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Microbiome Analysis Techniques and Discovery

Guest Editor:

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Deadline for manuscript submissions:
closed (25 March 2024)

Message from the Guest Editor

Dear Colleagues,

Metagenomics sequencing has evolved in pace with developments in next-generation sequencing and bioinformatic analysis. The identification of microbes at the genus and species level is achieved from environmental samples. In this Special Issue, we would like to put emphasis on currently established microbiome sequencing and analysis techniques such as the shotgun sequencing of DNA or RNA, metataxonomics (16S/18S/Internal Transcribed Spacer sequencing), and meta-transcriptomics (mRNA sequencing). Moreover, third-generation sequencing techniques with long-read sequencing approaches are also of novel interest. Finally, databases also play an important role for new and reusable sequencing data, enabling more robust comparative genomic and integrative functional studies.

The Earth Microbiome Project (EMP) is an ongoing global effort, with PathoMap or MetaSUB initiatives amongst others. We invite submissions of original research and methodological papers in the form of articles, communications, and perspective and review papers.

Dr. Christopher E. Mason
Guest Editor

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Editor-in-Chief

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Message from the Editor-in-Chief

Genes are central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fastmoving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised.

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