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New... ICPL™ Quadruplex technology improved with free Analysis Software

Biophoretics Inc. introduces the Serva ICPL™ Quadruplex Kit for simultaneous proteome analysis of four protein samples along with free ICPL*Quant* analysis software. The new ICPL*Quant* software and ICPL Quadruplex kit permit the user to quantify and identify: posttranslational modifications, processing variants, isoforms, membrane and low abundance proteins, and allow reducing proteome complexity by fractionation, enabling high- throughput quantitative protein profiling. Using isotope coded protein labelling (ICPL) of all lysine residues and N-termini of intact proteins, this technology is applicable to all protein samples including body fluids and tissue extracts, and is compatible with all protein separation methods. The main functionalities of the ICPL*Quant* software are peptide pattern searching (ICPL duplex, triplex, quadruplex), peptide quantification in an LC-run and merging with MASCOT protein results. ICPL*Quant* takes deisotoped data as input, generates precursor files for MS/MS and is able to import MASCOT result files for combining MS/MS and quantification results. By selecting only regulated precursors for subsequent MS/MS experiments, the software minimizes time consuming acquisition and interpretation of MS/MS data. The software was developed for analysis of LC/MS (MS¹) data of ICPL™ – labelled proteins (Brunner et. al., ICPL*Quant* – A software for non-isobaric isotope labelling proteomics, *Proteomics* 10, 2, (2010)). For more information or to down load the software free of charge go to:

Review and get software here.

<http://www.biochem.mpg.de/en/rg/lottspeich/technologies/ICPLQuant/index.html>

Get product and order information here.

http://www.biophoretics.com/pdfs/2010_06_18_0_498914.pdf

View ASCB poster presentation here.

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Never Stop Exploring...

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