



BBA GENE REGULATORY MECHANISMS

One of the ten topical journals of [BBA](#)

AUTHOR INFORMATION PACK

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DESCRIPTION

BBA Gene Regulatory Mechanisms includes reports that describe novel insights into **mechanisms** of transcriptional, post-transcriptional and translational **gene regulation**. Special emphasis is placed on papers that identify **epigenetic mechanisms** of gene regulation, including chromatin, modification, and remodeling. This section also encompasses mechanistic studies of regulatory proteins and protein complexes; regulatory or mechanistic aspects of RNA processing; regulation of expression by small RNAs; genomic analysis of gene expression patterns; and modeling of gene regulatory pathways. Papers describing gene promoters, enhancers, silencers or other regulatory DNA regions must incorporate significant functions studies.

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Biochemists, Molecular Biologists, and Geneticists

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Chromatin; nucleosome dynamics; transcription; DSB repair

Mark Parthun, Columbus, Ohio, USA

Epigenetics, Histone modifications, histone transport across the nucleus, Mass Spec analysis

Giovanni Perini, Bologna, Italy

Myc oncoproteins; Transcriptional repression; Epigenomics. Neuronal tumors; Transcriptome profiling

José Reyes, Sevilla, Spain

Epigenetics; Chromatin remodelling; Nucleosome positioning; Histone methylation; Transcription elongation

Karel Riha, Vienna, Austria

telomeres; DNA repair; meiosis

Stefan Roberts, Buffalo, New York, USA

Transcription; Core promoter; Tumor suppressor; Oncogene

Michael Schultz

transcription, chromatin, DNA damage response, metabolic regulation, yeast

Ed Seto, Washington, Washington, USA

Histone Deacetylase; Protein Acetylation; Protein Deacetylation; Gene Regulation

Yosef Shaul, Rehovot, Israel

transcription, DNA damage, gene therapy, tumor suppressors, and molecular mechanisms of virus host-cell interaction.

Wen-Hui Shen, Strasbourg, France

Plant biology, histone methylation, histone ubiquitylation, histone chaperones

Ravindra Singh, Ames, Iowa, USA

Yanming Wang, University Park, Pennsylvania, USA

David Wassarman, Madison, Wisconsin, USA

Transcription, splicing, alternative splicing, chromatin, Drosophila

Carol Wilusz, Fort Collins, Colorado, USA

mRNA stability, myotonic dystrophy, mRNA methylation, pluripotent stem cells, RNA-binding protein, post-transcriptional control

John Wyrick, Pullman, Washington, USA

Genome-wide mRNA levels in histone, mutant strains, Analysis of global protein-DNA interactions, bioinformatics software (to analyze microarray data), functional genomic tools

Rui-Ming Xu, Beijing, China

Epigenetics, chromatin structure, RNA processing, protein-RNA interactions, structural biology.

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BBA Gene Regulatory Mechanisms includes reports that describe novel insights into mechanisms of transcriptional, post-transcriptional and translational gene regulation. Special emphasis is placed on papers that identify epigenetic mechanisms of gene regulation, including chromatin, modification, and remodeling. This section also encompasses mechanistic studies of regulatory proteins and protein complexes; regulatory or mechanistic aspects of RNA processing; regulation of expression by small RNA's; genomic analysis of gene expression patterns; and modeling of gene regulatory pathways. Papers describing gene promoters, enhancers, silencers or other regulatory DNA regions must incorporate significant functions studies.

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Reference to a book:

[2] W. Strunk Jr., E.B. White, *The Elements of Style*, fourth ed., Longman, New York, 2000.

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[3] G.R. Mettam, L.B. Adams, How to prepare an electronic version of your article, in: B.S. Jones, R.Z. Smith (Eds.), *Introduction to the Electronic Age*, E-Publishing Inc., New York, 2009, pp. 281–304.

Reference to a website:

[4] Cancer Research UK, Cancer statistics reports for the UK. <http://www.cancerresearchuk.org/aboutcancer/statistics/cancerstatsreport/>, 2003 (accessed 13.03.03).

Reference to a dataset:

[dataset] [5] M. Oguro, S. Imahiro, S. Saito, T. Nakashizuka, Mortality data for Japanese oak wilt disease and surrounding forest compositions, *Mendeley Data*, v1, 2015. <https://doi.org/10.17632/xwj98nb39r.1>.

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