

FEE SCHEDULE 2023 | PROTEOMICS CENTER

ERASMUS MC - ROTTERDAM

| Sample preparation | | |
|--|--|----------------|
| | | EUR |
| Protein digestion, sample cleanup | | |
| | o 1-5 gel slice samples | 75 / sample |
| | o 6-10 gel slice samples | 50 / sample |
| | o >11 gel slice samples | 30 / sample |
| | o complete SDS-PAGE lane | 300 |
| | o other proteases (V8, Lys-N, Lys-C, pepsin, etc.) | 150 |
| | o In-solution digestion, 1-5 samples | 75 |
| | o In-solution digestion, >6 samples | 50 |
| | o On-bead digestion | 75 |
| Peptide fractionation of complex mixtures (WCE, tissue, etc.) | | |
| | o HILIC | 250 |
| | o RP, high pH elution | 300 |
| | o SCX, SAX | 300 |
| <p>For deep proteome coverage, we highly recommend fractionation of complex mixtures into at least 3 fractions.</p> | | |
| PTM enrichment | | |
| | o enrichment for phosphoproteomics (TiO ₂ , IMAC, etc.) | 250 |
| | o diGly, acetylated, methylated, etc. peptide enrichment with PTMscan (<u>including</u> reagents), per IP | 550 |
| | o diGly, acetylated, methylated, ... peptide enrichment with PTMscan (<u>excluding</u> reagents) | 250 |
| | o other PTM enrichment | <i>enquire</i> |
| Post-digestion labeling for quantitation (WCE, tissue, protein complex, etc.) | | |
| | o TMTPro (16- or 18-plex) labeling per sample | <i>enquire</i> |
| | o dimethyl labeling per sample | <i>enquire</i> |
| | o ¹⁸ O labeling per sample | <i>enquire</i> |
| <p>All additional, non-standard sample handling will be charged at € 65 per hour.</p> | | |
| Mass spectrometry | | |
| LC-MS (DDA/DIA on the Orbitrap Fusion Lumos Tribrid, Orbitrap Eclipse, Orbitrap Exploris 480 or Q Exactive Plus) | | |
| | 1 LC-MS (RP) run 60 min | 90 |
| | 1 LC-MS (RP) run 120 min | 135 |
| | 1 LC-MS (RP) run 180 min | 180 |
| PRM analysis (Orbitrap) | Selected set of target proteins (5 transitions per target) | <i>enquire</i> |
| Intact protein analysis | | 750 |

Data analysis

Standard data analysis includes identification and quantitation (SILAC, TMT and LFQ) for DDA and DIA analyses. The choice of software tool depends on the experimental design. We use MaxQuant, Proteome Discoverer / Mascot, PEAKS, Spectronaut, DIA-NN, Byonic, etc.

| | | |
|---|--|-----------|
| Additional downstream data analyses (statistical analysis, Perseus, etc.) | | 65 / hour |
| | | |

Two example applications:

Example 1: Complete gel lane

| | |
|------------------------------------|------------|
| Complete gel lane (>10 gel slices) | 300 |
| 10x LC-MS run (60 min) | 600 |
| Total | 900 |

Example 2: In-solution digest + HILIC fractionation of a complex sample

| | |
|------------------------|-------------|
| Protein digestion | 75 |
| HILIC fractionation | 250 |
| 6x LC-MS run (120 min) | 810 |
| Total | 1135 |

Terms & conditions

- Consultation regarding study design, data interpretation, and publication / public access is provided at no cost. Please note that charges include only a *minor* part of the reagent and personnel costs – the major part is covered by Erasmus MC core funding. The Proteomics Center realizes no profit whatsoever.
- The Proteomics Center runs all projects on a collaborative basis, which is expected to result in co-authorship if data generated by the Center are published in scientific papers. This scientific output allows our scientists to apply for research and infrastructure funding, which will ensure access to the state-of-the-art proteomics technology for Erasmus MC and external researchers.
- New collaborators are allowed to run one pilot experiment for free. If the results are satisfactory for both parties, the costs for subsequent experiments as indicated above will be charged to the collaborator.

For further information please contact the core facility director, Dr. Jeroen Demmers | email: j.demmers@erasmusmc.nl | <https://proteomics.center>

Visiting address

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