

FEE SCHEDULE 2021 | PROTEOMICS CENTER

ERASMUS UNIVERSITY MEDICAL CENTER ROTTERDAM

Sample preparation			
		EUR	
Protein digestion:			
	- Tryptic digestion of 1-5 gel band samples	90 per sample	
	- Tryptic digestion of 6-10 gel band samples	45 per sample	
	- Tryptic digestion of 10-20 gel band samples	30 per sample	
	- Tryptic digestion of one SDS-PAGE lane	300	
	- Digestion with other proteases (V8, Lys-N, Lys-C, pepsin, etc.)	150	
	- In-solution digestion	225	
	- On-bead digestion	225	
Peptide fractionation of complex mixtures (WCE, tissue, etc.):			
	- Fractionation by HILIC	300	
	- Fractionation by RP, high pH elution	300	
	- Fractionation by SCX or SAX	300	
For deep proteome coverage, we highly recommend fractionation of complex mixtures into <i>at least 6 fractions</i>.			
Peptide enrichment:			
	- TiO ₂ enrichment for phosphoproteomics	150	
	- diGly, acetylated, methylated, etc. peptide enrichment with PTMscan (<u>including</u> reagents)	1050	
	- diGly, acetylated, methylated, ... peptide enrichment with PTMscan (<u>excluding</u> reagents)	225	
	- Other types of enrichment: optional	<i>enquire</i>	
Post-digestion labeling for quantitation (WCE, tissue, protein complex, etc.):			
	- TMT labeling per sample	<i>enquire</i>	
	- Dimethyl labeling per sample	<i>enquire</i>	
	- 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 on the Orbitrap Fusion Tribrid, Orbitrap Fusion Lumos Tribrid or Q Exactive Plus (for complex proteomes and PTM analysis):			
	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 on Orbitrap Fusion Tribrid, Orbitrap Fusion Lumos Tribrid or Q Exactive Plus:			
	Setup of PRM analysis for ~10 target proteins (3-5 transitions per target)	1500	
	1 LC-MS (RP) run	90 / 135 / 180	

Intact protein analysis on the Orbitrap Fusion Tribrid:		750	
Data analysis			
Standard data analysis includes identification and quantitation by either SILAC, TMT, ¹⁸ O, dimethylation or LFQ. Software tools include MaxQuant, Mascot, Proteome Discoverer and PEAKS.			
Additional downstream data analyses (statistical analysis, Perseus, etc.):		75 per hour	

Two example applications:

Example 1: Complete gel lane for interactomics study

10 bands digestion total	300
10 LC-MS runs (Orbitrap)	300
Total	600

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

Protein digestion	225
HILIC fractionation	300
6 LC-MS runs (Fusion 120 min)	810
Total	1335

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. Consultation regarding study design, data interpretation, and publication / public access is provided at no cost. Charges include part of the reagent and personnel costs - the Center realizes no profit whatsoever.

New collaborators are allowed to run pilot experiments 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 Dr. Jeroen Demmers:
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