

Enhanced proteoform identification in top-down proteomic workflows using packed emitter columns.

Top-down proteomics has emerged as a powerful analytical approach for characterizing intact proteins and their proteoforms offering unique insights into protein structure, post-translational modifications (PTMs), and biological function. Proteoform identification is generally achieved by separation of intact proteins using reversed-phase liquid chromatography (LC) followed by fragmentation and detection on a mass spectrometer. One of the biggest challenges in the field is the inability to identify different proteoforms due to over-lapping separation profiles created by limited peak capacity. To address this, we developed a novel packed emitter chromatography column containing a C4 stationary phase. We demonstrate that this column achieves narrow peak widths and sensitive ionization enabling the efficient separation of complex intact proteins mixtures.

User consent

yes

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