Welcome to *Epigenomics*

*"*Epigenomics *will report on major challenges ahead and critical advances that are propelling research forward and further our understanding of the biological processes governed by epigenetic modifications".*

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We, as the senior editors of *Epigenomics*, are delighted to present you with the first issue of this new exciting journal that will focus on many of the various facets of epigenomics, one of the most rapidly advancing fields in biological and medical research.

Aims & scope of *Epigenomics*

With the availability of the reference sequence for human and many model organisms that heralded the post-genomic era, it has become increasingly clear that it is not the DNA sequence alone that determines the cellular phenotype. Epigenetic modifications add additional layers of information to the bare genomic sequence thereby dramatically extending the information potential of the genetic code. They permit cells to respond to certain internal as well as environmental cues and confer phenotypic plasticity. The field of epigenomics has gained great momentum in recent years and it has become clear that epigenetics plays a key role in normal development as well as in disease. The elucidation of the underlying molecular mechanisms is progressing at an unprecedented speed, but much remains to be discovered and understood. Each discovered part of the puzzle contributes to the insight that the gene regulatory network created by epigenetic modifications is much more complex than previously anticipated. However, epigenomics is beginning to generate a new understanding of the major role played by epigenetic changes in development and cell differentiation. This rapidly increasing knowledge holds the great promise of transforming our understanding of the major common diseases and opens up exciting new perspectives for tackling the big challenge of individualized patient management and treatment.

Epigenomics is an internationally peer-reviewed journal that focuses on all aspects of epigenetic research, spanning across the advances on the understanding of the molecular processes of epigenetic modifications such as DNA methylation, histone modifications and how small RNAs are involved in such as transcriptional regulation, cell differentiation and DNA replication and repair; effects of metabolic or environmental factors on persistent changes in the epigenome that might contribute to phenotypic variability or influence disease susceptibility. *Epigenomics* will report on and critically examine existing and upcoming technologies to enable innovation and evolution for epigenetic research. *Epigenomics* provides a critical overview of the latest and most significant advances in the search for epigenetic biomarkers and explores their potential application in the clinical setting. Innovative epigenetic therapies for diseases including antineoplastic treatment options will be a further focus of the journal. *Epigenomics* will report on major challenges ahead and critical advances that are propelling research forward and further our understanding of the biological processes governed by epigenetic modifications. The journal – currently published in six issues annually – delivers this information in concise, at-a-glance article formats – invaluable to a time constrained community.

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Epigenomics: a journal for the community

Epigenomics provides a forum to address the rapidly progressing research developments in this ever-expanding field. For this task, *Epigenomics* is highly fortunate to be served by an international editorial board drawn from the leading

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forces in research and development, whose diligence and discernment in the review process will greatly contribute to its success. The editorial board will coach the development of the journal and ensure a content of the highest quality, but the direction of the journal will also depend on the feedback that we hope to receive from our readers. We seek your expert input to learn what type of manuscripts and topics are the most beneficial to you, and those items that you feel are of less importance. This information helps to direct the board on what type of manuscripts we should actively solicit and topics on which we should focus. *Epigenomics* welcomes your submissions of research articles, reviews , special reports and perspectives in all areas of epigenomics. *Epigenomics* will also feature interviews with leading figures from both academy and industry and profile institutions and laboratories that focus on epigenetic research.

Why publish in *Epigenomics*?

The professional in-house editorial team of *Epigenomics* will accompany authors from submission to publication and inform authors regarding the status of the manuscript. All submitted articles will be subjected to rigorous and constructive peer review by at least three independent referees. The journal will make every effort to ensure a rapid publication in this competitive field of research (8–10 weeks from submission to acceptance). It should be noted that *Epigenomics* does not impose any page or submission fees. *Epigenomics* is published by Future Medicine Ltd (London, UK) renowned for its collection of journals providing healthcare practitioners and research professionals with a unique source of objective, cutting-edge information on exciting trends emerging in the light of advances in molecular medicine and clinical practice. Authors will benefit from excellent service from the editorial office during the entire publication process, the highest quality editing and reproduction, a professional and engaging layout, and a broad visibility of their research.

In this issue...

While the articles in this inaugural issue of *Epigenomics* deal with very different topics, it becomes evident from each of these contributions that the field of epigenomics is advancing at incredible speed and that this revolution of the field brings discoveries and possibilities, undreamed of only a very short time ago, but possibly also frightening to some people. *Epigenomics* is trying to contribute to the dissemination of this diversified and rapidly changing field of biomedical research that has profited from the development of new technologies, such as massively parallel sequencing technologies or the Illumina Infinium® epigenotyping chip, the latter described in the technology report by Marina Bibikova *et al.* [1]. Technologies have always advanced scientific discovery. The editorial by Clive Brown describes how new sequencing technologies have already revolutionized the field of epigenomics and we get a glimpse at the near-future development of third generation sequencers that will not only further increase sequencing capacity, but will also permit the direct detection of 5-methylcytosine in addition to the regular four bases of the genome [2]. A crucial issue in the near future is to develop infrastructures capable of mapping epigenetic modifications in different tissues and at different developmental stages, provide sophisticated bioinformatic support and to integrate the epigenomic data with genomic and transcriptomic information to decipher regulatory pathways and identify disease associated molecular changes. Two large epigenomic centers, the USC Epigenome Center (CA, USA) [3] and the Center for Epigenomics at Einstein (NY, USA) [4], created for this purpose are profiled in this inaugural issue of *Epigenomics*. The Center for Epigenetics at John Hopkins (MD, USA) is currently headed by Andrew Feinberg with whom you find a fascinating interview in this issue of *Epigenomics* where you learn how slime molds can bring you to genome-wide methylation scans at the epidemiological level in schizophrenia [5].

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It is, however, not always obvious how the number of differentially methylated loci identified in genome-wide scans can be used in clinical practice. At the moment, only a very few DNA methylation based biomarkers have been implemented in clinical practice. The review on biomarker development by Christoph Bock provides some guidelines and bioinformatic tools that might help to accelerate the process through the prioritization of candidate genes and automated optimization of assay [6]. One common way to assess the functional importance of genes identified in genome-wide studies as inactivated

by genetic or epigenetic modifications is the use of mouse models. The editorial by Randy Jirtle points out that this strategy may need to be revised as large differences in functional assays and therapeutic interventions are observed between mice and man [7]. This might be owing to different epigenomic environments in organisms and he reminds us that the 'proper study of mankind is man'.

In the very first research article of *Epigenomics,* Charles Caldwell and colleagues profile genome-wide methylation patterns in patients with B-cell chronic lymphocytic leukemia displaying variable expression levels of CD38 and identify some loci where DNA methylation patterns correlate with high or low CD38 expression [8]. This might spur further investigation in patient subgroups for the specific therapeutic reversal of these modifications. We would very much like to see many more excellent research articles such as the one in this issue and encourage you to submit your work to *Epigenomics*.

> *"Although epigenetics/epigenomics has been a rapidly advancing field of research in the past two decades, it is still in its infancy and many discoveries are still to be made."*

In recent years, we have come to understand much about the dynamic nature of epigenetic states, previously believed to be rather static. Epigenetic reprogramming is most prominent during early embryonic development and in primordial germ cells. Our current knowledge about these processes is reviewed by Michael Weber and colleagues [9]. Epigenetic modifications also provide the long term memory of a cell in response to physiological signals that are accumulated and dynamically modified during the entire life span of an organism. Epigenetics might thus also provide a biological memory for social exposure and 'behavioral interventions might lead to biochemical consequences' as pointed out in the thought-provoking editorial by Moshe Szyf [10]. The current knowledge about the interplay between environmental signals and epigenetic alterations leading to fine tuned interindividual differences in behavior, cognition and physiology is reviewed by Judy Sng and Micheal Meaney in this issue of *Epigenomics* [11]. The environmental signals perceived by the cells and memorized in the epigenome might not only have consequences for the organism during its life, but might also be transmitted to their offspring as a number of environmental factors and toxicants have the ability to modify epigenetic reprogramming at critical developmental periods as reviewed in the contribution by Michael Skinner and Carlos Guerrero-Bosagne [12].

Although epigenetics/epigenomics has been a rapidly advancing field of research in the past two decades, it is still in its infancy and many discoveries are still to be made. We hope you enjoy these and the other contributions in the first issue of *Epigenomics* and very much welcome your input and feedback for future features and articles.

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