

SIRIL AROCKIAM, Ph.D.

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RESEARCH FOCUS

I build GPU-accelerated machine learning systems for genomics and immunology, grounded in wet lab validation and cGMP industry experience. My work centers on learned representations of biological sequence and structure. I designed GenoCache, a learned-embedding alignment system that reaches 95 percent locus accuracy at 9 ms per long read on an A100 GPU on real Oxford Nanopore data, within 0.85x of minimap2's three decades of hand-tuned heuristics. In parallel, I built an end-to-end neoepitope discovery pipeline for HPV-driven cancers (VIRUSBreakead and GRIDSS, OptiType, pVACtools and NetMHCpan, top binder 5.98 nM at HLA-A*68:02), a single-cell annotation benchmark on PBMC scRNA-seq (Seurat, CellTypist, PyTorch baseline at 0.84 macro F1), and performed structural analysis of 109 TCR-pMHC crystal structures to push immunogenicity prediction beyond MHC binding affinity alone. Experienced in PyTorch, CUDA, FAISS, contrastive learning, transformer models for biology (HyenaDNA, DNABERT-2, scGPT), GPU profiling and tensor-core optimization, neoepitope prediction (pVACtools, NetMHCpan, HLA-Inception), single-cell analysis (Scanpy, Seurat, CellTypist), Python and R, AWS cloud, Oxford Nanopore long-read sequencing, and translational assay development under cGMP.

EDUCATION

Ph.D., Biological Design – Arizona State University, Tempe, AZ

Advisors: Prof. Karen S. Anderson, Prof. Jennifer Blain | Aug 2020 – Aug 2025

Dissertation: Point-of-Care Diagnostics for Early Detection of HPV-Driven Cervical and Oropharyngeal Cancer

- Conducted exploratory analysis of viral-human integration junctions from NGS data, investigating their potential as neoepitopes for cancer immunotherapy
- Expertise in primer design, assay optimization, POC and translational research

M.S., Biopharmaceutical Engineering – New Jersey Institute of Technology, Newark, NJ | May 2018

Thesis: Computational and Experimental Determination of the Mixing Efficiency of a Microfluidic Serpentine Micromixer

- Combined COMSOL modeling with experimental validation to optimize mixing efficiency in serpentine microchannels

B.Tech., Biotechnology – Anna University, India | June 2016

RESEARCH & PROFESSIONAL EXPERIENCE

Postdoctoral Research Scholar – Biodesign Institute, Arizona State University | Aug 2025 – Present

Computational Genomics, Translational Oncology & Immunogenomics

- Built end-to-end **neoepitope discovery pipeline** for HPV-driven cancers: VIRUSBreakead/GRIDSS for viral integration detection from WGS, OptiType for HLA typing, and pVACtools/NetMHCpan for prediction. Analyzed 4 HPV16/18 samples across integration hotspots (GLI2, KLF5, MYC) and identified **9 unique junction-spanning neoepitopes** (best: 5.98 nM, HLA-A*68:02). Also identified **novel E6/E7 epitopes for under-studied HLA alleles** (A*31:01, B*27:07). Extending the pipeline to TCGA-CESC/HNSC (n>600), integrating bulk RNA-seq to test whether integration burden plus host gene expression at integration loci predicts overall survival
- Developed rapid TB drug resistance detection using LAMP amplification coupled with Oxford Nanopore MinION sequencing with optimized rapid library preparation. Detected rifampicin resistance mutation S450L (66,000x depth) within **30 seconds** of sequencing. Sample to mutation detection under 2 hours
- Optimized high-throughput nucleic acid extraction and qPCR workflow on **Biomek i7** automated liquid handler: adapted MagMax extraction protocols (Thermo Fisher) to reduce per-sample reagent volumes for 96-well format, and developed TaqMan probe-based qPCR assays targeting HPV16/18 L1 and E7, enabling processing of **~6,000 saliva samples** for HPV-HNSC screening

- Led and executed MSD (Meso Scale Discovery) multiplex serology for HPV antibody profiling across **148 clinical samples** (HPV-16 E1/E2/E6/E7, HPV-18 L1, HPV-16 L1), correlating seroprevalence with qPCR positivity to evaluate HPV serology as a head and neck cancer screening tool

Graduate Research Assistant – Biodesign Institute, Arizona State University | Aug 2020 – Aug 2025

Molecular Diagnostics, Translational Oncology & Computational Genomics

- Developing cost-effective (**100x reduction**) and rapid sequencing library preparation method to identify viral-human integration junctions using **Oxford Nanopore MinION** for prognostic marker discovery and neoepitope identification in HPV-driven cervical and oropharyngeal cancers
- Designed and optimized **100+ LAMP/qPCR primer sets** achieving **single-digit copy sensitivity (1-10 copies)** for viral and pathogenic genome detection (HPV, COVID-19, Flu, Monkey Pox, TB, Mycobacterium)
- Engineered rapid nucleic acid extraction protocols (**under 10 min**) from diverse biological samples including saliva, cervical fluid, skin lesion and sputum with on-chip integration capability (*Analytical Methods*, 2025)
- Field-validated **SPRINT-HPV** on **over 150 patient samples** in resource-limited settings (AIIMS, India), achieving **100% sensitivity** and **94.5% specificity** for cervical samples benchmarked against **Roche Cobas**, and led large-scale population screening study analyzing **4,324 self-collected saliva samples** from diverse Arizona cohort for HPV16 prevalence using qPCR
- Developed multiplexed LAMP assays detecting **11 high-risk HPV types** with analytical sensitivity of **2.5 copies/μL**, matching FDA-approved reference standards
- Engineered portable diagnostic platform integrating microfluidic cartridge (**\$10-20/test**) with battery-powered detection unit (**\$200-300**), designed for resource-limited settings
- Developed custom lyophilization protocol on **SP Scientific Advantage Pro** for LAMP reagent stabilization (10% w/v lactose, <9% TTD variance vs. liquid), enabling ambient-temperature shipping and field deployment without cold-chain
- Performed on-chip skin lesion sample processing and adapted three **mpox LAMP assays** (Clade I, Clade II, pan-orthopoxvirus) onto portable POC platform, validated on **45 patient specimens** from the 2022 US outbreak, field-tested by **CDC collaborators** in the DRC (**5 samples, 100% concordance**)
- Developed custom **Cq-calling algorithm** for real-time LAMP fluorescence data with adaptive baseline noise estimation and slope-based amplification detection, enabling automated result interpretation on POC device
- Collaborated with interdisciplinary teams of electrical, biomedical, and mechanical engineers plus bioinformaticians on fully integrated sample-to-answer diagnostic platforms

Independent Projects

AI × Bio Hackathon (Evolved & NVIDIA) | Oct – Nov 2025

- Selected from **competitive applicant pool** for **NVIDIA-sponsored global hackathon** focused on AI applications in genomics, continued as independent research project
- Awarded **\$10,000 AWS credits** and **\$5,000 Modal (GPU cloud) credits** through competitive applications to support continued development
- Developed **embed-align (GenoCache)**, a GPU-accelerated genomic sequence alignment tool using learned 1D CNN embeddings with FAISS vector search and DP-chaining, reaching **95% locus accuracy** on real Oxford Nanopore long reads at 9 ms per read on an A100 (within 0.85x of minimap2 speed), with full SAM/CIGAR output. Earned \$15,000 in AWS and Modal cloud credits at the NVIDIA AI x Bio Hackathon
- Optimized end-to-end GPU pipeline achieving **9.0 ms/read on NVIDIA A100** (0.85x minimap2 speed): fp16 tensor-core inner-product search, numba-JIT chaining, and threaded edlib verification, representing a **4.8x speedup** over initial implementation through systematic profiling and optimization
- Conducted deep failure analysis identifying tandem repeat regions (subtelomeric, ~4kb period) as the architectural ceiling for embedding-based alignment, implemented minimizer-based rescue achieving 95.0% accuracy, with comprehensive benchmarking against minimap2

- Demonstrated that a lightweight learned encoder (0.5M params, 128-D embeddings) can approach the accuracy and speed of minimap2's decades-refined heuristics on real ONT sequencing data, a novel result with few comparable published work

TCR-pMHC Structural Analysis (Exploratory Computational Research) | 2026

- Analyzed 109 TCR-pMHC crystal structures from PDB to study CDR loop contact patterns and physicochemical properties at the TCR-peptide interface, confirming established P4-P8 dominant contact window and amino acid equivalence classes consistent with decades of structural immunology literature
- Exploring whether mRNA-level sequence features of TCR CDR regions correlate with 3D structural binding motifs and pMHC specificity, an open question at the intersection of transcriptomic and structural data that could improve neoepitope immunogenicity prediction beyond MHC binding affinity alone
- Building familiarity with structural immunology methods (ChimeraX, PDB analysis, contact mapping) to support future integration of TCR-seq data with structural modeling for neoepitope prioritization

scFM-Bench: Single-Cell Annotation Benchmark (Exploratory Computational Research) | 2026

- Built a single-cell cell-type annotation benchmark on PBMC scRNA-seq data, comparing reference-mapping methods (**Seurat v5** in R, **CellTypist**) with MLP baselines (PyTorch, TensorFlow). PyTorch MLP baseline reached **0.84 macro F1** on held-out cells. Extending the benchmark to single-cell foundation models (**scGPT**)
- Studying how single-cell annotation methods behave when reference panels are small, a setup typical for disease-specific cohorts where curated atlases are still being built
- Building familiarity with single-cell methods (Scanpy, AnnData, Seurat) and the foundation-model toolchain (scGPT, CellTypist) to support future integration of single-cell data with neoepitope and structural variant analysis

HonorHealth EHR Hackathon | First Place | 2025

- Won first place in the HonorHealth in-residence hackathon by building a patient pre-check-in system with intelligent routing (ER vs. urgent care vs. primary care) in one week, deployed as a real-world application prototype
- Built open-source **pptx-presentation skill** for Codex (OpenAI) with multi-agent architecture (art director, color theme, styling, layout QA) and 20+ automated QA scripts for typography, contrast, alignment, and readability, enabling design-quality scientific and business slide decks from natural language prompts

Molecular Visualization (Molecular Nodes / Blender)

- Used Molecular Nodes (Blender Geometry Nodes addon) for 3D protein structure visualization and animation, exploring geometry-based structural representation of HPV capsid proteins and molecular complexes

Industry & Earlier Research

Scientist II (Associate) – Merck & Co. | West Point, PA | April 2018 – Aug 2020

Assay Development & Process Optimization (Live-Attenuated VZV Vaccines)

- Executed cell-based flow cytometry assays (Guava easyCyte) for quantitative monitoring of VZV glycoprotein-E expression on MRC-5 cell substrates using monoclonal antibodies, supporting in-process potency testing and manufacturing process control for live-attenuated vaccine production
- Performed multiplexed gene expression profiling (NanoString nCounter, 120-gene RNA biomarker panel) to characterize host-cell transcriptional responses during vaccine production, establishing potency and toxicity scoring systems under cGMP conditions
- Conducted viral growth kinetics studies to optimize infection parameters and harvest timing, comparing traditional and novel cell culture methodologies to reduce process time and improve antigen yield, contributing data to process characterization protocols
- Served as Quality Lead for laboratory operations: trained 8 team members on cGMP analytical methods, coordinated inspection readiness for FDA, Russian regulatory authority, and external partner audits, supported deviation investigations and CAPA closure

- Authored and revised Standard Operating Procedures (SOPs), electronic batch records, and technical reports per cGMP and data integrity (ALCOA) requirements

Research Assistant – New Jersey Institute of Technology | Jan 2017 – Mar 2018

Microfluidics & Computational Modeling / Master's Thesis | Dr. Piero M. Armenante and Dr. Sagnik Basuray

- Developed and validated computational fluid dynamics models (COMSOL) for microfluidic mixing using serpentine channel designs, verified with experimental fluorescence data demonstrating integration of computational predictions with wet lab validation
- Engineered blood-brain barrier models in microdevices using mammalian endothelial cells for drug permeability studies, characterized tight junction protein expression via immunofluorescence imaging and electrochemical impedance spectroscopy
- Fabricated carbon nanotube biosensors using thiol chemistry for protein detection via impedance spectroscopy, conducted nanofabrication (photolithography, electron vapor deposition) in Class 100 cleanroom

Research Intern – National Institute for Research in Tuberculosis, Chennai, India | Nov 2015 – Mar 2016

- Developed LC-MS and RP-HPLC methods for quantifying pyrazinamide in human plasma samples for pharmacokinetic analysis. Optimized chromatographic parameters for improved sensitivity and reproducibility (Undergraduate Thesis)

TECHNICAL SKILLS

Molecular & Cellular Biology

- **Nucleic Acid Technologies:** DNA/RNA extraction, qPCR, LAMP, primer/probe design, NGS library preparation (Oxford Nanopore), sequencing, droplet digital PCR
- **Cell Culture:** Mammalian and bacterial cell culture, viral infection models, cell-based assays, flow cytometry
- **Protein Analysis:** Western blot, SDS-PAGE, ELISA, immunofluorescence microscopy
- **High-Throughput Assays:** NanoString gene expression, 96/384-well plate assays, automated liquid handling (Biomek i7, Kingfisher)

Computational & Bioinformatics

- **Viral Integration & Neoepitope:** VIRUSBreakend, GRIDSS (integration detection), OptiType (HLA typing), pVACtools, NetMHCpan, MHCflurry, HLA-Inception (neoepitope prediction)
- **NGS Analysis:** minimap2, BWA, SAMtools, bedtools, edlib (semi-global alignment), SAM/BAM generation, CIGAR string computation, Oxford Nanopore data processing
- **Single-Cell Analysis:** Scanpy, AnnData, Seurat (R), scGPT, CellTypist
- **Programming & AI:** Python, R, GPU computing (CUDA, PyTorch, TensorFlow), contrastive learning, 1D CNN encoders, transformer models (HyenaDNA, DNABERT-2, scGPT), vector databases (FAISS, IVF-PQ), numba JIT, Modal cloud GPU orchestration
- **Structural Bioinformatics:** PDB structure analysis, TCR-pMHC contact mapping, Molecular Nodes (Blender), UCSF ChimeraX
- **Modeling & Simulation:** COMSOL Multiphysics (fluid dynamics), computational assay design
- **Data Analysis:** Minitab, ImageJ, GraphPad Prism, Microsoft Office Suite
- **Laboratory Informatics:** MES, LIMS/ELN systems

Instrumentation & Techniques

- **Analytical:** LC-MS, RP-HPLC, UV-Vis spectroscopy, fluorescence microscopy (confocal, widefield), SEM, EDX
- **Specialized:** Electrochemical impedance spectroscopy, cell counting (Vi-Cell, hemocytometry), microfluidics, soft lithography, EVD
- **Immunoassays:** MSD (Meso Scale Discovery) multiplex serology, ELISA, Luminex bead-based assays, lateral flow assay development, ELISPOT
- **Regulatory:** cGMP laboratory practices, FDA audit readiness, quality control systems

PUBLICATIONS

Peer-Reviewed Articles

- **Arockiam, S.** et al. Rapid On-Chip Nucleic Acid Extraction for Point-of-Care Salivary Diagnostics. *Analytical Methods*, 17.21 (2025): 4321-4333.
- Nguyen, V. T., **Arockiam, S.**, Kumar, P., et al. Diagnostic Translational Considerations for Global Health Settings: Portable Detection of Human Papillomavirus for Cervical Cancer Screening in India. *JCO Global Oncology*, 11, e2500117 (2025).
- **Arockiam, S.** et al. Mixing Efficiency in Serpentine Microdevices. *Chemical Engineering Research and Design*, 167, 303-317 (2021).
- Cheng, Y. H., et al. (including **Arockiam, S.**). Effect of electrode configuration on nucleic acid detection sensitivity in porous interdigitated electrodes. *Biomicrofluidics* 13(6) (2019).
- Bhuvaneshwari, S., et al. (including **Arockiam, S.**). Studies on the Phytochemistry and Bioefficacy of Industrial Crops *Coffea canephora* and *Gravillea robusta* from Kolli Hills. *International Journal of Research in Pharmaceutical Sciences*, 5, 147-151 (2014).

Patents

- Anderson, K., Knappenberger, M., **Arockiam, S.** Methods for parallel LAMP assays at a single temperature using temperature-shifting agents. U.S. Patent App. 18/694,303 (2024).
- Anderson, K., Knappenberger, M., **Arockiam, S.** Silica-based chromatographic processes for isolating nucleic acid-protein complexes and detecting target nucleic acids. U.S. Patent App. 18/255,731 (2024).
- Arockiam, S. et al. Simple and rapid nucleic acid extraction method. (Patent pending).
- Arockiam, S. et al. HR-HPV detection and genotyping using RT-LAMP in laboratory and Point-of-Care (POC) settings. (Patent pending).

Manuscripts in Review/Preparation

- **Arockiam, S.** et al. Portable, Isothermal Amplification and Detection of High-Risk Human Papillomavirus. Preprint available at SSRN: <https://dx.doi.org/10.2139/ssrn.5456445> (In review).
- Knappenberger, M., **Arockiam, S.** et al. Portable Detection of Monkeypox Virus Clades using Bridging LAMP. (In review).
- Nguyen, V. T., **Arockiam, S.** et al. User-Actuated, Multiplexing Microfluidic Device for Point-of-Care Isothermal Nucleic Acid Detection. (In review).
- **Arockiam, S.** et al. Detection of Human Papillomavirus Type 16 in Self-Collected Saliva: Population-Based Prevalence Study in Arizona. (In preparation).
- **Arockiam, S.** et al. Computational Identification of Neoepitopes from HPV-Human Integration Junctions and Novel E6/E7 Epitopes for Under-Studied HLA Alleles. (In preparation).

Conference Proceedings

- **Arockiam, S.** et al. Colorimetric On-Chip Detection of HPV for POC Settings. *IEEE HI-POCT 2024*, 1-4.
- Nguyen, V. T., **Arockiam, S.** et al. Low-Cost Microfluidic Fluorescence Assay for Viral Screening. *IEEE HI-POCT 2024*, 49-52.
- Biswas, S., **Arockiam, S.**, & Christen, J. M. B. Magnetic Bead Characterization for Nucleic Acid Extraction in Microfluidic Devices. *IEEE MWSCAS 2021*, 408-411.

PRESENTATIONS

Oral Presentations

- "Point-of-Care Colorimetric Detection of High-Risk HPV" – IEEE HI-POCT 2024, Tucson, AZ.

Poster Presentations

- AAAS Annual Meeting – 2026 (Phoenix, AZ).
- Early Detection Research Network (EDRN) Conference – 2023, 2025 (Gaithersburg, MD).

- International Papillomavirus Conference (IPVC) – 2024 (Edinburgh, Scotland).
- Nature Bioengineering for Global Health Conference – 2023 (Nashville, TN).
- BMES Annual Meeting – 2024 (Baltimore, MD).
- IEEE Midwest Symposium on Circuits and Systems (MWSCAS) – 2023.
- Biodesign Fusion Conference – 2021, 2023 (Tempe, AZ).

LEADERSHIP, GRANTS & PROFESSIONAL DEVELOPMENT

Co-Founder & Director of Communications – Nucleate Arizona | Aug 2022 – Aug 2025

- Co-founded student-led nonprofit accelerating biotech entrepreneurship in Arizona
- Organized 10+ events engaging **400+ attendees**, bridging academia-industry gap
- Built partnership with AZBio, CEI, and industry leaders to strengthen Arizona's startup ecosystem

Participant – Nucleate Activator Program | Jan 2025 – May 2025

- Selected for flagship 6-month equity-free program supporting academic biotech translation
- Developing commercialization strategy for point-of-care diagnostic platform
- Training in market analysis, business development, fundraising, and validation strategies

Grant Development & Funding | 2024 – 2025

- Co-led **SBIR Phase I grant application** for point-of-care HPV detection from cervical samples, **awarded August 2025**
- Contributed to multiple **NIH grant proposals (R21, U01)** including technical sections, budget justifications, and specific aims development
- Developed commercialization strategies and regulatory pathways for diagnostic platforms targeting resource-limited settings

Venture Capital Fellow & Life Science Scholar – VC University, Cohort 16 | June 2024 – Sep 2024

- Awarded full-tuition **Life Science Scholarship** for aspiring life science VC investors
- Completed comprehensive training in venture finance, investment strategies, and deal structures
- Participated in 3-month mentorship with experienced VC professionals

Venture Fellow – Venture Cooperative (Laconia Capital) | May 2023 – July 2023

- Selected for competitive fellowship program focused on early-stage investment education
- Gained exposure to due diligence, portfolio management, and startup ecosystem dynamics

HONORS & AWARDS

- Life Science Scholarship – VC University (2024)
- Travel Awards – MWSCAS 2023, Nucleate Summits 2022-2025, ASU GPSA travel award
- Fulton Fellowship Award – Arizona State University (2020)
- Best Undergraduate Thesis Award & Presidential Showcase – Anna University (2016)
- BioSummit 3.0 Selection – MIT Media Lab (Selected from **600+ global applicants**)

PROFESSIONAL DEVELOPMENT & CERTIFICATIONS

- GMP Laboratory Control Systems – International Society for Pharmaceutical Engineering (ISPE)
- Six Sigma Yellow Belt – Institute of Industrial & Systems Engineers
- FDA Audit & Multi-Country Regulatory Inspection Experience

PROFESSIONAL SERVICE & OUTREACH

- Biodesign Open Door Event – Interactive immunology demonstrations for K-12 students (2023, 2025)

- Newark Arts Council – Community event coordination, Newark, NJ (2016)
- Chennai Flood Relief & Rescue – Volunteer coordinator, Aide et Action (2015)

REFERENCES

- Karen S. Anderson, M.D., Ph.D. – Karen.Anderson.1@asu.edu
- Jennifer Blain Christen, Ph.D. – Jennifer.BlainChristen@asu.edu
- Vel Murugan, Ph.D. – Vel.Murugan@asu.edu
- Joshua LaBaer, M.D., Ph.D. – Joshua.LaBaer@asu.edu