

FEE SCHEDULE 2024 | PROTEOMICS CENTER

ERASMUS MC - ROTTERDAM

Sample preparation		
		EUR
Protein digestion, sample cleanup		
	o 1-5 gel slice samples	115 / sample
	o 6-10 gel slice samples	75 / sample
	o >11 gel slice samples	45 / sample
	o complete SDS-PAGE lane	450
	o other proteases (V8, Lys-N, Lys-C, pepsin, etc.)	225
	o In-solution digestion, 1-5 samples	115
	o In-solution digestion, >6 samples	75
	o On-bead digestion	115
Peptide fractionation of complex mixtures (WCE, tissue, etc.)		
	o HILIC	375
	o RP, high pH elution	450
	o SCX, SAX	450
For deep proteome coverage, we highly recommend fractionation of complex mixtures into at least 3 fractions.		
PTM enrichment		
	o enrichment for phosphoproteomics (TiO ₂ , IMAC, etc.)	375
	o diGly, acetylated, methylated, etc. peptide enrichment with PTMscan (<u>including</u> reagents), per IP	825
	o diGly, acetylated, methylated, ... peptide enrichment with PTMscan (<u>excluding</u> reagents)	375
	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>
All additional, non-standard sample handling will be charged at € 65 per hour.		
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	135
	1 LC-MS (RP) run 120 min	200
	1 LC-MS (RP) run 180 min	270
PRM analysis (Orbitrap)	Selected set of target proteins (5 transitions per target)	<i>enquire</i>
Intact protein analysis		1125

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.)		95 / hour

Two example applications:

Example 1: Complete gel lane

Complete gel lane (>10 gel slices)	450
10x LC-MS run (60 min)	1350
Total	1800

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

Protein digestion	115
HILIC fractionation	375
6x LC-MS run (120 min)	1200
Total	1690

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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