

<b>CNB-CSIC PROTEOMICS FACILITY FARES 2021</b>	<b>CAMPUS DE EXCELENCIA UAM+CSIC</b>	<b>CSIC</b>	<b>PUBLIC*</b>	<b>PRIVATE</b>
<b>Protein and Peptide Molecular Weight Analysis by Mass Spectrometry</b>				
Molecular Weight Analysis By MS-MALDI-TOF	16	32	37	64
<b>Protein Identification</b>				
<b>Protein Identification by MS-MS/MS (MALDI-TOF/TOF)</b>				
Peptide Mass Fingerprinting MS-MS/MS (MALDI-TOF/TOF) Coomassie/Silver/Sypro	36	58	68	103
<b>Protein Identification by LC-ESI-MS/MS (protein extraction/lysis not incl.)</b>				
High Resolution, "Ultra-short" Gradient	136	155	181	241
High Resolution, Short Gradient	179	202	236	307
High Resolution, Medium Gradient	221	259	303	464
High Resolution, Long Gradient	398	487	570	798
<b>Others: Protein Fractionation</b>				
High pH Reversed-Phase Fractionation (HPLC)	185	190	222	334
High pH Reversed-Phase Fractionation (Spin-column)	88	90	105	158
<b>Protein Characterization</b>				
<b>Determination Of Phosphosites (protein extraction/lysis not incl.)</b>				
Simple Protein Mixture (Enrichment + LC-ESI-MS/MS, MR, Short Gradient)	258	290	339	469
Complex Protein Mixture (Enrichment + LC-ESI-MS/MS, HR, Medium Gradient)	300	347	406	622
Phosphopeptides Quantitation - LFQ (LC-ESI-MS/MS, High Resolution, Medium Gradient)	306	375	444	694
<b>Sequencing (protein extraction/lysis not incl.)</b>				
De novo Peptide Sequencing of a Simple Mixture (by LC-ESI-MS/MS, MR, Short Gradient)	194	225	264	330
<b>Electrophoresis</b>				
<b>SDS-PAGE (staining not incl.)</b>				
SDS-PAGE, minigel	16	20	23	50
SDS-PAGE, medium gel	36	38	44	78
SDS-PAGE, large gel	52	55	64	123
<b>Gel Staining</b>				
Silver or Fluorescent Gel Staining, minigel	29	31	36	54
Silver or Fluorescent Gel Staining, medium or large gel	33	35	41	57
Coomassie Gel Staining, minigel	12	21	24	34
Coomassie Gel Staining, medium or large gel	16	24	28	38
<b>Others</b>				
Cleanup/Concentration By SDS-PAGE Gel ("Stacking gel")	70	98	112	192
Fluorescent Gel Scanning (Typhoon)	-	52	60	100
<b>Differential Proteomics by Mass Spectrometry</b> (Relative quantitation of differences in protein abundance)				
<b>Isobaric chemical labelling (iTRAQ/TMT) (protein extraction/lysis incl.)</b>				
4 samples - iTRAQ-4plex Simple (LC-ESI-MS/MS, High Resolution, Long Gradient)	916	1240	1469	1971
4 samples - iTRAQ-4plex Fractionated (4 Fr.) (LC-ESI-MS/MS, High Resolution, Medium Gradient)	1377	1792	2128	3097
6 samples - TMT-6plex Simple (LC-ESI-MS/MS, High Resolution, Long Gradient)	1231	1720	2004	2661
6 samples - TMT-6plex Fractionated (4 Fr.) (LC-ESI-MS/MS, High Resolution, Medium Gradient)	1722	2324	2713	3859
8 samples - iTRAQ-8plex Simple (LC-ESI-MS/MS, High Resolution, Long Gradient)	1551	2175	2569	3381
8 samples - iTRAQ-8plex Fractionated (4 Fr.) (LC-ESI-MS/MS, High Resolution, Medium Gradient)	2074	2821	3340	4663
<b>Non-labelling (Label Free Quantitation) **price/sample (protein extraction/lysis incl.)</b>				
Label Free Quantitation - Simple (LC-ESI-MS/MS, High Resolution, Short Gradient)	211	267	316	424
Label Free Quantitation - Medium (LC-ESI-MS/MS, High Resolution, Medium Gradient)	231	295	350	547
Label Free Quantitation - Complex (LC-ESI-MS/MS, High Resolution, Long Gradient)	389	473	560	834
<b>Targeted Proteomics (sample preparation not incl.)</b>				
Method development for MRM quantification	200	242	282	359
Protein quantification by MRM (per sample)	43	56	65	86
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<b>IMPORTANT: These prices are subjected to changes in function of necessary additional sample preparation steps</b>				

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<b>Peptide Synthesis</b>					
<b>Single peptides (€/peptide)</b>					
<b>25µmol (15-20mg)</b>					
<b>CRUDE</b>	1-8 amino acids	90	100	130	160
	9-15 amino acids	126	140	182	224
	> 15 amino acids	180	200	260	320
<b>&gt;90%</b>	1-8 amino acids	162	180	234	290
	9-15 amino acids	198	220	286	352
	> 15 amino acids	252	280	364	448
<b>Peptide libraries 2µmol (1-2mg) (€/peptide) // AAA: amino acid analysis</b>					
<b>Light</b>					
<b>CRUDE</b>	23	25	33	40	
<b>&gt;90%</b>	54	60	78	96	
<b>&gt;90% + AAA</b>	86	97	119	146	
<b>Heavy (peptide C-term labeled with heavy Lys (+8Da) or Arg (+10Da))</b>					
<b>CRUDE</b>	40	45	59	72	
<b>&gt;90%</b>	72	80	104	128	
<b>&gt;90% + AAA</b>	104	117	145	178	
<b>Peptide modifications (€/modif.)</b>					
KLH/OVA/BSA conjugation	99	110	143	176	
Fluorescein conjugation (N-term)	67	74	96	118	
Fluorescein conjugation (Cys)	108	120	156	192	
Biotinylation (N term)	36	40	52	64	
Phosphorylation Ser/Thr/Tyr	45	50	65	80	
<b>Peptide arrays</b>					
Array up to 600 (deca-dodecapeptides)	450	500	600	800	
<b>Gluten Analysis</b>					
<b>Gluten Analysis By R5-ELISA</b>					
Analysis By Competitive R5-ELISA	33	38	50	65	
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