Antibody-Free Approach for the Global Analysis of Protein Methylation

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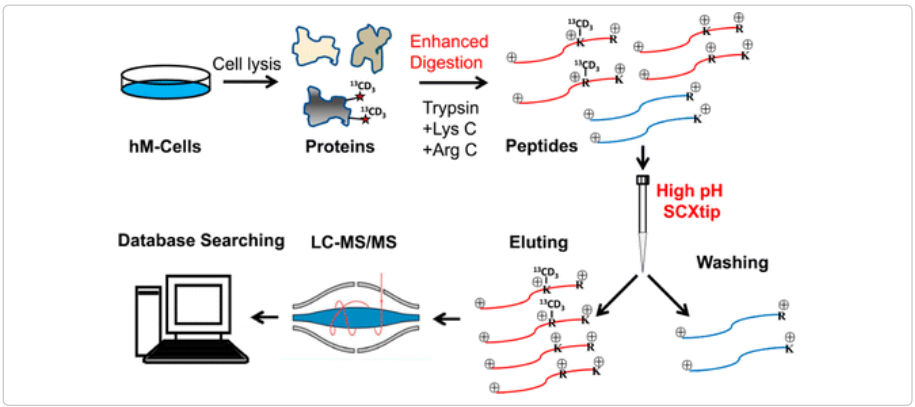
Abstract



Protein methylation is receiving more and more attention for its important regulating role in diverse biological processes including epigenetic regulation of gene transcription, RNA processing, DNA damage repair, and signal transduction. Global analysis of protein methylation at the proteome level requires the enrichment of methylated peptides with various forms; unfortunately, the immunoaffinity purification method can only enrich a subset of them due to lacking of pan specific antibody. Because methylation does not significantly alter the physicochemical properties of arginine or lysine residues, chemical approach for global methylome analysis is still at infancy. In this study, by exploiting the fact that the methylation on Arg and Lys prohibiting the cleavage by proteases for these sites, we developed an antibody-free method to enrich methylated peptides, which enabled the identification of 887 methylation forms on 768 sites from HepG2 cells. This technique allows the simultaneous analysis of both Lys and Arg methylation while it has better performance for the identification of Arg methylation. It should find broad applications in studying methylation regulated biological processes.

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