

FEE SCHEDULE 2020 | PROTEOMICS CENTER

ERASMUS UNIVERSITY MEDICAL CENTER ROTTERDAM

Sample preparation		
		EUR
Protein digestion:		
	- Tryptic digestion of 1-5 gel band samples	60 per sample
	- Tryptic digestion of 6-10 gel band samples	30 per sample
	- Tryptic digestion of 10-20 gel band samples	20 per sample
	- Tryptic digestion of one SDS-PAGE lane	200
	- Digestion with other proteases (V8, Lys-N, Lys-C, pepsin, etc.)	60
	- In-solution digestion	150
	- On-bead digestion	150
Peptide fractionation of complex mixtures (WCE, tissue, etc.):		
	- Fractionation by HILIC	200
	- Fractionation by RP, high pH elution	200
	- Fractionation by SCX or SAX	200
<p>For deep proteome coverage, we highly recommend fractionation of complex mixtures into <i>at least</i> 6 fractions.</p>		
Peptide enrichment:		
	- TiO ₂ enrichment for phosphoproteomics	100
	- diGly, acetylated, methylated, etc. peptide enrichment with PTMscan (including reagents)	700
	- diGly, acetylated, methylated, ... peptide enrichment with PTMscan (excluding reagents)	150
	- 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>
<p>All additional, non-standard sample handling will be charged at € 65 per hour.</p>		
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	60
	1 LC-MS (RP) run 120 min	90
	1 LC-MS (RP) run 180 min	120
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)	1000
	1 LC-MS (RP) run	60 / 90 / 120

Intact protein analysis on the Orbitrap Fusion Tribrid:	500
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.):	50 per hour

Two example applications:

Example 1: Complete gel lane for interactomics study

10 bands digestion total	200
10 LC-MS runs (Orbitrap)	200
Total	400

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

Protein digestion	150
HILIC fractionation	200
6 LC-MS runs (Fusion 120 min)	540
Total	890

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.

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