Aurelien Pelissier, Ph.D.

O-1 visa (U.S.) — work authorized

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https://www.aurelienpelissier.com
S Google Scholar Github
Linkedin M Medium

Experience:

- ML Scientist, **Google X (A-Life)** (2026–Present) | Perturbation & Synthetic Biology
- Postdoctoral Scientist, **Yale University** (Swiss-funded) (2023–2026) | GenAI & Foundation Models
- ML Scientist, **IBM Research Zurich** (2019–2023) | AI for Scientific Discovery

Education:

- PhD, AI & Computational Biology, **ETH Zurich** (2019–2023) [Thesis]
- BSc & MSc, Quantum Physics, **ENS Paris-Saclay** (2018)

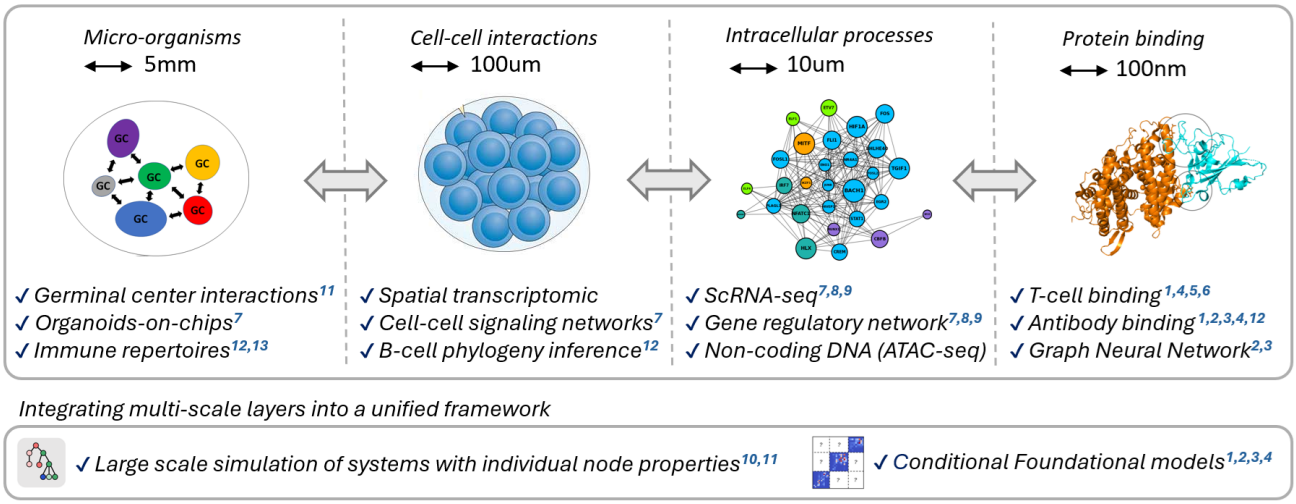
Highlights (Machine Learning):

- Fine-tuning **protein language models (PLMs)** for immunology tasks [1, 3, 4, 5]
- Multiple contributions in preparation for top venues ***Neurips 2026*** [1, 2]
  (*Conditional fine-tuning of generative PLMs & Graph-based metric-learning for TCR/antibody design*)
- **AIntibody Challenge**: 3rd place (generative antibody design) [2]
- Conference paper at ***SDM 2019*** (reinforcement learning) [19]

Highlights (Computational Biology):

- Published in ***Nature Communications*** (multiscale modeling) [13]
- Manuscripts under revision at ***Nature Methods*** and ***Cell Stem Cell*** (vascularized organoids) [6, 7, 8]
- Identified **BACH1** as a therapeutic target for rheumatoid arthritis; validated experimentally [10]
- Contributions to **Raman Spectroscopy** for thyroid cancer diagnosis (*Analytical Chemistry*) [17, 18]
- Contributed talks at top venues: ***ISMB*** (2021, 2022) [11, 13]

My current research bridges machine learning, bioinformatics and mathematical modeling frameworks to advance our understanding of immunology, with a particular focus on **Foundation Models** in the context of B/T-cell dynamics and perturbation modeling. I combine together interpretability methods, diffusion-inspired models, and graph neural networks to achieve efficient and flexible feature representations for **Generative AI** tasks in immunology.



Ultimately, my goal is to integrate together biological processes **spanning multiple scales**, such as cell population dynamics, cell-cell interactions, intracellular mechanisms, and protein binding, to construct a realistic *in-silico model* of the immune response.

Selected Publications [Google Scholar]

✉ *Indicates co-corresponding authors*
* *Indicates co-first authors; author order may be adjusted for CV.*

Generative AI | Masked Language Models | Graph Neural Networks

1 **Pelissier, A.***, Shao, Y.*, Chen, Y., & Martinez, M. R. (2025). Logit-preserving contrastive fine-tuning for generative and interpretable conditional masked language models. *In preparation for NeurIPS 2026.* [Poster] [Draft]

2 **Pelissier, A.***, Lui, C.*, Denzle, L., Shao, Y., Martin C.R., A., Paige, B., & Rodriguez Martinez, M. (2026). Abrank: A benchmark dataset and metric-learning framework for antibody-antigen affinity ranking. *In preparation for NeurIPS 2026 Datasets & Benchmarks Track*. doi:10.48550/arXiv.2506.17857

3 **Pelissier, A.***, Deutschmann, N.*, Weber, A., Gao, S., Bogojeska, J., & Martínez, M. R. (2024). Do domain-specific protein language models outperform general models on immunology-related tasks? *ImmunoInformatics*, 100036. doi:10.1016/j.immuno.2024.100036

4 Nielsen, M., Eugster, A., Jensen, M. F., Goel, M., Tiffeau-Mayer, A., **Pelissier**, **A.**, … Greiff, V. et al. (2024). Lessons learned from the IMMREP23 TCR-epitope prediction challenge. *ImmunoInformatics*, *16*, 100045. doi:10.1016/j.immuno.2024.100045
→ *Demonstrated the potential of protein language models to generalize TCR binding to "unseen" epitopes.*

5 Weber, A., **Pelissier, A.**, & Martinez, M. R. (2024). T-cell receptor binding prediction: A machine learning revolution. *ImmunoInformatics*, 100040. doi:10.1016/j.immuno.2024.100040

ScRNA-seq | Gene Regulatory Networks | Cell-Cell Signaling Networks

6 Quintard, C., Salewskij, K., Ramisch, S., Tenorio, E., Ren, J., Ania, B., … **Pelissier, A.**✉ & Penninger, M. J.✉. (2025). Modeling human hematopoiesis in bone marrow organoids. *Cell Stem Cell (in revision)*

7 Quintard, C., Wang, J., **Pelissier**, **A.**, Ren, J., Sebastien, R., Lee, J., … Penninger, M. J. (2025). Engineering vascularized organoids-on-chip with microfluidic perfusion. *Nature Methods (in revision)*

8 Wang, J., **Pelissier**, **A.**, SH. Lin, J., Quintard, C., Tamakhina, A., Wang, J., … Penninger, M. J. (2025). Organotypic vascularization improves human islet organoids survival and reverses diabetes. *Cell Stem Cell (in revision)*
→ [6, 7, 8] *Led the computational biology analysis, including scRNA-seq, cell-cell signaling network inference, RNA velocity, and gene regulatory network inference. Identified key transcription factors and pathways driving organogenesis, offering critical insights into developmental biology* [Figures].

10 **Pelissier, A.***, Laragione, T.*, Harris, C., Martínez, M. R., & Gulko, P. S. (2025). BACH1 as a key driver in rheumatoid arthritis fibroblast-like synoviocytes identified through gene network analysis. *Life Science Alliance*, *8*(1). doi:10.26508/lsa.202402808
→ *Identified computationally BACH1 inhibition as a promising therapeutic strategy for RA, validated in vitro and currently undergoing in vivo testing*

11 **Pelissier**, **A.**, Laragione, T., Gulko, P. S., & Martinez, M. R. (2024). Cell-specific gene networks and drivers in rheumatoid arthritis synovial tissues. *Frontier in Immunology*, 2024–12. doi:10.3389/fimmu.2024.1428773
→ *Contributed talk at ISMB2022 (Leading conference in computational biology, ranked A/A*).*

12 Laragione, T., Harris, C., **Pelissier**, **A.**, & Gulko, P. S. (2025). NUSAP1 regulates rheumatoid arthritis fibroblast-like synoviocyte phenotypes implicated in joint damage, glycolysis, and a cancer-associated transcriptomic signature. *Gene Reports*, 102270. doi:10.1016/j.genrep.2025.102270

Multi-Scale Stochastic Models & Non-Markovian Processes

13 **Pelissier**, **A.**, Phan, M., Beerenwinkel, N., & Rodriguez Martinez, M. (2026). Unifying non-markovian dynamics and agent heterogeneity in scalable stochastic simulation. *Nature Communication (in press).* doi:10.48550/arXiv.2212.05059
→ *Contributed talk at ISMB2021 (Leading conference in computational biology, ranked A/A*).*

14 **Pelissier**, **A.**, Akrout, Y., Jahn, K., Kuipers, J., Klein, U., Beerenwinkel, N., & Rodriguez Martinez, M. (2020). Computational model reveals a stochastic mechanism behind germinal center clonal bursts. *Cells*, *9*(6), 1448. doi:10.3390/cells9061448
→ *Outstanding Presentation & Third best poster award at ISMB2020.* [Certificate]

Immune Repertoires & B-Cell Phylogeny

15 **Pelissier, A.***, Stratigopoulou, M.*, Dimitriadis, E., Bende, R., van Noesel, C., Rodriguez Martinez, M., & EJ Guikema, J. (2023). Convergent evolution and B-cell recirculation in germinal centers in a human lymph node. *Life Science Alliance*. doi:10.26508/lsa.202301959

16 **Pelissier, A.***, Luo, S.*, Stratigopoulou, M., EJ Guikema, J., & Rodriguez Martinez, M. (2023). Exploring the impact of clonal definition on B-cell diversity: Implications for the analysis of immune repertoires. *Frontier in immunology*. doi:10.3389/fimmu.2023.1123968

ML for Raman Spectroscopy & Hyperspectral Imaging

17 **Pelissier, A.***, Hashimoto, K.*, Mochizuki, K.*, Taylor, J. N., Clément, J.-E., Kumamoto, Y., … Komatsuzaki, T. (2025). Beyond the nucleus: Cytoplasmic dominance in follicular thyroid carcinoma detection using single-cell Raman imaging across multiple devices. *Analytical Chemistry*, *97*(25), 12998–13009. doi:10.1021/acs.analchem.4c06544

18 Taylor, J. N., **Pelissier, A.**, Mochizuki, K., Hashimoto, K., Kumamoto, Y., Harada, Y., … Komatsuzaki, T. (2023). Correction for extrinsic background in Raman hyperspectral images. *Analytical Chemistry*, *95*(33), 12298–12305. doi:10.1021/acs.analchem.3c01406

Others

19 **Pelissier**, **A.**, Nakamura, A., & Tabata, K. (2019). Feature selection as monte-carlo search in growing single rooted directed acyclic graph by best leaf identification. In *Proceedings of the 2019 SIAM International Conference on Data Mining* (pp. 450–458). SIAM. doi:10.1137/1.9781611975673.51

20 Lehner, J., & **Pelissier**, **A.** (2022). Peer2Panel: Democratizing renewable energy investment with liquid and verifiable tokenized solar panels. *Whitepaper*. doi: 10.13140/RG.2.2.11113.06247

21 Sammut, R., Fenwarth, L., **Pelissier**, **A.**, Marceau, A., Duployez, N., Benachour, S., … Loschi, M. (2025). Clonal evolution of myeloid malignancies treated with microtransplantation: A single-centre experience. *Journal of Cellular and Molecular Medicine*, *29*(6), e70520. doi:10.1111/jcmm.70520

Invited Talks & Presentations

- **Keynote Speaker** — Representing IBM Research at the Biotechnet Meet-Up 2023.
  Presented: *AI-Driven Engineering of the Immune System*.
- **Invited Talk** — AstraZeneca Journal Club (2025).
  Presented: *Abrank: A metric-learning framework for antibody-antigen affinity ranking*.
- Contributed talk, ISMB 2022, *Cell-type Specific Gene Regulation in Rheumatoid Arthritis*.
- Contributed talk, ISMB 2021, *A Rejection Gillespie Algorithm for Non-Markovian Stochastic Processes*.
- **Outstanding Presentation & Best Poster Award** (Third Place), ISMB 2020, *Computational Model Reveals a Stochastic Mechanism Behind Germinal Center Clonal Bursts* [Poster][Certificate].
- Contributed poster, ISMB 2022, *Characterization of Antibody Specificity Leads to the Identification of Convergent Evolution in Germinal Centers* [Poster].
- **Invited Pitch** — Swiss Blockchain Federation (SBF) member event 2022.
  Presented: *Peer2Panel: Investing into a bright future* [Talk].

Awards, Trainings & Certifications

2026 **Recipient of U.S. O-1A Extraordinary Ability Classification**
Mountain View, CA, USA
Granted for demonstrated excellence and sustained international acclaim in Computational Biology.

2025 **Third Place, Challenge 2 — AIntibody Competition**
New Haven, CT, USA
Awarded for an experimentally validated antibody design with high affinity and developability scores.

Awards, Trainings & Certifications (continued)

2023 **Nomination for the ETH Silver Medal**
Zurich, Switzerland
Awarded to outstanding doctoral theses.

2020 **Best Poster Award (3rd place) at ISMB2020**
Montreal, Canada
Awarded for an outstanding presentation in *Computational Modeling of Biological Systems* [Certificate].

Innosuisse Entrepreneurship Program
Zurich, Switzerland
From Idea to Market, Business model development, Financial planning & Pitching [Certificate].
→ *Funded* ***Peer2Panel*** *[20] with the Innosuisse NTN Innovation Booster Blockchain grant (CHF 20k)*

2014 **Appointed Normalien (civil-servant trainee) at École Normale Supérieure.**
Paris-Saclay, France
Highly selective status conferred by the French Ministry of Education following a national competitive examination [Official Decree].

Skills & Interests

ML & Coding
Python, R, C++, Matlab, Fortran,
TensorFlow, PyTorch,
Masked Language Models, Generative AI,
Graph neural network, Geometric deep learning,
Stochastic processes, Bayesian statistics, Interpretable ML,
Transformers, LSTM, Reinforcement learning,
Quantum machine learning (See my article on Qiskit).

Computational Biology
Protein language models (PLMs), T-cell and Antibody binding,
ScRNA-seq, RNA velocity, Spatial transcriptomic,
ScATAC-seq, Non-coding DNA,
Gene regulatory networks, Cell-cell communication networks,
Immune repertoires, B-cell phylogeny inference,
Non-Markovian processes, Mechanistic models,
Raman Spectroscopy, Metabolics.

Work Experience

Appointments

2026 – Present **ML Scientist - Perturbation Modeling & Synthetic Biology**
A-Life, Google [X] *The Moonshot Factory, United States*

Mission: Enable at-scale biomanufacturing of mass-market biologics and chemicals (incl. pharmaceuticals and proteins) in bioreactors with engineered microorganisms (e.g., bacteria and yeast), reducing costs vs. traditional manufacturing.

Role 1: Integrate multi-modal cell foundation models with mechanistic and causal modeling to recommend genetic edits/perturbations and optimize growth conditions, accelerating design–build–test–learn (DBTL) in synthetic biology.

Role 2: Develop a real-time control loop (PID) using inline Raman spectroscopy feedback (via calibrated spectral models) to track product/byproduct/impurity concentrations and stabilize bioreactor operation.

Work Experience (continued)

2023 – 2026 **Postdoctoral Scientist - GenAI & Foundation Models**
Yale School of Medicine, United States
Leading the fine-tuning of masked language models (MLMs) for diverse downstream tasks across DNA and protein sequences, with an emphasis on retaining interpretability [1]. Demonstrated the benefits of representing antigen complexes as graphs, rather than relying solely on sequence-based approaches [2].
→ Organized team participation in the IMMREP25 T-cell prediction challenge and the AIntibody generative antibody design competition.

Life Sciences Institute, University of British Columbia, Canada
Organoid-on-chips for disease modeling - Prof. Josef Penninger.
Characterizing the benefits of high-flux environments for the growth of vascularized organoids and the organ specificity of their vascular networks using scRNA-seq, spatial transcriptomics, and cell–cell communication network analysis [7].
→ Contributed rigorous, in-depth computational analyses for multiple high-impact studies forthcoming in *Cell Stem Cell*, *Nature*, and *Nature Biotechnology* [Figures].

2019 – 2023 **Ph.D. Fellowship - AI & Computational Biology**
IBM Research Zurich & ETH Zurich, Switzerland
AI for Scientific Discovery – Prof. Maria Rodriguez Martinez.
Stochastic Modeling of the Humoral Immune Response: A Multi-scale Challenge [Thesis].
→ *Nominated for the 2023 ETH Silver Medal awarded to outstanding doctoral theses.*

2018 – 2019 **Research Scientist - AI & Raman Spectroscopy**
Imperial University of Hokkaido, Japan
Molecule & Life nonlinear science laboratory – Prof. Tamiki Komatsuzaki.
Accelerating cancer diagnosis measurement technologies by integrating single-cell Raman imaging with machine learning [17, 18].

Feb. – July 2018 **Master Thesis - Reinforcement Learning**
Imperial University of Hokkaido, Japan
Laboratory for Pattern recognition & Machine Learning - Prof. Atsuyoshi Nakamura.
Feature Selection as Reinforcement Learning by Bandit strategies and Monte Carlo tree search [19]. [Thesis] [Code] [Poster]

2016 – 2017 **Visiting International Student - Experimental Physics & Modeling**
University of British Columbia, Vancouver, Canada
Ultrafast Spectroscopy Laboratory – Prof. David Jones.
Study of High Harmonic Generation (HHG) in high repetition rate systems.
(A one year research program as part of my ENS degree).
[Thesis] [Code] [Poster]

Apr. – July 2016 **Research Internship - Experimental Physics & Modeling**
Ecole Polytechnique federale de Lausanne, Switzerland
Advanced Semiconductors for Photonics & Electronic (LASPE) - Prof. Nicolas Grandjean.
Impact of piezoelectric effects on Nitride-III Nanobeam optical properties.
[Thesis] [Code]

Blockchain

2022 – Present **Co-Founder - Peer2Panel**
The company aims at making investment in renewable energy secured, transparent and accessible to customers with capital of any size. With the acquisition of tokens backed by physical solar panels, clients can grow a renewable energy portfolio easily and affordably through the Ethereum blockchain [20]. [https://www.peer2panel.com]
→ *Funded with an Innosuisse NTN Innovation Booster Blockchain grant (CHF 20k)*
→ *Part of ETH AI Center's TalentKick*

Education

2019 – 2023 **Ph.D. Fellowship - AI & Computational biology**
ETH Zurich, Switzerland
Joint program with IBM Research.
Germinal center B cell evolution, Antigen-Antibody binding, Gene regulatory networks, Single cell transcriptomic, non-Markovian processes, Interpretable AI, Drug discovery.
→ *Nominated for the 2023 ETH Silver Medal awarded to outstanding doctoral theses.*
[Thesis]

2017 – 2018 **M.Sc. Quantum physics, Nanophysics**
University Grenoble - Alpes, France
Double degree with ENS Paris-Salclay.
Quantum information theory, Nanoelectronics, Nanomagnetism, Nanophotonics.

2014 – 2018 **Grande École Degree - Fundamental physics & Applications**
Ecole Normale Superieure (ENS), Paris-Saclay, France
PHYTEM (PHYsics, Theory, Experiment, Modeling).
Statistical physics, Solid state physics, Astrophysics, Particle physics, Semiconductors.

2012 – 2014 **Scientific CPGE**
Classe Préparatoire aux Grandes Écoles, Grenoble, France
Two years preparation to highly selective national competitive exam.