

A New Interface for Faster Proteoform Analysis

박해민[†]

충남대학교

(haemin.park@cnu.ac.kr[†])

Different proteoform products of the same gene can exhibit differing associations with health and disease, and their patterns of modifications may offer more precise markers of phenotypic differences between individuals. However, currently employed protein-biomarker discovery and quantification tools, such as bottom-up proteomics and ELISAs, are mostly proteoform-unaware. Moreover, the current throughput for proteoform-level analyses by liquid chromatography-mass spectrometry for quantitative top-down proteomics is incompatible with population-level biomarker surveys requiring robust, faster proteoform analysis. To this end, we developed immunoprecipitation coupled to SampleStream Mass Spectrometry as a high-throughput, automated technique for targeted quantification of proteoforms. The data show IP-SampleStream-MS to be a robust, scalable workflow for high-throughput associations of proteoforms to phenotypes.