Proteomic profiling of biological samples

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Cancer is expected to be the world's leading cause of death in the 21st century with 18.1 million new cases of cancer diagnosed globally and an estimated 9.2 million deaths from cancer.[1] Protein analysis may assist in identifying potential protein biomarkers that might be used for the improvement of early disease diagnosis, screening and monitoring and for the development of personalized therapies.

Mass spectrometry (MS)-based proteomics has become a crucial tool in biomarker discovery. However, proteomics faces several challenges. Protein solubility often needs to be promoted because proteins are frequently insoluble in their native form, which is accomplished by adding detergents and chaotropes to extraction buffers. Furthermore, proteomic analysis requires large sample amounts to obtain deep proteomic coverage while sample losses may occur during sample preparation steps, limiting the analysis of small sample amounts.

Here, we develop MS strategies for proteome processing of biological materials for the identification of biomarker proteins. We focused on the development of simple and reliable methods for proteome detection from minute samples.

[1] Bray, F.; Ferlay, J.; Soerjomataram, I.; Siegel, R. L.; Torre, L. A.; Jemal, A. Global Cancer Statistics 2018: GLOBOCAN Estimates of Incidence and Mortality Worldwide for 36 Cancers in 185 Countries. CA. Cancer J. Clin. 2018, 68 (6), 394–424. https://doi.org/10.3322/caac.21492.