

Post Doctoral position in 'Transcription and Chromatin' lab, Institut de Génétique Moléculaire de Montpellier

Role of secondary DNA structures in transcription and chromatin opening at the genome scale

The team Transcription and Epigenomics is interested in basal and activated transcription mechanisms as well as the regulation of gene expression through regulatory elements (promoters and enhancers). We are looking for a motivated and enthusiastic postdoc with good knowledge in genome editing and functional genomics.

The project aims at understanding the role of G-quadruplexes and their ligands in the regulation of genome expression in normal and cancerous cells. He/She will perform genome editing (CRISPR) and functional genomics experiments (ChIP-seq, RNA-seq, nucleosome mapping) to support its investigations in the laboratory. The applicant should have a PhD in Genetics/Molecular Biology, preferably in the fields of transcription/chromatin and/or functional genomics. He/she should be experienced with at least one the following techniques: molecular biology and biochemistry, CRISPR and gene editing, transcriptome or chromatin investigations using high-throughput sequencing approaches. Further knowledge in Bioinformatics analyses will be useful for the project but is not compulsory. The selected applicant will be offered a one year contract that could be renewed for one or two extra years. Send CV including 2 referees and motivation letter to jean-christophe.andrau@igmm.cnrs.fr.

Recent publications of the group:

[Alternative Enhancer Usage and Targeted Polycomb Marking Hallmark Promoter Choice during T Cell Differentiation.](#) Maqbool et al, **Cell Rep.** **2020** Aug 18;32(7):108048.

[The Landscape of L1 Retrotransposons in the Human Genome Is Shaped by Pre-insertion Sequence Biases and Post-insertion Selection.](#) Sultana et al, **Mol Cell.** **2019** May 2;74(3):555-570.e7

[Tyrosine-1 of RNA Polymerase II CTD Controls Global Termination of Gene Transcription in Mammals.](#) Shah et al, **Mol Cell.** **2018** Jan 4;69(1):48-61.e6.

[Lineage-specific enhancers activate self-renewal genes in macrophages and embryonic stem cells.](#) Soucie et al, **Science.** **2016** Feb 12;351(6274):aad5510.

[High-throughput and quantitative assessment of enhancer activity in mammals by CapStarr-seq.](#) Vanhille et al, **Nat Commun.** **2015** Apr 15;6:6905.