

## Bioinformatician position \_ Generation & *in-depth* characterization of pediatric organoid.

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### Keywords:

Pediatric Cancer, Organoids, Next Generation Sequencing, Illumina technologies

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### About the lab:

The establishment of cancer-derived organoids has recently begun to emerge as a prominent and promising tool to enhance our understanding of human cancers (*Broutier et al., nature protocols 2016 & Broutier et al., nature medicine 2017*). However, such models have as yet not been developed for pediatric cancers. The research program that we develop in the C<sup>3</sup> lab forms part of this perspective with the objective to elaborate innovative organoid models to address pediatric cancers specificities and complexity, with a special focus on the mechanisms of resistance to treatments. We are affiliated to the Cancer Research Centre of Lyon (CRCL –INSERM U1052 / CNRS 5286) and to the Centre Léon Bérard's Pediatric hospital (IHOPE). The CRCL is amongst the most prestigious cancer research center in France and the IHOPE is a major reference pediatric cancer center. Our group is therefore composed of both researchers, clinicians and pathologists.

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### Position Highlight:

Starting on October 2019. Our group need a bioinformatician and high-performance computing set up to interrogate the data publicly available and currently being generated in our in-house projects. Available for highly motivated bioinformatics post-doctoral fellow in the field of bioinformatics applied to Next Generation Sequencing and Illumina technology. The candidate will be responsible for processing and analyzing multi-scale omics data (including not limited to (WGS, WGBS, WES, RNA-seq, ATACseq, MethylationEPIC BeadChip...)). The successful applicant will strongly interact with the "Gilles Thomas" bioinformatics facility (Dir. Alain Viari) <http://www.cancer-research-lyon.com/fiches/FSLC-Fiche-GillesThomas.pdf>.

### Length/Period:

The successful applicant will initially have a 1-year contract, with the possibility of extension (+1 years).

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**Salary:** Salary will depend on candidate's experience.

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### Objectives:

To establish organoid lines from fresh biopsies and relevant control non-tumoral organoid lines from healthy tissues, the candidate will decipher active signaling cascades that could support cell growth, as reliable insights to find out the appropriate culture conditions. Moreover, to set-up the culture conditions it will be important to uncover the cell-of-origin of pediatric tumors. During tumorigenesis some DNA methylation patterns may be retained as a form of epigenetic memory, representing the history of the cancer cells. The candidate will use methylome data to uncover the distinct cellular sources of pathologies of interest. The candidate will be involved in training/advising wet-lab collaborators on basic bioinformatic analysis. The successful candidate will also have opportunity to develop their own research ideas as they fit within the general research interests of our group.

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### Candidate profile:

- Applicants should have demonstrated working experiences in Next Generation Sequencing/Illumina technology analyses. Extensive experience in sequencing data tools such as Picard tools, SAMtools, FastQC, aligners such as BWA, Tophat, STAR, variant calling pipelines such as GATK tools / Queue, SAMtools mpileup, annotation packages and resources such as Ensembl, GENCODE, BLAST, GSEA, mSigDB, GWAS catalog, OMIM, KEGG, online data resources such as GTEx, TCGA, GEO, dbGaP, genotype processing, QC and analysis tools such as PLINK, IMPUTE2, relevant R packages such as limma, edgeR, MatrixEql, RNAseq tools such as featureCounts, HTSeq, Cufflinks.
  - A good knowledge in statistics and in programming (bash, R, perl, C or python) is mandatory.
  - Basic knowledge in cancer biology and genetics is required.
  - The candidate should be highly self-motivated, with the ability to work independently and with our interdisciplinary team and wet-lab collaborators.
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**Elements to be provided for your application:** Interested candidates should send a single PDF file that includes a full curriculum vitae with publications, a short description of previous training & work experiences and the names, contact details and recommendation letters of 2 referees (former professor/advisor/mentor) to [laura.broutier@lyon.unicancer.fr](mailto:laura.broutier@lyon.unicancer.fr). Please indicate "BIOINFO POSITION\_C3 TEAM" in the subject line.