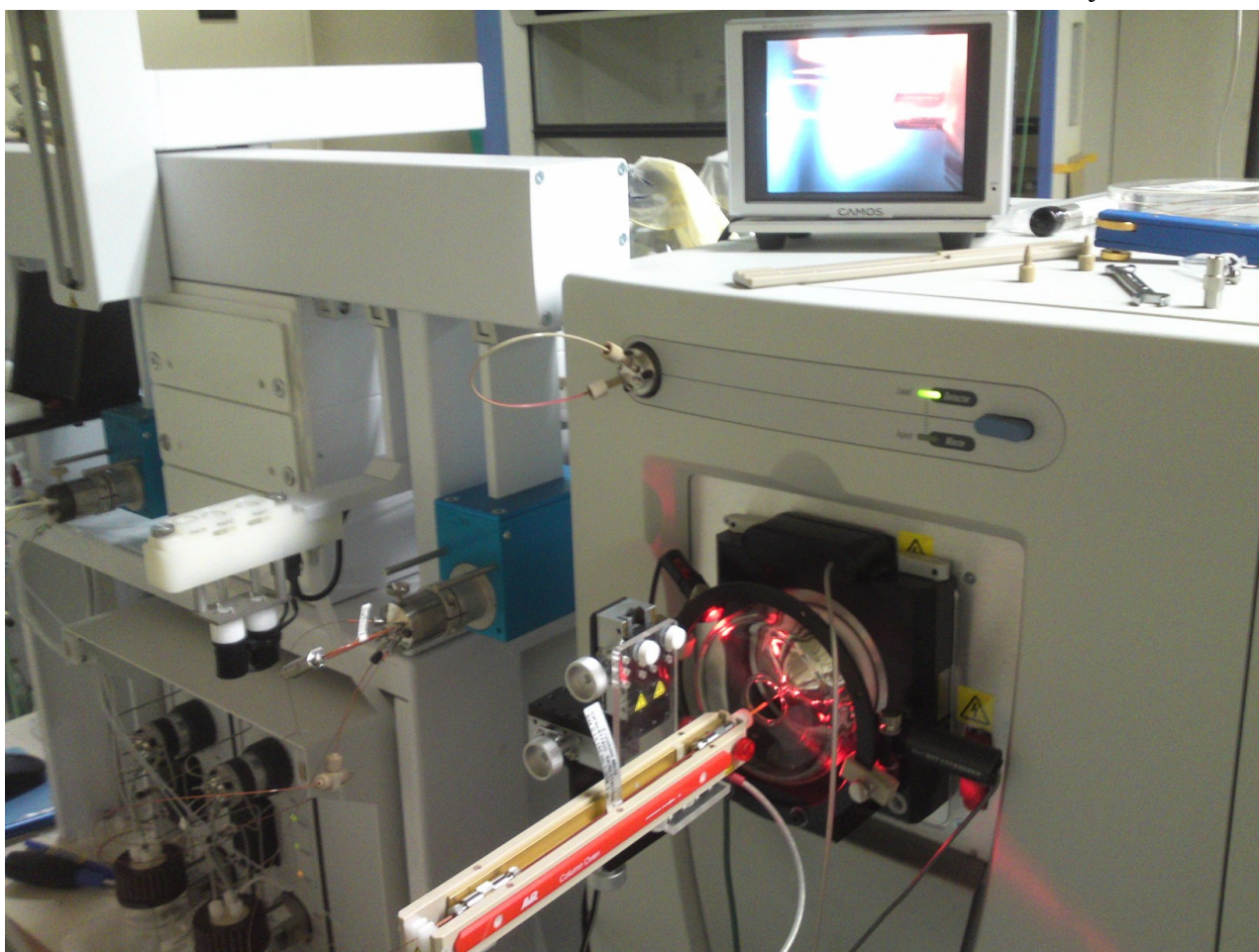


Studies on protein structure, function, and degradation mechanism.

Takashi NAKAZAWA [Chemistry Course]



Part of nano-LC-ESI-MS/MS instrument for protein analysis

It is possible to interpret almost every feature of living organisms in terms of protein structure, function, and interaction of proteins, which are expressed in the cell under the control of DNA encoding tens of thousand genes. Our research focuses on developing methods for the elucidation of structure-function relationship of proteins with the aid of state-of-art techniques of mass spectrometry and spectroscopic methods in conjunction with methodologies of organic chemistry. Some of our recent progresses include the proposal of “terminal proteomics” enabling to enhance the efficiency of protein identification by chemically labeling the N- and C-terminal amino acid residues for sequencing with mass spectrometry. Another one is the development of a method to characterize the acid-base of an amino acid residue in as protein as a function of hydrogen/deuterium exchange rate measured by mass spectrometry. We are now devoted to establishing “protein archaeology” of our own as an extension of protein science applied to proteins preserved in archaeological specimens.

Keywords : Protein, Organic chemistry, Biochemistry, Mass spectrometry, Archaeology