Fulvio Magni is one of the leading experts on mass spectrometry and its applications to biomedical research, not only in Italy but also in international MS communities, especially in the field of MS-Imaging. He has expertise on Clinical Chemistry and on Proteomics and Metabolomics. In the last years, he had several grants u**p** to more than 3.300.000€ and he is a PI of the Clinical Proteomics and Metabolomics Unit of the University of Milano-Bicocca.

EDUCATION
1991   PhD in Pharmacology and Toxicology, Faculty of Pharmacy, University of Milan, Italy
1984   Master in Chemistry and Pharmaceutical Technology, Faculty of Pharmacy, University of Milan, Italy

CURRENT POSITION(S)
2016-Present   Full Professor in Biochemistry, Department of Medicine and Surgery, University of Milano-Bicocca, Italy

He has experience on most of the proteomics strategies (proteins identification and PTMs characterization gel-based and gel-free separation (MudPIT), label-based and label-free quantitation, imaging-mass spectrometry, etc.). In the last years, he activated several lines of research in the Clinical Proteomics field aimed to search biomarkers in solid samples (tissues and cellular cultures) and in biological fluids. In collaboration with clinical (urologist and pathologist) and life science (biochemist and clinical biochemist) units he has begun a wide project aimed to define the proteome of the normal and of tumor kidney tissue (RCC). Today he has extended his activity to study the proteome of biological fluids (serum, plasma, urine and amniotic liquor) to search possible biomarkers in several pathologies: renal cell carcinoma, diabetic nephropathy, preterm premature rupture of membranes, and glomerulonephritis. Very recently, he has started the application of the "imaging by mass spectrometry" technique to investigate the spatial distribution of proteins analyzing directly the tissues. He is applying this new technology to study the thyroid and kidney tumors and glomerulonephritis aimed to biomarkers discovery for diagnosis, prognosis and to predict the response to therapy.

He was a member of the "Management Committee" of the following Cost Actions (BIOMEDICINE AND MOLECULAR BIOSCIENCES): **BM0702**: European kidney and urine proteomics (**www.eurokup.org**) and **BM1104**: Mass Spectrometry Imaging: New Tools for Healthcare Research. He is a member of the MC of the Cost Action CA16113 CliniMARK: 'good biomarker practice' to increase the number of clinically validated biomarkers'
He was a **PI of one units of the project: FP7-PEOPLE-2013-ITN;** Initial Training Networks (ITN); Title: Clinical and system –omics for the identification of the MOlecular DEterminants of established Chronic Kidney Disease.
He has experience on proposal writing either for national and international projects (see below). Moreover, he has collaboration with several SMEs.

<div align="center">

Recent Research grant as PI or coordinator
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2006-07:   **MURST** - PROGRAMMI DI RICERCA SCIENTIFICA DI RILEVANTE INTERESSE NAZIONALE - COFIN04 (DM n. 582/2006 del 26 MARZO 2006) *Titolo progetto: Ricerca sistematica di marcatori molecolari del carcinoma renale con nuove tecniche proteomiche e genomiche*.
2009-2013   **FIRB - Fondo per gli Investimenti della Ricerca di Base** (Decreto Direttoriale 1 dicembre 2006 prot. n. 2689/Ric./2006) *Titolo progetto: Rete Nazionale per lo studio della Proteomica Umana (*RBRN07BMCT_011)
2009-2012   **Istituto Italiano di Tecnologia** *(IIT) piano strategico 2009-2011. Progetti SEED: "*Isoelectric focusing chip-array for protein profiling of biological samples with MALDI detection"
2011-2013   Progetto finanziato da Regione Lombardia nell'ambito del "Fondo per la promozione di Accordi Istituzionali" istituito con DGR N. 5200/2007, integrato con DGR N. 8545/2008, approvato con Decreto N. 4779/2009 . Progetto NEDD
2013-2017   **FP7-PEOPLE-2013-ITN;** Funding scheme: Initial Training Networks (ITN); Title: Clinical and system –omics for the identification of the MOlecular DEterminants of established Chronic Kidney Disease.
2017-2020   **Bando AIRC 2016** "Application of a proteomic-based thyroid lesions classifier in cytopathology by MALDI-imaging".