

Summer Research Program

(SRP)

EPFL
School of Life Sciences
Impact Report 2025

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A word from the program directors

Since the establishment of the Summer Research Program (SRP) in 2006, more than 420 international students have had the opportunity to visit EPFL and, for a brief 2-month period, become a part of its ecosystem. 2025 marked our 20th anniversary year and stands as a milestone achievement for the program, receiving over 1300 applications from scholars worldwide. We believe that this level of interest speaks to the academic merits of the program and the stellar reputation of EPFL research. Through a careful selection process, 26 exceptional students representing 20 countries were invited to join host labs at the School of Life Sciences over this past summer.

SRP features a comprehensive professional development program. In addition to expanding their practical skills through participation in research projects and access to state-of-the-art infrastructure on campus, SRP scholars also attend workshops on career development, scientific integrity, leadership, and ecology. Their training is complemented with regular social events such as beach BBQs and visits to the breathtaking alpine villages. Through these experiences, SRP participants connect with their peers, both scientifically and culturally, forge long-lasting friendships and build bridges of understanding.

To celebrate our **20th anniversary**, we were honored to host Nobel Prize laureate Professor Jacques Dubochet, who shared invaluable career perspectives and engaged directly with our students in an intimate meeting. This exchange offered our participants a rare glimpse into the trajectory of scientific excellence and the perseverance required to reach the highest levels of research achievement.

The program concluded with two celebratory events that captured the spirit of what SRP has built over two decades. The traditional closing symposium brought together over 100 collaborators and visitors to witness our students present their research projects to the EPFL scientific community at large. This year, we expanded our celebrations with a special alumni event that drew more than 30 former participants back to campus. These alumni, now at various stages of their careers, shared their experiences across diverse professional paths: some have continued in academia, others have launched entrepreneurial ventures, and many have joined leading companies in their fields.

As we enter our third decade, we remain committed to assembling dynamic programs that catalyze the personal and professional growth of these future scientists, building on the strong foundation established over the past 20 years.



Aleksandar Antanasijevic



Gioele La Manno





Summer Research Program

This summer, our laboratories welcomed 26 outstanding future researchers representing 20 different nationalities. The SRP strives to discover and nurture talent and potential worldwide, from all backgrounds.

Benefits to the Students

The participants:

- Gain hands-on interdisciplinary research experience.
- Put classroom learning into action to solve current research problems.
- Improve critical thinking skills by evaluating scientific information, designing experiments and testing hypotheses.
- Experience the excitement and challenges of scientific research gaining insight into what a research career entails.
- Present their research to the local scientific community during lab meetings and at the closing symposium.
- Prepare for future independent research projects and advanced research in graduate school.

Selection criteria

Fellowships are awarded on a competitive basis, applicants are required to have completed two years of undergraduate study in a life sciences program, be in the top 5% of their class, demonstrate a strong potential and have a keen interest in a life sciences career.

Facts

Over the last 20 years, SRP has grown to be a truly international program.

- 16% of the participants return to the EPFL to continue their studies in some capacity.
- 421 students were selected from over 11'267 applicants.
- A living stipend is provided and the majority of travel expenses are covered by program sponsors and the School of Life Sciences.
- Housing in Lausanne for the duration of the stay is provided.
- The working language is English.

Hands-on research experience

SRP Students dive into eight weeks of hands-on research, each matched to a lab that suits their background and interests. As part of a research team, under the mentorship of lab heads or group members, they work on specific projects within our five institutes. They explore interdisciplinary questions in neuroscience, global health, bioengineering, and cancer research.

Weekly Talks & Workshops

Weekly workshops bring students together with EPFL faculty, visiting external experts, and EPFL alumni. Topics range from scientific integrity to climate and sustainability challenges, as well as career testimonials from principal investigators and alumni. These workshops inspire a strong sense of community and prepare students for leadership roles in life sciences.

Visits and Cultural Activities

Students visit research hubs like Campus Biotech in Geneva and the Agora Cancer Research Center in Lausanne, experiencing the importance of collaboration in sciences. Social events, such as BBQs, a Swiss mountain hike, and cultural awareness activities, encourage community building and broaden cultural perspectives.

Joint Symposium with UNIL's SUR Program

A highlight at the end of the summer, the Joint Symposium with the Summer Undergraduate Program (SUR) of the University of Lausanne provides a platform for students to present their research findings, network with peers, and gain valuable presentation experience.



List of participants

	Name	Country	Lab	Sponsor
IBI	Lazo Bakhtiar Ali	Irak	Maerkl	McCall MacBain Foundation
	Jasmine Della Valle	Italy	Dal Peraro	Fondation pour des bourses d'études italo-suisse
	Jia Run Dong	Canada	Tang	McCall MacBain Foundation
	Ricardo Gonzalez Hidalgo	Mexico	Radenovic	Institute of Bioengineering
	Julia Christine Jamieson	USA	Sakar	Institute of Bioengineering
	Diana María Juárez Polo	Mexico	Fantner	McCall MacBain Foundation
	Zhuowen Li	China	Ijspeert	McCall MacBain Foundation
	Samin Mahdipour Aghabagher	Iran	Schrimpf	Fondation Protechno
	Gilda Quezada Correa	Ecuador	Bastings	Institute of Bioengineering
	Anna Claire Woolley	USA	Barth	Institute of Bioengineering
ISREC	Sayani Bose	India	Briskin	Fondation ISREC
	Camilla Brückmann de Mattos	Brazil	Gönczy	Fondation ISREC
	Febrina Margaretha	Indonesia	Thomä	Fondation ISREC
GHI	Abdinoor Kassim Dagane	Kenya	Antanasijevic	Tomorrow Foundation
	Carl Damell	Sweden	Persat	Global Health Institute
	Rachelle Fernández-Vargas	Costa Rica	Paoli	McCall MacBain Foundation
	Anna Sushnova	Ukraine	Van der Goot	Anonymous Donor
Neuro-X	Anuj Prafulla Chavan	India	Van de Ville	McCall MacBain Foundation
	Héloïse Hughes	South Africa/CH	Nakatsuka	Neuro-X Institute
	Mayuka Otsuki	Japan	Blanke	Neuro-X Institute
BMI	Iliana Hernandez	USA	McCabe	Brain Mind Institute
	Marcello Lattanzi	Italy	Zenk	Fondation pour des bourses d'études italo-suisse
	Francesco Pieracciani	Italy	La Manno	Fondation pour des bourses d'études italo-suisse
	Teoman Soydan	Turkey	Priestley	Brain Mind Institute
	Bernadett Tőkés	Hungary	Herzog	Brain Mind Institute
	Montserrat Trejo Valencia	Mexico	Gräff	Anonymous Donor

IBI: Institute of Bioengineering

ISREC: Swiss Institute for Experimental Cancer Research

GHI: Global Health Institute

Neuro-X: Institute of Neurosciences, Neurotechnology and Neurocomputation for medicine

BMI: Brain Mind Institute

Participating professors

IBI



Patrick
Barth



Maartje
Bastings



Matteo
Dal Peraro



Georg
Fantner



Auke
Ijspeert



Sebastian
Maerkl



Aleksandra
Radenovic



Selman
Sakar



Martin
Schrimpf



Li
Tang

ISREC



Cathrin
Briskén



Pierre
Gönczy



Nicolas
Thomä

GHI



Aleksandar
Antanasijevic



Lucas
Paoli



Alexandre
Persat



Gisou
van der Goot

Neuro-X



Olaf
Blanke



Nako
Nakatsuka



Dimitri
Van de Ville

BMI



Johannes
Gräff



Michael
Herzog



Gioele
La Manno



Brian
McCabe



James
Priestley



Fides
Zenk

Participating students

IBI



Lazo Bakhtiar
Ali



Jasmine
Della Valle



Jia Run
Dong



Ricardo
Gonzalez Hidalgo



Julia Christine
Jamieson



Diana María
Juárez Polo



Zhuowen
Li



Samin Mahdipour
Aghabagher



Gilda
Quezada Correa



Anna Claire
Woolley

ISREC



Sayani
Bose



Camilla
Brückmann de Mattos



Febrina
Margaretha

GHI



Abdinoor Kassim
Dagane



Carl
Damell



Rachelle
Fernández-Vargas



Anna
Sushnova

Neuro-X



Anuj Prafulla
Chavan



Héloïse
Hughes



Mayuka
Otsuki

BMI



Iliana
Hernandez



Marcello
Lattanzi



Francesco
Pieracciani



Teoman
Soydan



Bernadett
Tőkés



Monserrat
Trejo Valencia



Lazo Bakhtiar ALI

Lebanese American University

Maerkl Laboratory of Biological Network Characterization (LBNC)

Supervisor: Fanjun Li

Lazo is supported by McCall MacBain Foundation

Abstract :

We present an integrated framework for high-throughput analysis of transcription terminators. Libraries are designed using Sobol sampling of literature-derived sequence and structural parameters, targeting short, efficient terminators and unexplored motif-hairpin combinations. Each construct carries unique barcodes for accurate tracking and is ligated upstream of genes for in vitro transcription. Polyadenylation and dual-UMI template switching enable precise RNA quantification by sequencing. Per-base readouts are then used to fine-tune DNA and RNA foundation models, providing scalable design-test-learn cycles for predictive terminator engineering.

Massively Parallel Terminator Libraries for AI-Driven Sequence-Function Discovery

Lazo B. Ali, Fanjun Li, Sebastian J. Maerkl

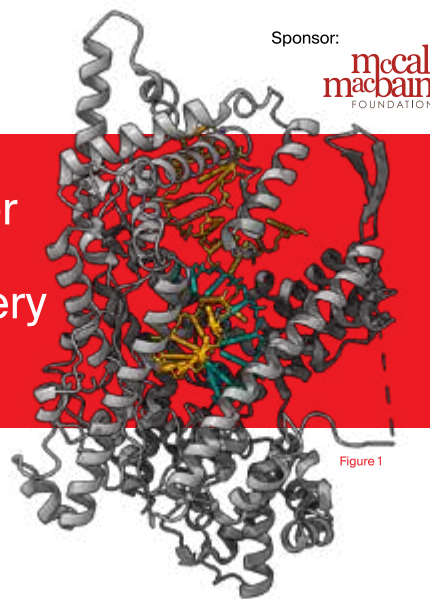


Figure 1

Abstract

We present a computational-experimental framework for high-throughput mapping of transcription terminators. Libraries are de novo designed via Sobol sampling of a literature-derived parameter space, targeting short, efficient terminators and exploring novel structural-sequence combinations. Internally barcoded oligonucleotide pools are synthesized, PCR-amplified, ligated to promoter-gene constructs, and transcribed in vitro. RNA products undergo polyadenylation and dual-UMI template-switching reverse transcription, followed by two-step PCR to append Illumina adapters. Sequencing data yield per-base read depth profiles, which fine-tune DNA and RNA foundation models through low-rank adaptation (LoRA), enhancing design-space modeling and evaluating model capacity to capture termination function. This scalable design-test-learn pipeline generalizes to diverse sequence-function relationships and, with sufficient scale and diversity, enables training of problem-specific predictive models for biological engineering.

Design



Rationale for Methodology

- **T7 RNAP:** High fidelity, processive, single-protein polymerase, widely used in cell-free systems. (Figure 1)
- **Limitation:** Promoter control is efficient, but terminator is weak → hinders precise multi-gene expression.
- **Terminator Classes:**
 - Class I (HP): Hairpin terminators.
 - Class II (CS): Conserved pause signal. (5'-TATCTGTT-3')
- **Problem:** Native and synthetic terminators have low/moderate termination efficiency (TE), efficient ones >100 nt, too long for small genes (e.g., tRNA)
- **Measurement gap:** TE often from gels/fluorescence → lacks per-base resolution, RNA-seq studies limited to small design subspaces, fail to explore known efficient CS-HP combinations.
- **Design space:** Efficiency shaped by complex interactions: HP stability, GC content, CS placement/tandem spacing, promoter distance, upstream context, poly-U tails...
- **Evidence:** One-variable designs fail, rational constructs show unpredictable TE. No single variable correlates strongly with TE. (Figure 2)
- **Need:** Vast, systematic libraries → capture latent interactions, feed AI, enable robust sequence-to-function discovery.



Figure 2. TBE-Urea PAGE analysis of T7 RNAP terminator constructs.

1. Native T7 RNAP terminator.
2. HP50: best TE from Calvo/Chen et al. >100 nt.
3. 510-M89-T16: best TE from Teramachi & Gonchooski, 107 nt spacer, M89 = modified HP T16 = terminator HP5. Doesn't include CS.
4. Variant with CS-replacing M89.
5. Variant with CS embedded in M89 with minimal HP disruption.
6. Variant with CS inserted after T16, before poly-U.

Multiple bright bands indicate distinct transcript products; higher termination efficiency is indicated by stronger shorter bands and reduced long run-off transcripts. All constructs have significant run-off product.

CS in 4 and 5 show the emergence of distinct 'spine' run-off products. In 3, run-off product is less bright.

Sampling Strategy:

Sobol low-discrepancy sampling for even coverage. Vector maps to design under constraints.

Barcode Design:

Terminator flanked by dual 8-nt barcodes. GC-balanced, minimum hamming distance.

Test

In Vitro Transcription:

Terminator-gene constructs are transcribed with T7 RNAP. Generates run-off and terminated RNA species. Poly-A tailing with post-IVT to standardize 3' ends.

Library Preparation (RT-TSO):

Reverse transcription with template-switching oligos for unbiased 5' prime capture. Captures all unique RNA species and minimizes PCR bias. Dual-UMIs Enable accurate molecule counting by correcting for PCR duplicates and base-call errors of each other.

Sequencing:

Two-step PCR appends Illumina adapters and sample indices. Libraries are pooled and sequenced (PE RNA-seq). Reads mapped to barcode-flanked constructs for TE and per-base depth calculations.

Learn



Model Fine Tuning:

Use Low-Rank Adaptation (LoRA) to efficiently fine-tune pretrained RNA and DNA foundation models on termination assay data. Incorporate per-base read depth vectors as training targets. Compare the variety of foundational models on termination prediction pre- and post-fine-tuning.

Visualization and Feature Analysis:

Generate UMAP embeddings of sequence space to visualize structural and sequence diversity. Construct saliency maps to highlight features (e.g. HP stability, CS placement, poly-U length, others...) most predictive of TE.

In Silico Prediction:

Fine-tuned models used to predict TE of novel designs. Generate novel designs based on terminator space of least confidence. Enables iterative design-test-learn cycles to rapidly converge on highly accurate sequence-to-function model.

Assess Current Models:

Consider training novel models in case of low generalizability of current models.

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■ Laboratory for
Biological Network
Characterization



Jasmine DELLA VALLE

University of Pisa

[Dal Peraro Lab for Biomolecular Modeling](#)

Supervisors: Edoardo Cavani, Maria J. Marcaida

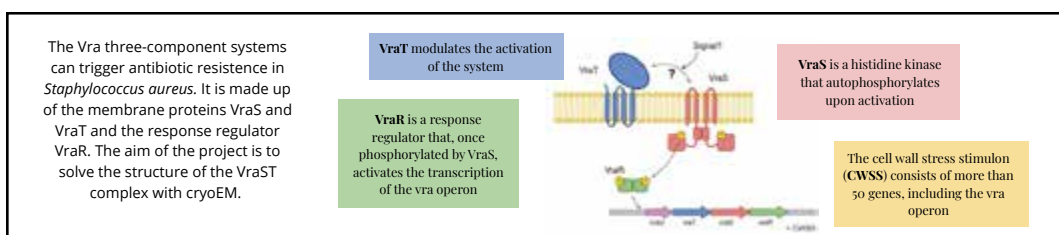
*Jasmine is supported by Fondation pour des bourses
d'études italo-suisse*

Abstract :

The Vra three-component system is an important regulator of antibiotic resistance in *Staphylococcus aureus*. It includes the dimeric histidine kinase VraS, the response regulator VraR, and VraT, a membrane protein essential for system activation. This project aims to resolve the VraS-T complex structure using cryo-EM, which will provide valuable insights into how the system functions. I optimized a purification protocol for five different orthologous systems with the aim of enhancing protein expression and stability, and to improve sample quality for cryo-EM analysis.

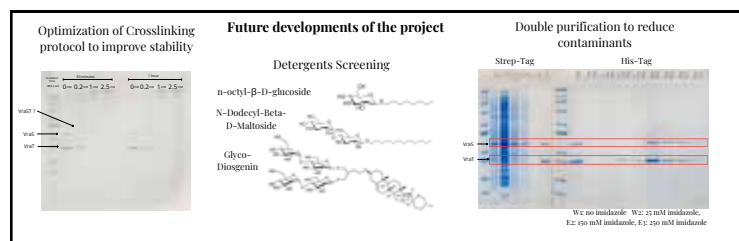
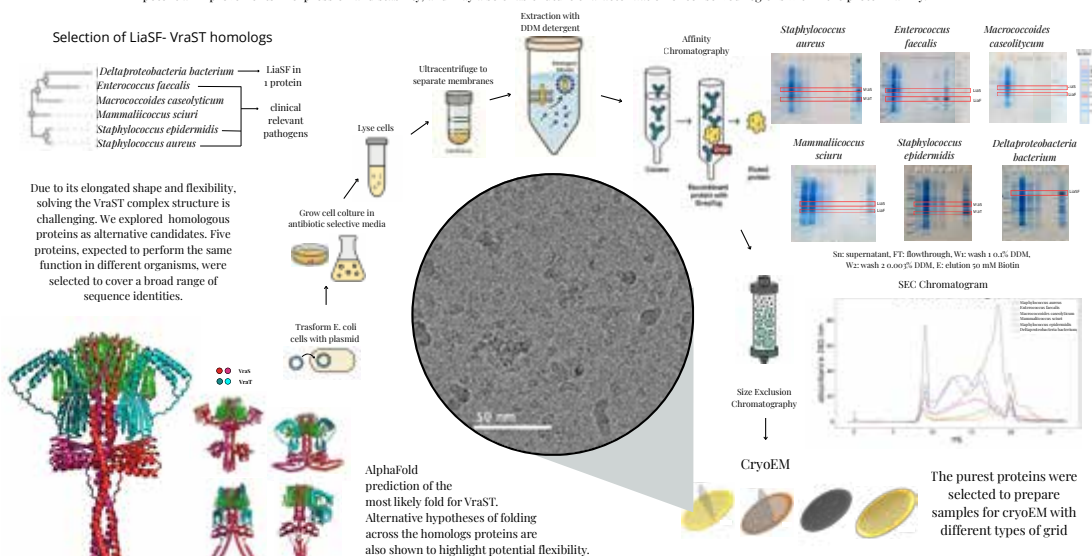
Structural characterization of protein receptors involved in β -lactam antibiotic resistance

Jasmine Della Valle^{2,1}, Edoardo Cavani¹, Juan F. Bada Juarez¹, Maria J. Marcaida¹, Leticia I. Llarrull³, Matteo Dal Peraro¹
¹Laboratory for Biomolecular Modeling, EPFL ²Scuola Normale Superiore di Pisa, ³Instituto de Biología Molecular y Celular de Rosario

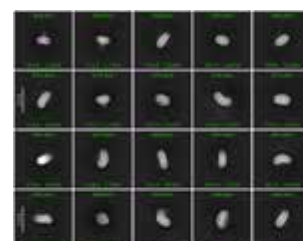


Evaluation of expression and purification performance across VraST homologs

The recombinant protein expression and purification protocol previously validated for VraST was applied to 5 homologs. This approach aims to assess potential improvements in expression and stability, and may also enable future characterization of conserved regions within the protein family.



Examples of 2D classes obtained with CryoSPARC from data collection on *S. aureus* VraST



S. Gardete et al. Role of VraSR in Antibiotic Resistance and Antibiotic-Induced Stress Response in *Staphylococcus aureus* (2006)
 McCallum N, et al. Mutational analyses of open reading frames within the vraSR operon and their roles in the cell wall stress response of *Staphylococcus aureus*. (2011)
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Acknowledgement: The DCI team EPFL, The entire LBM lab.



Jia Run DONG

University of Manchester

[Tang Lab of Biomaterials for Immunoengineering](#)

Supervisor: Yu Hu

Jia Run is supported by McCall MacBain Foundation

Abstract :

Although chimeric antigen receptor (CAR)-T cell therapy has revolutionized treatment for hematological cancers, solid cancers nonetheless remain difficult to treat. To address this, we investigated the in vitro effects of a largely unstudied cytokine family on CAR-T cell effector function and identified at least one member with the potential to enhance antitumor immunity in vivo. Our results suggest that this cytokine family could serve as a promising avenue for the development of improved CAR-T cell therapy against solid cancers.

Jia Run Dong^{1,2}, Yu Hu¹, Li Tang¹1. Laboratory of Biomaterials for Immunoengineering, École Polytechnique Fédérale de Lausanne
2. The University of Manchester**Introduction****Chimeric antigen receptor (CAR)-T cells:**

- T cells engineered with synthetic receptors that recognize specific tumor antigens (Fig. 1) [1]
- Effective against hematological cancers but struggle against solid tumors and often do not elicit long-lasting responses [2,3]

Previous research:

- IL10-expressing CAR-T cells developed in Tang lab showed enhanced, durable antitumor activity *in vivo* [4]
- Cytokine 2, from a relatively underexplored cytokine family, have been reported to enhance CAR-T cell antitumor efficacy, though other related cytokines, cytokines 1 and 3, have yet to be tested for similar effects

Overall aim of project:

- Measure and compare the effector function of CAR-T cells expressing cytokine 1, 2, or 3 with conventional CAR-T cells as well as our lab's IL10-expressing CAR-T cells

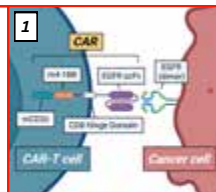


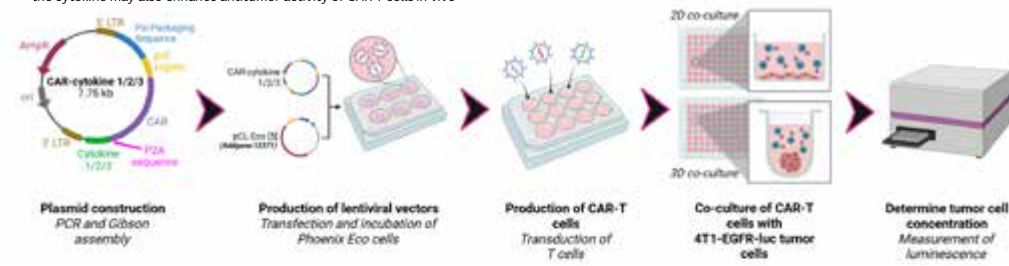
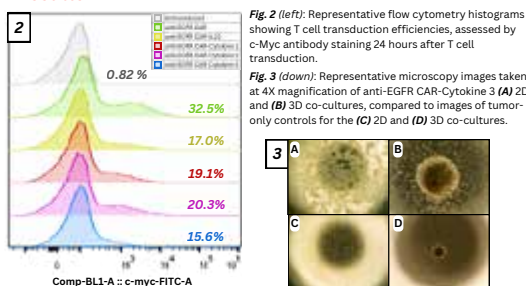
Fig. 1: Simplified diagram of a conventional second-generation CAR.

Aims

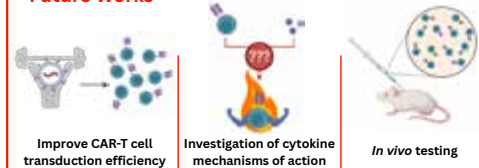
- To generate armored CAR-T cells expressing cytokine 1/2/3
- To use *in vitro* methods to investigate the tumor cell killing efficacy of the cytokine-expressing CAR-T cells
- To compare effector functions of the armored CAR-T cells and predict their potential *in vivo* performance

Methods**Proof of concept: *in vitro* 2D and 3D co-culture of anti-EGFR CAR-T cells expressing cytokine 1/2/3 with 4T1-EGFR-luc tumor cells**

- Utilization of 4T1-EGFR-luc, a luciferase-expressing tumor cell line, allows the easy quantification of tumor cell presence through a bioluminescence assay
- If CAR-T cells expressing cytokine 1/2/3 produce a significant decrease in luminescence compared to wild-type anti-EGFR CAR-T cells, especially in the 3D co-culture, the cytokine may also enhance antitumor activity of CAR-T cells *in vivo*

**Results****Conclusion**

- Among the cytokine family tested, only cytokine 1 enhanced CAR-T cell function against 2D tumor cell cultures, while only cytokine 3 provided a significant increase in CAR-T cell function against 3D tumor spheroids
- CAR-T cells expressing cytokine 3 may demonstrate the highest antitumor activity *in vivo*, as spheroids better model tumor structure, but more replicates are necessary to conclude that other members of the cytokine family do not provide similar effects
- Interestingly, cytokine 2 did not show significant effects on CAR-T cell effector function - may need further investigation
- T cell transduction efficiencies were lower than expected - may be able to improve by using fresh cell lines for lentiviral production and a lengthened incubation time after transduction
- Future research of this cytokine family may provide us with a more diverse weapons arsenal to use against solid cancers

Future Works**Acknowledgements**

I would like to express my utmost gratitude to the members of Tang lab; notably Dr. Yu Hu for her invaluable mentorship and time, Prof. Li Tang for welcoming me into the lab and providing the facilities and resources necessary for my project, and Dr. Zheng Yu for generously sharing his cell cultures. I am also incredibly grateful to Ms. Alice Emery Goodman as well as Profs. Aleksandar Antanasijevic and Gioele La Manno for their time and dedication in organizing and bringing to life the amazing EPFL Summer Research Program. Finally, I would like to give my thanks to the McCall MacBain Foundation for providing the funds that made my whole SRP journey possible. Figures were created with Biorender.com, Graphpad Prism, and FlowJo.

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- [4] Zhou X, Chen L, Antanasijevic A, Tang S, Yu Y, Zhou M, et al. B220-expressing CAR-T cells mediate depletion and mediate durable clearance of solid tumors and metastases. *Nature Immunology*. 2020;21(1):1-12.
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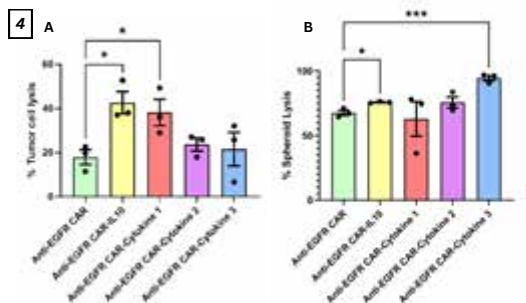


Fig. 4: Distinct cytokines enhance CAR-T cell effector function in 2D versus 3D tumor cell cultures. (A) Cytokine 1 enhanced CAR-T cell killing efficiency against 2D tumor cell cultures (1:2 cell:tumor cell ratio), while (B) Cytokine 3 significantly improved CAR-T cell killing of 3D tumor spheroids (1:1 cell:tumor cell ratio). Percent lysis of tumor cells was measured using a bioluminescence assay after 24 hours of co-culture. Anti-EGFR CAR-IL10 was included as a positive control. Data shown as mean ± SEM of triplicate wells and analyzed using two-tailed unpaired t-tests.



Ricardo GONZALEZ HIDALGO

Universidad de las Américas Puebla

[Radenovic Lab of Nanoscale Biology](#)

Supervisors: Lely Feletti, Eugene Glushkov

Ricardo is supported by the Institute of Bioengineering

Abstract :

The thermodynamics of living cells is still not fully understood and is actively debated. However, intracellular thermal events from internal cellular processes may play a role in thermal signaling, and precise tools to study them are needed. The project investigates these processes using a Diamond Heater-Thermometer and Fluo-4 staining to monitor calcium (Ca^{2+}) release in living cells and organoids. Differences in calcium signaling responses across cell types (HeLa, COS-7, and mammary gland organoids) highlight the complexity of cell-specific thermodynamic behavior.

To respect the confidentiality of unpublished results, we have included a concise abstract instead of the full poster for this project



Julia Christine JAMIESON

University of Florida

[Sakar Lab of Microbiorobotic Systems](#)

Supervisor: Adrien Mery

Julia is supported by the Institute of Bioengineering

Abstract :

Microfluidic-generated alginate hydrogel fibers with a cell core are a promising material to construct higher-order structures in tissue engineering. Due to their manipulatable motion and potential to stimulate in vitro tissue models, we generated fibers from fibroblasts that contract when exposed to light. Over 34 days, the proliferation of the cell-based fibers (100 μm wide and up to a meter long) was observed. The study illuminated the fibers' growth patterns and identified collection and display methods to optimize fiber generation.

To respect the confidentiality of unpublished results, we have included a concise abstract instead of the full poster for this project



Diana María JUÁREZ POLO

Universidad de las Américas Puebla

Fantner Lab of Bio- and Nano- Instrumentation

Supervisor: Prabhu Swain

Diana is supported by McCall MacBain Foundation

Abstract :

Understanding the structure of biological materials is crucial, but conventional imaging methods can damage delicate samples. This project tested a new system combining Atomic Force Microscopy (AFM) and Scanning Electron Microscopy (SEM), using chitosan nanoparticles as a model, we showed that AFM/SEM improves navigation and imaging compared to AFM alone. These results represent a first step towards applying cryo-SEM/AFM for high-resolution visualization of cells and tissues while preserving their native structure.

COMPARATIVE ANALYSIS OF AFM AND AFM/SEM FOR BIOLOGICAL-BASED SAMPLE CHARACTERIZATION: TOWARDS CRYO-SEM/AFM

Diana María Juárez Polo¹, Prabhu Prasad Swain¹, and G. E. Fantner¹

¹Laboratory for Bio- and Nano-Instrumentation, École Polytechnique Fédérale de Lausanne, Switzerland

GENERAL OBJECTIVE

To **demonstrate** the advantages of **AFM integrated in SEM** for the characterization of biological samples, as a step towards high-resolution visualization of biological structures with minimal structural damage using **cryo-SEM/AFM**.

INTRODUCTION

- AFM and SEM separately are widely used for nanoscale surface and structural analysis.
- AFM provides **high vertical resolution** (nanometer-scale) but limited field of view.
- SEM images larger areas with good **depth of field** but lower vertical resolution.
- Integrating AFM into SEM combines the strengths: **SEM guides the AFM tip** (already achieved), while AFM adds topographical and mechanical info.
- **Biological samples** are delicate and non-conductive, requiring gentle imaging techniques. **Cryogenic conditions** (cryo-SEM/AFM) preserve hydrated structures, enabling high-resolution imaging with minimal damage.

METHODS (SETUP)



Figure 1. AFM/SEM chamber view, showing the sample stage inside the electron microscope.



Figure 2. SEM visualization of the AFM cantilever, obtained during training, illustrating precise tip positioning on regions of interest.

CHITOSAN NANOPARTICLES SYNTHESIS

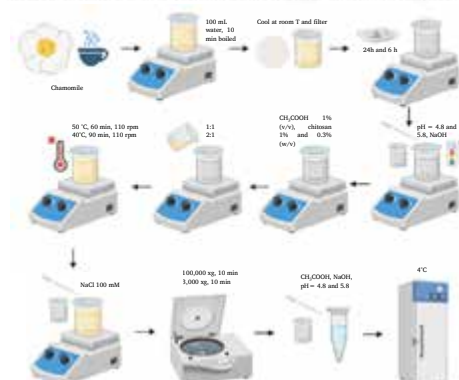


Figure 3. Schematic representation of the green synthesis of chitosan nanoparticles, created with BioRender.

RESULTS



Figure 4. SEM image of chitosan nanoparticles with heterogeneous size and morphology.



Figure 5. 2D image obtained with the AFM/SEM setup.

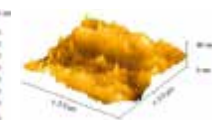


Figure 6. 3D image obtained with the AFM/SEM setup.

AFM/SEM Scan vs AFM-only Scan

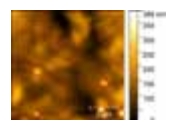


Figure 7. 2D AFM image at 20 μm scan size.



Figure 8. 2D AFM image at 80 μm scan size.

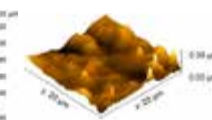


Figure 9. 3D AFM image at 20 μm scan size.

FUTURE PERSPECTIVES

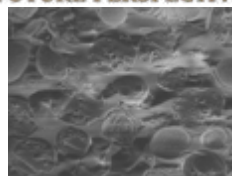


Figure 10. Cryogenic SEM image of yeast cells, acquired during training, demonstrating structural preservation in hydrated biological samples.

Cryo-SEM/AFM will enable high-resolution visualization of biological samples (cells and tissues) in their native structure, without causing damage.

CONCLUSIONS

- AFM-only imaging **limitations**: 2D images appeared blurred and required larger scan sizes (80 μm) to detect enough nanoparticles.
- AFM/SEM imaging **avoided** scanning artifacts thanks to **SEM guidance**, enabling precise XY positioning of the AFM tip and selective characterization of individual nanoparticles.
- Topographic analysis confirmed the **presence of dispersed chitosan nanoparticles** with heterogeneous size and volume distribution.
- **Manual and software-based measurements** revealed discrepancies, but consistently indicated nanoscale dimensions and occasional aggregates.
- **AFM/SEM integration improves** particle localization and reliability of topographic characterization, making it a **promising approach** for studying delicate **biological materials**.

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Supervisor: Qiyuan Fu

Zhuowen is supported by McCall MacBain Foundation

Abstract :

To quantitatively investigate salamander locomotion across diverse terrains, we developed a salamander robot for validating central nervous system models. My work focuses on improving the robot's limbs by reducing their rotational inertia to enable both crawling and swimming. A tendon-driven transmission system was implemented, achieving a 46% reduction in limb inertia while simultaneously increasing the joint torque margin by 1.9 times. This design advances the biomimetic study of salamander locomotion in both terrestrial and aquatic environments.

Design of a Lightweight, Agile Robotic Salamander Limb for Multi-Modal Locomotion

Zhuowen Li, Qiyuan Fu, Auke Ijspeert

INTRODUCTION

Q1 Why design a Salamander Robot?

Experiments in real-world environments are yet difficult to model Agile locomotion of animals numerically.

Q2 Why focus on the limbs?

Challenge for trade off between Power for terrestrial locomotion vs. Lightness for versatile transitions.



Biology

Inspiring Design
Understanding Locomotion

Robotics

OBJECTIVE

Four DOF: 3 DOFs at the hip joint and 1 at the knee

Length: a closely scaled up replica of the animal's limbs

Range: replica of joint angle trajectories for Salamander



Fig1. Hind limb skeleton of right leg of transformed specimen. I1 is shoulder width, 48.5mm, I2 is upper limb length 116mm, I3 is low limb length 100mm

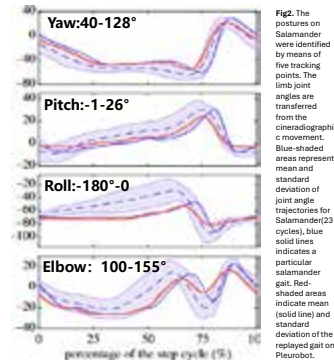


Fig2. The postures on Salamander were identified by means of five tracking points. The limb joint angles are transferred from the cineradiography movement. Blue shaded areas represent mean and standard deviation of joint angle trajectories for Salamander (23 cycles), blue solid lines indicates a particular salamander gait. Red shaded areas indicate mean (solid line) and standard deviation of the replayed gait on Pleurobot.

DESIGN

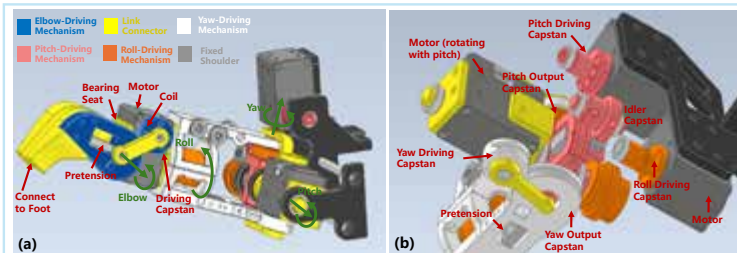


Fig3. (a) Overall oblique isometric view of the design (b) Bottom view of the Hip joint (with some components hidden)

Cable Transmission Mechanism (Compared with Gear, Worm Gear, link, Timing Belt)

Advantages

Long-distance and High torque transmission, No-backlash, High Flexibility

Favorable Outcome

- Lighten the structure without sacrificing power
- Amplify torque of robot limbs' joints

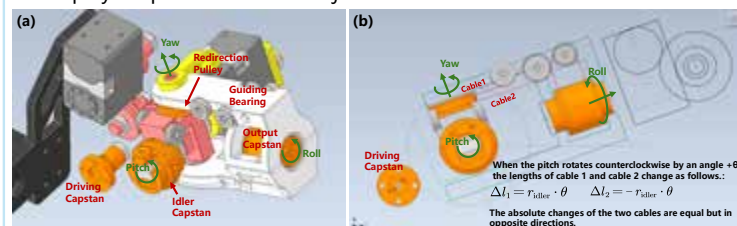


Fig4. (a) The mechanism involved in the roll degree of freedom (highlighted in orange). (b) Since its rotation axis is at the distal end, guiding bearings and redirection pulleys are needed to guide the rope along the designed route. Additionally, the roll DOF is coupled with pitch and yaw, so decoupling is essential. Since the ropes can only provide tension, to properly control the roll rotation, one cable must be wound while the other is unwound. Therefore, decoupling principle shown in (b) meets the requirement of cable-driven actuation.

Active compensation decoupling

Decouple by actively controlling servo to rotate corresponding angles

RESULT

- Complete fabrication and assembly
- Developing the motors control program in future



Fig5. Photo of the current prototype. The structure is entirely 3D-printed using PLA. The rope has a diameter of 1.2 mm and a load capacity of 45 kg.

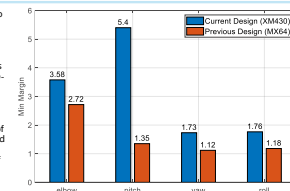


Fig6. Comparison of servo torque margins: original design and new design. For each joint, the maximum velocity and torque were extracted from the locomotion data of the salamander robot. Based on the maximum velocity and the current gear ratio, the motor output speed was calculated. Using the motor performance graph (DYNAMIXEL XM430), the corresponding minimum output torque was then determined. By comparing this torque with the required torque, the torque margin was obtained.

[1] Y.-J. Kim, "Anthropomorphic Low-Inertia High-Stiffness Manipulator for High-Speed Safe Interaction," in IEEE Transactions on Robotics, vol. 33, no. 6, pp. 1358-1374, Dec. 2017, doi: 10.1109/TRO.2017.2732354.
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Supervisor: Abdülkadir Gökce

Samin is supported by Fondation ProTechno

Abstract :

This project aims to recreate human visual experience using artificial intelligence. To achieve this, we used a dataset of brain activity recorded with fMRI while people viewed natural images. By applying multimodal models, we reconstructed the original picture from the fMRI input. This approach bridges neuroscience and artificial intelligence, offering new insight into how the brain encodes vision and demonstrating that it is possible to recreate aspects of perception directly from neural activity.



Reconstructing Visual Experience from Brain Activity using Multimodal AI

Samin Mahdipour Aghabagher¹, Abdülkadir Gökçe²

¹Department of Computer Science and Operational Research, Université de Montréal, Mila Quebec AI Institute, Canada.

²School of Computer and Communication Sciences, EPFL (Swiss Federal Institute of Technology Lausanne), Switzerland

The NeuroAI group aims to computationally understand the neural mechanisms of human intelligence by bridging Deep Learning, Neuroscience, and Cognitive Science. We build artificial neural networks whose internal representations mirror brain activity and whose outputs align with human behavior.

INTRODUCTION

The 4M framework¹ is a scalable, any-to-any multimodal model that aligns diverse data types within a unified token space. In this project, we extend 4M by introducing fMRI as a new modality.

By mapping brain activity into the shared token vocabulary, we enable direct alignment between neural signals and visual embeddings.

This allows us to ask a fundamental question: **can we reconstruct what the brain sees?** Using fMRI recordings as input, we leverage 4M to generate reconstructions of the visual stimuli, bridging human perception and multimodal AI.



Figure 1 - Illustration of multimodal AI: brain activity (fMRI) is processed and translated into different modalities such as images and text.

DATASET

The Natural Scenes Dataset (NSD)

The Natural Scenes Dataset (NSD)² is a large-scale 7T fMRI resource providing whole-brain, high-resolution data (1.8 mm voxels, 1.6 s TR) from 8 adults. Over 30–40 sessions, participants viewed up to 30,000 natural images during a recognition task. NSD's data and quality make it a key benchmark for studying visual representations and testing computational models of perception.

Next Steps

In next steps, we will add an fMRI module to the multimodal model and train it to align fMRI tokens with image representations using contrastive alignment and token-prediction objectives; the aligned embedding conditions the image decoder to generate a reconstruction of the original scene.

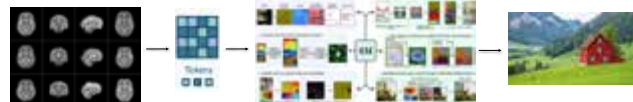


Figure 6 - Final framework, fMRI tokens drive a Multimodal AI to reconstruct the image.

METHODOLOGY

Visual cortex ROI masking

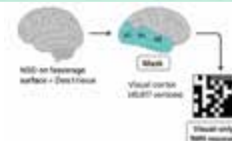


Figure 2 - Extracted visual-only data from the NSD betas by mapping them to the fsaverage³ cortical surface and applying the Destrieux⁴ (a2009s) atlas mask.

Three baseline approaches for learning fMRI representations were evaluated:

Principal Component Analysis (PCA)⁵ + Multi-Layer Perceptron (MLP)⁶

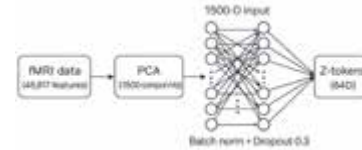


Figure 3 - PCA + MLP pipeline for encoding fMRI visual data into 64-D tokens.

Vision Transformer⁷ with Vector Quantization⁸ (ViT-VQ)

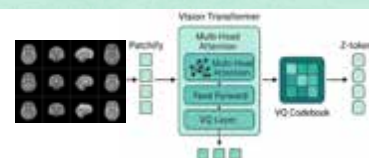


Figure 4 - ViT-VQ pipeline for encoding fMRI visual data into Z-tokens.

Variational Autoencoder⁹ with Vector Quantization (VQ-VAE)



Figure 5 - VQ-VAE pipeline for encoding fMRI visual data into Z-tokens.

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Gilda QUEZADA CORREA

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Supervisors: Bhanu Pothineni, Yuduo Chen, Yameng Lou

Gilda is supported by the Institute of Bioengineering

Abstract :

DNA origami nanostructures hold great promise for biomedical applications, yet their limited enzymatic stability and uncertain cellular uptake remain major barriers. This project addressed these challenges by evaluating the degradation of DNA disks in nuclease-rich environments and by studying how different fluorophores affect their cellular interactions and uptake. Together, these investigations provide fundamental insights to improve the design, robustness, and functionality of DNA nanostructures, helping advance their potential use in targeted drug delivery and diagnostic applications.

Engineering and Evaluating DNA Origami Nanostructures: Enzymatic Stability and Impact of Fluorophore on Cellular Uptake

EPFL

Gilda Quezada Correa^{1,2} and Maartje M. C. Bastings¹

¹ Programmable Biomaterials Laboratory, EPFL, Switzerland. ² KAUST, Saudi Arabia

**PROGRAMMABLE
BIOMATERIALS
LABORATORY**

1. DNA ORIGAMI NANOTECHNOLOGY

DNA origami is a method that folds a long single-stranded DNA scaffold into precise 2D or 3D shapes using short staple strands, allowing nanoscale control over structure and surface functionality.



Key Features:

- **Programmability:** arbitrary shapes and patterns can be designed in silico.
- **Biocompatibility:** DNA is inherently safe and biodegradable.
- **Functionalization:** chemical groups, fluorophores, peptides, or drugs can be attached with spatial precision.
- **Optimized morphology:** shape can be tuned for surface interactions and efficient cellular uptake.

Current Challenges:

- **Stability:** DNA origami is highly vulnerable to nuclease digestion in biological fluids.
- **Surface modifications:** even small chemical tags (like fluorophores) can drastically alter interaction and uptake with cells.

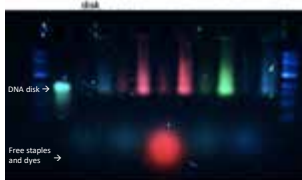
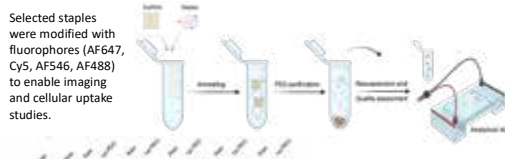


OBJECTIVES:

- **Evaluate enzymatic stability:** study how DNA origami disks degrade in nuclease-rich biological environments.
- **Investigate fluorophore impact:** determine how the chemical structure of fluorophores influences cellular uptake.

2. SYNTHESIS AND PURIFICATION

Selected staples were modified with fluorophores (AF647, Cy5, AF546, AF488) to enable imaging and cellular uptake studies.

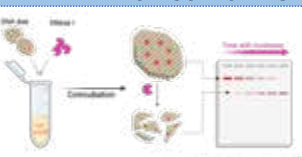


Excess staples and free fluorophores are removed by PEG precipitation. DNA disks are collected from the pellet for downstream use.

Before purification: Fluorescence at the gel bottom (free staples and dyes)

After purification: Disk band only

3. NUCLEASE DEGRADATION



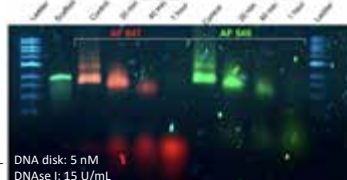
DNase I cleaves the DNA backbone, causing the origami disks to break apart [2].

The vulnerability of DNA origami to nucleases in biological fluids could limit in vivo applications.

The disk band gradually disappears over time.

Low-molecular-weight fragments increases as disks degraded.

After 1 h, the original disk band was completely disappeared for both AF647- and AF546-labeled disks.



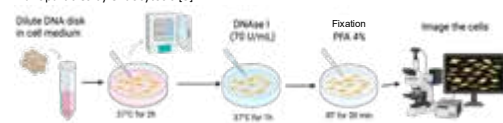
DNA disk: 5 nM
DNase I: 15 U/mL

CONCLUSIONS

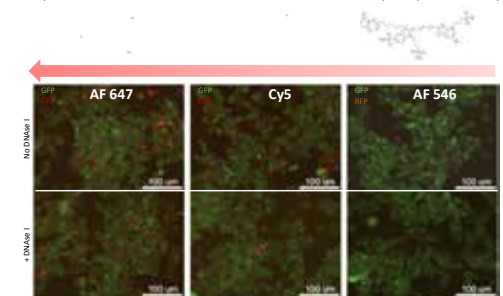
- Mapping enzymatic stability identifies conditions to preserve structural integrity in biological environments.
- Analyzing fluorophore-dependent uptake highlights how chemical modifications influence internalization and informs rational design for improved delivery and imaging.

4. CELLULAR UPTAKE

MutuDC dendritic cells were used for the experiments, as they efficiently internalize nanoparticles by endocytosis [3].



Fluorophore-labeled DNA disks were incubated with the cells to compare uptake efficiency.



AF647-labeled DNA disks exhibited the highest uptake, likely due to their hydrophobicity, and favorable charge distribution that enhance membrane interactions. Based on these findings, AF647 is recommended for labeling DNA disks in future cellular studies.

Besides, the fluorescence signal indicates that some disks may form aggregates, which could also hinder cellular uptake.

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Supervisors : Naman Mishra, Shuhao Zhang

Anna is supported by the Institute of Bioengineering

Abstract :

G-protein coupled receptors (GPCRs) are key to how our cells sense and respond to signals, and they are major targets for medicines. My project combines lab experiments with advanced computer models to design new, stable GPCRs from scratch, a process called *de novo* design, overcoming the limits of natural receptors. By creating GPCRs that switch between active and inactive states, this research could provide more reliable tools for science and inspire new therapeutic opportunities.

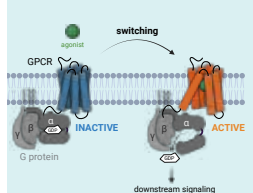
INTRODUCTION

GPCRs:

- G protein-coupled receptors (GPCRs) transduce extracellular signals into intracellular responses
- Targeted by ~30-40% of all modern drugs
- Shift from inactive to active primarily by moving transmembrane 6 outward

de novo design:

- Overcomes constraints of natural receptors with novel and tailored properties



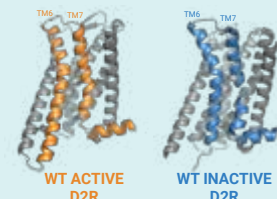
OBJECTIVES

Computational

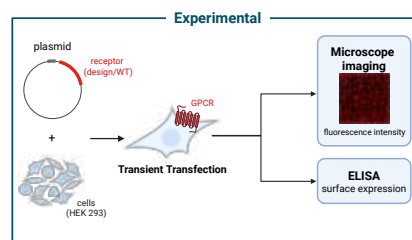
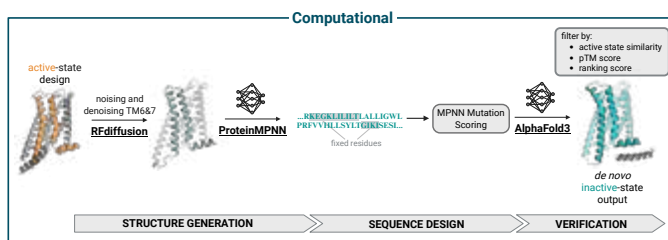
Design a stable inactive state from a stable active-state design with the smallest number of mutations.

Experimental

Validate *de novo* single-state GPCR designs.



METHODS



RESULTS

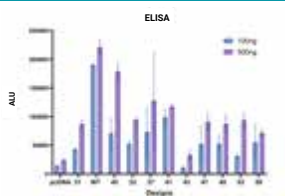


Fig. 1. ELISA for cell-surface expression. Positive control WT-D2R, negative control pcDNA.

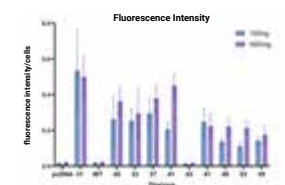


Fig. 2. Per cell fluorescence intensities. Positive control 31 (intermediate plasmid), negative control WT-D2R and pcDNA.

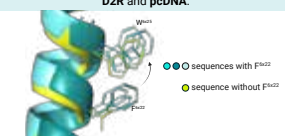


Fig. 3. WT-like upward shift of W219 and F216 was designed for a better clash with the ligand.

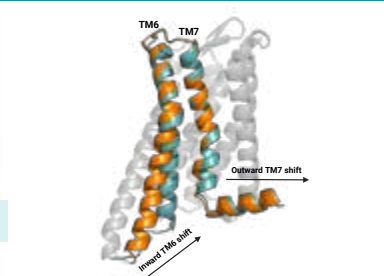


Fig. 4. RFDiffusion with Monomer ROG guiding potentials was used to generate the inactive state backbones.

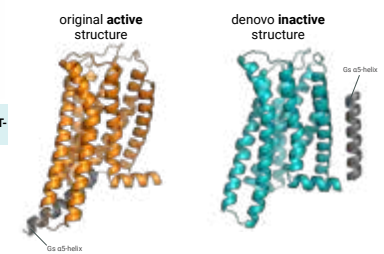


Fig. 4. Generated inactive designs could no longer accommodate the Gs α5-helix in the G-protein binding site, when predicted with AlphaFold3 single sequence mode.

CONCLUSIONS

- Single-state design 45 showed the strongest expression (Fig. 1–2).
- Upward shift of W²¹⁹ is essential for inactivation, enabled by the presence of F²¹⁶ (Fig. 3).
- Inward movement of TM6 and outward movement of TM7 are required for inactivation (Fig. 4); designs with insufficient TM6 shift remained active.
- The pipeline can successfully generate *de novo* inactive state structures which failed to accommodate the Gs helix (Fig. 5).
- Multi-state MPNN with active and inactive designs could result in switchable sequences.

Integrating structural features from the best-expressing designs with our computational pipeline will enable the creation of functional *de novo* GPCRs in the future.

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Supervisor: Pranay Dey

Sayani is supported by Fondation ISREC

Abstract :

Synthetic progestins in hormonal contraceptives exhibit divergent androgenic activities with implications for breast carcinogenesis. Using qRT-PCR and immunofluorescence in mammaplasty and ER+ PDX models, we show that chronic Levonorgestrel exposure, particularly in combination with estradiol, markedly upregulates Ki67, PGR, and pERK, indicating enhanced proliferative and MAPK signaling. In contrast, Drospirenone fails to elicit such effects and suppresses Ki67 induction. These data identify Levonorgestrel as a driver of early breast tumorigenesis, highlighting androgenic progestins as critical risk determinants in contraceptive safety.

Chronic Exposure to Levonorgestrel (androgenic progestin) but not an antiandrogenic progestin (Drospirenone) leads to early breast carcinogenesis

Sayani Bose, Pranay Dey(pranay.dey@epfl.ch), Cathrin Brisken(cathrin.brisken@epfl.ch)

L'exposition chronique au lévonorgestrel (progestatif androgénique), mais non à un progestatif antiandrogénique (drospirénone), conduit à une carcinogenèse mammaire précoce.

Chronische Exposition gegenüber Levonorgestrel (androgenes Gestagen), jedoch nicht gegenüber einem antiandrogenen Gestagen (Drospirenon), führt zu einer frühen Brustkarzinogenese.

Introduction

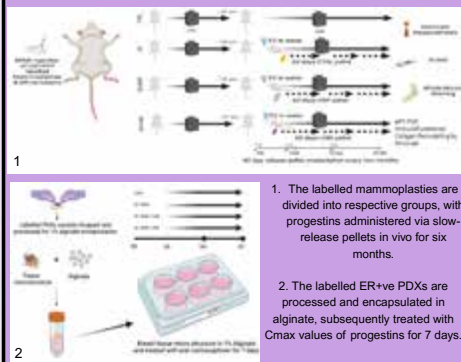
- Hormonal contraceptives often contain synthetic progestins, which can differ in their androgenic or antiandrogenic properties. Their long-term impact on breast tissue biology remains a key concern in cancer research.
- We hypothesize that Levonorgestrel exposure might promote early breast carcinogenesis, whereas Drospirenone does not exhibit this effect.
- Significance: These findings emphasize the importance of considering the androgenic profile of progestins in contraceptives and hormone therapies when evaluating breast cancer risk.



Research Approach

- qRT-PCR to analyse the proliferation and activation of hormone signaling after progestin treatment
- Immunofluorescence to check the hormone receptor levels and activation of growth factor signaling and proliferation by Ki67

Methods



- The labelled mammoplasties are divided into respective groups, with progestins administered via slow-release pellets in vivo for six months.
- The labelled ER+ve PDXs are processed and encapsulated in alginate, subsequently treated with Cmax values of progestins for 7 days.

Results

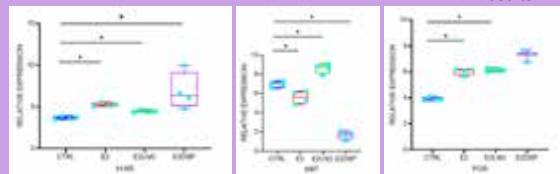


FIGURE 1 : Box and violin plots showing the relative expressions of the genes H-R, Ki67 and PGR in the conditions Control(CTRL), Estradiol(E2), Estradiol+Levonorgestrel(E2LNG), and Estradiol+Drospirenone(E2DSP). The treatment was carried out for 7 days. The qPCR was done in T218 treated in alginate after 7 days of treatment.

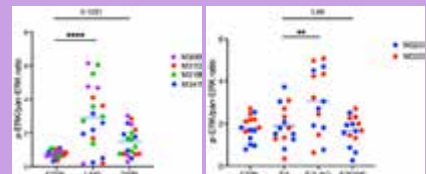


FIGURE 2 : Plots showing the ratio of Phospho-ERK(p-ERK) over total ERK(pan-ERK) in different mammoplasties samples (M308, M310, M318, M341, M320, M330) in the conditions CTRL, LNG, DSP, E2, E2LNG AND E2DSP after the analysis of immunofluorescence data. The treatment for mammoplasties were carried out for 6 months.

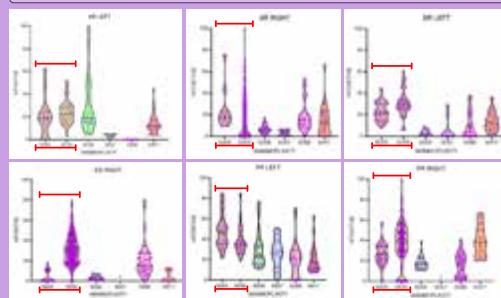


FIGURE 3 : Plots showing the %positive cells in different mammoplasties patients (M320, M330, M356, M357, M388, M411) to show the variation of steroid hormone receptors.

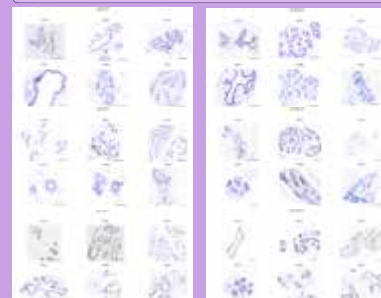


FIGURE 4 : Reference images for the different mammoplasties conditions corresponding to the different steroid hormone receptors.

Conclusion

- FIGURE 1: The plots show E2LNG strongly enhances proliferation, while Drospirenone E2DSP suppresses the Ki67 gene. Both E2 and progestins increase PGR expression, with Drospirenone showing the highest induction. ($p < 0.05$ for all the plots)
- FIGURE 2: pERK is the proliferation marker. Both the plots show that LNG greatly increases the Phospho-ERK (PERK) levels in the patients. In the second plot we can also see a slight(not significant) changes caused by E2. The changes cause by LNG are significantly ($p < 0.05$) more.
- FIGURE 3: The plots show the variation of steroid hormone receptors in different patients. We know that the Estrogen Receptor(ER) and Progesterone Receptor(PR) status changes all throughout menstruation cycle but the Androgen receptor(AR) status remain relatively stable. So we can rely on the information provided by this study on AR status to correlate the influence of AR signaling on breast cell proliferation post contraceptive treatment.
- FIGURE 4: Representative images showing the hormone receptor status in different patients.

References

- Shenavand, M., De Maribus, F., Constandin, C., Scabia, V., Laviollet, A. S., Laschi, C., Ayyanar, A., Battista, L., Rithoul, W., Gailloud-Mathieu, M. C., Bucher, P., Fohs, M., Ambrosini, G., Sftomas, G., & Brisken, C. (2021). Contraceptive progestins with androgenic properties stimulate breast epithelial cell proliferation. *EMBO molecular medicine*, 13(7), e14314. <https://doi.org/10.15252/emmm.202114314>
- Scabia, V., Ayyanar, A., De Martino, F. et al. Estrogen receptor positive breast cancers have patient specific hormone sensitivities and rely on progesterone receptor. *Nat Commun* 13, 3127 (2022). <https://doi.org/10.1038/s41467-022-30898-0>
- Hickey, T. E., Robinson, J. L., Carroll, J. S., & Tilley, W. D. (2012). Minireview: The androgen receptor in breast tissue: growth inhibitor, tumor suppressor, oncogene? *Molecular endocrinology* (Baltimore, Md.), 26(5), 1252–1267. <https://doi.org/10.1210/me.2012.1107>



Camilla BRÜCKMANN DE MATTOS

Universidade Federal do Rio Grande do Sul

Gönczy Lab of Cell and Developmental Biology

Supervisor: Samya Aich

Camilla is supported by Fondation ISREC

Abstract :

Centrioles are cylindrical organelles that duplicate once per cell cycle, with mother centrioles templating new procentrioles. While component-parts are known, which proteins are sufficient for centriole assembly is unclear. Using a synthetic SUMO/SIM condensate system to reroute PLK4 or SAS-6 to non-centriolar sites, we demonstrate that SAS-6 is not sufficient to direct centriole assembly, whereas PLK4 is sufficient to form distinct foci within droplets that recruit SAS-6 and CEP152. This highlights the system's utility in dissecting individual protein contributions to centriole assembly.

SUMO/SIM condensate system as a method to evaluate SAS-6 and PLK4 sufficiency in centriole assembly

Les systèmes de condensats SUMO/SIM comme méthode pour évaluer la suffisance de SAS-6 et PLK4 dans l'assemblage du centriole
SUMO/SIM-Kondensatsysteme als Methode zur Bewertung der Suffizienz von SAS-6 und PLK4 bei der Zentriolenassemblierung

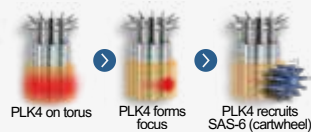
Camilla Brückmann de Mattos^{1,2}, Samya Aich² and Pierre Gönczy²

¹ Laboratory of Cell Signaling and Plasticity, Universidade Federal do Rio Grande do Sul, Brazil
² Laboratory of Cell and Developmental Biology, École Polytechnique Fédérale de Lausanne

INTRODUCTION

Centrioles are cylindrical microtubule-based organelles, present in pairs, that are **essential** for cell signaling, motility, division, and serve as **platforms for procentriole formation**.

CENTRIOLE ASSEMBLY



SUMO/SIM CONDENSATES AS A PROTEIN REROUTING SYSTEM

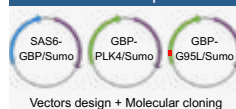


OBJECTIVE

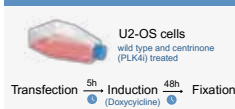
Determine whether SAS-6 and PLK4 are sufficient for centriole protein recruitment and ectopic centriole assembly using the SUMO/SIM system

METHODS

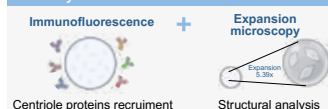
1 Plasmid Development



2 Cell Transfection



3 Analysis

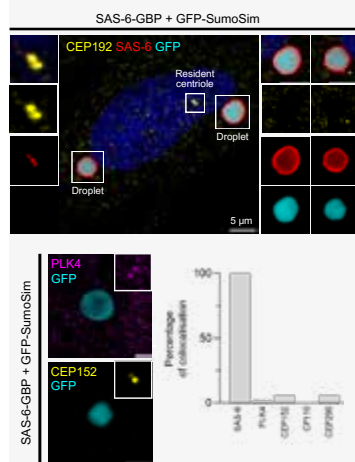


4 Imaging

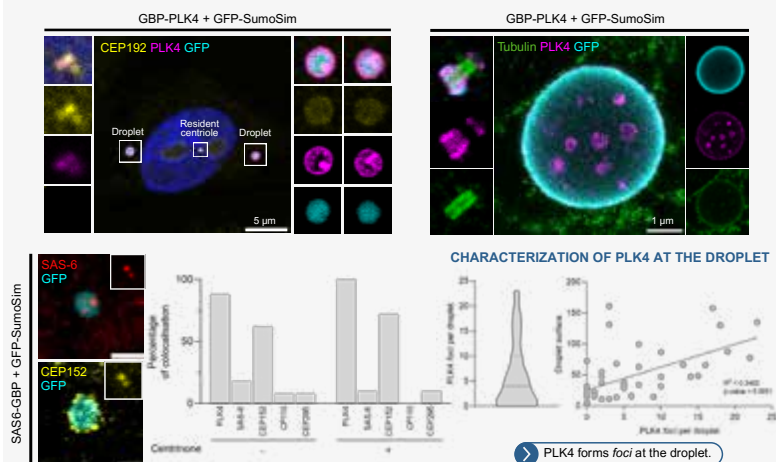


RESULTS

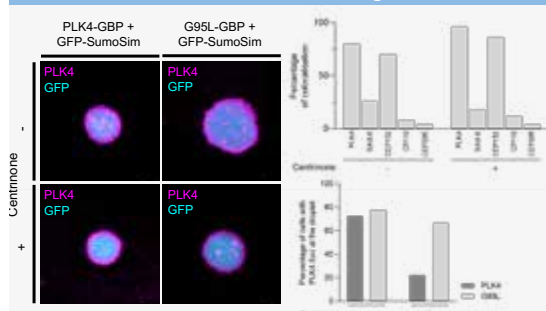
SAS-6 rerouting



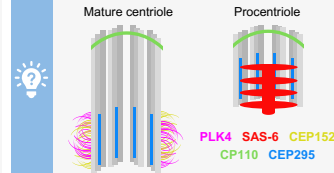
PLK4 rerouting



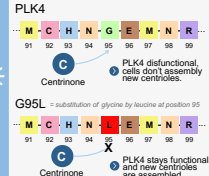
PLK4 G95L rerouting



CENTRIOLE PROTEINS ANALYSED



WHAT IS G95L?



CONCLUSIONS

- SAS-6 is not sufficient for ectopic centriole assembly.
- PLK4 is partially sufficient for ectopic centriole assembly, being able to recruit CEP152 and SAS-6.

REFERENCES





Febrina MARGARETHA

i3I Indonesia International Institute for Life Sciences

Thomä Lab – Paternot Chair in Cancer Research

Supervisor: Alexandra Bendel

Febrina is supported by Fondation ISREC

Abstract :

Some cellular proteins contain pockets that can be exploited in drug discovery, allowing inhibitors to bind and block their functions. This is crucial when dysfunctional proteins drive disease. Yet, many disease-relevant proteins lack such pockets. For these, molecular glues represent a new drug class. They promote protein-protein interactions without relying on structural binding pockets, thereby modulating activity or triggering degradation. Developing such glues remains challenging, so our goal is to create systematic methods to screen for them rationally.

Deciphering molecular glue-mediated protein-protein interactions through dihydrofolate reductase-based protein-fragment complementation assay (DHFR-PCA)

Febrina Margaretha^{1,2}, Marvel Ehab Sobhy Hanna^{2,3}, Alexandra Bendel², Nicholas Thomä²

¹ Department of Bioinformatics, School of Life Sciences, Indonesia International Institute for Life Sciences; ² UPTHOMAS, Swiss Institute for Experimental Cancer Research, École Polytechnique Fédérale de Lausanne; ³ John A. Paulson School of Engineering and Applied Sciences, Harvard College

INTRODUCTION

BACKGROUND

- Targeted protein degradation:** usage of **small-molecule** drugs to induce the selective **degradation** of **disease-related** proteins
- Molecular glues** (MGs): small molecules that **induce** protein-protein interactions (PPIs) on targets that **usually do not interact**
- MG degrader: MG major class that works by promoting **ubiquitination** and degradation of the **protein of interest** (POI)

MOLECULAR GLUE DEGRADER MECHANISM



RESEARCH MOTIVATION

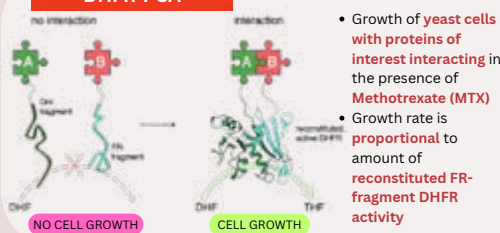
- MGs reprogram protein-protein interaction binding surfaces, stabilizing **weak interactions**
- A novel therapeutic strategy to target **>85%** of proteins, which are deemed **"undruggable"** and lacking **"binding pockets"** (e.g. transcription factor, membrane proteins)
- MGs are rather **discovered serendipitously**

OBJECTIVES

- Proof of concept: Establish a **yeast-based binding assay** for **existing glue-induced interaction** (FKBP12-FK506-Calcineurin)
- Expand the **target space** of a glueable E3 ligase (VHL) by stabilizing **weak interactions** through **covalent bonds**

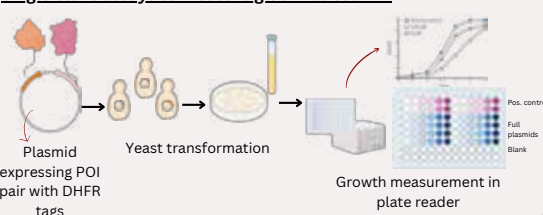
METHODOLOGY

DHFR-PCA



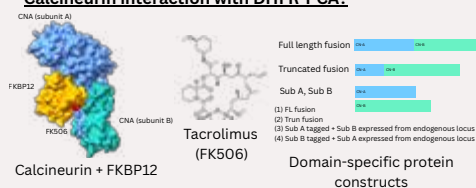
- Growth of **yeast cells** with **proteins of interest** interacting in the presence of **Methotrexate (MTX)**
- Growth rate is **proportional** to amount of **reconstituted FR-fragment DHFR activity**

Single clone assays to measure glue-induced PPI

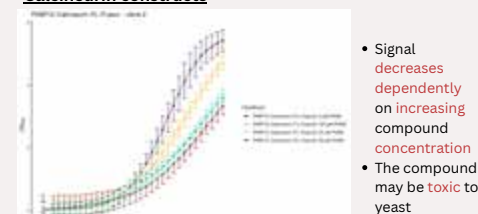


RESULTS

Proof-of-concept: Can we measure the FKBP12-FK506-Calcineurin interaction with DHFR-PCA?

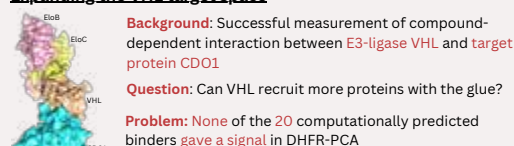


FK506 dimerization mediated binding in FKBP12-Calcineurin constructs

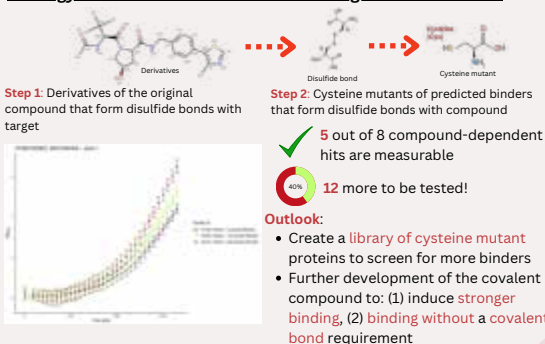


Outlook: Make a yeast mutant strain with FK506-resistant FKBP12 and/or calcineurin → repeat experiment in a mutant background

Expanding the VHL target space



Strategy: Stabilize weak interactions through covalent bonds





Abdinoor Kassim DAGANE

University of Debrecen

Antanasijevic Lab of Virology and Structural Immunology

Supervisors: Ammar Khobieh, Tiago Lopes Monteiro, Lh  a Warnery

Abdinoor is supported by Tomorrow Foundation

Abstract :

The rabies virus glycoprotein (RABV-G), the sole surface antigen, mediates host entry and is the main target for neutralizing antibodies and vaccines. Its unstable pre-fusion trimer limits structural analysis and immunogenicity. We engineered stabilized RABV-G variants via site-directed mutagenesis, expressed them in HEK293T cells, and purified them for analysis by chromatography, SDS-PAGE, and Western blot. ELISA and electron microscopy confirmed structural and antigenic integrity. These variants demonstrated improved purity and antigenicity, advancing rational development of next-generation rabies vaccines and therapeutics.

Structural Analysis of the Rabies Virus Glycoprotein

Abdinoor Kassim Dagane^{1,2}, Ammar Khobieh¹, Tiago Lopes Monteiro¹, Lh  a Warnery¹
Professor: Aleksandar Antanasijevic¹

¹ Antanasijevic Lab – Virology and Structural Immunology, EPFL, Switzerland; ² University of Debrecen, Hungary

Abstract

The rabies virus glycoprotein (RABV-G) is the sole surface antigen of rabies virus, mediating host-cell entry and serving as the primary target for neutralizing antibodies and vaccine design. Its pre-fusion trimeric state is structurally unstable, limiting high-resolution characterization and, potentially, its capacity to induce neutralizing antibodies. To address this, we engineered stabilized RABV-G variants through site-directed mutagenesis. Verified plasmid constructs were expressed in HEK293T cells under optimized transient transfection conditions, followed by affinity purification and analysis via size-exclusion chromatography, SDS-PAGE, and Western blot to evaluate size and homogeneity. Selected constructs were then probed with monoclonal antibodies in ELISA and electron microscopy experiments to verify the presence of appropriate structural and antigenic features in designed constructs. The generated designs show significant improvement compared to WT rabies glycoprotein, in terms of purity and antigenicity, thereby providing an important first step towards the rational design of next-generation rabies vaccines and therapeutics.

Background

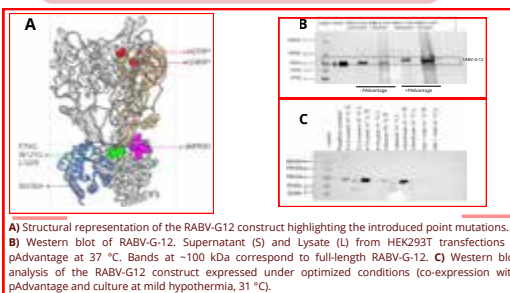
- Rabies virus infection is almost always fatal if untreated, causing >50,000 deaths per year.
- The rabies virus glycoprotein (RABV-G) mediates viral entry and is the main target of neutralizing antibodies.
- Current rabies vaccines rely on RABV-G but can trigger non-neutralizing immune responses due to its structural heterogeneity.
- Stabilizing RABV-G in its prefusion conformation may lead to more effective and durable vaccines.
- This project investigates an engineered RABV-G variant (RABV-G-12) to improve protein stability, expression, and suitability for structural studies.

Objective

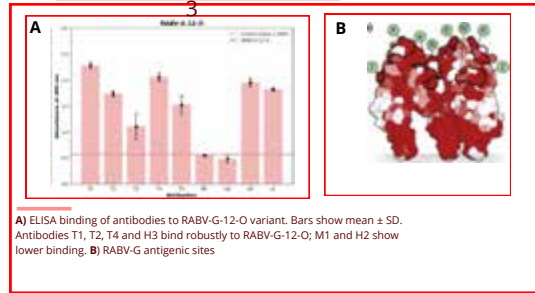
Engineer and characterize stabilized RABV-G variants suitable for structural analysis and antibody complexing.

Results

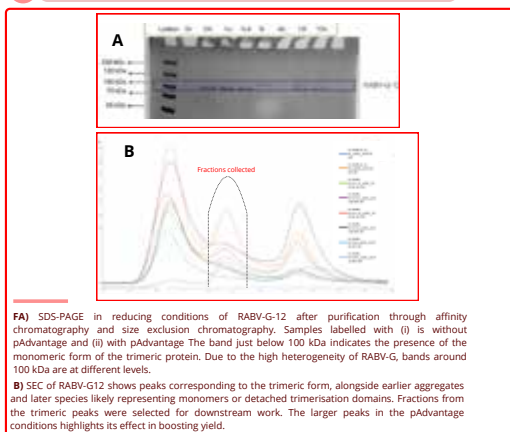
1 Expression of stabilized RABV-G construct



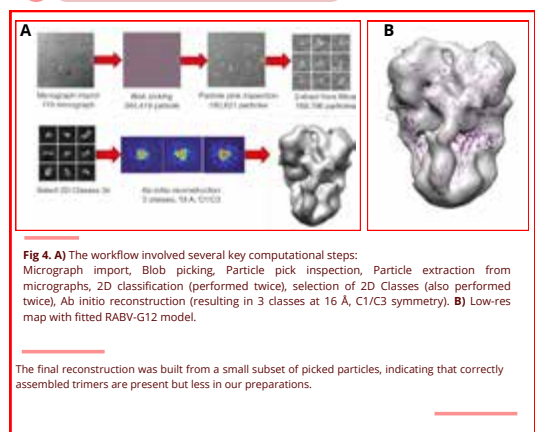
Antigenic analysis using ELISA



2 Purification of the stabilized RABV-G construct



4 Structural analysis of RABV-G



CONCLUSION

The stabilized RABV-G12 variant can be successfully expressed and purified while retaining its antigenicity. Negative-stain electron microscopy revealed trimeric particles; however, only a minor proportion of selected particles contributed to the final 2D classes, suggesting a low yield of correctly assembled trimers. Although co-expression with pAdvantage enhanced overall protein expression, further optimization of folding and secretion pathways will be critical to improving the recovery of properly assembled trimeric fractions. Ongoing work involves testing additional stabilizing mutations to further characterize structural integrity and antigenic properties.



• Rabies Virus Overview: Structure, Transmission, Pathogenesis, Symptoms, etc [WWW Document], n.d., CUSABIO. URL <https://www.cusabio.com/infectious-diseases/rabies-virus.html> (accessed 8.7.25).
 • de Melo, G.D., Hellert, J., Gupta, R., Corti, D., Bourhy, H., 2022. Monoclonal antibodies against rabies: current uses in prophylaxis and in therapy. *Current Opinion in Virology* 53, 101204. <https://doi.org/10.1016/j.coviro.2022.101204>





Carl DAMELL

Uppsala University

Persat Lab of Microbial Mechanics

Supervisor: Miro Plum

Carl is supported by the Global Health Institute

Abstract :

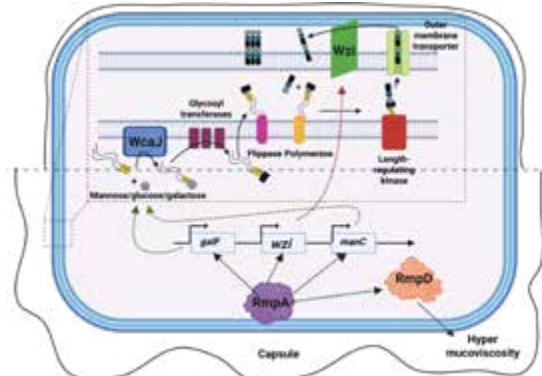
Hypervirulent *Klebsiella pneumoniae* (hvKp) causes severe, invasive infections in otherwise healthy people. This project aims to expand our knowledge on how capsule morphology affects hvKp infection in the lungs. Capsule synthesis genes, *wcaJ* and *wzi*, and capsule regulating genes, *rmpA* and *rmpD*, were knocked out. Lung transwells were then infected with the knockout mutants and studied using spinning disc confocal microscopy. The results indicate that knockouts in both synthesis genes and regulatory genes decrease the invasiveness of the hvKP.

Capsule morphology affects *Klebsiella pneumoniae* lung infections

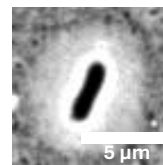
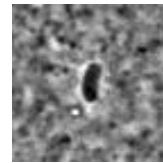
Carl Damell¹, Miro Plum², Alexandre Persat²

²Global Health Institute, School of Life Science, EPFL, Lausanne, Switzerland

How does capsule morphology affect *Klebsiella pneumoniae* in lung infections?

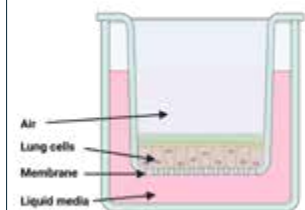


- *wcaJ* is the initiating step in capsule synthesis
- *wzi* anchors polysaccharides to the membrane
- *rmpA* and *rmpD* regulate capsule synthesis and mucoviscosity respectively

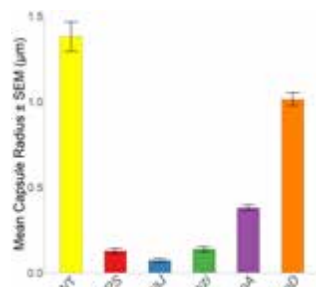


Approach

1. Construct *K. pneumoniae* mutants ($\Delta wcaJ$, Δwzl , $\Delta rmpA$, $\Delta rmpD$).
2. Capsule properties: sedimentation, string test, capsule size and growth rate.
3. Infection of lung transwells with mutants and microscopy.



Indian ink capsule quantification

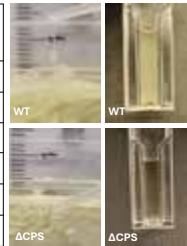


- All mutants have altered capsule morphology

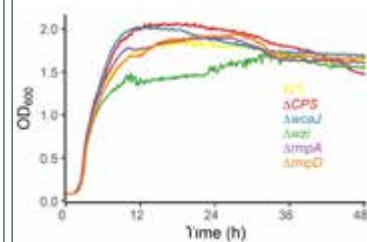
String test and sedimentation

Strain	String test	OD ₆₀₀		
WT	Pos.	1.00		
ΔCPS	Neg.	0.04		
$\Delta wcaJ$	Neg.	0.02		
Δwzi	Pos.	0.65		
$\Delta rmpA$	Neg.	0.04		
$\Delta rmpD$	Pos.	0.22		

- Small capsule mutants can still be mucoviscous.
- This depends on which gene is deleted

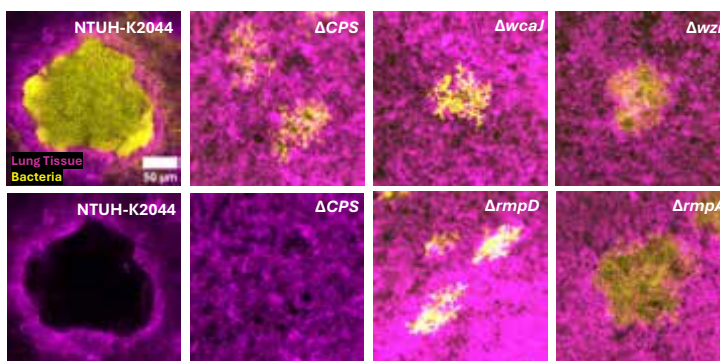


Growth in liquid media



- Changes in capsule production alters growth
- Changes in capsule regulation does not alter growth

Characterization of lung infection in capsule mutants



- Defects in capsule regulation and production leads to:
 - Smaller colonies
 - No invasion in lung tissue

Conclusion

- Alterations of capsule morphology changes mechanical properties, growth and infection.
- Reduced capsule hvKp colonies are smaller in lung infections compared to WT.
- Reduced capsule hvKp do not invade lung tissue during infection.

Acknowledgements

Prof. Alexandre Persat, Dr. Miro Plum and the SRP.

References

Rendueles, O. Deciphering the role of the capsule of *Klebsiella pneumoniae* during pathogenesis: A cautionary tale. *Molecular Microbiology* **113**, 883–888 (2020).

Dorman, M. J., Feltwell, T., Goulding, D. A., Parkhill, J. & Short, F. L. The Capsule Regulatory Network of *Klebsiella pneumoniae* Defined by density-TraDISort. *mBio* **9**, e01863-18 (2018).

Capsule schematic and lung transwell schematic were created in <https://BioRender.com>



Rachelle FERNÁNDEZ-VARGAS

University of Costa Rica

Paoli Lab of Microbiome Immunity and Ecology

Supervisors: Agatha BredeI

Rachelle is supported by McCall MacBain Foundation

Abstract :

The ocean microbiome sustains life on Earth, yet microbial immunity against viruses across ecological gradients remains poorly understood. This project investigates the variation of microbial immune systems across the planktonic matter continuum, focusing on free-living versus particle-attached lifestyles. Using metagenomic datasets, we characterized the composition and density of defense systems across oceanic size fractions. Results show that particle-associated bacteria exhibit enriched and distinct repertoires of antiviral defenses, highlighting ecology as a key driver of microbial immunity in marine environments.

How does ecology shape microbial immunity across the planktonic matter continuum?

Rachelle Fernández-Vargas, Agathe Bredel & Lucas Paoli

École Polytechnique Fédérale de Lausanne, Switzerland

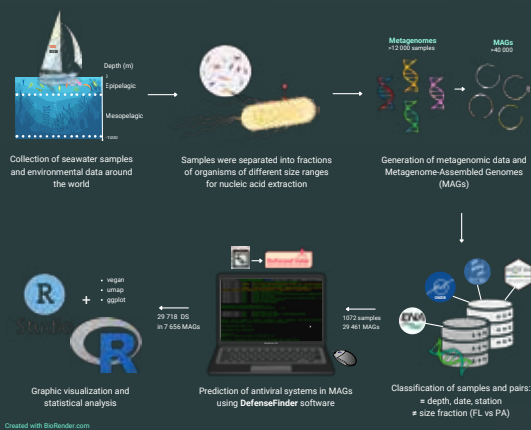
INTRODUCTION

- The **ocean microbiome sustains life on Earth**, driving global biogeochemical cycles and food webs.
- Interactions between **microbes and their viruses** shape oceanic community composition and ecosystem function.
- Bacteria have evolved a variety of **antiviral defense systems** (immunity) to survive in virus-rich environments, such as CRISPR and restriction modification (RM).
- However, the variation of these defense systems across **ecological gradients and bacterial lifestyles**, remain poorly understood.

AIM

- To investigate how antiviral defense systems varies across the planktonic matter continuum and whether lifestyle (free-living (FL) or particle attached (PA) bacteria) influences microbial immunity in the ocean.

METHODS



CONCLUSION

- Defense system composition varies across size fractions.
- PA samples tend to cluster together, while FL and Mixed are more heterogeneous.
- RM, Cas, CBASS, AbiE, and SoFI are enriched in PA samples; RADAR, Gao-TerY, and VP1840 in others.
- PA fractions show higher defense system density than FL in overall and under the same ecological conditions, suggesting bacterial lifestyle as a key driver of antiviral defense repertoires.

Acknowledgements

I thank Dr. Lucas Paoli and doctoral assistant Agathe Bredel for their mentorship throughout this project.

RESULTS

1 Clustering of defense systems across size fractions

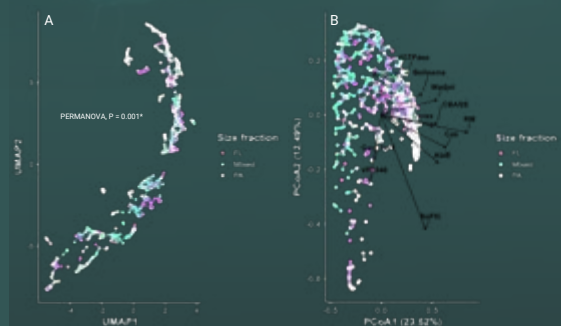


Fig. 1. (A) UMAP of defense system density profiles, with samples colored by size fraction. (B) PCoA based on a Bray-Curtis distance matrix, with vectors representing the most abundant defense systems. PERMANOVA indicated significant compositional differences among size fractions ($R^2 = 0.058$, $p = 0.001$, 999 permutations).

2 Density of defense systems across size fractions and pairs

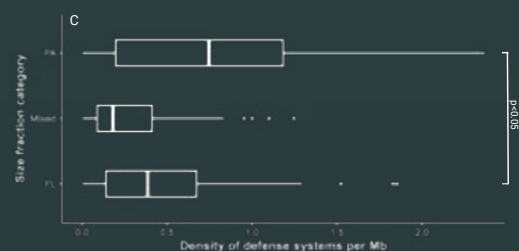


Fig. 2. Average density of defense systems per size fraction. Density was calculated as the number of defense systems per sample normalized by total genome size (Mb), considering only samples with ≥ 10 genomes. Wilcoxon rank-sum test revealed significant differences among fractions ($p < 0.05$).

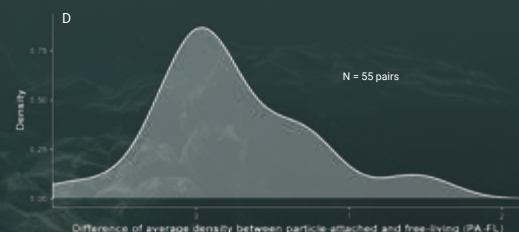


Fig. 3. Distribution of pairwise differences in defense system density (PA - FL). Paired samples were matched by ecological conditions (depth, station, date) but differed in size fraction.



Anna SUSHNOVA

University of Kyiv

[Van der Goot Lab of Cell and Membrane Biology](#)

Supervisors: Laurence Abrami, Jerome Archambeau

Anna is supported by an Anonymous Donor

Abstract :

S-acylation (palmitoylation) is a reversible post-translational modification in which palmitic acid is attached to cysteine residues by palmitoyl acyltransferases (PATs) with a conserved DHHC domain. TMEM214, a transmembrane ER protein implicated in ER morphology and lysosomal distribution, contains 15 cytosolic cysteines as potential modification sites.

We identified specific PATs mediating TMEM214 S-acylation and mapped candidate cytosolic residues. Furthermore, S-acylation was found to alter TMEM214 perinuclear localization, suggesting a regulatory role in ER organization.

To respect the confidentiality of unpublished results, we have included a concise abstract instead of the full poster for this project



Anuj Prafulla CHAVAN

University of Toronto

[Van de Ville Lab of Medical Image Processing](#)

Supervisor: Maria Giulia Preti

Anuj is supported by McCall MacBain Foundation

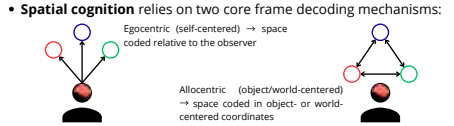
Abstract :

Human spatial cognition relies on the integration of egocentric and allocentric reference frames to support perception and navigation. Disruptions in these mechanisms are associated with attentional and navigational deficits, emphasizing the importance of investigating underlying effective connectivity (EC). Recent evidence implicates the Posterior Intra-Temporal (PIT) area as a potential hub for allocentric processing within the attentional control network. We use functional MRI and Dynamic Causal Modeling to examine PIT's interactions during spatial perception visual tasks involving faces/houses. Testing competing EC models across 3,4-node architectures, this work aims to examine connectivity contributions to reference frame transformations and the broader dynamics of spatial cognition.

Allocentric and Egocentric Reference Frames

Introduction:

- The brain uses both **egocentric** and **allocentric** frames to visually perceive and navigate spatially.
- Spatial cognition** relies on two core frame decoding mechanisms:

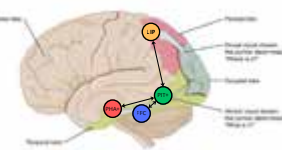


Disruptions in these mechanisms → clinical implications

- Disrupted Attentional Modulation
- Erroneous Spatial Cognition and Reasoning
- Navigation deficits

Theory, Recent Advances, Past Investigations

Classical brain networks with lateral view of human brain with labelled lobes and visual processing pathways [1]



- Ventral occipito-temporal stream → object identity ("What is it?")
- Dorsal occipito-parietal stream → spatial location ("Where is it?")
- Recent advances [2] suggest **Posterior Infero-Temporal (PIT)** area as a **new attentional control node** which:
 - shows **strong attention-related modulation** (not feature-specific responses).
 - structurally connected** to parietal (LIP) and frontal nodes → **suggesting a three-node attention network** (ie. fronto-parietal network → attentional control).

Objectives

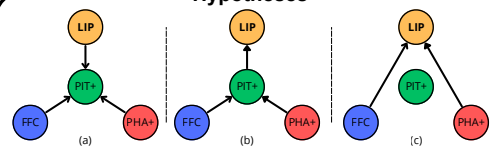
- How do PIT, LIP, FFC (faces), and PHA (houses) interact during egocentric vs. allocentric tasks?
- Does PIT serve as an allocentric computing hub, or simply relay information during egocentric processing?

Methods and Approach

Shows the methodological analysis pipeline

- MRI Scans - Subjects performed spatial perception tasks with visual stimuli (faces and houses) with contrasted egocentric and allocentric judgment.
- General Linear Model (GLM) estimated activation patterns for each condition and specified a design for subject level DCM.
- ROI Definition & BOLD Time Series Extraction - ROIs time series were extracted for each subject.
- Dynamic Causal Modeling (DCM) - Designed and estimated competing hypothesis with (i) 3-Nodal (ii) 4-Nodal models.

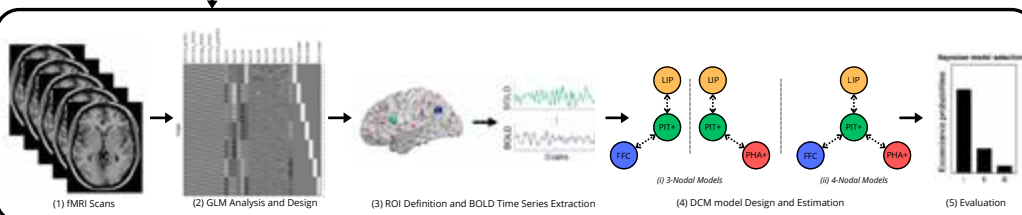
Hypotheses



Competing hypotheses models of statistically significant directional pathways (Effective Connectivity). From left to right (a) Allocentric Computing, (b) Egocentric Relay, (c) Egocentric Direct

- Allocentric Computing:** During allocentric processing, PIT will receive visual information about the object's identity from FFC and PHA and space information from LIP.
- Egocentric Relay:** During egocentric processing, LIP will receive visual information about the object's identity from FFC and PHA through PIT.
- Egocentric Direct:** LIP receives visual information about the object's identity from FFC and PHA.

LIP: Lateral Intraparietal, PIT+: Posterior Infero-Temporal Area, FFC: Fusiform Face Cortex, PHA+: Posterior Hypothalamic Area



Dynamic Causal Modelling

- First-level modeling** was performed **subject-wise** and session-wise to capture individual variability.
- Models were constructed separately for **left and right hemispheres**.
- 3-node models** were designed to **test simplified hypotheses** (PIT-LIP-PHA/FFC).
- 4-node models** were built to **incorporate full network interactions** (PIT, LIP, FFC, PHA).
- Each **model was fitted to observed fMRI BOLD time series**, and connectivity parameters were estimated.
- Subject-wise session data was augmented** to reperform methods for better design.

Current Results and Future Work

- Preliminary model fitting (session-wise) estimation **achieved minimal fit** between observed and simulated data.
- Perform estimation on augmented session data** per subject and **finalize DCM fitting**.
- Complete Bayesian statistics on subject-level and group-level analyses across all participants** and conditions.
- Quantify exceedance probabilities to **identify the best-fitting hypothesis**.
- Refine model space by testing reduced vs. extended connectivity patterns.

References

- [1] Marin, G., Vuilleumier, P., Sani, I. et al. Human Spatial Cognition: Behaviors and Neural Networks of Allocentric Space Processing. Masters Thesis, Department of Neurosciences, Faculty of Medicine, University of Geneva
- [2] Sani, I., Stemmann, H., Caron, B. et al. The human endogenous attentional control network includes a ventro-temporal cortical node. Nat Commun 12, 360 (2021). <https://doi.org/10.1038/s41467-020-20583-5>



Héloïse HUGHES

Amherst College

Nakatsuka Laboratory of Chemical Nanotechnology

Supervisor : Jokubas Surgailis

Héloïse is supported by the Neuro-X Institute

Abstract :

Electrochemical sensors enable quantification of molecules by converting chemical interactions into measurable electrical signals, enabling monitoring of neurotransmitters such as dopamine – a critical molecule for brain health. Aptamers are DNA sequences engineered to undergo conformational changes upon binding specific target molecules, while molecularly imprinted polymers (MIPs) are synthetic materials embedded with target-shaped cavities for selective detection. By integrating hybrid aptamer-MIP sensing layers onto electrodes, our goal was to develop a durable, selective, and miniaturizable dopamine biosensor.

Aptamer-Integrated Molecularly Imprinted Polymer Sensors for Dopamine Detection

EPFL

Héloïse Hughes, Jokūbas Surgailis, Nako Nakatsuka
Laboratory of Chemical Nanotechnology (CHEMINA), Neuro-X Institute, EPFL

CHEMINA

Introduction

Electrochemical neurotransmitter sensors enable quantification of molecules by converting chemical signals into measurable electrical signals, to contribute towards the understanding of neuroscience through in vitro or in vivo monitoring. Such devices require fast and sensitive responses while being miniaturized and affordable. An aptamer and Molecularly Imprinted Polymers (MIPs) sensor was developed to detect dopamine, which is involved in neurodegenerative diseases such as Parkinson's Disease. Aptamers are DNA sequences that change conformation when bound to a specific target molecule, while MIPs are polymers imprinted with the shape of the target molecule to enable specific detection. Hybrid aptamer-MIP sensing layers are integrated onto single electrodes and act as a sensors, creating a selective but durable biosensor.

Optimizing Polymer Thickness

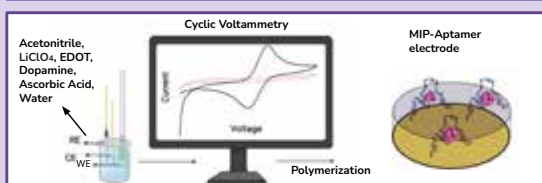


Fig 2: Electropolymerization with three electrode setup using cyclic voltammetry in a polymer solution containing dopamine, which causes the aptamer to change conformation during polymerization

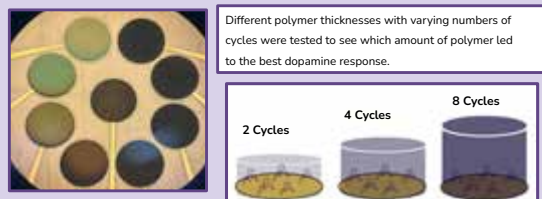


Fig 3: Range of polymer thickness on the gold electrode: from 2 to 10 cycles (left to right) of cyclic voltammetry.

Fig 4: Schematic of different polymer thicknesses, quantified by number of cycles in cyclic voltammetry

Nonspecific Binding with Serotonin



Fig 8: Schematic of device response to dopamine vs. serotonin

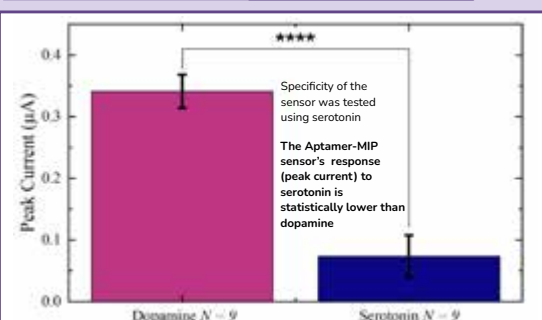


Fig 9: Bar chart of peak current for the Aptamer-MIP device, dopamine and serotonin, Tukey's HSD, $p < 0.05$

Conclusion

- The aptamer-molecularly imprinted polymer electrode shows the largest response to dopamine, compared to other conditions
- The designed electrode shows some signs of specificity: larger response to dopamine than serotonin

References

- Nako Nakatsuka *et al.*, Aptamer-field-effect transistors overcome Debye length limitations for small-molecule sensing, *Science* 362,319-324(2018).
- Shen, M. and X. Kan, Aptamer and molecularly imprinted polymer: Synergistic recognition and sensing of dopamine. *Electrochimica Acta*, 2021. 367: p. 137433.

Acknowledgements:

EPFL School of Life Sciences Summer Research Program



Future Directions

- Further tests for non-specific binding with more structurally similar molecules: L-Dopa, norepinephrine
- Make this aptamer-MIP-modified electrode the gate for an organic electrochemical transistor (OECT) to amplify the detection

Acknowledgements:

EPFL School of Life Sciences Summer Research Program



Method

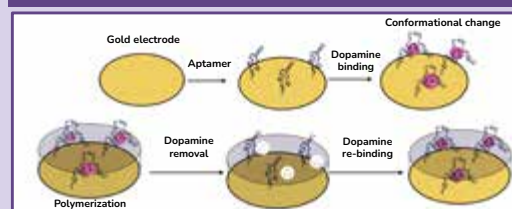


Fig 1: Method schematic: aptamer functionalization, electropolymerization, dopamine sensing

Comparing Different Sensor's Response to Dopamine

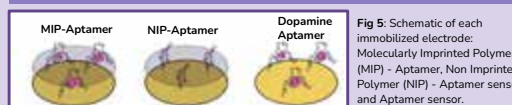


Fig 5: Schematic of each immobilized electrode: Molecularly Imprinted Polymer (MIP) - Aptamer, Non Imprinted Polymer (NIP) - Aptamer sensor and Aptamer sensor.

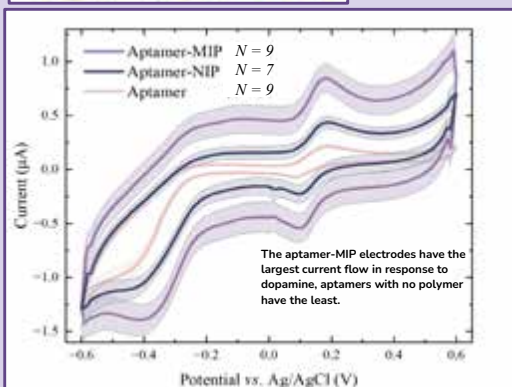


Fig 6: Cyclic voltammogram of 3 devices, last of 10 cycles with a standard deviation across nine or seven trials

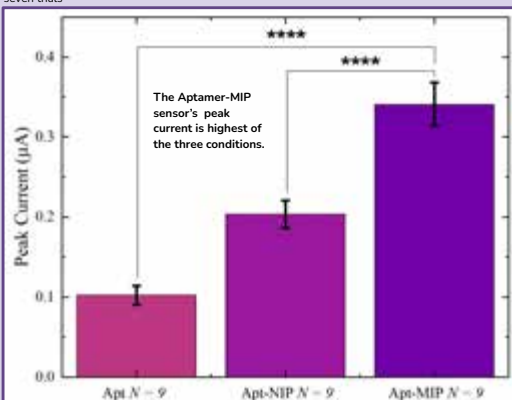


Fig 7: Bar chart of peak current for the Aptamer, Aptamer-MIP and Aptamer-NIP electrodes, Tukey's HSD, $p < 0.05$



Mayuka OTSUKI

Oberlin College

[Blanke Lab of Cognitive Neuroscience](#)

Supervisors: Haotian Yao, Bruno Herbelin

Mayuka is supported by the Neuro-X Institute

Abstract :

Studying the human vestibular system is challenging because physical movements create both mechanical and physiological noises. This project exploits the post-rotation effect—the sensation of spinning after physical movement stops—to record clean brain signals while participants are equipped with an EEG cap sitting in a rotating chair. We developed a system that wirelessly syncs EEG data with a precisely controlled rotating chair. This method enables future studies on how the brain integrates vestibular information to form a coherent sense of self.

Recording the neural responses evoked by natural vestibular stimuli in humans during rotation post-effects

Mayuka Otsuki¹, Haotian Yao¹, Bruno Herbelin¹, Olaf Blanke¹

¹Laboratory of Cognitive Neuroscience, EPFL;

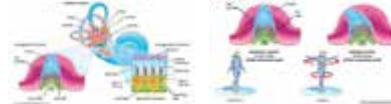


1 Introduction

- The vestibular sense is crucial for our sense of balance, spatial orientation, and self-consciousness.
- Understanding its neural basis is a significant challenge in understanding our body consciousness
- Traditional methods of studying the vestibular sense with EEG are hampered by "noise" from physical movement.
- **Our research focuses on the "post-rotation effect"**—the sensation of movement that persists after rotation has stopped¹.
- This allows us to isolate the brain activity related purely to the sensation of balance, providing a clean and clear signal for us to study¹.

2 Background

The fluid in your semicircular canals has **inertia**. When you stop spinning, this fluid doesn't stop immediately—it keeps swirling for a moment. This continued motion pushes the cupula in the **opposite direction**, sending a false signal to your brain that you're now spinning the other way. This is the post-rotation effect.



3 Method Overview

1. Hardware & Equipment

- A unique, self-contained recording system was built and **mounted on the rotating chair** to capture clean EEG during motion.
- **ANT Neuro 64-channel EEG**
- **Mobile Streaming** (a mini-computer mounted on the chair)

2. Programming & Automation

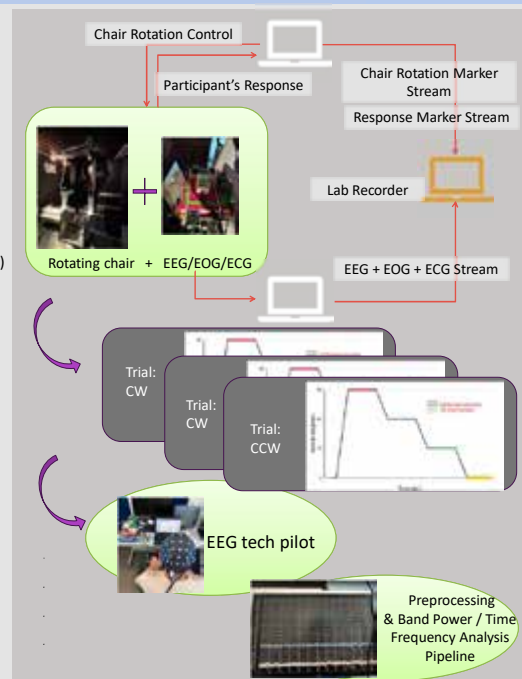
- **Synchronized Control**: Custom C# application in Unity to control the chair's "raised cosine" rotation profile while sending synchronized event markers over **Lab Streaming Layer (LSL)**, enabling a wireless stream of information.
- **Unified Recording**: Implemented LSL for time-stamped data file (.xdf)

3. Recording Protocol

- **Trial Structure**: Each trial consisted of a timed sequence of acceleration, constant-speed rotation, deceleration, and rest.
- **Randomized Conditions** by direction (Clockwise/Counter-clockwise).
- **Calibration Program**: Before each experiment session, participants reported their subjective sensation of rotation to optimize the duration of constant-speed rotation and rest.

4. Preprocessing & Data Analysis

- A custom pipeline was written in Python using the MNE library.
- **FASTER³-inspired Automated Artifact Removal**:
 - Filtering (0.1-40 Hz band-pass, 50 Hz notch)
 - Bad channel interpolation
 - Independent Component Analysis (ICA) and automatic artifact rejection based on EOG/ECG to remove eye-movement and heartbeat-related noise.
- **Band Power Analysis, Time Frequency Analysis**



4 Results & Discussion

- Successfully established a **synchronized EEG and rotating chair**.
- Developed a **robust data-preprocessing pipeline that effectively removes artifacts from the chair rotation**.
- Future Directions: Conduct a full-scale study with more participants. Explore how this research can contribute to our understanding of human self-consciousness.

References

1. Gale, S., Piss, M., Schurger, A., Gay, A., Pallard, A., Herbelin, B., Guyot, J.-P., Lopez, C., & Blanke, O. (2016). Oscillatory neural responses evoked by natural vestibular stimuli in humans. *Journal of Neurophysiology*, 115(3), 1228–1242. <https://doi.org/10.1152/jn.00153.2015>
2. LabStreamingLayer: LabStreamingLayer Super Repository Comprising Submodules for LSL and Associated Apps. n.d. Github. Accessed August 21, 2025. <https://github.com/NeuroLab/LSL>
3. Nolan H, Whelan R, Reilly RB. FASTER: Fully Automated Statistical Thresholding for EEG artifact Rejection. *J Neurosci Methods*. 2010 Sep 30;192(1):152-62. doi: 10.1016/j.jneumeth.2010.07.015. Epub 2010 Jul 21. PMID: 20654646.

Partner/Sponsor:





Iliana HERNANDEZ

Southwestern University, Texas

McCabe Lab of Neural Genetics and Disease

Supervisors: Rebecca Smith, Evelyn Ruchti

Iliana is supported by the Brain Mind Institute

Abstract :

Dale's Principle proposes that neurons release the same neurotransmitter at all synapses, but evidence of dual release challenges this view. In *Drosophila melanogaster*, scientists have debated whether segregated neurotransmission occurs. Using the UAS genetic reporter system, we examined neuronal populations for signs of dual signaling. While reporter leakiness posed challenges, our data identified cases suggesting segregated neurotransmission, providing important insight into neurotransmitter organization in *Drosophila*.

Dual Neurotransmission in *Drosophila melanogaster*

Iliana Hernandez, Evelyn Ruchti, Rebecca Smith, Brian McCabe

Laboratory for Neural Genetics and Disease

1 Introduction



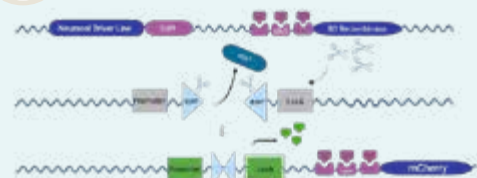
Dale's Principle (1935): Neurons release the *same* neurotransmitters at all synapses

Modern Evidence: Some organisms can *co-release* multiple transmitters from the same pre-synaptic terminal

Current Belief: *Drosophila Melanogaster* does not use any form of dual transmission

Segregated Neurotransmission: Different transmitters routed to different post-synaptic targets by the same pre-synaptic neuron

2 UAS Gene Tool



Steps

Driver line → activates in chosen neurons (circadian, sensory, etc.)

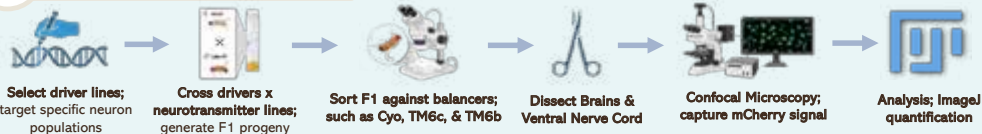
GAL4 transcribes **UAS** sequence → expresses **B3 recombinase enzyme**

B3 recombinase removes neurotransmitter region → **LexA** is promoted

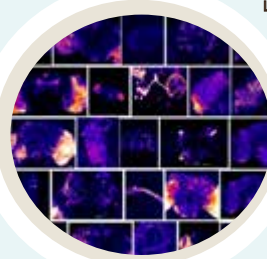
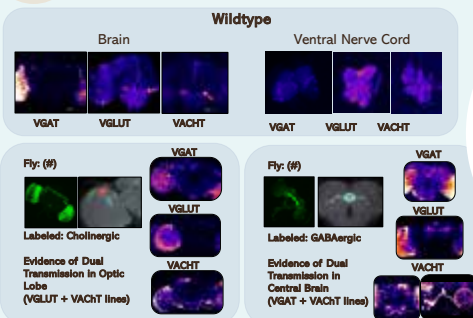
LexA → **LexOP** → drives **mCherry reporter (red)**

Do *Drosophila* neurons use segregated neurotransmission? If so, which neurons - and does the UAS system provide a clearer way to visualize it?

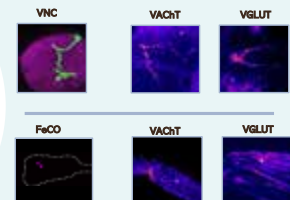
3 Methods



4 Results



Sensory Neuron Line: Hook
Labeled: Cholinergic



Evidence of Dual Transmission in
VNC & Femoral Chordotonal Organ
(VGLUT + VACHT lines)

5 Conclusion

- Reporter construct was **leaky**, complicating interpretation
- Despite this, some lines show evidence of **dual/segregated transmission**
- Findings suggest Dale's Principle may **not be absolute** in *Drosophila*
- Data provides a **foundation** for improved tools and validation

5 Future Direction

- New genetic system:** avoid LexA/LexOP leakiness
- Engineer flies to label all **three neurotransmitters** in distinct colors
- Protein tagging to confirm presence of proteins, not just gene activity
- Broader screening of neuron types to map dual transmission across circuits

References

- Chen C., et al., "Functional architecture of neural circuits for leg proprioception in *Drosophila*," *Current Biology* 31(10), 2215–2228 (2021). pmc.ncbi.nlm.nih.gov/articles/PMC8411111/
- Janelia Research Campus, *FlyLight Project* (including Virtual Fly Brain & NeuronBridge tools), janelia.org.
- Xiao, N., et al., "A single photoreceptor splits perception and circadian photoentrainment by co-transmitting two neurotransmitters," *Nature*, 623, 562–570 (2023).



Marcello LATTANZI

University of Pisa

Zenk Lab NeuroNA Chair in Epigenomics of Neurodevelopmental disorders – EpiGN

Supervisors: Marlena Judith Wisser Lübke

Marcello is supported by Fondation pour des bourses d'études italo-suisses

Abstract :

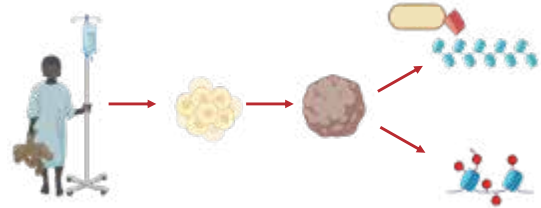
Chromatin remodelers play a crucial role in neurodevelopment and neuronal function. To investigate their contribution, knockout (KO) cell lines were generated and analyzed through optimized chromatin fractionation. Results revealed reduced histone variant incorporation in KO cells, indicating disrupted chromatin regulation. Using inducible NGN overexpression, iNeurons were derived under guided and unguided conditions, with unguided differentiation producing more mature neuronal morphologies. Ongoing work explores whether overexpression of remodelers can rescue KO phenotypes during organoid formation, offering insights into neurodevelopmental disorders.

Understanding the Role of the Chromatin Remodelers in Neurodevelopment and Disease

Marcello Lattanzi¹, Dr. Marlena Judith Wisser Lübke², Prof. Fides Zenk²
Scuola Normale Superiore (SNS), Pisa, Italy¹, Swiss Federal Institute of Technology Lausanne (EPFL), Lausanne, Switzerland²

Introduction

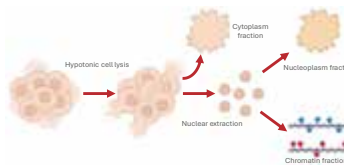
- Postmortem tissue and animal models give **limited insight** into this disorder.
- Cortical organoids** provide a suitable in vitro model for studying neurodevelopment.
- Some chromatin remodelers are essential for mature neuronal function.
- Remodeler KO cell lines were generated through genetic manipulation.



Methods

Chromatin Extraction to Quantify Bound Histone variants

Figure 2: chromatin fractionation was used to separate cellular components into 3 fractions: cytoplasm, nucleoplasm and chromatin. In this way, the integration of histone variants into chromatin can be studied.



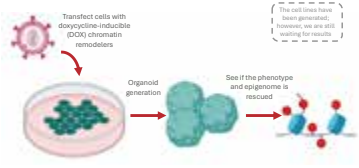
Generation of Inducible Neurons (iNeurons)

Figure 3: lentiviral DOX-inducible NGN overexpression in iPSCs accelerates iNeuron generation from iPSC's. Guided (with morphogens) and unguided protocols were tested to compare the resulting neuronal populations.



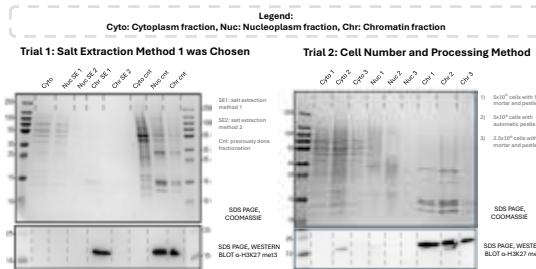
Overexpression of Chromatin Remodelers in KO Cell Lines

Figure 4: lentiviral DOX-inducible chromatin remodelers overexpression was used to test if KO phenotypes can be rescued during organoid formation.

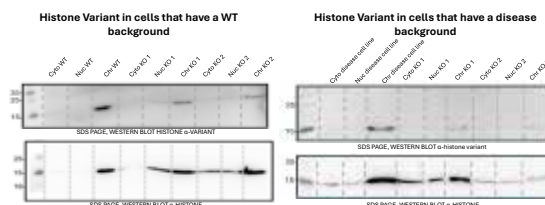


Results

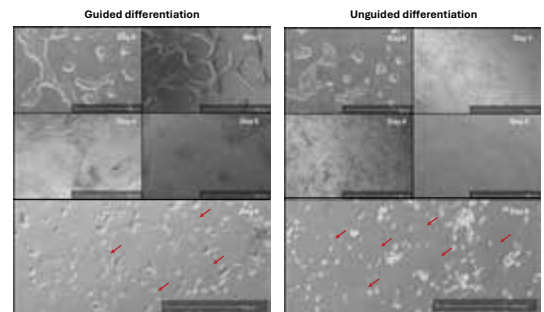
Chromatin Fractionation Trials



Histone variant incorporation is reduced in KO cells



iNeurons



Conclusions

- The protocol for chromatin fractionation was successfully optimized
- There is a **depletion of the histone variant** in the chromatin fraction when **the chromatin remodeler is knocked out**
- The unguided protocol for iNeuron generation seems to have **more mature neurons** (longer axons); however, qPCR needs to be done to determine which type of neurons are generated





Francesco PIERACCIANI

Scuola Normale Superiore/University of Pisa

[La Manno Lab of Brain Development and Biological Data Science](#)

Supervisor: Luca Fusar Bassini

Francesco is supported by Fondation pour des bourses d'études italo-suisse

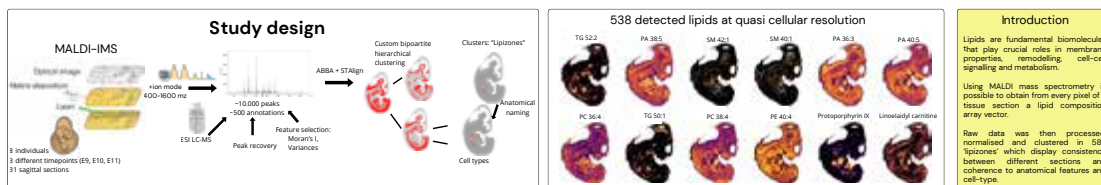
Abstract :

Lipids are fundamental biomolecules that play crucial roles in cellular processes, however their role in development has been elusive. Here we tried to understand their contribution to organogenesis by studying their abundance, spatial localisation and temporal variance. The collected lipidomic data have been first computationally analysed and subset in clusters, the 'lipizones'; the principles dictating the splits have been then investigated with a focus on heart anatomy, cell-type variety and developmental pathways.

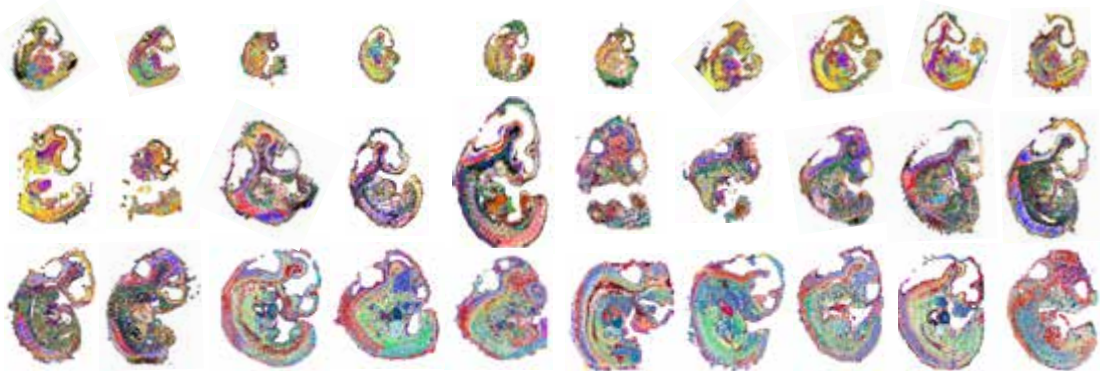
The Lipidomic Achitecture Of The Developing Mouse

Francesco Pieracciani^{1,2}, Luca Fusar Bassini³, Alessandro Valente³, Giovanni D'Angelo^{3*}, Gioele La Manno^{3*}

¹Scuola Normale Superiore, ²University of Pisa, ³EPFL



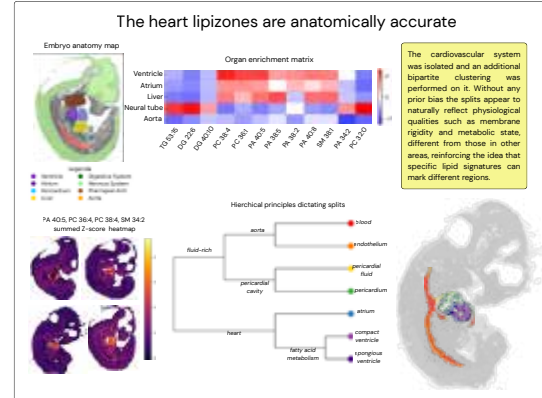
Embryonic lipozones are organised according to anatomy, metabolism and developmental origin



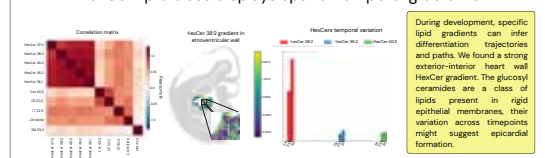
Lipozones are spatially cohesive and coherent between sections



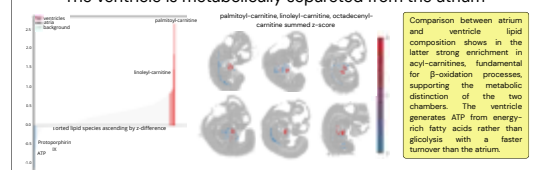
The heart lipozones are anatomically accurate



HexCer lipid class displays spatio-temporal gradients



The ventricle is metabolically separated from the atrium





Teoman SOYDAN

Vassar College

[Priestley Lab of Neurobiology of Memory](#)

Supervisor: Daniel Molinuevo Gomez

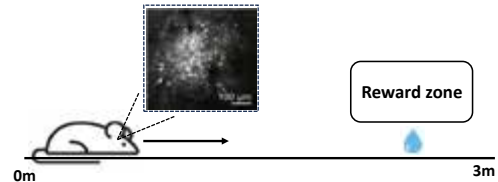
Teoman is supported by the Brain Mind Institute

Abstract :

As rodents forage environments, it has been found that the hippocampus, a brain region involved in memory formation, accurately encodes allocentric location. However, this “place coding” has been found to be deeply influenced by the animal’s arousal levels. Consequently, developing models to assess mouse engagement states can be key to deciphering hippocampal function. Here, we leveraged Hidden Markov Models to infer mouse engagement states solely from behavioral data and used them to showcase how hippocampal remapping emerges upon disengagement.

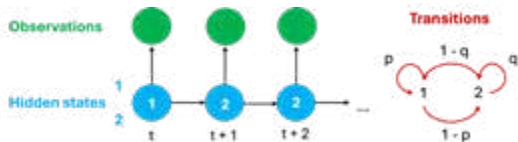
Introduction

- As rodents forage environments, the hippocampus **accurately encodes allocentric location**. [1,2]
- However, this “place coding” is deeply **influenced by the animal’s arousal levels**. [3,4]
- In this project, we will:
 - Develop a model to infer mouse engagement states** from behavioral observations.
 - Assess position decoding based on mouse engagement states.**

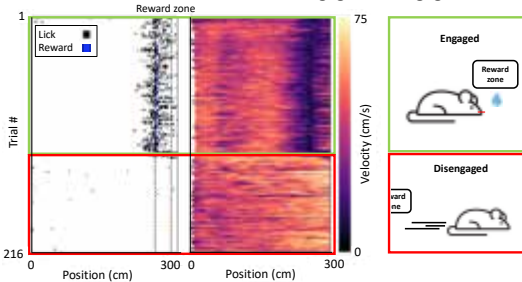


Aim 1: Methods

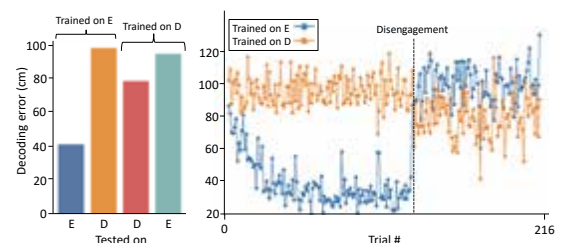
1. Hidden Markov Model



2. Characterization of hidden states: engaged/disengaged



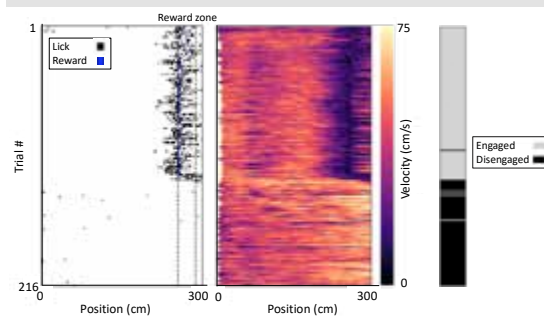
Aim 2: Results



Discussion

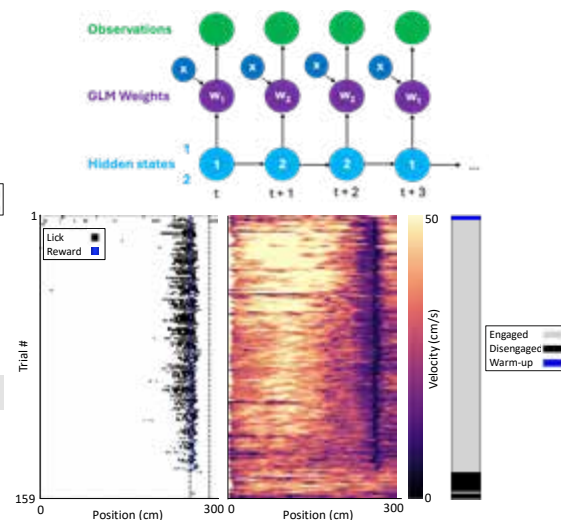
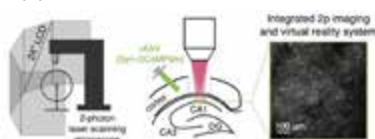
- Behavioral variability in our tasks can be accounted for with the use of HMMs.
- An animal’s active engagement with its environment is crucial for maintaining cognitive maps.
- Future directions:
 - Develop model into a GLM-HMM [5]
 - Cross-validation to systematically determine number of states [5]

Aim 1: Results



Aim 2: Methods

- Filter dataset based on mouse engagement states
- Compare position decoding accuracy when engaged (E) vs. disengaged (D)



Acknowledgements: I would like to thank the Directors of SNP and Alice Emery-Goodman for organizing this program, Olivier Ulrich and Mag Lane for always being open to answering my questions, James Priestley for having me in his lab, Hamza Bennani for letting me use his position decoding model for my project and contributing to it with the plots, Jiaran Xu for being an awesome roommate, and most importantly, Dani Molinuevo Gomez for being such an inspiring mentor. I hope I get to be a mentor like you one day.

References: [1] O’Keefe, J., & Dostrovsky, J. (1971). The hippocampus as a spatial map. Preliminary evidence from unit activity in the freely-moving rat. *Brain Research*, 34(1), 171–175. [2] Muller, R., & Kubie, J. (1987). The effects of changes in the environment on the spatial firing of hippocampal complex-spike cells. *The Journal of Neuroscience*, 7(7), 1551–1568. [3] Petrus, N. L., Yuan, X. C., & Harvey, C. D. (2022). Hippocampal place codes are gated by behavioral engagement. *Nature Neuroscience*, 25(5), 565–566. [4] Huber, R., Ziemann, K., Mazzucato, L., McCormick, D. A., & Jaramillo, S. (2024). Decision-making dynamics are predicted by arousal and unstructured movements. *Cell Reports*, 43(2), 113709. [5] Ashwood, J. C., Roy, N. A., Stone, L. R., Uribe, A. E., Churchland, A. K., Reigert, A., & Pillow, J. W. (2022). Mice alternate between discrete strategies during perceptual decision-making. *Nature Neuroscience*, 25(2), 201–212.



Bernadett TÖKÉS

Károli Gáspár University

[Herzog Lab of Psychophysics](#)

Supervisor: Martina Morea

Bernadett is supported by the Brain Mind Institute

Abstract :

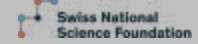
When we look at objects in cluttered scenes, recognition often fails because of visual crowding. Traditionally, this has been explained by a simple pooling of nearby features. However, new research shows that context matters: crowding is strong when target and surrounding elements group, and weaker when they separate. We tested whether a brief preview of surrounding elements could reduce crowding and whether EEG can reveal the brain dynamics underlying this grouping process.

Neural dynamics of segmentation in visual perception

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Laboratory of psychophysics
 Prof. Michael H. Herzog



Introduction

- **Visual crowding:** we struggle to recognize a target when nearby elements (flankers) interfere.
- **Traditional view:** it is caused by pooling of low-level features.
- **New evidence:** context really matters, crowding is strong when target and flankers group, weaker when they segregate.

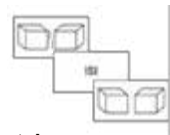


Hypothesis (H1): A brief preview of flankers helps grouping and reduces crowding.

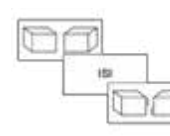
Research Question (RQ): Can EEG capture the neural dynamics of this process?

Conditions

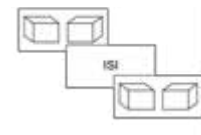
Preview



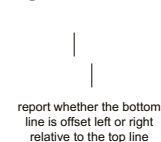
Postview



Control

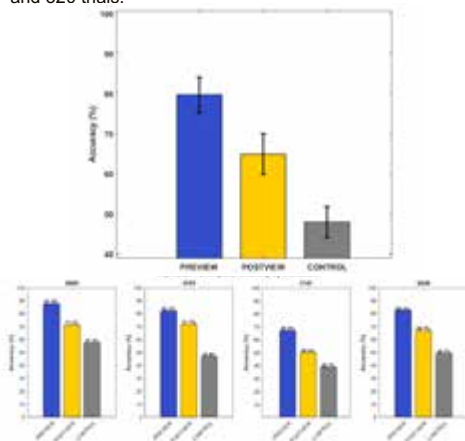


Target



Accuracy

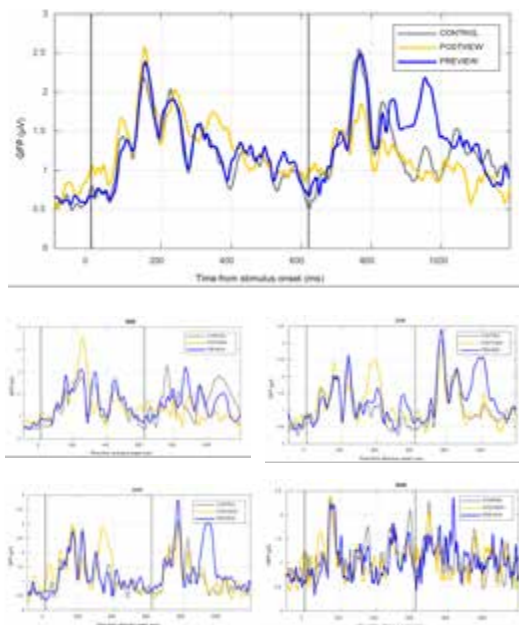
Accuracy of correct responses (n=4) across the 8 blocks and 320 trials.



GFP



Global Field Power (GFP) averaged across all electrodes. Vertical lines mark the stimulus presentation time.



Conclusions

Our aim was to assess neural dynamics of grouping in a crowding paradigm. Previous research has shown that a brief preview of the flankers can boost segregation and ultimately reduce crowding, whereas showing the flankers after the target does not. Such grouping processes may be visible in the global dynamics of brain responses. However, given the small sample size and the low quality of the recordings, a clear pattern across participants was not discernible. A larger study will be needed to validate whether the neural signatures observed indeed reflect temporal dynamics of grouping in visual perception.

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Monserrat TREJO VALENCIA

University Veracruzana

Gräff Lab of Neuroepigenetics

Supervisor: Cesar Sierra

Monserrat is supported by an Anonymous Donor

Abstract :

Memory linking allows the brain to associate experiences within a short time window, supported by epigenetic regulation. In hippocampal engram neurons after contextual fear conditioning, H3K27ac increased after 2h but markedly decreased after closing of the memory linking window, while HDAC2 showed the opposite pattern. Elevated HDAC2 would reduce H3K27ac and thereby chromatin accessibility, and transcription of plasticity-related genes. These results provide novel hints on the molecular mechanisms mediating memory linking, revealing a pivotal role of epigenetic changes in this process.

Dynamic Balance of HDAC2 and H3K27ac Shapes Memory Linking in Hippocampal Engram Neurons

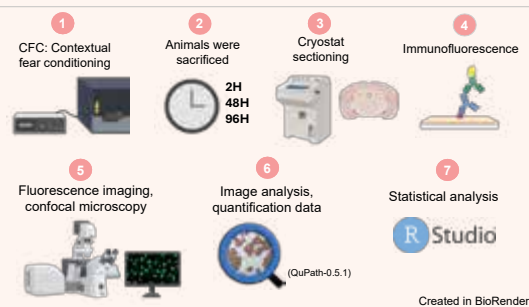
Monserrat Trejo Valencia¹, Cesar Sierra¹, Johannes Gräff¹

¹Laboratory of Neuroepigenetics, Brain Mind Institute, School of Life Sciences, École Polytechnique Fédérale de Lausanne (EPFL), Switzerland

Introduction

• **Memory linking** is the ability to associate two experiences if they occur within a limited temporal window (**~6 hours**), a process dependent on overlapping neuronal ensembles (*engram cells*) (Cai et al., 2016; Rashid et al., 2016).
 • **Epigenetic regulation** is essential for stabilizing memory traces. **Histone acetylation** at enhancers, such as **H3K27ac**, increases chromatin accessibility and enables transcription of plasticity-related genes (Fischer et al., 2010; Gräff & Tsai, 2013).
 • In contrast, **histone deacetylases (HDACs)**, particularly **HDAC2**, remove acetyl groups from histones. Reduced H3K27ac lowers chromatin accessibility and impairs the transcription of memory-related genes, ultimately limiting neuronal plasticity (Guan et al., 2009).
 • The **dynamic balance between H3K27ac (opening chromatin) and HDAC2 (closing chromatin)** may determine how long neurons remain in a permissive state for memory linking.
 • Using **GFP-labeled engram neurons**, we investigated the temporal changes of H3K27ac and HDAC2 at 2 h, 48 h, and 96 h after contextual fear conditioning (CFC).

Method



Results

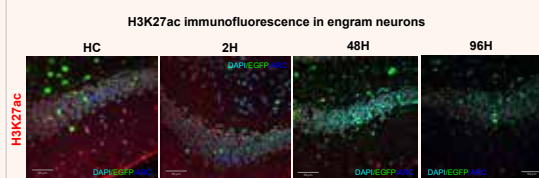


Figure 2. Representative confocal images (40x) showing H3K27ac (red), GFP-labeled engram neurons (green), ARC (blue), and DAPI (bright blue) in the dentate gyrus at baseline (HC), 2 h, 48 h, and 96 h after contextual fear conditioning. Scale bar: 50 μm.

Dynamics of H3K27ac levels in GFP+ and GFP- neurons across timepoints

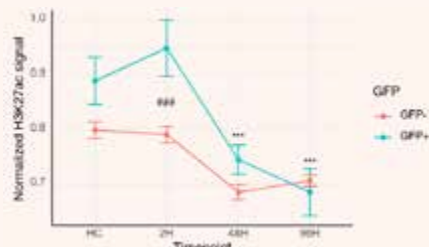


Figure 3. Normalized H3K27ac signal in GFP+ and GFP- neurons across experimental timepoints (HC, 2h, 48h, 96h). Data are expressed as mean ± SEM. Statistical analysis was performed using two-way ANOVA followed by Tukey's post-hoc test. Asterisks indicate intra-group differences within GFP+ across timepoints (**p < 0.001 vs HC and 2h). Hash symbols indicate inter-group differences between GFP+ and GFP- at the same timepoint (###p < 0.001).

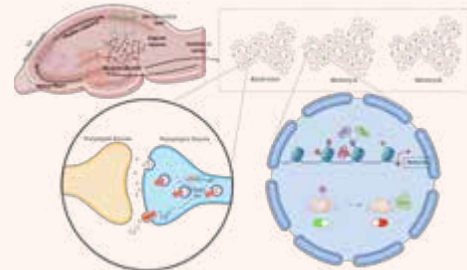


Figure 1. Memory linking depends on overlapping engram neurons within a ~6 h window. Epigenetic regulation stabilizes these traces: H3K27ac promotes chromatin accessibility and gene expression, whereas HDAC2 removes acetyl groups to repress transcription. The balance between H3K27ac and HDAC2 may shape the temporal dynamics of memory linking, here assessed in GFP-labeled engram neurons after contextual fear conditioning.

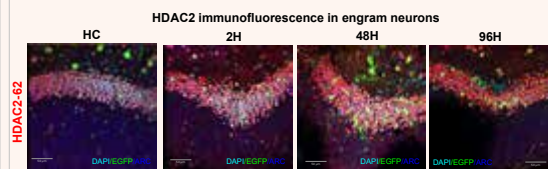


Figure 4. Representative confocal images (40x) showing HDAC2 (red), GFP-labeled engram neurons (green), ARC (blue), and DAPI (bright blue) in the dentate gyrus at baseline (HC), 2 h, 48 h, and 96 h after contextual fear conditioning. Scale bar: 50 μm.

Dynamics of HDAC2 levels in GFP+ and GFP- neurons across timepoints

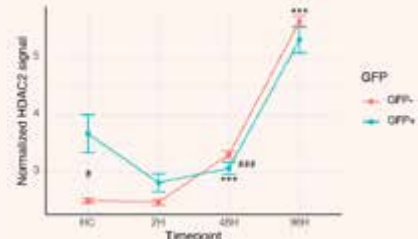


Figure 5. Normalized intensity values of HDAC2 in GFP+ and GFP- neurons at 2 h, 48 h, and 96 h after CFC, relative to control (HC). Data were analyzed using two-way ANOVA (factors: condition × cell group) followed by Tukey post-hoc tests. Significance: intra-group comparisons across timepoints (**p < 0.001) and inter-group comparisons at the same timepoint (#p < 0.05, ###p < 0.001).

Discussion

- The **increase in HDAC2 in GFP+ neurons** leads to the removal of acetyl groups, causing the **decrease of H3K27ac**. This reduction in acetylation results in decreased chromatin accessibility, limiting the transcription of memory-related genes and ultimately restricting neuronal plasticity.
- **Opposing dynamics of H3K27ac and HDAC2** highlight coordinated epigenetic regulation.
- Differences between **GFP+ and GFP-** show that changes are specific to memory-encoding neurons.
- Supports the idea that **epigenetic plasticity** underlies **experience-dependent memory processes** and could be **therapeutically targeted**.

Conclusion

Our results show that epigenetic regulation is dynamic during memory consolidation, with H3K27ac decreasing and HDAC2 increasing specifically in GFP+ neurons. This provides evidence that epigenetic mechanisms selectively shape neuronal ensembles involved in memory. These findings highlight the potential of targeting epigenetic regulators to improve cognitive deficits, and emphasize the importance of considering temporal windows in neuroepigenetic studies to better understand memory at the molecular level.

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Donors

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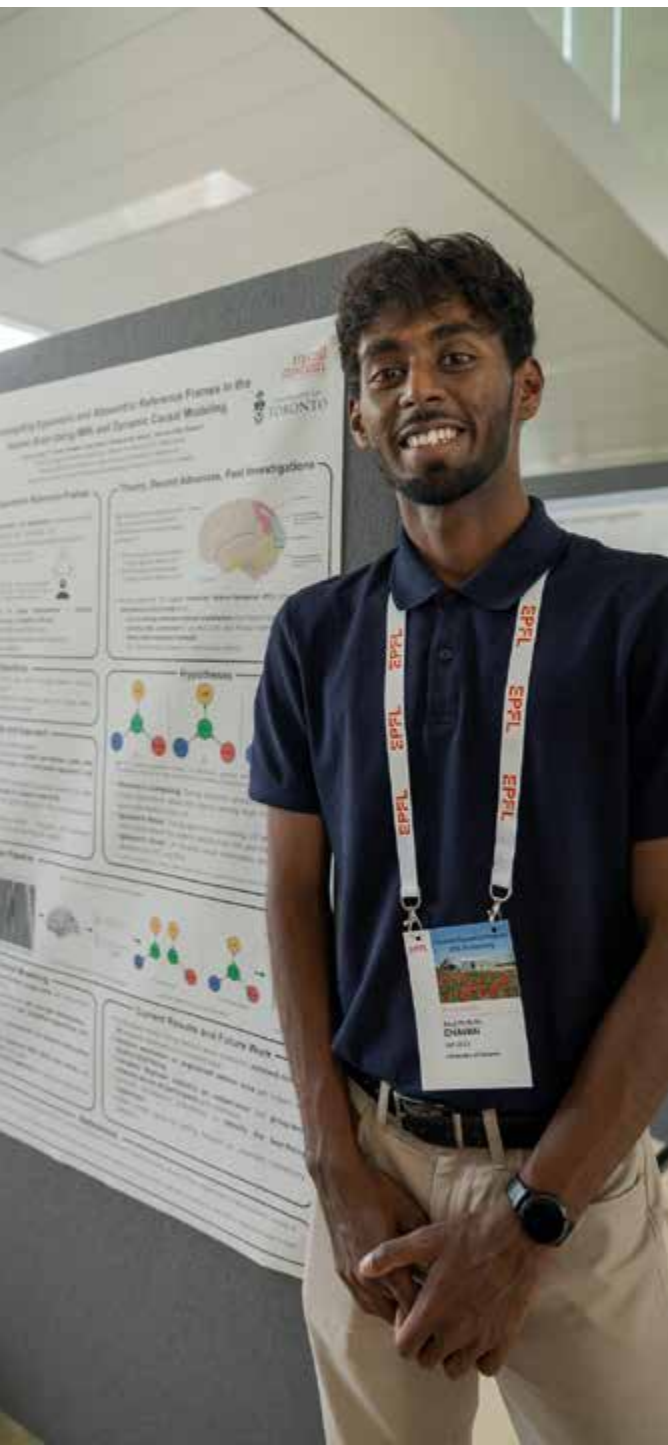
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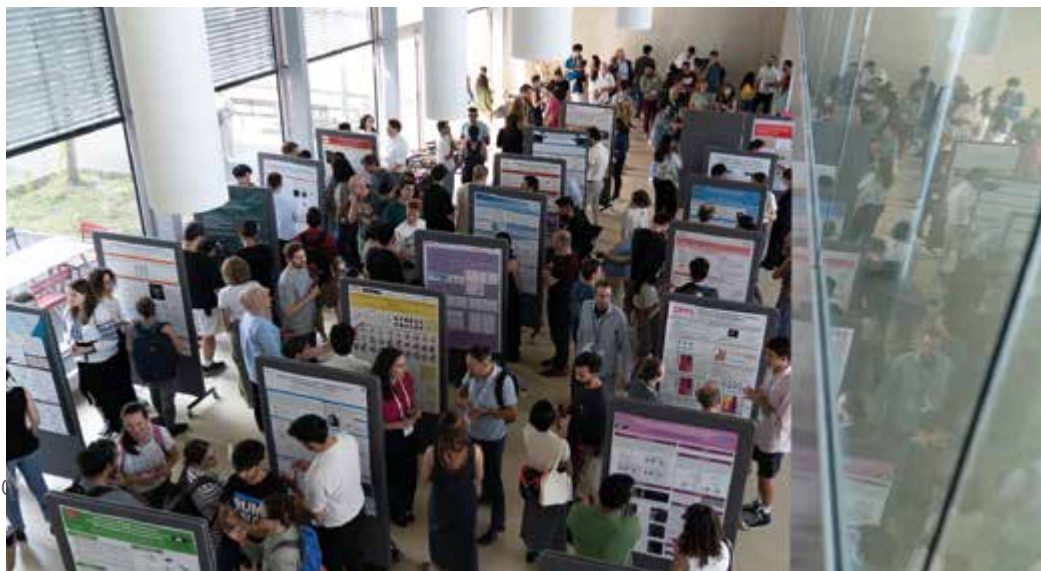
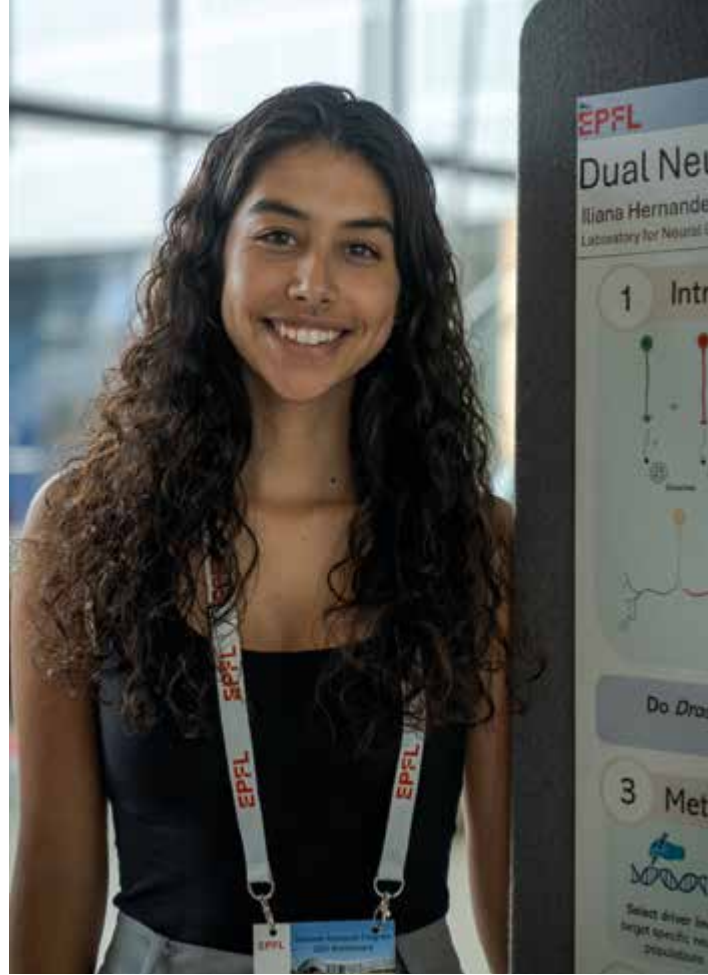
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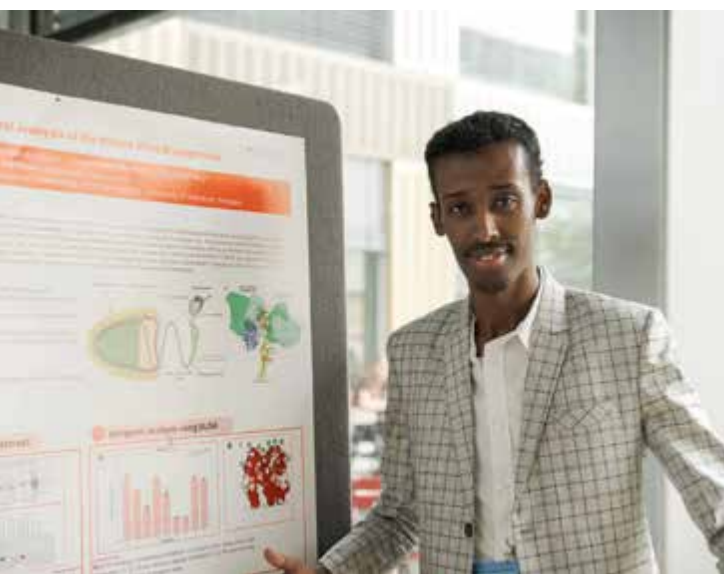
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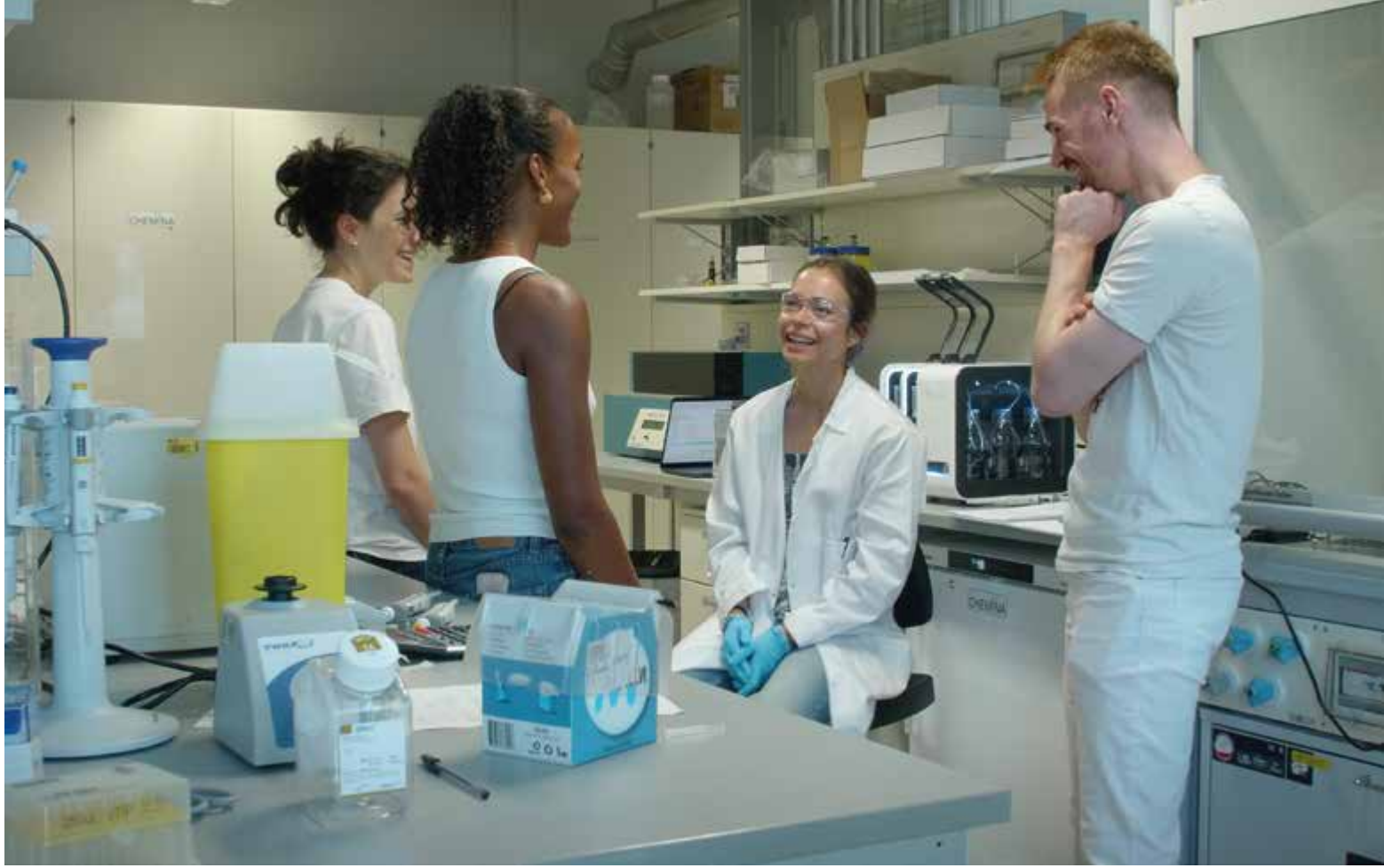
Tomorrow Foundation











Thank you

From the students

“

The best part of SRP was getting to do research in such a world-class environment. Seeing how curiosity and teamwork drive discovery made me realize how much dedication it takes to be a scientist. It really motivated me to aim higher in my studies and career.

“

What surprised me most was how much I grew, not just academically but as a person. I learned that I can adapt quickly to new places and that I love being surrounded by people who share my passion for science. Every challenge taught me something valuable.

“

SRP gave me the chance to work hands-on with advanced techniques and gain confidence in the lab. I also discovered how important collaboration and mentorship are for learning and growing as a researcher.

“

One thing that stood out to me was how SRP encouraged independence and problem-solving. I learned to trust my ideas and think critically while sharing and learning from my peers. Being part of such an international community was amazing, it taught me so much about different cultures and perspectives.

From the supervisors

“

Supervising SRP students pushes you to match their enthusiasm. Their curiosity is contagious and brings great energy to the lab. Working together on new experiments often sparks fresh ideas and helps shape exciting new directions for our research.

“

SRP students bring such fresh perspectives to the lab. Their curiosity challenges how we think and often opens new directions. It's inspiring to see their enthusiasm and to share in the excitement of discovery together.

“

Mentoring SRP students felt like attending a mini-conference, so many new ideas! Designing a focused project for them was rewarding and helped me see my own research differently, breaking big questions into clear, manageable steps.

“

Working with these bright students is always enriching. Their questions often reveal things we hadn't noticed and inspire new ways of thinking. It's a genuine exchange of ideas that reawakens our own curiosity as researchers.

Where are they now?

The SRP didn't just accelerate my career, it affirmed my place in a community of thinkers, builders, and changemakers. It reminded me that talent knows no boundaries, and that with the right support, lives can be transformed - mine included.

Aleksandra Vancevska

Psychotherapist in Private Practice and Podcaster
SRP 2012



Twenty years after joining the SRP, I remain deeply grateful for an experience that sparked my curiosity for research and international collaboration, motivating me to pursue my master's thesis abroad and shaping both my academic and personal journey.

Christoph Bernoulli

Associate Director, Global Filling Process and Technology Owner, CSL
SRP 2006



My first research experience was the SRP internship at EPFL on breast cancer, which inspired me to pursue science and has now brought me in a full circle to a Marie Skłodowska-Curie PhD in breast cancer at IDIBAPS in Barcelona.

Lidia Trombello

*Marie Curie PhD fellow, IDIBAPS
SRP 2019*



The EPFL Summer Research Program shaped my entire research journey: from my MSc at Oxford to my PhD at DKFZ. It gave me rare early access to world-class labs and a real taste of scientific life, inspiring me to pursue research with purpose and passion.

Shivohum Bahuguna

*Business development & Client
engagement, DKFZ
SRP 2017*



Alice Emery- Goodman

Summer Research Program

Coordinator



When I came to EPFL in 2009 and was handed the reins of the Summer Research Program (SRP) for the School of Life Sciences, I had no idea that it would become such a large part of my life. At the time, we were receiving only about 350 paper applications which more than doubled when we went on-line a few years later, and now stands at over 1'100 every January. We have never had to advertise the program; the success of the SRP spread on its own by the alumni themselves when they returned home after their 2 months in Lausanne.

More often than not, the SRP is a transformative experience both scientifically and personally for the student. It helps students discern their goals and dreams and it gives them the tools and experience to open those doors.

Over the 15 years, both I and SRP have grown and developed our sense of “mission”. The original *raison d'être* is to showcase the outstanding research done here at SV to the world and make connections between universities while giving talented students a chance to experience research first-hand. With SRP, we hope to attract excellent students back for our PhD programs. As good as these goals are, after a few years, I realized that SRP could be even more.

In a world where polarization, conflicts and mistrust of people who are different from ourselves is increasing, programs like SRP can help to build bridges of understanding between stereotypically opposing groups. By working together, living together, and playing together, SRP students develop long-lasting friendships which will serve them and others long after their summer is over. Moreover, we here in Switzerland have a responsibility to extend a helping hand to talented students world-wide, especially to those who do not have opportunity in their home country. We keep these principals in the back of our minds as we go through the selection process and plan the weekly workshops.

It is exciting to see that the SRP will celebrate its 20th anniversary next year and I am honored to have been given the chance to be such a big part of it. It has been a gift to be trusted to coordinate SRP over the years and I sincerely hope that SRP will continue its multifaceted mission for many years to come, making its small contribution towards a world that is more understanding, curious and kind. Receiving the EPFL Outstanding Commitment Award in 2024 has been a deeply meaningful recognition of this journey and a welcome acknowledgment of the importance of SRP at EPFL.

Alice Emery-Goodmann

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Coordination: Alice Emery-Goodman

Workshops: uentin Barraud, Laura Batti, Michele De Palma, Daniele Desravines, Giulia Di Domenicantonio, Mai-Phuong Dinh, Benoît Duc, Susan Gasser, Eleonora Ghisoni, Fernanda Herrera, Anna Kounina-Masse, Achilleas Laskaratos, Jean-François Mayol, Dimitrios Noukakis, Gaspard Pardon, Olivier Reynaud, Théo Ribierre, Flavie Robert, Amanda Skarda, Fides Zenk

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