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# Preface

Phosphorylation is recognized as one of the most prevalent and versatile means to regulate protein function. Alteration in the normal target protein phosphorylation state is also established as a major contributor to disease and, as a consequence the enzymes that add a phosphate group to proteins, the protein kinases, are considered the second largest drug target of the pharmaceutical industry. Given the role of protein kinases, it is natural to think then that the enzymes that remove phosphate from proteins are equally important and thus are likely contributors to disease when functioning aberrantly. The acceptance of the protein phosphatases as equal in importance to protein kinases and as potential drug targets has been slow in coming. Nevertheless, a number of important research articles over the last few years have dramatically shifted this paradigm [for instance see, MacKeigan et al. *Nat. Cell Biol.* 7(6):591–600]. With a growing interest in protein phosphatase function, *Protein Phosphatase Protocols* represents a timely revisit to phosphatase methodologies.

I have tried to assemble a series of articles covering a broad range of protein phosphatase methodologies (proteomics, genomics, biochemistry, RNAi and genetics) with examples from several model organisms, including yeast, *Drosophila*, plant and human cells. By including a variety of approaches across many organisms, I was able to get contributions from many of the leading and emerging protein phosphatase researchers from around the world, but at the same time this meant that many were unable to contribute to this volume. Undoubtedly, research by other phosphatase laboratories is referenced within many of these chapters. I hope that the techniques explained here generate ideas on new approaches to protein phosphatase research in your laboratory.

***Greg Moorhead***