Erasmus+

INSTITUT Pasteur

Education

DEPARTMENT

Projects 2025-2026

RESEARCH CENTRE

Legal name: **Institut Pasteur**

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Country: **France**

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Brief description of your Institution

The Institut Pasteur is a private non-profit foundation that contributes to the prevention and treatment of diseases through research, education, and public health activities. Its campus in Paris hosts more than 3000 individuals, 146 research units, organized in 13 departments.
Research: priority is given to fight infectious diseases, as well as to study the impact of climate change on health, the origin of pathologies (cancer, genetic, neurodegenerative, and allergic diseases) and to explore health and diseases at extremities of life (Pasteur 2030 Strategic Plan).
Education: every year 600 young scientists from all over the world follow high-level courses in various fields related to research in microbiology, immunology, cellular biology, epidemiology, genetics, and disease control. Over 850 trainees from 77 different countries come to perfect their skills or conduct their Master or Doctoral trainings in the Institute's laboratories.

Description of the work program(s)

See projects on following pages

N° of placements available for work programs:

The laboratories at the Institut Pasteur have proposed 36 projects for Erasmus internships. Students may also contact other laboratories at Pasteur to apply for an internship, even if the laboratories have not presented a project (https://research.pasteur.fr/en/team-heads).

FACILITIES

- **Accommodation**: a limited number of rooms for rent are reserved for Pasteur at the student residence "Cité Universitaire"
- **Canteen**: partially subsidized canteen is available on the Pasteur Campus
- **Additional salary:** additional salary of approximately 600 euros/month (for internships longer than 60 days) is paid by the host lab (4.35 euros/hour, 7 hours/day)

Institut Pasteur, 2025-2026

Title of the work program 1

Study of the impact of two probiotics on the invasive process of *Entamoeba histolytica* using human colon-on-chip model

Description of the work program

Entamoeba histolytica is a protozoan parasite that colonizes the human colon. It is estimated that around 60 % of the population in developing countries might be harboring *Entamoeba* in an asymptomatic manner, and only ~20% of the cases develop intestinal amoebiasis which is characterized by colonic mucosa invasion and destruction. The stimuli triggering the parasite to switch from commensal to virulent state are unknown. In asymptomatic infection, *E. histolytica* interacts with and feeds on bacterial microbiota. In the pathogenesis, the parasite overcomes the colonic barrier using a combination of proteases (for review Labruyère et al, 2017). In vitro studies highlight that *Escherichia coli* attenuates *E. histolytica* cytotoxicity and that some pathogenic bacteria increase it. A comparative metagenomic study between a cohort of healthy individuals and individuals positive for *E. histolytica* reported significant decreases in bacteria species producing mainly butyrate *(Bacteroides, Clostridium,* and *Lactobacillus*) and, in contrast, an increase in *Bifdobacterium.* However, these studies cannot conclude whether dysbiosis promotes amoebiasis or is a result of it. *Lactobacillus* and *Bifidobacterium* are probiotics, which may protect the host against pathogen by different mechanisms such as competition with pathogen for nutrient and niche, the regulation of the gut environment, and the immune response of the host.
Our hypothesis is that the outcome of amoebiasis could be influenced by the composition of the gut bacterial microbiome. We have first explored the direct impact of *L. rhamnosus* and *B. longum* on *E. histolytica* virulence. Our preliminary results show that the presence of the probiotics change cysteine proteases activity of *E. histolytica*.

The student will address her/his project following two axes:

1- The study of the impact of the bacteria on *E. histolytica* virulence: she/he will identify and quantify two virulence factors of *E. histolytica* (intracellular and secreted) in their presence.
2- The study of the invasive process of *E. histolytica* in the presence of the bacteria: she/he will use: human colon-on-chip model which reproduces the tree-dimensional colonic architecture and can be mechanically stretch to mimic peristalsis; Real time and fixed samples imaging, spinning disk confocal microscope, and image quantification plugins; The infection dynamics (under stretch and not) will be quantified by different measures over the time such as bacterial colonization area, amoeba displacement and tissue connectivity.

Tutor/supervisor

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Institut Pasteur, 2025-2026

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Selected publications or patents of the Research Group offering the work program

1. M. Manich, P. Bochet, A. Boquet-Pujadas, T. Rose, G. Laenen, N. Guillén, JC.Olivo-Marin and E. Labruyère. Fibronectin induces a transition from amoeboid to a fan morphology and modifies migration in *Entamoeba histolytica*. **PLoS Pathog**. **2024.** DOI: 10.1371/journal.ppat.1012392.
2. Samba-Louaka A, Labruyère E, Matondo M, Locard-Paulet M, Olivo-Marin JC, Guillen N. Encystation and Stress Responses under the Control of Ubiquitin-like Proteins in Pathogenic Amoebae. **Microorganisms. 2023**. PMID: 38004682.
3. Mukherjee S, Sarkar R, Manich M, Labruyère E, Olivo-Marin JC. Domain Adapted Multitask Learning for Segmenting Amoeboid Cells in Microscopy. **IEEE Trans Med Imaging**. **2023**. PMID: 36044485.
4. Boquet-Pujadas A, Feaugas T, Petracchini A, Grassart A, Mary H, Manich M, Gobaa S, Olivo-Marin JC, Sauvonnet N, Labruyère E. 4D live imaging and computational modeling of a functional gut-on-a-chip evaluate how peristalsis facilitates enteric pathogen invasion. **Science Advences**. **2022**. PMID: 36269830
5. Apte A, Manich M, Labruyère E, Datta S. PI Kinase-EhGEF2-EhRho5 axis contributes to LPA stimulated macropinocytosis in Entamoeba histolytica. **PLoS Pathog. 2022**. PMID: 35594320.

Scientific or technical background required for work program

Cell biology, Microbiology

Institut Pasteur, 2025-2026

Title of the work program 2

Lipid Regulation of Lysosomes and Amyloid Beta

Description of the work program

Alzheimer's disease (AD) is a devastating brain disorder that causes memory loss and cognitive decline. Current treatments can only relieve symptoms – they do not stop or slow the disease itself. A key feature of AD is the buildup of harmful protein clumps in the brain, known as amyloid plaques and neurofibrillary tangles. These plaques form when a normal protein, called APP, is broken down in a way that produces toxic fragments known as amyloid beta (AB). These fragments tend to stick together and accumulate between brain cells, damaging them over time.
We still don't fully understand what triggers this toxic process. However, because these events happen in the membrane surrounding brain cells, we believe that changes in the composition of these membranes – especially their fat (lipid) content – may play a key role in either the production of these toxic aggregates, or their internalization and processing by neighboring cells. In this project, we will study how changes in brain cell membranes affect the production of AB. We will also explore whether these changes interfere with the cells' ability to clear toxic proteins, and whether correcting them can help prevent or slow the disease.
By uncovering how brain cell membrane influence AD progression, our work could open the door to new treatments that target the disease at its roots – not just its symptoms.

Tutor/supervisor

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Selected publications or patents of the Research Group offering the work program

- Palese F., Rokotobe M., Zurzolo C. Transforming the concept of connectivity: unveiling tunneling nanotube biology and their roles in brain development and neurodegeneration. Physiol Rev, 2025 DOI: 10.1152/physrev.00023.2024
- Palese F., et al. A protective role for N-acylphosphatidylethanolamine phospholipase D in 6-OHDA-induced neurodegeneration. Sci Rep, 2019 DOI: 10.1038/s41598-019-51799-1
- Palese F., et al. NAPE-specific phospholipase D regulates LRRK2 association with neuronal membranes. Adv Pharmacol, 2021 DOI: 10.1016/bs.apha.2020.09.003

Scientific or technical background required for work program

Students are expected to be familiar with cell culture techniques and working under sterile conditions. A solid understanding of wet lab methods such as Western blotting and RT-PCR is highly valued. Experience with immunofluorescence and confocal microscopy is also appreciated.

Institut Pasteur, 2025-2026

Title of the work program 3

Exploring the neuroimmune mechanisms of mood disorders

Description of the work program

Our reasoning for examining mental illness, and mood disorders in particular, from the perspective of the body-brain axis dysfunction also lies in the recognition that these disorders frequently emerge as chronic conditions, often triggered by maladaptive immune responses. In the case of depression, the role of inflammation has been established in various studies, in the context of the relationship between gut microbiota dysregulation and increased intestinal permeability. **We hypothesize in this Erasmus project that inflammation arising at the periphery could impact the central nervous system through various mechanisms that we seek to pinpoint**. Exploring the connections between the periphery and the brain could provide insights into future adjunctive strategies via the manipulation of the immune system, or lifestyles, thus offering opportunities for novel and holistic approaches to treat mental health.

Tutor/supervisor

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Five selected publications of the Research Group offering the work program

1. Siopi E, *et al.* & Lledo PM (2023). Gut microbiota changes require vagus nerve integrity to promote depressive-like behaviors in mice. *Molecular Psychiatry* (doi: 10.1038/s41380-023-02071-6).
2. Gabanyi I, *et al.* & Lledo P-M (2022). Bacterial sensing via neuronal Nod2 contributes to appetite and body temperature regulation. *Science* 376(6590): eabj3986.
3. de Melo GD, *et al.* & Lledo P-M (2021). COVID-19-related anosmia is associated with viral persistence and inflammation in human olfactory epithelium and brain infection in hamsters. *Science Transl Med*, 13(596): eabf8396.
4. Chevalier G, *et al.* & Lledo PM (2020) The impact of gut microbiota on depressive-like behaviors and adult hippocampal neurogenesis requires the endocannabinoid system. *Nature Communication* 11, 6363.
5. Siopi E, *et al.* & Lledo PM (2020) Changes in gut microbiota by chronic stress impair the efficacy of fluoxetine. *Cell Report* 30, 3682-3690.

Scientific or technical background required for work program

- Mouse behaviour analysis
- Histology

Institut Pasteur, 2025-2026

Title of the work program 4

Host response to tuberculosis

Description of the work program

Tuberculosis (TB), caused by *Mycobacterium tuberculosis* (MTB), is one of the deadliest diseases caused by a single infectious agent, alongside COVID-19. According to the latest WHO report, 10 million new TB cases were recorded, and the disease claimed 1.3 million lives in 2023. Despite considerable efforts, TB remains a major public health issue. There is still no fully effective vaccine against TB, and multidrug-resistant (MDR) strains of MTB continue to emerge. Combating tuberculosis, therefore, requires new strategies and a better understanding of host-pathogen interactions.
In our laboratory, we are developing several projects aimed at:

1. Finding new molecules that enhance the resistance or bactericidal functions of innate immune cells and/or improve the efficacy of anti-tuberculosis drugs,
2. Understanding and evaluating the long-term impacts of the disease on the body,
3. Studying the role of NK cells in TB.

Depending on the length of the internship, candidates will work on one of these projects. They will use a combination of cellular biology, microbiology, and immunology techniques. They will notably learn how to isolate human cells from blood, differentiate these cells into macrophages (the main targets of the bacteria), and infect them with fluorescent MTB strains or attenuated bacteria. The interactions between MTB and its host will then be studied using advanced imaging techniques. The murine model of TB will also be used for some of these projects. Other approaches commonly used in the laboratory include genomics (RNA sequencing), and flow cytometry.

Tutor/supervisor

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Selected publications or patents of the Research Group offering the work program

1 Maure, A. et al. A host-directed oxadiazole compound potentiates antituberculosis treatment via zinc poisoning in human macrophages and in a mouse model of infection. PLoS Biol. Apr 29;22(4):e3002259 (2024).
2 Giraud-Gatineau, A. et al. The antibiotic bedaquiline activates host macrophage innate immune resistance to bacterial infection. eLife 9, doi:10.7554/eLife.55692 (2020).
3 Bottai, D. et al. TbD1 deletion as a driver of the evolutionary success of modern epidemic Mycobacterium tuberculosis lineages. Nat Commun 11, 684, doi:10.1038/s41467-020-14508-5 (2020).
4 Coya, J. M. et al. Tri-mannose grafting of chitosan nanocarriers remodels the macrophage response to bacterial infection. J Nanobiotechnology 17, 15, doi:10.1186/s12951-018-0439-x (2019).
5 Groschel, M. I. et al. Recombinant BCG Expressing ESX-1 of *Mycobacterium marinum* Combines Low Virulence with Cytosolic Immune Signaling and Improved TB Protection. Cell Rep 18, 2752-2765, (2017).

Scientific or technical background required for work program

- Strong motivation, scientific curiosity and interest in microbiology or immunology
- Good verbal and written English communication skills are expected
- Research experience in cell culture and/or animal manipulation is regarded very favorably

Institut Pasteur, 2025-2026

Title of the work program 5

In search of mechanisms driving diversity of cilia and flagella

Description of the work program

Cilia and **flagella** are sophisticated organelles made of 9 doublet microtubules and composed of up to 1,000 proteins. They perform multiple functions in motility, sensing or morphogenesis. Despite their conservation in most eukaryotes, they display amazing variations between species or between cell types of the same organism.

The goal of the project is to look for mechanisms that could explain this diversification by performing structural and functional comparisons of cilia and flagella, with a specific focus on **intraflagellar transport** (IFT), the machinery responsible for their construction. IFT is the movement of protein complexes (termed trains) dragged by molecular motors on ciliary microtubules (tracks), allowing the delivery of precursors for incorporation at the distal tip, which is the building site. Our team has shown that IFT trains circulate at high frequency but are restricted to some doublet microtubules in the protist *Trypanosoma brucei* (Bertiaux et al., 2018a). This restriction is put in place after the entry of trains in the flagellum (Alves et al., 2025). We proposed that this restriction would allow faster evolution of flagella (Mallet & Bastin, 2022).

The host team has collected several parasitic and free protists with flagella of different architecture. The student will use several electron and light microscopy approaches including **expansion microscopy** to reveal and explore the organisation of their flagella thanks to a collection of antibodies already available. Functional impact of the morphological differences will be evaluated with a combination of fluorescent protein tagging to monitor **protein trafficking** and **Crispr-Cas9** approaches.

Environment: the host lab has exhaustive expertise in molecular and cellular biology, as well as in imaging at multiple level (live imaging, expansion microscopy, super-resolution, scanning and transmission electron microscopy) and has access to high-end facilities of the Institut Pasteur. It has trained numerous students over the years coming from more than 15 countries and 5 continents.

Lab website: https://research.pasteur.fr/en/team/trypanosome-cell-biology/
Social network: https://bsky.app/profile/bastinlab.bsky.social

Tutor/supervisor

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Institut Pasteur, 2025-2026

Selected publications or patents of the Research Group offering the work program

1. **Bertiaux, E**., **Mallet, A., Fort, C.**, Blisnick, T., Bonnefoy, S., Jung, J., Lemos, M., Marco, S., Vaughan, S., Trepout, S., Tinevez, J.Y., and Bastin, P. (2018). Bidirectional intraflagellar transport is restricted to two sets of microtubule doublets in the trypanosome flagellum. **J Cell Biol** *217*, 4284-4297. Top 5% Altmetrics.
2. **Bertiaux, E**., Morga, B., Blisnick, T., Rotureau, B., and Bastin, P. (2018). A Grow-and-Lock Model for the Control of Flagellum Length in Trypanosomes. **Curr Biol** *28*, 3802-3814 e3803.
3. **Mallet, A.**, and Bastin, P. (2022). Restriction of intraflagellar transport to some microtubule doublets: An opportunity for cilia diversification? **Bioessays** *44*, e2200031. Front cover.
4. Bonnefoy, S., Alves, A.A., Bertiaux, E., and Bastin, P. (2024). LRRC56 is an IFT cargo required for assembly of the distal dynein docking complex in Trypanosoma brucei. **Mol Biol Cell** *35*, ar106.
5. **Abbuhl, D**., Pruzincova, M., Stepanek, L., Bouscasse, E., Azevedo, R., Matondo, M., Varga, V., Bonnefoy, S., and Bastin, P. (2025). A novel approach to tagging tubulin reveals MT assembly dynamics of the axoneme in Trypanosoma brucei. **J Cell Sci**. *in press*
6. Alves, A.A., Jung, J., Moneron, G., Vaucelle, H., **Fort, C., Buisson, J**., Schietroma, C., and Bastin, P. (2025). Intraflagellar Transport Selectivity Occurs with the Proximal Portion of the Trypanosome Flagellum. **J Cell Biol** *in press*.

Names of former PhD students in bold

Scientific or technical background required for work program

Cellular and molecular biology, microscopy

Institut Pasteur, 2025-2026

Title of the work program 6

Manipulation of host lipid metabolism by an intracellular bacterium

Description of the work program

Chlamydia trachomatis causes the most common bacterial sexually transmitted infection worldwide. The bacteria undergo an obligate intracellular developmental cycle in epithelial cells of the genital tract (1). They develop inside a vacuolar compartment and use a virulence associated non-flagellar type 3 secretion system (T3SS) to translocate proteins into the cytoplasm of their host cell. These so-called "effector" proteins manipulate host pathways to the benefit of the bacteria and are often made of several domains, each engaged in a specific function. TaiP is a 68 kDa protein made of two domains of about equal size and we showed this protein was an effector associated to *C. trachomatis* virulence (2). We discovered that its carboxy-terminal domain targeted one host protein called ATG16L1. By binding ATG16L1 we showed that TaiP allowed some vesicular traffic to be re-routed towards the vacuole in which the bacteria develop (3).
The internship will focus on the second domain of TaiP, whose function has not yet been characterized. We recently discovered that it bound a host lipid metabolism enzyme. The intern will use molecular biology and biochemistry tools to delineate the interacting domains within the two proteins. In parallel, the intern will investigate the consequences of this interaction on lipid metabolism in the host and whether it contributes to lipid acquisition by the bacteria.

Tutor/supervisor

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Selected publications or patents of the Research Group offering the work program

Publications related to the project:

1. Triboulet, S., and Subtil, A. (2019) Make It a Sweet Home: Responses of Chlamydia trachomatis to the Challenges of an Intravacuolar Lifestyle. *Microbiol Spectr* **7**
2. Cossé, M. M., Barta, M. L., Fisher, D. J., Oesterlin, L. K., Niragire, B., Perrinet, S., Millot, G. A., Hefty, P. S., and Subtil, A. (2018) The Loss of expression of a single type 3 effector (CT622) strongly reduces *Chlamydia trachomatis* infectivity and growth. *Front Cell Inf Microbiol* **8**, 145
3. Hamaoui, D., Cossé, M. M., Mohan, J., Lystad, A. H., Wollert, T., and Subtil, A. (2020) The *Chlamydia* effector CT622/TaiP targets a nonautophagy related function of ATG16L1. *Proc. Natl. Acad. Sci. U. S. A.* **117**, 26784-26794

Scientific or technical background required for work program

Past experience in tissue culture, and in cell biology technics, is recommended.

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Institut Pasteur, 2025-2026

Title of the work program 7

Functional Impacts of Ribosomal RNA Modifications in *Vibrio cholerae*

Description of the work program

Background & Rationale
Ribosomal RNA (rRNA) modifications are known to fine-tune ribosome activity under environmental stress but appear to be functionally redundant during normal growth conditions. In Vibrio cholerae, these modifications may influence translation fidelity, speed, and adaptability, with potential consequences for antibiotic susceptibility and virulence.
Deletion or inactivation of specific rRNA modification genes could lead to codon-specific or context-dependent translation changes. Some mutants may exhibit slower but more accurate protein synthesis, while others may favor speed at the cost of fidelity. These functional differences may become more pronounced under antibiotic stress or during infection, revealing phenotypes relevant to resistance, sensitivity, and virulence factor regulation.

Objectives
Tool Development. Construct CRISPR interference (CRISPRi) plasmids to inactivate multiple rRNA modification genes and assess basic growth phenotypes.
Ribosome Function Analysis.
-Develop puromycin incorporation assays coupled with flow cytometry to q Quantify global translation activity.
-Use existing fluorescent reporter systems to evaluate ribosome processivity, recycling at stop codons, and rescue mechanisms (e.g., non-stop GFP, tmRNA reporter, bicistronic translation reporter).
-Virulence Factor Expression. Assess expression levels of key virulence-associated proteins using targeted Western blotting or fluorescent reporters. Follow-up studies may extend to infection models.

Methods & Techniques
Molecular Biology: CRISPRi plasmid construction, mutant strain generation.
Phenotypic Characterization: Growth curves, viability assays.
Fluorescence-Based Measurements: Plate reader assays, flow cytometry.
Protein Expression Analysis: Western blotting, reporter-based quantification.

Expected Outcomes
- Identification of functional roles for individual and combined rRNA modifications in *V. cholerae*.
- Characterization of trade-offs between translation speed and accuracy in different mutants.
- Insights into links between ribosome regulation, antibiotic response, and virulence factor production.

Adaptability

The project is modular: each objective can be pursued independently and yields interpretable results. This flexibility makes it suitable for internships of varying durations, from short-term exploratory projects to longer, in-depth investigations.

Lab website: https://research.pasteur.fr/en/team/epitranscriptomic-and-translational-responses-to-antibacterial-stress/

Tutor/supervisor

The laboratory is located at IBPC (CNRS), 13 rue Pierre et Marie Curie, 75005 Paris. The lab is part of the Genomes and Genetics department of Institut Pasteur.

Institut Pasteur, 2025-2026

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Selected publications or patents of the Research Group offering the work program

de Crécy-Lagard* V, Baharoglu* Z, Yuan Y, Boël* G, Babor J, Bacusmo JM, Dedon PC, Ho P, Hummels KR, Kearns D. Are Bacterial Processes Dependent on Global Ribosome Pausing Affected by tRNA Modification Defects? J Mol Biol. 2025 Apr 9:169107. doi: 10.1016/j.jmb.2025.169107. PMID: 40210524.

Fruchard L, Babosan A, Carvalho A, Lang M, Li B, Duchateau M, Giai-Gianetto Q, Matondo M, Bonhomme F, Hatin I, Arbes H, Fabret C, Corler E, Sanchez G, Marchand V, Motorin Y, Namy O, de Crécy-Lagard V, Mazel D, Baharoglu Z. Aminoglycoside tolerance in Vibrio cholerae engages translational reprogramming associated with queuosine tRNA modification. eLife. 2025 13:RP96317. https://doi.org/10.7554/eLife.96317.3

Babosan A, Fruchard L, Krin E, Carvalho A, Mazel D, Baharoglu Z. Nonessential tRNA and rRNA modifications impact the bacterial response to sub-MIC antibiotic stress. microLife. 2022. doi: 10.1093/femsml/uqac019. Selected for best article award in microLife for 2022. HAL. pasteur-03897869

Lang MN, Krin E, Korlowski C, Sismeiro O, Varet H, Coppee JY, Mazel D, Baharoglu Z. Sleeping ribosomes: Bacterial signaling triggers RaiA mediated persistence to aminoglycosides. Iscience. 2021;24(10). doi: 10.1016/j.isci.2021.103128. HAL. pasteur-03349141

Scientific or technical background required for work program

- Interest in microbiology, molecular biology, and bacterial physiology
- Foundational knowledge of molecular biology (DNA, RNA, protein synthesis) and bacterial genetics
- Basic microbiology skills (e.g., aseptic technique, handling bacterial cultures)
- Conceptual understanding of protein expression and translation
- Students should be comfortable working in a biosafety level 2 (BSL-2) laboratory
- Enthusiasm, attention to detail, and commitment to precise experimental work

Institut Pasteur, 2025-2026

Title of the work program 8

Who builds blood before birth? Probing the role of embryonic progenitors in shaping stem cell behavior.

Description of the work program

Traditionally, hematopoietic stem cells (HSCs) have been associated with both the generation of the blood system during development and its lifelong maintenance. However, recent studies — including our own — have challenged this view. We found that during embryogenesis, it is not HSCs but embryonic multipotent progenitors (eMPPs) that sustain late gestation blood and immune cell production. HSCs are indeed present in the fetal liver at this stage, but rather than driving hematopoiesis, they expand to establish the long-term adult stem cell pool.

The goal of this internship is to explore what happens to HSCs if eMPP activity is reduced during development. Do HSCs adapt and enter the game earlier to compensate? Or is their role developmentally programmed to remain "on standby" until after birth, regardless of the embryonic context?

To answer this, the student will:

- Use mouse models and antibody-based approaches to reduce eMPP activity.
- Analyze HSC expansion and differentiation using flow cytometry and cell-cycle reporters.

The project will give hands-on training in developmental hematology, advanced flow cytometry, and in vivo perturbation strategies. It will also introduce the student to state-of-the-art tools such as fluorescent cell-cycle reporters.

By testing how HSCs respond to the absence of eMPP activity, the project will shed light on the division of labor between stem cells and progenitors during development, with potential implications for regenerative medicine.

Tutor/supervisor

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Selected publications or patents of the Research Group offering the work program

- Soares-da-Silva F., Nogueira G., Marie-Pierre Mailhe, Freyer L., Perkins A., Hatano S., Yoshikai Y., Pereira P., Bandeira A., Elsaid R.[#], Gomez-Perdiguero E., Cumano A.[#]. Distinct origin and fate for fetal hematopoietic progenitors. *biorxiv* 2025, **doi:** https://doi.org/10.1101/2025.01.08.631951. (Under review). [#]**Corresponding authors.**

- Soraes-da-Silva, F.*, Elsaid, R.*, Peixoto, M. *, Nogueira, G. *, Pereira, P., Bandeira, A. and Cumano, A. Assembling the layers of the hematopoietic system: a window of opportunity for thymopoiesis in the embryo. Immunol Rev. 2023 May;315(1):54-70. doi: 10.1111/imr.13187. PMID: **36869420.** HAL Id: pasteur-04019883. ***equal contribution**.
- Elsaid, R.[#], Meunier, S., Defranoux, O., Soraes-da-Silva, F., Perchet, T., Iturri, L., Freyer, L., Vieira, P., Pereira, P., Golub, R., Bandeira, A., Perdiguero, E. and Cumano, A[#]. A wave of bipotent T/ILC-restricted progenitors shapes the embryonic thymus microenvironment in a time-dependent manner. *Blood 2021;*137(8): 1024–1036. doi.org/10.1182/blood.2020006779**.** PMID: 33025012. HAL Id: pasteur-03064548. [#]**Corresponding authors.**
- Soraes-da-Silva, F., Freyer, L., Elsaid, R.**,** Defranoux, O., Iturri, Lorea., Sismeiro, O., Pinto-do-O, P., Perdiguero, E. and Cumano, A. Yolk sac but not hematopoietic stem cell-derived progenitors, sustain erythropoiesis throughout murine embryonic life. *J Exp Med 2021* Apr 5;218(4):e20201729. doi: 10.1084/jem.20201729. PMID: **33566111.** HAL Id: hal-03139070.

Scientific or technical background required for work program

Candidates should be currently enrolled in a Master's program in Biology, Biotechnology, Biomedical Sciences, or a closely related field, and must have previous laboratory experience, being comfortable with standard molecular and cellular biology techniques, lab safety protocols, and basic data analysis. Experience with flow cytometry, including sample preparation, data acquisition, and analysis, as well as knowledge or prior work related to developmental hematopoiesis or stem cell biology, is optional but strongly recommended. Candidates should be proficient in English for scientific communication, able to work both independently and collaboratively in a lab environment, and motivated to engage in experimental design, troubleshooting, and scientific reporting.

Erasmus+

Institut Pasteur, 2025-2026

Title of the work program 9

Understanding the fundamental role of ATRX in the de novo initiation of epigenetic silencing

Description of the work program

Overall, this project finds itself at the intersection of three basic research questions. The first question pertains to the mechanism(s) of the *de novo* initiation of epigenetic silencing (which can be transcriptional [heterochromatin-mediated] or post-transcriptional [RNAi-mediated]). The second question is about the mechanism of action of the conserved chromatin remodeler ATRX (alpha-thalassemia mental retardation X-linked), which serves several critical functions in eukaryotes, including the *de novo* initiation of epigenetic silencing. The third question deals with the nature of the primary signal that triggers such silencing. Here we are very interested in discovering the mechanism by which repetitive DNA becomes subject to silencing in a wide range of eukaryotes, from protists to humans. Specifically, we wish to test the hypothesis that the triggering signal is produced by the direct homologous dsDNA-dsDNA pairing of intact identical repeats. Such a discovery will illuminate a new fundamental property of DNA (which may also underpin other processes, such as pairing of homologous chromosomes in meiosis). We have obtained experimental evidence that these three questions are indeed connected. While the specific topic of this Erasmus+ project will be a subject to further discussion with a prospective candidate, possible research themes may include the following: (1) characterize protein composition of a model chromatin locus undergoing ATRX-dependent silencing, (2) characterize additional critical factors required for ATRX-dependent silencing, (3) reconstitute the remodeling/silencing cycle *in vitro*, (4) obtain further experimental support for homologous dsDNA-dsDNA pairing as a signal for silencing *in vivo*.

In the lab, we utilize the fungus *Neurospora crassa* as an exceptionally advantageous model organism, and all *in-vivo* work for this project is expected to be done in *N. crassa* as well. The reasons why *N. crassa* is the best model organism to pursue the aforementioned questions are the following. First, throughout evolution, *N. crassa* managed to retain all main epigenetic processes, including fully functional RNAi, DNA methylation, constitutive (“H3K9me3”), and facultative (“H3K27me3”) heterochromatin. Second, all these processes can be inactivated (individually or altogether) without causing substantial fitness defects to *N. crassa* in the lab, and, thus, they can be dissected without running into side effects that often complicate their analysis in “higher” eukaryotes. Third, *N. crassa* features several extremely efficient genome-defense mechanisms that use these pathways to effectuate silencing. This is a very important point: while *N. crassa* appears to share its basic epigenetic toolbox with plants and animals (including humans), it uses it much more efficiently than any other model organism to combat incoming deleterious genetic elements, thus representing another precious gift of Nature to Science (https://www.nobelprize.org/uploads/2018/06/brenner-lecture.pdf). Fourth, *N. crassa* is haploid and has a relatively small genome that is free of naturally occurring repetitive DNA and gene paralogs, thus greatly simplifying its genetic analysis. Fifth, *N. crassa* represents an established model organism, which is very easy to grow, transform, and manipulate in the lab.

This project is based on our two papers (PMID: 34385329 & 39052837), where we show that SAD-6, a Neurospora ATRX ortholog, can trigger both the formation of heterochromatin and the initiation of RNAi at loci that appear to be perturbed. Critically, we were able to manipulate the state of the affected loci precisely (which is not the case in plants and animals, in which large amounts of repetitive DNA are involved, being notoriously hard to tackle experimentally). As the result, we have proposed a general model in which the silencing is induced by the act of ATRX-

dependent remodeling rather than a mere existence of a perturbed chromatin state. Intriguingly, we have discovered that SAD6/ATRX is also absolutely required for a pathway that connects homologous DNA pairing to the initiation of constitutive heterochromatin in *N. crassa* during a process known as repeat-induced point mutation (unpublished). We have also conducted a forward genetics screen to identify new factors in this ATRX-dependent silencing and found many of them to have direct orthologs in humans. These results place our lab at the leading edge of the field, and we are looking forward to finally elucidating the role of ATRX in the *de novo* initiation of transcriptional and post-transcriptional silencing in *N. crassa* and other eukaryotes.

Tutor/supervisor

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☒ I authorise the IP Erasmus+ team to publish the project proposal on the pasteur.fr website

Selected publications or patents of the Research Group offering the work program

[Research papers]

[1] Carlier F, Castro Ramirez S, Kilani J, Chehboub S, Loïodice I, Taddei A, Gladyshev E. 2024. Remodeling of perturbed chromatin can initiate de novo transcriptional and post-transcriptional silencing. PNAS 121: e2402944121. doi: 10.1073/pnas.2402944121.

[2] Rhoades N, Nguyen TS, Witz G, Cecere G, Hammond T, Mazur AK, Gladyshev E. 2021. Recombination-independent recognition of DNA homology for meiotic silencing in Neurospora crassa. PNAS 118: e2108664118. doi: 10.1073/pnas.2108664118.

[3] Carlier F, Nguyen TS, Mazur AK, Gladyshev E. 2021. Modulation of C-to-T mutation by recombination-independent pairing of closely positioned DNA repeats. Biophys J. 120: 4325-4336. doi: 10.1016/j.bpj.2021.09.014.

[Reviews]

[4] Mazur AK, Gladyshev E. 2023. C-DNA may facilitate homologous DNA pairing. Trends Genet. 39: 575-585. doi: 10.1016/j.tig.2023.01.008.

[Preprints]

[5] Mazur AK, Maaloum M, Gladyshev E. (2024). Properties of DNA in concentrated aqueous solutions of LiCl suggest transition to C-DNA. doi: 10.1101/2024.09.20.613475. bioRxiv.

Scientific or technical background required for work program

An ideal candidate should have background in eukaryotic molecular genetics or biochemistry. Prior experience in fungal genetics is a plus not it is not required.

Erasmus+

Institut Pasteur, 2025-2026

Title of the work program 10

Impact of repeated acoustic trauma on presbycusis

Description of the work program

Institut presentation

The Hearing Institute (Institut de l'Audition, IdA, Paris 12eme) is a new center for basic and translational neuroscience research in the field of hearing, which opened in 2020 at the initiative of the Fondation Pour l'Audition and the Institut Pasteur. The overarching goal of the Institute is to elucidate the principles underpinning the workings of the auditory system, auditory perception and cognition from the molecular to the cognitive level. Optical techniques are key for this endeavor.

Scientific Context

Age-related hearing loss (presbycusis) progressively impairs auditory function in approximately one-third of individuals over 65. A central feature of this pathology is damage to cochlear hair cells. Epidemiological studies indicate that environmental factors—particularly repeated exposure to loud noise—contribute to its variability and severity, although the underlying mechanisms remain poorly understood. Emerging evidence suggests that temporary threshold shifts (TTS) caused by acoustic overexposure (e.g., concerts, machinery) disrupt tip links—nanoscale protein complexes (CDH23/PCDH15) essential for sound transduction. While this disruption is reversible, we hypothesize that repeated TTS episodes may compromise tip link integrity and ultimately accelerate presbycusis. This project seeks to elucidate how recurrent acoustic trauma affects tip link structure and regeneration.

Internship Objectives

The student will characterize the structural and functional consequences of acoustic trauma on hair cell tip links in mouse models. Key aims include:

1. Quantifying tip link breakage after single/repeated TTS using super-resolution microscopy.
2. Correlating ultrastructural damage with functional hearing thresholds.

Methodology

The internship integrates three experimental phases:

- **Acoustic Trauma Induction:** The student will expose mice to calibrated noise (8–16 kHz, 95 dB SPL, 2 hours) to induce TTS. Auditory Brainstem Responses (ABRs) and otoacoustic emissions will monitor pre/post-trauma hearing thresholds.

- **Cochlear Dissection & Immunolabeling:** The student will carry out dissection of cochlea and immunostaining of CDH23, PCDH15, and actin. She/he will then visualize the sample under confocal or STED microscope.
- **Structural-Functional Correlation:** Using confocal/STED imaging, the student will quantify tip link integrity via CDH23/PCDH15 colocalization. Time-series sampling (1h–48h post-trauma) will track regeneration dynamics. Data will be cross-referenced with ABR thresholds to establish mechanistic links between tip link disruption and hearing loss.

Training and Skills Development

The student will gain rare expertise in auditory neuroscience techniques: murine auditory phenotyping, cochlear dissection, microscopy (confocal/STED), and quantitative image analysis. They will participate in interdisciplinary team meetings, contributing to experimental design and data interpretation.

Tutor/supervisor

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☒ I authorise the IP Erasmus+ team to publish the project proposal on the pasteur.fr website

Selected publications or patents of the Research Group offering the work program

1. Gourévitch, B., Edeline, J.-M., Occelli, F. & Eggermont, J. J. Is the din really harmless? Long-term effects of non-traumatic noise on the adult auditory system. *Nat. Rev. Neurosci.* **15**, 483–491 (2014).
2. Brunstein, M. & Oheim, M. Dependence of descriptors of co-localization on microscope spatiotemporal resolution and the choice of regions of interest: Brunstein and Oheim. *Microsc. Res. Tech.* **80**, 220–230 (2017).
3. Wagner, E. L. & Shin, J.-B. Mechanisms of Hair Cell Damage and Repair. *Trends in Neurosciences* **42**, 414–424 (2019).

Scientific or technical background required for work program

We seek a master's student in neuroscience, cell biology, or biomedical engineering with a strong academic record. Prior experience in histology or microscopy is advantageous but not essential. The ideal candidate should be meticulous, with problem-solving aptitude and enthusiasm for translational sensory research.

Institut Pasteur, 2025-2026

Title of the work program 11

Emotional processing in mood disorders

Description of the work program

Understanding the neural circuits that link internal and external stimuli with positive or negative emotional value to guide behavior is one of the central questions in contemporary neuroscience. Emotional expressions are considered windows into the affective state of an individual across species—from insects to humans. Notably, emotional processing is a core domain disrupted in mood disorders.

Human and animal studies have shown that the olfactory and emotional systems are closely interconnected, sharing common neural substrates. Disruption of the olfactory system can lead to significant behavioral changes in animals, and in humans, there is a strong, reciprocal link between impaired olfaction and various psychiatric disorders.

This project aims to uncover how the mammalian brain assigns emotional value to stimuli under both normal and pathological conditions. We are particularly interested in olfactory perception and its connection to emotional states. By combining behavioral analyses in mice, animal models of mood disorders, intersectional viral vector strategies, neuroanatomy, in vivo imaging, and optogenetic/chemogenetic tools, our research seeks to establish causal links between the activity of defined neural circuits, full-body physiological responses, and behavior.

Tutor/supervisor

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Institut Pasteur, 2025-2026

Selected publications or patents of the Research Group offering the work program

Bigot M, De Badts C-H, Benchetrit A, Vicq E, Moigneu C, Meyrel M, Wagner S, Houenou J, Lledo P-M, Henry C*, **Alonso M*.** Disrupted basolateral amygdala circuits supports negative valence bias in depressive states. Transl Psychiatry. 2024 14: 382. *Last coauthors

Bigot M, Vicq E, Lledo PM, **Alonso M*,** Henry C*. Assessing positive and negative valence systems to refine animal models of bipolar disorders: the example of GBR 12909-induced manic phenotype. Sci Rep 2022, 12: 7364. *Last coauthors

Grelat A, Benoit L, Wagner S, Moigneu C, Lledo P-M*, **Alonso M*.** Adult-born neurons boost odor-reward association. PNAS 2018 115, 2514-2519. *Last coauthors

Alonso M, Lepousez G, Wagner S, Bardy C, Gabellec M-M, Torquet N, Lledo P-M. Activation of adult-born neurons facilitates learning and memory. Nat. Neurosci. 2012 15, 897–904.

Alonso M, Ortega I, Grubb M, Bourgeois JP, Chaneau P, Lledo PM. Turning astrocytes from the rostral migratory stream into neurons: a role for the olfactory sensory organ. J Neurosci 2008 28:11089-102.

Scientific or technical background required for work program

We are seeking a motivated Master's student to join our research project focused on deciphering emotional circuits in the rodent brain. Candidates should have a solid background in neuroscience, including knowledge of neuroanatomy, behavioral neuroscience, and neurophysiology. Prior experience with rodent handling and behavioral assays is highly desirable. Familiarity with experimental techniques such as immunohistochemistry, viral tracing, or in vivo imaging is a strong plus. Basic data analysis skills (e.g., Python, MATLAB, or R) and understanding of statistical methods are required. Prior knowledge of mouse model for psychiatric disorders is particularly valuable and will be considered an asset.

Institut Pasteur, 2025-2026

Title of the work program 12

Biomolecular condensates in viral infection

Description of the work program

HIV basic science research not only uncovers novel mechanisms exploited by the virus but also serves as a powerful tool for studying key cellular processes, including phase separation mechanisms (Scoca et al., 2023), innate immunity (Ay et al., 2025), nuclear translocation (Blanco-Rodriguez et al., 2020; Lelek et al., 2015; Zila et al., 2021), and the size and dynamics of the nuclear pore complex (Kreysing et al., 2025; Zila et al., 2021). HIV-based tools, with appropriate modifications, are even being applied clinically, such as in gene therapy (Di Nunzio et al., 2008; Morgan et al., 2021).
However, many intranuclear viral processes remain unclear, and further investigation could help elucidate the mechanisms of viral invasion and develop more effective strategies to counteract them. Recent discoveries also from our laboratory highlighted the formation of nuclear biomolecular condensates once the virus enters the nucleus of an infected cell. This phenomenon has been shown to occur in vivo (Ay et al., 2024). Importantly these membraneless organelles seems to exert key roles for the viral infection and for the host cell.

In order to further leverage the power of the virus-host relationship as a conduit for scientific discovery at the molecular, subcellular and cellular scales, here we propose a multidisciplinary strategy that combines cryo-EM studies and cutting-edge fluorescence imaging technologies capable of dynamically interrogating steps of the viral life cycle.

Tutor/supervisor

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Selected publications or patents of the Research Group offering the work program

[1] Elena Rensen, Florian Mueller, Viviana Scoca, Jyotsana Parmar, Philippe Souque, et al.. Clustering and reverse transcription of HIV-1 genomes in nuclear niches of macrophages. *EMBO Journal*, 2021, 40 (1), pp.e105247. ⟨10.15252/embj.2020105247⟩. ⟨**pasteur–03088393**⟩

[2] Francesca Di Nunzio. Stress–induced condensate switch awakens sleeping viruses. *Cell Host & Microbe*, 2023, 31 (5), pp.679–680. ⟨10.1016/j.chom.2023.04.008⟩. ⟨**pasteur–04126658**⟩

[3] Francesca Di Nunzio, Vladimir Uversky, Andrew Mouland. Biomolecular condensates: insights into early and late steps of the HIV–1 replication cycle.. *Retrovirology*, 2023, 20 (1), pp.4. ⟨10.1186/s12977–023–00619–6⟩. ⟨**pasteur–04126418**⟩

[4] Viviana Scoca, Francesca Di Nunzio. Characterization of Nuclear HIV–Induced Membraneless Organelles Through Fluorescence Microscopy. Vinayaka R. Prasad; Ganjam V. Kalpana. *HIV Protocols*

[4th edition], 2807, Springer, pp.113–125, 2024, Methods in Molecular Biology, 978–1–0716–3861–3. ⟨10.1007/978–1–0716–3862–0_8⟩. ⟨**pasteur–04598269**⟩

[5] Thierry Mourer, Francesca Di Nunzio. La capside du VIH–1. *Médecine/Sciences*, 2025, 41 (3), pp.219–222. ⟨10.1051/medsci/2025028⟩. ⟨**hal–05001671**⟩

[6] Guillermo Blanco–Rodriguez, Anastasia Gazi, Blandine Monel, Stella Frabetti, Viviana Scoca, et al.. Remodeling of the core leads HIV–1 pre–integration complex in the nucleus of human lymphocytes.. *Journal of Virology*, 2020, [Epub ahead of print], pp.JVI.00135–20. ⟨10.1128/JVI.00135–20⟩. ⟨**pasteur–02548457**⟩

[7] Viviana Scoca, Renaud Morin, Maxence Collard, Jean–Yves Tinevez, Francesca Di Nunzio. HIV–induced membraneless organelles orchestrate post–nuclear entry steps. *Journal of molecular cell biology*, 2023, 14 (11), pp.mjac060. ⟨10.1093/jmcb/mjac060⟩. ⟨**hal–04264224**v3⟩

[8] Selen Ay, Julien Burlaud–Gaillard, Anastasia Gazi, Yevgeniy Tatirovsky, Céline Cuche, et al.. In vivo HIV–1 nuclear condensates safeguard against cGAS and license reverse transcription. *EMBO Journal*, 2024, ⟨10.1038/s44318–024–00316–w⟩. ⟨**pasteur–04826770**⟩

[9] Chiara Tomasini, Céline Cuche, Selen Ay, Maxence Collard, Bin Cui, et al.. Decoding the biogenesis of HIV–induced CPSF6 puncta and their fusion with the nuclear speckle. 2025. ⟨**pasteur–05117096**v1⟩

Scientific or technical background required for work program

We are looking for highly motivated and team player individuals with a strong motivation in the following fields:

- virology
- biochemistry
- cell biology
- molecular biology
- image and signal processing
- biophysics

Institut Pasteur, 2025-2026

Title of the work program 13

Application of deep mutational scanning to emerging RNA viruses

Description of the work program

Viruses emerging and re-emerging into the human population generally exhibit genotypic changes which result in phenotypes previously unobserved or different to previously circulating strains. Such mutations are often relevant to public health responses and in some cases, result in immune escape e.g. neutralizing polyclonal sera or monoclonal antibodies or reduction in the efficacy of treatments, among other effects.

Systematic experimental evolutionary approaches such as deep mutational scanning (DMS) can be utilised to investigate the impact of single amino acid mutations, insertions and deletions from a known viral background. DMS generates a catalogue of per-residue functional scores that can then be used to rapidly map the consequences of amino-acid mutations observed in nature without the immediate necessity for laboratory characterization, potentiating public health responses. DMS has been extensively applied to SARS-CoV-2 during the COVID-19 pandemic and has allowed early identification of variants with public health importance.

The general objective of this project is to contribute to the development and optimization of deep mutational scanning-based assays for the definition of evolutionary space around existing genotypes from RNA viruses of public health importance.

This project is laboratory based and thus will develop the student's general molecular biology skills i.e. cloning, PCR, cell culture, NGS library preparation, pseudovirus production. The laboratory additionally has the capacity for dry-lab based skills that the student would be able to participate in if it matches their interests.

Tutor/supervisor

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YES I authorise the IP Erasmus+ team to publish the project proposal on the pasteur.fr website

Selected publications or patents of the Research Group offering the work program

- Taieb F, Baidaliuk A, Durand A, Prot M, Jidar K, Hochedez P, Consigny PH, Itani O, Simon-Loriere E. Phylogenetic analysis of chikungunya virus in travellers returning from La Reunion Island. J Travel Med. 2025 Aug 1:taaf079. doi: 10.1093/jtm/taaf079. PMID: 40748267.

- Tey Putita Ou, Julia Guillebaud, Artem Baidaliuk, Sothyra Tum, Dany Chheang, Deborah Delaune, Matthieu Prot, Rafael Rahal Guaragna Machado, Leakhena Pum, Vibol Hul, Thavry Hoem, Sovann Ly, Heidi Auerswald, Gavin James Smith, Philippe Dussart, Erik A Karlsson, Véronique Chevalier, Julien Cappelle, Veasna Duong, Etienne Simon-Lorière. Characterization and evolutionary history of novel SARS-CoV-2-related viruses in bats from Cambodia. bioRxiv 2025.04.15.648942; doi: https://doi.org/10.1101/2025.04.15.648942
- Planas D, Staropoli I, Michel V, Lemoine F, Donati F, Prot M, Porrot F, Guivel-Benhassine F, Jeyarajah B, Brisebarre A, Dehan O, Avon L, Bolland WH, Hubert M, Buchrieser J, Vanhoucke T, Rosenbaum P, Veyer D, Péré H, Lina B, Trouillet-Assant S, Hocqueloux L, Prazuck T, Simon-Loriere E, Schwartz O. Distinct evolution of SARS-CoV-2 Omicron XBB and BA.2.86/JN.1 lineages combining increased fitness and antibody evasion. Nat Commun. 2024 Mar 13;15(1):2254. doi: 10.1038/s41467-024-46490-7. PMID: 38480689
- Gámbaro F, Pérez AB, Prot M, Agüera E, Baidaliuk A, Sánchez-Seco MP, Martínez-Martínez L, Vázquez A, Fernandez-Garcia MD, Simon-Loriere E. Untargeted metagenomic sequencing identifies Toscana virus in patients with idiopathic meningitis, southern Spain, 2015 to 2019. Euro Surveill. 2023 Nov;28(45):2200913. doi: 10.2807/1560-7917.ES.2023.28.45.2200913. PMID: 37943504.

Scientific or technical background required for work program

Skills listed below are advantageous but not a pre-requsitite of the program:

- General molecular biology techniques
  - Cloning
  - PCR
  - Nucleic acid extraction
  - Gel electrophoresis
- Cell culture and aseptic technique

Institut Pasteur, 2025-2026

Title of the work program 14

Standardisation of common immunomonitoring study protocols

Description of the work program

Immunomonitoring studies allow for a detailed analysis of immune responses within the context of clinical, translational and systems immunology studies. Monitoring an individual's immune response over the course of vaccination, infection or treatment can help to explain mechanisms of treatment action and/or possible resistance or hypersensitivity. A variety of immunological techniques and technologies are involved in order to gain a deep understanding of the complexity of the immune response to treatment/infection. To accurately compare results between participants in the same study and between different immunomonitoring studies, it is crucial to standardise the protocols applied to each technology.

As part of the European Vaccine Hub consortium, our unit will be involved in immunomonitoring. Our primary goal is therefore to establish a standard operating procedure (SOP) for each technology to be applied. The list includes, but is not limited to:

- Spectral cytometry
- ELISpot
- ELISA
- Proteomics (Luminex, Olink)
- scRNAseq

The selected candidate will have the opportunity to:

- Participate in development of at least one SOP
- Work in P2 laboratory with human samples
- Use ID7000 (Sony BioTecnology) spectral cytometer
- Analyse high-dimensional flow cytometry data

Tutor/supervisor

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Selected publications or patents of the Research Group offering the work program

Standardized high-dimensional spectral cytometry protocol and panels for whole blood immune phenotyping in clinical and translational studies.

Dott T, **Culina S**, Chemali R, Mansour CA, Dubois F, Jagla B, Doisne JM, Rogge L, Huetz F, Jönsson F, Commere PH, Di Santo J, Terrier B, Quintana-Murci L, Duffy D, Hasan M; Milieu Intérieur Consortium. Cytometry A. 2023 Sep 26. doi: 10.1002/cyto.a.24801. Online ahead of print. PMID: 37751141

Scientific or technical background required for work program

Basic knowledge of immunology

Institut Pasteur, 2025-2026

Title of the work program 15

Structural basis behind the entry of retroviruses to target cells.

Description of the work program

Retroviruses reverse transcribe their genetic material (RNA) into double-stranded DNA and integrate it into the host genome. They encode a glycoprotein that recognizes host proteins (receptors) and fuses the viral membrane with the target cell, allowing entry and starting the infectious cycle. These viruses have tremendous medical relevance, since they affect millions of people, causing severe immunodeficiency (Human Immunodeficiency Virus, HIV) and cancer (Human T-cell leukemia virus, HTLV). Besides, our genomes harbour remnants of ancient retroviral integrations, called endogenous retroviruses (ERVs), that were domesticated to fulfil new functions.

This work program aims to study retroviral glycoproteins and to elucidate details on viral fusion mechanisms using structural biology techniques, such as X-ray crystallography and cryo-electron microscopy (cryo-EM). According to the student's interest, they will be able to join projects to (1) engineer retroviral glycoproteins to determine their structure, (2) validate structures of glycoprotein-receptor complexes by mutagenesis and biophysical and cellular assays, (3) determine the structure of retroviral glycoproteins and antibodies that block their activity, or (4) advance in the design of antigens for potential vaccine applications. In this way, the student will contribute to a better understanding on the entry of important human pathogens and the development of strategies for their prevention and treatment.

Tutor/supervisor

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☒ I authorise the IP Erasmus+ team to publish the project proposal on the pasteur.fr website

Selected publications or patents of the Research Group offering the work program

1) Dufloo J*, **Fernández I***, Arbabian A, Haouz A, Gimenez-Lirola LG, Rey FA, Sanjuan R. *Dipeptidase 1 is a functional receptor for coronavirus PHEV*. BioRxiv 2025.01.09.632101. doi: 10.1101/2025.01.09.632101 (Nature Microbiology, in press).

2) **Fernández I***, Saunders N*, Duquerroy S, Bolland WH, Arbabian A, Baquero E, Blanc C, Lafaye P, Haouz A, Buchrieser J, Schwartz O, Rey FA. *Structural basis of TMPRSS2 zymogen activation and recognition by the HKU1 seasonal coronavirus*. Cell. 2024 Aug 8;187(16):4246-4260.e16. doi: 10.1016/j.cell.2024.06.007. Epub 2024 Jul 3. PMID: 38964326.

3) **Fernández I#**, Bontems F, Brun D, Coquin Y, Goverde CA, Correia BE, Gessain A, Buseyne F, Rey FA, Backovic M#. *Structures of the Foamy virus fusion protein reveal an unexpected link with the F protein of paramyxo- and pneumoviruses*. Sci Adv. 2024 Oct 11;10(41):eado7035. doi: 10.1126/sciadv.ado7035. Epub 2024 Oct 11. PMID: 39392890; PMCID: PMC11468914.

4) **Fernández I**, Dynesen LT, Coquin Y, Pederzoli R, Brun D, Haouz A, Gessain A, Rey FA, Buseyne F, Backovic M. *The crystal structure of a simian Foamy Virus receptor binding domain provides clues about entry into host cells*. Nat Commun. 2023 Mar 6;14(1):1262. doi: 10.1038/s41467-023-36923-0. PMID: 36878926.

5) Lorin V*, **Fernández I***, Masse-Ranson G, Bouvin-Pley M, Molinos-Albert L, Planchais C, Hieu T, Péhau-Arnaudet G, Hrebík D, Girelli Zubani G, Fiquet O, Guivel-Benhassine F, Sanders R, Walker B, Schwartz O, Scheid J, Dimitrov J, Plevka P, Braibant M, Seaman M, Bontems F, Di Santo J, Rey F, Mouquet H. Epitope Convergence of Broadly HIV-1 Neutralizing IgA and IgG Antibody Lineages in a Viremic Controller. Journal of Experimental Medicine, 2022 Mar 7;219(3):e20212045. doi: 10.1084/jem.20212045.

Scientific or technical background required for work program

We are looking for highly motivated students interested in biochemistry and structural biology, who have analytical skills, an independent spirit and experience in a research laboratory. The work proposal will be tailored to the candidate's interest, so students with multiple backgrounds are encouraged to apply. Previous experience on structural biology techniques is not required but skills concerning molecular biology (cloning, transfection), expression and purification of recombinant proteins (chromatography, SDS-PAGE, Western Blot) or cell culture will be highly advantageous.

Institut Pasteur, 2025-2026

Title of the work program 16

Deciphering stromal cell heterogeneity and plasticity at single cells level in tissue homeostasis and disease

Description of the work program

Project Overview: This study aims to investigate the cellular and molecular mechanisms underlying stromal cell diversity and function at homeostasis and in different types of pathologies, such as tissue repair and cancer. **Research Objectives:** 1) Identify and characterize stromal cell subpopulations using scRNA-seq data from previously generated datasets. 2) Investigate the transcriptional programs governing stromal cell plasticity during the transition from tissue-supportive to pathology associated phenotypes. 3) Elucidate the molecular mechanisms by which stromal cells contribute to pathogenesis through secretory factor-mediated and cell adhesion-mediated pathways. 4) Generate stromal cell signatures and intercellular communication networks. **Methodology:** We will analyze existing scRNA-seq datasets to characterize stromal cell subpopulations across healthy, regenerating, and malignant tissues. Computational analysis will include cell clustering and annotation using Seurat, trajectory inference to track cell differentiation pathways, intercellular communication analysis and functional enrichment analysis (GSEA) to identify key regulatory pathways. When applicable, integration of spatial transcriptomics data will provide tissue architecture context. **Expected Impact:** This research will provide insights into stromal cell biology, potentially identifying novel therapeutic targets for cancer treatment and tissue regeneration strategies.

Tutor/supervisor

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Selected publications or patents of the Research Group offering the work program

Di Carlo SE, Raffenne J, Varet H, Ode A, Cabrerizo Granados D, Stein M, Legendre R, Tuckermann J, Bousquet C, Peduto L. 2023. Depletion of slow-cycling PDGFRa^{+}ADAM12^{+} mesenchymal cells promotes antitumor immunity by restricting macrophage efferocytosis. **Nature Immunology** 24(11):1867-1878.

Jacob JM, Di Carlo SE, Stzepourginski I, Lepelletier A, Ndiaye PD, Varet H, Legendre R, Kornobis E, Benabid A, Nigro G, Peduto L. 2022. PDGFRα-induced stromal maturation is required to restrain postnatal intestinal epithelial stemness and promote defense mechanisms. **Cell Stem Cell**, 29(5): 856-868.

Scientific or technical background required for work program

Candidates should possess a computational biology degree with strong R programming skills and previous experience with single cells RNAseq analysis. Experience with Seurat package, Monocle, CellChat, GSEA or other trajectory analysis tools and pathway enrichment methods would be advantageous for this project.

Institut Pasteur, 2025-2026

Title of the work program 17

A bacterial genetics approach to study interactions between virulence factors in *Pseudomonas aeruginosa*

Description of the work program

Bacterial pathogens employ various mechanisms to deliver virulence factors to the eukaryotic host cells they are infecting. The type III secretion system (T3SS) is a needle-like apparatus produced by certain bacteria, which allows the injection of effectors/virulence factors into the host cell. We are interested in the role of T3SS injected effectors/virulence factors in the pathogenesis of *Pseudomonas aeruginosa*, a pathogen that plays a major role in infections of patients suffering from cystic fibrosis.

One of these effectors, ExoY has the ability to generate different cNMPs (cGMP, cAMP, cUMP and cCMP in this order of preference *in vitro*). The nucleotidyl cyclase activity (NC) of ExoY is activated only inside host cells, but not inside bacteria, a mechanism necessary to protect bacteria from unphysiological levels of cNMPs. We identified several proteins interacting with ExoY. We would now like to understand the role of the interaction between ExoY and these proteins. For this purpose, precise mutants need to be created on the bacterial chromosome using a two-step allelic exchange method. The mutant phenotype of validated mutants will be studied by evaluating the effects on secretion of ExoY and/or other T3SS injected effectors.

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Selected publications or patents of the Research Group offering the work program

1. Belyy, A., Raoux-Barbot, D., Saveanu, C., Namane, A., Ogryzko, V., Worpenberg, L., David, V., Henriot, V., Fellous, S., Merrifield, C., Assayag, E., Ladant, D., Renault, L., and **Mechold, U.** (2016) Actin activates Pseudomonas aeruginosa ExoY nucleotidyl cyclase toxin and ExoY-like effector domains from MARTX toxins. *Nat Commun* **7**, 13582

2. Belyy, A., Mechold, U., Renault, L., and Ladant, D. (2018) ExoY, an actin-activated nucleotidyl cyclase toxin from P. aeruginosa: A minireview. *Toxicon* **149**, 65-71

3. Belyy, A., Santecchia, I., Renault, L., Bourigault, B., Ladant, D., and **Mechold, U.** (2018) The extreme C terminus of the Pseudomonas aeruginosa effector ExoY is crucial for binding to its eukaryotic activator, F-actin. *J. Biol. Chem.* **293**, 19785-19796

4. Raoux-Barbot, D., Belyy, A., Worpenberg, L., Montluc, S., Deville, C., Henriot, V., Velours, C., Ladant, D., Renault, L., and **Mechold, U.** (2018) Differential regulation of actin-activated nucleotidyl cyclase virulence factors by filamentous and globular actin. *PLoS One* **13**, e0206133

5. Silistre, H., Raoux-Barbot, D., Mancinelli, F., Sangouard, F., Dupin, A., Belyy, A., Deruelle, V., Renault, L., Ladant, D., Touqui, L., and **Mechold, U.** (2021) Prevalence of ExoY Activity in Pseudomonas aeruginosa Reference Panel Strains and Impact on Cytotoxicity in Epithelial Cells. *Front Microbiol* **12**, 666097

Scientific or technical background required for work program

The successful candidate should have good English language skills, a solid knowledge in molecular biology, or biochemistry or genetics, should be rigorous and organized and eager to learn new methods.

Institut Pasteur, 2025-2026

Title of the work program 18

Unveiling the ecological role of a novel antimicrobial compound in *Veillonella parvula*'s competitive dynamics within the oral microbiome

Description of the work program

Veillonella parvula is a ubiquitous, Gram-negative, anaerobic bacterium found in various sites in the human body, notably the oral cavity. It thrives by metabolising lactate — a by-product of streptococcal fermentation — into weaker acids (e.g. acetate and propionate), and it is an essential component of dental plaque biofilms, contributing to their formation and architecture. *V. parvula* indeed interacts with multiple partners in dental plaque, such as Streptococci and Actinomyces species, influencing the colonisation of dental plaque by potential oral pathogens, such as the cariogenic bacterium *Streptococcus mutans* and the periodontopathogen *Porphyromonas gingivalis*. Our research group has begun to study the physical interactions of *V. parvula* with its potential partners and has identified some of the molecular factors responsible for specific interactions. However, the potential interference mechanisms between oral bacteria remain understudied. While studying the Bfv two-component system (TCS) regulon of *V. parvula*, we detected the activation of an operon potentially involved in the production, processing, and export of a 60-amino-acid lantibiotic. Lantibiotics such as nisin are known to behave as antimicrobial agents that can affect the dynamics of the microbiota.

The aim of this internship is to characterise this potential lantibiotic, including its activity, regulation, and capacity to modulate the interactions of *V. parvula* with other relevant oral bacteria.

The student will participate in constructing mutants of the lantibiotic system in wild-type (wt) and Δ*bfv* strains. We will then assess whether the constructed strains interfere with the growth of various oral bacteria, including pathogenic bacteria such as *S. mutans* and *P. gingivalis*, and whether this depends on the lantibiotic system. If so, we will determine whether this inhibitory activity is contact-dependent and investigate the activity and host range of V. parvula culture supernatants. Using the chosen microorganisms, we will attempt to identify mutants that resist to this lantibiotic in order to determine its molecular target(s) and mode of action. We will follow the production of the lantibiotic using an antibody raised against a 60 amino acid (aa) synthetic peptide, in order to evaluate the regulation of its production and the environmental and other conditions that influence this regulation. We will also assess the production and effects of this lantibiotic in monospecies and multispecies biofilms using an *in vitro* dental plaque model on hydroxyapatite disks that mimic dental surfaces. Finally, we will evaluate the conservation and evolution of this type of lantibiotic system within bacterial diversity.

Through this project, we aim to demonstrate *V. parvula*'s antimicrobial activity against oral pathogens, identify the target and mode of action of this lantibiotic, and show that it can enhance V. parvula's competitive fitness in biofilms. Overall, this project could provide valuable insights into how commensals regulate oral pathogens, informing the development of probiotic or anti-biofilm therapies.

Tutor/supervisor

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Institut Pasteur, 2025-2026

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Selected publications or patents of the Research Group offering the work program

1. Taib N, Megrian D, Witwinowski J, Panagiotis A, Poppleton D, Borrel G, Beloin C, Gribaldo S*. Genome-wide analysis of the Firmicutes illuminates the Gram-negative/Gram-positive transition. Nature Ecology & Evolution. 2020. Dec;4(12):1661-1672. doi: 10.1038/s41559-020-01299-7. PMID: 33077930.
2. Witwinowski J, Sartori-Rupp A, Taib N, Pende N, Tham TN, Poppleton D, Ghigo JM, Beloin C*, Gribaldo S*. An ancient divide in outer membrane tethering systems in Bacteria suggests a possible mechanism for the diderm-to-monoderm transition. Nature Microbiology. 2022. 7(3):411-422. doi: 10.1038/s41564-022-01066-3. Epub 2022 Mar 4. PMID: 35246664.
3. Bayard-Bernal J, Thiebaud J, Brossaud M, Beaussart A, Caillet C, Waldvogel Y, Travier L, Létoffé S, Fontaine T, Rokbi B, Talaga P, Beloin C, Mistretta N*, Duval JFL* and Ghigo JM*. Bacterial capsular polysaccharides with antibiofilm activity share common biophysical and electrokinetic properties. Nature Communications. 2023. 3;14(1):2553. doi: 10.1038/s41467-023-37925-8. PMID: 37137893; PMCID: PMC10156666
4. Chekli Y, Stevick RJ, Kornobis E, Briolat V, Ghigo JM, Beloin C*. Escherichia coli aggregates mediated by native or synthetic adhesins exhibit both core and adhesin-specific transcriptional responses. Microbiology Spectrum. 2023. 11(3): e0069023. doi: 10.1128/spectrum.00690-23. Epub ahead of print. PMID: 37039668; PMCID: PMC10269875.
5. Silale A, Zhu Y, Witwinowski J, Smith R, Newman KE, Bhamidimarri SP, Baslé A, Khalid S, Beloin C*, Gribaldo S*, van den Berg B*. 2023. An ancestral dual function of OmpM as outer membrane tether and nutrient uptake channel in diderm Firmicutes. Nature Communications. 2023. 6;14(1):7152. doi: 10.1038/s41467-023-42601-y. PMID: 37932269; PMCID: PMC10628300.
6. Chekli Y, Thiriet-Rupert S, Caillet C, Quilès F, Le Cordier H, Deshayes E, Bardiaux B, Pédron T, Titecat M, Debarbieux L, Ghigo JM, Francius G, Duval JFL, Beloin C*. Biophysical insights into sugar-dependent medium acidification promoting YfaL protein-mediated Escherichia coli self-aggregation, biofilm formation and acid stress resistance. Nanoscale. 2024 16(37):17567-17584. doi: 10.1039/d4nr01884b. PMID: 39225712. https://pasteur.hal.science/hal-04693551v2.
7. Krasekamp KP, Beaud Benyahia B, Taib N, Audrain B, Bardiaux B, Rossez Y, Izadi-Pruneyre N, Lejeune M, Trivelli X, Chouit Z, Guerardel Y, Ghigo JM, Gribaldo S*, Beloin C*. 2023. The Mla system in the diderm Firmicute Veillonella parvula reveals and ancestral transenvelope bridge for phospholipid trafficking. Nature Communications. 2023. 23;14(1):7642. doi: 10.1038/s41467-023-43411-y. PMID: 37993432; PMCID: PMC10665443. https://pasteur.hal.science/hal-04301455.
8. Dorison L, Béchon N, Martin-Gallasiaux C, Chamorro Rodriguez S, Vitrenko I, Ouazahrou R, Villa R, Deschamps J, Briandet R, Gribaldo S, Ghigo JM, Beloin C*. Identification of V. parvula and S. gordonii adhesins mediating co-aggregation and its impact on physiology and mixed biofilm structure. mBio. 2024 11:e0217124. doi: 10.1128/mbio.02171-24. Epub ahead of print. PMID: 39526776.
9. Megrian D, Taib N, Witwinowski J, Beloin C, Gribaldo S*. One or two membranes? Diderm Firmicutes challenge the Gram-positive/Gram-negative divide. Molecular Microbiology. 2020;113(3):659-671 doi: 10.1111/mmi.14469. PMID: 31975449.
10. Beaud Benyahia B, Taib N, Beloin C, Gribaldo S*. Terrabacteria: redefining bacterial envelope diversity, biogenesis and evolution. Nat Rev Microbiol. 2025 Jan;23(1):41-56. doi: 10.1038/s41579-024-01088-0. Epub 2024 Aug 28. PMID: 39198708.

Scientific or technical background required for work program

- **Technical Skills**: Anaerobic microbiology, molecular microbiology, genomic analysis.
- **Analytical Skills**: Data interpretation, ecological modeling of microbial interactions.
- **Professional Development**: Scientific writing, presentation at lab meetings, collaboration.

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Institut Pasteur, 2025-2026

Title of the work program 20

Crucial role of σ^B and its activation pathway in controlling key steps of the infectious cycle of *Clostridioides difficile*

Description of the work program

Clostridioides difficile (*CD)* is a strictly anaerobic, spore-forming Bacillota. It is the leading cause of post-antibiotic diarrhea in adults and pseudomembranous colitis. Spores are the forms in which the bacteria persist and are transmitted. *CD* colonizes the digestive tract in conditions of microbiota dysbiosis following antibiotic therapy. After spore germination in the small intestine in the presence of bile salts, the vegetative cells are subjected to numerous stresses: antimicrobial peptides, variations in osmolarity and pH, low O_2 tension in the small intestine (5%) and near the epithelial cells of the colon (1-2%). In addition, toxin production will promote severe inflammation leading to the production of reactive oxygen species (ROS), NO, and HOCl. *CD* has detection, protection, and detoxification mechanisms. The sigma factor of the general stress response, σ^B, plays a central role in O_2 tolerance and resistance to ROS and NO by regulating their detoxification pathways, and it also contributes to intestinal colonization. The σ^B activation pathway involves an anti-sigma factor RsbW, an anti-anti-sigma factor RsbV, and a phosphatase, RsbZ. In the absence of stress, RsbW sequesters σ^B. In response to stress, RsbZ dephosphorylates RsbV, allowing it to bind RsbW and liberate σ^B. Free σ^B then associates with RNA polymerase to transcribe the σ^B regulon. The signaling pathway activating RsbZ remains poorly characterized. As part of this internship, we aim to better characterize the signaling pathway leading to σ^B activation. We will test the impact of signaling molecules related to infection (O_2, ROS, cecum extracts) on σ^B targets and try to identify sensor proteins detecting these signals. The role of RsbW, which appears to be atypical in *CD,* will be also studied by combining phenotypic tests and transcriptional analysis.

The four O_2 reductases of *CD* that are expressed under the control of σ^B were detected on the surface of the spore. In the presence of primary bile salts, *CD* spores germinate in the small intestine, where they are exposed to O_2 tensions of around 5%. We therefore wish to study i) the expression of O_2 reductase genes during sporulation using reporter genes (expression compartment, sigma factors involved….) ii) the role of these proteins during germination in the presence of O_2 and iii) the rapid induction of σ^B targets following germination using single cell strategy. This will give us a better understanding of the factors important for germination and the role of σ^B in this key step of the infectious cycle.

This work will establish the crucial role of σ^B and its activation pathway during infection, particularly in protecting against and detoxifying the major stresses encountered by *CD* in the gastrointestinal tract.

Tutor/supervisor

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Institut Pasteur, 2025-2026

Selected publications or patents of the Research Group offering the work program

N. Kint, C. Alves Feliciano, M. C Martins, C. Morvan, S. Fernandes, F. Folgosa, B. Dupuy, M. Texeira and **I. Martin-Verstraete**. How anaerobic *Clostridioides difficile* deals with low O_2 tensions. mBio. 2020. Sep 8;11(5):e01559-20.

T. Garcia-Garcia, S. Poncet, E. Cuenot, T. Douché, Q Giai Gianetto, J Peltier, P. Courtin, M-P Chapot-Chartier, M. Matondo, B Dupuy, T Candela and **I. Martin-Verstraete**. Ser/Thr kinase-dependent phosphorylation of the peptidoglycan hydrolase CwlA controls its export and modulates cell division in *Clostridioides difficile*. mBio. 2021. 12(3):e00519-21.

T. Garcia-Garcia, T. Douché, Q. Giai Gianetto, S. Poncet, N. El Omrani, W. K. Smits, E. Cuenot, M. Matondo and **I. Martin-Verstraete**. In-depth characterization of the *Clostridioides difficile* phosphoproteome to identify Ser/Thr kinase substrates. Mol Cell Proteomic. 2022 Nov;21(11):100428.

C. Anjou, A. Lotoux, A. Zhukova, M. Royer, L. C. Caulat, E. Capuzzo, C. Morvan and **I. Martin-Verstraete**. The multiplicity of Thioredoxin systems meets the specific needs of Clostridia. Plos Pathogen. 2024 Feb 8;20(2):e1012001

L C. Caulat, A. Lotoux, M. M. Martins, N. Kint, C. Anjou, M. Teixeira, F. Folgosa, C. Morvan and **I. Martin-Verstraete**. Physiological role and complex regulation of the O_2-reductases in the obligate anaerobe *Clostridioides difficile.* mBio. 2024 Aug 27:e0159124. doi: 10.1128/mbio.01591-24

A. Lotoux, L C. Caulat, C. Martins-Alves, C. Alves Feliciano, C. Morvan, F. Folgosa, and **I. Martin-Verstraete**. Defense arsenal of the strict anaerobe, *Clostridioides difficile,* against reactive oxygen species encountered during its infection cycle. 2025. mBio.Mars 20:e0375324

Scientific or technical background required for work program

Skills in molecular biology and microbiology will be required for the work program

Institut Pasteur, 2025-2026

Title of the work program 19

Study of In Vivo Replication Mechanisms of a ZTGC-DNA Phage

Description of the work program

2-aminoadenine replaces completely adenine in the genome of several lytic bacteriophages including S-2L lytic for *Synechococcus elongatus*, ΦVC8 lytic for *Vibrio cholerae* and many others.
The extraordinary aspect of 2-aminoadenine (hereafter abbreviated as Z) incorporation in DNA is that it deviates from Watson and Crick's base pairing. The evolutionary success of these phages demonstrates that the presence of Z in DNA is compatible with normal DNA function, to a certain extent. However, this compatibility is not trivial, as the substitution of adenine by Z increases the thermostability of the DNA due to a third hydrogen bond in the Z:T pair. Indeed, the presence of the 2-amino group in the minor groove alters the conformational properties of the double helix, leading to modified recognition by proteins and small molecules. As a result, ZTGC-DNA is resistant to restriction enzymes that have an A in their recognition site. Additionally, the presence of Z in the DNA hinders access to the floor of the groove. It is therefore highly likely that these modifications in protein-DNA interactions have broader consequences on processes such as recombination, transcription, and DNA replication. This suggests that the proteins involved in these processes must adapt to the presence of Z in DNA, although the extent of this selective pressure remains to be determined.
We previously proposed a biosynthetic pathway for dZMP and we now want to elucidate how the viral DNA replication machinery incorporates this modified base.

The objective of the internship will be to define the set of genes required for in vivo replication and to characterize their specificity for modified DNA. This will include primase-polymerase, DNA polymerase, ssDNA-binding protein, and helicase. In addition to these known replication factors, we will investigate whether other genes with unknown functions are also required. The goal is to determine the minimal set of genes necessary for ZTGC replication, including the origin of replication, and to assess their specificity for this modified DNA.

Tutor/supervisor

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Institut Pasteur, 2025-2026

Selected publications or patents of the Research Group offering the work program

Kaminski PA. Mechanisms supporting aminoadenine-based viral DNA genomes. Cell Mol Life Sci. 2021 Dec 15;79(1):51. doi: 10.1007/s00018-021-04055-7. PMID: 34910247; PMCID: PMC11072226. HAL Id : pasteur-03549987

Czernecki D, Bonhomme F, **Kaminski PA**, Delarue M. Characterization of a triad of genes in cyanophage S-2L sufficient to replace adenine by 2-aminoadenine in bacterial DNA. Nat Commun. 2021 Aug 5;12(1):4710. doi: 10.1038/s41467-021-25064-x. PMID: 34354070; PMCID: PMC8342488. HAL Id : pasteur-03327945

Pezo V, Jaziri F, Bourguignon PY, Louis D, Jacobs-Sera D, Rozenski J, Pochet S, Herdewijn P, Hatfull GF, **Kaminski PA**, Marliere P. Noncanonical DNA polymerization by aminoadenine-based siphoviruses. Science. 2021 Apr 30;372(6541):520-524. doi: 10.1126/science.abe6542. PMID: 33926956. HAL Id : pasteur-03228903

Sleiman D, Garcia PS, *Lagune M*, Loc'h J, Haouz A, Taib N, Röthlisberger P, Gribaldo S, Marlière P, **Kaminski PA**. A third purine biosynthetic pathway encoded by aminoadenine-based viral DNA genomes. Science. 2021 Apr 30;372(6541):516-520. doi: 10.1126/science.abe6494. PMID: 33926955. HAL Id : pasteur-03228896

Czernecki D, Legrand P, Tekpinar M, Rosario S, **Kaminski PA**, Delarue M. How cyanophage S-2L rejects adenine and incorporates 2-aminoadenine to saturate hydrogen bonding in its DNA. Nat Commun. 2021 Apr 23;12(1):2420. doi: 10.1038/s41467-021-22626-x. PMID: 33893297; PMCID: PMC8065100. HAL Id : hal-03208082

Scientific or technical background required for work program

Molecular biology techniques and microbiology

Institut Pasteur, 2025-2026

Title of the work program 21

Protein Diversification: Why human autophagy has six ATG8 proteins

Description of the work program

Autophagy (old Greek term for “self-eating”) is an intracellular recycling system that delivers cytoplasmic material to the lysosomes for degradation. It is an essential mechanism to maintain cellular homeostasis by degrading endogenous substrates, such as damaged organelles/aggregated proteins and exogenous substrates like bacteria/viruses that escaped phagosomes. During autophagy, the cargo is enclosed by a double membrane-sac called an autophagosome that delivers the cargo to lysosomes.

Autophagy is highly conserved from yeast to man. A dedicated machinery, composed of more than forty AuTophGy related (ATG) proteins, coordinates the formation of autophagosomes. *The hallmark of autophagy is the conjugation of Atg8 proteins to the membrane lipid phostatidylethanolamine (PE).* Atg8 is involved in the protein scaffold on model membranes in in vitro system and this autophagic membrane coat is essential for the maturation of autophagosomes. Interestingly, human cells express six ATG8 homologs of unknown function in two subfamilies, LC3 (LC3A, LC3B and LC3C) and GABARAP (GABARAP, GABARAP-L1 and GABARAP-L2). ATG8 proteins regulate various stages during autophagosome biogenesis, including cargo selection, phagophore expansion, maturation, and fusion with lysosomes. Work over the past years points to a division of labour between ATG8 proteins. LC3 proteins promote phagophore expansion while GABARAP proteins coordinate maturation and fusion with lysosomes. However, the specific molecular function of these proteins remains poorly understood.

The major aim of this study is to reveal the functional diversity of ATG8s through a combination of in vitro reconstitution system and cell biology.

The project involves the generation of human ATG proteins toolbox – purification of various ATG proteins in bacteria and insect cell lines, and generation of different lipid model membranes. By using hexa ATG8 knock out cell lines we would like to decipher the function of each ATG8 at cellular level. Overall the combination of in vitro reconstitution system and cell biology techniques might help to understand the specific functions of each ATG8s at molecular level.

Tutor

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Selected publications or patents of the Research Group offering the work program

- **Mohan J,** Moparthi SB, Girard-Blanc C, Campisi D, Blanchard S, Nugues C, Rama S, Salles A, Pénard E, Vassilopoulos S, Wollert T. ATG16L1 induces the formation of phagophore-like membrane cups. *Nat Struct Mol Biol.* 2024 Sep;31(9):1448-1459.

- Kaufmann, A., Beier, V., Franquelim, H. G. & Wollert T. Molecular Mechanism of Autophagic Membrane-Scaffold Assembly and Disassembly. *Cell* **156**, 469–481 (2014).

Scientific or technical background required for work program

A solid background in biological sciences is crucial for effectively engaging with advanced biochemistry. Incoming student is expected to have a foundational understanding of biochemistry and cell biology. These principles form the basis for understanding the ATG8 code in human at their molecular and functional levels. Importantly, student should be proficient in fundamental laboratory techniques, and highly motivated to learn new methods and techniques**.** Prior experience with scientific writing and data presentation will further enhance the engagement with the program's research-focused elements.

Together, this multidisciplinary background ensures that student is well equipped to explore the functional diversity of ATG8 in human autophagy and contribute to the advancement of biochemistry in both academic and applied contexts.

Institut Pasteur, 2025-2026

Title of the work program 22

Characterization of HIV-1 and SARS-CoV-2 receptors

Description of the work program

Our group focuses on the dissection of the viral entry process with the aim to identify new therapeutic targets. The entry of HIV-1 and SARS-CoV-2 requires the interaction of a viral glycoprotein (gp120/Spike) with cellular receptors: CD4 and CCR5 for HIV-1, ACE2 for SARS-CoV-2. The objective of the internship will be to characterize the mechanisms that regulate the cell surface expression of these receptors by studying their organization at the plasma membrane (distribution, stoichiometry, dynamics) depending on different parameters (ligands, partners, membrane composition). For this, molecular biology, cell biology, and imaging approaches will be developed.

Tutor/supervisor

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Selected publications or patents of the Research Group offering the work program

- J. Groen, *et al*. Bridging the resolution gap in cryo-CLEM by introducing cryo-SXT: cryo-CLXEM. BioRxiv doi.org/10.1101/2025.09.05.673626.
- G. Nardi, *et al*. Characterizing particle dynamics in live imaging through stochastic physical models and machine learning. doi.org/10.1101/2024.12.17.628916
- Blachier, S, *et al*. Intranasal delivery of a broadly neutralizing single domain antibody targeting ACE2 protects against SARS-CoV-2 infection. BioRxiv. doi.org/10.1101/2024.10.11.617877
- Momboisse F, Nardi G, Colin P, Hery M, Cordeiro N, Blachier S, Schwartz O, Arenzana-Seisdedos F, Sauvonnet N, Olivo-Marin JC, Lagane B, Lagache T, Brelot A. Tracking receptor motions at the plasma membrane reveals distinct effects of ligands on CCR5 dynamics depending on its dimerization status. Elife. 2022 Jul 22;11:e76281. doi: 10.7554/eLife.76281.
- Gaelle Boncompain, Floriane Herit, Sarah Tessier, Aurianne Lescure, Elaine Del Nery, Pierre Gestraud, Isabelle Staropoli, Yuko Fukata, Masaki Fukata, Anne Brelot, Florence Niedergang, and Franck Perez. (2019). Targeting CCR5 trafficking to inhibit HIV-1 infection. Science Advances, Oct 16;5(10).
- Brelot A, Chakrabarti LA (2018). CCR5 revisited: How mechanisms of HIV Entry govern AIDS pathogenesis J Mol Biol. 2018 Aug 17;430(17):2557-2589.
- Jin J, Momboisse F, Boncompain G, Koensgen F, Zhou Z, Cordeiro N, Arenzana-Seisdedos F, Perez F, Lagane B, Kellenberger E, Brelot A. (2018). CCR5 adopts three homodimeric conformations that control cell surface delivery. Science Signaling May 8;11(529).
- Jin J, Colin P, Staropoli I, Lima-Fernandes E, Ferret C, Demir A, Rogée S, Hartley O, Randriamampita C, Scott MG, Marullo S, Sauvonnet N, Arenzana-Seisdedos F, Lagane B, Brelot A. (2014). Targeting spare CC chemokine receptor 5 (CCR5) as a principle to inhibit HIV-1 entry. J Biol Chem. Jul 4;289(27):19042.

Scientific or technical background required for work program

A background in biochemistry, in the molecular pharmacology of G protein-coupled receptors, and/or imaging would be advantageous. The candidate should be able to interact with members of an interdisciplinary partnership and possess excellent interpersonal and scientific communication skills.

Institut Pasteur, 2025-2026

Title of the work program 23

Host-mimetic microfluidics to investigate mycobacterial persistence

Description of the work program

CONTEXT

Tuberculosis (TB) is caused by *Mycobacterium tuberculosis* (Mtb) and remains one of the leading infectious killers worldwide, with almost 11 million new cases and 1.25 million deaths reported in 2023 (**1**). The crisis is worsening due to the rise of increasingly drug-resistant strains, which are harder to treat and require long, toxic, and often unsuccessful therapies (**2**). One of the main challenges in TB treatment is the ability of Mtb to persist in the host and evade drug action. Beyond genetic mutations that lead to resistance, Mtb can survive antibiotic treatment through phenotypic drug tolerance, in which a subset of bacterial cells survives therapy due to transient non-genetic changes (**3**). These subpopulations can later resume growth, causing disease relapse and promoting resistance (**4**).

In the lab, we investigate the functional role of phenotypic variation in mycobacterial survival. Traditional laboratory models provide important insights but do not fully capture the complexity of the lung environment, where Mtb infection occurs. Mechanical forces from breathing, extracellular matrix properties, and interactions between different host cells strongly influence how Mtb grows, manipulates host microenvironments and immunity, and responds to drugs (**5**). Microfluidic devices simulating the lung microenvironment offer a valuable opportunity to study early host-pathogen interactions at high resolution, providing insights into infection physiology (**6**).

The hosting lab has developed approaches to study phenotypic variation in mycobacterial cells using time-lapse microfluidic microscopy and fluorescent reporter strains (**7**). This work also led to the identification of a promising compound that decreases phenotypic variation and weakens Mtb, making it more susceptible to existing therapy (**8**). More recently, we have developed an alveolus-on-chip prototype, which combines host-like conditions with live-cell imaging. This model will allow direct observation of mycobacterial subpopulations within distinct cellular microenvironments.

AIM

The aim of this Erasmus project is to contribute to the functional characterization of the alveolus-on-chip model and begin testing it as a host-biomimetic platform to study early infection stages and persistence using a relevant mycobacterial model organism. We will analyze host responses, including cytokine production, reactive species formation, and relevant tissue mechanical properties. The project will assess how different functional compartments of the chip respond to mycobacterial infection and subsequent antibiotic perfusion. This will help identify host niches that favor bacterial survival versus killing. This project will ultimately provide new insights into mycobacterial cell dynamics under host-relevant conditions.

APPROACHES

The project will use a custom-built alveolus-on-chip platform designed to mimic essential lung features while enabling high-resolution imaging. Host cells will be cultured under controlled mechanical and extracellular matrix conditions. Mycobacterial cells will be fluorescently labeled to allow monitoring by live-cell imaging. Time-lapse microscopy will track the fate of individual bacteria in different microenvironments, in the presence or absence of relevant anti-tubercular drugs. In parallel, host cell responses will be assessed using live-cell probes, antibodies, and molecular quantification techniques.

EXPECTED OUTCOME AND SIGNIFICANCE

This project is expected to provide initial insights into how lung-like mechanical forces and tissue microenvironments influence the early stages of mycobacterial infection, the emergence of persistent subpopulations, and their response to therapy. Understanding these interactions could reveal which host niches favor bacterial survival and how certain mycobacterial cells evade treatment. In the future, this work will support the application of new host-biomimetic models, advance our knowledge of early TB pathogenesis, and help the development of more effective therapeutic strategies.

LEARNING OPPORTUNITIES

In the Microbial Individuality and Infection team, the Erasmus student will gain hands-on experience in microfabrication, host cell culture, mycobacterial genetics, fluorescent reporter use, quantitative live-cell imaging, and molecular and cell biology techniques. The student will work in an interdisciplinary environment at the interface of microbiology, bioengineering, and infection biology, providing a strong background for future research, including a potential PhD. This Erasmus project will allow the student to contribute to the development and application of an original alveolus-on-chip platform, enabling further studies on TB pathogenesis, drug responses, and disease control strategies.

REFERENCES

1. World Health Organization. Global Tuberculosis Report 2024. (https://iris.who.int/bitstream/handle/10665/379339/9789240101531-eng.pdf?sequence=1).

2. Dartois, V. A. & Rubin, E. J. Anti-tuberculosis treatment strategies and drug development: challenges and priorities. *Nat Rev Microbiol* **20**, 685–701 (**2022**) DOI: 10.1038/s41579-022-00731-y.

3. Dhar, N., McKinney, J. & Manina, G. Phenotypic heterogeneity in *Mycobacterium tuberculosis*. *Microbiol Spectr* **4**, (**2016**) DOI: 10.1128/microbiolspec.TBTB2-0021-2016.

4. Balaban, N. Q. *et al.* Definitions and guidelines for research on antibiotic persistence. *Nat Rev Microbiol* **17**, 441–448 (**2019**) DOI: 10.1038/s41579-019-0196-3.

5. Mishra, R. *et al.* Mechanopathology of biofilm-like *Mycobacterium tuberculosis* cords. *Cell* **186**, 5135-5150.e28 (**2023**) DOI: 10.1016/j.cell.2023.09.016.

6. Leung, C. M. *et al.* A guide to the organ-on-a-chip. *Nat Rev Methods Primers* **2**, 1–29 (**2022**) DOI: 10.1038/s43586-022-00118-6.

7. Manina, G., *et al.* Preexisting variation in DNA damage response predicts the fate of single mycobacteria under stress. *The EMBO Journal* **38**, e101876 (**2019**) DOI: 10.15252/embj.2019101876.

8. Mistretta, M. *et al.* Dynamic microfluidic single-cell screening identifies pheno-tuning compounds to potentiate tuberculosis therapy. *Nat Commun* **15**, 4175 (**2024**) DOI: 10.1038/s41467-024-48269-2.

Institut Pasteur, 2025-2026

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Selected publications or patents of the Research Group offering the work program

Team members; *First author; †Correspondence

Mistretta M, Cimino M, Campagne P, Volant S, Kornobis E, Hebert O, Rochais C, Dallemagne P, Lecoutey C, Tisnerat C, Lepailleur A, Ayotte Y, LaPlante SR, Gangneux N, Záhorszká M, Korduláková J, Vichier-Guerre S, Bonhomme F, Pokorny L, Albert M, Tinevez JY, †Manina G. Dynamic microfluidic single-cell screening identifies pheno-tuning compounds to potentiate tuberculosis therapy. **Nat Commun.** (**2024**) 15(1):4175. DOI: 10.1038/s41467-024-48269-2. PMID: 38755132.

Mistretta M, Gangneux N, †Manina G. Microfluidic dose-response platform to track the dynamics of drug response in single mycobacterial cells. **Sci Rep.** (**2022**) 12(1):19578. DOI: 10.1038/s41598-022-24175-9. PMID: 36379978.

Griego A, Douché T, Gianetto QG, Matondo M, †Manina G. RNase E and HupB dynamics foster mycobacterial cell homeostasis and fitness. **iScience.** (**2022**) 25(5):104233. DOI: 10.1016/j.isci.2022.104233. PMID: 35521527.

†*Manina G, Dhar N. Single-Cell Analysis of Mycobacteria Using Microfluidics and Time-Lapse Microscopy. **Methods Mol Biol.** (**2021**) 2314:205-229. DOI: 10.1007/978-1-0716-1460-0_8. PMID: 34235654.

†*Manina G, Griego A, Singh LK, McKinney JD, Dhar N. Preexisting variation in DNA damage response predicts the fate of single mycobacteria under stress. **EMBO J.** (**2019**) 38(22):e101876. DOI: 10.15252/embj.2019101876. Epub 2019 Oct 4. PMID: 31583725.

Manina G and Mistretta M. Multiplexable microfluidic culture chamber for imaging monolayer growth of single cells, published on **19.11.2020**. Patent number EP3969174; US20220195486 (https://patentscope.wipo.int/search/en/detail.jsf?docId=WO2020229629&tab=PCTBIBLIO).

Scientific or technical background required for work program

The ideal candidate should have experience in one or more of the following areas: genetics, microbiology, cell biology, or microfluidics. Knowledge of sterile laboratory techniques is required, and skills in bioinformatics applied to image analysis and statistics would be an advantage. The student must also have a good command of both written and spoken English, work well in a team, and demonstrate scientific curiosity and dedication to research.

Institut Pasteur, 2025-2026

Title of the work program 24

Unveiling the mechanisms for Poxviruses entry and neutralization

Description of the work program

We study Poxviruses, a family of DNA viruses that includes human pathogens such as Variola virus (VARV), the causative agent of smallpox, and monkeypox (MPXV), responsible for several outbreaks in last years. Smallpox has been one among the deadliest contagious disease worldwide, having caused millions of deaths before his eradication, achieved thanks a huge vaccination campaign. The virus was considered eradicated in 1980 with consequent termination of the vaccination program, leaving generations of individuals susceptible to infection. MPXV is a zoonotic disease, with clinical symptoms similar to VARV. In 2022 and 2024 it has been declared by the World Health Organization (WHO) as a Public Health Emergency of International Concern. The fear that VARV could be used as a biological weapon along with the increasing MPVX outbreaks, have stimulated active research on safe and efficient new generation vaccines.

Poxviruses are very large viruses comprising more than 200 proteins. This complexity is mirrored by an intricate life cycle with two distinct antigenic forms, the mature virion (MV) and the enveloped virus (EV). The two forms show distinctive surface proteins and functions, the first having a pivotal role in inter-individual and the latter in intra-individual dissemination. On the MV there is a complex of 11 proteins (entry fusion complex, EFC) which mediates fusion of the viral membrane with the target cell membrane. Although the components of the EFC have been identified, their individual role in viral fusion and cell entry has not been completely elucidated. Furthermore, the importance of a strong antibody response in protection has been put in evidence by several experimental observations. In our unit, we use Vaccinia virus (VACV) as a model system to study virus biology and entry and identify potential targets for new generation vaccines. We combine cell biology and structural approaches to identify viral envelope regions that could be the targets for the development of antiviral treatments.

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Selected publications or patents of the Research Group offering the work program

Structural basis of poxvirus fusion regulation and anti-A16/G9 antibody-mediated neutralization and protection.
Meola et al, Cell, 2025 DOI: 10.1016/j.cell.2025.07.040

Mechanisms of tecovirimat antiviral activity and poxvirus resistance.
Vernuccio R et al, Nat Microbiol, 2024 DOI: 10.1038/s41564-025-01936-6

MPXV Infection stimulates a more robust and durable neutralizing antibody response compared to MVA-BN vaccination.
Selverian CN et al, J Infec Dis, 2024. PMID: **39422181** DOI: 10.1093/infdis/jiae515

Institut Pasteur, 2025-2026

Production and Purification of Hantavirus Glycoproteins in Drosophila melanogaster S2 cells.
Meola A et al., Methods Mol Biol, 2024 DOI: 10.1007/978-1-0716-3666-4_1

Scientific or technical background required for work program

To join us, we require basic expertise in cell handling and protein purification. The ability to analyze proteins by SDS-PAGE and Western Blot would be very appreciated. Knowledge of Biolayer Interferometry (BLI) would be a plus. Skills in either X-ray crystallography or cryo-EM will be acquired on site according to the project evolution.

Institut Pasteur, 2025-2026

Title of the work program 25

Insight into the unique biology and ecology of a human gut methanogenic archaeon

Description of the work program

The Archaea are largely known as microorganisms thriving in extreme environments but are in fact ubiquitously found in nature. Importantly, archaeal methanogens are also stable members of the human gastrointestinal tract. *Methanomassiliicoccales* is one of the two main lineages of methanogens in the human gut and one of the most recently discovered order of methanogens. Only two species of this order were isolated, *Methanomethylophilus alvi* being the only one that specialized to live in the gut environment. *Methanomassiliicoccales* are strict anaerobes, having the capacity to use several energetic substrates among which trimethylamine (TMA).Trimethylamine is a bacterial metabolite involved in the development of cardiovascular diseases and its depletion by *Methanomassiliicoccales* might be protective for human health. However, our current knowledge about the cell biology and ecology of *Methanomassiliicoccales* is very limited. Preliminary microscopic observations of these cells have revealed unusual features including dynamic cell morphologies ranging from cocci to pleiomorphic shapes with membrane protrusions. Correlation networks have also revealed co-abundance pattern between *Methanomassiliicoccales* and syntrophic bacteria. This project aims to explore how *Methanomassiliicoccales* interact with syntrophic bacteria (e.g TMA producers), both metabolically and physically, with a focus on the role and determinants of *M. alvi* atypical cellular shapes.

In the first part of the internship, the *M. alvi*, will be grown in monoculture with different nutrients, energetic stress and physicochemical conditions. Modifications of the cell shape will be determined by light microscopy and cryo-electronic microscopy. Next, modification of *M. alvi* cell shape during co-culture with syntropohic bacteria will be assessed. The best selective conditions for different shapes will be identified, changes in the protein composition of the cell envelope of the different phenotypes and modification of metabolic pathways will be explored using proteomics and transcriptomic, respectively.

In the second part of the internship, live imaging of *M. alvi* will be developed to study the dynamics of cell shape modification and cell division under different conditions. This will involve the utilisation of specific anaerobic device in Pasteur and cutting-edge microfluidics approach at ICMCB (CNRS-Université de Bordeaux). Particular attention will be given to the dynamics of formation of the extrusions and other unusual and unique cell phenotypes as well as cell division using fluorescent dyes. Live-imaging will help to determine whether membrane extrusions are stimulated by bacteria and potentially involved in interspecies exchanges. Live-imaging experiments, using real anoxic conditions inside microfluidic devices, will be carried out at ICMCB (CNRS-Université de Bordeaux), in collaboration with Anaïs Cario during two months of the internship.

Tutor/supervisor

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Institut Pasteur, 2025-2026

Selected publications or patents of the Research Group offering the work program

1. Baquero DP, **Borrel G**, Gazi A, Martin-Gallausiaux C, (…) Gribaldo S, Krupovic M. Biogenesis of DNA-carrying extracellular vesicles by the dominant human gut methanogenic archaeon. *Nature Communications*, 2025; 16:1. https://doi.org/10.1038/s41467-025-60272-9
2. **Borrel G**[#], Fadhlaoui K, (…) Brugère J-F. Methanomethylophilus alvi gen. nov., sp. nov., a Novel Hydrogenotrophic Methyl-Reducing Methanogenic Archaea of the Order Methanomassiliicoccales Isolated from the Human Gut and Proposal of the Novel Family Methanomethylophilaceae fam. nov. *Microorganisms*, 2023; 11:2794.
3. *Thomas CM*, Desmond-Le Quemener E, Gribaldo S, and **Borrel G**. Factors shaping the abundance and diversity of the gut archaeome across the animal kingdom. *Nature Communications*, 2022; 13:3358. https://doi.org/10.1038/s41467-022-31038-4
4. **Borrel G**, Brugère J-F, Gribaldo S, Schmitz RA, Moissl-Eichinger C. The host-associated archaeome. *Nature Review Microbiology*, 2020; 18:622–636. https://doi.org/10.1038/s41579-020-0407-y.

Scientific or technical background required for work program

A background in microbiology is required. Knowledge in microorganism cultivation (in particular anoxic conditions), microscopy and basic molecular biology would be appreciated.

Institut Pasteur, 2025-2026

Title of the work program 26

Mitochondrial Metabolism and Inflammation in a Synucleinopathic Neuroimmune Axis

Description of the work program

Parkinson's disease (PD) is a neurodegenerative disease that kills dopaminergic neurons, with α-synuclein (α-syn) aggregates perturbing neuronal degradative pathways and damaging mitochondrial functions, leading to neuroinflammation. Our lab has demonstrated that α-syn and mitochondria can be transferred between microglia and α-syn-burdened neurons via tunneling nanotubes (TNTs) to aid in clearance. CD4+ T cells also play a significant role in the initial inflammatory response to α-syn-laden neurons; however, their functional properties diminish over time in PD patients. Here, we seek to elucidate the effects of α-syn on the neuronal-microglia-CD4+ T cell network, specifically on mitochondrial metabolism and inflammatory responses. We found that α-syn can be internalized in Jurkat (CD4+ T) cells and colocalize with lysosomes after 9 hours. When re-exposed to α-syn and subsequently co-cultured with SH-SY5Y cells, Jurkat cells display enlarged, circular mitochondria that localize more towards the immunological synapse. The cellular body extends towards the neuronal cells and the TNT number per cell increases; however, additional exposures to α-syn reduces these, suggesting possible exhaustion. With repeated exposures, Th1 lineage and exhaustion markers increase, as has been shown in circulatory CD4+ T cells in PD patients. When tri-cultured with SH-SY5Y and HMC cells, Jurkat cells preferentially form TNTs with SH-SY5Y cells, with mitochondria found in several TNT-like connections only in the presence of HMC cells. These preliminary data suggest that upon α-syn presentation, CD4+ T cells become activated, undergo mitochondrial reprogramming, and provide mitochondria to α-syn-laden neuronal cells. However, CD4+ T cells seem to become exhausted with continued exposure to α-syn. Mitochondrial metabolism and inflammatory responses will be further investigated to determine factors driving CD4+ T cells towards exhaustion in PD. Tri-culture systems will be utilized along with FACS and flow cytometry to analyze the expression of activation/exhaustion and Th-subtype markers as well as Seahorse to characterize the metabolic profiles of each cell type. In this way, we aim to understand how metabolic reprogramming and inflammatory cascades are affected by a synucleinopathic environment between neuronal, microglial, and CD4+ T cells.

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Institut Pasteur, 2025-2026

Selected publications or patents of the Research Group offering the work program

Chakraborty R, Nonaka, T, Hasegawa, M, and Zurzolo, C, *Tunnelling nanotubes between neuronal and microglial cells allow bi-directional transfer of alpha-Synuclein and mitochondria.* Cell Death Dis, 2023. **14**(5): p. 329. 10.1038/s41419-023-05835-8. https://www.ncbi.nlm.nih.gov/pubmed/37202391

Chakraborty R, Maya S, Testa V, Montero-Munoz J, Nonaka, T, Hasegawa, M, Consiglio A, and Zurzolo, C, α-Synuclein aggregates induce mitochondrial damage and trigger innate immunity to drive neuron–microglia communication. bioRxiv, **doi:** https://doi.org/10.1101/2025.06.23.661105

Dilsizoglu Senol A, Samarani, M, Syan, S, Guardia, CM, Nonaka, T, Liv, N, Latour-Lambert, P, Hasegawa, M, Klumperman, J, Bonifacino, JS, and Zurzolo, C, *alpha-Synuclein fibrils subvert lysosome structure and function for the propagation of protein misfolding between cells through tunneling nanotubes.* PLoS Biol, 2021. **19**(7): p. e3001287. 10.1371/journal.pbio.3001287. https://www.ncbi.nlm.nih.gov/pubmed/34283825

Scientific or technical background required for work program

Proficiency in cell culture work, RNA extraction, RT-qPCR, and confocal imaging.

Institut Pasteur, 2025-2026

Title of the work program 27

Dynamics of transcription and DNA motion at pluripotency genes using live imaging.

Description of the work program

In spite of intense investigations, it remains unclear whether and how the interaction between promoters and distant enhancers has a role in transcription. Until recently, this problem has been mainly addressed using techniques relying on cell fixation and DNA Next Generation Sequencing. Thanks to recent development of imaging technologies, it has become possible to observe the motion of DNA sequences and the production of mRNA molecules at a gene locus in live cells. In the 6-months of stay in the lab, the student will contribute to the production and analysis of a mouse embryonic stem cell line whose genome is engineered in such a way that both the transcription and the location of enhancer and promoter of a specific pluripotency gene can be observed and monitored in space and time, using **advanced fluorescence microscopy**. **Cell line engineering** will consist in the insertion of exogenous repetitive arrays at the endogenous gene locus using CRISPR-Cas9, followed by the random insertion of the fluorescent reporter which is able to bind those sequences. The two steps will require cloning of the construct to be inserted, as well as the optimization via different rounds of transfection and microscopic assessment. The aim is a **quantitative measurement of DNA motion and transcription**. The quantitative aim has specific requirements, whose understanding will be an important component of the traineeship.
If the engineered cell line will already be ready (this will depend on the time of joining the lab), there are other two possible projects for the student, equally important for the development of the big project:

i. The student will induce molecular perturbations (such as the elimination of transcription factors or chromatin modification) to understand the molecular players of transcriptional regulation at the gene locus (enhancer communication versus other mechanisms)
ii. As a complementary approach to live-imaging, the student will implement a single molecule RNA FISH approach to monitor transcriptional dynamics.

The student will be directly supervised and work together with Sara Formichetti, a postdoc in the Unit for the Physics of Biological Function, directed by Thomas Gregor at Institut Pasteur in Paris (France). Sara will teach the student all the necessary techniques and guide her/him through all challenges encountered.

The candidate will be immersed in a highly interdisciplinary team, composed of biologists, physicists, engineers, and computer scientists. All have the same mission of a quantitative understanding of gene expression during development. The student will be encouraged to participate in discussions with all lab members. He/she will also be immersed in the lively and highly international environment of Institut Pasteur. According to project progress, there could be the possibility of an extension in case of mutual agreement.

Tutor/supervisor

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Institut Pasteur, 2025-2026

Selected publications or patents of the Research Group offering the work program

Chen, H. et al. Dynamic interplay between enhancer-promoter topology and gene activity. Nat. Genet. 50, 1296–1303 (2018).

Scientific or technical background required for work program

Scientific:

- cellular biology
- molecular biology of transcription and chromatin in eukaryotes i.e. the transcription and mRNA cycle, the regulation of gene expression by non-coding regulatory sequences.

Technical:

- Experience with mammalian cell culture.
- Experience with standard molecular biology techniques: PCR, qPCR, cloning.

Motivation to work on a project that could involve a lot of cell culture as well as technical troubleshooting.
Motivation to learn the biophysical approach to molecular biology and challenge her/himself with new advanced techniques, including single molecule microscopy.

The candidate will go through a VC interview to assess further his/her motivation and background.

Institut Pasteur, 2025-2026

Title of the work program 28

Development of multistage mRNA vaccines for Plasmodium falciparum malaria

Description of the work program

There is a need to develop malaria vaccines with high efficacy. We propose to develop a multivalent mRNA vaccine for P. falciparum malaria based on the pre-erythrocytic antigen, PfCSP, and the essential blood stage invasion ligand, PfRH5, which will together target both sporozoites and blood stages. Targeting parasites at both the pre-erythrocytic and blood stages is likely to provide synergy leading to high efficacy.

The goal of developing an effective multi-stage vaccine against P. falciparum malaria will be accomplished by achieving the following specific objectives:

1.) **Evaluate the immunogenicity and efficacy of PfCSP mRNA constructs in mice and identify optimal constructs for further development:** mRNA constructs encoding truncated and full-length PfCSP will be fused to HBsAg to produce VLPs that display PfCSP epitopes on the surface. mRNAs formulated in lipid nanoparticles (LNPs) will be used to immunize C57BL/6 and Balb/c mice. Sera from immunized mice will be tested for recognition of recombinant PfCSP by ELISA and native PfCSP on sporozoites by immunofluorescence assay (IFA). Immunised mice will be challenged with Pb-PfCSP sporozoites to evaluate efficacy. PfCSP constructs that yield high efficacy in the mouse model will be selected for further development. Immune responses to PfCSP-mRNA constructs will be evaluated by testing antibodies from mice for recognition of PfCSP by ELISA and immunofluorescence assay. IgG isotypes will be determined and antibodies will be tested in functional cytotoxicity assays with transgenic Pb-PfCSP sporozoites.

2.) **Evaluate immunogenicity of PfRH5 mRNA constructs in mice and identify an optimal construct that elicits efficient growth inhibition:** LNP formulations of mRNA constructs designed to express PfRH5 fused to ferritin to produce NPs or expressed on mammalian cell surface by fusion with SS and TMD from influenza virus hemagglutinin at the N- and C-terminus will be used to immunize mice. Sera will be tested for recognition of PfRH5 by ELISA and IFA with P. falciparum blood stages. Anti-PfRH5 sera will also be tested for inhibition of PfRH5-Basigin binding and *P. falciparum* growth *in vitro.* Constructs that are immunogenic and yield optimal growth inhibition will be selected for further development.

Tutor/supervisor

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Institut Pasteur, 2025-2026

Selected publications or patents of the Research Group offering the work program

1. Martinez FJ, White M, Guillotte-Blisnick M, Huon C, Boucharlat A, Agou F, England P, Popovici J, Hou MM, Silk SE, Barrett JR, Nielsen CM, Reimer JM, Mukherjee P, Chauhan VS, Minassian AM, Draper SJ, **Chitnis CE. 2024.** PvDBPII elicits multiple antibody-mediated mechanisms that reduce growth in a Plasmodium vivax challenge trial. NPJ Vaccines. 9(1):10.
2. Hou M, Barrett J, Themistocleous Y, Rawlinson TA, Diouf A, Martinez FJ, Nielsen CM, Lias AM, King LDW, Kingham L, Poulton ID, Khozoee B, Goh C, Hodgson S, Mac Lochlainn DJ, Salkeld J, Guilotte-Blisnick M, Huon C, Mohring F, Reimer JM, Chauhan VS, Mukherjee P, Biswas S, Taylor IJ, Lawrie AM, Cho JS, Nugent FL, Long CA, Moon RW, Miura K, Silk SE, **Chitnis CE***, Minassian AM*, Draper SJ*. 2023. Vaccination with *Plasmodium vivax* Duffy-binding protein inhibits parasite growth during Controlled Human Malaria Infection. **Sc. Trans. Med**. 15(704):eadf1782. *Corresponding authors.
3. Wagner MP, Formaglio P, Gorgette O, Dziekan JM, Huon C, Berneburg I, Rahlfs S, Barale JC, Feinstein SI, Fisher AB, Ménard D, Bozdech Z, Amino R, Touqui L, **Chitnis CE.** 2022. Human peroxiredoxin 6 is essential for malaria parasites and provides a host-based drug target. **Cell Reports.** 39(11):110923.
4. More KR, Kaur I, Giai Gianetto Q, Invergo BM, Chaze T, Jain R, Huon C, Gutenbrunner P, Weisser H, Matondo M, Choudhary JS, Langsley G, Singh S, **Chitnis CE**. 2020. Phosphorylation-Dependent Assembly of a 14-3-3 Mediated Signaling Complex during Red Blood Cell Invasion by Plasmodium falciparum Merozoites. **mBio.** 11(4):e01287-20.
5. Singh P, Alaganan A, More KR, Lorthiois A, Thiberge S, Gorgette O, Guillotte Blisnick M, Guglielmini J, Aguilera SS, Touqui L, Singh S, **Chitnis CE**. 2019. Role of a patatin-like phospholipase in *Plasmodium falciparum* gametogenesis and malaria transmission. **Proc Natl Acad Sci (USA)**. 116(35):17498-17508.

Scientific or technical background required for work program

The candidate should have strong theoretical knowledge in one or more of the following areas of modern biology: molecular biology, microbiology, biochemistry, immunology. The candidate should have some laboratory experience in life sciences. Most importantly, the candidate should be motivated to learn and be passionate about research in his/her chosen field.

Institut Pasteur, 2025-2026

Title of the work program 29

Developing a novel measles-based vaccine platform, resistant to measles preimmunity and amenable to intranasal delivery.

Description of the work program

The large global burden of viral infections and especially the COVID-19 pandemic shows the need for new approaches in vaccine development. Plug-and-play vaccine platform technology that would enable fast development of a vaccine candidate against an emerging pathogen, large-scale immunization of pediatric and adult populations and induction of mucosal responses in the respiratory tract, is a grail.

The measles vector (MV) platform technology derived from the safe and highly efficacious live-attenuated measles virus vaccine has long held promise as a universal vaccine platform. However, our phase I clinical study of the V591 measles-vectored COVID-19 vaccine candidate expressing a prefusion stabilized full-length spike protein, revealed a significant impact of pre-existing anti-measles immunity* on the response to V591, leading to discontinuation of further development (Launay, 2022) and highlighting the caveat of the original MV platform.

The Erasmus+ student will contribute to explore some of the possible modifications to the measles vector to enable it to escape pre-existing immunity and be delivered by the respiratory route.

This work will involve engineering and characterization of new vectors, both *in vitro* and in animal models. It will rely on a diversity of techniques, from molecular and cellular virology to immunology.

* (induced by previous exposure to the pediatric measles vaccine)

Tutor/supervisor

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Selected publications or patents of the Research Group offering the work program

- Ku et al. intranasal vaccination with a lentiviral vector protects against sars-cov-2 in preclinical animal models. *Cell Host & Microbe*, 2021, Feb 10;29(2):236-249.E6.
- Gransagne et al. Development of a highly specific and sensitive VHH-based sandwich immunoassay for the detection of the SARS-CoV-2 nucleoprotein. *Journal of Biological Chemistry*, 2022, 298 (1), pp.101290.
- Launay et al. Safety and Immunogenicity of a measles-vectored Sars-Cov-2 vaccine candidate, V591 / TMV-083, in healthy adults: results of a randomized, placebo-controlled Phase I study. *Ebiomedicine*, 2022, Jan;75:103810.
- Brunet et al. A measles vectored vaccine candidate expressing prefusion stabilized SARS-CoV-2 spike protein brought to Phase I/II clinical trials: Candidate selection in a preclinical murine model. *J Virol, 2024,* 14;98(5):e0169323.
- Nambulli et al. A measles vectored vaccine candidate expressing prefusion stabilized SARS-CoV-2 spike protein brought to Phase I/II clinical trials: Protection of African green monkeys from COVID-19 disease. J. Virol, 2024, 14;98(5):e0176223.

Scientific or technical background required for work program

Hands-on experience with virology techniques, protein western blotting, immunofluorescence would be an asset. Training to work in BSL3 will be provided for students able to stay more than 6 months.

Institut Pasteur, 2025-2026

Title of the work program 30

IL-23 signalling in human immune cells - physiological role and pathological consequences

Description of the work program

IL-23 receptor (IL-23R) polymorphisms are associated with chronic inflammatory diseases (CID) such as psoriasis, spondyloarthritis (SpA) and Crohn's disease. In parallel, evidence from Il23/Il23r-deficient mice uncovered the importance of IL-23 in the pathogenesis of CID. These findings led to the development and clinical success of IL-23 blockers.

More recent studies have pointed to crucial roles of innate-like immune cells expressing the IL-23R in the pathogenesis of CID. Systemic expression of IL-23 induced enthesitis in a mouse model by acting on a CD3+CD4-CD8-RORγt+ resident T cell population (Sherlock et al, Nat. Med., 2012). In humans, RORγt+ subsets of $\gamma\delta$-T cells and invariant Natural Killer T cells (iNKT) were identified in the inflamed joints of spondyloarthritis (SpA) patients (Venken et al, Nat. Commun., 2021). Also, Mucosal-associated invariant T (MAIT) cells have been found to express the highest levels of *IL23R* transcripts and display a competent IL-17 response in synovial fluid from SpA patients (Rosine et al, Arthritis Rheumatol., 2019).
Latest findings from our lab demonstrated that IL-23 stimulation of human MAIT cells enhanced their inflammatory functions by upregulating the expression of MHC-II genes and the AP-1 family of transcription factors (Camard et al, iScience, 2025).

However, little is known about whether IL-23 targets are shared across different human cell types. Thus, in this work, we aim to better understand the role of IL-23 in iNKT cells, another known IL-23R-responsive population.

Overall, the aim of the project is to define the effects of IL-23 on immune cell functions in human to better understand its role in the pathogenesis of chronic inflammatory diseases. In particular, the Erasmus+ student will assess the effects of IL-23 on innate-like T cells: MAIT and iNKT.

Tutor/supervisor

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Selected publications or patents of the Research Group offering the work program

Camard L, Stephen T, Yahia-Cherbal H, Guillemot V, Mella S, Baillet V, Lopez-Maestre H, Capocefalo D, Cantini L, Leloup C, Marsande J, Garro K, Sienes Bailo J, Dangien A, Pietrosemoli N, Hasan M, Wang H, Eckle SBG, Fourie AM, Greving C, Joyce-Shaikh B, Parker R, Cua DJ, Bianchi E, Rogge L, IL-23 tunes

inflammatory functions of human mucosal-associated invariant T cells., iScience 2025 Feb; 28(2): 111898.

Rosine N, Rowe H, Koturan S, Yahia-Cherbal H, Leloup C, Watad A, Berenbaum F, Sellam J, Dougados M, Aimanianda V, Cuthbert R, Bridgewood C, Newton D, Bianchi E, Rogge L, McGonagle D, Miceli-Richard C, , Characterization of Blood Mucosal Associated Invariant T (MAIT) cells in Axial Spondyloarthritis and of resident MAITs from control axial enthesis., Arthritis Rheumatol 2022 Feb; ():

Scientific or technical background required for work program

We are looking for a highly motivated student with a solid knowledge of immunology. Previous experience in cell culture, flow cytometry and molecular biology techniques such as western blots would be very helpful but is not mandatory.

The student will be hosted in a multidisciplinary lab, where they will receive training in fundamental immunological methods routinely applied in the field.

Institut Pasteur, 2025-2026

Title of the work program 31

How behavioural responses to emerging pathogens drive epidemic risk: a data-driven infectious disease modelling study

Description of the work program

Overview: This project seeks to integrate data from a human behaviour survey into an infectious disease transmission model to predict how human behaviour influences which pathogen phenotypes lead to greatest epidemic risk. This modelling project is best suited to graduate students working in epidemiology, applied mathematics, economics, ecology or a related quantitative field.

Background: Infectious disease dynamics are shaped by how individuals choose to modify their behaviour, or not, when faced with epidemic risk. For respiratory pathogens, behaviours such as social distancing and face mask wearing not only modify one's own risk of infection, but also influence patterns of transmission throughout populations. In epidemic contexts, there is strong evidence of a positive relationship between disease severity and one's propensity to adopt transmission prevention behaviours. This finding suggests that emerging pathogens of intermediate virulence may pose the greatest epidemic risk, consistent with longstanding ecological theory. However, the relationship between pathogen severity and epidemic risk remains poorly quantified, due in large part to a lack of data regarding how individuals modify their behaviour in response to different kinds of infectious diseases.

Project: The starting point for this project is a discrete choice experiment conducted in the UK, in which a nationally representative sample of adults were surveyed about their willingness to wear facemasks and practice social distancing during the next respiratory virus pandemic. The successful candidate will use these data to develop and parameterise an infectious disease transmission model describing the first wave of a hypothetical "Disease-X" pandemic. Epidemic simulations will be conducted, accounting for heterogeneity in the epidemiological characteristics of Disease-X, and incorporating feedback loops created by human behavioural responses to the emerging outbreak. This modelling framework will allow for data-driven prediction of which pathogen phenotypes could lead to greatest transmission risk and disease burden during the next pandemic.

Learning opportunities: This project is an opportunity to develop quantitative modelling skills in the context of a research project with clear public health utility. The candidate will have the opportunity to work with diverse datasets, including behavioural data, demographic data and epidemiological data. Creative thinking will be required to integrate these datasets into a transmission dynamic modelling framework. There will be opportunities for collaboration with leading researchers within and beyond Institut Pasteur.

Lab environment: Institut Pasteur is a global centre of excellence in infectious disease research. This projects sits within the Epidemiology and Modelling of Antibacterial Evasion (EMAE) team – a diverse group of epidemiologists, modellers and clinicians working on various topics in infectious diseases and global health – and will be conducted in collaboration with researchers at the University of Oxford. Located in central Paris, Institut Pasteur is a thriving environment for young and early-career researchers, offering high-quality IT infrastructure, comfortable office space, flexible work-from-home arrangements and an active social network of graduate students and post-docs.

Erasmus+

Institut Pasteur, 2025-2026

Tutor/supervisor

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Selected publications or patents of the Research Group offering the work program

Selected publications:

- Smith DRM et al. Health and economic impacts of Lassa vaccination campaigns in West Africa. *Nature Medicine* 2024; DOI: 10.1038/s41591-024-03232-y.
- Smith DRM et al. Collateral impacts of pandemic COVID-19 drive the nosocomial spread of antibiotic resistance: a modelling study. *PLOS Medicine* 2023; 20:e1004240.
- Smith DRM et al. Rapid antigen testing as a reactive response to surges in nosocomial SARS-CoV-2 outbreak risk. *Nature Communications* 2022; 13:1-10.
- Smith DRM et al. Microbiome-pathogen interactions drive epidemiological dynamics of antibiotic resistance: a modelling study applied to nosocomial pathogen control. *eLife* 2021; 10:e68764.

Scientific or technical background required for work program

Required:

- Statistical or mathematical modelling experience
- Coding proficiency (e.g. R, Python, C++)
- English proficiency

Preferred:

- Background knowledge in infectious disease epidemiology
- Dynamic modelling experience (e.g. differential equations, individual-based models)

Institut Pasteur, 2025-2026

Title of the work program 32

Role of macrophages and IL23 in chronic inflammatory diseases

Description of the work program

Chronic inflammatory diseases (CIDs) are clinically heterogeneous conditions arising from aberrant immune responses and sharing common inflammatory pathways. Genome-wide association studies in humans and mouse models of autoimmune disease demonstrated that interleukin-23 (IL-23) dependent signaling plays a key role in the pathogenesis of CIDs such as psoriasis, psoriatic arthritis, axial spondyloarthritis and Crohn's disease.

Multiple types of adaptive immune cells are target of IL23 and may play a role in CID pathogenesis, including $CD4^+$ T cells and innate-like lymphocytes, such as MAIT and iNKT, express IL-23 receptor (IL-23R) and produce IL-17 upon IL-23 stimulation. Among innate lymphoid cells, ILC3 express high levels of IL23R on their surface. Macrophages can also play a role in CID pathogenesis and modulation. These cells are abundant in inflammation sites in psoriasis or arthritis and are a major source of IL-23. However, it is currently unclear whether human macrophage express IL-23R and whether they respond to IL-23 stimulation.

To address the role of macrophages and their potential regulation by IL-23, human macrophages subsets generated ex-vivo from peripheral blood monocytes, or primary macrophages isolated from synovial fluid will be analyzed.
The following points will be investigated:

1. Expression of IL23R by different macrophage subtypes at RNA and protein level.
2. Effect of IL-23 stimulation on macrophage subsets. We will analyze variation of the transcriptome by RNA-seq and/or secretion of specific cytokines/chemokines, with or without IL-23 stimulation.
3. Phenotypic analysis of monocyte-macrophage subsets in synovial fluids from psoriatic arthritis patients and analysis of the expression of IL23R by these cells.

These studies are expected to improve our knowledge on molecular and cellular mechanisms underlying CID pathogenesis and possibly provide new targets for diagnosis and/or therapy.

Tutor/supervisor

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Selected publications or patents of the Research Group offering the work program

1. Bianchi, E., and L. Rogge. 2019. The IL-23/IL-17 pathway in human chronic inflammatory diseases—new insight from genetics and targeted therapies. Genes Immun. 20: 415–425.

2. Rosine, N., H. Rowe, S. Koturan, H. Yahia-Cherbal, C. Leloup, A. Watad, F. Berenbaum, J. Sellam, M. Dougados, V. Aimanianda, R. Cuthbert, C. Bridgewood, D. Newton, E. Bianchi, L. Rogge, D. McGonagle, and C. Miceli-Richard. 2022. Characterization of Blood Mucosal-

Associated Invariant T Cells in Patients With Axial Spondyloarthritis and of Resident Mucosal-Associated Invariant T Cells From the Axial Entheses of Non-Axial Spondyloarthritis Control Patients. Arthritis Rheumatol. 74: 1786–1795.

3. Mezghiche, I., H. Yahia-Cherbal, L. Rogge, and E. Bianchi. 2024. Interleukin 23 receptor: Expression and regulation in immune cells. Eur. J. Immunol. 54: 2250348.

4. Camard, L., T. Stephen, H. Yahia-Cherbal, V. Guillemot, S. Mella, V. Baillet, H. Lopez-Maestre, D. Capocefalo, L. Cantini, C. Leloup, J. Marsande, K. Garro, J. Sienes Bailo, A. Dangien, N. Pietrosemoli, M. Hasan, H. Wang, S. B. G. Eckle, A. M. Fourie, C. Greving, B. Joyce-Shaikh, R. Parker, D. J. Cua, E. Bianchi, and L. Rogge. 2025. IL-23 tunes inflammatory functions of human mucosal-associated invariant T cells. iScience 28: 111898.

Scientific or technical background required for work program

The ideal candidate is a biology student with some background in immunology. Previous experience with mammalian cell culture and flow cytometry is also welcome, as well as some knowledge in basic cell biology, biochemistry and/or molecular biology techniques (eg RTqPCR).

Institut Pasteur, 2025-2026

Title of the work program 33

Functional study of cellular factors and organelles hijacked by hepaciviruses upon hepatocyte infection

Description of the work program

Chronic hepatitis C is a human liver disease resulting frequently in metabolic disorders, such as steatosis, an abnormal lipid accumulation in hepatocytes. Lipid droplets, which are key subcellular organelles involved in the handling of lipids, as well as cellular lipoproteins are essential for hepatitis C virus (HCV) morphogenesis. Mechanistic aspects of the rewiring of hepatocyte organelles, factors and pathways by HCV, as well as their pathological consequences are not fully understood. We identified the interactomic network of HCV nonstructural protein 5A (NS5A) in infected hepatoma cells by mass spectrometry. We now investigate the functional role of selected hepatic factors linked to the biogenesis, degradation or function of lipid droplets and peroxisomes in the life cycle of HCV.
Depending on the time frame of the internship, the Erasmus+ student will either contribute to this study of selected HCV NS5A cellular interacting partners or establish fluorescent reporter cultured cell systems enabling live imaging of infection in order to study the dynamics of lipid droplet remodeling driven by HCV or a rat hepacivirus (RHV).

Tutor/supervisor

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Selected publications or patents of the Research Group offering the work program

- Brunet *, Choucha *, Gransagne * *et al.* A measles-vectored vaccine candidate expressing prefusion-stabilized SARS-CoV-2 spike protein brought to phase I/II clinical trials: candidate selection in a preclinical murine model. *J. Virol.*, 2024, May 14;98(5):e0169323. PMID: 38563763
- Nambulli *et al.* A measles-vectored vaccine candidate expressing prefusion-stabilized SARS-CoV-2 spike protein brought to phase I/II clinical trials: protection of African green monkeys from COVID-19 disease. *J. Virol.*, 2024, May 14;98(5):e0176223. PMID: 38563762
- Launay *et al.* Safety and immunogenicity of a measles-vectored SARS-CoV-2 vaccine candidate, V591 / Tmv-083, in healthy adults: Results of a randomized, placebo-controlled Phase I study. *Ebiomedicine*, 2022, Jan;75:103810. PMID: 35045362
- Lesage *et al.* Discovery of genes that modulate Flavivirus replication in an interferon-dependent manner. *J. Mol. Biol., 2022 Mar 30;434(6):167277. PMID: 34599939*
- Escriou *et al.*, Patent: Measles-vectored COVID-19 immunogenic compositions and vaccines. PCT/EP2021/053540 filed on February 12, 2021.
- Boukadida *et al.* NS2 proteases from hepatitis C virus and related hepaciviruses share composite active sites and previously unrecognized intrinsic proteolytic activities. *PloS Pathog., 2018,* 14(2):E1006863. PMID: 29415072
- Aicher *et al.* Differential regulation of the Wnt/ß-catenin pathway by hepatitis C virus recombinants expressing core from various genotypes. *Sci. Rep., 2018,* Jul 25;8(1):11185. PMID: 30046100

Erasmus+

Institut Pasteur, 2025-2026

Scientific or technical background required for work program

Hands-on experience with molecular biology techniques, cell culture and/or fluorescent microscopy would be an asset.

Institut Pasteur, 2025-2026

Title of the work program 34

Shaping Stimulation for Hearing Implants

Description of the work program

Some people with severe deafness receive a medical device called a *cochlear implant* that recreates a sensation of sound by stimulating the hearing nerve with electrical currents. The processor of the implant executes a sound coding algorithm that performs the conversion of sound into a spatio-temporal sequence of electrical pulses, replacing the natural mechano-transduction of sound that occurs naturally in a healthy ear. Although the recovered experience of sound is life-changing for the recipient, the outcomes are far from restoring the equivalent of natural, healthy hearing. Part of the limitations might arise from an inaccurate representation of the sound for the hearing nerve, due to suboptimality of the sound coding algorithm or to the specific physiology and hearing pathology of the recipient. Our aim is to build, refine, and exploit models that predict the neural representation of cochlear implant stimulation, capturing both physical and physiological phenomena. In order to determine physiological model parameters, we will develop a new experimental technique to perform and analyse electrophysiological measurements from human implant recipients. By exploiting universal and personalized models, we will propose new principles and algorithms for sound coding that achieve a more useful and naturalistic neural representation, as well as strategies for fitting stimulation parameters to the physiology of individual recipients.

Tutor/supervisor

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Selected publications or patents of the Research Group offering the work program

Arzounian, D., Guérit, F., Deeks, J. M., Garcia, C., de Groote, E., Bance, M., & Carlyon, R. P. (2025). Measurement of phase-locked neural responses to cochlear-implant stimulation from multiple stages of the auditory system. Hearing Research, 109338. https://doi.org/10.1016/j.heares.2025.109338

Gaultier, C., & Goehring, T. (2024). Recovering speech intelligibility with deep learning and multiple microphones in noisy-reverberant situations for people using cochlear implants. The Journal of the Acoustical Society of America, 155(6), 3833–3847. https://doi.org/10.1121/10.0026218

Institut Pasteur, 2025-2026

Prof. Paul Avan, Center for Research and Innovation in Human Audiology, Real-time artificial intelligence-based speech enhancement methods for hearing aid improvement: https://research.pasteur.fr/en/project/refined/

Scientific or technical background required for work program

The project may be suitable for a wide range of scientific profiles training in medicine, engineering, physics, computer science, mathematics, computational biology, neuroscience, or audiology. Specific project aims may be adapted to the profile and skills of the candidate. Programming skills will be essential in all cases.

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Institut Pasteur, 2025-2026

Title of the work program 35

Can’t hear it? Tune the network to the proper connectivity.

Description of the work program

Context

The auditory cortex (AC) plays a pivotal role in processing complex sounds [1,2]. Within the AC, distinct neuronal populations respond to sound patterns, converting spatio-temporal auditory information into population codes. Our lab combines advanced tools to simulate large biophysical networks and identify optimal parameter sets [3]. Preliminary findings suggest that short-term synaptic plasticity, recurrent connectivity, and dendritic memory each contribute uniquely to sound integration. However, a major limitation of biophysical networks is their lack of task-dependent, learned recurrent connectivity.

This challenge can be addressed using ad-hoc approaches that extend supervised training to spiking networks, such as surrogate gradient methods [4]. While these techniques are not yet widely adopted in neuroscience, they offer a promising path forward. This algorithm can be implemented in biophysically constrained networks that follow strict rules on the dynamics of cells and synapses. Although such networks may have lesser performance than more abstract ones in sound discrimination, they retain biological interpretability and support meaningful inferences on the actual cortical dynamics.

In this project, we leverage supervised learning in spiking neural networks to train biophysical networks for sound recognition. Our goal is to uncover which properties of recurrent connectivity are essential for sound discrimination.

References

[1] Bagur, S. et al. A spatial code for temporal information is necessary for efficient sensory learning. Science Advances 11, adr6214 (2025).
[2] Lamothe, C., Bagur, S., Gosselin, E. & Bathellier, B. Sound offset responses become highly informative in the auditory cortex. bioRxiv 10.1101/2025.05.19.654889 (2025).
[3] JuliaSNN Documentation
[4] Neftci, E. O., Mostafa, H. & Zenke, F. Surrogate Gradient Learning in Spiking Neural Networks: Bringing the Power of Gradient-Based Optimization to Spiking Neural Networks. IEEE Signal Processing Magazine 36, 51–63 (2019).

Plan of work

The student will work in Julia, a modern and efficient language for scientific computing. They will use JuliaSNN [4], a robust library for spiking neural network simulations, to implement a network model with surrogate gradient backpropagation. This will be achieved using Flux.jl, a fast and flexible machine learning library for Julia.
Once the network is established, the student will train it on a comprehensive dataset of single-unit recordings from the thalamus and compare the resulting network activity with voltage traces recorded in the auditory cortex.

The project will be supervised by Dr. Quaresima, the lead developer of JuliaSNN. Our lab has already acquired the thalamus and auditory cortex datasets, and our expertise covers the full scope of the project. Throughout this project, the student will gain hands-on experience running machine learning pipelines using a state-of-the-art library and implementing a cutting-edge algorithm (gradient descent) to tackle a key question in auditory neuroscience.

Erasmus+

Institut Pasteur, 2025-2026

Tutor/supervisor

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Selected publications or patents of the Research Group offering the work program

[1] Bagur, S. et al. A spatial code for temporal information is necessary for efficient sensory learning. Science Advances 11, adr6214 (2025).

[2] Lamothe, C., Bagur, S., Gosselin, E. & Bathellier, B. Sound offset responses become highly informative in the auditory cortex. 2025.05.19.654889 Preprint at 10.1101/2025.05.19.654889 (2025).

[3] https://juliasnn.github.io/SpikingNeuralNetworks

Scientific or technical background required for work program

The student must have excellent computational skills and a keen enthusiasm for biology. They must be willing to study autonomously to learn the Julia language and utilize the library.

Erasmus+

Institut Pasteur, 2025-2026

Temporal integration of complex sound patterns relies on recurrent activity and dendritic memory in biophysical networks optimized for sound discrimination

The auditory cortex (AC) is crucial for processing complex sounds [1-2]. Different neuronal populations in the AC activate in response to sound patterns, transforming spatio-temporal auditory information into population codes [3-4]. Theoretical research suggests that time-dependent neural processing requires memory integration on the input's timescale, supported by biophysical processes such as short-term synaptic plasticity, recurrent connectivity, and dendritic memory [5-8]. However, how they contribute to integrating complex sounds is unknown.

We address this question by probing thousands of network models with a high-throughput approach to parameter optimization. Networks are composed of 2500 excitatory and inhibitory cells, comprising fast-spiking and adapting interneurons, endowed with short/long-term synaptic plasticity. Excitatory and fast-spiking neurons receive real spike-trains recorded in mice's thalamus during passive listening of 88 distinct sounds. We compare networks with random, tonotopically organized, and purely feed-forward connections. For each arrangement, excitatory neurons feature either point neurons or three-compartment models with dendritic nonlinearity. Evidence-based objective functions guide the optimization of parameters; maximizing sound discrimination, minimizing the cross-entropy between the model's firing rates and AC recordings, and enforcing the spiking asynchronous-irregular regime.

Population activity following a sound presentation (offset activity) can be distinguished for 80% of the presented sounds. Networks with dendrites perform twice as well as point neurons in sound recognition during the offset response phase and exhibit a firing rate distribution more in line with recordings. Point neurons, on the other hand, achieve the task only when firing rates exceed 15 Hz and before stimulus offset. Recurrent connections also contribute to sound discrimination. Spatially organized networks outperform purely feedforward networks, while random connectivity decreases sound decodability. Early results suggest that synaptic plasticity contributes only marginally to sound recognition, whether in the short or long term. Facilitating recurrent synapses grants good recognition in a broad parameter set, although optimized non-plastic networks perform similarly. In conclusion, our results suggest that dendritic integration contributes to the maintenance of auditory information in the brain network over intermediate time scales.

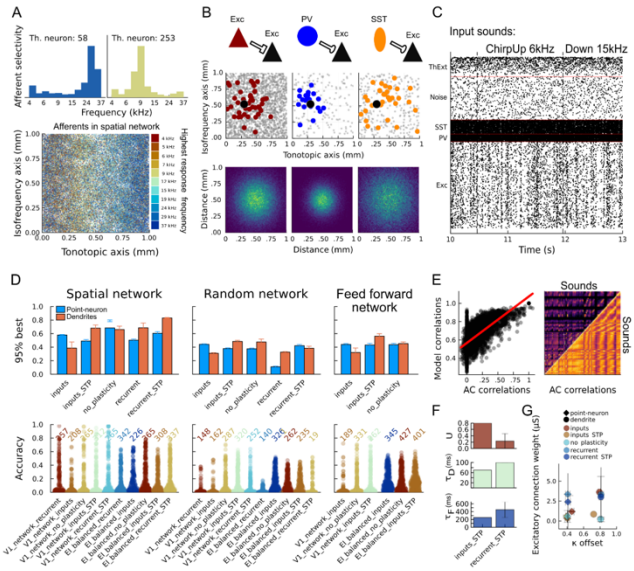


Figure 1: (A) Tonotopic structure of thalamic afferents; (B) Spatial recurrent connectivity; (C) Example of sound presentation and network activity; (D) Model comparison and task accuracy; (E) Model and AC representation similarity. Optimal parameters for short term plasticity (F) and recurrent weights (G).

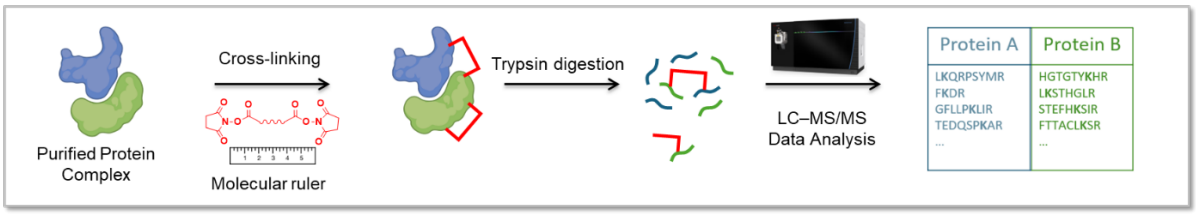
Institut Pasteur, 2025-2026

Title of the work program 36

Pushing the boundaries of cross-linking mass spectrometry to better understand virulence factor dynamics in *Neisseria meningitidis*

Description of the work program

Introduction. Protein interactions are essential for cellular function, serving as fundamental mechanisms by which organisms perform complex cellular tasks. These interactions occur through precise physical contacts that allow proteins to recognize, bind, and collaborate, ultimately forming sophisticated molecular networks. Understanding the nature and mechanisms of protein interactions is crucial for comprehending biological processes at the molecular level.
Cross-linking mass spectrometry (XL–MS) has emerged as an innovative and powerful technique for investigating protein–protein interactions. A small chemical linker serves to covalently link two interacting protein sites, preserving critical information about their spatial interaction. Advanced mass spectrometric analysis can then detect and interpret cross-linked peptides, providing detailed insights into the specific domains and regions involved in protein interactions.



Generic workflow to capture and detect protein–protein interactions by cross-linking mass spectrometry.

Our research is focused on studying the structure and dynamics of bacterial virulence factors with XL–MS. Bacteria utilize virulence factors to invade, damage, and evade host immune responses. *Neisseria meningitidis* is a gram-negative bacterium which causes invasive meningococcal disease in humans. Type IV pili—filamentous fibers extended into the extracellular space—are its main virulence factor. Type IV pili function as external attachment points for bacteria, enabling them to form microcolonies and to adhere to human cells. Pilus biogenesis in *Neisseria meningitidis* is a highly dynamic process relying on many interaction partners involved in pilus assembly, extrusion into the extracellular space, and pilus disassembly. The pilus fiber itself majorly consists of the protein PilE. Our research has thoroughly characterized the sequence and structure of the PilE protein both in isolated and fiber-assembled form. However, dynamic PilE protein interactions within the scope of pilus biogenesis remain incompletely understood. Overcoming this knowledge gap is vital to better understand its role in the context of infection.

Project Aim. The aim of your project is to push the boundaries of XL–MS to better understand PilE interactions in the scope of pilus biogenesis and *Neisseria* virulence.

Your project will include the following tasks, focusing both on analytical method development and biological application:

- Identification of novel interaction sites of the PilE protein
- Identification and mapping of PilE interaction sites along its filamentous assembly

- Dissection of pilus–pilus interactions in bacterial cell culture
- Translation and optimization of an analytical workflow (from sample preparation to bioinformatic data analysis) to identify PilE cross-links *in vitro* and in live cells (based on in-house workflows using our enrichable cross-linker NNP9)
- Testing and application of novel cross-linkers specifically designed to study pilus biogenesis

Investigating interactions of dynamic filamentous structures presents significant analytical challenges, and your research will focus developing novel XL–MS approaches making it possible to study those interactions. The primary objective is to uncover novel interaction sites of the PilE protein, providing crucial insights into pilus biogenesis mechanisms. To complete your ambitious tasks, you will greatly benefit from our developed XL–MS workflows to study bacterial virulence in *Neisseria meningitidis*. Cell culture and live cell experiments will be conducted in the laboratory of Guillaume Duménil (Pathogenesis of Vascular Infections), pioneers in understanding the fundamental biological processes in *Neisseria meningitidis* related to virulence. Our long-standing research collaboration has been remarkably productive, revealing a multitude of novel insights into the virulence mechanisms of *Neisseria meningitidis*.

Over the course of the project, you will be introduced to the entire workflow of XL–MS, ranging from biological sample preparation and cross-linking, over mass spectrometric sample preparation, instrumental analysis, and data analysis. By project completion, you will have developed a versatile, interdisciplinary skill set that seamlessly integrates analytical chemistry and chemical biology, positioning you advantageously for future scientific endeavors.

Who are we?
Our research unit at Institut Pasteur, led by Julia Chamot-Rooke, is a close-knit team with a welcoming and familiar environment. Our team comprises a diverse mix of international students, postdoctoral researchers, and permanent staff. Our scientific mission focuses on the development of state-of-the-art analytical methods in our primary fields of interest, top-down mass spectrometry and cross-linking mass spectrometry. Situated within the rich scientific ecosystem of Institut Pasteur, we offer a tight intersection between fundamental research and technology. Our research network also extends beyond the institute, encompassing diverse fields such as synthetic chemistry and advanced bioinformatics. To pursue our mission, we are equipped with state-of-the-art mass spectrometers, including the Orbitrap Astral or the timsTOF Ultra 2.

Located in the heart of Paris, the institute offers:

- Easy access to a vibrant urban landscape, with numerous cafes, bars, and restaurants; just steps away from the campus
- Easy accessibility of the campus by public transportation and by bike
- Numerous training courses to further develop your skills and explore other fields and techniques
- Weekly seminars with invited speakers coming from all over the world
- A lively student community that organizes regular get together and social events for you to connect and to have fun
- A multitude of non-scientific activities like sport groups or a music lab, among others
- Administrative assistance and assistance for housing (special offers for students)

Please join us to develop the mass spectrometric techniques of the future!

Erasmus+

Institut Pasteur, 2025-2026

Tutor/supervisor

Project Supervisor:

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☒ I authorise the IP Erasmus+ team to publish the project proposal on the pasteur.fr website

Selected publications or patents of the Research Group offering the work program

[1] Nouchikian, L., Fernandez-Martinez, D., Renard, P.-Y., Sabot, C., Duménil, G., Rey, M., & Chamot-Rooke, J. (2024). Do Not Waste Time–Ensure Success in Your Cross-Linking Mass Spectrometry Experiments before You Begin. *Analytical Chemistry*, 96(6), 2506–2513.

[2] Rey, M., Dhenin, J., Kong, Y., Nouchikian, L., Filella, I., Duchateau, M., Dupré, M., Pellarin, R., Duménil, G., & Chamot-Rooke, J. (2021). Advanced in Vivo Cross-Linking Mass Spectrometry Platform to Characterize Proteome-Wide Protein Interactions. *Analytical Chemistry*, *93*(9), 4166–4174.

[3] Nury, C., Redeker, V., Dautrey, S., Romieu, A., van der Rest, G., Renard, P. Y., Melki, R., & Chamot-Rooke, J. (2015). A novel bio-orthogonal cross-linker for improved protein/protein interaction analysis. *Analytical Chemistry*, *87*(3), 1853–1860.

[4] Fernandez-Martinez, D., Kong, Y., Goussard, S., Zavala, A., Gastineau, P., Rey, M., Ayme, G., Chamot-Rooke, J., Lafaye, P., Vos, M., Mechaly, A., & Duménil, G. (2024). Cryo-EM structures of type IV pili complexed with nanobodies reveal immune escape mechanisms. *Nature Communications 2024 15:1*, *15*(1), 1–15.

[5] Jurėnas, D., Rosa, L. T., Rey, M., Chamot-Rooke, J., Fronzes, R., & Cascales, E. (2021). Mounting, structure and autocleavage of a type VI secretion-associated Rhs polymorphic toxin. *Nature Communications 2021 12:1*, *12*(1), 1–11.

Scientific or technical background required for work program

What do we expect from you?:
We seek an enthusiastic candidate passionate about interdisciplinary research at the intersection of biology, chemical biology, and analytical chemistry.

Ideally, you will have:

- Prior experience or strong interest in mass spectrometric techniques (e.g., analytical chemistry, OMICS approaches); no biological background required

- Willingness to work with pathogenic bacteria in a biosafety level 2 laboratory
- Openness to comprehensive training in both biological and instrumental methodologies

We value candidates who:

- Are eager to develop independent research skills
- Can bring innovative ideas and creative problem-solving approaches
- Are interested in pursuing a PhD project with us

Key requirements:

- Fluent English communication (oral and written); French language skills are not required

We offer you a great opportunity to grow and develop/carry through your own scientific ideas in a highly cross-intersectional field. This will give you an ideal scientific profile to follow up with a doctoral research project. Furthermore, you will be able to present your research project during scientific meetings and congresses.