By linking a protein of interest into a dense, cross-linked network of a swellable polyelectrolyte hydrogel, biological specimen can be physically expanded allowing for magnified imaging with subdiffraction-resolution on conventional microscopes. Since its first introduction in 2015\cite{1}, expansion microscopy (ExM) has shown impressive results including the magnified visualization of pre- or post-expansion labeled proteins and RNAs with fluorescent proteins, antibodies, and oligonucleotides, respectively, in isolated organelles, cells, pathogens, tissues, and human clinical specimen\cite{2,3}. In addition, various protocols have been developed to anchor proteins or RNA into charged polyacrylamide hydrogels enabling expansion factors of up to 20-fold\cite{4,5}. Thus, ExM enables confocal diffraction-limited fluorescence imaging with spatial resolutions comparable to that of super-resolution microscopy methods. By careful optimization of the expansion protocol U-ExM demonstrated that even ultrastructural details of multiprotein complexes such as centrioles can be truthfully preserved\cite{6}. Combined with super-resolution microscopy methods such as STED and SIM, ExM provides a simple and efficient way for three-dimensional (3D) multicolor nanoscale imaging with 10-20 nm spatial resolution. In combination with single-molecule localization microscopy method such as dSTORM, ExM has the potential to approach the resolution of electron microscopy. However, current attempts to demonstrate ExM-dSTORM remained challenging because of protein and fluorophore loss during digestion or denaturation, gelation, and the incompatibility of expanded polyelectrolyte hydrogels with photoswitching buffers. I will summarize our recent efforts to track down the molecular architecture of the synaptonemal complex by ExM-SIM. Furthermore, I will show nanoscale imaging of cellular and bacterial membranes by ExM-SIM and finally show that ExM-dSTORM with post-expansion immunolabeling enables super-resolution imaging of endogenous proteins with minimal linkage error.