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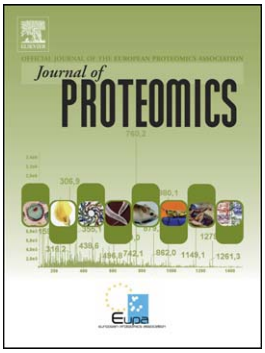

Editorial: Breakthroughs in top-down proteomics

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Breakthroughs in Top-down Proteomics

Editorial

Top-down proteomics has been rapidly evolving and attracting new researchers and interest from different areas of biology, especially biomedicine. The ability to discriminate proteoforms at the genetic and post-translational modification level for all proteins in the human body while elucidating their functional cross-talk aspects at a given time and condition, as advocated by top-down proteomics, will definitely broaden the knowledge of the human proteome in health and diseases.

Several distinct proteoforms for each protein might exist and specific proteoforms of the same protein can be qualitatively or quantitatively related to different pathological mechanisms and thus be used as biomarkers for a distinct disease. However, proteoform variants have been escaped full detection using conventional high throughput 'bottom-up'- based proteomics since this technology produce mass spectra measurements for particular peptides to infer the identity of proteins and not necessarily of corresponding proteoforms. In contrast, top-down proteomics by investigating intact proteins instead of peptides provide information about all proteoform variants of a particular protein.

However, the complexity and diversity of the biological environment where proteins function, often in large dynamic range of mass and concentration associated with a plethora of post-translational modifications and sequence variations, make high throughput top-down proteomics still challenging using the current available pre-fractionation/separation systems and mass spectrometers.

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