

## Núria López-Bigas

Núria Lopez-Bigas is an ICREA Research Professor at IRB Barcelona and full professor at the Pompeu Fabra University (UPF). She has a PhD in Biology from the University of Barcelona and expertise in Medical Genetics and Computational Biology and Bioinformatics. During her PhD work, Núria studied the molecular causes of hereditary deafness at Xavier Estivill's group. Next, she moved to the European Bioinformatics Institute in Hinxton (Cambridge, UK) to work on Computational Genomics in Christos A. Ouzounis's lab and then to the CRG (Barcelona) in Roderic Guigó's group. Nuria joined the UPF in April 2006 as a Ramón y Cajal Researcher and was appointed ICREA Research Professor in October 2011, and her lab moved to IRB Barcelona in November 2016. In 2015, she was awarded an ERC Consolidator Grant. She currently leads the European project CGI-Clinics , which joins cancer hospitals across Europe to develop and implement a data-driven cancer genome interpretation for clinical decision making. She co-leads the Cancer Grand Challenge project PROMINENT.

She received the Lilly Foundation Biomedicine Award (2023), the City of Barcelona award (2022), the National "Doctores Diz Pintado" Cancer Research Prize (2020) and the XI Banco Sabadell Foundation Award for Biomedical Research (2016). Nuria Lopez-Bigas was elected member of the European Molecular Biology Organization (EMBO) in 2016, Fellow of the International Society of Computational Biology (ISCB) in 2021, and member of the Spanish Royal Society of Sciences in 2024. In 2022 she received the ISCB Innovator Award. Núria López-Bigas research is focused on the study of cancer from a genomics perspective. She is particularly interested in the identification of cancer driver mutations, genes and pathways across tumor types and understanding the mutational processes leading to accumulation of mutations in tumors, the development of machine learning models to identify driver mutations in cancer genes applied to precision oncology, and the study of somatic mutations that lead to clonal expansions in normal tissues.