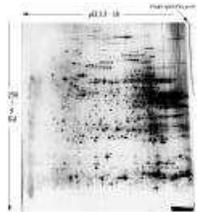


Proteomics

Our proteome service includes optimization of **sample extraction**, **protein quantification** and **sample clean-up**.

1- and 2-dimensional gel-electrophoresis on small, medium and



large scale gels can be done. The service includes staining (Coomassie, silver, Sypro-Ruby, ProQ Diamond, Flamingo, DIGE etc.), scanning, electroblotting, and western-blot analyses.

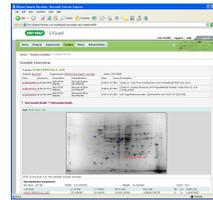
For quantitative **image analysis** we compare 2D-gels with the software packages ProteomWeaver and PDQuest .

For **spot-picking** the data can be directly transferred to a spot-cutter, which picks up to 600 spots/h. Furthermore, the cutter is also capable to pick membranes (NC and PVDF) for on-membrane proteolytic digest.



Up to 384 **proteolytic in-gel digests** can be performed overnight with a roboter for automatic MALDI-

TOF-MS peptide fingerprints and MS/MS analyses combined with database searches for protein identification.



All analysis data are stored in a central **database** (iDQuest) which the client can access via an internet-browser.

N-Terminal Edman sequencing



The amino acid sequence of proteins and peptides can be determined by Edman sequencing. If the N-terminus is not blocked, this is still the method of choice for identification of the N-terminus.

HPLC separation techniques

We offer HPLC methods for isolation of proteins, peptides and other biomolecules.

The methods include gelpermeation-, ion-exchange-, normal- and reverse-phase-chromatography.



LC-MALDI coupling

For LC-MALDI coupling we have a nano-LC system which can be coupled with a fraction



collector which allows direct spotting of complete LC-runs on a MALDI-TOF target to obtain a higher sequence coverage compared to total digest MS analysis.

Posttranslational modifications

We have methods to localize and analyze phosphorylation sites, O- and N-glycans and disulfide linkages.

C. elegans Lab

Our *Caenorhabditis elegans* lab is focused on the investigation of host-parasite interactions between nematode parasites and their hosts. We have a large set of *E. coli* RNAi feeding strains to knock-down specific proteins.

The Protein Analytics Team



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Pricing

Clients can choose between different cost models:

Academic co-authorship:

Academic clients usually prefer this model, but the client is obliged to offer co-authorship for the scientists of the **Protein Analytics** group who are involved in the analyses for any publication using results generated in the **Protein Analytics** group.

Academic

Academic clients who do not plan to publish the analyses data have to choose this model.

Industry

Non-academic clients have to choose this cost model.



From complete organisms to protein structures ...

