

Special Issue

Metagenomics: New Trends and Solutions: 2nd Edition

Message from the Guest Editors

Metagenomics has shown significant progress in describing microbial communities from a great variety of environments. It can reveal pathogenic or biotechnologically relevant strains among harmless bacteria of the same species using alignment-free computational approaches. Genome-resolved metagenomics yields complete genomes of so far uncultured bacteria and yet unstudied phages, as well as deciphers genetic mobility and metabolic interactions within complex communities. Novel computational approaches allow for efficient reconstruction of patterns of microbial consortia development in the historical aspect, including propagation of phage infections or pathogen outbreaks. A particularly intriguing emphasis in metagenomics is connected with mutual events of transcript-based signaling and regulation between particular microorganisms in complex communities, as well as between prokaryotes and their hosts. Yet, novel directions of investigations and methodological approaches are emerging and there are many more to come. We encourage the authors to submit results in the already traditional fields and, especially, pioneering investigations that lay groundings for cutting-edge topics.

Guest Editors

Dr. Olga Ozoline

Institute of Cell Biophysics, Russian Academy of Sciences, Moscow 142290, Russia

Dr. Konstantin S. Shavkunov

Institute of Cell Biophysics of the Russian Academy of Sciences, Pushchino Scientific Center for Biological Research RAS, Pushchino, Russia

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Editor-in-Chief

Prof. Dr. Lluís Ribas de Pouplana

Institute for Research in Biomedicine (IRB Barcelona), The Barcelona
Institute of Science and Technology, 08028 Barcelona, Spain

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