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One postdoctoral position is available in our laboratory on the topic of the molecular control of adult neural stem cell (aNSC) activation and aging

Open position from now and for 2 years with a one year-renewable contract

Laboratory Research: Our laboratory is interested in the biology of neural stem cells during development and in the adult brain. Our studies focus on the mechanisms controling neural stem cell quiescence versus activation and on the role of neurovascular interactions in neural stem cell behavior. We are using molecular genetic approaches in mice and zebrafish as well as molecular analyse of human brain biopsies.

In collaboration with A. Eichmann's group (Yale Cardiovascular Medicine), we have shown that neural and endothelial cells use common signaling molecules, including the Netrin receptor UNC5B, Robo4, and Neuropilin1/2 to regulating capillary and lymphatic patterning and guidance. We have also found that vascular endothelial growth factor-C (VEGF-C), the key inducer of lymphatic vessel development, and its high-affinity receptor VEGFR-3, are critically required for neurogenesis. VEGF-C directly acts on VEGFR3-expressing neural stem cells (NSCs) in mice and humans, opening potential approaches for repair of neurodegenerative diseases.

Publications: Han J, *Cell Rep*. 2015 Feb 24;10(7):1158-72; Ristori E, *Dev Cell*. 2015 Mar 9;32(5):546-60; Bouvrée K., Circ *Res*. 2012 Aug 3; 111(4): 437-45; Eichmann A. and Thomas J-L. *Cold Spring Harb Perspect Med* 2013 Jan 1; 3(1): a006551; Calvo CF, Gene*s Dev*. 2011 Apr 15;25(8):831-44; Le Bras B, *Nat. Neuroscience* 2006; 9: 340-348; Lu X, *Nature* 2004; 432: 179-86.

Project. Molecular control of adult neural stem cell (aNSC) activation and aging

The overall goal of this proposal is identify the gene networks and the specific genes governing the balance between activation and quiescence in brain NSCs during their lifespan in mice and humans. The NSC-reporter mouse Vegr3YFP is used to identify and isolate mouse NSCs or sample intracellular NSC material for Single-cell RNA sequencing and histone modification analysis (ATAC-seq and ChIPseq), while frozen human brain samples are collected at embryonic, fetal and post-natal stages as a source of nuclei for Single nuclei-RNA sequencing. *Partner at Yale*: Nenad Sestan. The candidate will work with a team of bioinformaticists and take advantage of computers and softwares available in the Sestan lab.

Profile required: Applicants should either have experience in bioinformatics and data analysis or have strong background in theoretical computer science or combinatorics and burning desire to work in the field of bioinformatics. The applicants interested in new algorithmic approaches to transcriptome analysis are particularly sought. Applicants are expected to have proficiency with one or multiple computer languages such as R and Python, and to demonstrate ability to analyze genomic/transcriptomic data (through read alignment, dimension reduction, clustering analysis, differential expression analysis, etc..).

Qualifications: a PhD in Computer Science/Mathematics (or a related field) and some experience in computer programming. At least 2 good papers as a first author. English: fluent; Letters of reference (2-3).

Please send your CV, cover letter and letters of reference to
jean-leon.thomas@yale.edu
Object: post-doctoral application