

Characterizing disease-associated changes in post-translational modifications by mass spectrometry.

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Streszczenie

Exploring post-translational modifications (PTMs) with the use of mass spectrometry (PTMomics) is a rapidly developing area, with methods for discovery/quantification being developed and advanced on a regular basis. PTMs are highly important for the regulation of protein function, interaction and activity, both in physiological and disease states. Changes in PTMs can either cause, or be the result of a disease, making them central for biomarker studies and studies of disease pathogenesis. Recently, it became possible to study multiple PTMs simultaneously from low amount of sample material, thereby increasing coverage of the PTMome obtainable from a single sample. Thus, quantitative PTMomics holds great potential to discover biomarkers from tissue and body fluids as well as elucidating disease mechanisms through characterization of signaling pathways. Areas covered: Recent mass spectrometry-based methods for assessment of the PTMome, with focus on the most studied PTMs, are highlighted. Furthermore, both data dependent and data independent acquisition methods are evaluated. Finally, current challenges in the field are discussed. Expert commentary: PTMomics holds great potential for clinical and biomedical research, especially with the generation of spectral libraries of peptides and PTMs from individual patients (permanent PTM maps) for use in personalized medicine.

Słowa kluczowe

DDA strategies, DIA strategies, Post-translational modification, clinical proteomics, enrichment strategies, mass spectrometry

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