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(54) Title: TANDEM MASS TAG MULTIPLEXED QUANTITATION OF POST-TRANSLATIONAL MODIFICATIONS OF PROTEINS

(57) Abstract: Disclosed are methods of quantifying multiple quality attributes, such as post translational modifications, of multiple samples in a single mass spectrometry (MS) run, including contacting two or more samples with a digesting solution under conditions sufficient to digest samples, wherein each sample is digested separately and the digesting solution is a Tris-free buffer solution; contacting each of the two or more digested samples with a specific Tandem Mass Tag (TMT) labeling reagent under conditions sufficient to label peptides within each of the digested samples with the specific TMT labeling reagent; quenching labeling of peptides within each of the two or more digested samples; combining equal volumes of the two or more labeled, digested samples into a single combined sample solution; and analyzing the single combined sample solution by targeted mass spectral analysis, thereby allowing multiple quality attributes of the two or more samples to be quantified in a single mass spectrometry (MS) run.



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