

A post-doctoral position is open in our team « Mechanisms of genome expression and integrity" at the Institut de Génétique Moléculaire of Montpellier, France (IGMM, CNRS/University of Montpellier,). Our team has recently moved from Paris for a challenging and exciting new start in the great living and scientific environment of Montpellier in the south of France. We study the **molecular mechanisms** of transcription and gene expression in general, using yeast as a model system, but with present and future openings to the mammalian system.

It is now clear that RNA polymerase II transcribes most of the genome, largely beyond the limits of geness coding for functional product. These transcription events generate non-coding RNAs that are often rapidly degraded, whose functions and raison-d'être are not completely understood. We have provided important contributions to the discovery of pervasive, non-coding transcription, and studied how it is originated and functions. We are now turning our attention to the crosstalks between transcription, replication, genome stability and genome organization. How generalized transcription influences these other processes that share the use of the DNA template? How these processes are coordinated to avoid disruptive, mutual interference? We are also interested in the physiology of R-loops, genotoxic structures containing RNA-DNA hybrids that are formed during transcription. We address these questions with a variety of methodologies, using current and advanced biochemistry (e.g. in vitro transcription termination), molecular biology and genome-wide approaches, some of which have been originally developed in the team. The successful candidate will have the opportunity to learn these techniques and/or collaborate with other members of the team in shared projects.

The Institut de Génétique Moléculaire de Montpellier (<u>https://www.igmm.cnrs.fr/en/</u>) is a center of excellence for fundamental research in molecular and cellular biology. The scientific interests of IGMM groups cover a large variety of subjects, from RNA to transcription and gene expression, from immunology to virology and cancer biology. The multidisciplinary and international scientific environment provides rich and stimulating training opportunities for young scientists. The Institute also provides a very friendly and socially-active environment. The post-doc will have access to state-of-theart core facilities (including, but not limited to, live-cell imaging, proteomics, genomics) either in-house or



in neighboring Institutes of the Montpellier area through the BioCampus managing facility. **Montpellier is an exceptional** scientific environment, internationally recognized and certainly one of the best in Europe.



The town is a great and affordable place for living, with a beautiful historical center and a living and culturally-active environment, very student-friendly. Montpellier is located in an exceptional geographic

position, with farms, vineya

position, with close-by beaches, a beautiful countryside with farms, vineyards and freshwater – lakes and rivers – locations.

The applicants should hold a PhD and have some **expertise in biochemistry, molecular biology and genomics.** Basic **knowledge of some bioinformatic tools and/or programming skills would be welcome**. Working knowledge of the English language (scientific, oral and written) is necessary, but **knowledge of French is not required**. **Enthusiasm, motivation and willingness to contribute to a dynamic and enjoyable working environment are qualities we value.** The candidate should show autonomy, but a successful integration into the team projects is essential.

We propose a 12-month, renewable contract for a post-doctoral position with a salary defined by CNRS rules. **The position is open immediately but the starting date is to some extent flexible.** Applications should include a CV and a letter of motivation summarizing your scientific interests, as well as the contact information of at least 2 scientists for reference.

Contact : domenico.libri@igmm.cnrs.fr

Web page: DLOP lab

Twitter:@DomenicoLibri @LabLibri

A few recent references:

Aiello, U., Challal, D., Wentzinger, G., Lengronne, A., Appanah, R., Pasero, P., Palancade, B., and Libri, D. (2022). Sen1 is a key regulator of transcription-driven conflicts. Mol Cell 82, 2952-2966.e6. https://doi.org/10.1016/j.molcel.2022.06.021.

Xie, J., Aiello, U., Clement, Y., Haidara, N., Girbig, M., Schmitzova, J., Pena, V., Müller, C.W., Libri, D., and Porrua, O. (2022). An integrated model for termination of RNA polymerase III transcription. Sci Adv 8, eabm9875. https://doi.org/10.1126/sciadv.abm9875.

Villa, T., Barucco, M., Martin-Niclos, M.-J., Jacquier, A., and Libri, D. (2020). Degradation of Non-coding RNAs Promotes Recycling of Termination Factors at Sites of Transcription. Cell Rep *32*, 107942.

Han, Z., Jasnovidova, O., Haidara, N., Tudek, A., Kubicek, K., Libri, D., Stefl, R., and Porrua, O. (2020). Termination of non-coding transcription in yeast relies on both an RNA Pol II CTD interaction domain and a CTD-mimicking region in Sen1. EMBO J. e101548.

Appanah, R., Lones, E.C., Aiello, U., Libri, D., and De Piccoli, G. (2020). Sen1 Is Recruited to Replication Forks via Ctf4 and Mrc1 and Promotes Genome Stability. Cell Rep 30, 2094-2105.e9.

Wang, S., Han, Z., Libri, D., Porrua, O., and Strick, T.R. (2019). Single-molecule characterization of extrinsic transcription termination by Sen1 helicase. Nat Commun 10, 1545.

Candelli, T., Gros*, J., and Libri*, D. (2018). Pervasive transcription fine-tunes replication origin activity. Elife 7.

Challal, D., Barucco, M., Kubik, S., Feuerbach, F., Candelli, T., Geoffroy, H., Benaksas, C., Shore, D., and Libri, D. (2018). General Regulatory Factors Control the Fidelity of Transcription by Restricting Non-coding and Ectopic Initiation. Mol. Cell 72, 955-969.e7.