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🌐 Website coming soon!

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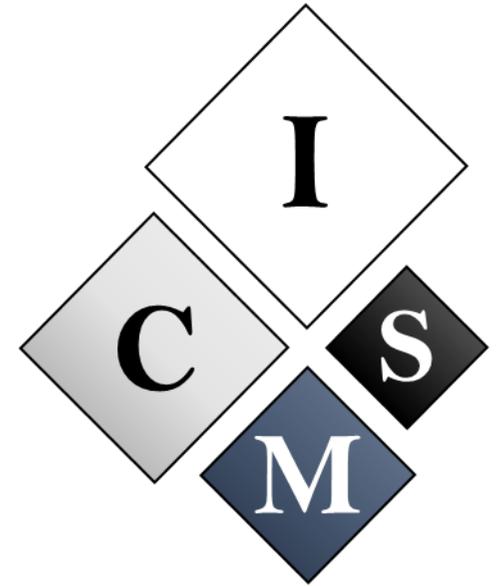
Management committee

Rita Grandori

Marina Lasagni

Marina Lotti

Andrea Marco Zanchi



Interdepartmental Center of Mass Spectrometry



TSQ Quantum™ Access MAX

SAMPLE PREPARATION

Single drop liquid phase microextraction (SDLPME)	€ 40
Dispersive liquid-liquid microextraction (DLLME)	€ 72
Solid phase extraction (SPE)	€ 80
Solid phase microextraction (SPME)	€ 80
Dispersive solid phase extraction (DSPE)	€ 80
Dispersive solid phase microextraction (DSPME)	€ 80
Labeling for unknowns quantitation	€ 180

MASS SPECTROMETRY ANALYSIS

ESI-MS by in flow infusion	€ 80
ESI-MS/MS by in flow infusion	€ 80
HPLC-MS/MS: standard gradient	€ 200
UHPLC-MS/MS: standard gradient	€ 220

DATA ANALYSIS

Interpretation of ESI-MS/MS spectrum for small molecules	€ 64
Interpretation of chromatogram	€ 60

ANALYSIS PACKAGES

Development of UHPLC/HPLC-MS quantitation method (15 determinations included)	€ 4900
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The **Orbitrap Fusion™ Tribid™** mass spectrometer enables the analysis of molecules and supramolecular complexes in the 50-6,000 m/z range, with high resolution (up to R=450,000), scan rate (MSn up to 20 Hz), mass accuracy (< 3 ppm), dynamic range (> 5,000) and sensitivity (100 fg total amount of the reserpine standard). The instrument is characterized by a great flexibility of scan protocols based on multiple fragmentation modes (CID, HCD, ETD) and their combinations, two different collision cells (quadrupole and linear ion trap) and two different mass analyzers (linear ion trap and Orbitrap). These features support bottom-up, top-down and middle-down proteomics studies and enable high-throughput and in-depth analysis of small molecules, peptides, proteins and other polymers, post-translational modifications, protein-ligand interactions. Quantitative proteomics analyses can be implemented by either stable-isotope or label-free approaches. The instrument is equipped with a regular and a nano-electrospray ionization (ESI) sample source and can be coupled to a nano-flow UHPLC EASY-nLC 1000, enabling automated, high-performance LC/MS analyses of complex biological matrices.

The **TSQ Quantum™ Access MAX** instrument is a Triple Quadrupole analyzer equipped with a HESI ionization probe and a 90° high-efficiency square quadrupole collision cell. The instrument enables the analysis of molecules in the mass range 10–3,000 m/z at 5,000 μ /s scan rate and 25 ms polarity switching time. Scan functions include full scan MS in Q1 or Q3, selected ion monitoring (SRM) in Q1 or Q3, selected reaction monitoring (SRM), product ion scanning, precursor ion scanning and neutral loss scanning. In SRM mode, it is possible to define up to 3,000 timed segments and 2 ms dwell times. These features support targeted analysis of hundreds of compounds in a single run. In addition, the quantitation-enhanced data-dependent MS/MS (QED-MS/MS) provides simultaneous compound identification and quantification. The mass spectrometer is coupled with a UltiMate 3000 with LPG-3400SD Gradient Pump, which supports 4 eluents via a proportioning valve with a settable flow of 0.001 to 10.000 mL/min at pressures up to 620 bar. This LC system supports standard LC applications and offers full compatibility with fast UHPLC separations.

Orbitrap Fusion™ Tribid™

SAMPLE PREPARATION

Buffer exchange/desalting	€ 32
Spot/band picking from acrylamide gel	€ 8
In-gel digestion and peptides extraction	€ 72
In-solution digestion	€ 64
Second enzyme digestion	€ 32
Peptide enrichment*	€ 48
Labeling for protein quantitation (iTRAQ)	€ 200
Labeling for protein quantitation (TMT)	€ 160

MASS SPECTROMETRY ANALYSIS

ESI-MS by direct infusion	€ 80
ESI-MS/MS by direct infusion	€ 80
nanoLC-MS/MS: 60 min gradient	€ 160
nanoLC-MS/MS: 90 min gradient	€ 200
nanoLC-MS/MS: 120 min gradient	€ 240
nanoLC-MS/MS: PTM mapping	€ 400
nanoLC-MS/MS: targeted quantitation	€ 400
nanoLC-MS/MS: label-based quantitative proteomics	€ 400
nanoLC-MS/MS: label-free quantitative proteomics	€ 640

DATA ANALYSIS

Analysis of MS spectra	€ 32
Analysis of MS/MS spectra	€ 64
Database search	€ 32
PTM mapping	€ 64
Targeted quantitation	€ 96
Label-based quantitative proteomics	€ 64
Label-free quantitative proteomics	€ 96

ANALYSIS PACKAGES

Intact protein exact mass determination: sample purification by ZipTip and MS by direct infusion	€ 90
Phosphorylation characterization: phosphopeptide enrichment and nanoLC-MS/MS	€ 480
SDS-PAGE band ID: in-gel digestion and nanoLC-MS/MS	€ 304
iTRAQ or TMT protein quantitation: labelling and sample preparation, nanoLC-MS/MS (duplicate run)	€ 640
Label-free protein quantitation: nanoLC-MS/MS (duplicate run)	€ 704

A discount will be applied for orders with a high number of analyses