

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

Institut Pasteur & ENS Paris

Paris, France

POST-DOC RESEARCHER IN ROMAIN KOSZUL AND NATHALIE SPASSKY LABORATORIES

Sep 2020 - Oct 2021

- 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)• R (expert), Python (intermediate)• High-Performance Computing (slurm)
Bioinformatics	<ul style="list-style-type: none">• 8+ years using R/Bioconductor• Genome-wide sequencing in-depth analysis (RNA/ATAC/ChIP/single-cell)• Automation of mapping and analysis pipelines• Advanced data visualization
Data analysis	<ul style="list-style-type: none">• Data mining using R (5 years) or Python (2 years)• Data visualization using 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">• Static web: HTML5, CSS, Bootstrap, Wordpress, HUGO
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

Peer-reviewed publications

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

Generating fragment density plots in R/Bioconductor with VplotR	<i>Journal of Open-Source Software</i>
10.21105/JOSS.03009	2021
<i>Jacques Serizay</i> , Julie Ahringer	
periodicDNA: an R/Bioconductor package to investigate k-mer periodicity in DNA	<i>F1000Research</i>
10.12688/F1000RESEARCH.51143.1	2021
<i>Jacques Serizay</i> , Julie Ahringer	
Distinctive regulatory architectures of germline-active and somatic genes in C. elegans	<i>Genome Research</i>
10.1101/GR.265934.120	2020
<i>Jacques Serizay</i> , Yan Dong, Jürgen Jänes, Michael Chesney, Chiara Cerrato, Julie Ahringer	
A protein assembly mediates Xist localization and gene silencing	<i>Nature</i>
10.1038/S41586-020-2703-0	2020
Amy Pandya-Jones, Yolanda Markaki, <i>Jacques Serizay</i> , Tsothe Chitiashvili, 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	<i>Journal of Cell Biology</i>
10.1083/JCB.201908078	2020
Alejandro Athie, Francesco P Marchese, Jovanna González, Teresa Lozano, Ivan Raimondi, Prasanna Kumar Juvvuna, Amaya Abad, Oskar Marin-Bejar, <i>Jacques Serizay</i> , 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	<i>eLife</i>
10.7554/ELIFE.37344	2021
Jürgen Jänes †, Yan Dong †, Michael Schoof ‡, <i>Jacques Serizay</i> ‡, 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	<i>Current Opinion in Cell Biology</i>
10.1016/J.CEB.2018.03.009	2018
<i>Jacques Serizay</i> , Julie Ahringer	

Bioinformatic resources

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

Scientific communication

2nd annual Qlife conference		Online
TALK: CO-OPTING THE MITOTIC MACHINERY TO DIFFERENTIATE (SELECTED)		2021
Systems Biology: Global Regulation of Gene Expression		CSHL, New York
POSTER: DISTINCT REGULATORY ARCHITECTURES OF GERMLINE AND SOMA GENES IN <i>C. elegans</i> (SELECTED)		2020
International <i>C. elegans</i> Conference		UCLA, California
TALK: DISTINCT REGULATORY ARCHITECTURES OF GERMLINE AND SOMATIC GENES (SELECTED)		2019
Research in Genetics Conference		Cambridge, UK
POSTER: TISSUE-SPECIFIC CHROMATIN ORGANIZATION IN <i>C. elegans</i> (SELECTED)		2018
International <i>C. elegans</i> Conference		UCLA, California
POSTER: PROFILING TISSUE-SPECIFIC CHROMATIN PARAMETERS DURING <i>C. elegans</i> DEVELOPMENT (SELECTED)		2017
Shell Research Conference		Cambridge, UK
POSTER: FUNCTIONAL ROLES OF CHROMATIN DYNAMIC ORGANIZATION IN TISSUE-SPECIFIC GENE REGULATION (SELECTED)		2017

Teaching

2021	Single-cell RNA-seq analysis with R/Bioconductor	Physalia Courses
2021	NGS analysis for gene regulation and epigenomics	Physalia Courses
2020	Introduction to Multi-omics Data Integration and Visualisation	European Bioinformatics Institute, UK
2018-2019	1A Biology of the Cells	University of Cambridge, UK
2017-2019	Supervision of master students (4-6 months lab internships)	University of Cambridge, UK
2016-2019	Supervision of 1st year undergraduate students	University of Cambridge, UK
2015-2016	Teaching for BTEC Higher National Diploma, Biotechnology	Gifs/Yvette, France

Extracurricular Activity

Fovea Paris		https://foveaparis.com/
FOUNDING MEMBER		2016 - PRESENT
<ul style="list-style-type: none">• Micro-entrepreneur in jewelry crafting.• Hand-crafting limited series of jewelry recycling beetle elytra		
Generative art		https://jserizay.com/galleries
EXPLORING ART WITH R		2020 - PRESENT
<ul style="list-style-type: none">• dnaRt: DNA Networks & Assisted Representation of Time: Creating unique art based on DNA sequence similarities• mondrianRt: In silico generation of Mondrian-styled art• seuratify: Turn any photo into a Seurat-styled image• movieaRt: Investigating movies through their colors		
Movie databases analysis		Movie packages on Github
ANALYSIS AND INTERACTIVE EXPLORATION OF MOVIE DATABASES		2018 - PRESENT
<ul style="list-style-type: none">• moviestats: Movie box-office data investigation package• movierecommendations: Interactive, network-based movie recommendations		