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## **Advances in Ancient Genomes**

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Deadline for manuscript submissions:

closed (15 January 2024)

## **Message from the Guest Editors**

Dear Colleagues,

In recent years, the rapidly increasing advancements of next-generation sequencing (NGS) technologies have revolutionized our approach to ancient DNA research. Much research has contributed to overcoming earlier limitations, including the degradation and preservation of endogenous ancient DNA molecules, as well as the contamination by modern DNA. With the technological improvements regarding the capacity of recovery and the analysis of the ancient molecules, it is now possible to retrieve complete genomes from fossil remains or even sediment. Palaeogenomics offers a high-resolution means to uncover long-standing issues of confusion. Ancient genomes are providing a more comprehensive and a more complete perspective on the evolutionary history of modern and extinct species. This Special Issue will collect reviews and original contributions concerning the study of advances in ancient genomes of different organisms, considering accomplishments and challenges, methodological approaches, bioinformatics and analytical tools, and the current status and future prospects of paleogenomic research.













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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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