Preface

Current Proteomics is a well-known peer reviewed international journal from Bentham Science Publishers. It was first launched in 2004. During the past two decades, it has been successfully publishing original research work and review articles devoted to proteomics, nearly and bioinformatics fields. In recent years this area of research has gained significant interest and close attention due to its implication in health and diseases. Moreover, there has been incredible technological and computational advance in the field. In fact, studies on these topics led to the development of new tools, novel techniques, methodologies, software and databases that inspired further work and investigation. These have improved our understanding of the mechanism of diseases, associated pathologies and their biochemical pathways, leading to more efficient diagnosis and alternate therapies with new targets. Current Proteomics provided a perfect platform for researchers to publish their work in the field for the benefit of others. These are original research findings, review articles, in-depth analysis, research perspectives and book reviews on topics related to peptide/protein chemistry, enzymology, proteomics, bioinformatics and computational chemistry with special emphasis on new development and progress in the field. Several papers on hot topic subjects and key areas of current relevance are published on a regular basis. Moreover, the journal welcomes contributions for publication on invited thematic issues of high interest and significance. This is accomplished with the expert guidance and advice of an eminent or internationally well-renowned scientists in the field. Together these made key impacts on research and the scientific community in the field. Current Proteomics has received an explosion of research data and results about new techniques, new disease biomarkers, target identification, methods and technologies with potential health and therapeutic benefits. This new issue with a wide range of studies, as detailed below, is no exception to that, particularly in this era of global pandemic due to Covid-19 infection. The journal faced a lot of challenges and adverse conditions in its daily activity, yet in the end, it came out successfully by publishing high quality research work from around the world. This latest issue, the first of the new-year 2022 (volume 19, number 1), contains 10 interesting research articles, including one review paper on protein aggregation and its implications in health and diseases. These articles contain new research data and results covering diverse disease fields consistent with the journal’s main objective and mandate. There were contributions from various countries, including Mexico (3), Turkey (2), Pakistan (2), Canada (1), China (1) and Taiwan (1).

The first article is the review work from Canada by Basak and Basak which summarizes various aspects of research advancements on protein self-assembly and associated neurological dementia and pathologies. The second article by Zhou et al. from Taiwan investigated the proteins altered in MDA-MB-231 triple negative breast cancer cells following treatment with the anticancer drug cryptotanshinone. They also explored the key pathways and identified specific molecular markers involved in cryptotanshinone treatment. Their studies, in vitro, revealed that cryptotanshinone could trigger rapid and irreversible apoptosis in MDA-MB-231 cells in an irreversible manner via inhibition of cell metabolism. The third paper by He et al. from China identified several key proteins which may be associated with the incidence and progression of the femoral neck bone tissues of patients suffering from hyperuricaemia. These proteins are linked to cytoskeleton formation, energy metabolism, or signal transduction confirming their roles in the disease. 50 biological processes, including peroxisome proliferator-activated receptor (PPAR) signalling and fatty acid metabolism, have been implicated. The fourth article by Silva-Gaona et al. from Mexico conducted research study to determine the effects of curcumin on the liver protein profile of diabetic db/db mice. Their results showed that among all differentially expressed proteins, curcumin reverted the altered expression of seven proteins derived from the liver. The fifth article was also a contribution from Mexico by the research team of Polanco et al. who demonstrated that SARS CoV-2 structural, non-structural, and putative proteins are characterized by a unique Polarity Index Method (PIM®) profile when compared to those of SARS-CoV-1 and MERS-CoV. The authors concluded that this profile may be useful for the identification of viral proteins linked to SARS-CoV-2 infection and pathogenesis. The following paper (Sixth article), also from Mexico by the same group, was dedicated to the characterization of proteins from human DNA and RNA viruses using the tool of bioinformatics based on UniProt database. Their work showed that polarity and charge profile might represent a physicochemical metric that can be used to effectively identify specific viral groups from their protein sequences. The seventh article was a contribution from Ergul et al. of Turkey, who has identified critical amino acid residues in Hsp70 protein’s (an anti-apoptotic factor) Nucleotide binding domain that can be useful in designing improved and efficient drugs for cancer treatment. The eighth article was from Yazgan et al. of Turkey, who studied cytotoxic and apoptotic effects of Iris Taochia plant extracts on human breast cancer (MCF-7) Cells. Their data showed that Iris Taochia extract reduced cell viability as well as induced apoptotic pathways, which can act as a potential regulator of cancer cell mortality. The ninth article consisted of a study conducted by the research team of Nanzoor et al. from Pakistan who analysed the expression profiles of various proteins in Schizophrenia Brain following treatment with 4-hydroxynonenal (HNE) and their relevance to redox dysregulation. They proposed the role of HNE-modified proteins with the pathology of schizophrenia. In the last and tenth article, also from Pakistan, Naz et al. carried out epidemiological and Pangenome Landscape analysis of Staphylococcus aureus and Identification of a Conserved Novel Candidate for Vaccine development against infection caused by this microorganism.
Overall, the above ten articles of this issue of Current Proteomics provided useful data and research findings in respective domains that will, no doubt, draw the attention and keen interest of researchers in academic, pharmaceutical, and biotechnological fields. In conclusion, we sincerely believe that with this issue, Current Proteomics will continue to serve the interests of scientists, biochemists, medical professionals, molecular and cellular biologists, and others who are engaged in research, involving proteins, enzymes, proteomics as well as computational chemistry and bioinformatics. These novel efforts are aimed at improving people’s lives throughout the world and all population.

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