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Evolution of Epigenetic Mechanisms and Signatures

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submissions:

closed (31 August 2020)

Message from the Guest Editors

Many mechanisms have been elucidated governing genome activity regulation at the levels of chromatin organization, the transcription of DNA, RNA stability and translation. These include but are not limited to DNA methylation and hydroxymethylation; histone modifications; and various types of non-coding RNAs like circular RNAs, small interfering RNAs, and micro RNA machinery. Numerous applications have been found in fundamental studies, bioengineering, and molecular diagnostics.

Many epigenetic mechanisms have been investigated in detail in such biologically distinct objects as mammals (human, mouse), teleosts (zebrafish), insects (drosophila), nematodes (*C.elegans*), and plants (*Arabidopsis*). This has been immensely enhanced by the recent progress in massive parallel screening technologies such as next-generation sequencing and modern proteomic approaches. In this Special Issue, the authors are invited to submit all formats of manuscripts dealing with the evolutionary aspects of epigenetic mechanisms. Both bioinformatic and experimental research papers and reviews will be accepted.



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Special Issue



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Cells has become a solid international scientific journal that is now indexed on SCIE and in other databases. We have successfully introduced a special issues format so that these issues serve as mini-forums in specific areas of cell science. *Cells* encourages researchers to suggest new special issues, serve as special issues editors, and volunteer to be reviewers. Our main focus will remain on cell anatomy and physiology, the structure and function of organelles, cell adhesion and motility, and the regulation of intracellular signaling, growth, differentiation, and aging. We are open to both original research papers and reviews.

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