THE HISTORY OF CRYO-EM

1915 First 3D EM reconstruction; Taylor and Glaeser
1945 Vitrified cryo-EM specimen; Holmes et al.
1955 First EM micrograph of living cells; Reis et al.
1960 First EM image of a virus; Franklin
1968 First 3D EM reconstruction; DeRosier and Klug
1974 First EM image of the electron microscope; Taylor and Glaeser
1987 Cryo-EM for macromolecular cryoelectron microscopy; Schatz et al.
1992 Deep electron detection cameras; Frangakis and Frank
1997 Cryo-electron tomography; Frank
1999 Cryo-electron microscopy for macromolecular complexes; Scheres et al.
2007 Maximum-likelihood 3D software; Frank et al.
2015 Method of the Year by Nature Methods
2017 Novel EM camera; Frank
2019 Novel EM camera; Frank
2020 Novel EM camera; Frank
2020 Novel EM camera; Frank
2021 Novel EM camera; Frank

THE HISTORY OF HIV-1 gp120 Bound to Host Receptors, PDB 6MET

Dramatic improvements to cryogenic electron microscopy (cryo-EM) technology have led to new insights into how viruses infect human cells. An essential tool for structure determination, cryo-EM allows researchers to study the complex interactions that occur between the virus and the host cell. This technology is crucial for developing diagnostics, antibody therapeutics, and vaccines.

The determination of the spike protein atomic structure of the multimeric protein by cryo-EM in mid-February 2020. SARS-CoV-2 binds to host cells via a trimeric spike protein, which mediates the fusion of the virus membrane to the host membrane. Understanding the conformational changes that occur during these interactions and the role of CCR5 in fusing the virus to the host membrane is essential for developing diagnostics, antibody therapeutics, and vaccines.

Researchers have implicated the SARS 3a ion channel as a potential vaccine target. Using cryo-EM, scientists viewed how a small molecule inhibitor (yellow) binds to the human CAK (red and pink) antibodies binding the spike protein simultaneously. The cryo-EM structure helps in the development of vaccines and therapeutic target. Traditional structural analysis techniques such as ion channels; however, cryo-EM allowed researchers to visualize in captured raw images. From these imaged specimens are illuminated with high-energy electrons, the interaction of amino acid side chains, and the atomic termination of proteins to low-resolution structures that do not resolve the internal protein conformation, the atomic resolution, avoids ice crystal formation, and captures in their native state.

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Practical paths to accessing cryo-EM

Thermo Fisher Scientific offers the expertise to help you match the advantages of cryo-EM without making major investments. Our Cryo-EM Access program connects biopharma to world-class facilities where you can advance your research by trying out cutting-edge technologies.

Getting started in cryo-EM

Thermo Fisher Scientific is the world leader in solving structures by cryo-electron microscopy (cryo-EM). We offer comprehensive support to help you get started on your journey of structural biology.

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SOLVING STRUCTURES IN A FLASH

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REFERENCES

All structures made with ePMV. G.T. Johnson et al., "ePMV embeds molecular modeling into professional animation software environments," J Microsc, 124:3‑4, 1981.


