
Preface

Research in stem cell biology has generated immense interest recently due to the potential of stem cells to treat human diseases such as neurodegenerative disease, cardiovascular disease, and cancer. Advancements in stem cell research aid our understanding of genetics and developmental biology, and, because stem cells have the ability to repopulate tissues, there is an expectation that stem cells research will translate into clinical therapies. However, much work is required to understand the underlying transcriptional programs of stem cells that promote self-renewal vs. differentiation. Investigating how epigenetic and transcriptional landscapes are patterned in stem cells and committed lineages will provide insight into how these features regulate unique cellular expression programs during development, and contribute to the diverse cellular repertoire that exists in mammals. Next-generation sequencing technologies have recently been used to survey global expression and protein–DNA binding interactions at nucleotide resolution in stem cells. Use of these emerging technologies has shed light on stem cell transcriptional networks that define primitive vs. committed epigenetic landscapes. Moreover, recent advancements in reprogramming and transdifferentiation have armed stem cell biologists with additional tools to develop solutions for regenerative medicine purposes. The aim of this volume is to provide a resource for biologists to interrogate stem cell transcriptional networks.

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Methods and Protocols

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