

Jérôme GARIN

Laboratoire d'Étude de la Dynamique des Protéomes (EDyP ; U880 CEA/INSERM/UJF)
Grenoble (France)

Mass spectrometry–based proteomics turns quantitative

Mass spectrometry has served as a major tool for the discipline of proteomics to catalogue proteins in an unprecedented scale. The development of high throughput proteomics methodologies has generated a concomitant need for protein quantification. A few recently developed methodologies offering the opportunity to obtain quantitative proteomic information will be presented. A special focus will be dedicated to the intensified efforts which are done worldwide to establish robust approaches for absolute protein quantification of proteomes. These efforts are especially critical in the context of systems biology, and for the successful promotion of candidate proteins into clinically relevant biomarkers.