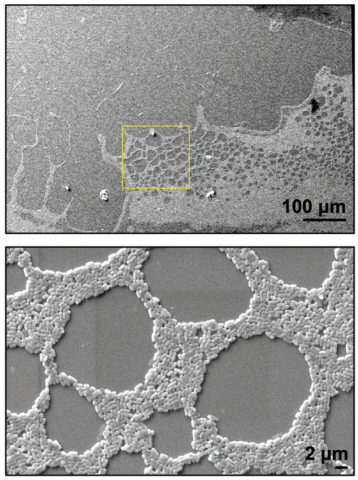
Highlights from Microscopy AND Microanalysis

Biological Applications

Structural Analysis of Gliding Motility of a Bacteroidetes Bacterium by Correlative Light and Scanning Electron Microscopy (CLSEM) by Devanshi Khare, Pallavi Chandwadkar, and Celin Acharya, *Microsc Microanal* | https://doi.org/10.1017/S1431927622000095.

We used correlative light and scanning electron microscopy (CLSEM) to illustrate dynamic spatial and temporal analysis of microbial processes by light microscopy, and ultrastructural details with scanning electron microscopy. CLSEM provided complementary information from the same region of interest at any fixed point in time. The members of the Bacteroidetes phylum move on the solid surfaces by gliding motility, leading to the formation of spreading colonies. We evaluated the structural features of the spreading colony edges in a uranium-tolerant Bacteroidetes bacterium, *Chryseobacterium* sp. strain PMSZPI, by CLSEM (Figure). We successfully acquired an optimal overlay/correlation of the light/fluorescence microscopy information of the cellular organization at the colony edges in the absence and presence of uranium. The rod-shaped cells at the colony edges were perfectly packed in hexagonal clusters, aligning with the neighboring cells, and formed regular lattice patterns. Subsequently, imaging of the correlated regions was done at higher resolution in the scanning electron microscope to obtain more comprehensive information.

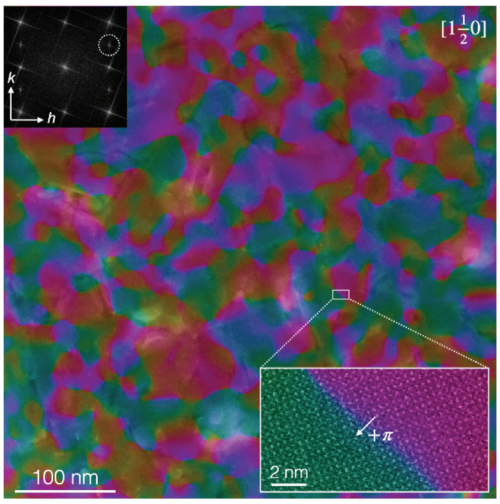


CLSEM of spreading colony edges of gliding *Chryseobacterium* PMSZPI in the presence of uranium. Overlay of LM and SEM images after correlation is shown (top). The yellow square (top) shows the area selected for higher-resolution imaging with SEM (bottom). The rod-shaped cells of PMSZPI appeared to be packed in regular lattices creating a "mesh"-like pattern.

Materials Applications

Disentangling Coexisting Structural Order Through Phase Lock-In Analysis of Atomic-Resolution STEM Data by BH Goodge, I El Baggari, SS Hong, Z Wang, DG Schlom, HY Hwang, and LF Kourkoutis, *Microsc Microanal* | https://doi.org/10.1017/S1431927622000125.

Phase demodulation analysis of atomic-resolution S/TEM images is a powerful way of visualizing crystalline lattice inhomogeneities such as defects and strain fields in real space. Many quantum materials, however, are described by complex and often coexisting structural order parameters, including not just the primary atomic lattice but also subtle structural distortions that form periodic superstructures. We demonstrate the extension of conventional geometric image phase analysis to secondary and superlattice frequency components beyond the primary lattice frequencies by a frequency lock-in method. Our technique is sensitive to phase slips and dislocations in superlattice order (for example, pm-scale antipolar displacements) even in regions of atomically pristine crystalline lattice (Figure). With the advantages of a Fourier-based technique, this method provides quantitative mapping of competing modes of atomic-scale superstructure order and disorder across mesoscale fields of view. This approach will enable direct visualization of the interplay between coexisting order parameters and provide new insights into the multiscale hierarchies of emergent phenomena in complex materials.



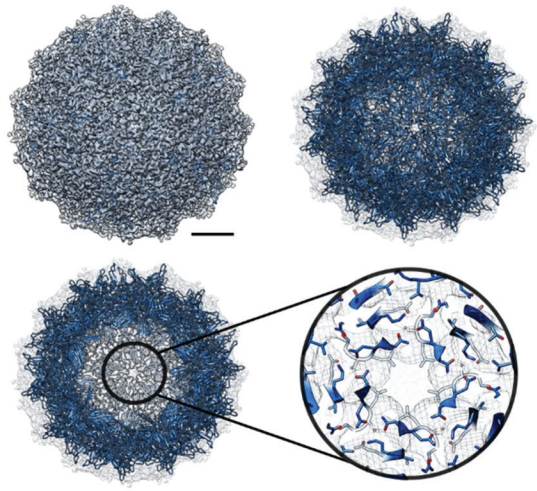
Phase lock-in mapping of the [1½0] superlattice peak describing antipolar displacements in a free-standing oxide membrane. Rich heterogeneity in the superlattice order can be observed across the 0.5 × 0.5 µm² atomic-resolution ADF-STEM image. The inset shows a region of pristine crystallinity with a discontinuity of the antipolar displacements identified by a π phase slip.

Microscopy AND Microanalysis

Techniques

Automated Tools to Advance High-Resolution Imaging in Liquid by GM Jonaid, MA Casasanta, WJ Dearnaley, S Berry, L Kaylor, MJ Dressel-Dukes, MS Spilman, JL Gray, and DF Kelly, *Microsc Microanal* | https://doi.org/10.1017/S1431927621013921.

Liquid-electron microscopy (Liquid-EM) is an exciting area in the materials imaging field providing unprecedented views of molecular processes. Time-resolved insights from Liquid-EM studies are a strong complement to the remarkable results achievable with other imaging techniques. Here, we describe opportunities to expand Liquid-EM technology by enhancing current practices with automated tools. Our results describe high-resolution structures of human viruses and individual proteins in liquid droplets by improving procedures for specimen preparation, data collection procedures, and computational processes. To develop these strategies, we used biological specimens relevant for drug delivery and the treatment of COVID-19. We also provide the first view of therapeutic protein candidates live in solution (Figure). Improving our understanding of the physical properties of macromolecules in a liquid state, as maintained in the human body, has broad societal implications for human health and disease. Major findings from this work entail insights for visualizing biological materials as well as quantifiable measures to assess their physical changes.



High-resolution structure of AAV determined from particles in solution. Slices through the AAV assembly with the atomic model (blue; pdb code, 3KIC, all chains) placed in the EM map (gray). A magnified region near the 5-fold axis shows some side chains present and distinct within the density. Scale bar = 5 nm.