

LGB

Laboratoire de génét et biologie cellu

PARTNERS

The LGBC develops projects in collaboration with different partners:

- With the team of Maxime Breban (U1173 INSERM/UVSQ), we use the *Drosophila* model system to study the activities of the HLA-B27 antigen, the main genetic predisposing factor to ankylosing spondylitis, an inflammatory rheumatic disease. This study identified a specific HLA-B27 interactor in *Drosophila* that has a human homolog capable of interacting with HLA-B27, a receptor of the TGFbeta/Activin/BMP pathway. Functional studies showed the ability of HLA-B27 to deregulate these signaling pathways in patient cells, which may explain aspects of ankylosing spondylitis (Grandon et al. 2019). The project funded by the French National Research Agency is continuing with the objective of further characterizing these deregulations.

- With Fabienne Misguich and Jean-Louis Herrmann (U1173 INSERM/UVSQ), we are using *Drosophila* as a model organism for *Mycobacterium abscessus* infection, in particular to identify factors that allow *Mycobacterium abscessus* to resist the innate immune response and the humoral (antimicrobial peptides) or cellular (plasmacytes)

immune response during infection (Touré et al. 2023)

- In the framework of the "Sideroflexins, mitochondria, and cell fate" axis, we collaborate through a project funded by the French National Research Agency with Nathalie Bonnefoy and Geneviève Dujardin (I2BC, Gif-sur-Yvette), Géraldine Liot (CEA, Fontenay-aux-Roses), Marie-Pierre Golinelli (ICSN, Gif-sur-Yvette) and Ioana Ferecatu (Faculty of Pharmacy Paris 5, Paris).

- In the framework of the "Mitochondria and ER stress resolution" axis, we collaborate with Jérôme Estaquier (Laval University, Quebec) to study the role of the ATF5 protein in HIV infection and with Loïc Paulevé to model in silico the signaling network centered around ATF5 (LaBRI, Bordeaux). This approach allows integrating results from the literature into a simulated network to predict expected results in vivo and test these predictions in immortalized or primary cultured cells.