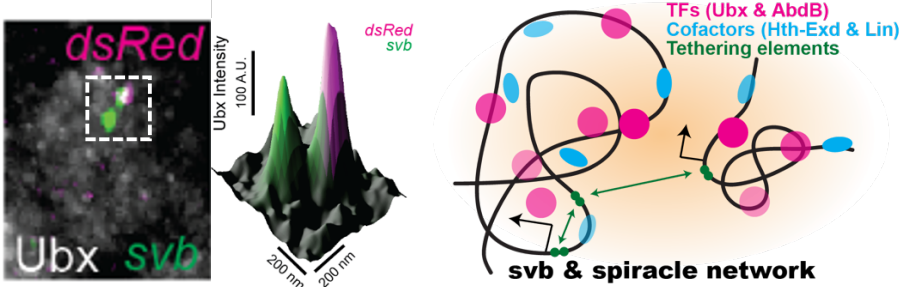


2027 Internship Offer

Master 1: YES – Duration: 5 months **Master 2:** YES – Duration: 6 months

Team, Contact	Albert TSAI, CRBM, albert.tsai@crbm.cnrs.fr
Title	Developing a toolset to dissect the spatial coordination between genomic loci during embryo development
Research Themes and questions	Multiple genes can colocalize in the nucleus, making gene expression and embryo development more resilient to environmental and genetic changes. However, the mechanism behind this pairing is not known. We identified tethering elements (TEs) that surround enhancers and promoters of developmental genes on the chromatin as candidate regulatory elements promoting these interactions. We are developing imaging approaches to track and dissect how TEs promote pairing and ensure its specificity.
Methods and experimental approaches	We use <i>Drosophila melanogaster</i> embryos, a model organism with conserved regulatory pathways for embryo development and powerful genetic editing tools. We will first perform cloning to generate transgenic constructs containing different configurations of TEs, enhancers, and promoters taken from the developmental gene <i>shavenbaby</i> (<i>svb</i>). After generating transgenic flies, we will employ a genetic approach coupled with confocal microscopy to determine the ability of the different transgenes to colocalize with the endogenous <i>svb</i> locus. We will also assay how TEs pairing with the <i>svb</i> locus alters transcription using RNA FISH.
Illustration	 <p>The illustration consists of three parts. On the left, a confocal microscopy image shows a nucleus with dsRed (magenta) and Ubx svb (green) colocalizing. A dashed white box highlights a region of interest. In the middle, a 3D surface plot shows Ubx intensity (100 A.U.) with a scale bar of 200 nm. On the right, a schematic diagram of the <i>svb</i> & spiracle network shows TFs (Ubx & AbdB) in magenta, Cofactors (Hth-Exd & Lin) in blue, and Tethering elements in green.</p>
1-3 Publications	<ol style="list-style-type: none"> 1. Tsai A., <i>et al.</i>, (2017) Nuclear microenvironments modulate transcription from low-affinity enhancers. <i>eLife</i>, doi: 10.7554/eLife.28975 2. Tsai A., <i>et al.</i> (2019) Multi-enhancer transcriptional hubs confer phenotypic robustness. <i>eLife</i>, doi: 10.7554/eLife.45325 3. Li X. & Levine M., (2024) What are tethering elements? <i>Curr Opin Genet Dev.</i>, doi: 10.1016/j.gde.2023.102151