

Vincent Turon-Lagot, Ph.D.

Molecular Virologist · Experimental Platform Builder · Live-Cell Imaging · Scientific AI

vincentturonlagot.com · [LinkedIn](#) · [GitHub](#)

PROFILE

Experimental biologist with more than eight years in virology, cell engineering, and large-scale assay development, with a habit of measuring the tools as carefully as the biology. Built a comparative CRISPRi platform across three DNA viruses, a live-cell RNA-virus reporter, analysis pipelines used across Biohub, and an ongoing multi-agent hypothesis generator over my own screen data—then audited that system across 142 runs and documented, in numbers, where its reasoning fails.

CORE EXPERTISE

Experimental	CRISPRi screening · high-throughput assay development · cell engineering · live-cell imaging · FACS · small-molecule screening · viral infection models · molecular cloning · mechanistic validation
Computational	Python · pandas / NumPy · scikit-learn · Cellpose · Ultrack · napari · HPC / SLURM · Git · CLI tooling · dashboards · reproducible analysis
Scientific AI	Multi-agent orchestration · real tool calling · critic debate · deterministic guardrails against fabrication · literature grounding · quantitative reliability audits

PROFESSIONAL EXPERIENCE

Senior Scientist · Scientist II · Scientist I — Biohub, San Francisco

January 2023 – present · Arias Group

Experimental platform development

- Developed an ongoing comparative CRISPRi platform targeting more than 3,000 proteostasis-network genes across HSV-1, HCMV, and Vaccinia virus while holding the cell model, perturbation format, library, selection strategy, and FACS readout constant. Biological triplicates identified nine validated shared host factors.
- Led mechanistic follow-up of prioritized hits using quantitative imaging, molecular biology, and orthogonal analytical assays; characterized host-trafficking processes and a retrograde-transport inhibitor with activity across multiple viruses. Manuscript in preparation.
- Designed a flow-cytometry compound screen, identified antiviral hits without measurable cytotoxicity, and contributed to validation in a skin-organoid model with collaborators at UC Irvine.
- Led V-SWITCH, a single-vector OFF-to-ON reporter validated with Dengue, Zika, West Nile, and HCoV-OC43. The system supports live imaging, FACS isolation, and CRISPR screening; preprint and public analysis workflow released in 2026.
- Expanded CRISPRi screening capabilities with focused sgRNA sublibraries, quantitative FACS and optical readouts, and inducible perturbation systems.
- Manage a Research Associate through hit-to-lead experimental work; presented at GRC Viruses & Cells 2025 and ASCB 2025.

Computational analysis and scientific AI

- Built the open-source V-SWITCH pipeline for multidimensional microscopy data: Cellpose segmentation, Ultrack tracking, fluorescence-trajectory extraction, sigmoid fitting, activation detection, and response classification.
- Trained a random-forest cell-death classifier on 224 live-cell trajectories, reaching 0.909 ± 0.015 ROC-AUC and 0.832 ± 0.008 balanced accuracy.
- Built and continue to develop a 13-stage multi-agent hypothesis-generation workflow with specialized analysis roles, three independent critics, literature-grounded evidence review, and three hypotheses now under experimental validation.
- Engineered deterministic guardrails around generative steps, including ground-truth re-derivation of effect directions, citation filtering against returned results, PubMed verification, evidence quoting, confound filters, and deterministic statistics rendering.
- Audited the system across 142 runs: 1,094 direction inversions caught in 4,752 hypothesis rounds; two independently implemented citation checks converging at 24–26% claim failure; and 1,055 hypothesis-replacement events. Documented which guardrails underperform and which gates lack telemetry.

Postdoctoral Research Fellow — University of California, San Francisco

October 2021 – January 2023

- Conducted a genome-wide CRISPR screen and analyzed the resulting datasets to identify genes driving sensitivity to a novel anti-cancer drug conjugate targeting KRAS-driven tumors; evaluated toxicity and molecular inhibition through quantitative assays alongside a medicinal-chemistry team.

Ph.D. Researcher — INSERM U1110, Institute of Viral & Liver Disease / Strasbourg University

Strasbourg, France · 2016 – 2020

- Ran high-throughput genetic and small-molecule screening that produced a hepatitis D virus infection inhibitor now in preclinical evaluation; contributed to identification of estrogen receptor alpha and CAD as HDV host factors and antiviral targets, and to work on HBV evasion of cGAS sensing.
- Built mammalian cell-line models with lentiviral vectors and CRISPR-Cas9; trained and supervised four researchers; coordinated a €250K public-private collaboration with Sanofi.

EDUCATION, AWARDS & LANGUAGES

Ph.D., Molecular Biology & Virology — Strasbourg University, 2020 · M.S., Biology of Microorganisms (Virology) — Strasbourg University, 2016 · Deep Learning Specialization — DeepLearning.AI, 2026

1st Prize for Innovation, Doctoriales d'Alsace (2018) · Ministerial Research Fellowship, €140K, French Ministry of Research (2016) · French (native) · English (fluent, IELTS 8.0) · Spanish (beginner)

SELECTED PUBLICATIONS

- Cid-Rosas M, et al.; Turon-Lagot V, Arias C. V-SWITCH: a single-vector OFF-to-ON fluorescent reporter of live RNA virus infections. *bioRxiv*, 2026.
- Liu C, Hillsley A, et al.; Turon-Lagot V, et al. A multimodal perturbation atlas defines the phenotypic resolution of cellular morphology. *bioRxiv*, 2026.
- Najarro G, Brackett K, et al.; Turon-Lagot V, et al. BiP/GRP78 is a pro-viral factor for diverse dsDNA viruses that promotes survival and proliferation upon KSHV infection. *PLoS Pathogens*, 2024.
- Verrier ER, Weiss A, et al.; Turon-Lagot V, et al. Combined small-molecule and loss-of-function screen uncovers estrogen receptor alpha and CAD as host factors for HDV infection. *Gut*, 2020.
- Turon-Lagot V, et al. Targeting the host for new therapeutic perspectives in hepatitis D. *Journal of Clinical Medicine*, 2020.
- Verrier ER, Yim SA, et al.; Turon-Lagot V, et al. Hepatitis B virus evasion from cGAS sensing in human hepatocytes. *Hepatology*, 2018.

ADDITIONAL

Open source: github.com/vturonlagot — V-SWITCH analysis pipeline (MIT), Zenodo-archived; ongoing multi-agent screen-analysis workflow with quantitative reliability audit. Based in San Francisco.