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Sensitivity booster for mass detection enables unambiguous analysis of peptides, proteins, and antibodies

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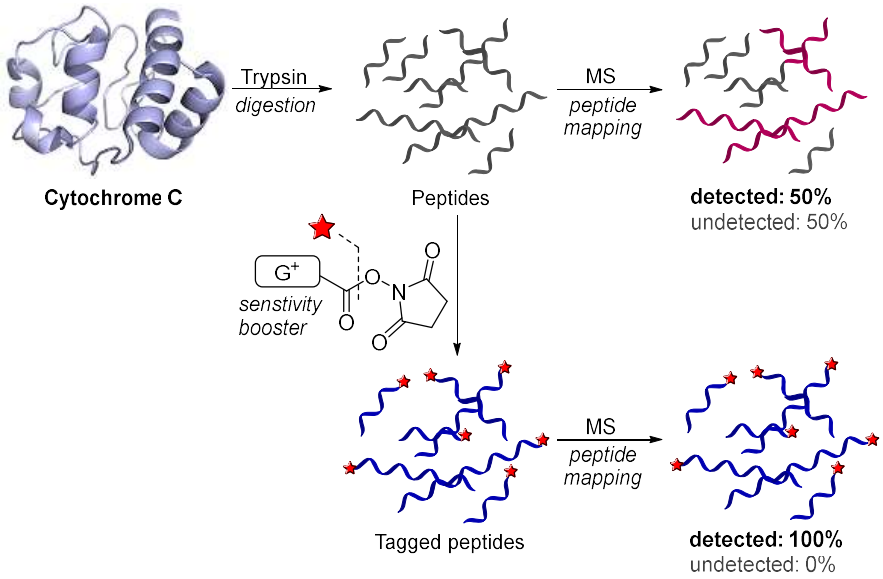
Proteins play a critical role in central dogma and regulate diverse biological processes. Their detection and unambiguous analysis at low concentration provide the gateway for multiple investigations. A prominent example in this perspective involves the identification of biomarkers.[1,2] Besides, the area of protein bioconjugation would be immensely benefited by a kit that could resolve the loss of information during peptide mapping and sequencing. The rapid analysis and high sensitivity exhibited by mass spectrometry (MS) have made it the first choice for qualitative and quantitative analysis of peptides and proteins. However, it frequently encounters the challenges due to insufficient ionization and ion suppression. A few tags based on imidazolium derivatives, piperazine derivatives, and quaternary ammonium salts have been developed to address this concern.[3-5] In this perspective, we have developed a tagging reagent that enables the detection of peptide up to attomolar concentration. It overpowers the inherent differences in the ionization of various peptides in a proteolytic digest. This feature empowers the detection of ~90-100% sequences during the peptide mapping. It also translates in a simplified and consistent detection of fragments during the sequencing of a peptide by MS-MS. We demonstrated that the mapping of primary sequence in a monoclonal antibody, trastuzumab, can be enhanced from ~20% to ~70% using our kit.



Scheme. Sensitivity booster for enhancing the peptide mapping.

References and Notes:

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