

# SENIOR COMPUTATIONAL BIOLOGIST POSITION

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## Background

ErVaccine Technologies is a start up company integrated in Centre Léon Bérard, Lyon, France, which develops new immunotherapeutic approaches targeting human endogenous retroviruses (HERV) and other non-conventional tumor antigens (Bonaventura et al, Sci Adv 2022; Alcazer et al, Am J Hematol 2022). For more information see: <http://ervaccinetechnologies.com/>

## The Role

As a key member of the bioinformatics team, you will contribute to the bioinformatics development at ErVaccine. You will be in charge of the *in silico* identification of original therapeutic targets in cancer that will be further validated by the preclinical team. You will also contribute to the development of new methods to analyze HERV expression and identify new targets and biomarkers. You will be expected to develop the infrastructure and the pipelines already proposed by the team. A strong implication in the overall project will be asked.

## First developments

- Integrate and optimize the current HERVs-analysis pipeline in different diseases
- Propose some new lists of targets in different cancers
- Establish a new method to integrate pan-HLA targets
- Develop single cell analyses of HERV retrotranscriptome
- Interact with experts on different projects such as proteomics and TCR modelling
- Prepare *in silico* data for regulatory reports
- Participate actively in scientific communications and publications
- Keep the links with the local bioinformatics teams at Centre Leon Berard

## Position Requirements

- Solid mathematical training with a PhD in bioinformatics, computer science or related fields with significant experience in genomics
- Post-doc experience
- Good background in biology
- Excellent working proficiency in R, python, bash or other scripting language in CLI environment commonly used in bioinformatics pipelines
- Familiarity with high-performance computing resources and linux environment
- Proficient in Next-generation sequencing data analysis (RNA-seq and single cell RNA-seq), from quality check to data analysis
- Strong ability to work independently and share results to both bioinformaticians and biologists
- Statistical intuition, deep understanding of core statistical principles, and extensive experience with core methods (e.g., linear regression, GLMs, dimensionality reduction, tree-based models, bootstrapping, maximum likelihood estimation, Bayesian modeling...) and machine learning/deep learning approaches
- English written and spoken (scientific level)

Candidates should address their CV and contact information to Rasha Boulos, PhD, at [rasha.boulos@ervaccinetechnologies.fr](mailto:rasha.boulos@ervaccinetechnologies.fr)