| PROTEOMICS FACILITY FARES 2025 | CNB/CBM | H2020 | CSIC/UAM* | PUBLIC | PRIVATE |
|---|---|---|---|---|---|
| **Protein Identification** | | | | | |
| **Protein Identification by LC-ESI-MS/MS** (sample preparation incl.) | | | | | |
| **High Resolution, "*Ultra-short*" Gradient** | 162 | 182 | 190 | 236 | 281 |
| **High Resolution, Short Gradient** | 209 | 229 | 245 | 297 | 354 |
| **High Resolution, Medium Gradient** | 259 | 280 | 304 | 363 | 432 |
| **High Resolution, Long Gradient** | 468 | 488 | 549 | 633 | 754 |
| **Protein Characterization** | | | | | |
| **Determination Of Phosphosites** (protein identification analysis not incl.) | | | | | |
| **Phosphopeptide Enrichment** | 95 | 102 | 111 | 132 | 157 |
| **Interactomics** | | | | | |
| **X-linking Analysis** | 200 | 225 | 235 | 292 | 347 |
| **Differential Proteomics by Mass Spectrometry** (Relative quantitation of differences in protein abundance) | | | | | |
| **Isobaric chemical labelling (TMT)** (sample preparation incl.) | | | | | |
| **Per sample - TMTpro Simple** (LC-ESI-MS/MS, High Resolution, Long Gradient) | 224 | 245 | 263 | 318 | 378 |
| **Per sample - TMTpro Fractionated (5 Fr.)** (LC-ESI-MS/MS, High Resolution, Medium Gradient) | 310 | 331 | 364 | 429 | 510 |
| **Targeted Proteomics** (sample preparation incl.) | | | | | |
| **Method development for PRM quantification** | 244 | 265 | 287 | 343 | 409 |
| **Protein quantification by PRM (per sample)** | 93 | 114 | 110 | 148 | 176 |
| **Peptide Synthesis** | | | | | |
| **Single peptides (€/amino acid)** | | | | | |
| **25µmol (15-20mg) (>90% purity)** | 17 | 20 | 20 | 26 | 34 |
| **Peptide libraries 2µmol (1-2mg) (€/peptide) // AAA: amino acid analysis** | | | | | |
| **Light >90% purity** | 60 | 69 | 70 | 90 | 115 |
| **Heavy >90% purity** (peptide C-term labeled with heavy Lys (+8Da) or Arg (+10Da)) | 80 | 89 | 94 | 115 | 148 |
| **Amino acid analysis quantitation** | 39 | 39 | 46 | 51 | 56 |
| **Peptide modifications** | | | | | |
| **Per modification** | 79 | 85 | 93 | 116 | 142 |
| **Peptide arrays** | | | | | |
| **Array up to 600** (deca-dodecapeptides) | 469 | 536 | 550 | 695 | 894 |
| **Gluten Analysis** | | | | | |
| **Gluten Analysis By R5-ELISA** | | | | | |
| **Analysis By Competitive R5-ELISA** | 39 | 48 | 46 | 62 | 68 |
| **Other Analysis** | | | | | |
| **Data Re-analysis** (hourly rate) | | | | | |
| **Data re-analysis (search, quantification, etc.)** | 35 | 39 | 41 | 50 | 60 |

**IMPORTANT: Rates applicable as of April 1, 2025 (rates are rounded to euros)**

**\* Rates applicable to CSIC centers or centers located on the UAM Campus**