List of references

- **Blalock W. L, Piazzi M, et al.** Identification of the PKR nuclear interactome reveals roles in ribosome biogenesis, mRNA processing and cell division. J Cell Physiol. 2014
- **Colangelo T, Polcaro G, et al.** Proteomic screening identifies calreticulin as a miR-27a direct target repressing MHC class I cell surface exposure in colorectal cancer. Cell Death Dis. 2016
- **Fontana S, Saieva L et al.** Contribution of proteomics to understanding the role of tumor-derived exosomes in cancer progression: state of the art and new perspectives. Proteomics. 2013
- **Garcia-Rua V, Feijoo S, et al.** Metabolic alterations derived from the absence of Two-Pore Channels (TPCs) at the cardiac level: proteomics approach. BBA Proteins and Proteomics. 2016
- **Huttenhain R. S, Surinova R, et al.** N-glycoprotein SRMAtlas: a resource of mass spectrometric assays for N-glycosites enabling consistent and multiplexed protein quantification for clinical applications. Molecular and Cellular Proteomics. 2013
- **de Jager W, Bourcier K, et al.** Prerequisites for cytokine measurements in clinical trials with multiplex immunoassays. BMC Immunol. 2009
- **Kelder T, Verschuren L, et al.** Network signatures link hepatic effects of anti-diabetic interventions with systemic disease parameters. BMC Syst Biol. 2014
- **Lombardi G, Lanteri P, et al.** Blood biochemical markers of bone turnover: pre-analytical and technical aspects of sample collection and handling. Clinical Chemistry and Laboratory Medicine. 2012
- **Mancone C, Ciccosanti F, et al.** Applying proteomic technology to clinical virology. Clin Microbiol Infect. 2013
- **Marziali G, Signore M, et al.** Metabolic/ Proteomic Signature Defines Two Glioblastoma Subtypes With Different Clinical Outcome. Sci Rep. 2016
- **Martins R. P, Collado-Romero M, et al.** Proteomic analysis of porcine mesenteric lymph-nodes after Salmonella typhimurium infection. Proteomics. 2012
- **Mato E, Barceló-Batllori S, et al.** The proteomic 2D-DIGE approach reveals the protein voltage-dependent anion channel 2 as a potential therapeutic target in epithelial thyroid tumours. Mol Cell Endocrinol. 2015
- **Milone M. R, Pucci B, et al.** Proteomic analysis of zoledronic-acid resistant prostate cancer cells unveils novel pathways characterizing an invasive phenotype. Oncotarget. 2016
- **Rodolfo C, Ciccosanti F, et al.** Proteomic analysis of mitochondrial dysfunction in neurodegenerative diseases. Expert Rev Proteomics. 2010
- **Rylova G. T, Ozdian L, et al.** Affinity-Based Methods in Drug-Target Discovery. Current Drug Targets. 2015
- **Segura V, Medina-Aunon J. A, et al.** Surfing transcriptomic landscapes. A step beyond the annotation of Chromosome 16 proteome. Journal of Proteome Research. 2014
- **Van Gool A. J, Hendrickson R. C, et al.** The proteomic toolbox for studying cerebrospinal fluid. Expert Rev Proteomics. 2012
- **Velez P, Ocaranza-Sanchez R, et al.** 2-DIGE-based proteomic analysis of intracoronary versus peripheral arterial blood platelets from acute myocardial infarction patients: upregulation of platelet activation biomarkers at the culprit site. PROTEOMICS. 2016
- **Wessels H. J. C. T, Vogel R. O, et al.** Analysis of 953 human proteins from a mitochondrial HEK293 fraction by complexome profiling. PLOS One. 2013

eatris

European infrastructure for translational medicine

www.eatris.eu, info@eatris.eu, +31 (0)20 4442254

De Boelelaan 1118, 1081 HZ Amsterdam, The Netherlands

How can **proteomics** support your **biomarker research** project?

eatris

PROTEOMIC BIOMARKERS:

QUANTIFY, STANDARDISE AND TRANSLATE TO PRACTICE

FROM MOLECULAR TARGETS TO CLINICAL BIOMARKERS

Proteomics facility at Radboudumc, Nijmegen, The Netherlands

EATRIS institutes offer services and research collaboration in the analysis of protein targets and biomarkers. It includes their identification and validation in relevant preclinical and clinical situation, together with the development of customized proteomic methods for disease diagnosis, prognosis and prediction of therapeutic response. This approach holds the potential for supporting personalized medicine therapies by using each patient's unique proteomic signature. The integration of proteomics into clinical research and practice is not trivial and involves many steps and stakeholders, EATRIS is optimally suited to solve that challenge, being a well organized infrastructure with close collaborations among analytical chemists, biochemists, statisticians, medical and bioinformaticians, translational and clinical researchers.

A selection of EATRIS institutes

Institute of Molecular and Tranlational Medicine (IMTM), Olomouc, Czech Republic
University of Turku and Turku University Hospital, Turku, Finland
Fondazione IRCCS Fondazione Pascale, Napoli, Italy
Fondazione IRCCS Lazzaro Spallanzani, Rome, Italy
University Medical Center Utrecht (UMCU), Utrecht, The Netherlands
Istituto Ortopedico Galeazzi, Milan, Italy
Radboudumc, Nijmegen, The Netherlands
Health Research Institute of Santiago de Compostela (IDIS), Santiago de Compostela, Spain.
Rizzoli Orthopedic Institute (IOR), Bologna, Italy
Vall d'Hebron Research Institute (VHIR), Barcelona, Spain
UMC Utrecht, Utrecht, The Netherlands
Istituto Superiore di Sanità (ISS), Rome, Italy
Instituto Ramón y Cajal (IRYCIS), Madrid, Spain
Bellvitge Biomedical Research Institute (IDIBELL), Barcelona, Spain

How can proteomics help with your biomarker search project?

- Detailed analysis and characterization of single proteins to whole proteome from various matrices;
- Labeling for proteins quantification – compare diseased vs. normal tissues in one experiment;
- Label-free quantification – where unmodified samples are priority;
- Targeted quantification of peptides representing protein biomarkers;
- Enrichment and analysis of post-translation modifications including glycosylations, phosphorylations, ubiquitinylations;
- Development and optimization of protein biomarker assays;
- Optimization of protein biomarker validation in (pre)clinic;
- Analysis of protein-protein interactions by NMR, full length proteins as single or protein complexes;
- Mass spectrometry imaging of tissues;
- Metabolomics profile by signals of single aminoacids;

Quality aspects of the EATRIS proteomic core facilities

- Access to a broad scale of high-end and (ultra) high resolution proteomic equipment including Orbitrap, MALDI-TOF, Q-TOF, QqQ, nano-HPLC/ Ion Trap 3D;
- multiplex immunoassays;
- Shared best practices and protocols among the EATRIS proteomic laboratories;
- Ensurance that isotope labeling of proteins does not affect function and behavior;
- Seamless transition from cell-culture to tissue and/or serum experiments;
- Precise targeted quantification with isotope labeled internal standards;
- Precise liquid handling using robots enables good standardization;
- Experience transition from biomarker discovery to validation phases;
- Close integration of analytical capabilities and data analysis workflows;

NMR 600Mhz Bruker at Fondazione IRCCS Fondazione Pascale, Napoli, Italy