

Pitfalls in Proteomics 1

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Editorial

High-throughput technology of protein identification using MALDI-TOF or MALDI-TOF-TOF is a major advent allowing rapid analysis of hundreds of proteins “overnight”. Automation is thought to be high advanced but there are more and more doubts evolving.

Results from automation have to be interpreted with care, software has to be taken with caution and raw data have to be carefully and individually checked. Do we have to go back to the past and analyse each protein individually?

Now, technology, hardware, is advanced we have to carefully and rapidly work on identification software and “software” in the scientists’ brains.

Identification of pitfalls in proteomics is mandatory and the many newcomers in the booming proteomic area have to be trained to prevent overload literature with identifications just based upon “highest score” printed out from instruments.

These editorial words declare the aim to invite scientists in the area to submit short communications that will be handled rapidly to inform the young proteomic community about pitfalls in proteomics.

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