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Bioinformatician

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*Biotechnologist with training in Molecular Genetics and Bioinformatics. Interested in omics data analysis to study the mechanisms of gene regulation in mammals.*

## Education

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**MSc. Bioinformatics and Biostatistics**, *Universitat Oberta de Catalunya*, Online 2018 - 2022  
**MSc. Molecular Genetics and Biotechnology**, *Universidad de Sevilla*, Seville (Spain) 2017 - 2018  
**BSc. Biotechnology**, *Universitat de Girona*, Girona (Spain) 2012 - 2017

## Employment

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*Institut Josep Carreras*

**Badalona (Spain)**

**Bioinformatician**

08/2021 - Present

- Study of the Piwi-interacting RNAs (piRNAs) and their variation across closely-related species.
- Analysis of small RNA-seq data for the study of piRNAs.
- Approach to reduce gene length differences for differential expression analysis with multiple species.

*Istituto Europeo di Oncologia*

**Milan (Italy)**

**Bioinformatician**

07/2019 - 07/2021

- Study of different signaling pathways in the development of cancer and stem cell differentiation.
- Analysis and integration of RNA-seq, ChIP-seq and ATAC-seq data.
- Development of a pipeline to process and analyze ATAC-seq data.
- Comparison of different software for ATAC-seq peak calling.
- Comparison of sequencing depths for RNA-seq and their impact on differential expression analysis.

*Instituto de Biomedicina de Sevilla*

**Seville (Spain)**

**Research assistant**

07/2018 - 10/2018

- Study of protein Ccr4 and its influence in nucleosome positioning and transcriptional regulation in yeast.
- Computational analysis of MNase-seq data.

**Master's thesis student**

09/2017 - 07/2018

- Study of protein Xrn1 and its influence in nucleosome positioning and transcriptional regulation in yeast.
- Computational analysis of MNase-seq data.
- MNase-qPCR experiments: DNA digestion, primer design, qPCR.

*Institut d'Investigació Biomèdica de Girona*

**Girona (Spain)**

**Research internship student**

07/2017 - 09/2017

- Identification of new factors (genetic and bacterial) related to adipose tissue physiology and obesity.
- DNA and RNA extraction from animal and human biopsies/feces.

*Microbial. Sistemes i aplicacions analítiques, S.L.*

**Girona (Spain)**

**Bachelor's thesis student**

01/2017 - 06/2017

- Analysis of the mucosa-associated microbiota from human intestinal biopsies
- DNA extraction, qPCR, analysis of sequencing data.

**Internship student**

09/2016 - 06/2017

- Analysis of pathogens in food and water samples. Food Forensics.
- DNA extraction, qPCR, molecular cloning, bacterial culture.

## Publications

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### JOURNAL ARTICLES

Begley *et al.* 2020 **Xrn1 influence on gene transcription results from the combination of general effects on elongating RNA pol II and gene-specific chromatin configuration.** *RNA Biology*. DOI: [10.1080/15476286.2020.1845504](https://doi.org/10.1080/15476286.2020.1845504).

## Projects

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### ACADEMIC PROJECTS

#### Analysis of the variation in piRNA expression across three *Mus* species

- Master's thesis (UOC, 2022).
- Supervisor: Dr. Tanya Vavouri.
- Grade: 9.7/10, *with honours*.

#### Influence of Xrn1 in nucleosome positioning across *Saccharomyces cerevisiae* genome and its effects in transcription

- Master's thesis (US, 2018).
- Supervisors: Dr. Sebastián Chávez de Diego and Dr. Gabriel Gutiérrez Pozo.
- Grade: 9.2/10.

#### Butyrate-induced changes in the diversity of the intestinal mucosa-associated microbiota in colorectal cancer patients submitted to a lateral ileostomy

- Bachelor's thesis (UdG, 2017).
- Supervisor: Prof. Jesús García-Gil.
- Grade: 9.4/10.

## Skills

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### Languages

- Catalan (*native*) - Spanish (*bilingual*) - English (*IELTS 7.5 - C1*) - Italian (*basic*)

### Bioinformatics

- *Omics data analysis*: Microarray, (small) RNA-seq, ChIP-seq, ATAC-seq, MNase-seq - *Genomic Browsers*: IGV, UCSC Genome Browser - *Other*: Analysis of sequences, ENSEMBL Compara, Biomart

### Informatics

- *Languages*: R/Bioconductor, Bash, Python (*basic*) - *Other*: R Markdown, Snakemake, Conda, Docker, Singularity, Git, HPC, LaTeX

## References

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Available upon request.