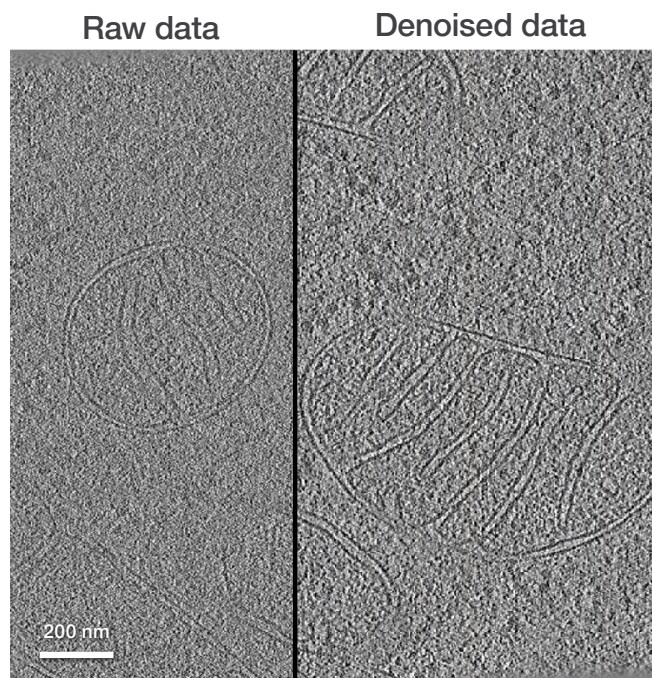
How does Amira Software improve data quality for robust image analysis?

Cryo-ET datasets provide outstanding structural detail, enabling the visualization and investigation of biological structures at nanometer resolution. However, cryo-ET datasets are challenging to interpret due to their low signal-to-noise ratio and low intrinsic contrast.

Amira Software provides dedicated image pre-processing tools to help you analyze cryo-ET data:

- AI-based denoising methods, including Noise2Void and Noise2Clean
- Broad range of classical image processing filters, including a Gaussian filter and non-local means filter
- Dedicated membrane and structure enhancement filters to improve the visibility of cellular structures such as membranes

Together, these capabilities help you improve data interpretability, reveal low-contrast cellular features, and prepare datasets for accurate segmentation and quantitative analysis.

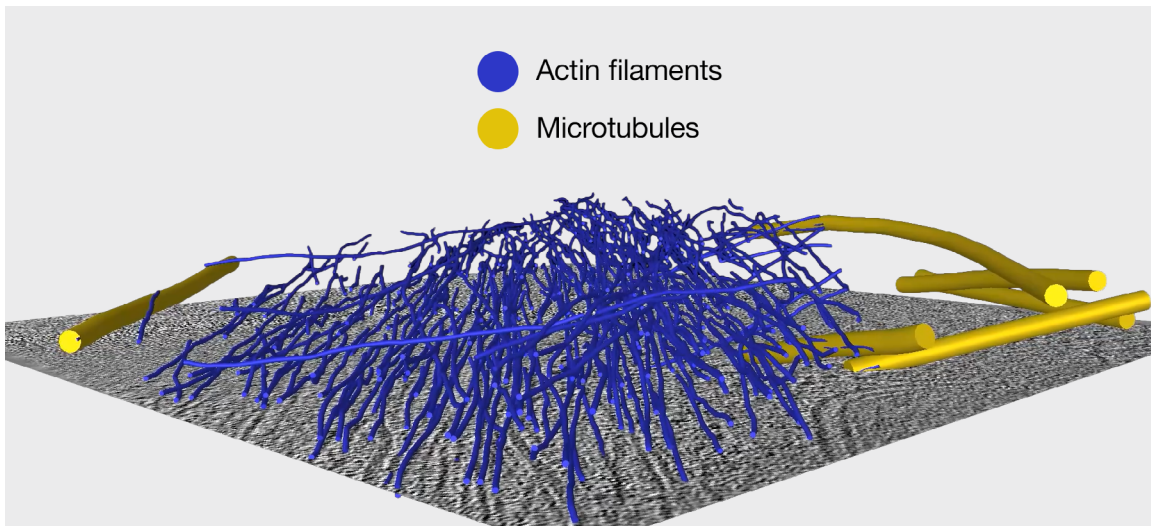


2D image extracted from a 3D cryo-ET tomogram. Image acquired using a Krios Cryo-TEM and denoised with Amira Software. Data from EMPIAR-11370.

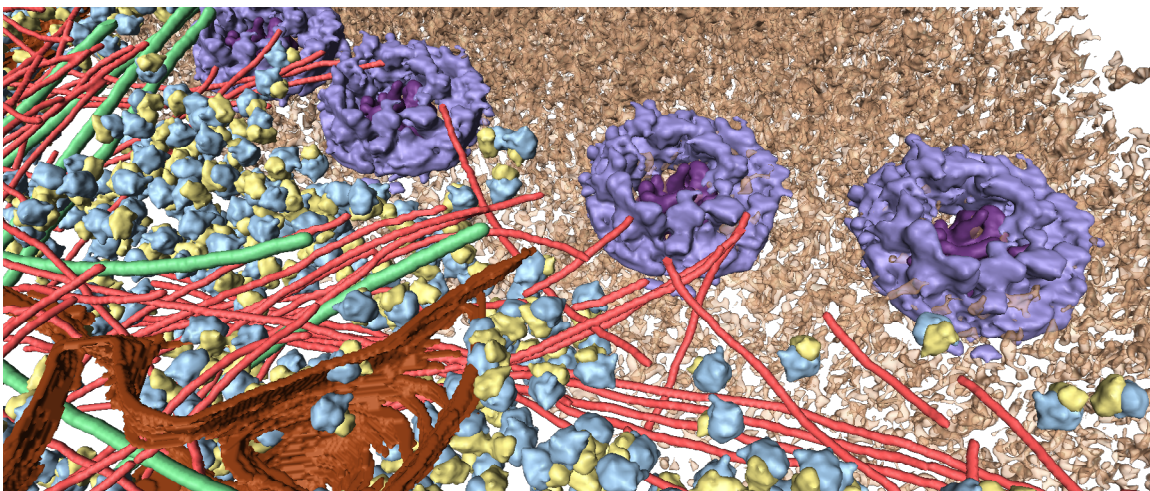
How can AI accelerate segmentation of complex cellular structures?

Cellular structure segmentation encompasses a wide range of challenges rather than a single, uniform problem. Cells contain components that differ substantially in shape, size, and connectivity. Some structures, such as nuclei, are compact and well separated, whereas others, including cytoskeletal filaments and vascular-like networks, are highly elongated, branching, and interconnected. This structural diversity fundamentally influences the choice of segmentation strategies.

Methods that perform well for isolated, approximately spherical objects may not be suitable for thin, continuous, or densely connected structures. In these cases, preserving the underlying geometry and topology is essential. Effective segmentation approaches must maintain structural continuity, accurately resolve branch points and crossings, and distinguish genuine biological connections from image noise and reconstruction artifacts.



Actin filaments and microtubules identified and visualized in Amira software. Image from EMPIAR 10989 image archive.



Visualization of the nuclear periphery of a HeLa cell revealed by cryo-electron tomography. Segmentation and 3D reconstruction performed using Amira Software. Data courtesy of Dr. J. Mahamid, Department of Molecular Structural Biology, Max Planck Institute for Biochemistry, Martinsried, Germany.

Amira Software provides AI-assisted segmentation and advanced structural analysis, including:

- Comprehensive annotation tools with AI-assisted object selection
- Deep learning-based segmentation of multiple biological structures, including organelles, membranes, viruses, and other cellular features
- Flexible model training in 2D, 2.5D, and 3D
- Automated tracing of filamentous structures, such as actin filaments and microtubules

You can efficiently analyze cryo-ET datasets using AI models trained from a small set of manually annotated examples. Once trained, the models automatically segment and classify multiple cellular structures throughout the volume, supporting faster, reproducible analysis while dramatically reducing the time required for data interpretation.

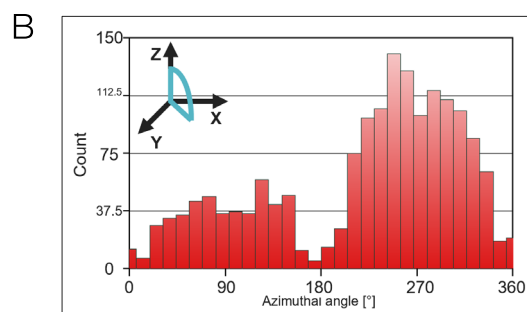
How can biological insights be extracted through quantitative analysis?

Segmented macromolecular complexes, particles, organelles, and cellular features can be classified and quantified for efficient and reproducible analysis. Automated analysis tools support accurate and reproducible data interpretation, particularly in crowded cellular environments with numerous detected structures. By efficiently organizing and classifying segmented features, they reduce the risk of manual errors and support reliable analysis of complex cryo-ET datasets.

Amira Software provides a comprehensive set of quantitative analysis tools that help you:

- Measure membrane thickness, morphology, and structural organization
- Analyze filament length, orientation, tortuosity, and network architecture
- Quantify object size, shape, volume, and distribution
- Evaluate distances and spatial relationships between cellular structures
- Analyze clustering and density of organelles, vesicles, and molecular complexes
- Export quantitative results, plots, and statistics for reporting and publication

These capabilities help researchers characterize cellular structures, investigate spatial relationships, and compare biological features across samples, conditions, and experimental replicates.



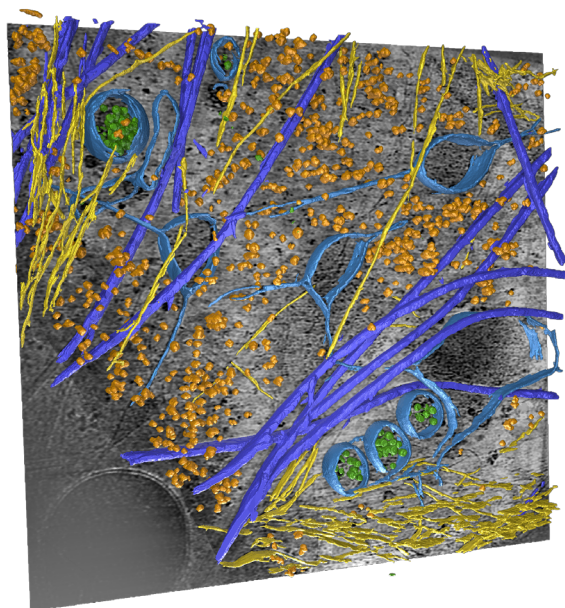
(A) 3D visualization of actin filaments color-coded for the azimuthal angle to highlight the direction of actin polymerization. (B) Quantitative data collected in a plot. Tomogram acquired using a Krios Cryo-TEM, actin filament detection and quantification performed with Amira Software. Data courtesy: Dr. Marion Jasnin, MPI for Biochemistry, Martinsried, Germany. Jasnin et al. *Structure*, 2019

How can reproducible workflows improve cryo-ET studies?

Amira Software delivers consistent analysis across tomograms, experimental replicates, and research projects, which helps researchers standardize image processing, segmentation, and quantification workflows; reduce variability; improve efficiency; and collect reproducible scientific results.

Key workflow capabilities include:

- Creation of reusable analysis recipes for common cryo-ET workflows
- Standardized processing and segmentation across multiple tomograms
- Consistent application of image enhancement and quantification parameters
- Scalable analysis of experimental replicates and large datasets
- Reduced manual intervention through workflow automation
- Improved reproducibility and confidence in quantitative results.



Rhinovirus-infected cos cells. Tomogram acquired with the Krios Cryo-TEM and segmented and visualized in Amira Software. Image from EMPIAR 12270 image archive.

Features

Data import and handling

- Import and analysis of 2D to 5D datasets from electron microscopy, light microscopy, CT, and MRI
- Support for large datasets and most established microscopy file formats

Filtering and pre-processing

- Image alignment, filtering, noise reduction, and artifact correction
- Multi-scale data preparation from subcellular structures to large tissue volumes
- AI-based denoising

AI-based segmentation

- AI-driven segmentation for complex 2D and 3D microscopy data
- Deep learning workflows with minimal ground-truth annotation
- Multi-class segmentation of organelles, membranes, particles, and biological structures
- Robust performance on noisy and low-contrast datasets, including cryo-FIB-SEM data

Experience what Amira Software can do for your cryo-ET datasets. [Contact us](#)

Measurement and analysis

- More than 200 built-in quantitative measurements
- Custom, user-defined measurements for application-specific analysis
- Extraction of volumes, surface areas, shapes, and spatial relationships at scale

Visualization and presentation

- High-resolution 2D and 3D visualization of volumetric datasets
- Animation and movie generation for communication and reporting

Workflow automation and usability

- Recipe-based automated workflows for efficiency and reproducibility
- Intuitive user interface for both novice and experienced users

Applications and support

- Applicable across cell biology, neuroscience, structural biology, plant science, pharma, and biotech
- Professional training, consulting, and custom development services.

 Learn more at thermofisher.com/amira

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