
Preface

Cells respond to environmental cues through a complex and dynamic network of signaling pathways that normally maintain a critical balance between cellular proliferation, differentiation, senescence, and death. One current research challenge is to identify those aberrations in signal transduction that directly contribute to a loss of this division-limited equilibrium and the progression to malignant transformation. The study of cell-signaling molecules in this context is a central component of cancer research. From the knowledge of such targets, investigators have been able to productively advance many insightful hypotheses about how a particular cancer cell may misinterpret, or respond inappropriately to, growth regulatory cues in their environment. Despite these key insights, the rapidly evolving nature of cell signaling research in cancer has necessitated a continuous revision of these theoretical constructs and the updating of methods used in their study. One contemporary example of the evolution of this field is provided by an analysis of the Human Genome Project data, which reveal a previously unsuspected diversity in the multigene families encoding for most signaling pathway intermediates. In assessing the usefulness of a particular methodological approach, therefore, we will need to keep in mind that there is a premium on those protocols that can be easily adapted for the analysis of multiple members within a gene family. *Cancer Cell Signaling: Methods and Protocols* brings together several such methods in cell signaling research that are scientifically grounded within the cancer biology field. The first part of this volume is generally concerned with methods and techniques for the investigation of apoptosis and cell death. The second part contains a complementary set of protocols for manipulating and/or monitoring oncogenic signals in cancer cells. In the third, methods for studying protein–protein interactions are covered. Finally, in part four, there is a detailed protocol for capturing pure samples of malignant cells from frozen tissue specimens and two alternative techniques for analyzing their genomic DNA.

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