

Ferran Nadeu did a bachelor in Biotechnology (University of Barcelona), a master of science in Bioinformatics (Pompeu Frabra University), and a PhD in Biomedicine (University of Barcelona, Dr. Elías Campo lab). He is currently a junior researcher at the Fundació Recerca Clínic Barcelona-Institut d'Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS). He has published >90 articles in top journals in the field of hematology and cancer genomics including Nature Medicine, Nature Genetics, Blood, Nature Communications, among others, as first and/or corresponding author (times cited: >3,300; H-index: 30). Dr. Nadeu has participated as invited speaker, oral presenter, and poster presenter in national and international meetings such as the European Hematology Association (EHA), International Workshop on CLL (iwCLL), American Society of Hematology (ASH), European Research Initiative on CLL (ERIC), and 'Sociedad Española de Hematología y Hemoterapia' (SEHH). Dr. Nadeu has received 14 national and international awards for young investigators including the Young Investigator Award awarded by the Catalan Society of Biology and the American Association for Cancer Research (AACR)-Pezcoller Foundation Scholar-in-Training Award. His research has received the financial support of the European Research Council (ERC, Starting Grant), Instituto de Salud Carlos III (ISCIII, Miguel Servet), EHA, AACR, SEHH, and Lady Tata Memorial Trust, among others. Dr. Nadeu has served as a referee for high-impact journals and national/international congresses. He has supervised multiple high-school scientific projects, final degree projects, final master thesis, and PhD students. He has licensed the use of the IgCaller algorithm for its commercial use. His research focuses on understanding the (immuno)genomic determinants of B-cell leukemia/lymphoma initiation, diversification, and progression before and after therapy through the use of novel methodologies and bioinformatic tools. Dr. Nadeu also aims to translate these new tools and knowledge into easy-to-implement assays for the routine molecular characterization of these neoplasms, as accomplished with the IgCaller algorithm and the all-CLL next-generation sequencing panel.