# HIV persistence in bacteria specific CD4+ T cells

11<sup>th</sup> HIV Persistence during therapy workshop

Armando Espinosa Ortiz

Chomont's lab

Wednesday 11<sup>th</sup> December

# **Conflicts of interest**

None to disclose

# A summary for all

#### What was our question?

Can cells that recognize bacteria found in the gut contribute to HIV pathogenesis and persistence?

#### What did we find?

These cells can be infected by HIV, are preferentially lost during untreated infection and not fully restored by treatment initiation

Moreover, infected bacteria-specific cells can carry genetically intact HIV genomes in PWH on ART

#### - Why is it important?

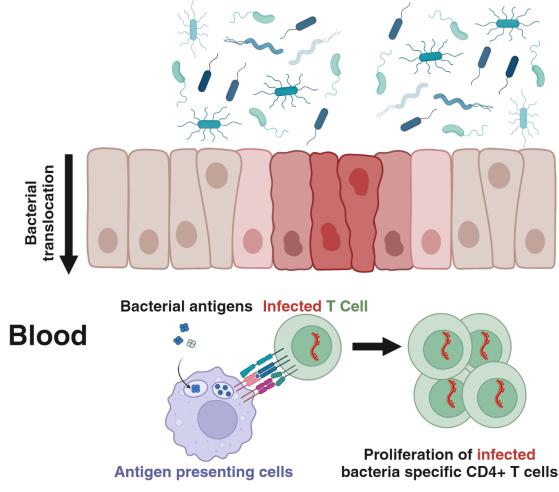
A better characterization of the reservoir cells can help us design new therapies. For example, by modulating the bacterial flora of PWH on ART

# **Rationale and hypothesis**

- Most HIV reservoir cells are clonal however, the majority of the antigen specificities of these cells are still unknown (Maldarelli, 2014; Mendoza, 2020; Simonetti, 2021; Gantner, 2020)

# **Rationale and hypothesis**

### **Gut lumen**



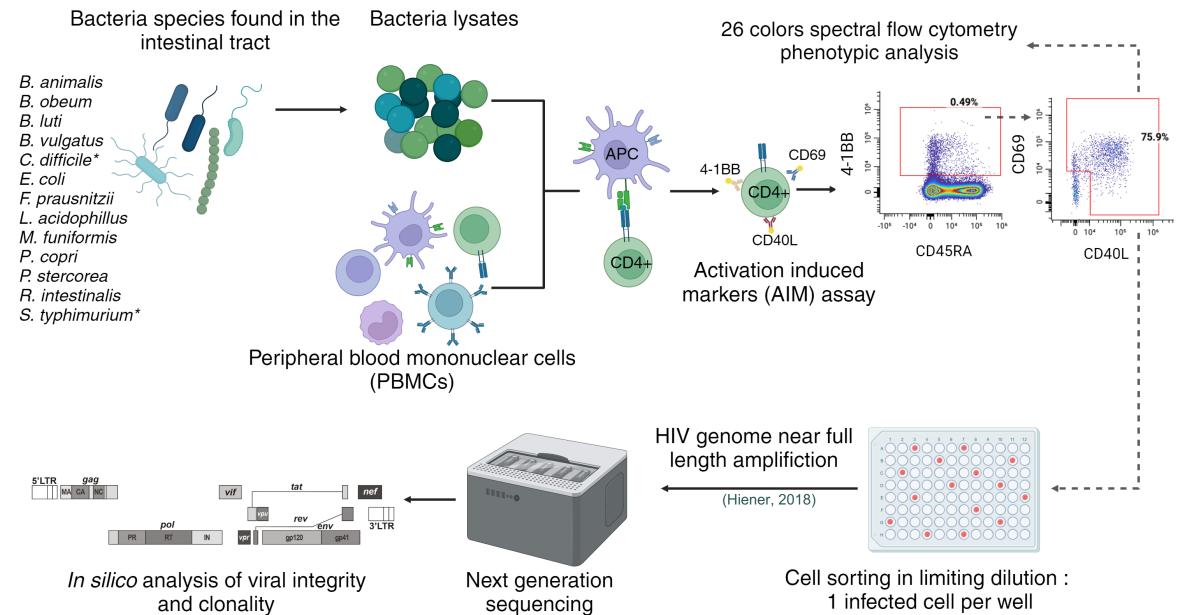
- The gut is home to an important number of CD4+ T cells. Notably cells with high susceptibility for HIV infection (Chun, 2008; Brenchley, 2006; Planas, 2017)

#### - The gut is a major source of antigens

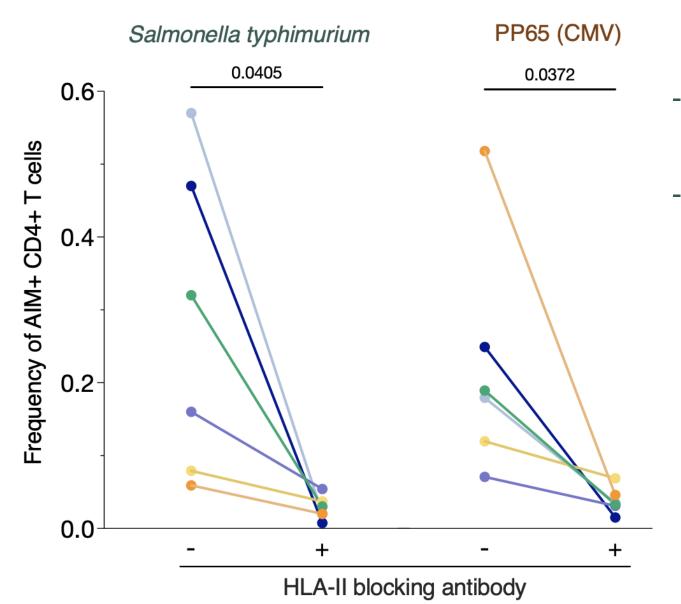
- During HIV infection the gut epithelia is altered leading to the translocation of bacterial products into the blood (Brenchley, 2006)

We hypothesized that gut-bacteria specific CD4+ T cells are preferentially infected and are HIV reservoirs in PWH on ART

## **Methods**

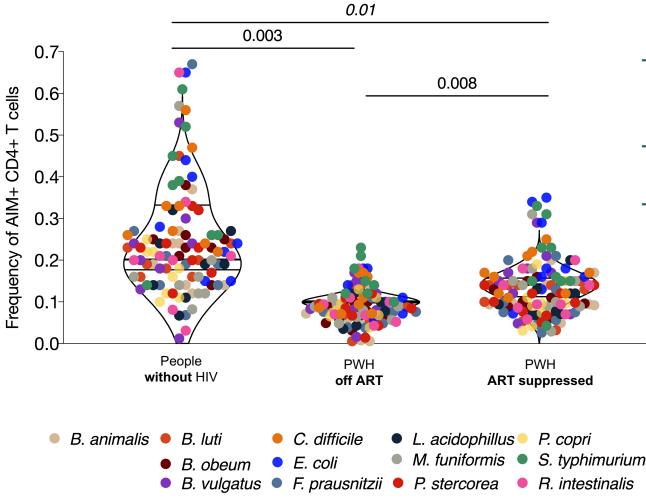


# Validation of the AIM assay



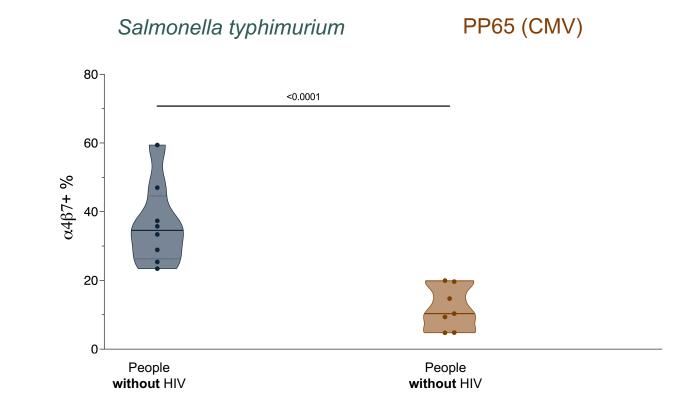
- Antibody blockade of HLA-II a loss of the AIM signal
- This suggest that the activation by the AIM assay is TCR-mediated

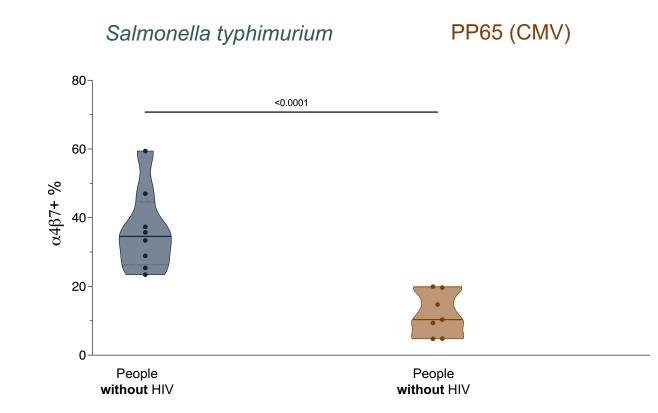
# Frequencies of gut-bacteria specific CD4+ T cells



- HIV infection is associated with lower frequencies of gut-bacteria specific CD4+ T cells
- ART only partially restores this phenomenon
- This depletion may be due to the preferential infection by HIV and subsequent death of these cells

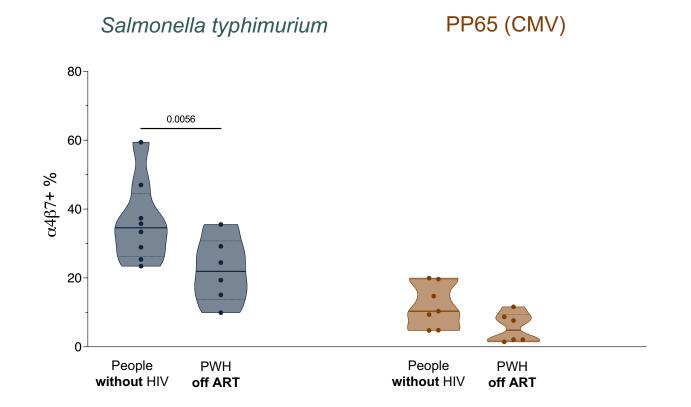
n=8 for each group



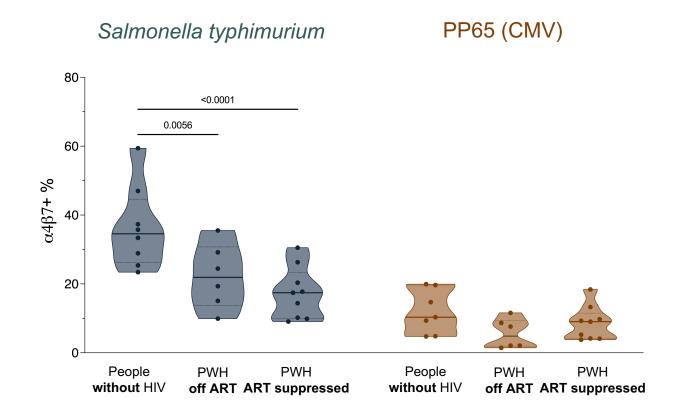


-  $\alpha 4\beta$ 7+ cells have been shown to be enriched in total HIV DNA (Xie, 2021; Asowata, 2021; Jiminez-Leon, 2024)

- Salmonella Typhimurium specific CD4+ T cells expressed higher level of this gut homing integrin than CMV specific CD4+ T cells

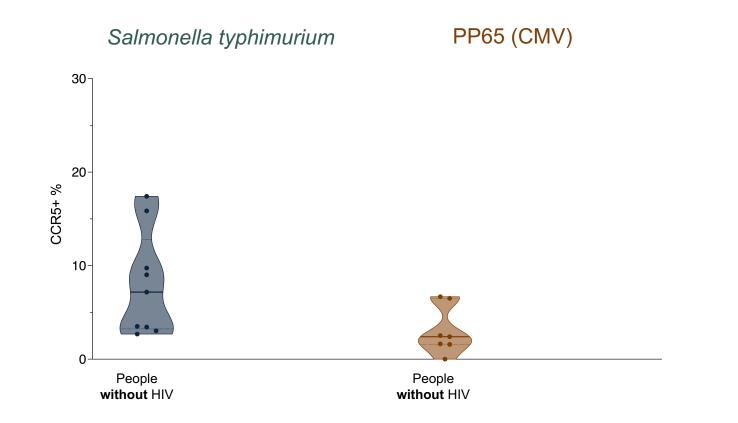


- We see a decrease of the frequency of  $\alpha 4\beta$ 7+ cells in PWH off ART



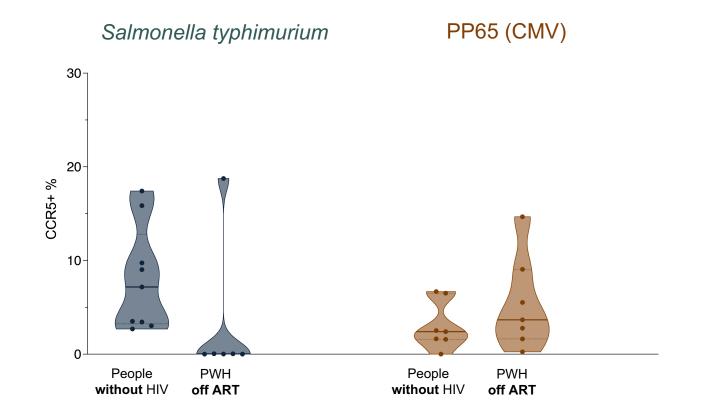
- This is maintained in ART suppressed individuals for bacteria specific CD4+ T cells but not CMV specific cells

## **Depletion of susceptible CD4+ T cells**



- There was a trend for higher CCR5 expression in *Salmonella typhimurium* specific CD4+ T cells rather than in CMV specific CD4+ T cells

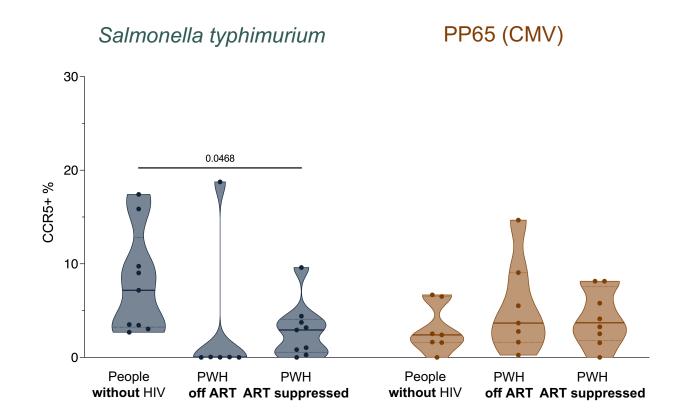
# **Depletion of susceptible CD4+ T cells**



- CCR5 expression on Salmonella typhimurium is decreased in PWH

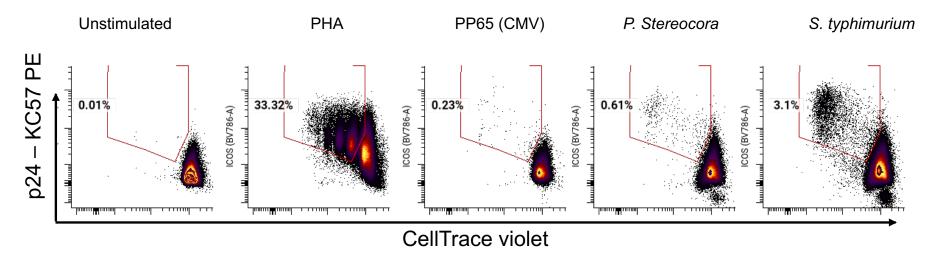
- This suggest a depletion of CCR5+ Salmonella typhimurium specific CD4+ T cells

## **Depletion of susceptible CD4+ T cells**



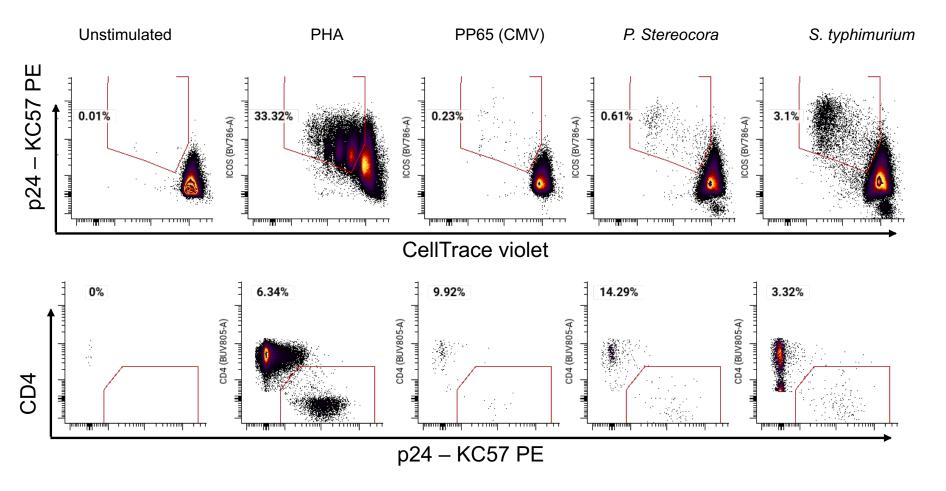
- This phenomenon is maintained in ART supressed individuals for *Salmonella Typhimurium* specific CD4+ T cells but not for CMV specific CD4+ T cells

# *In vitro* infection of gut-bacteria specific CD4+ T cells



CCR5 tropic TF virus (HIV-1 33931N)

# *In vitro* infection of gut-bacteria specific CD4+ T cells

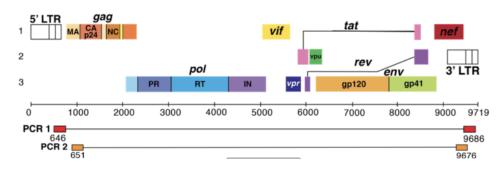


CCR5 tropic TF virus (HIV-1 33931N)

# **Contribution to HIV reservoir**

We performed near-full length amplification of HIV genomes on sorted bacteria specific CD4+ T cells

using an approach developed by the Palmer group, and adapted in our lab (Hiener et al. 2018, Dufour et al. 2023)



Near-full length HIV genome amplification

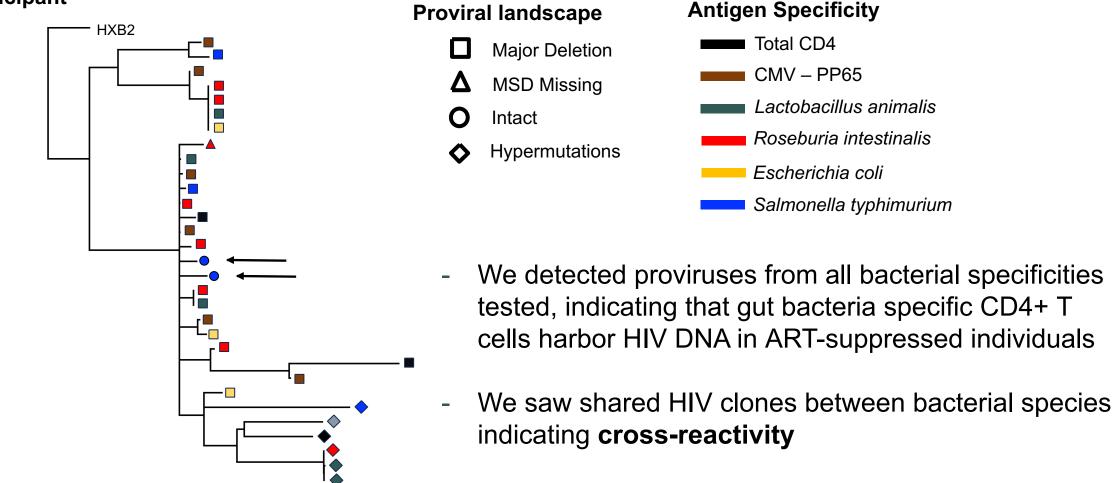
This approach followed by next-generation sequencing (PacBio and Nanopore) allows us to determine:

- Intactness of proviruses
- Clonality of HIV reservoir cells

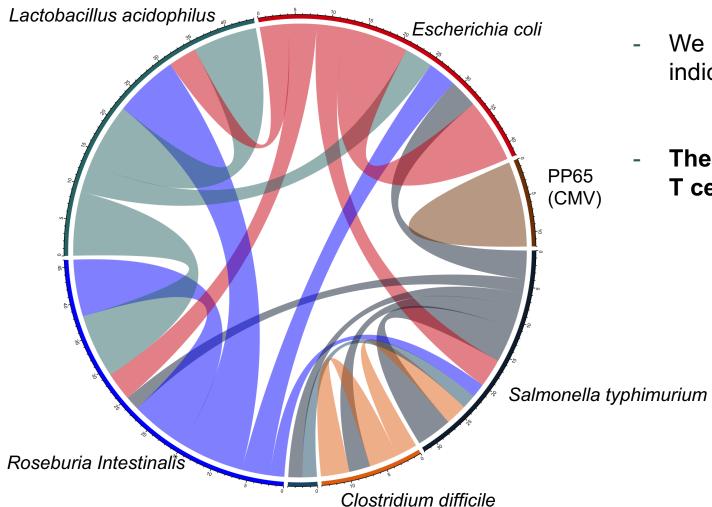
# **Proviral landscape**

0.02

One participant

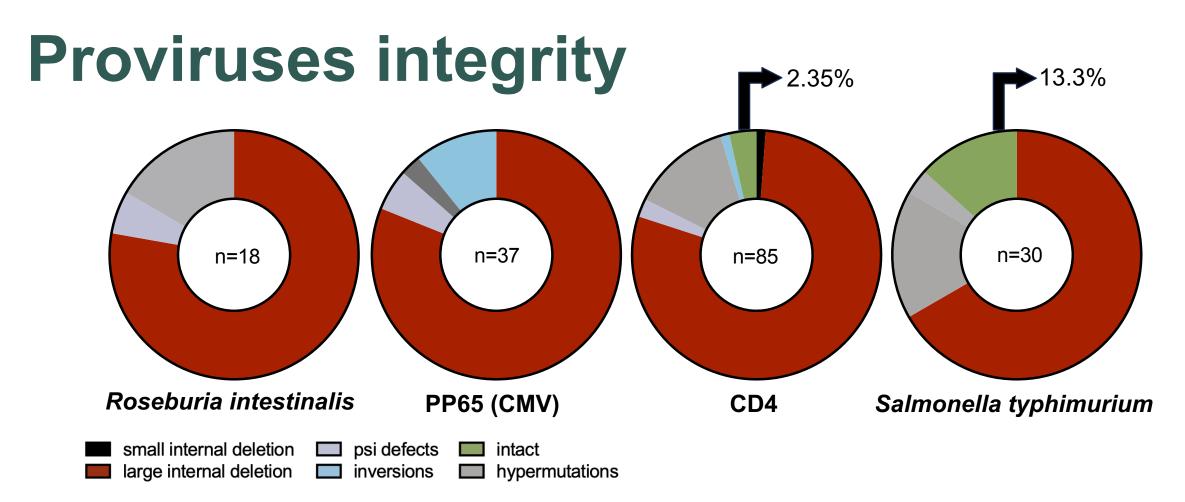


# **Cross reactivity**



- We saw shared HIV clones between bacterial species indicating **cross-reactivity**
- These clones were not found in PP65 specific CD4+ T cells

Interactivity map showing clonal proviruses only



- Among 200 sequences retrieved from 5 participants, we detected 6 distinct genetically inferred intact proviruses in 3 participants
- 4 of them were retrieved in S. typhimurium specific cells from 2 participants
- Why S. Typhimurium specific CD4+ T cells would be a preferential reservoir for HIV?

# Conclusions

- Bacteria specific CD4+ T cells are preferentially depleted during untreated HIV infection and not fully restored by ART
- These cells express markers associated with HIV permissiveness and can be infected in vitro
- We retrieved proviruses from all bacterial specificities tested, demonstrating that **gut bacteria specific CD4+ T cells carry HIV DNA**
- These bacteria-specific infected cells can undergo clonal proliferation
- Intact proviruses were found in S. typhimurium specific CD4+ T cells.
- Immune reconstitution is incomplete since the functions of gut-bacteria specific CD4+ T cells remain altered in ART-suppressed individuals

# **Next steps**

- We plan to sort gut bacteria-specific CD4+ T cells from participants in acute HIV infection (<2 months) to determine if the depletion of these cells occurs at the earliest stage
- We will perform TCR sequencing on gut bacteria specific CD4+ T cells to measure crossreactivity between bacterial species
- In addition, we are planning to perform AIM assays followed by provirus sequencing in gut isolated cells from ART suppressed individuals

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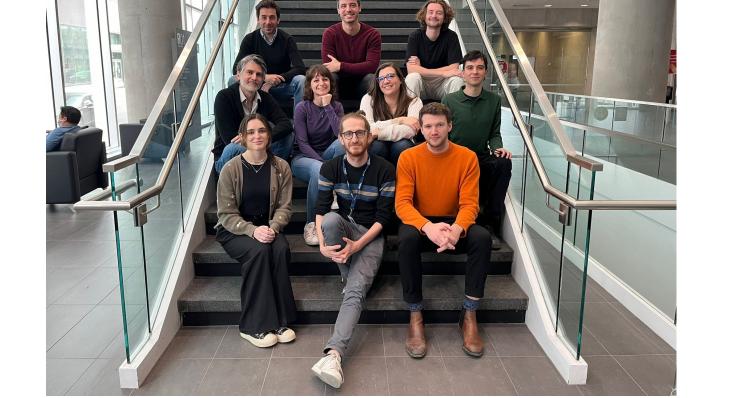
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