

Title:

Mass Spectrometry and its modern evolution --
from Atomic Bomb to Proteomics and Beyond.

Abstract:

Mass spectrometry is one of the most useful tools ever developed.

In the past century, we have witnessed its broad usability ranging from element purification to application in biology.

In addition to a very brief historical reviews, I will mainly discuss its use in proteomics and systems biology. Key problems in utilizing mass spectrometry in these area such as sensitivity and statistical accuracy will be described in particular. To address problems associated with peptide identification confidence that is of immense importance in modern proteomics, we have developed methods, RAId and RAId_DbS, aiming to solve those problems.

Comparison of our methods to other existing tools in terms of peptide Identification and statistical accuracy will be shown.