Development of the heart and its error-free operation throughout the life of an animal are subjects of intense research. Biomedical researchers and clinicians employ a number of methodologies and tools to study gene expression and regulation in cardiac cells and tissues. ‘Cardiac Gene Expression: Methods and Protocols,’ is a comprehensive compilation of various experimental and in silico methods relating to cardiac gene expression. It is part of the Humana series of volumes in ‘Methods in Molecular Biology,’ and clearly and meticulously examines these methods to explore the underlying theories of cardiac development and function. A number of experts have contributed towards an efficient and effective delivery of the concepts, protocols and tools. The book is well organized and covers most of the salient features of cardiac gene expression in an easily readable format. References are provided in each chapter for the reader to access research findings relevant to the discussion.

The book is organized into six parts: Cardiac Gene Expression (Part I), Cardiac Gene Regulation (Parts II and III), In Silico Assessment of Regulatory cis-Elements and Gene Regulation (Part IV), Cardiac Single Nucleotide Polymorphisms (Part V) and Gene Overexpression and Targeting in the Myocardium (Part VI). There are a total of 20 chapters in the book written by experts in the cardiac gene expression arena. Each part has a varying number of chapters under a unifying theme describing diverse protocols and methods. Most chapters are laid out in a uniform format with sections of Introduction, Materials, Methods and Notes. The Notes section strengthens this compilation as it imparts the authors’ wisdom through ‘short cuts’ and ‘warnings’ that are not explicitly mentioned in the protocols.

Part I provides a global perspective to cardiac gene expression protocols with chapters on microarray analysis using the Affymetrix GeneChip probes, serial analysis of gene expression (SAGE) library construction, cDNA subtractive hybridization for functional genomics and statistical methods employed on microarray data. Although there is some overlap in the material covered in different chapters, the description of the methodologies is extremely detailed and highly thorough. Besides the wet laboratory protocols, tools for the computational analysis of data are also well documented. Parts II and III discuss cardiac gene regulation from the mRNA measurement (Part II) and promoter characterization (Part III) angles. In Part II, chapters pertaining to quantification of mRNA using reverse transcription PCR, quantitative real time PCR and RNase protection assay along with mRNA/DNA localization by in situ hybridization are dealt with extremely well. Chapters on the use of gel mobility shift assays for characterizing cis and trans elements in transcriptional regulation, primer extension analysis and RNase protection assay for transcriptional start site identification and characterization of cardiac-specific promoters with reporter constructs are included in Part III. Unfortunately, there is only cursory coverage of in silico tools for the identification of transcription factor (TF) binding sites and no discussion of chromatin immunoprecipitation followed by promoter array analysis (ChIP-on-chip). A discussion of the latter topic would have been timely and useful, since this technique helps identify target genes that are binding to and transcriptionally activated or repressed by a given TF in a physiological setting.

Computational methods and tools to study cardiac gene regulation are described in Part IV, with a chapter on comparative genomics and a second on developing computational resources particularly with respect to constructing the Human Cardiac Gene Expression Knowledge Base (CaGE). The comparative genomics topic is covered in a fairly thorough
fashion with discussion of databases and tools, such as the comparative genomic browsers, rVISTA etc. and strategies for successful phylogenetic shadowing. Although a few Perl scripts are shown as examples of data extraction from online public domain databases, there is no in-depth discussion of data integration issues in the second chapter. This is disappointing, because the authors could have covered open source mechanisms such as BioPerl and distributed annotation servers (DAS) in this chapter. In Part V, an excellent discussion on mathematical modelling of metabolic networks in the context of assessment of SNPs involved in perturbing one or more of the components, and a description of the MALDI-TOF MS method for SNP discovery are presented. Here, readers could have benefited from a chapter on genome-wide association studies that identify variations in the human genome related to disease phenotypes. The final part, Part VI, is the most biomedically relevant, since it includes chapters on the over expression and targeting of genes in the heart. There are chapters on the conditional targeting of cardiac specific genes using the Cre recombinase to create transgenic mice and the isolation of neonatal rat ventricular cardiomyocytes. The last two chapters in this part delve into adeno-associated virus (AAV) and lentivirus as a delivery vehicle for genes into cardiomyocytes and the rodent heart.

This book could be employed as an excellent laboratory resource by graduate students, fellows and clinical and basic science researchers studying gene expression and regulation in cardiac cells and tissues. Its contents are laid out in a thorough and straightforward style and the coverage of topics is fairly exhaustive. Most chapters are highly detailed in explaining the experimental protocols (or in silico methods) and point out the intricacies and difficulties inherent in them. Though some additional information could make this book stronger, I highly recommend it as an essential handbook for research methods in cardiac gene expression.

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