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# Editorial for "Advances in OMICs-based disciplines"

The completion of the Human Genome Project at the turn of the 21st century was a crucial moment in the birth of "OMICs-based" sciences [1,2]. Following the establishment of genomics-based studies, numerous other disciplines evolved including proteomics, transriptomics, lipidomics, glycomics and metabolomics [3]. Today, the field of "OMICs" research is more complex than ever before. "OMICs" approaches have enabled scientists to comprehensively analyze the functions of thousands of genes, proteins or metabolites simultaneously, instead of studying single molecules as was the case before. The resultant large-scale data collections and analyses have fundamentally altered our way of thinking, and have had enormous impact on both basic- and translational-biomedical research and, more recently, on personalized medicine [4].

Nowadays, "OMICs" based research is rapidly evolving due to the development of novel tools and technologies. In this first special issue of BBRC dedicated to the "OMICs"-based sciences, we present a critical review of the current field as well as descriptions of new approaches for use in the analysis and manipulation of genomes, proteomes and glycomes. The issue starts with a review article by Catherman et al. describing advances in promising new "top down" proteomics approaches [5], followed by two research papers, the first describing the use of mass spectrometry to analyze in-depth proteomes of ovarian cancer cell line exosomes [6], and the second describing the KYSS method – a new computational tool for the evaluation of large scale proteomics datasets and assessment of LC-MS/MS proteome analysis [7]. These three articles are followed by a review by Basini & Cameron, showing how mass spectrometry can be used to study a "sport-ome", which they define as a metabolome and proteome complement analyzed in exercising athletes [8]. The next two contributions describe a database of biologically and structurally characterized peptide-binding sites, called PeptiSite [9], and an *in silico* drug screening method for human membrane proteins [10]. Following these articles, four contributions describe the use of either conventional, split-ubiquitin-based two-hybrid assays and computational approaches to identify, analyze and visualize protein–protein interactions of various yeast and human proteins [11–14]. These are then followed by two articles, one by Kasper et al. describing the miRNA regulation of the human glycome [15], and the other review article providing a general overview of miRNA target predictions [16]. The final three articles in this issue then describe the development of an antigen microarray approach for high-throughput monoclonal antibody selection [17], a CRISPR/Cas-based system for generation of genome-modified mice [18], and, lastly, a phage display approach that lead to the identification of a novel fibroblast growth factor-binding peptide with anti-tumor effect [19].

In summary, I hope that the information presented in this special issue will serve as a valuable resource for both current "OMICS"-based researchers, as well as those in other disciplines seeking to improve their knowledge of this dynamic and exciting field of research. One thing is certain – as the "OMICS"-based approaches continue to grow in both application and scope, they help scientists to reshape our current understanding of complex biological processes, and therefore promise great biomedical benefits in the future.

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