



GENomique
EPIdémologique
des maladies
Infectieuses



Centre
International
de Recherche
en Infectiologie

Post-doctoral position in Viral Metagenomics

Description:

The HAP2 European research project aims to develop host-directed drugs and biomarkers to enhance the prevention and treatment of hospital-acquired pneumonia (HAP) (<https://hap2-project.com/>). Our research team is involved in the biomarker work package and has been generating viral metagenomics data on this cohort. We also lead research projects using metatranscriptomics, metagenomics, and/or metabarcoding data to explore viral pathogenesis and respiratory diseases on several other clinical cohorts (including patients hospitalized for bronchiolitis, influenza disease, and pre-term newborn).

The postdoctoral fellow will be in charge of the analysis of multi-omics data of the human microbiome (including metabarcoding, metagenomics, metatranscriptomics, and transcriptomics) in these different clinical studies, with the help of bioinformaticians and virologists of the team.

Contract: **2 years**.

Profile:

- PhD in Virology with experience in interpretation of omics data analyses
or PhD in Bioinformatics or Computational biology with experience in metagenomics
- Good programming skills (R, python)
- Experience in omics data analysis (e.g. (meta)genomics, (meta)transcriptomics, proteomics, metabolomics, epigenomics, genotyping data)
- Experience in clinical datamining/machine learning, biomarker detection is a plus

Environment:

You will join the GenEPII sequencing platform <https://genepii.univ-lyon1.fr> and the VirPath research team of the CIRI- International Center for Infectiology Research (<https://ciri.ens-lyon.fr>). You will be based at the *Hopital de la Croix Rouse* (69004 Lyon) within the Hospices Civils de Lyon. The genEPII team includes microbiologists, bioinformaticians, engineers and technicians working on microbiology genomics. The platform is associated with four National Reference Centers (NRC), including the NRC for respiratory viruses and has been heavily involved in SARS-CoV-2 genome sequencing. The lab has on-site robotic sample processing, high-throughput computing resources as well as next-gen sequencing facilities (NextSeq, NovaSeq, oxford nanopore gridion).

How to apply:



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Please send an email to Dr Laurence Josset (laurence.josset@chu-lyon.fr) attaching the following documents:

- A cover letter
- A curriculum vitae
- Contact information for 3 references

If you have any questions please contact Dr Laurence Josset (laurence.josset@chu-lyon.fr)

Deadline

Review of applications begins immediately and continues until March 31st, 2023.

Recent publications from the lab related to the field

Langevin S, Pichon M, Smith E, [...] **Josset L** « Early Nasopharyngeal Microbial Signature Associated with Severe Influenza in Children: A Retrospective Pilot Study ». *The Journal of General Virology* 98, n° 10 (2017): 2425-37. <https://doi.org/10.1099/jgv.0.000920>.

Bal A, Pichon M, Picard C, [...] **Josset L** « Quality Control Implementation for Universal Characterization of DNA and RNA Viruses in Clinical Respiratory Samples Using Single Metagenomic Next-Generation Sequencing Workflow ». *BMC Infectious Diseases* 18, n° 1 (2018): 537. <https://doi.org/10.1186/s12879-018-3446-5>.

Bal A, Sarkozy C, **Josset L**, [...] Brengel-Pesce K « Metagenomic Next-Generation Sequencing Reveals Individual Composition and Dynamics of Anelloviruses during Autologous Stem Cell Transplant Recipient Management ». *Viruses* 10, n° 11 (2018): E633. <https://doi.org/10.3390/v10110633>.

Bal A, Oriol G, **Josset L**, [...] Assant S « Metagenomic Investigation of Torque Teno Mini Virus-SH in Hematological Patients ». *Frontiers in Microbiology* 10 (2019): 1898. <https://doi.org/10.3389/fmicb.2019.01898>.

Charre C, Ginevra C, Sabatier M, [...] **Josset L** « Evaluation of NGS-Based Approaches for SARS-CoV-2 Whole Genome Characterisation ». *Virus Evolution* 6, n° 2 (2020): veaa075. <https://doi.org/10.1093/ve/veaa075>.

Sabatier M, **Bal A**, **Destras G** [...] **Josset L** « Comparison of Nucleic Acid Extraction Methods for a Viral Metagenomics Analysis of Respiratory Viruses ». *Microorganisms* 8, n° 10 (2020): E1539. <https://doi.org/10.3390/microorganisms8101539>.

Bal A, **Destras G**, Sabatier M, [...] **Josset L**, Morfin F. «Metagenomic Analysis Reveals High Abundance of TTMV in the Respiratory Tract of Children with Acute Respiratory Illness». *Viruses*, 2022

Bal, A ; Simon, B ; Destras, G ; Chalvignac, R ; Semanas, Q ; Oblette, A [...] **L. Josset**, Detection and prevalence of SARS-CoV-2 co-infections during the Omicron variant circulation in France., *Nat Commun*, 2022, 13, 6316