Special Issue

The Optimized Production, Purification, Characterization and Application of Proteins/Enzymes

Message from the Guest Editor

A general protocol for protein purification involves the isolation of these macromolecules from a wide range of sources, which include animal organs, plants, bacteria, viruses, and other sources. The purification step is essential and preliminary to an accurate characterization of a protein that, because of the intrinsic features of each protein, involve the use of multiple techniques. These include ELISA for the identification of the protein; UV and VIS spectrophotometry for the calculation of the protein concentration; SDS-PAGE, SEC, and MS for the determination of the molecular weight; chemical and/or enzymatic digestion in combination with HPLC and MS for peptide mapping; the Edman chemistry for the analysis of the primary sequence; and CD, X-ray diffraction, and NMR for the determination of secondary and tertiary structures.The aim of this Special Issue is to attract contributions on all aspects of protein purification and characterization, with special emphasis on the application of the most sophisticated technologies that allow for addressing the purification processes characterized by peculiar difficulties.

Guest Editor

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Deadline for manuscript submissions

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Message from the Editor-in-Chief

As the premier open access journal dedicated to experimental organic chemistry, and now in its 25th year of publication, the papers published in *Molecules* span from classical synthetic methodology to natural product isolation and characterization, as well as physicochemical studies and the applications of these molecules as pharmaceuticals, catalysts and novel materials. Pushing the boundaries of the discipline, we invite papers on multidisciplinary topics bridging biochemistry, biophysics and materials science, as well as timely reviews and topical issues on cutting edge fields in all these areas.

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