dia-PASEF for improved thorough proteomics

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Fundamental challenges in MS-based proteomics include the high sample complexity, the large dynamic range in protein concentration, and the resulting big-data computational analysis.

Deeper proteome coverage can help understand the mechanisms behind biological processes and can support targeted efficient treatment approaches. Developments in mass spectrometers towards higher sensitivity, faster sequencing speed and larger peak capacity address many of these challenges.

One example of complex sample is blood plasma: this is the key sample of interest in clinical proteomics research applications. As plasma's availability, accessibility and physiological role make it an attractive support to perform diagnosis, prognosis or theragnosis assays, Label-Free Quantification Proteomics now appears to be a method of choice to search for candidate biomarkers and comprehensive proteome analysis still remains challenging due to the large dynamic range of concentration.

dia-PASEF approach, allows visualizing molecules in very low amounts in the presence of more abundant proteins, as a way to discover biomarkers in plasma, using a high throughput approach, from injection to data processing.

Another example of improved proteomics relates to the cell population heterogeneity in diseases such as cancer, with a direct impact on successful therapies and appearance of resistances. The next step in translational approaches is analyzing single cells from FFPE tissue. dia-PASEF® on the timsTOF Ultra is revolutionizing low-input tissue proteomics and becoming an essential solution for molecular medicine labs.

Sample preparation involves having access to isolate single cells and analyze them separately by MS. The analysis of protein group and precursor identification rates in FFPE mouse liver tissue, dissected by laser capture microdissection, with varying cell equivalents, demonstrated increased protein group abundance and correlation of protein abundance between different cell equivalents.

In conclusion, a dia-PASEF approach digs deeper into the proteome coverage, provides more confidence in data, and increases data completeness by reducing the number of missing values. 4D proteomics considers four dimensions of data, and allows separations of coeluting isobars for confident annotations.

Agradecimentos: