

Role of ribosome and translation in cancer

Keywords: bioinformatics, data science, NGS, ribosomal RNA, epitranscriptomics, translational control, cancer

A **research engineer position in bioinformatics** is open to work at the interface of one team (Ribosome, Translation and Cancer) and two platforms (Bioinformatics and RibosOMICS) of CRCL in Lyon, France. The research programs will focus on the understanding of the role of ribosomal RNA epitranscriptomics and translation in cancer. The successful applicant will join a multidisciplinary group to implement novel technologies at CRCL for routine use. In particular, the objectives are (i) to develop methods that will be further included in bioinformatics tools, in particular R packages from a pool of already existing in-house packages, and (ii) to analyze datasets dedicated to RNA-seq based technologies: RiboMethSeq (rRNA 2'Ome), HydraPsiSeq (rRNA pseudouridylation) and translaticomics (polysome profiling, RiboSeq, RiboSTAMP). The successful candidate will work closely with the [Gilles Thomas Bioinformatics platform](#), a dynamic environment comprising 14 bioinformaticians, bioanalysts, biostatisticians, and developers. Since its inception in 2009, the platform has cultivated multidisciplinary expertise and established advanced skills to leverage the vast amounts of data generated from large-scale genomic projects in cancer research and immuno-oncology.

Main tasks

- Development of methodologies specifically dedicated to rRNA epitranscriptomics and translaticomics
- Development of functions/pipelines to automate analysis tasks when they become routines
- Perform bioinformatic/biostatistic analyses of the data, from raw sequencing data to biologically usable results
- Possibility to help the group to develop, implement and maintain tools, including software solutions (Nextflow, R package, Bioconductor...) and web interfaces
- Writing analysis reports

Required technical skills

- Hold a Master degree (Bac+5) in bioinformatics (or equivalent experience/field)
- Very good programming skills in R and/or Python, ideally in R package development (Bioconductor or CRAN)
- Knowledge of bioinformatics tools, in particular in the NGS domain
- Good knowledge of statistical laws/methods associated with NGS sequencing data analysis (especially RNAseq)
- Knowledge of descriptive statistics and machine learning methods
- Familiar with the work on linux environments and cluster computing
- Expertise in manipulation and visualization of NGS data or other large scale biologic data with R
- Good knowledge in English (at least writing and reading)

Desirable knowledge, skills and abilities

- Ability to work independently at the interface of an interdisciplinary research group
- Ability to present to non-expert audiences
- Scientific precision, seriousness and curiosity, good oral and written communication abilities
- Knowledge and/or interest in Cancer biology
- Enthusiasm for visual analytics and data science

Lab/Location: The three teams are located on the Centre Léon Bérard hospital campus (Grange-Blanche) in Lyon, France

Working language: French or English

Working commitment / Duration: Full-time position; 12 months (renewable)

Contacts: Applicants should send a cover letter and a CV to

- **Plat. RibosOMICS unit** (<https://www.crcl.fr/en/ribosomics-platform/>): ribosomics@lyon.unicancer.fr

Closing date: July 15, 2024 / **Starting date:** between September 2024 and December 2024