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Domain Organization of the Genome - from Random Neighborhood to Joint Regulation

Guest Editor:

Dr. Tatyana D. Kolesnikova

Institute of Molecular and Cellular Biology, Siberian Branch of Russian Academy of Sciences, Novosibirsk 630090, Russia

Deadline for manuscript submissions:

closed (20 July 2021)

Message from the Guest Editor

The genomes of higher eukaryotes are highly heterogeneous in nucleotide composition and gene density. Based on analysis of the distribution of chromatin proteins, the genome can be divided into discrete chromatin types. There is also a tendency for the majority of housekeeping genes to lie in the domains of permanently open chromatin and form clusters of permanently active genes, while tissue-specific genes more often lie in closed domains and open chromatin locally where they are expressed.

In this issue, I propose to publish works devoted to the study of different types of genome clustering into domains with different properties. I am particularly interested in papers that discuss the mechanisms of boundary formation between domains and the importance of these boundaries for the correct regulation of gene expression. A very intriguing subject is the evolutionary direction, which shows how important such clustering is for the regulation of individual genes, and how the regulation of genes changes when they enter new conditions.



mdpi.com/si/67967

Special Issue



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Editor-in-Chief

Prof. Dr. Selvarangan Ponnazhagan

Department of Pathology, The University of Alabama at Birmingham, 1825 University Blvd, SHEL 814, Birmingham, AL 35294-2182, USA

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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Genes Editorial Office
MDPI, Grosspeteranlage 5
4052 Basel, Switzerland

Tel: +41 61 683 77 34
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