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Keyword: | [TOP](#) > [Available Issues](#) > [Table of Contents](#) > [Abstract](#)

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[\[PDF \(478K\)\]](#) [\[References\]](#)**Traceable Amino Acid Analyses of Proteins and Peptides by Isotope-Dilution Mass Spectrometry Using Precolumn Derivatization Reagent**[Tomoya KINUMI^{1\)}](#), [Ryota ICHIKAWA^{2\)}](#), [Hirokazu ARIMOTO^{2\)}](#) and [Akiko TAKATSU^{1\)}](#)*1) Bio-Medical Standard Section, National Metrology Institute of Japan (NMIJ), National Institute of Advanced Industrial Science and Technology (AIST)**2) Graduate School of Life Sciences, Tohoku University***(Received May 11, 2010)****(Accepted July 12, 2010)**

We have developed an accurate and traceable quantitation method of proteins and peptides by isotope-dilution mass spectrometry with the precolumn derivatization for hydrolyzed amino acid. This method utilized *N*-butylnicotinic acid *N*-hydroxysuccinimide ester iodide as the derivatization reagent and C-30 reversed phase column for the separation. Quantitative results of porcine insulin and human serum albumin obtained from the hydrolyzed six or seven amino acids showed a good agreement, with less than 3% of the expanded uncertainties. This method allows more accurate and more robust amino acid analysis in comparison with non-labeled methods.

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