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Advanced Research on Mitochondrial Genome

Guest Editor:

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Message from the Guest Editor

The expansion of high-throughput sequencing into the life sciences, together with the diminishing costs of short-read sequencing, explains why complete or nearly complete mitochondrial genomes are quickly and steadily becoming markers of choice for the examination of within-species population structures and among-species phylogenetic relationships. The accurate assembly, in silico annotation, manual curation, and detailed characterization of mitochondrial genomic features is highly relevant for phylomitogenomic and many other downstream analyses. The present Special Issue of the journal *Genes*, entitled “Advanced Research on Mitochondrial Genome”, will host articles in which the authors provide an accurate and detailed characterization of mitochondrial genomes from a wide variety of marine, freshwater, and terrestrial vertebrate and invertebrate animals. Studies that provide an accurate assembly of mitochondrial genomes and a detailed characterization of their features will result in relevant biological insight.



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Special Issue



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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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