Special Issue

Tools for understanding PTM crosstalk

Message from the Guest Editors

It is now well established that PTMs act in combination on proteins for modulation and regulation purposes. The next challenge is to identify the constraints that rule their cooperative and/or antagonist effects. This is illustrated in attempts to decipher the “histone code” that would explain the combined effects of methylation, acetylation, ADP-ribosylation, ubiquitination, citrullination and phosphorylation of histone tails. In fact, the elucidation of PTM crosstalk requires dedicated effort not only in improving detection and characterization methods but also in apprehending the interplay between modified proteins and modifying enzymes. This special issue will cover PTM detection methods mostly using MS technology, particularly top down strategies that have been successful in characterizing modified histones, along with innovative bioinformatics tools supporting data analysis as well as PTM prediction. It also welcomes manuscripts reflecting current research on how PTM combinations are generated and affect protein function and interactions. This covers studies in protein science in the broadest sense and is equally applicable to prokaryotic or eukaryotic

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About the Journal

Message from the Editorial Board

Proteomes is an international, peer-reviewed, open access journal that was first published in 2013 by MDPI. *Proteomes* addresses all aspects of proteome analysis with a special focus on the quantification and characterisation of the proteome at the level of proteoforms. We encourage submission of articles that accurately quantify and characterise the proteome, as well as new and updated methods and technologies that enhance the accurate quantification and characterisation of the proteome and thereby provide evidence directly facilitating the understanding of biological mechanisms. Articles emphasising a multi/transdisciplinary approach combining different omics techniques are welcomed.

Editors-in-Chief

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