

LAB. di SPETTROMETRIA di MASSA					
DESCRIZIONE PRESTAZIONE	RESPONSABILE	U.M.	COSTO TOT. € (IVA escl.)	ICMS COD. TARIFF.	Note
In-gel protein Identification by bottom-up or middle-down MS - method development and analytical setting	Grandori Rita	€	500,00 €	ICMS.01A	
In-gel protein Identification by bottom-up or middle-down MS - sample preparation and MS data collection: band excision, washing, reduction, alkylation, in-gel digestion (trypsin); peptides extraction and desalting; nUHPLC-MS/MS analysis (short gradient, HCD fragmentation, duplicate run)	Grandori Rita	€/band	200,00 €	ICMS.02A	
▼ In-gel protein Identification by bottom-up or middle-down MS - alternative/additional digestion protocol	Grandori Rita	€/sample	50,00 €	ICMS.02B	▼ € 50-200 1-4
In-gel protein Identification by bottom-up or middle-down MS - phosphopeptides-enrichment (TiO2)	Grandori Rita	€/sample	90,00 €	ICMS.02C	
In-gel protein Identification by bottom-up or middle-down MS - glycopeptides-enrichment (HILIC)	Grandori Rita	€/sample	160,00 €	ICMS.02D	
▼ In-gel protein Identification by bottom-up or middle-down MS - alternative/additional enrichment protocol	Grandori Rita	€/sample	90,00 €	ICMS.02E	▼ € 90-360 1-4
In-gel protein Identification by bottom-up or middle-down MS - additional fragmentation (CID, ETD)	Grandori Rita	€/analysis	50,00 €	ICMS.02F	
In-gel protein Identification by bottom-up or middle-down MS - data analysis: data processing; database search and protein identification; interpretation and report drafting	Grandori Rita	€/search	50,00 €	ICMS.03A	
In-gel protein Identification by bottom-up or middle-down MS - PTM mapping	Grandori Rita	€/search	100,00 €	ICMS.03B	
In-solution protein Identification by bottom-up or middle-down MS - method development and analytical setting	Grandori Rita	€	500,00 €	ICMS.04A	
In-solution protein Identification by bottom-up or middle-down MS - sample preparation and MS data collection: in-solution reduction, alkylation, digestion (trypsin); peptides desalting; nUHPLC-MS/MS analysis (short gradient, HCD fragmentation, duplicate run)	Grandori Rita	€/sample	150,00 €	ICMS.05A	
▼ In-solution protein Identification by bottom-up or middle-down MS - alternative/additional digestion protocol	Grandori Rita	€/sample	50,00 €	ICMS.05B	▼ € 50-200 1-4
In-solution protein Identification by bottom-up or middle-down MS - phosphopeptides-enrichment (TiO2)	Grandori Rita	€/sample	90,00 €	ICMS.05C	
In-solution protein Identification by bottom-up or middle-down MS - glycopeptides-enrichment (HILIC)	Grandori Rita	€/sample	160,00 €	ICMS.05D	
▼ In-solution protein Identification by bottom-up or middle-down MS - alternative/additional enrichment protocol	Grandori Rita	€/sample	90,00 €	ICMS.05E	▼ € 90-360 1-4
In-solution protein Identification by bottom-up or middle-down MS - additional fragmentation (CID, ETD)	Grandori Rita	€/analysis	50,00 €	ICMS.05F	
In-solution protein Identification by bottom-up or middle-down MS - data analysis: data processing; database search and protein identification; interpretation and report drafting	Grandori Rita	€/search	50,00 €	ICMS.06A	
In-solution protein Identification by bottom-up or middle-down MS - PTM mapping	Grandori Rita	€/search	100,00 €	ICMS.06B	
Qualitative proteomics by bottom-up or middle-down MS - method development and analytical setting	Grandori Rita	€	500,00 €	ICMS.07A	
Qualitative proteomics by bottom-up or middle-down MS - sample preparation and MS data collection: in-solution reduction, alkylation, digestion (trypsin); peptides desalting; nUHPLC-MS/MS analysis (long gradient, HCD fragmentation, duplicate run)	Grandori Rita	€/sample	300,00 €	ICMS.08A	
Qualitative proteomics by bottom-up or middle-down MS - albumin and IgG immunodepletion (for biofluids)	Grandori Rita	€/sample	110,00 €	ICMS.08B	
▼ Qualitative proteomics by bottom-up or middle-down MS - alternative/additional digestion protocol	Grandori Rita	€/sample	50,00 €	ICMS.08C	▼ € 50-200 1-4
Qualitative proteomics by bottom-up or middle-down MS - phosphopeptides-enrichment (TiO2)	Grandori Rita	€/sample	90,00 €	ICMS.08D	
Qualitative proteomics by bottom-up or middle-down MS - glycopeptides-enrichment (HILIC)	Grandori Rita	€/sample	160,00 €	ICMS.08E	
▼ Qualitative proteomics by bottom-up or middle-down MS - alternative/additional enrichment protocol	Grandori Rita	€/sample	90,00 €	ICMS.08F	▼ € 90-360 1-4
Qualitative proteomics by bottom-up or middle-down MS - additional fragmentation (CID, ETD)	Grandori Rita	€/analysis	50,00 €	ICMS.08G	
Qualitative proteomics by bottom-up or middle-down MS - data analysis: data processing; database search and protein identification; interpretation and report drafting	Grandori Rita	€/search	100,00 €	ICMS.09A	
Qualitative proteomics by bottom-up or middle-down MS - PTM mapping	Grandori Rita	€/search	200,00 €	ICMS.09B	
Label-free quantitative proteomics by bottom-up or middle-down MS - method development and analytical setting	Grandori Rita	€	1.500,00 €	ICMS.10A	
Label-free quantitative proteomics by bottom-up or middle-down MS - sample preparation and MS data collection: in-solution reduction, alkylation, digestion (trypsin); peptides desalting; nUHPLC-MS/MS analysis (long gradient, HCD fragmentation, duplicate run)	Grandori Rita	€/sample	300,00 €	ICMS.11A	
Label-free quantitative proteomics by bottom-up or middle-down MS - albumin and IgG immunodepletion (for biofluids)	Grandori Rita	€/sample	110,00 €	ICMS.11B	
▼ Label-free quantitative proteomics by bottom-up or middle-down MS - alternative/additional digestion protocol	Grandori Rita	€/sample	50,00 €	ICMS.11C	▼ € 50-200 1-4
Label-free quantitative proteomics by bottom-up or middle-down MS - phosphopeptides-enrichment (TiO2)	Grandori Rita	€/sample	90,00 €	ICMS.11D	
Label-free quantitative proteomics by bottom-up or middle-down MS - glycopeptides-enrichment (HILIC)	Grandori Rita	€/sample	160,00 €	ICMS.11E	
▼ Label-free quantitative proteomics by bottom-up or middle-down MS - alternative/additional enrichment protocol	Grandori Rita	€/sample	90,00 €	ICMS.11F	▼ € 90-360 1-4
Label-free quantitative proteomics by bottom-up or middle-down MS - additional fragmentation (CID, ETD)	Grandori Rita	€/analysis	50,00 €	ICMS.11G	
Label-free quantitative proteomics by bottom-up or middle-down MS - data analysis: data processing; database search and protein identifications; determination of relative normalized abundance; interpretation and report drafting	Grandori Rita	€/search	250,00 €	ICMS.12A	
Label-free quantitative proteomics by bottom-up or middle-down MS - PTM mapping	Grandori Rita	€/search	200,00 €	ICMS.12B	
Label-based quantitative proteomics by bottom-up or middle-down MS - method development and analytical setting	Grandori Rita	€	1.500,00 €	ICMS.13A	
Label-based quantitative proteomics by bottom-up or middle-down MS - sample preparation and MS data collection: in-solution reduction, alkylation, digestion (trypsin); peptides desalting; nUHPLC-MS/MS analysis (long gradient, HCD fragmentation, duplicate run)	Grandori Rita	€/analysis	1.700,00 €	ICMS.14A	
Label-based quantitative proteomics by bottom-up or middle-down MS - TMT labelling (up to 10 compared samples)	Grandori Rita	€/sample	100,00 €	ICMS.14B	
Label-based quantitative proteomics by bottom-up or middle-down MS - iTRAQ labelling (up to 4 compared samples)	Grandori Rita	€/sample	450,00 €	ICMS.14C	
Label-based quantitative proteomics by bottom-up or middle-down MS - albumin and IgG immunodepletion (for biofluids)	Grandori Rita	€/sample	110,00 €	ICMS.14D	
▼ Label-based quantitative proteomics by bottom-up or middle-down MS - alternative/additional digestion protocol	Grandori Rita	€/sample	50,00 €	ICMS.14E	▼ € 50-200 1-4
Label-based quantitative proteomics by bottom-up or middle-down MS - phosphopeptides-enrichment (TiO2)	Grandori Rita	€/sample	90,00 €	ICMS.14F	
Label-based quantitative proteomics by bottom-up or middle-down MS - glycopeptides-enrichment (HILIC)	Grandori Rita	€/sample	160,00 €	ICMS.14G	
▼ Label-based quantitative proteomics by bottom-up or middle-down MS - alternative/additional enrichment protocol	Grandori Rita	€/sample	90,00 €	ICMS.14H	▼ € 90-360 1-4
Label-based quantitative proteomics by bottom-up or middle-down MS - additional fragmentation (CID, ETD)	Grandori Rita	€/analysis	50,00 €	ICMS.14I	
Label-based quantitative proteomics by bottom-up or middle-down MS - data analysis: data processing; database search and protein identifications; determination of relative normalized abundance; interpretation and report drafting	Grandori Rita	€/search	800,00 €	ICMS.15A	
Label-based quantitative proteomics by bottom-up or middle-down MS - PTM mapping	Grandori Rita	€/search	200,00 €	ICMS.15B	
Targeted quantitative proteomics by bottom-up MS - method development and analytical setting	Grandori Rita	€	4.500,00 €	ICMS.16A	
Targeted quantitative proteomics by bottom-up MS - sample preparation and MS data collection: in-solution reduction, alkylation, digestion (trypsin); peptides desalting; targeted nUHPLC-MS/MS analysis (long gradient, HCD fragmentation, duplicate run)	Grandori Rita	€/sample	200,00 €	ICMS.17A	
Targeted quantitative proteomics by bottom-up MS - albumin and IgG immunodepletion (for biofluids)	Grandori Rita	€/sample	110,00 €	ICMS.17B	
▼ Targeted quantitative proteomics by bottom-up MS - alternative/additional digestion protocol	Grandori Rita	€/sample	50,00 €	ICMS.17C	▼ € 50-200 1-4
Targeted quantitative proteomics by bottom-up MS - phosphopeptides-enrichment (TiO2)	Grandori Rita	€/sample	90,00 €	ICMS.17D	
Targeted quantitative proteomics by bottom-up MS - glycopeptides-enrichment (HILIC)	Grandori Rita	€/sample	160,00 €	ICMS.17E	
▼ Targeted quantitative proteomics by bottom-up MS - alternative/additional enrichment protocol	Grandori Rita	€/sample	90,00 €	ICMS.17F	▼ € 90-360 1-4
Targeted quantitative proteomics by bottom-up MS - additional fragmentation (CID, ETD)	Grandori Rita	€/analysis	50,00 €	ICMS.17G	
Targeted quantitative proteomics by bottom-up MS - data analysis: data processing; quantification of targeted proteins; interpretation and report drafting	Grandori Rita	€/search	50,00 €	ICMS.18A	
Targeted quantitative proteomics by bottom-up MS - PTM mapping	Grandori Rita	€/search	100,00 €	ICMS.18B	
▼ Functional annotation of proteomic results (networks, biological processes, pathways)	Grandori Rita	€/analysis	100,00 €	ICMS.19A	▼ € 100-1000 1-10
Native MS of proteins and protein complexes - method development and analytical setting	Grandori Rita	€	500,00 €	ICMS.20A	
Native MS of proteins and protein complexes - sample preparation and MS data collection: protein desalting and buffer exchange; sample preparation before injection (dilution, denaturant and/or ligand addition etc.); nano-ESI MS analysis (duplicate)	Grandori Rita	€/sample	120,00 €	ICMS.21A	
Native MS of proteins and protein complexes - protein-protein or protein-ligand dissociation by CID	Grandori Rita	€/analysis	50,00 €	ICMS.21B	
Native MS of proteins and protein complexes - data analysis: data processing, mass deconvolution; conformational ensemble deconvolution by Gaussian fitting; estimation of solvent accessible surface area; interpretation and report drafting	Grandori Rita	€/sample	384,00 €	ICMS.22A	
Native MS of proteins and protein complexes - titration for folding or binding analysis	Grandori Rita	€/set	100,00 €	ICMS.22B	
Proteoforms characterization by top-down MS - method development and analytical setting	Grandori Rita	€	1.500,00 €	ICMS.23A	
Proteoforms characterization by top-down MS - sample preparation and MS data collection: desalting, buffer exchange, denaturation; nano-ESI MS analysis (duplicate)	Grandori Rita	€/sample	120,00 €	ICMS.24A	
Proteoforms characterization by top-down MS - nano-ESI MS/MS analysis by HCD fragmentation (per proteoform)	Grandori Rita	€/analysis	50,00 €	ICMS.24B	
Proteoforms characterization by top-down MS - nano-ESI MS/MS analysis by CID fragmentation (per proteoform)	Grandori Rita	€/analysis	50,00 €	ICMS.24C	
Proteoforms characterization by top-down MS - supercharging agent addition; nano-ESI MS/MS analysis by ETD fragmentation (per proteoform)	Grandori Rita	€/analysis	70,00 €	ICMS.24D	
Proteoforms characterization by top-down MS - data analysis: data processing, mass deconvolution; interpretation and report drafting	Grandori Rita	€/sample	50,00 €	ICMS.25A	
Proteoforms characterization by top-down MS - confirmation of protein identity from MS/MS spectra; PTMs identification and mapping	Grandori Rita	€/sample	280,00 €	ICMS.25B	
Proteoforms characterization by top-down MS - deconvolution of isobaric proteoform mixtures	Grandori Rita	€/sample	200,00 €	ICMS.25C	
Protein structural analysis by covalent labelling - method development and analytical setting	Grandori Rita	€	4.500,00 €	ICMS.26A	
Protein structural analysis by covalent labelling - sample preparation and data collection: protein covalent modification (amino-groups, carboxyl-groups, etc.); in-solution reduction, alkylation, digestion (trypsin); peptides desalting; nUHPLC-MS/MS analysis (short gradient, HCD fragmentation, duplicate run)	Grandori Rita	€/sample	400,00 €	ICMS.27A	
▼ Protein structural analysis by covalent labelling - alternative/additional digestion protocol	Grandori Rita	€/sample	50,00 €	ICMS.27B	▼ € 50-200 1-4
Protein structural analysis by covalent labelling - additional fragmentation (CID, ETD)	Grandori Rita	€/analysis	50,00 €	ICMS.27C	
Protein structural analysis by covalent labelling - data analysis: data processing; determination of relative normalized abundance; interpretation and report drafting	Grandori Rita	€/set	800,00 €	ICMS.28A	
Structural proteomics by limited proteolysis (LiP)-MS - method development and analytical setting	Grandori Rita	€	4.500,00 €	ICMS.29A	

Structural proteomics by limited proteolysis (LiP)-MS - sample preparation and data collection: limited proteolysis (proteinase K) and complete digestion (trypsin); reference complete digestion (trypsin); peptides desalting	Grandori Rita	€/sample	150,00 €	ICMS.30A	
Structural proteomics by limited proteolysis (LiP)-MS - untargeted nUHPLC-MS/MS analysis on sample and reference (duplicate run)	Grandori Rita	€/sample	500,00 €	ICMS.30B	
Structural proteomics by limited proteolysis (LiP)-MS - targeted nUHPLC-MS/MS analysis on sample and reference (duplicate run)	Grandori Rita	€/sample	250,00 €	ICMS.30C	
▼ Structural proteomics by limited proteolysis (LiP)-MS - alternative/additional digestion protocol	Grandori Rita	€/sample	50,00 €	ICMS.30D	▼ € 50-200 1-4
Structural proteomics by limited proteolysis (LiP)-MS - data analysis: data processing; determination of proteolytic sites and differential analysis; interpretation and report drafting	Grandori Rita	€/set	800,00 €	ICMS.31A	
H/D exchange analysis on intact protein - method development and analytical setting	Grandori Rita	€	2.500,00 €	ICMS.32A	
H/D exchange analysis on intact protein - sample preparation and data collection: protein desalting and lyophilization; sample preparation for isotopic labelling (exchange-in or exchange-out)	Grandori Rita	€/sample	50,00 €	ICMS.33A	
H/D exchange analysis on intact protein - nano-ESI MS analysis in real time	Grandori Rita	€/sample	150,00 €	ICMS.33B	
H/D exchange analysis on intact protein - aliquot sampling, quenching and nano-ESI MS analysis	Grandori Rita	€/aliquot	100,00 €	ICMS.33C	
H/D exchange analysis on intact protein - ETD fragmentation on selected masses & charge states	Grandori Rita	€/analysis	100,00 €	ICMS.33D	
H/D exchange analysis on intact protein - data analysis: data processing; interpretation and report drafting	Grandori Rita	€/sample	100,00 €	ICMS.34A	
H/D exchange analysis on intact protein - analysis of protein conformational dynamics	Grandori Rita	€/sample	200,00 €	ICMS.34B	
H/D exchange analysis on intact protein - solvent-exposed region mapping	Grandori Rita	€/sample	500,00 €	ICMS.34C	
Small molecules analysis from purified samples - method development and analytical setting	Grandori Rita	€	100,00 €	ICMS.35A	
Small molecules analysis from purified samples - sample preparation for direct injection	Grandori Rita	€/sample	40,00 €	ICMS.36A	
Small molecules analysis from purified samples - low resolution ESI-MS analysis (TSQ Quantum Access Max)	Marina Lasagni	€/sample	60,00 €	ICMS.36B	
Small molecules analysis from purified samples - high resolution ESI-MS analysis (Orbitrap Fusion)	Grandori Rita	€/sample	100,00 €	ICMS.36C	
Small molecules analysis from purified samples - ESI-MS/MS analysis by CID fragmentation (TSQ Quantum Access Max)	Marina Lasagni	€/analysis	60,00 €	ICMS.36D	
Small molecules analysis from purified samples - ESI-MS/MS analysis by CID fragmentation (Orbitrap Fusion)	Grandori Rita	€/analysis	100,00 €	ICMS.36E	
Small molecules analysis from purified samples - additional ESI-MS/MS analysis by HCD/ETD fragmentation (Orbitrap Fusion)	Grandori Rita	€/analysis	140,00 €	ICMS.36F	
Small molecules analysis from purified samples - data analysis: data processing, mass deconvolution	Grandori Rita	€/sample	50,00 €	ICMS.37A	
Small molecules analysis from purified samples - interpretation of MS/SM spectra and report drafting	Grandori Rita	€/analysis	100,00 €	ICMS.37B	
Targeted small molecules quantitation in complex mixtures - method development and analytical setting (15 determinations included)	Marina Lasagni	€	3.900,00 €	ICMS.38A	
Targeted small molecules quantitation in complex mixtures - single drop microextraction	Marina Lasagni	€/sample	40,00 €	ICMS.39A	
Targeted small molecules quantitation in complex mixtures - dispersive liquid-liquid microextraction	Marina Lasagni	€/sample	70,00 €	ICMS.39B	
Targeted small molecules quantitation in complex mixtures - solid-phase (micro)extraction	Marina Lasagni	€/sample	80,00 €	ICMS.39C	
Targeted small molecules quantitation in complex mixtures - dispersive solid-phase (micro)extraction	Marina Lasagni	€/sample	80,00 €	ICMS.39D	
Targeted small molecules quantitation in complex mixtures - HPLC-MS/MS, standard gradient	Marina Lasagni	€/sample	200,00 €	ICMS.39E	
Targeted small molecules quantitation in complex mixtures - UHPLC-MS/MS, standard gradient	Marina Lasagni	€/sample	220,00 €	ICMS.39F	
Targeted small molecules quantitation in complex mixtures -labelling for unknowns quantitation	Marina Lasagni	€/sample	140,00 €	ICMS.39G	
Targeted small molecules quantitation in complex mixtures - data analysis: data processing; quantitation of targeted molecules; interpretation and report drafting	Marina Lasagni	€/sample	130,00 €	ICMS.40A	