

양이온 비드를 이용한 소변 펩타이드 동정의 개선

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Improving Urinary Peptide Identification using Strong Cation Exchange (SCX) Bead

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Human urine has been analyzed to identify disease biomarkers (prostate cancer, diabetes, renal disease etc.). The endogenous urinary peptide may provide clinically useful biomarkers for any renal diseases. Peptide preparation protocol is independent of tandem mass spectrometry (MS/MS) parameters. In this study, we improved identification of urinary peptides in the human urine. Urine samples were collected from 3 male healthy donors and analyzed through three different 3 preparation methods (C18 alone, C18+MCX and C18+SCX bead) with LC-MS/MS. We identified 2 proteins in C18 alone, 6 proteins in C18+MCX and 14 proteins in C18+SCX bead including protein for Tamm-horsfall protein (UMOD). Among the three methods, using a SCX beads method is more useful. This approach is suitable in development of biomarkers specific for diseases using clinical peptidomics research. Further determinations of the clinical study from large numbers of clinical samples are required.

Key Words: 질량분석기, 펩티도믹스, 바이오마커
LC-MS/MS, Peptidomics, Biomarker