## SERVA ICPL™ Quadruplex Kit - Now with a fourth label!

The powerful ICPL ™-technology for comparative quantification of proteins is now available with a fourth label. Applying the ICPL™ Quadruplex method the simultaneous quantitative analysis of four independent proteome samples can be performed by stable isotope protein labelling of all lysine residues and protein N-termini. The ICPL™-technology combines the power of stable isotope labelling with the concept of reducing the proteome complexity by fractionation of intact proteins.

## Data evaluation with ICPLQuant –freeware and easy to use

A new software - ICPLQuant – was developed for analysis of LC/MS data of ICPLTM – labelled proteins (Brunner et. al., ICPLQuant – A software for non-isobaric isotope labelling proteomics, Proteomics 10, 2, (2010)).

**The software tool is free of charge and can be downloaded from:**

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

The main functionalities are peptide pattern searching (ICPL duplex, triplex, quadruplex), peptide quantification in an LC-run and merging with MASCOT protein results. ICPLQuant 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.
Up to now, ICPLQuant is able to handle data generated by MALDI (Applied Biosystems 4700/4800, Bruker Ultraflex) and ESI (Thermo Orbitrap) machines.

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