

Fast and Simple Method on Tryptic Digestion of Protein for MALDI-MS using Temperature Controllable Microchip

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In the research of proteomics, mass spectrometry is an essential analysis method for protein identification. We demonstrate a novel method on tryptic digestion of protein for MALDI-TOF(matrix assisted laser desorption/ionization time of flight) mass spectrometry using temperature controllable microchip. Tryptic digestion is the inevitable procedure for protein samples preparation for mass spectrometry analysis. Sample preparation using temperature controllable microchip is simple and fast than conventional chemical denaturation of protein. We obtained the digested protein without any other chemical process and purification. We could observe more peptides matched with their theoretical mass in the case of thermally denaturated tryptic digestion compared to nondenaturated digestion of both proteins. We think this chip-based thermal denaturation can be applied to proteomics and various studies about protein with mass spectrometer.

Reference

1. Zee-Yong Park, Thermal Denaturation: A Useful Technique in Peptide Mass Mapping, *Anal. Chem.* Vol.72, No. 11, June 1, 2000.