Post-doctoral position at the Institute of Biology Paris-Seine (IBPS)
Title: Deciphering the translational fingerprint of cell division with an Attribute Network-Based Ranking (ANeR) method

IBPS brings together almost all the research in Biology of the Pierre et Marie Curie Campus within Sorbonne University. Located in Paris downtown by the Seine river, IBPS hosts over 500 people across 5 laboratories and 6 technological platforms. It provides a highly collaborative, international and interdisciplinary life science environment.
https://www.ibps.sorbonne-universite.fr/en

Laboratory
Because of the interdisciplinary approach of the project, the post-doctoral researcher will be co-supervised by two researchers: Enrico Daldello, from the "Biology of the oocyte" team (Laboratory of Developmental Biology - IBPS), and Juliana Bernardes, from the "Statistical genomics and biological physics" team (Laboratory of Computational and Quantative Biology - IBPS).

Project
The selected candidate will work on the identification of new translated proteins controlling cell division through an interdisciplinary research program coupling mathematical model predictions with cell biology approaches. Cell division is a crucial biological process that underlies the existence of all organisms and is highly conserved across evolution. The initiation of cell division is dependent on the activation of Cdk1, the universal master regulator of all eukaryotic cell divisions. The activation of Cdk1 is controlled by a complex network of proteins that are regulated by post-translational mechanisms and protein translation. Specifically, blocking protein translation halts Cdk1 activation in both mitosis and meiosis.
However, the identity of the proteins whose translation is required for Cdk1 activation remains an open question in the field, with only a few having been identified through biochemical methods. In recent years, the rise of -omic technologies has enabled to study this fundamental cellular process at a genome-wide scale.
We have started to develop a new computational approach (*Attribute Network-Based Ranking - ANeR*) that uses machine learning and graph theory to identify novel regulators of cell division that are controlled at the protein translation level, using the vast collection of -omics datasets available in the literature.
The selected candidate will finalize the optimization parameters of ANeR. He/she will experimentally validate its predictions using a translation reporter technique that we developed for *Xenopus* oocytes. He/she will compare ANeR predictions of the *Xenopus* oocyte model to other existing models, as the principal component analysis (PCA), with the global aim of deciphering the translational fingerprints of cell division.

Candidate profile

Expertise in molecular biology is necessary. The successful applicant must be interested in expanding his/her biological skills on the application of computation approaches. Ability to work independently within a team environment and good communication skills are required.
English: good level (French speaking is not required).

Contract information
- Starting date: September 1st, 2023 to January 1st, 2024
- Duration: 12 to 16 months (end of the contract: December 31th, 2024).
- Working time: full time
- Benefits: Salary based on experience, according to the Sorbonne University guidelines.

Application

Please send your application including the following items to Enrico M. Daldello (enrico.daldello@upmc.fr):
- a description of your previous research experience and your general research interests (2 pages maximum),
- a curriculum vitae,
- the list of your publications,
- at least two contacts for references (including phone number and email).

References

Meneau, Ferdinand, Aude Dupré, Catherine Jessus, and Enrico Maria Daldello. "Translational Control of Xenopus Oocyte Meiosis: Toward the Genomic Era." *Cells* 9, no. 6 (June 19, 2020): 1502. https://doi.org/10.3390/cells9061502.

Xiong, Zhuqing, Kai Xu, Zili Lin, Feng Kong, Qiujun Wang, Yujun Quan, Qian-qian Sha, et al. "Ultrasensitive Ribo-Seq Reveals Translational Landscapes during Mammalian Oocyte-to-Embryo Transition and Pre-Implantation Development." *Nature Cell Biology*, June 13, 2022. https://doi.org/10.1038/s41556-022-00928-6.