



CHEMICAL ANALYTICS

PROTEOMICS AND ANALYTICAL BIOCHEMISTRY

ESTABLISHED METHODS AND INSTRUMENTATION & ESTABLISHED WORKFLOWS FOR PROTEOMICS PROJECTS

Our research laboratory offers a range of latest proteomics methods and technologies together with proteomics project consulting and management. Our key techniques are:

ELECTROPHORESE

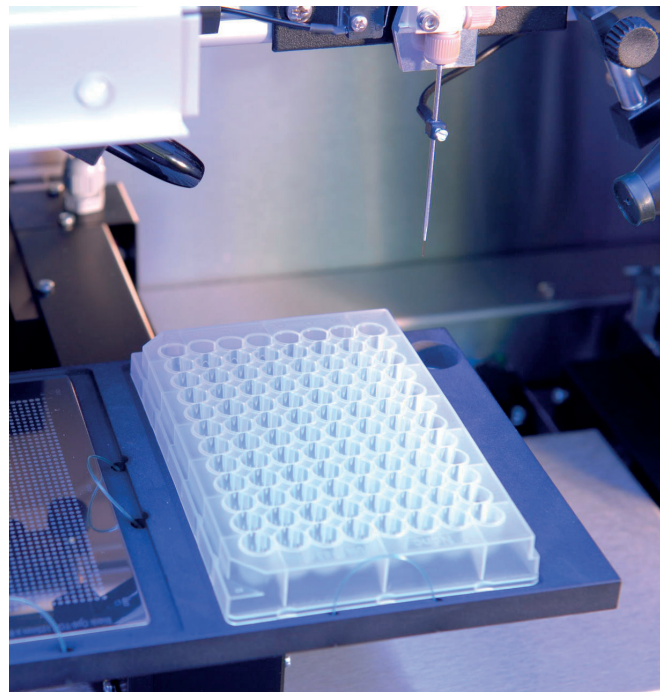
1D- and 2D-PAGE (e.g. vertical and horizontal carrier ampholyte IEF, IPG-IEF, SDS-PAGE with various buffer systems, large sized 2D-PAGE for simultaneously running up to twelve gels, all gel staining techniques).

PROTEIN- AND PEPTID-HPLC

RP-HPLC, IEX-HPLC, affinity chromatography (e.g. for depletion of high abundant proteins in serum or plasma), HPLC on monolytical columns, nano-HPLC separations All techniques are available both on analytical as well as preparative scale .

MASS SPECTROMETRY

ESI-MS: High resolution high mass accuracy mass spectrometry (LTQ-Orbitrap)
MALDI-MS (4800 MALDI TOF/TOF Analyzer)
Identification of PTMs
Protein quantification via stable isotope labelling techniques (e.g. iTRAQ, ICPL, ICAT)



BIOINFORMATICS

Quantitative image analysis of 1D- and 2D-gels
Mass spectra evaluation via e.g. Mascot, Sequest, ProteinPilot, de novo sequencing
Biomarker discovery via multivariate statistics (e.g. PCA, PLS-DA)

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ESTABLISHED WORKFLOWS FOR PROTEOMICS PROJECTS:

We offer a large variety of different workflows for proteomics projects, e.g.:

Development of image analysis software for 1D- and 2D-gels

One of our latest projects was dedicated to the development of a 1D-image analysis software for the detection of doping with recombinant erythropoietin. The software was used at the IAAF World Championships in Athletics (Helsinki 2005) and the Olympic Winter Games (Torino 2006).

Quantitative proteomics for biomarker discovery

Digging deeper into proteomes by multidimensional fractionation techniques is one of the key elements for quantifying low abundant regulatory proteins. Our workflows include both gel based and non-gel based techniques and are selected according to the analytical needs and our customers' ideas. They are based on stable isotope labelling techniques on intact protein level or on peptide level after enzymatic digestion.

To mention just a few of our workflows: SDS-PAGE-MS, IPG-MS, 2D-PAGE-MS, multidimensional chromatography (mRP, SCX, RP, perfusion chromatography, multi affinity chromatography, etc.).

Quantisation is usually done by HT-MALDI TOF/TOF mass spectrometry as well as latest ESI techniques (e.g. PQD, HCD) and dedicated bioinformatics software.

Characterization and identity confirmation of recombinant protein pharmaceuticals)

The identity of generic protein/peptide based pharmaceuticals has to be strictly controlled. We compare these generic or non-generic pharmaceuticals with their non-generic analogues (e.g. erythropoietin, hCG, hGH, LH, FSH). A set of orthogonal techniques is usually employed (e.g. IEF-PAGE, 2D-PAGE, ESI-MSn, MALDI-TOF MS, HPLC on monolytic columns).

Proteomic profiling and classification

We use high resolution high mass accuracy mass spectrometry for this purpose. A series of several thousand characteristic masses per sample are being statistically evaluated and used for discrimination and grouping purposes.



CONTACT

Seibersdorf Labor GmbH
Chemical Analytics
2444 Seibersdorf, Austria

DR. CHRISTIAN REICHEL

Phone: +43 50550 - 3572
+43 50550 - 3500 (Secretary)
Fax: +43 50550 - 3566
E-mail: christian.reichel@seibersdorf-laboratories.at
Web: www.seibersdorf-laboratories.at/proteomics