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Book Reviews

S. Brackman, A. Schwienhorst (Eds.), Evolutionary Methods in Biotechnology: Clever Tricks for Directed Evolution, Wiley-VCH, Weinheim, Germany (xiii + 214 pp., £90-00, ISBN 3-527-30799-0).

The Darwinian model of evolution is now understood at the molecular level by the study of genetic evolution throughout species. The current use and development of molecular biology strategies to manipulate nucleic acids allows identification of specific DNA markers from separate species. Such techniques are often regrouped under the term 'Directed evolution', which in this book involves optimisation strategies used to generate, screen, and modify nucleic acid libraries.

Evolutionary Methods in Biotechnology: Clever Tricks for Directed Evolution is composed of 13 chapters that present novel techniques and applications for directed evolution of nucleic acids. This volume is complementary to *Directed Molecular Evolution of Proteins*. A short introduction is followed by a first section that focuses upon methods for generation of molecular diversity, such as random mutagenesis, DNA shuffling applications, and DNA recombination by staggered extension process (StEP) methods. DNA shuffling mimics the processes of natural evolution by generating diverse recombined nucleic acid products using restriction enzymes and DNAses. On the other hand, StEP processes involve short cycle PCR. Subsequent chapters deal with screening and/or mass screening technologies such as FACS-based screening of combinatorial peptides and proteins, selection of phage displayed enzymes and selection of target-binding nucleic acids. Target-binding nucleic acids (also known as aptamers) exhibit a defined structure due to their nucleotide sequence and are thereby capable of binding specific nucleic acids or proteins. The following three chapters present the use of computer-based methods to design random codons for subsets of amino acids, and to predict the structure of random generated mutant proteins and RNA molecules. The final chapter presents patenting issues in evolutionary biotechnology, including requirements for patentable products such as novelty, inventiveness and utility.

A CD-ROM containing software tools for library design, mutants selection and predictive algorithms as well as references accompanies this volume. This is a practical oriented book, since it presents currently employed protocols, and will therefore be of particular interest to researchers and students involved in the use of such directed evolution technologies.

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M. Niaounakis , C.P. Halvadakis, Olive-Mill Waste Management, Literature Review and Patent Survey, Typophyto-George Dardanos Publications, Athens, Greece, 2003 (xv +430 pp., Currently Not For Sale—Free under Request (500 copies only), ISBN 960-402-123-0).

Amongst the 1743 metric tons of olive oil produced worldwide annually, 98% is produced in the Mediterranean region; Spain, Italy, Greece, Turkey and Tunisia being the biggest producers. The olive oil manufacturing process yields three materials; the olive oil (20%), solid waste (30%) and aqueous liquor (50%). Though other products such as pomace or stones can be extracted from the solid phase, the remaining solid wastes and liquors phases as well as the water used during the extraction process, are generally not used and are collectively known as 'olive-mill waste water' (OMWW). OMWW generation represents 0.55–2 L/kg of olive, and has raised ecological concerns because of its phenolics and acids content that have phytotoxic and biotoxic effects. It is estimated that the load of phenolic compounds within the OMWW is about 1000 times larger than that of domestic sewage. There are now several existing processes that can provide a solution to the OMWW problem. These include detoxification processes, recycling and recovery of valuable components and production process modifications.

Olive-Mill Waste Management initially presents background information about the olive oil production industry