# Making the most of your experiments: powerful processing of proteomics data for optimal performance

**Prof. Lennart Martens** (Department of Biochemistry, Faculty of Medicine and Health Sciences, Ghent University, Ghent, Belgium)

High-throughput proteomcis studies are capable of generating large volumes of data quickly, and the latest instruments and methods allow investigations of the proteome that span more than an astonishing ten orders of magnitude. However, both the amount of data as well as the complexity of the methodologies employed, require advanced and powerful data processing to extract useful information from an experiment. Indeed, data processing, analysis and interpretation often forms the bottleneck in present-day proteomics experiments. Here, several end-user oriented tools, algorithmic approaches and detailed data analyses will therefore be presented that show how to obtain the most from your experiments, while also highlighting issues and caveats that need to be taken into account. It will thus be shown that highly powerful data processing of proteomics data is already available to any interested scientist, thus highlighting the usefulness of proteomics as a unique analytical research tool in the life sciences.