

# David Mas-Ponte

Bioinformatics - Genomics - Biotechnology

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## Education

- 2017–2022 **Ph.D. in Biomedicine**  
Universitat de Barcelona, Barcelona, Spain.  
*Current*
- 2015–2017 M.Sc. in Bioinformatics for Health Sciences  
Universitat Pompeu Fabra, Barcelona, Spain.  
*Specialization in Genomics - GPA: 9 / 10*
- 2011–2015 B.Sc. in Biotechnology  
Universitat Autònoma de Barcelona, Spain.  
International exchange (6 months), McGill University, Montreal, Canada  
*GPA: 8.5 / 10*

## Research Experience

- 01 2022 - **Stanford University** - *Visiting Student Researcher*  
As part of my Ph.D. research I am visiting the laboratory of Ashby Morrison where I am participating in the study of mutagenesis susceptibility for UV lesions in both human cells and tissues. I am analysing a comprehensive datasets of genomic and epigenomic data to quantify their importance in the determination of somatic mutation rates.
- 08 2017 - **Institute for Research in Biomedicine** - *Ph.D. Student*  
My Ph.D. project is enclosed in the field of computational genetics, studying how mutational processes shape the eukaryotic genomes. We use statistical and machine learning techniques to extract patterns from massive genomic data sets. In particular, we are interested in unraveling mechanisms of local hypermutation both somatically and in populations. **Fran Supek's Lab (AGENDAS)**.
- 2016 - 2017 **Centre for Genomic Regulation (CRG)** - *Master Science Research Thesis*  
My Master Thesis was focused in the link between lncRNAs' subcellular localization and their function. I have also developed a web-based DB using R and SQL to make subcellular expression data available to the scientific community. **Roderic Guigo's Lab, tutored by Rory Johnson**.
- 2015-2016 **Institute of Evolutionary Biology (IBE)** - *Part time Research Internship*  
I studied the evolutionary processes surrounding the RHD gene in Western Mediterranean populations in order to unravel demographic (*drift*) or adaptive (*selection*) processes. **David Comas' Lab**

## Code

- R, Python, Bash & nextflow  
●●○ Docker, git &  $\LaTeX$   
●○○ SQL, JavaScript & HTML/CSS

## Languages

- Catalan | Mother tongue  
Spanish | Bilingual Proficiency  
**English** | **Proficient (CAE-C2 2021)**

## Selected Publications

Find a complete list at [orcid.org/0000-0001-7409-305X](https://orcid.org/0000-0001-7409-305X). Lead author publications highlighted in **bold**.

- 2020 | **David Mas-Ponte and Fran Supek. DNA mismatch repair promotes apobec3-mediated diffuse hypermutation in human cancers. *Nature genetics*, 52(9):958–968, 2020 - Peer-reviewed Journal**
- Joana Carlevaro-Fita, Andrés Lanzós, **David Mas-Ponte**, Rory Johnson, and PCAWG Consortium. Cancer LncRNA Census reveals evidence for deep functional conservation of long noncoding RNAs in tumorigenesis. *Communications Biology*, 3(1):56, February 2020. ISSN 2399-3642. doi: 10.1038/s42003-019-0741-7 - Peer-reviewed Journal
- 2019 | Marina Salvadores, **David Mas-Ponte**, and Fran Supek. Passenger mutations accurately classify human tumors. *PLOS Computational Biology*, 15(4), April 2019. doi: 10.1371/journal.pcbi.1006953- Peer-reviewed Journal
- Irene Franco, Hafdis T. Helgadóttir, **David Mas-Ponte**, Fran Supek, and Maria Eriksson. Whole genome DNA sequencing provides an atlas of somatic mutagenesis in healthy human cells and identifies a tumor-prone cell type. *Genome Biology*, 20(1):285, 2019. ISSN 1474-760X. doi: 10.1186/s13059-019-1892-z - Peer-reviewed Journal
- 2017 | **David Mas-Ponte, Joana Carlevaro-Fita, Emilio Palumbo, Toni Hermoso Pulido, Roderic Guigo, and Rory Johnson. LncATLAS database for subcellular localization of long noncoding RNAs. *Rna*, 23(7):1080–1087, 2017. Publisher: Cold Spring Harbor Lab - Peer-reviewed Journal**

## Selected Conferences

- 2021 | David Mas-Ponte Fran Supek. Clustered apobec mutagenesis in human tumors. In *EACR Bioinformatics Conference*, Virtual conference, May 2021 - Peer-reviewed Conference - Short talk
- 2019 | David Mas-Ponte and Fran Supek. HyperMut: a method to detect localized hypermutation with stringent control for confounders. In *ISMB/ECCB*, Basel, Switzerland, July 2019 - Peer-reviewed Conference - Poster
- 2018 | David Mas-Ponte and Fran Supek. Association of localized hypermutation patterns with transcription programs of tumor samples. In *EMBL Conference: From Functional Genomics to Systems Biology*, Heidelberg, Germany, November 2018 - Peer-reviewed Conference - Poster

## Other scientific contributions & Awards

- 2021 | **SCB award to the best scientific article - Nominee**  
The *Societat Catalana de Biologia* (SCB) is the society that groups all professional and academic biologist in Catalonia. Every year, they award a recognition to the best scientific article in life sciences published in an international journal. In 2021, my paper (*Mas-Ponte Nature Genetics 2020*) got selected as one of the nominees for this award
- 2018-2019 | **ENABLE 2019 - Scientific Organizing Committee**  
ENABLE is an international scientific conference for Ph.D. Students from all over the world co-organized by 4 European research centers (IRB Barcelona, RIMLS, CPR, and SEMM) funded by the European Union Horizon 2020 program. The third edition was held in the city of Nijmegen in the Netherlands with a total of 229 Ph.D. students and postdocs coming from 26 different countries.