CRYO ELECTRON MICROSCOPY
(ribosomes et al. as brownian particles)

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Introduction to high-resolution cryo-electron microscopy

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ABSTRACT

For many years two techniques have dominated structural biology – X-ray crystallography and NMR spectroscopy. Traditional cryo-electron microscopy of biological macromolecules produced macromolecular reconstructions at resolution limited to 6–10 Å. Recent development of transmission electron microscopes, in particular the development of direct electron detectors, and continuous improvements in the available software, have led to the "resolution revolution" in cryo-EM. It is now possible to routinely obtain near-atomic-resolution 3D maps of intact biological macromolecules as small as ~100 kDa. Thus, cryo-EM is now becoming the method of choice for structural analysis of many complex assemblies that are unsuitable for structure determination by other methods.

https://www.nobelprize.org/nobel_prizes/chemistry/laureates/2017/

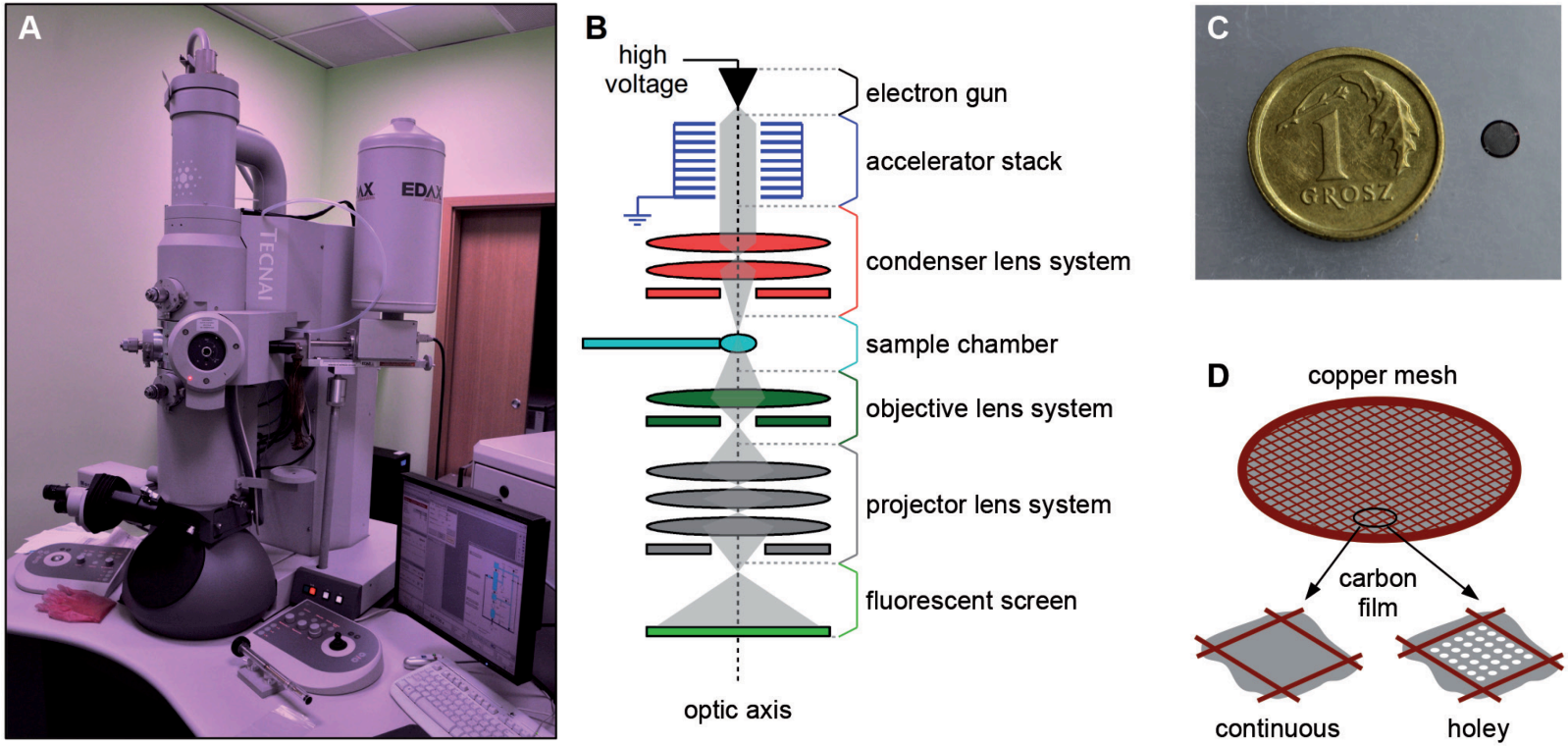
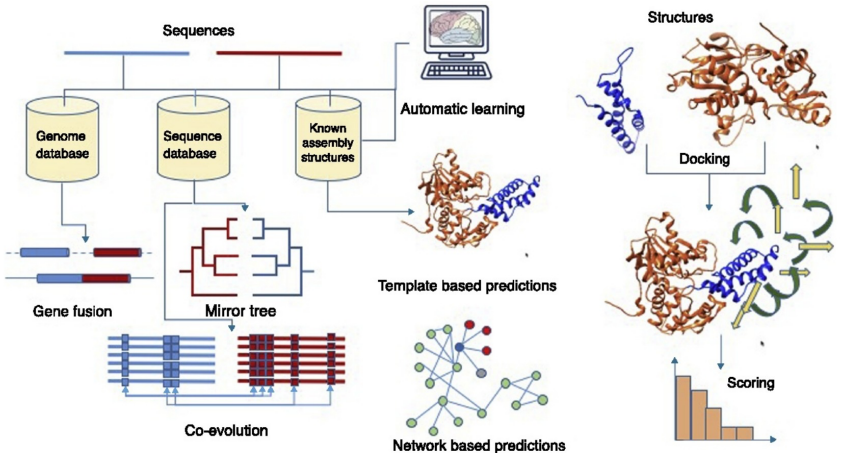


Figure 1. Transmission electron microscope and TEM grids. A. Tecnai 120 kV D1203 BioTwin microscope in the Department of Histology and Embryology, Medical University of Silesia, Zabrze, Poland. B. General layout of a transmission electron microscope. C. A picture of square mesh copper support TEM grid. D. Two types of carbon coating in TEM grids.

The computational prediction of protein assemblies

Anna Tramontano[1,2]

The function of proteins in the cell is almost always mediated by their interaction with different partners, including other proteins, nucleic acids or small organic molecules. The ability of identifying all of them is an essential step in our quest for understanding life at the molecular level. The inference of the protein complex composition and of its molecular details can also provide relevant clues for the development and the design of drugs. In this short review, I will discuss the computational aspects of the analysis and prediction of protein–protein assemblies and discuss some of the most recent developments as seen in the last Critical Assessment of Techniques for Protein Structure Prediction (CASP) experiment.



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