Biomedical Genomics Group, Cancer Program
Institute for Research in Biomedicine (IRB Barcelona), 08028 - Barcelona. **T** 934039912**.**
nuria.lopez@irbbarcelona.org http://bbglab.irbbarcelona.org

SHORT SUMMARY

Nuria Lopez-Bigas is a biologist with a PhD in molecular genetics. She transitioned into bioinformatics during her postdoc at the European Bioinformatics Institute (EBI). Since 2006, she leads a research group in Barcelona focused on the study of cancer from a genomics perspective. Her lab has done important contributions in the identification of cancer genes and driver mutations across cancer types, in the interpretation of tumor genomes for precision cancer medicine, in the discovery of the variation of mutation rate along the genome, in the identification of mutational signatures of cancer treatment and in the identification of genes and mutations involved in clonal hematopoiesis.

ACADEMIC POSITIONS AND EDUCATION

2016-present	**Group Leader** (ICREA Research Professor) Biomedical Genomics Group Institute for Research in Biomedicine (IRB Barcelona) Barcelona, Spain
2023-present	**Full professor** at the University Pompeu Fabra Barcelona
2016 - 2023	**Associate professor** at the University Pompeu Fabra Barcelona
2011- 2016	**Group Leader** (ICREA Research Professor) Biomedical Genomics Group Universitat Pompeu Fabra Barcelona, Spain
2006-2011	**Group Leader** (Ramon y Cajal Researcher) Biomedical Genomics Group Universitat Pompeu Fabra Barcelona, Spain
2005-2006	**Postdoctoral Researcher** (Human Frontiers Science Program - HFSP) Centre for Genomic Regulation (CRG) Barcelona, Spain (Laboratory of Roderic Guigó)
2002-2005	**Postdoctoral Researcher** (Human Frontiers Science Program - HFSP) European Bioinformatics Institute (EBI) Cambridge, UK (Laboratory of Christos A. Ouzounis)
1998-2002	**PhD student** at Oncologic Research Institute (Laboratory of Xavier Estivill). PhD from University of Barcelona Barcelona, Spain
1994-1998	**B.Sc. Biology** University of Barcelona Barcelona, Spain

SHORT STAYS IN OTHER SCIENTIFIC INSTITUTIONS

2024-25 (12 months)	**Visiting Scholar** at University of California San Francisco (UCSF), USA
2017 (3 months)	**Visiting Professor** at Cancer Research UK Cambridge Institute, UK
2013 (3 months)	**Visiting Researcher** (EMBO Short Term Fellowship) at MRC – Laboratory of Molecular Biology, Cambridge UK Sarah Teichmann Lab
2001 (2 months)	**Visiting PhD student** at INSERM U254 (Montpellier, France) Prof. Remy Pujol and Dr. Lionel Simonneau lab
2000 (2 months)	**Visiting PhD student** (EMBO Short Term Fellowship) at Sackler School of Medicine, Tel Aviv University, Israel Karen Avraham Lab
1997 (3 months)	**Summer student** at Fred Hutchinson Cancer Research Center (FHCRC, Seattle, USA) Ronald Reeder Lab
1996 (3 months)	**Summer student** at Fred Hutchinson Cancer Research Center (FHCRC, Seattle, USA) David Martin Lab

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HONORS, AWARDS AND DISTINCTIONS

2024	Elected member of the Spanish Royal Academy of Sciences (RAC)
2024	Elected member of the Barcelona Royal Academy of Sciences and Art (RACAB - pending entrance speech)
2023	Biomedicine Award of Lilly Foundation
2022	CGI-clinics EU project granted (coordinator role)
2022	Cancer Grand Challenge Award (co-leading project PROMINENT)
2022	City of Barcelona Award
2022	Innovator Award of the International Society of Computational Biology (ISCB)
2022	Aspire Award ASPIRE Award from The Mark Foundation for Cancer Research
2021	Elected fellow of the International Society of Computational Biology (ISCB)
2019	VIII National "Doctores Diz Pintado" Cancer Research Prize
2016	XI Banc de Sabadell Award for Research in Biomedicine
2016	Elected Member of the European Molecular Biology Organization (EMBO)
2015	European Research Council Consolidator Grant (ERC-consolidator)
2011	Selected Senior Research Professor at ICREA (Catalan Institute for Research and Advanced Studies). The mission of ICREA is “to select and hire the most talented and extraordinary scientists and academics to work in Catalonia”
2011	Catalan National Award for Young Research Talent (*Premi Nacional de Recerca al Talent Jove*)
2006	Career Development Award from the Human Frontiers Science Program Organization (HFSPO)
2006	EMBO Short Term Fellowship to visit the Laboratory of Molecular Biology (LMB-MRC)
2005	Selected for Ramon y Cajal Researcher. Competitive call from the Spanish Ministry of Science to incorporate in the Spanish Research system young researchers with an outstanding track record
2003	Long Term Fellowship Award from the Human Frontiers Science Program Organization (HFSPO)
2000	EMBO Short Term Fellowship to visit Sackler School of Medicine, Tel Aviv University, Israel.

PROFESSIONAL ACTIVITIES AND COMMUNITY SERVICE (selected)

2017 - present	Chair of the Research Integrity Committee at the Institute for Research in Biomedicine
2017 - present	Member of the Scientific Board of the Spanish Society Against Cancer (AECC)
2021 - present	Board member of the European Association of Cancer Research (EACR)

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2021 - present	Member of the Scientific Council of Gustave Roussy Cancer Center, Paris, France
2024 – present	Leader of National Mirror Group 9. Use case- Cancer (1+Milion Genome Initiative)
2023 - present	Member of the International Scientific Advisory Board at IFOM, Milan (Italy)
2021 - present	Member of the Scientific Advisory Board, CRUK Manchester Institute
2020 - present	Member of the Scientific Advisory Board, VHIO Barcelona
2020 - present	Mentor of the LEAP mentorship program - EMBL
2019 - 2022	Member of the Scientific Advisory Board of Finland Institute of Molecular Medicine
2019	Member of the Scientific Advisory Board of Open Targets (UK) 2016 and
2018	Panel Member for the evaluation of the European Research Council Consolidator Grants
2017	Panel Member for the recruitment of Junior Research Leaders for “la Caixa”
Several years	Evaluator for Wellcome Trust
Several years	Evaluator for Cancer Research UK (CRUK)
Several years	Panel member for the evaluation of Ramon y Cajal Grants and Project Grants from the Spanish Ministry

COMPETITIVE GRANTS AS PRINCIPAL INVESTIGATOR

- PROMINENT: Discovering the molecular signatures of cancer PROMotion to INform prevENTion. Cancer GrandChallenges. Co-funded by CRUK, NIH and AECC. Budget for the Group: £ 4,702,838.25. Co-leader. Total project budget: ~25M $.
- Data-driven cancer genome interpretation for personalised cancer treatment. Horizon Europe HORIZON-HLTH-2021-CARE-05. 2022-2027. Budget for the Group: 2.872.675 €. Coordinator of the Consortium. Ref: 101057509. Total project budget: ~10M €.
- CHEMOHEALTH. Effectos of chemotherapies in healthy tissues. MICINN PID2021-126568OB-I00. 2022-2025. 484.000 Eur. Co-Principal Investigator.
- CIBERONC. Group of the consortium CIBERONC. ISCIII-MICINN. From 2022. Principal Investigator.
- Atheroclonal. Somatic mutations and clonal hematopoiesis as drivers of atherosclerosis: from the laboratory to the clinic. MICINN, Lineas Estratégicas. 2022-2024. 156.601 €. Principal Investigator. Project Coordinator: Jose Javier Fuster, CNIC.
- Myoclonal Somatic mutations and clonal hematopoiesis as predictors and drivers of heart failure progression. La Caixa Foundation HR22-00732. 2022-2025. Project Coordinattor: Jose Fuster.
- IMPACT-Data. Infraestructura de Medicina de Precisión asociada a la Ciencia y Tecnología (IMPaCT) de la Acción Estratégica en Salud. 2021-2024. 97.350 €. Project coordinator: BSC.
- EOSC4Cancer. HORIZON-INFRA-2021-EOSC-01. 2022-2025. 65.000 €. Coordinator: Alfonso Valencia.

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- SGR2021. AGAUR. 2022-2025. 60.000 €
- Identifying and functionally characterising colorectal cancer driver mutations. Wellcome Trust. 2019-2024. 277.000 €. Principal investigator. Project coordinator: Professor Richard Houlston.
- Computational Oncology Training Alliance (CONTRA). H2020 Innovative Training Network ITN-766030. European Commission. 01/01/2018-31/12/2021. 495.745 €. Principal investigator.
- Identifying noncoding cancer drivers NONCODRIVERS. ERC Consolidator Grant 682398. European Commission. 01/12/2016-30/11/2021. 1.995.828 €. Principal investigator.
- Discovering the mechanisms of tumorigenesis by driver mutations across tissues. ASPIRE Awards The Mark Foundation for Cancer Research. 2022-2023. 195.308,08 $. Principal Investigator.
- Damage, repair and mutations caused by alkylating agents along the genome. MINECO RTI2018-094095-B-I00. 01/01/2019-31/08/2022. 387.000 €. Principal Investigator.
- Exploring mechanisms of resistance in adult and pediatric T-Acute Lymphoblastic Leukemia. Asociación Española Contra el Cáncer (AECC). 01/11/2016- 31/10/2022. 216.000 €. Principal investigator.
- BioMedTec, Cancer Genome Interpreter. IRB Barcelona Fundació La Caixa. 2017
- Improving the interpretation of tumor genomes for precision cancer medicine. (SAF-2015-66084-R) MINECO (2016-2018)
- Creating medically-driven integrative bioinformatics applications focused on oncology, CNS disorders and their comorbidities (MedBioinformatics) (H2020 - PHC-32-2014 – 634143). European Commission (2015-2018)
- Conveni programa pilot EDI: IntOGen: integrative oncogenomics cancer browser (EDI-PILOT-2014-9) AGAUR (2014)
- Consolidated group grant for the Computational Genomics group (2014 SGR 1121) AGAUR (2014-2016)
- The Cancer Genome Interpreter (2013110) Fundació La Marató TV3 (2014-2017)
- Plan Nacional: Genómica Integrativa del Cancer en la era de la secuenciación masiva (SAF2012-36199). MICINN (2013-2015)
- Plan Nacional: Integración de datos genómicos para el estudio del Cancer (SAF2009-06954) Spanish Ministry of Science (MCI) (2010-2013)
- INNOCASH: Sistema informático para el manejo, gestión y explotación de datos genómicos (INC-0436 FASE II). Fundación Española para la Ciencia y la Tecnologia (FECYT) (2010-2012)
- FPI grant for Carlota Rubio (BES-2013-063354) MINECO (2013-2017)
- Marie Curie grant (Tecniospring) for David Tamborero. (TECSPR13-1-0011) European Commission & ACC10. 2014-2016.
- Causes & Mechanisms of Tumour development: a computational "Human Frontier Science Program". Human Frontiers Science Program Career Development Award. (2006-2010)

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PHD THESIS SUPERVISED

Currently supervising four PhD students: Olivia Dove, Stefano Pellegrini, Raquel Blanco and Ferriol Calvet

13 PhD Thesis completed

2019-2023	Co-Director of the thesis of Hanna Kranas. Title: Computational studies of DNA damage and repair of alkylating agents and UV light University Pompeu Fabra
2019-2022	Co-Director of the thesis of Claudia Arnedo. Title: Clustering of somatic mutations across cancer genomes University Pompeu Fabra
2019-2022	Co-Director of the thesis of Jose Bonet. Title: Computational studies of DNA modifications and mutations in bulk and single-cell data University Pompeu Fabra
2017-2021	Co-Director of the thesis of Inés Sentís. Title: The evolution of T-cell acute lymphoblastic leukemia in adult patients under treatment University Pompeu Fabra
2017-2021	Co-Director of the thesis of Oriol Pich. Title: The role of mutational processes in the evolution of somatic tissues and malignancy University Pompeu Fabra
2016-2020	Co-Director of the thesis of Joan Frigola. Title: Coding and noncoding drivers: identification and downstream effects University Pompeu Fabra
2014 - 2017	Director of the thesis of Carlota Rubio-Perez. Title: “In silico drug prescription to cancer patients”. University Pompeu Fabra.
2012 - 2015	Director of the thesis of Christian Pérez Llamas. Title “Computational approaches for integrative cancer genomics”. Defended successfully at the UPF on 18th December 2015
2011 - 2014	Director of the thesis of Michael P Schroeder. Title: “Analysis and visualization of multidimensional cancer genomics data”. Co-supervised with Dr. Abel Gonzalez-Perez, UPF. Defended successfully at the UPF on 21st November 2014
2009 - 2014	Director of the thesis of Alba Jené-Sanz. Title: “Integrative study of the regulatory and epigenomic programs involved in cancer development”. Defended successfully at the UPF on 29th April 2013
2008 - 2013	Director of the thesis of Khademul Islam. Title: “Delineating epigenetic regulatory mechanisms of cell proliferation and differentiation”. Co-supervised with Dr. Elizaveta Benevolenskaya, University of Illinois Chicago. Defended successfully at the UPF on 25th June 2012
2007 - 2011	Director of the thesis of Gunes Gundem. Title: “Integration of genomic data for the study of cancer”. University Pompeu Fabra. Defended successfully at the UPF on 29th September 2011
2003 - 2007	Codirector of Dr. Simon J. Furney thesis. Title: “In silico analisis of human disease and cancer genes”. Defended successfully in the Faculty of Medicine of the University College Dublin on 8th February 2007

TRAINING FUTURE SCIENTIFIC LEADERS

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Past trainees	**Position after leaving my lab**
Francisco Martínez-Jiménez	Postdoc at UMC Utrecht – Currently Group Leader at VHIO Barcelona
Sabarinathan Radhakrishnan	Principal Investigator (National Centre for Biological Sciences, Tata Institute of Fundamental Research, Bangalore, India)
Hanna Kranas	Postdoc at Josep Carreras Leukaemia Research Institute (Porta lab)
Oriol Pich	Postdoc at Crick Institute London (Charles Swanton Lab)
Claudia Arnedo-Pac	Postdoc at Cambridge University (Sarah Aitken Lab)
José Bonet Giner	Data architect at Tetrascience, a scientific AI company
Santiago Gonzalez	Computational Biologist at C2i Genomics
Joe Usset	Computational Biologist at Hartwig Medical Foundation
Inés Sentís	Postdoc at CNAG Barcelona (Holger Heyn Lab)
David Tamborero	Scientist, Karolinska Institute, Sweden
Loris Mularoni	Bioinformatics Specialist at Center for Regenerative Medicine Barcelona
Joan Frigola	Postdoc at VHIO, Barcelona (Enriqueta Felip Lab) currently Senior Scientist at AstraZeneca
Carlota Rubio-Perez	Postdoc at VHIO, Barcelona (Joan Seoane Lab) – Currently Oncologist at Clinic Hospital in Barcelona
Michael P. Schroeder	Postdoc (Charité University Hospital, Berlin) – Currently Analytics, ML & Data Science Expert at ERNI
Gunes Gundem	Postdoc at Wellcome Trust Sanger Insitute (UK) – Currently Senior Research Fellow (MSKCC, New York)
Christian Perez-Llamas	Senior Software/Data Engineer – Currently at Schibsted Media Group
Alba Jené Sanz	Bioinformatics Unit Coordinator at Barcelona Supercomputing Center
Khademul Islam	Associate Professor (University of Dhaka) – Currently Full Professor
Simon J. Furney	Postdoc at CRUK Manchester Institute - Currently Principal Investigator (Royal College of Surgeons in Ireland)

ORGANIZER OF INTERNATIONAL CONFERENCES (selected)

2024	Co-organizer Barcelona Biomed Conference on CANCER PROMOTION: understanding cancer promotion to inform prevention
2024	Co-organizer Cancer Genomics, Multiomics and Computational Biology Bergamo, Italy : 30 April - 2 May 2024
2022	Co-organizer EACR Congress Translating Biology to Medicine. June 2022 Sevilla, Spain.
2021	Organizer Bioinformatics in Cancer EACR Conference, online
2017 - 2023	Co-organizer. Biannual Cancer Genomics EMBL Conference, Heidelberg (Germany)
2019	Conference Chair, Advances in Computational Biology Conference, ISCB. Barcelona, Spain
2018	Conference Chair, Next Generation Sequencing Conference, ISCB. Barcelona, Spain
2017	Co-organizer. ICREA conference: Across Tumor Heterogeneity and Evolution in Cancer: From In Silico Studies to Clinical Impact, School of Medicine. Barcelona, Spain

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2016 Co-organizer. IV Bioinformatics and Genomics Symposium, Barcelona (Spain)

2014 Co-organizer. Beyond the Genome: Cancer Genomics. Harvard Medical School, Boston, USA

TECHNOLOGY TRANSFER ACTIVITIES

- CancerGenomeInterpreter (CGI): Platform to facilitate the interpretation of alterations in a patient's tumor (https://www.cancergenomeinterpreter.org). CGI is extensively used in research and clinical settings, with more than 10,000 users per year during the last three years (measured by Google Analytics). We have issued agreements with more than 10 companies and foundations for the use of CGI, including Genomics England (the UK National Initiative for Whole-genome sequencing in the National Health Service (NHS)) and Hartwig Medical Foundation, which provides tumor whole-genome sequencing in clinical practice in partnership with 43 hospitals in the Netherlands. In 2022 an EU project, CGI-Clinics was awarded 10M Euros to further develop and implement CGI in the clinic. CGI-Clinics joins together cancer hospitals in France, Germany, England, Greece and Spain, and cancer patient associations, to develop a carefully designed 5 years project to implement the comprehensive and systematic data-driven interpretation of cancer genomes for precision cancer medicine into clinical settings.
- IntOGen: A framework that uses somatic mutations to identify cancer driver genes and their cancer mutational patterns. (https://www.intogen.org). IntOGen methods and the pipeline are provided to the community with a free license that allows academic and commercial use. IntOGen had more than 100,000 unique visitors (according to Google Analytics) in the last years from all around the world.
- Contract of service with INIVATA, clinical cancer genomics company on non-invasive tumour analysis from circulating DNA in Cambridge, UK. October 2014.
- Innovation Teams Program 2014. Catalan Research Foundation. Program to support knowledge transfer. INNOCASH 2010-2011.
- Computational system for managing and exploiting genomic data for personalized medicine. Research Collaboration with Sistemas Genómicos, a biotech company in Valencia, Spain.

INVITED SPEAKER AT MAJOR INTERNATIONAL CONFERENCES (Selected)

2024 Keynote Speaker at Cancer Evolution: From Genome to Ecology 2024 conference, Hinxton (UK)

2024 Invited Speaker at EACR Cancer Genomics, Multiomics and Computational Biology, Bergamo (Italy)

2023 Invited Speaker at VIB Tumor Heterogeneity, Leuven (Belgium)

2023 Invited Speaker at 127th International Titisee Conference "Somatic Mosaicism", Titisee (Germany)

2023 Invited Speaker at the 10th InterAcademy Workshop, The Korean Academy of Science and Technolog (KAST), Frankfurt (Germany)

2023 Invited Speaker at 4th Crick International Cancer Conference, London, (UK)

2023 Invited Speaker at EACR annual meeting Torino (Italy)

2023 Invited Speaker at Gordon Research Conference on Epithelial Differentiation and Keratinization, Barcelona (Spain)

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2023 Invited Speaker at Cancer Dependency Map Symposium, Milan (Italy)

2023 Invited Speaker and discussant. Forbeck Foundation meeting "Mutational signatures in pediatric cancer-from etiology to therapeutic implications" Asilomar Conference Grounds (USA)

2022 Invited Speaker, 34th EORTC-NCI-AACR symposium on Molecular targets and Cancer Therapeutics (ENA 2022), Barcelona (Spain)

2022 Keynote Speaker Congress Translating Biology to Medicine. June 2022 Sevilla (Spain)

2022 Keynote speaker. Mechanisms of Mutagenesis and Their Clinical Implications. Mutagenesis Gordon Research Seminar (USA)

2022 Invited Speaker. EMBO Workshop: The many faces of cancer evolution, Rimini (Italy)

2021 Invited Speaker. Symposium on Mutation Signatures and Cancer. National Cancer Institute, NIH. 2021 Bioinformatics in Cancer EACR Conference

2021 EACR 2020 Virtual Congress. 18-19 June 2020

2020 Discussion Leader. CSHL Biology of Genomes Conference (USA)

2019 EMBL Cancer Genomics Conference 2019 (Germany)

2019 EACR conference. Defence is the Best Attack: Immuno-Oncology Breakthroughs. Barcelona (Spain)

2019 Heterogeneity and Evolution in Cancer Conference at CNIO, Madrid (Spain)

2019 III Optimizing Immunotherapy New Approaches, Biomarkers, Sequences and Combinations. IMIM, PRBB Barcelona (Spain)

2019 V Simposio Nacional de Genómica Aplicada en Oncología (CNIO), Madrid (Spain)

2019 Medical Genetics Session, New Horizons in Genomics, QMUL London (UK)

2019 EACR conference. Tracking Cancer: Detection and Monitoring, from Diagnosis to Therapy, EACR, Barcelona (Spain)

2019 Keynote Speaker. First Zürich Precision Oncology Symposium, Comprehensive Cancer Center Zürich (Switzerland)

2018 Keynote Speaker. Molecular Analysis for Personalised Therapy (MAP) Congress by ESMO. Paris (France)

2018 49th International Symposium of the Princess Takamatsu Cancer Research Fund, Tokyo (Japan)

2018 Cell Symposia: TCGA Legacy. Multi-omic studies in Cancer, Washington (USA)

2018 EMBO Workshop, Cellular signaling and Cancer Therapy, Dubrovnik (Croatia)

2018 European Association of Cancer Research (EACR) Biennial Congress, Amsterdam (Netherlands)

2018 Keynote Speaker. RECOMB-CCB Cancer Computational Biology, Paris (France)

2018 The Impact of Genomics Data on Health: The Role of the European Genome-Phenome Archive (EGA). Barcelona (Spain)

2017 Cancer Genomics Conference EMBL, Heidelberg (Germany)

2017 Louis Jeantet Symposium, University Medical Center, Geneva (Switzerland)

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2017 St. Gilles Thomas Symposium, Perspectives in cancer genetics and genomics. Paris (France)

2017 CRG Symposium: 7th International Workshop on Genomic Epidemiology, Barcelona.

2107 Keynote Speaker. BC2 Basel Computational Biology Conference, Basel (Switzerland)

2017 Genomics of Common Diseases, Welcome Genome Campus, Cambridge (UK)

2017 EACR: Cancer Genomics 2017, Cambridge (UK) 2017 Invited Speaker Major Symposium at AACR Annual meeting 2017, Washington (USA)

2017 Gene-Regulatory Systems in Development. Carmona (Spain)

2017 EACR, Making it Personal, Cancer Precision Medicine. Meet the expert session. Amsterdam (Netherlands) 2017 ICREA-FIJC Conference, Across tumor heterogeneity and evolution in cancer: from in silico studies to clinical impact, Barcelona (Spain)

2017 HUGO-HGM, From Genomics to Therapy, Barcelona (Spain)

2016 Genetics Society Autumn Meeting Functional genetic variation in the non-coding genome. London (UK).

2016 Canceromatics III: Tumor Heterogeneity, CNIO, Madrid (Spain).

2016 Keynote Speaker. European Conference on Computational Biology - ECCB2016, The Hague (Netherlands).

2016 Keystone Symposium: Understanding the Function of Human Genome Variation, Uppsala (Sweden).

2016 Systematic Functional Annotation of Cancer Variants, "Tumor genomes shed light into mutational processes and cancer vulnerabilities", Cancer Systems Genetics, Heidelberg (Germany).

2016 1st European Conference for Translational Bioinformatics, MBI, Copenhagen (Denmark)

2016 Applied Bioinformatics in Life Sciences, Leuven, (Belgium).

2016 Keystone Symposium: The Cancer Genome, Fairmont Banff Springs, Banff, Alberta, (Canada).

2016 Festival of Genomics, London (United Kingdom).

2015 EMBL Cancer Genomics conference.

2015 EMBO meeting 2015 meeting. Birmingham, UK

2015 Advances in Genome Biology and Technology (AGBT) meeting. Marco Island, Florida.

INVITED SEMINARS (Selected)

2024 Harvard Medical School, Boston, USA

2024 San Francisco, UCSF, Diller Comprehensive Cancer Center, USA

2024 University of Colorado, Department of Biochemistry and Molecular Genetics, USA

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2024 University of Illinois Chicago, Biochemistry and Molecular Genetics Depart., USA

2024 San Francisco, UCSF ImmunoX Program Seminar, USA

2024 Cardiff University, virtual Science Seminar Talk

2023 Berlin Institute for Medical Systems Biology, Berlin, Germany

2023 Izmir University, Izmir, Turkey

2023 Koç University, Istanbul University, Istanbul, Turkey

2023 CRUK Cambridge Institute, UK - United Kingdom

2023 Wellcome Trust Sanger Institute, UK - United Kingdom

2023 EMBL Science by the beach, Barcelona - Spain 2021 Broad Institute Seminar Series on Medical and Population Genetics, USA

2021 Netherlands Cancer Institute (NKI), NKI Seminars, Netherlands

2021 SMB Faculty Seminar Series". Washington University, USA - United States of America (on-line)

2020 CNIO Distinguished Seminars, Madrid, Spain

2019 Quantitative biology, Bioinformatics, and Genomics Seminar series, DKFZ, Heidelberg, Germany

2019 Ludwig Institute Seminar Series at the University of Oxford

2019 Memorial Sloan Kettering Cancer Center, New York (USA)

2018 Invited lecture at Barts Cancer Institute (BCI), London

2018 The University of Texas MD Anderson Cancer Center, Texas (USA)

2017 The Gurdon Institute, Cambridge, UK

2017 Wellcome Sanger Institute, Hinxton, UK

2017 The Francis Crick Institute, London, UK 2016 Institute Gustave Roussy, Paris, France

2016 Austrian Academy of Sciences, Research Center for Molecular Medicine, Vienna

2016 Cornell University, New York, USA

PUBLIC ENGAGEMENT AND OUTREACH ACTIVITIES (selected)

- Multiple newspaper / radio / documentary appearances showcasing our research (Meet Our Scientists, La Vanguardia, El País, El Punt Avui TV, TVE, TV3, Catalunya Radio...).
- Showing our lab and explaining our work to the general public during PRBB Open Day (2014, 2015, 2016) and IRB Open Day (2017-2023).
- Showing the work of our lab at “Fira de la Rercerca en Directe” at Science Museu–Cosmocaixa (2019-2023).
- Multiple seminars at primary schools and high schools about science and cancer genomics.
- Authored a chapter titled «*La misteriosa periodicitat del genoma*» explaining our research for the general public in the book “*Deu aportacions catalanes a la ciència actual*” ed. Galaxia Gutenberg.

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TEACHING ACTIVITIES

2007-present	Coordinator of Elements of Biocomputing Course - Master in Bioinformatics for Health Sciences at University Pompeu Fabra
2017-present	Co-coordinator of Bioinformatics and High-throughput data analysis - Master in Translational Medicine at University of Barcelona
2018,19	Speaker at Seminar series of the Inter-University Bioinformatics Degree (UPF, UPC, UAB and UB)
2017,18,19	Speaker at Master in Bioinformatics UAB
2014	Teacher at Master in OMICS Data Analysis (UVIC)

PUBLICATIONS

Publications summary
Nuria Lopez-Bigas has authored more than 160 publications. Articles she has co-authored had been cited more than 37,000 times. H-index: 74 (according to google scholar).

For a complete list of publications, visit:
PubMed: http://www.ncbi.nlm.nih.gov/pubmed/?term=Lopez-Bigas
Google Scholar: http://goo.gl/hrCQr7
ORCID: 0000-0003-4925-8988

10 RECENT SELECTED PUBLICATIONS WITH FEW DESCRIPTIVE SENTENCES

Members of Lopez-Bigas lab are shown in **bold** #join supervisor *Corresponding author

Joseph Usset, **Axel Rosendahl Huber, Maria A Andrianova**, Eduard Batlle, Joan Carles, Edwin Cuppen, Elena Elez, Enriqueta Felip, Marina Gómez-Rey, Deborah Lo Giacco, Francisco Martinez-Jimenez, Eva Muñoz-Couselo, Lillian L Siu, Josep Tabernero, Ana Vivancos, **Ferran Muiños**, **Gonzalez-Perez* A, López-Bigas* N.** Five latent factors underlie response to immunotherapy. **Nature Genetics**, **2024**

Only a subset of the cancer patients treated with immunotherapy response to the treatment. The group of Lopez-Bigas embarked on a comprehensive computational analysis to understand which features of the patient and the tumor define treatment response and survival. They discovered that all biomarkers associated with immunotherapy response and survival collapse into five orthogonal latent factors: tumor mutation burden, T cell effective infiltration, transforming growth factor-beta activity in the microenvironment, prior treatment and tumor proliferative potential. They then built a machine learning classifier that combines the five latent factors to predict response and survival in patients treated with immune checkpoint inhibitors.

Mònica Sánchez-Guixé, Ferran Muiños, Morena Pinheiro-Santin, Víctor González-Huici, Carlos J Rodriguez-Hernandez, Alexandra Avgustinova, Cinzia Lavarino, **Abel González-Pérez#,** Jaume Mora*, **Núria López-Bigas#*.** Origins of second malignancies in children and mutational footprint of chemotherapy in normal tissues. **Cancer Discovery 2024**

Cancer in childhood is fortunately relatively rare, suffering two tumors during infancy is extremely surprising. This work describes the study of the cases of four children who have experienced two cancers during childhood. To understand why, Lopez-Bigas team sequenced

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whole-genome sequencing of the two tumors and normal tissue of the four children. Using sofisticated computaional techniques they partially reconstructed the evolutionary history of those tumors, finding different cancer evolutionary trajectories in each case. This study also shows that healthy tissues of the patients accumulated mutations due to chemotherapy treatment. Understanding the effect of chemotherapy in healthy tissues is important as a step to uncover the causes of late side effects of the treatment.

Muiños F*, Martínez-Jiménez F, Pich O, Gonzalez-Perez A#*, Lopez-Bigas N#*. In silico saturation mutagenesis of cancer genes. **Nature 2021**

Not all mutations in cancer genes are cancer driver mutations. Sorting out which are and which aren't is critically important for precision cancer medicine and to understand the mechanisms of tumorigenesis. The group of Nuria Lopez-Bigas have addressed this by discovering (using machine-learning models inspired by evolutionary biology), directly from the somatic mutations in tumors, which are the features that define driver mutations in each gene/cancer type. With models trained per gene/tumor type, they can perform "In silico saturation mutagenesis" to identify all driver mutation in each cancer gene, and study the interplay between mutational processes and driverness.

Martínez-Jiménez F, Muiños F, Sentís I, Deu-Pons J, Reyes-Salazar I, Arnedo-Pac C, Mularoni L, Pich O, Bonet J, Kranas H, Gonzalez-Perez A#*, Lopez-Bigas N#*. A compendium of mutational cancer driver genes. **Nature Reviews Cancer 2020**

This manuscript describes the comprehensive approach, named IntOGen, to identify cancer genes across tumor types by detecting signals of positive selection in the pattern of mutations. It reports the results of analyzing more than 28000 tumor genomes with this approach leading to the identification of 568 cancer genes. In addition, it provides an historical review of cancer gene identification.

Pich O, Reyes-Salazar I, Gonzalez-Perez A#* & Lopez-Bigas N#*. Discovering the drivers of clonal hematopoiesis. **Nature Communications 2022**

Clonal hematopoiesis (CH) has emerged as a prevalent condition across human populations, associated with the development of cardiovascular morbidity, hematopoietic malignancies and aging. Although few genes are known to drive CH upon mutations in Hematopoietic Stem Cells, this list is probably reduced to the tip of the iceberg of mutation frequency. Lopez-Bigas team reasoned that the clonal expansion that drives clonal hematopoiesis is reminiscent of that observed in tumors, and therefore methods to detect positive selection in the mutations of genes across tumors could be used to identify the complete list of CH-related genes. They have repurposed paired tumor/blood genome sequencing data to identify somatic mutations in healthy blood across 12,000 patients. Next, they identified CH driver genes by detecting signals of positive selection in blood somatic mutations. This approach works remarkably well; it recovers all known CH genes, and discovers novel interesting candidates, some of which are supported by prior studies. They also demonstrated that employing all the genes in this novel compendium greatly increases the sensitivity in the detection of CH across donors.

Pich O, **Muiños F**, Lolkema MP, Steeghs N, **Gonzalez-Perez A#, Lopez-Bigas N#***. The mutational footprints of cancer therapies. **Nature Genetics 2019**

Cancer therapies produce late side effects which in some cases appear even decades after the patient was treated. These side effects are especially well documented in childhood cancer survivors and include secondary neoplasms, mental disabilities and cardiac problems among others. The mechanisms on how cancer therapies exert these late side effects are not known. Many chemotherapies and also radiotherapy produce mutations in surviving tumor and healthy cells of the patient and it is reasonable to think that these mutations might be involved in causing some of these late side effects. In this work the team measured for the

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first time the mutation burden caused by cancer therapies in patient cells. To do that they analyzed more than 3500 whole-genomes of treated metastatic patients to uncover the mutational footprints (or mutational signatures) of the cancer treatments. These signatures allowed them to measure the mutational toxicity of these treatments across patients and organs.

The importance of this work relies not only on the results it reports (namely new mutational signatures of most commonly used chemotherapies and the mutation burden they exert in patient cells) but also in that it paves the way to explore the mechanistic link between cancer treatments and their late side effects.

Gonzalez-Perez A*, Sabarinathan R*, Lopez-Bigas N*. Local Determinants of the Mutational Landscape of the Human Genome. **Cell 2019**

This manuscript is an invited review. It explores recent results, some from Lopez-Bigas lab, on the large variability of mutation rate along the genome. They start by describing the different mutational processes affecting cells from different tissues in our body and the DNA repair pathways involved in fixing DNA damage and mismatches. Next, they detail how chromatin conformation, the presence of nucleosomes and DNA structure interfere both with DNA damage and DNA repair shaping the rate at which mutations are accumulated in our genome.

Pich O, Muiños F, Radhakrisnan S, Reyes-Salazar I, Gonzalez-Perez A#, Lopez-Bigas N#*. Somatic and germline mutation periodicity follow the orientation of the DNA minor groove around nucleosomes. **Cell 2018**

This work started when Nuria Lopez-Bigas and her team realized that there is a stunning 10bp periodicity in the rate of somatic mutations in nucleosome covered regions. They observed this initially in tumor genomes. They thought it may be related to the long-studied WW 10bp periodicity in the eukaryotic genomes. Thus, they wanted to determine the causes of this periodicity and its link with the evolution of eukaryotic genomes. The analysis of somatic mutations in thousands of tumors, variation and divergence in Human and Arabidopsis, and maps of DNA damage in human and yeast cells, allowed them to conclude that the structure of DNA and the way it wraps around the nucleosomes is a major influence to DNA damage (UV-light damage) and to the efficiency of DNA repair (Nucleotide Excision Repair and Base Excision Repair), thus leading to a periodic mutation pattern.

The importance of this work is twofold: from one side it is a major advance in our understanding of DNA damage and DNA repair (and on particular on how the structure of DNA and its wrapping around histones affects them) and from another side it provides an explanation on how these factors shape the evolution of eukaryotic genomes leading to patterns like the mysterious 10bp WW periodicity.

Frigola J, Sabarinathan R, Mularoni L, Muiños F, Gonzalez-Perez A, López-Bigas* N. Reduced mutation rate in exons due to differential mismatch repair. **Nature Genetics**, **2017**

This manuscript describes that exons and introns have a different rate of somatic mutations. This difference is most prominent in tumors with mutations in the polymerase (e.g. POLE). POLE mutant tumors accumulate a large number of mutations due to mismatches created during replication. The team finds that the mutation rate difference between exons and introns is caused by differential activity of mismatch repair in those regions. The importance of this manuscript is framed in the increase in our understanding on DNA repair along the genome and how it shapes the rate of mutations in different regions.

Sabarinathan R, Mularoni L, Deu-Pons J, Gonzalez-Perez A, Lopez-Bigas N*. Nucleotide excision repair is impaired by binding of transcription factors to DNA. **Nature**, **2016**

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This work was initially motivated by the interest of the group in finding driver mutations in non-coding regions. When analyzing mutations in promoters in melanoma samples they found a high number of mutations in transcription factor binding sites (TFBS). They suspected that this accumulation was not related to their role as cancer driver mutations. Thus, they turned our attention to Nucleotide Excision Repair, the pathway involved in repairing UV-light DNA adducts. They showed that when there is a protein binding to the DNA (i.e. a transcription factor) NER activity is impaired, thus leading to a more than fivefold increase in the mutation rate in TFBS.

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