A novel strategy for quantitative proteomics using isotope-coded protein labels

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Stable isotope labelling in combination with mass spectrometry has emerged as a powerful tool to identify and relatively quantify thousands of proteins within complex protein mixtures. Here we describe a novel method, termed isotope-coded protein label (ICPL), which is capable of high-throughput quantitative proteome profiling on a global scale. Since ICPL is based on stable isotope tagging at the frequent free amino groups of isolated intact proteins, it is applicable to any protein sample, including extracts from tissues or body fluids, and compatible to all separation methods currently employed in proteome studies. The method showed highly accurate and reproducible quantification of proteins and yielded high sequence coverage, indispensable for the detection of post-translational modifications and protein isoforms. The efficiency (e.g. accuracy, dynamic range, sensitivity, speed) of the approach is demonstrated by comparative analysis of two differentially spiked proteomes.
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