Justus-Liebig-University Giessen, Faculty of Medicine,
Institute of Biochemistry, Friedrichstrasse 24, 35392 Giessen
https://www.uni-giessen.de/fbz/fb11/institute/biochemie/forschung/corefacilityproteomics/indexcorefacilityproteomics

Biochemisches Institut
FB 11

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Core Facility Proteomics

LC-ESI-MS-based Proteomics

Priority ☐ normal ☐ high **Internal sample number…………………………..**

Client

Name*   ………………………….   email*   …………………………………….

Institution*   …………………………………………………………………………….

Address*   …………………………………………………………………………….

Phone, fax*   ………………………….

Cost model*:   ☐ Inst. Biochemistry

☐ Industry   ☐ other: …………………

Sample [a]

☐   Extract   ☐ other: ……………………………………………………..

No of samples   ……..   Sample name   …………………………………….

Origin* (NCBI taxonomy ID)   …………………………………………………….

Sample preparation* …………………………………………………………………….

…………………………………………………………………………………………..

…………………………………………………………………………………………..

known contaminants*   ☐   salt

☐   detergents

☐   other: …………………………………………….

known modifications* ☐   …………………………………………………….

Radioactivity*   ☐ no   ☐ yes

☐ hazardous   ☐ infectious   ☐ cancerous

☐ dry   soluble in   ☐ Lysis buffer ☐ 0.1% TFA ☐   other: ……………….

☐ dissolved in   ☐ Lysis buffer ☐ 0.1% TFA ☐   other: ……………….

Storage* ☐ -80°C ☐ -20°C ☐ 4-8°C ☐ RT

* required

[a] Detailed information about the sample is a prerequisit for successful analysis. Clients are strongly encouraged to discuss sample preparation with the core facility: proteomics@biochemie.med.uni-giessen.de

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Analysis

Extraction:

☐ Lysis buffer   ☐ other: …………………………………………………………..

      Vol.: ………..

Precipitation:

☐ Acetone   ☐ Chlorform/Methanol

☐ Protein determination   Concentration ……........

Chemical modifications:

☐ Reduction/carbamidomethlyation   ☐ other: …………………………………………

Proteolytic digest:

☐ digest in solution   ☐ digest in gel   ☐ FASP

☐ Trypsin   ☐ other ……………………..

☐ ZipTip desalting (..... % of sample)

☐ lyophilisation

☐ reconstitution in …………………………………………..

Isotopic labelling:

☐ TMT …. plex   ☐ other ……………….

Fractionation:

☐ high-pH fractionation

LC-ESI-MS:

….. %/ug of sample/analysis

….. h gradient

Specific MS parameters: …………………………………………………………………..

                                 …………………………………………………………………..

* required

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Bioinformatic analysis

☐ Proteome Discoverer

    ☐ MASCOT

    ☐ Sequest

    ☐ PMI-Byonic

    ☐ XlinkX

☐ PMI-Byonic

☐ PEAKS

☐ …………………

☐ specific analysis parameters: …………………………………………………………..

Aim of analysis: …………………………………………………………………..

                     ………………………………………………………………….

                     ………………………………………………………………….

Results

☐ by phone   ☐ by email   ☐ by fax

☐ data upload ………………………………………………………………………….

Signature client   …………………………….   **Date**: ……………………

Fax signed form to: 0641-99-47489 or send by email

* required

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