Methods in *Protein Science*

Protein Science has always been interested not only in results in protein science, but also in better ways to obtain these results.

To make this clearer we are designating a new category of manuscript, namely “Methods and Applications”.

The first two such reports appear in this issue of the journal.

In the first article (pp. 231-238), Frances Arnold's group at CalTech introduces a method for identifying regions of a protein structure that can be shuffled to make chimeric proteins from two or more homologous parents. The approach does not rely on detailed atomic models and is applicable to relatively distantly-related proteins. In an example used to illustrate the new method, an X-ray crystal structure allows detailed visualization of the designed chimera.

The second Methods report (pp. 222-230) is from the groups of Wayne Anderson at Northwestern University and Wladek Minor at the University of Virginia. This article addresses an important problem in structural proteomics, namely how to identify the function of an enzyme for which one knows the structure but little else. In this case the structure gave some clues as to the general class of the enzyme, allowing the authors to develop a

broad-substrate screen that identified potential substrates for bacterial enzymes of this superfamily.

In general, articles in the “Methods and Applications” section will describe new methods and approaches that are expected to have broad applicability in understanding various aspects of protein structure and function. They could, for example, describe methods related to protein engineering or protein purification or protein characterization or protein folding, or methods for structure determination and analysis by a variety of different techniques. The main requirement is that the work be novel and of broad applicability to protein science. The utility of the new method should be illustrated by specific examples. If the work includes the use of novel computational procedures then the related software should be available from a specified website or sufficient information about the new algorithm should be provided so that the results reported could be reproduced by an expert in the field. The format of the manuscripts will be the same as for full-length articles.

We warmly encourage authors to make contributions to the journal in this area.

Brian W. Matthews
Editor-in-Chief