

Special Issue

Cryo-EM and Molecules: Current Progress and Perspective

Message from the Guest Editors

Electron microscopy (EM) is one of the oldest methods to determine protein structures and provide initial insights into the structures of large biomolecular complexes, such as ribosome and proteasome. The recent revolution of resolution in cryo-EM has tremendously enhanced our ability to examine the structures of large protein complexes in atomic details, which was a huge challenge or almost impossible using other conventional methods. The whole structural biology community has now shifted toward using cryo-EM to determine protein structure, resulting in the number of protein structures newly deposited in PDB databases by cryo-EM exceeding that by X-ray crystallography. This is truly the era of Renaissance in structural biology, and cryo-EM will continue to play a major role in investigating the mechanism of protein complexes. Furthermore, cryo-electron tomography (Cryo-ET) combined with other optical microscopic tools has begun to emerge as an excellent or maybe the sole tool to investigate protein structures in near-atomic resolution without taking proteins out of cells.

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Deadline for manuscript submissions

closed (30 April 2022)



International Journal of Molecular Sciences

an Open Access Journal
by MDPI

Impact Factor 4.9
CiteScore 9.0
Indexed in PubMed



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*International Journal of
Molecular Sciences*
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