

초청강연초록

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Recent Technology and Trends In Proteomics Research

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The driving forces in proteomics are mainly mass spectrometry technology and bioinformatics.

However, display and separation of the highly complex protein mixtures have equal importance. Two-dimensional electrophoresis is still the most powerful method to resolve and purify the components of complex protein mixtures. Sample preparation is an important part of the procedure, which greatly influences the quality of the separation and the reproducibility. New developed narrow interval pH-gradient gel strips allow the detection of lower expressed gene products. Image analysis of the separation pattern has been identified as the bottleneck of the entire procedure: because of time consumption and human interference. Newly developed fully automated software removes this bottleneck completely. The image data are further processed, the x/y-coordinated of these spots are exported to the spot picking robot, which automatically finds and excises the protein spots of interest. The entire spot handling process, including in-gel digestion, mixing the peptides with matrix and spotting those on MALDI targets, can be fully automated in order to reduce human errors and to allow sample traceability. New hardware and software for mass spectrometry with MALDI ToF allow automated spot identification via peptide mass profiling and amino acid sequence data. New chemistry for derivatisation of the peptides makes post source decay happen in a better controlled way than in the past. New electrospray ionization mass spectrometers coupled to fast liquid chromatography allow analysis of intact proteins and complexes.

Finally, the entire proteomics workflow from sample receiving to protein identification and characterization can be monitored and controlled with laboratory workflow system software. Thus, within a short period of time proteomics had been developed from a combination of a few hands-on procedures to a professional high-throughput approach on a high industrial standard.