

Jacques Serizay

POST-DOCTORATE RESEARCHER IN GENOMICS

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Education

University of Cambridge

Cambridge, UK

PHD IN GENOMICS

2016-2020

- **PhD thesis:** *Spatiotemporal control of gene expression in C. elegans.*
- Julie Ahringer lab, Gurdon Institute / Department of Genetics

Ecole Normale Supérieure de Paris-Saclay & Magistère Européen de Génétique

Paris, France

MSc IN GENETICS

2014-2016

- **MSc thesis:** *Functional role of BAP1 in the control of gene transcription.*
- Graduated second out of 25
- Graduated with **highest honors**
- **First** (UK) / *summa cum laude* (USA)
- Partnership with Pasteur Institute

Research Experience

ENS Paris & Institut Pasteur

Paris, France

POST-DOC RESEARCHER IN NATHALIE SPASSKY AND ROMAIN KOSZUL LABORATORIS

Sep 2020 - PRESENT

- Implementation of bio-computational approaches to study temporal gene regulation in single-cell RNA-seq.
- Optimization & analysis of chromatin interaction landscapes from genome-wide and capture Hi-C experiments.
- Conceptualization & development of bio-computational approaches to improve network-based identification of moving elements in datasets from metagenomic sequencing

University of Cambridge

Cambridge, UK

PHD STUDENT IN JULIE AHRINGER LAB

Sep 2016 - Aug 2020

- Development and troubleshooting of a FACS-based nucleus sorting procedure in *C. elegans*.
- Profiling of chromatin landscape (accessibility, protein binding, histone modifications) and transcriptome (RNA-seq) in isolated tissues of *C. elegans*.
- Conception & development of bio-computational approaches to cross-analyse ATAC-seq and RNA-seq datasets and integrate them along with public Transcription Factor databases.
- Conception & development of a bio-computational approach to resolve tissue-specific chromatin interactions *in silico*.
- Implementation of single-cell RNA-sequencing techniques (10X Genomics) to profile transcriptomic variations during *C. elegans* embryonic development at single-cell resolution.

Institut Curie

Paris, France

MASTER STUDENT IN RAPHAËL MARGUERON LAB

Jan 2016 - May 2016

- Development and troubleshooting of ChIP-seq in haploid human cell cultures.
- Implementation of SILAC & Mass spectrometry in haploid human cell cultures.
- ChIP-seq and RNA-seq data analysis and visualization.

University of California Los Angeles

Los Angeles, California

PLACEMENT YEAR IN KATHRIN PLATH LAB

Sep 2014 - Jul 2015

- Implementation and troubleshooting of Xist lncRNA Antisense Purification (RAP-seq).
- Implementation and troubleshooting of Nascent-RNA sequencing upon induction of stem cell differentiation and activation of X Chromosome Inactivation.
- ChIP-seq, RNA-seq and CLIP-seq data analysis and visualization.
- DNA/RNA-FISH of lncRNAs and single gene loci.

University of Navarra

Pamplona, Spain

SHORT INTERNSHIP IN MAITE HUARTE LAB

Jun 2014 - Aug 2014

- Project: Long intergenic non-coding RNA frequently amplified or deleted in cancerous cells play a role in cancer phenotypes.
- Techniques: RT-qPCR, Analysis and visualization of amplified and deleted loci in various cancer types

Institut Curie

Paris, France

SHORT INTERNSHIP IN EDITH HEARD LAB

Jun 2013 - Aug 2013

- Project: Study of random monoallelic expression of autosomal genes.
- Techniques: Western blots, Molecular cloning, Sanger sequencing, DNA- & RNA-FISH

Skills

Basic computing	<ul style="list-style-type: none">• Linux, Bash, (advanced), High-Performance Computing• R (expert), Python (intermediate)
Bioinformatics	<ul style="list-style-type: none">• R/Bioconductor• Automation of mapping and analysis pipelines• Advanced data visualization• Genome-wide sequencing in-depth analysis (RNA/ATAC/ChIP/others)
Data analysis	<ul style="list-style-type: none">• Data mining and visualization (R, Python)• Interactive dashboards (Shiny, Dash)• SQL databases (sqlite3, MySQL)
Workflow management	<ul style="list-style-type: none">• Pipeline automation (Nextflow, Snakemake)• Containerization (Docker, Singularity)
Web	<ul style="list-style-type: none">• HTML5, CSS, Bootstrap, Wordpress
Languages	<ul style="list-style-type: none">• English: fluent (TOEFL 2016: 110/120)• French: native• Spanish: intermediate

Awards & funding

2018	1st place , Cambridge Genomics Hackathon >sudo: sequence	Cambridge, UK
2016	£50,976 , Medical Research Council Doctoral Training Grant	Cambridge, UK
2016	£6,000 , Sackler Fund	Cambridge, UK
2012	€63,168 , Fellowship from École Normale Supérieure Paris-Saclay	Paris, France

Publications

†, ‡ indicate authors who contributed equally to the study.

Generating fragment density plots in R/Bioconductor with VplotR *Journal of Open-Source Software*
IN REVIEW 2021
Jacques Serizay

periodicDNA: an R/Bioconductor package to investigate k-mer periodicity in DNA *F1000Research*
IN PRESS 2021
Jacques Serizay, Julie Ahringer

Distinctive regulatory architectures of germline-active and somatic genes in *C. elegans* *Genome Research*
10.1101/GR.265934.120 2020
Jacques Serizay, Yan Dong, Jürgen Jänes, Michael Chesney, Chiara Cerrato, Julie Ahringer

A protein assembly mediates Xist localization and gene silencing *Nature*
10.1038/s41586-020-2703-0 2020
Amy Pandya-Jones, Yolanda Markaki, *Jacques Serizay*, Tsothe Chitashvili, Walter R Mancina Leon, Andrey Damianov, Constantinos Chronis, Bernadett Papp, Chun-Kan Chen, Robin McKee, Xiao-Jun Wang, Anthony Chau, Shan Sabri, Heinrich Leonhardt, Sika Zheng, Mitchell Guttman, Douglas L Black, Kathrin Plath

Analysis of copy number alterations reveals the lncRNA ALAL-1 as a regulator of lung cancer immune evasion *Journal of Cell Biology*
10.1083/JCB.201908078 2020
Alejandro Athie, Francesco P Marchese, Jovanna González, Teresa Lozano, Ivan Raimondi, Prasanna Kumar Juvvuna, Amaya Abad, Oskar Marin-Bejar, *Jacques Serizay*, Dannys Martínez, Daniel Ajona, Maria Jose Pajares, Juan Sandoval, Luis M Montuenga, Chandrasekhar Kanduri, Juan J Lasarte, Maite Huarte

Chromatin accessibility dynamics across *C. elegans* development and ageing *eLife*
10.7554/ELIFE.37344 2018
Jürgen Jänes †, Yan Dong †, Michael Schoof †, *Jacques Serizay* ‡, Alex Appert, Chiara Cerrato, Carson Woodbury, Ron Chen, Carolina Gemma, Ni Huang, Djem Kissiov, Przemyslaw Stempor, Annette Steward, Eva Zeiser, Sascha Sauer, Julie Ahringer

Genome organization at different scales: nature, formation and function *Current Opinion in Cell Biology*
10.1016/J.CEB.2018.03.009 2018
Jacques Serizay, Julie Ahringer

Bioinformatic resources

periodicDNA	R package to study k-mers periodicity at small and large scale in genomes	https://jserizay.com/periodicDNA/
VplotR	R package to easily generate V-plots of paired-end sequencing data	https://jserizay.com/VplotR/
RegAtlas	Developmental and tissue-specific regulatory atlas in <i>C. elegans</i> - Shiny app	https://ahringerlab.com/RegAtlas/
C. elegans browser	Genome browser for exploratory data analysis of developmental and tissue-specific chromatin organization in <i>C. elegans</i>	https://ahringerlab.com/Browser/

Scientific communication

Systems Biology: Global Regulation of Gene Expression

POSTER (SELECTED)

CSHL, New York

2020

International *C. elegans* Conference

TALK: DISTINCT REGULATORY ARCHITECTURES OF GERMLINE AND SOMATIC GENES (SELECTED)

UCLA, California

2019

Research in Genetics Conference

POSTER (SELECTED)

Cambridge, UK

2018

sciLife / LMB Bioscience Symposium

POSTER

Cambridge, UK

2017

International *C. elegans* Conference

POSTER (SELECTED)

UCLA, California

2017

Shell Research Conference

POSTER (SELECTED)

Cambridge, UK

2017

Teaching

Introduction to Multi-omics Data Integration and Visualisation

European Bioinformatics Institute, UK

1A Biology of the Cells

University of Cambridge, UK

Supervision of master students (4 6 months lab internships)

University of Cambridge, UK

Supervision of 1st year undergraduate students

University of Cambridge, UK

Teaching for BTEC Higher National Diploma, Biotechnology

Gif s/ Yvette, France

Extracurricular Activity

Fovea Paris

<https://foveaparis.com/>

FOUNDING MEMBER

2016 - PRESENT

- Micro-entrepreneur in jewelry crafting.
- Hand-crafting limited series of jewelry recycling beetle elytra

Box-office predictions

<https://github.com/js2264/moviestats>

UNDER DEVELOPMENT

2018 - PRESENT

- Movie box-office data investigation
- R package using machine-learning algorithms to predict movies box-office successes/failures

dn&art: DNA Networks & Assisted Representation of Time

<https://jserizay.com/dnart>

UNDER DEVELOPMENT

2020 - PRESENT

- Generative art in R/Bioconductor
- Creating individualized art based on DNA sequence similarities