CRBM
Centre de Recherche de Biologie cellulaire de Montpellier
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UNIVERSITÉ DE MONTPELLIER

2027 Internship Offer

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

Team, Contact	Borensztein Team – Reprogrammation épigénétique et développement Contact: Hegias Mira-Bontenbal, hegias.mira-bontenbal@igmm.cnrs.fr, & Helmlinger Team - Régulation de l'expression des gènes Contact : Peggy Raynaud, peggy.raynaud@crbm.cnrs.fr
Title	Involvement of the transcriptional coactivator SAGA in X chromosome reactivation
Research Themes and questions	In female mammals, one X chromosome is epigenetically silenced through X chromosome inactivation (XCI), initiated at embryo implantation. During primordial germ cell (PGC) development, this silencing is reversed through X chromosome reactivation (XCR), a process that remains poorly understood despite its critical implications for female meiosis and fertility. Using a genome-wide CRISPR/Cas9 knockout screen in an *in vitro* PGCLC differentiation system, the Borensztein's group (where Hegias Mira-Bontenbal [HMB] is based - IGMM) identified two core subunits of the SAGA chromatin-modifying complex, SUPT3 and SUPT7L, as required for XCR, representing the first link between SAGA and this process. SAGA co-activator complex regulates transcription through histone acetylation and deubiquitination, both of which are relevant to XCI and XCR dynamics.
Methods and experimental approaches	This M2 project, a collaboration between HMB and SAGA expert Peggy Raynaud (PR; Helmlinger group - CRBM), aims to validate and dissect SAGA's role in XCR. Using a well-established hybrid ESC-to-PGCLC differentiation model with dual fluorescent reporters, the student will combine siRNA knockdowns, endogenous degron engineering, and allele-specific CUT&RUN-seq for H3K9ac to determine how SAGA contributes to XCR during female germline development.
Illustration	
2-3 Publications	✓ Roidor C, Syx L, Beyne E, **Raynaud P**, Zielinski D, Teissandier A, Lee C, Walter M, Servant N, Chebli K, Bourc'his D, Surani MA, Borensztein M. **2025** *Temporal and regional X-linked gene reactivation in the mouse germline reveals site-specific retention of epigenetic silencing.* Nat Struct Mol Biol. 2025 May;32(5):926-939. doi: 10.1038/s41594-024-01469-2. Epub 2025 Jan 21. ✓ Detilleux D, **Raynaud P**, Pradet-Balade B, Helmlinger D. **2022** *The TRRAP transcription cofactor represses interferon-stimulated genes in colorectal cancer cells.* Elife, Mar 4;11:e69705.