



***In Situ* Cryo-Electron Tomography: A Post-Reductionist Approach to Structural Biology**

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Abstract

Cryo-electron tomography is a powerful technique that can faithfully image the native cellular environment at nanometer resolution. Unlike many other imaging approaches, cryo-electron tomography provides a label-free method of detecting biological structures, relying on the intrinsic contrast of frozen cellular material for direct identification of macromolecules. Recent advances in sample preparation, detector technology, and phase plate imaging have enabled the structural characterization of protein complexes within intact cells. Here, we review these technical developments and outline a detailed computational workflow for *in situ* structural analysis. Two recent studies are described to illustrate how this workflow can be adapted to examine both known and unknown cellular complexes. The stage is now set to realize the promise of visual proteomics—a complete structural description of the cell's native molecular landscape.

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Introduction

Understanding complex networks requires detailed knowledge about the properties and interactions of each of the network's components. This is especially true in molecular cell biology, where individual proteins are often involved in multiple cellular processes, frequently swapping interaction partners and changing states of assembly [1,2]. Structural biologists have traditionally approached this cellular complexity in a reductionist manner by characterizing purified molecular components [3]. This “divide and conquer” strategy has been highly successful, as evidenced by the impressive number of entries in the Protein Data Bank [4]. However, the reductionist approach has several intrinsic limitations. Labile and membrane-embedded complexes can be easily damaged or distorted from their functional conformations during purification. Moreover, complexes frequently lose their biologically relevant associations once they are removed from the crowded cellular environment. It is well known in protein crystallography that missing cofactors can weaken the integrity of structures, while packing forces can stabilize non-physiological conformations [5].

Cryo-electron tomography (cryo-ET) avoids these pitfalls by imaging unperturbed cells, preserving the full spectrum of each molecule's conformations and interactions [6–8]. With several recent technological advances increasing both the versatility and the image quality of cryo-ET, it is now possible to identify and characterize macromolecules within a wide variety of cell types [9–16]. Computational tools including template matching, subtomogram averaging, and classification enable the generation of molecular-resolution structures that accurately represent the physiological conformations of complexes within their functional environments [17–19]. In this review, we present a practical workflow for *in situ* structural analysis, with an eye toward the future of visual proteomics [20,21].

Preparation of Thin Vitreous Samples and Cryo-ET Data Acquisition

Sample preparation for cellular cryo-ET follows a relatively straightforward workflow that is compatible with most cell types (Fig. 1). Cells that grow in solution,

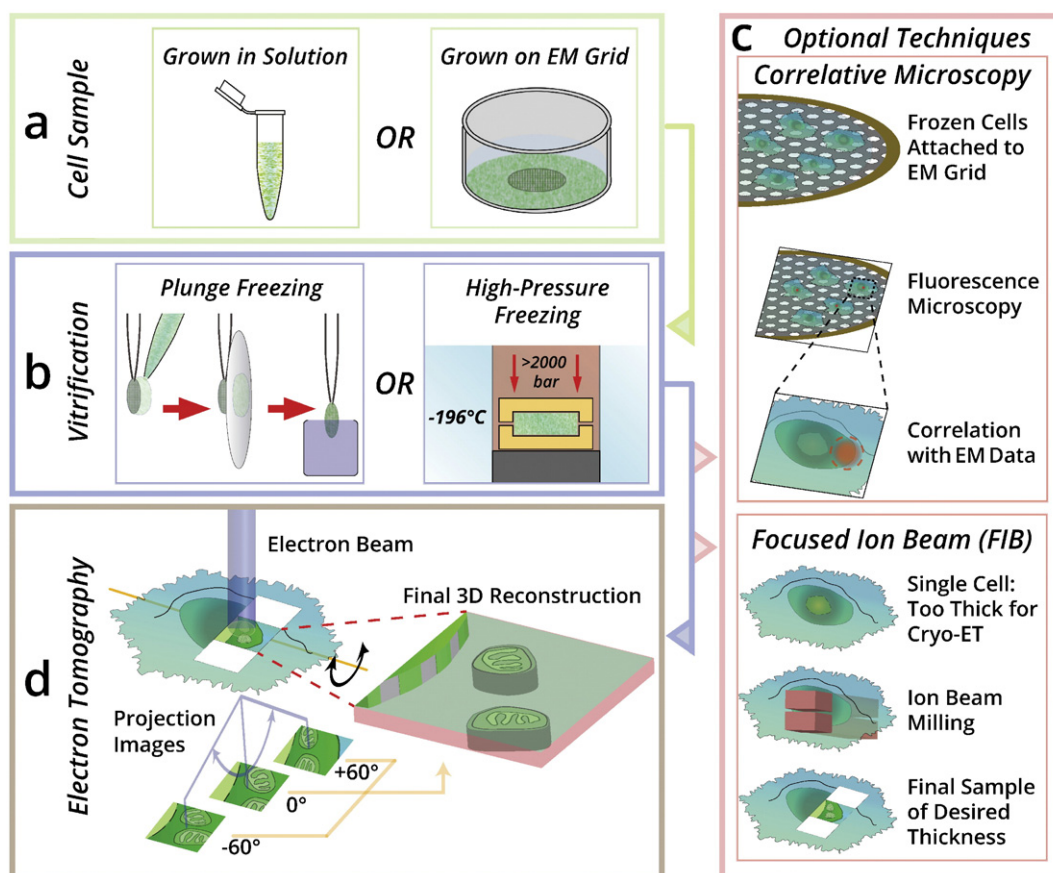


Fig. 1. Sample preparation and data acquisition workflow for *in situ* cryo-ET. Arrows point to the subsequent step in the workflow. (a) The cell sample can be provided either in solution (left box) or as an adherent culture grown on top of a gold EM grid (right box). (b) Vitrification methods. Left box: plunge freezing, where an EM grid with cells is attached to a tweezer (left), excess liquid is removed with filter paper (center), and the grid is rapidly plunged into coolant, which can be liquid ethane or a mixture of liquid ethane and liquid propane (right). Right box: HPF is used to vitrify thicker specimens, including tissue. The cells are immersed in cryo-protectant solutions, such as high-molecular-weight dextran and hexadecene, then subjected to >2000 bar of pressure while being rapidly cooled with a stream of liquid nitrogen. The pressure is then released and amorphous ice is formed within 20 ms [37]. (c) Top box: correlative microscopy can be used to identify target structures by their fluorescence signal (red dots), which aids in locating regions of interest for cryo-FIB milling and cryo-ET. Bottom box: during cryo-FIB milling, a vitrified cell (top) is eroded with a Gallium ion beam (center, red traces), thinning the sample and making the cell body accessible for cryo-ET observation (bottom). (d) The principle of electron tomography. The vitrified sample (cyan cell) is tilted around a fixed axis (orange line). An electron beam (blue) penetrates the sample and projection images are recorded through a series of tilt angles (bottom). A tomogram displaying the 3D cellular volume can be reconstructed by aligning and back-projecting these tilt-series images (right).

including bacteria, archaea, yeast, and many protists, are cultured in their standard medium and applied to carbon-coated copper electron microscopy (EM) grids just prior to freezing (Fig. 1a and b) [10,22–25]. Alternatively, adherent cells, such as *Dictyostelium*, mammalian cell lines, and neurons, are grown on top of carbon-coated gold EM grids, which are less cytotoxic than copper (Fig. 1a) [11,12,26–28]. The cells are then vitrified in glass-like amorphous ice, which is free of damaging ice crystals and does not discretely scatter the electron beam, facilitating cryo-ET imaging [29,30]. Vitrification immobilizes the sample, while preserving native molecular structures, maintaining a hydrated state, and decreasing the radiation sensitivity to incident electrons [29,31].

Vitrification of cells is commonly performed by one of two methods, plunge freezing or high-pressure freezing (HPF) (Fig. 1b). Plunge freezing is suitable for cells up to 10 μm in diameter [29,32,33]. Equipment for manual plunge freezing is now readily accessible, with homemade designs providing a cost-effective setup [34]. Automated plunge freezing devices enable control of humidity, temperature, blotting strength, and blotting time, improving sample reproducibility [35,36]. Alternatively, HPF is capable of freezing multi-cellular organisms and tissue up to 200 μm in thickness [37,38]. However, subsequent thinning is mandatory and usually performed with a cryo-ultramicrotome, which cuts vitreous sections that are susceptible to compression and crevasse

deformations [39–41]. A few strategies have been developed to avoid these artifacts when thinning HPF material, including a lift-out approach combining cryo-focused ion beam (FIB) milling with a cryo-micromanipulator [42–44].

Once vitreous cells are on the EM grid, an optional next step is to localize structures of interest using correlative fluorescence microscopy (FM) (Fig. 1c, top). Fluorescently labeled molecules within the frozen cells are imaged by cryo-FM, and this information is subsequently used to locate positions of interest on the EM grid inside the electron microscope [45–49]. The recent adaptation of sub-diffraction-limit FM to cryogenic samples should greatly increase the precision of correlation [50].

While some prokaryotic cells and eukaryotic cellular protrusions are small enough to be imaged whole by cryo-ET [9,11,23,24,27,51], most cells must be thinned to render them transparent to the electron beam. Cryo-FIB milling (Fig. 1c, bottom) is the method of choice, enabling compression-free thinning of samples directly on the same grid that will be used for tomography [52–54]. Gallium ions are used to ablate material to any specified thickness, typically producing 100- to 300-nm-thick windows into the native cellular interior [55,56].

After thinning, the grids are transferred into the transmission electron microscope and tilt-series images are acquired (Fig. 1d). These images are then aligned and reconstructed to generate three-dimensional (3D) views of the sample, called tomograms. Frozen biological material is easily damaged by electron radiation [57–60]. A common rule of thumb is that tilt-series acquisition should not exceed $100 \text{ e}^-/\text{\AA}^2$, although the dose limit varies with specimen type and may be substantially lower to preserve high-resolution information [58,59,61–63]. This radiation sensitivity places constraints on many cryo-ET acquisition parameters, including the magnification (image pixel size), the tilt scheme, and the amount of signal to noise in the images [57]. As a result, cryo-tomograms are often noisy and have low contrast, presenting challenges to tilt-series alignment and identifying macromolecules within the tomogram volumes. Thicker cellular volumes require higher electron dose to yield the same amount of image signal, further limiting cryo-ET acquisition.

Two recent technical developments, direct electron detectors and the Volta phase plate, have dramatically improved the image quality of cryo-ET [64–67]. Direct electron detectors are cameras that use complementary metal-oxide semiconductor (CMOS) sensors to convert electrons directly into digital signals [68]. Their major advantages over charged couple devices (CCDs) include enhanced sensitivity that reduces the electron dose required for a given set of acquisition parameters, improved detection precision that produces sharper images, and a fast frame readout that allows for image drift

correction [69,70]. Several studies have demonstrated the potential of these new cameras for single-particle cryo-EM, yielding subnanometer-resolution protein structures [64,66,71–76] and heralding the beginning of the cryo-EM “resolution revolution” [77,78]. The gains of applying direct electron detectors to cryo-ET have been similarly impressive [9,15,79–82], although there is still substantial room for resolution improvement in computational steps such as tilt-series alignment.

Previously, the only way to improve the contrast of cryo-EM images without increasing the electron dose was to use more defocus. However, this limits the image resolution, as there is a negative correlation between defocus and resolution. The Volta phase plate decouples this relationship by providing visually impressive contrast during in-focus acquisition, thus producing images of both high contrast and high resolution [9,10,15,67]. This boost in low-frequency contrast provides major advantages for both tilt-series alignment and structure identification.

Detection of Macromolecules Inside Cells

Several consecutive image-processing steps are necessary for the detection of macromolecules within cellular tomograms (Fig. 2). Tilt-series that were recorded with defocus can be subjected to contrast transfer function correction to improve their resolution [57,83,84]. This step is unnecessary for in-focus images acquired with the Volta phase plate. Denoising procedures (Fig. 2a), such as bandpass frequency filtering, non-local means filtering, and iterative reconstruction schemes [85–91], can be performed during or after tomogram reconstruction. Proper denoising can aid in tomogram interpretation and is particularly useful for the segmentation of supramolecular structures and organelles [11,92,93].

While tomogram segmentation (Fig. 2b) is optional, there are several reasons to mask cellular compartments. Segmentation can be utilized to selectively search for macromolecules inside specific organelles or the cytoplasm [9,16,94]. Restricting the search volume to the cell body also reduces false positives [9,94], excluding gold fiducial markers and grid contaminants that are often assigned high scores by template matching (Fig. 2c) [95–97]. Tomogram segmentation can be performed either manually or automatically, with several toolboxes available [98]. The latest automatic segmentation algorithms produce accurate results, which can be refined by providing boundary conditions [93,99]. However, manual segmentation may still be required for more complex cellular architecture that requires interpretation and *a priori* knowledge [10,93,99].

Template matching (Fig. 2c) is the computational method of searching for molecular complexes inside tomographic volumes [100,101]. A template is

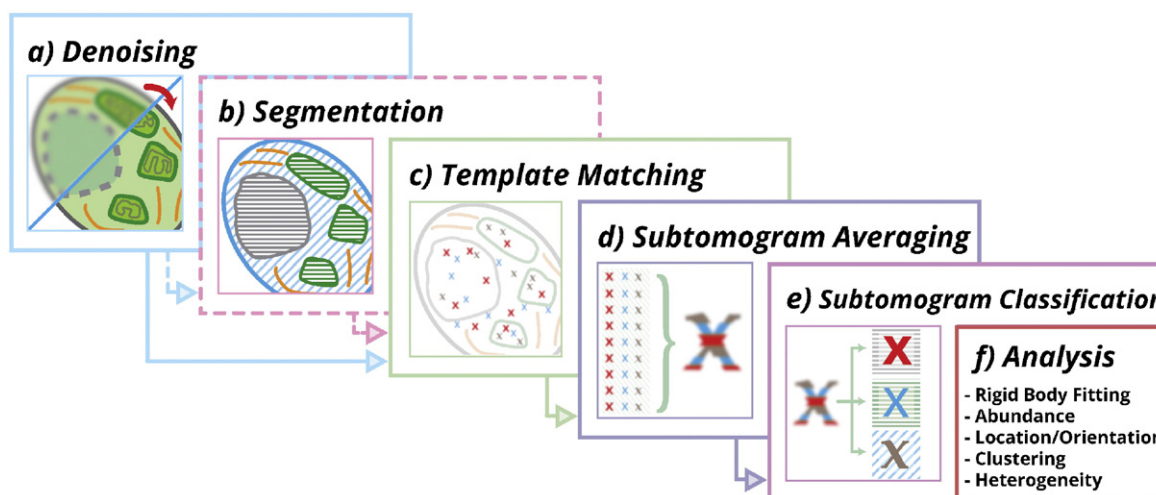


Fig. 2. Image-processing workflow for *in situ* cryo-ET. Each element is connected by either a dashed or a continuous arrow, indicating an optional or mandatory step, respectively. (a) Denoising can be applied either pre-reconstruction or post-reconstruction to provide signal enhancement. (b) Segmentation facilitates template matching and analysis of select cellular compartments (diagramed as colored areas). (c) Template matching and subsequent manual sorting generates a list of possible candidates for the desired macromolecule (illustrated with the letter “x”). (d) Subtomogram averaging initially uses all candidates regardless of conformation or assembly state to generate an inhomogeneous lower-resolution average (“x” with a mix of shapes and colors). (e) Subtomogram classification is capable of separating the dataset into homogeneous subsets, as indicated by the three sorted “x” classes with well-resolved averages. (f) Analysis steps include fitting atomic structures to the subtomogram averages and using the positions and orientations from template matching to quantify *in situ* concentrations, distributions, and interactions.

created using known information about a macromolecule, such as its crystal structure, rough morphology, or known binding partners [100]. As described later in this review, templates may also be generated *de novo* from the tomogram (Fig. 4) [16]. The template matching algorithms perform cross-correlation calculations to compare the template with each position in the tomogram, resulting in a correlation volume where each pixel is assigned a similarity score [20,101,102]. Subvolumes corresponding to the highest scores are then extracted from the tomogram and can be manually screened prior to further analysis to remove obvious false positives [9,16,103,104].

Once the subvolumes have been extracted, they are subjected to subtomogram averaging (Fig. 2d). Averaging methods use cross-correlation measurements to maximize the spatial overlap between all the subvolumes and the reference volume. Multiple rounds of iterative optimization are performed; each round yields a more refined subtomogram average, which in turn is used as a reference for the next round of alignment [19,105,106]. Different methods have been developed to perform subtomogram averaging in either real space or orthogonal coordinate systems [104–106].

Unlike purified complexes, macromolecules within the native cellular environment may show a high degree of heterogeneity in their conformations, interaction partners, and states of assembly. Thus, all initial subtomogram averages should be subjected to an additional classification step (Fig. 2e) to divide the

dataset into more homogeneous subsets [9,19,107]. During classification, scoring functions iteratively sort the subvolumes into classes based on relative similarity [18,104,108]. The recently developed auto-focused 3D classification algorithm reduces human interaction to a minimum by using the differences within a group of aligned subvolumes, given by the gray-value variance of their average, to automatically generate masks for the scoring function [18]. Even subtle assembly and conformational differences can be reliably detected and separated by this algorithm [18,107]. Additional rounds of classification may be applied to create even more homogeneous sub-classes, provided that there are still enough subvolumes remaining to allow for proper alignment [9,107]. Finally, rigid body or flexible fitting can be used to dock atomic structures of subunits into the classified averages [109–111], aiding in the characterization of different conformations or assembly states [9,112].

Two major concerns that need to be taken into consideration during the averaging of both single particles and subtomograms are anisotropic resolution and model bias. An inhomogeneous distribution of orientations in the dataset causes anisotropic resolution, where some regions of the final average are better resolved than others. This phenomenon is most commonly encountered in single-particle cryo-EM [113], where isolated complexes sometimes assume similar orientations in the thin ice of the EM grid. *In situ* cryo-ET has the advantage that complexes suspended within the cellular volume

usually do not have preferred orientations, and even if they do, these orientations will vary between cells. Therefore, subtomogram averaging can produce relatively isotropic structures from only a moderate number of *in situ* subvolumes [9,107,114].

Averaging a large dataset of pure noise images can accurately reproduce the structure of the reference used for alignment, a phenomenon known as model bias [115–117]. Single-particle cryo-EM studies may be especially prone to this artifact, as high-resolution structures are generated from near-focus images with limited contrast, making structural features nearly indistinguishable from noise [78]. Model bias can be minimized in cryo-ET by using the Volta phase plate to boost low-frequency contrast, low-pass filtering the template before searching the tomogram, template matching with a truncated structure (e.g., a single-capped 26S proteasome), and initially aligning the subvolumes to a spherical or random reference (Fig. 3a) [78,114].

In addition to the generation of subtomogram averages, *in situ* cryo-ET presents the unique opportunity to place these structures into their cellular context (Fig. 2f). Template matching identifies molecular positions and orientations with subnanometer precision, enabling the assignment of each macromolecule to its cellular location. This exact determination of origin is unmatched by biochemical fractionation; for example, cryo-ET reliably discriminates between ribosomes bound to the nuclear envelope and ribosomes bound to the endoplasmic reticulum. The spatial information from template matching can be combined with tomogram segmentation to determine the precise concentrations of molecular complexes within defined cellular compartments [9,11,107]. Template matching can also be used to analyze the clustering of macromolecules, as well as the positioning of macromolecules relative to other complexes, membranes, or the cytoskeleton. Mapping the *in situ* distributions of macromolecules in different conformations or assembly states may provide important insights into the spatial regulation of protein function inside the cell. Importantly, the plotting of positions and orientations can be expanded to include multiple different types of macromolecules within the same volume, creating interaction maps of the native cellular environment. Further expanding this analysis to the description of all detectable molecular complexes is the goal of visual proteomics [20,118], which will be discussed in the final section.

***In Situ* Characterization of Known Complexes: 26S Proteasomes in Neurons**

A recent study characterizing 26S proteasomes in neurons showcases the strength of *in situ* subtomogram

averaging and classification [9]. In this section, we outline this study's computational workflow, which can be adapted to the investigation of other complexes with known structures (Fig. 3). The 26S proteasome is a macromolecular complex responsible for the regulated degradation of proteins that are misfolded, damaged, or no longer needed [119,120]. These protein substrates are marked for destruction by the covalent attachment of ubiquitin and subsequently bind to the 19S regulatory particle (RP), a subcomplex of the 26S holoenzyme that caps the 20S core particle [120,121]. The substrates then undergo ATP-dependent unfolding and are fed into the 20S particle, a barrel-shaped chamber containing proteolytic degradation sites [120,121].

To visualize the 26S proteasomes *in situ*, thin regions of cultured mammalian neurons were imaged by cryo-ET with the Volta phase plate. The single-particle cryo-EM structure of the 26S proteasome [122] was then used to generate a low-pass-filtered, single-capped 26S model for template matching. Both the large size (2.5 MDa) and unique shape of the 26S holocomplex aided in its identification. To eliminate the possibility of model bias, the first round of subtomogram averaging used a neutral initial reference that was generated by randomly averaging all of the subvolumes (Fig. 3a, left) [105]. The data-driven alignment converged remarkably fast, where the sixth iteration already displayed a low-resolution, single-capped 26S proteasome. By the 20th iteration, no major changes in the alignment could be observed, resulting in an average of the holoenzyme with a single clearly visible RP on top of the 20S core particle (Fig. 3a, right).

The variance map calculated from the average (Fig. 3b, right) indicated a major structural component at the position of the second RP (Fig. 3b, green circle). The first round of classification was able to identify the cause of this heterogeneity: the dataset contained two different assembly states, the more abundant single-capped and less frequent double-capped 26S proteasomes (Fig. 3b, green inset). The *in situ* ratio of these two assembly states was consistent with previous observations of isolated 26S complexes [112,123–125].

Using a similar strategy, the dataset was subjected to another classification aimed at disentangling the highly variable 19S RP complex (Fig. 3b, red circles and red inset). Variances in the average were traced to two major classes that showed significant conformational differences. To address the functions of these classes, the two *in situ* conformational states were compared with atomic models of the 19S RP previously acquired from single-particle cryo-EM (Fig. 3c) [112]. Using rigid body fitting, both *in situ* conformations were successfully assigned a functional role. Whereas one class matched the 19S RP not bound to substrate (ground

state), the second class had a conformation that resembled the 19S RP during substrate commitment or translocation (substrate-processing state). This class also displayed a large density not present in the single-particle structure that likely corresponded to substrates or proteasome-interacting proteins. This was the first study to successfully localize the

26S proteasome *in situ*, enabling structural characterization of native structures at the single protein level. These insights may have implications for neuronal function, as the 26S proteasome plays a major role in numerous synaptic processes, and its malfunction is linked to several neurodegenerative diseases [126,127].

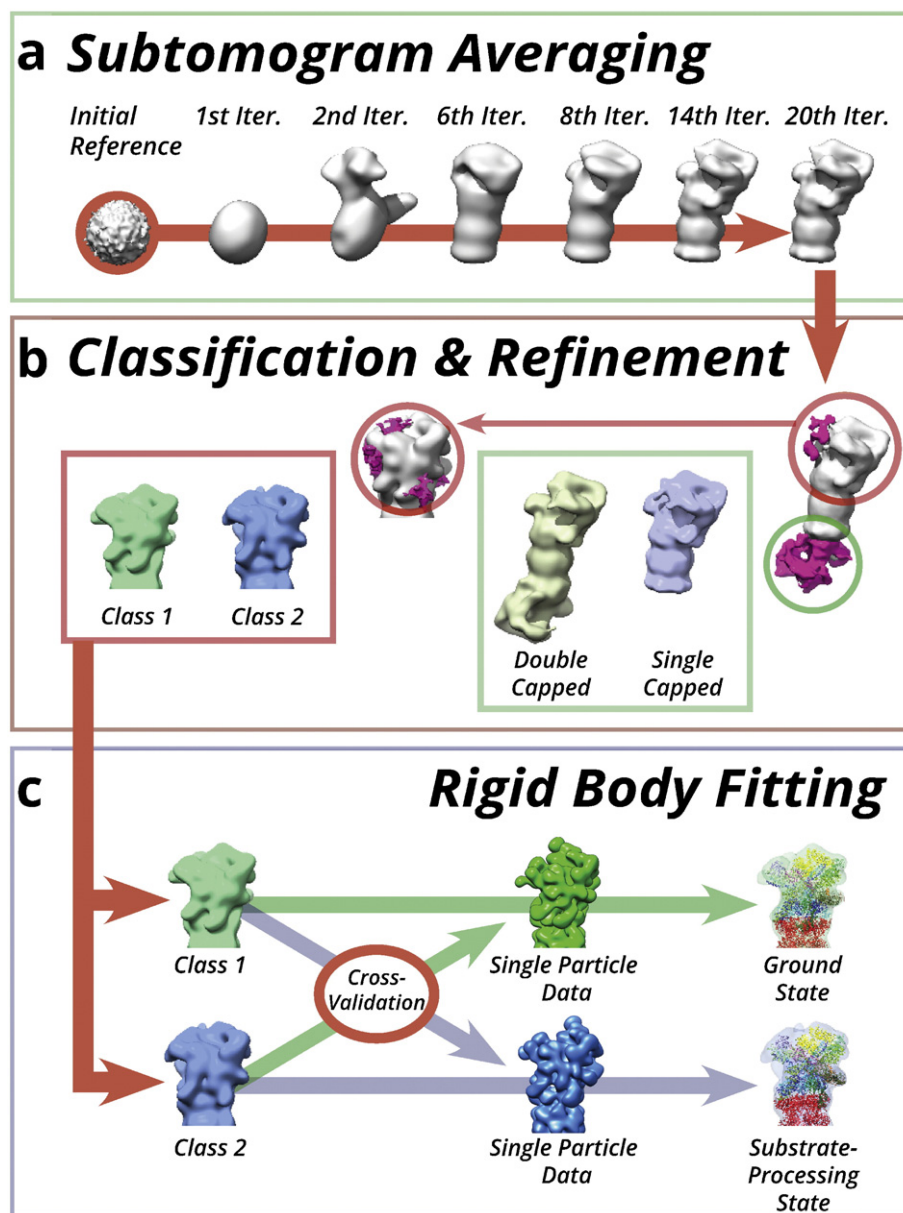


Fig. 3. Workflow for the *in situ* characterization of 26S proteasomes in intact neurons [9]. (a) Subtomogram averaging produced a viable average from a randomized initial template within several iterations (from left to right). (b) The previously calculated average was subjected to classification and refinement. From right to left: the variance map (variance in magenta) guided the positioning of two masks used for the classification (green and red circles). This enabled the dataset to be split into assembly state classes (double capped and single capped) and conformation classes (class 1 and class 2). (c) Atomic structure models from single-particle cryo-EM were fit into the two conformation classes with rigid body fitting and cross-validation. During cross-validation, class 1 and class 2 were compared to single-particle models of the proteasome in different conformational states [112]. Both conformation classes could be assigned to a functional state: the substrate-free ground state and the substrate-processing state.

De Novo Analysis of Unknown Structures: Golgi Intracisternal Protein Arrays

In situ subtomogram averaging is also capable of characterizing previously unknown structures. In a recent cryo-ET study, intracisternal protein arrays were observed within the Golgi apparatus of FIB-milled *Chlamydomonas reinhardtii* cells (Fig. 4a) [16]. These structures were both abundant and highly regular, enabling *de novo* structure generation.

The initial template was a single low-pass-filtered subvolume containing two cisterna membranes connected by a protein array (Fig. 4b, top). After the first round of template matching, candidate subvolumes were extracted, manually inspected, and averaged. The resulting subtomogram average was subsequently low-pass filtered and used as a refined template to

repeat the template matching (Fig. 4b). This iterative template generation improved the detection of the protein arrays, revealing an asymmetric structure linking the two membranes, with alternating long and short proteins projecting into the cisterna lumen (Fig. 4b and c). The structure also showed periodicity along the cisterna membrane, which was measured by performing an autocorrelation of the average (Fig. 4c). Using this information, the subtomogram average was further refined to account for translational symmetry (Fig. 4c).

The array's intracisternal projections are most likely interlinked protein complexes that hold the two cisterna membranes together by zipper-like interactions. These interactions appear to determine the narrow spacing of the central cisterna regions (Fig. 4d) and thus may force cargo that is

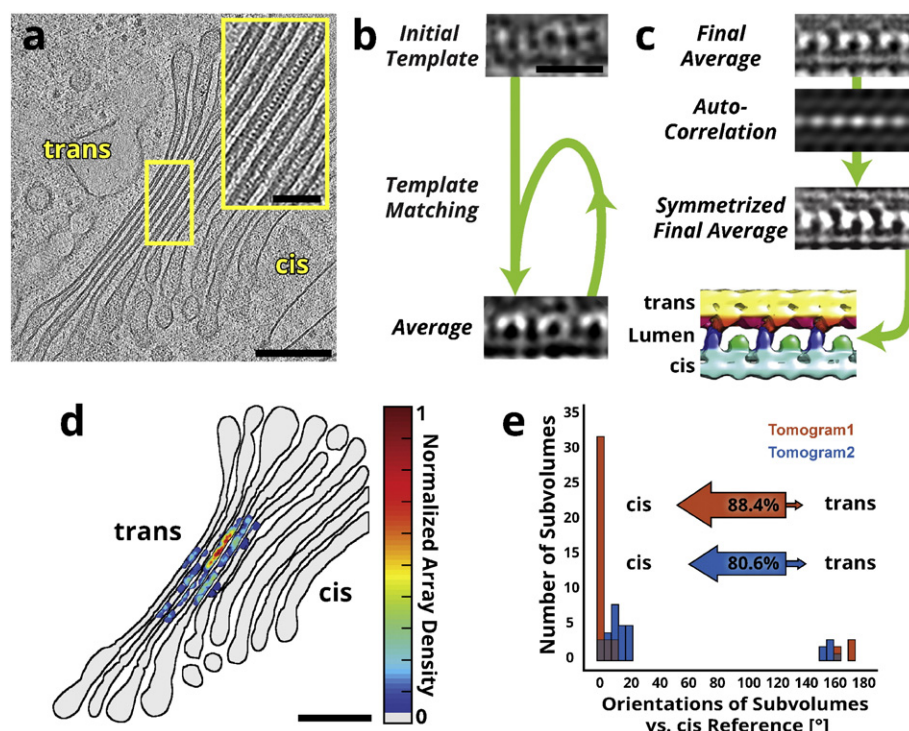


Fig. 4. *In situ* characterization of Golgi intracisternal protein arrays [16]. (a) Overview slice from a tomogram of a *Chlamydomonas* Golgi apparatus, revealing highly ordered membrane-associated complexes between the cisterna membranes. The region within the yellow box is shown enlarged in the inset. Scale bars: 200 nm, inset: 50 nm. (b) Iterative *de novo* template generation. The first round of template matching was performed with a single low-pass-filtered subvolume as an initial template (top). The resulting average (bottom) was used to initiate the second round of template matching, refining the average. Scale bar: 20 nm. (c) Translational symmetry of the final average (top) was measured by performing an autocorrelation of the volume (center). This translational repeat was then used to generate a final symmetrized average (bottom). The annotated 3D structure shows zipper-like interactions with clear asymmetry across the cisterna from *cis* to *trans* (*cis*-side and *trans*-side bilayers: light blue and yellow, respectively; luminal protein complexes: magenta, orange, blue, and green). (d) Heatmap displaying the protein array localization from template matching. The arrays clustered in “hot spots”, which were only found within the narrow central cisterna regions. Scale bar: 200 nm. (e) Histogram showing protein array orientations from template matching. Most arrays from two separate Golgi reconstructions (“tomogram 1” and “tomogram 2”) had the same preferred orientation, with larger luminal proteins projecting from the *cis*-side of the cisterna. (a), (d), and (e) are reproduced or modified from Ref. [16].

transiting the Golgi toward the bud sites at the cisterna periphery. Plotting the positions and orientations of the array-containing subvolumes in two tomograms revealed that all the arrays were asymmetric and most of them were facing the same direction (Fig. 4e). This observation has big implications for Golgi biology, as it indicates that the two membranes of the same cisterna have different compositions. The most promising putative candidates for the arrays are glycosyltransferases, which have compatible structures and have been shown to form homo-oligomeric and hetero-oligomeric complexes in the Golgi [128–131]. If the arrays are indeed composed of glycosyltransferases, the cooperative assembly of these proteins into higher-order structures may affect their enzymatic activity. While this study provided the first insights into intracisternal arrays and their possible biological functions, additional work is required to further characterize these structures and determine their molecular identity.

New Frontiers for Visual Proteomics

The functions of cellular complexes did not evolve in isolation. Thus, we believe that the holy grail of structural biology should be to directly observe molecular structures within their functional environments. Thanks to advances in sample preparation and cryo-ET, this vision is starting to become a reality. Although current studies have only examined a few types of macromolecules, extrapolating the *in situ* approach to its natural conclusion brings us to the concept of visual proteomics: the parallel identification and characterization of every molecular complex inside the cell. Visual proteomics is not a new idea [20,21,118], but until recently, researchers lacked the data quality and computational power to put this idea into practice. With continuing advances on both fronts, we are now approaching a convergence of cryo-ET and image analysis where it will be possible to determine the positions, conformations, and interactions of many macromolecules within a single cell through direct visualization [20,21].

What is possible when cell biology enters the age of visual proteomics? First and foremost, we may discover a new world of macromolecular and supramolecular structures, which have been missed by techniques that rely on biochemical purification or labeling of known proteins. We already see evidence that this may be the case, as the Golgi intracisternal arrays could only be identified by *in situ* cryo-ET. Visual proteomics will also mark the dawn of “big data” in EM. Cellular cryo-tomograms have exceptionally high information density. New computational tools will be required to effectively mine this information, revealing the relationships of every macromolecule with each other and with the local cellular environment.

In addition to advances in image processing, bioinformatic and statistical approaches may prove useful for building interaction networks from dense landscapes of visual information. This visual proteomic catalog will serve as rich source of experimental input for multi-scale modeling efforts that aim to bridge the cellular and molecular scales, explaining cellular phenomena by modeling the interplay of molecular complexes [132–134].

When the hardware and software of *in situ* cryo-ET become high throughput and readily accessible to the majority of researchers, we anticipate that this technique will be integrated into the core methodology of cell biology. Biochemistry provides many indirect ways to probe binary molecular interactions. However, while this approach can successfully dissect molecular function, it lacks cellular context and can be prone to artifacts, requiring *in vivo* validation. FM, with several recent advances in sub-diffraction-limit imaging, is invaluable for tracking the dynamics and spatial relationships of known proteins in living cells. However, this mode of visualization lacks molecular resolution and can only simultaneously examine a few specifically labeled molecular species. *In situ* cryo-ET complements both of these traditional approaches by providing a complete molecular-resolution view of every macromolecule within the unperturbed cellular environment.

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Abbreviations used:

cryo-ET, cryo-electron tomography; EM, electron microscopy; HPF, high-pressure freezing; FIB, focused ion beam; FM, fluorescence microscopy; RP, regulatory particle.

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