

## **Proteomic profile of acute myeloid leukaemia: a review update**

### **ABSTRACT**

Proteome analysis is a complex and dynamic process that encompasses several analytical platforms that include protein sequencing, structural or expression proteomics, protein modification, sub-cellular protein localization, protein-protein interaction and biological functional proteomics. In fact, expression proteomics is extensively applied in a majority of biomarker detection studies because it provides a detailed overview of differentially expressed proteins in cellular pathways and disease processes. Proteomics are also effective and dynamic in protein-protein interactions and cross-talks between interacting molecules of the cell. Proteomics has evolved into a crucial tool used to investigate the biochemical changes that possibly lead to development of cancer biomarkers. This review draws attention to the progress and advancements in cancer proteomics technology with the aim of simplifying the understanding of the mechanisms underlying the disease and to contribute to detection of biomarkers in addition to the development of novel treatments. Given that proteome is a dynamic entity of cellular functions in health and disease, it is capable of reflecting the immediate environmental state of cells and tissues as shown in this review. The review shows the possibility of elucidating the pathophysiology of acute myeloid leukaemia (AML) through proteome expressions, thus confirming the viability of proteome analysis in profiling AML.

**Keyword:** Acute myeloid leukaemia; Proteomics; Expression profile; Protein sequencing; Proteinprotein interaction; Biomarkers