Transcriptomic and Proteomic Expression Analyses for Advanced Structure & Activity Relationship Study and Biomarker Identification

Takashi Owa (Laboratory of Seeds Finding Technology, Eisai Co., Ltd.)

Exploiting tremendous resources of the decoded human genome sequence for improving human health and quality of life is a central subject in current life science and medical science. The research concept of chemical biology with biologically active small molecules is now recognized as a complement to genomics-based approach toward uncovering unknown gene functions, biological pathways, and genomic networks. In chemical biology studies, organic small molecules are tested as stimulants or perturbagens to induce gain-of-function or loss-of-function of their protein targets. In addition to several genetic manipulations such as overexpression and knockout, this kind of inducible system appears to be extremely important for functional genomics. The impact of this small molecule-based approach on drug discovery should be substantial because the study process and utilized technologies are closely related to research programs in pharmaceutical industry. Bioinformatics analyses of a huge amount of transcriptomic and proteomic expression data sets provide an unprecedented opportunity for profiling small molecule's biological effects on the genome-wide format, thereby making it possible to explore undeveloped chemical space, novel druggable targets, and effective biomarkers. In this lecture our attempt on sulfonamide-focused compound libraries will be presented, with particular focus on the application of DNA microarray analysis and quantitative proteomic analysis in medicinal chemistry task force for efficient drug discovery and development.