Special Issue

Molecular Studies of Microbial Communities

Message from the Guest Editor

Species within the kingdoms Archaea, Bacteria, and Fungi are ubiquitous in nature. They fulfil key environmental functions related to nutrient cycling, have beneficial to pathogenic associations with other macroscopic organisms, and thrive in habitats devoid of macroscopic life, such as hot acidic springs. Unfortunately, most microorganisms are unculturable using current laboratory techniques, a fact that has slowed the pace of research. However, due to the advancements in molecular sequencing and big data processing, it is now possible to investigate the unculturable microbial communities and their relationships to other organisms using environmental sequencing techniques. Using these methods, researchers can identify shifts in community structure, species composition, and investigate species distributional patterns among others. Therefore, this Special Issue focuses on using molecular techniques, including environmental sequencing, to uncover the microbial diversity associated with animals, insects, plants, and other environmental habitats. Manuscripts that focus on archaeal, bacterial, and fungal communities are welcome.

Guest Editor

Dr. Daniel B. Raudabaugh
Department of Botany and Plant Pathology, Purdue University, 500 Oval Dr, West Lafayette, IN 47909, USA

Deadline for manuscript submissions

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International Journal of Molecular Sciences
Editorial Office
MDPI, Grosspeteranlage 5
4052 Basel, Switzerland
Tel: +41 61 683 77 34
ijms@mdpi.com

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The *International Journal of Molecular Sciences* (*IJMS*) is an open access journal, which was established in 2000. The journal aims to provide a forum for scholarly research on a range of topics, including biochemistry, molecular and cell biology, and molecular biophysics. *IJMS* publishes both original research and review articles, and regularly publishes special issues to highlight advances at the cutting edge of research. We invite you to read recent articles published in *IJMS* and consider publishing your next paper with us.

Editor-in-Chief

Prof. Dr. José L. Quiles
Department of Physiology, Institute of Nutrition and Food Technology
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Avda. Conocimiento s/n, 18100 Armilla, Granada, Spain

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