

CURRENT PROTEOMICS: A New Journal for the Publication of Review Articles on Proteomics

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"The time has come," the Walrus said,

"To talk of many things:"

-Lewis Carroll

(from *Through the Looking-Glass
and What Alice Found There, 1872*)



The word proteome was coined about ten years ago from the words protein and genome. The number of proteomics papers published in 2002, based on Medline entries for proteome and proteomics were about a thousand, compared to only a few five years before that. Since the first book on proteomics was published in 1997, there are now several. There has been an explosion of information in proteomics. Scientific literature describing original work in this area are scattered over many publications, including several primary journals dedicated solely to proteomics that have come up in the last couple of years. With this large and increasing amount of literature in proteomics, the Bentham Science Publishers and I have recognized the need for a journal that publishes review articles in proteomics covering all the latest progress in the field. The launch of *CURRENT PROTEOMICS* is therefore very timely, and together with the support of an internationally recognized editorial board and Bentham Science Publishers, we aim to make the journal a great success.

Long before the techniques of nucleic acid sequence analysis were at all conceivable, protein sequence determination was at the forefront of research and offered a powerful tool for formulating and testing hypotheses about the function of genes. In the mid-nineteen forties, Frederick Sanger invented chemical methods that led to his Nobel Prize winning work on the primary structure of insulin, the first protein whose complete amino acid sequence was determined. An elegant approach that used sequential degradation of amino terminal residues of proteins was described in 1950 by Pehr Edman. Automated Edman degradation continued to be the capstone for determination of primary structure of proteins for several decades. However, rapid large-scale identification of proteins and their primary structures was not possible until the early nineteen nineties. This fundamental change in protein analysis was possible primarily due to a number of critical technical breakthroughs in mass spectrometry around that time, together with improvements in two dimensional gel electrophoretic techniques for separation of proteins, availability of complete genome sequences of organisms as well as dramatic improvements in the power of the desktop personal computers. Rapid technological advancements like these together with the accompanying changes in experimental biological approaches led to the emergence and subsequent formidable growth of the field of proteomics. What started with mass spectrometry based reliable large scale methods for protein identification at high sensitivity (expression proteomics), has grown enormously to open up new avenues of structural, functional and computational proteomics within a short time. I have absolutely no doubt that in the field of proteomics, technology will continue to drive biology, and biology will continue to drive technology. In the short span of less than ten years, the impact of proteomics on biology has been very remarkable. Integral to the developments of proteomics has been introduction of novel technology and instrumentation in many areas. All these are covered in the broad scope of the journal. It is my goal that the journal will provide a multidisciplinary medium for the biologists to keep themselves up-to-date with how their research could benefit from the emerging technologies; and for the technologists to understand the hurdles faced by the biologists.

I plan to dedicate certain issues of the journal to honor scientists who have carried out pioneering work that has remarkable impact on the development of protein science. In this regard, I think it is very fitting to dedicate the inaugural issue of this new journal in the memory of one of the greatest protein chemists of our times, my beloved mentor, the late Professor Rodney Porter, F.R.S., Nobel-Laureate. It is also an expression of my deep personal gratitude for his guidance and supervision in the art and science of protein chemistry, when I was a graduate (doctoral) student in his laboratory at the University of Oxford.

Many years ago when I was an undergraduate, I was very much attracted to the following quote in the beginning of the text book - Organic Chemistry by Dr. I.L. Finar:

“A Man would do nothing,
if he waited until he could do it so well
that no one would find fault
with what he has done.”

-Cardinal Newman

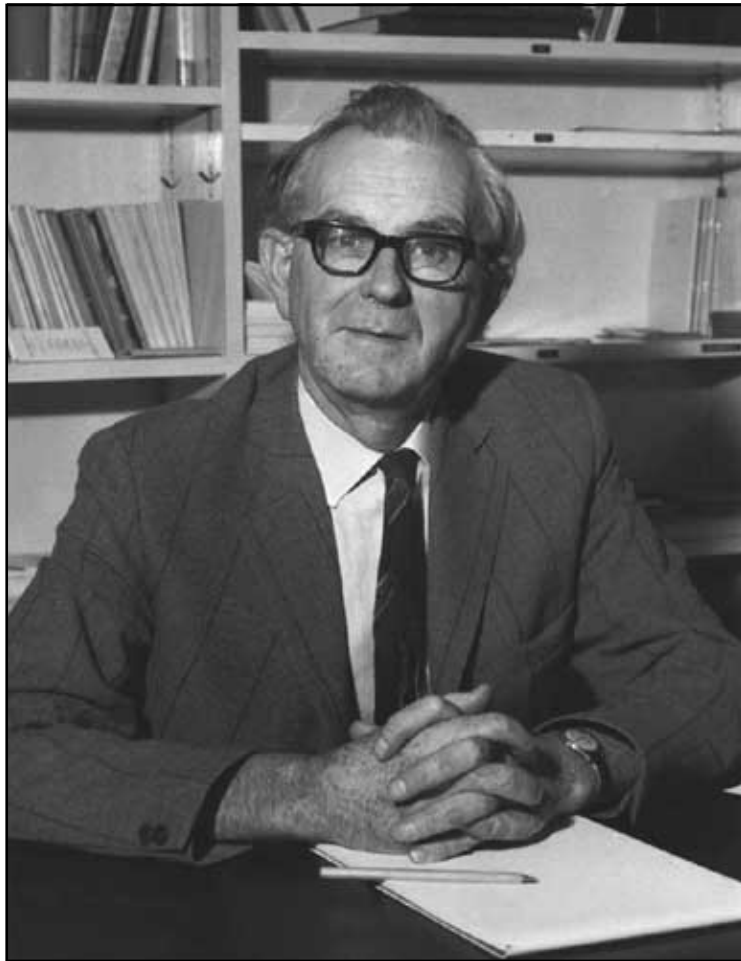
I, along with the Managing Editor, Dr. Bulbul Chakravarti and the Publication Manager of the journal, Afsheen Zain Uddin, as well as Bentham Science Publishers' entire production team aim to continually strive for excellence. However, as in all human endeavors, I am sure there will be mistakes and pitfalls. I would personally welcome any constructive criticism that the readers will be willing to provide. That is the only way we would be able to achieve perfection.



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The inaugural issue of *CURRENT PROTEOMICS* is dedicated to the memory of
“Prof”
Professor Rodney Robert Porter, C.H., F.R.S.
1917-1985

**Nobel Prize in Physiology or Medicine (1972) for “discoveries concerning the
chemical structure of antibodies”**