# Preface

NIH Director Elias Zerhouni, speaking at the annual meeting of the Association of American Medical Colleges in late 2002, addressed the need for the development of new and revolutionary research tools to understand complex biological systems that can then be applied to cure diseases. "Among revolutionary methods of research, we need to accelerate proteomics and large-scale technology for the postgenomic era," he noted, reminding the audience that sequencing the genome is essentially only "getting the parts list."

It was in this spirit of enthusiasm that the groundwork for this volume was begun earlier that year, by selecting well-recognized authors, who have contributed mightily to the field of proteomics, and identifying areas of interest and potential growth that could lead to a useful methods handbook.

*Proteomics,* as a word and as a discipline, is new to most of us and we expect that many will find this volume a useful dictionary for understanding the work of others as well as a map for setting out on our own research programs. From the start, it was our goal to produce a volume that would be valuable both to the neophyte and the seasoned worker. We encouraged the authors to include hints and tricks that might not be obvious in those original publications that did not describe the procedure in the detail reported here.

This editor, who marveled at the speed that the human genome was sequenced, realized that he was looking only at the blueprint for the Taj Mahal, not seeing a photo, much less actually having an experience in Agra. The beauty of the detail is the study of Proteomics.

The editor wants to thank the authors for interrupting their busy schedules to participate in this important project and the publisher for recognizing the need for placing it on a high priority timetable.

*P. Michael Conn*