



Marta Cascante is Full Professor at the Department of Biochemistry and Molecular Biology at University of Barcelona and leader of the Integrative Systems Biology, Metabolomics and Cancer team. She has authored over 250 publications, two of them cited in “Stryer” biochemistry textbook. She is partner of European translational research projects (H2020) in the field of systems medicine and metabolomics and member of the editorial advisory boards of Metabolomics and BMC systems Biology. She has been distinguished in 2015 with Icrea Academia Prize and with the Narcis Monturiol Medal of the Catalan Government for her scientific merits.

Research interests are focused on cancer and metabolic diseases with the goal of elucidating the networks and pathways that are fundamental in their development and progression. More specifically, the Integrative Systems Biology, Metabolomics and Cancer team’s mission is to devise new therapeutic strategies to forestall therapeutic resistance in cancer through integrative approaches that afford a rational identification of molecular targets, with emphasis on metabolic regulators, for effective synergistic combinations with chemotherapeutics with demonstrated efficacy and/or natural products. To tackle our mission, our team assembles high-level expertise in comprehensive metabolic analysis, bio-computational approaches, generation of cellular and pre-clinical animal models, functional genomics and drug discovery. We have generated proof-of-principle evidences that resulted in publications and a patent application of the effectiveness of this approach. We intend to generalize our approaches to inhibitors currently in use as first-in-line or emerging therapies, by unveiling and targeting the corresponding adaptive metabolic responses in order to overcome therapeutic resistance in cancer. Furthermore, in the framework of H2020 project “PheNoMenal”, coordinated by EBI, her team is contributing to develop and deploy an e-infrastructure that makes it feasible for healthcare researchers to process analyze and mine molecular phenotyping data, to facilitate large-scale data analysis in the coming age of Precision Medicine.