International Journal of
Molecular Sciences

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Cryo-EM and Molecules: Current Progress and Perspective

Guest Editors:

Prof. Dr. Weontae Lee
Department of Biochemistry, College of Life Science and Biotechnology, Yonsei University, Seoul 03722, Republic of Korea

Prof. Dr. Ji-Joon Song
Department of Biological Sciences, Korea Advanced Institute of Science and Technology (KAIST), 291 Daehakro, Daejeon 34141, Korea

Deadline for manuscript submissions:
closed (30 April 2022)

Message from the Guest Editors

Dear Colleagues,

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 a was 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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Editor-in-Chief

Prof. Dr. Maurizio Battino
Department of Odontostomatologic and Specialized Clinical Sciences, Sez-Biochimica, Faculty of Medicine, Università Politecnica delle Marche, Via Ranieri 65, 60100 Ancona, Italy

Message from the Editor-in-Chief

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Journal Rank: JCR - Q1 (Biochemistry and Molecular Biology) / CiteScore - Q1 (Inorganic Chemistry)

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International Journal of Molecular Sciences Editorial Office
MDPI, Grosspeteranlage 5
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