15-16 months contract "Ingenieur d'étude"
« Structural Basis for viral genome tethering to host chromatin »

A position is available under the supervision of **Dr. Paul Lesbats** in the team of Dr. Vincent Parissi at the Fundamental Microbiology and Pathogenicity (MFP) laboratory in Bordeaux, France.
The hosting laboratory main interests are revolving around host-pathogens interactions with a focus on retrovirus-cellular chromatin interplays [1–5].

Overview:
Chromatin tethering of viral genomes is a phenomenon observed among several DNA viruses and retroviruses. Our recent data showed that the retrovirus Prototype Foamy Virus (PFV) Gag protein directly binds host nucleosomes during mitosis [3]. By X-ray crystallography we determined that the docking station PFV Gag on the cellular histones is a conserved cavity made by H2A and H2B called "acidic patch". Abolishment of this interaction by designing point substitutions on Gag dramatically affects the distribution of integration sites. While the exact molecular mechanisms involved are still not properly understood these data underline a fundamental role of the viral structural proteins in the integration process.

Project:
The candidate will continue the development a new imaging technique using the ANCHOR system from NeoVirtech. This is part of the ongoing CaPTIVE ANR grant and will be the basis for a follow up project.

Qualifications:
We are looking for a self-motivated hard working candidate. Strong background in cellular biology and immunofluorescence microscopy is mandatory.

This opening is funded by the ANR (Agence Nationale de la Recherche) for up to 16 months.
Please send a cover letter describing past research accomplishments and future research interests, CV, and a list of 2-3 references by email to : paul.lesbats@u-bordeaux.fr.

1. Lesbats, P.; Botbol, Y.; Chevereau, G.; Vaillant, C.; Calmels, C.; Arneodo, A.; Andreola, M.L.; Lavigne, M.; Parissi, V. Functional Coupling between HIV-1 Integrase and the SWI/SNF Chromatin Remodeling Complex for Efficient in Vitro Integration into Stable Nucleosomes. *PLoS Pathog* **2011**, *7*, e1001280.
2. Benleulmi, M.S.; Matysiak, J.; Robert, X.; Miskey, C.; Mauro, E.; Lapaillerie, D.; Lesbats, P.; Chaignepain, S.; Henriquez, D.R.; Calmels, C.; et al. Modulation of the Functional Association between the HIV-1 Intasome and the Nucleosome by Histone Amino-Terminal Tails. *Retrovirology* **2017**, *14*, 54, doi:10.1186/s12977-017-0378-x.
3. Lesbats, P.; Serrao, E.; Maskell, D.P.; Pye, V.E.; O'Reilly, N.; Lindemann, D.; Engelman, A.N.; Cherepanov, P. Structural Basis for Spumavirus GAG Tethering to Chromatin. *PNAS* **2017**, *114*, 5509–5514, doi:10.1073/pnas.1621159114.
4. Mauro, E.; Lesbats, P.; Lapaillerie, D.; Chaignepain, S.; Maillot, B.; Oladosu, O.; Robert, X.; Fiorini, F.; Kieffer, B.; Bouaziz, S.; et al. Human H4 Tail Stimulates HIV-1 Integration through Binding to the Carboxy-Terminal Domain of Integrase. *Nucleic Acids Res.* **2019**, *47*, 3607–3618, doi:10.1093/nar/gkz091.
5. Lagadec, F.; Parissi, V.; Lesbats, P. Targeting the Nucleosome Acidic Patch by Viral Proteins: Two Birds with One Stone? *mBio* **2022**, *13*, e0173321, doi:10.1128/mbio.01733-21.