Protein Engineering Handbook

Stefan Lutz and Uwe Bornscheuer did a great job! By convincing many of the key players in the field to contribute to this two-volume masterpiece, they managed to assemble basically all aspects of modern protein engineering technology under one roof, that is, between four hard covers. The topics treated range from "Computational Protein Design" to "Engineering Enantioselectivity in Enzyme-Catalyzed Reactions", and from "Protein Folding"—illuminated from various angles—to "Evolutionary Methods". Merely by glancing over the chapter titles, the interested reader will notice that the two volumes cover not only those topics that are a must-read for newcomers to the field but also highly specialized topics, where even professionals may find and pick nuggets related to their own research. It is a major achievement by the editors to have unified this impressive span of topics when designing this book. This will ensure that the *Protein Engineering Handbook* has a firm position nearest to the desk on the shelves of many protein engineers!

The book's versatility is reflected not only in the wide range of topics treated, but also in each individual chapter. Without picking a specific one, I can say that each author or co-author seems to have worked out extremely carefully a perfect mixture that includes a substantial part explaining the basic essentials of her/his topic. This is usually nicely illustrated by clear figures or tables and a well-balanced specialized part, which provides methodological details of theory and practice and a wide range of valuable references.

This book series on protein engineering has appeared at the right time, even if perhaps a little late for one or two readers, as many protein engineers have waited a long time for a book dealing with their favorite playground. There are, of course, numerous publications and reviews covering individual parts of this seemingly endless realm of science, but they never give you the overview "at a glance" as this series can do. Protein engineers have been around since the beginning of modern molecular biology, and structurally oriented scientists discovered that 1 plus 1 may be much more than 2. Specifically modifying the primary sequence in the protein of interest and using the outcome as a small step towards understanding the structure–function relationships of proteins is still an ever-young discipline whose attractiveness was never jeopardized in all those years. Even more: with every new mutant polypeptide that is designed, expressed, and characterized, new insights are gained and even more absorbing questions can be posed!

The *Protein Engineering Handbook* is actually in very good company: in recent years Wiley-VCH has published a whole range of book series in the broad field of "proteins". These range from *Protein Analytics to Structural Genomics* to *Enzymes in Industry Bioinformatics*, *Handbook of Proteins*, and *Protein Folding*. In this context, the present *Protein Engineering Handbook* is perfectly embedded.

The term "Handbook" in the title can be taken literally! As mentioned above, the user might often pick it up to start reading about a certain topic, but it also will certainly lie open next to the researcher's pipette in order to follow one of the protocols that are outlined. Thus, it becomes "handy", both for lecturers *and* for students!

The major drawback of a book series such as this is to some extent generic: it is that the literature references are not all as up-to-date as one might wish. Apparently it takes a rather long time-frame to assemble this amount of knowledge and to get it published. In this aspect, I see room for improvement for authors, editors, and publishers. Everybody would profit if the processing of volumes such as the one discussed here could be quicker.

I am convinced that Stefan Lutz and Uwe Bornscheuer have succeeded in putting together a "[…] book series [that] might offer some new inspiration[…]" as they modestly claim in their introductory words. It definitely opens up routes towards the wide field of protein engineering for interested researchers. Admittedly, the editors did not achieve the impossible, namely to cover *every*-thing related to the topic, but they got far, very far! Furthermore, when the *Protein Engineering Handbook* is viewed against the background of recent hardcover publications, the picture comes close to being complete.

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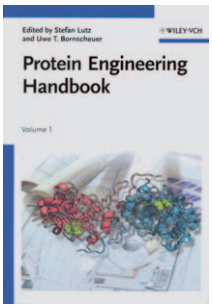

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