



genes



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Hox and TALE Gene Function in Evolution, Development, and Disease

Guest Editor:

Message from the Guest Editor

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Deadline for manuscript
submissions:

closed (20 May 2023)

The family of evolutionarily highly conserved Hox genes, since their discovery almost 40 ago, has attracted, and continues to attract, much interest. This is not only because of the crucial role played by this unique gene family in the development of the main body axis of essentially all studied animal species, but also its involvement in a number of human disorders, ranging from genetic diseases to cancer.

We aim to cover the most recent progress in the study of the function Hox genes and of their close partners, the TALE homeobox genes. Thus, contributions describing advances in our understanding of the regulation of Hox and/or TALE gene expression, of the transcriptional regulation by Hox and/or TALE proteins, of post-transcriptional mechanisms affecting Hox and/or TALE gene function that involve non-coding RNAs (miRNAs, lncRNAs), and of epigenetic regulatory mechanisms controlling Hox and/or TALE expression, from an evo–devo perspective and/or in developmental or disease processes, are all welcome.

Contributions can be in the form of research articles, reviews, and the description of new methodologies, including mathematical models.



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Special Issue



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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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