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Opportunity Title: USDA-ARS Computational Biology & Machine Learning for Avian Influenza Surveillance
Opportunity Reference Code: USDA-ARS-HQPD-2026-0428

Organization U.S. Department of Agriculture (USDA)

Reference Code USDA-ARS-HQPD-2026-0428

How to Apply ***To submit your application, scroll to the bottom of this opportunity and click APPLY.***

A complete application consists of:

- An application
- Transcript(s) – For this opportunity, an unofficial transcript or copy of the student academic records printed by the applicant or by academic advisors from internal institution systems may be submitted. Click here for detailed information about acceptable transcripts.
- A current resume/CV, including academic history, employment history, relevant experiences, and publication list
- Two educational or professional recommendations

All documents must be in English or include an official English translation.

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Application Deadline 1/15/2027 3:00:00 PM Eastern Time Zone

Description ***Applications are reviewed on a rolling-basis and applications may close before the deadline.**

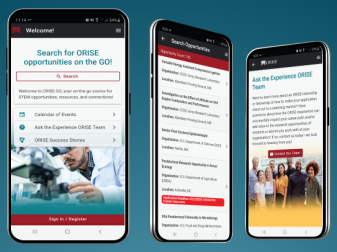
ARS Office/Lab and Location: A research opportunity is currently available with the U.S. Department of Agriculture (USDA), Agricultural Research Service (ARS), Genomics and Bioinformatics Research Unit, located in Gainesville, Florida.

The Agricultural Research Service (ARS) is the U.S. Department of Agriculture's chief scientific in-house research agency with a mission to find solutions to agricultural problems that affect Americans every day from field to table. ARS will deliver cutting-edge, scientific tools and innovative solutions for American farmers, producers, industry, and communities to support the nourishment and well-being of all people; sustain our nation's agroecosystems and natural resources; and ensure the economic competitiveness and excellence of our agriculture. The vision of the agency is to provide global leadership in agricultural discoveries through scientific excellence.

Research Project: The H5N1 outbreak in U.S. dairy cattle showed that influenza can establish itself in mammalian hosts and that our surveillance tools must keep pace with a changing virus. This fellowship combines two efforts: making PCR-based diagnostics and sequencing assays robust to viral mutation, and tracking viral adaptation to mammals through structural modeling. You will have the freedom to set the balance between them with your mentor, based on your strengths and early results.

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Project 1: Predicting assay failure as the virus mutates. With your mentor, you will learn how to build machine-learning models that predict how primer-template mismatches reduce amplification and extension efficiency in avian influenza assays, so likely failures can be flagged before they affect testing. You will use a large molecular training dataset and validate against new data from federal partner labs at the National Poultry Research Center and National Animal Disease Center. This is one of a set of foundational PCR modeling projects pairing optimization and ML methods for multiplex primer design: our group recently published PRISM (Chen et al., *Bioinformatics*, 2026), a submodular-optimization framework that designs multiplex primers. A central question is how to bring mismatch-aware predictions into this design framework. This learning experience is a collaboration with Dr. David Suarez, who developed the key avian influenza diagnostic tests.

Project 2: Predicting receptor-binding shifts. With your mentor, you will learn how to develop structure-based approaches to estimate how hemagglutinin and neuraminidase variants interact with avian-type (a2,3) and human-type (a2,6) sialic acid receptors, toward scalable monitoring of mammalian adaptation. This is a new direction for the lab, and we are still identifying potential structural-biology collaborators. Methods may include AlphaFold-based modeling, glycan-aware docking or co-folding, and OpenMM with AMBER-family force fields.

Several past mentees came in from a wet-lab or biology background and left with strong computational skills - training people across that boundary is as much a part of this fellowship as the research itself. Fellows publish as first author, and leave with an open-source tool and a dataset others will use. We support travel to present and collaborate closely with the University of Florida Emerging Pathogens Institute and the Microbiology and Cell Science department. Our workflows are Python-based and moving toward Rust; we provide training either direction, and we use AI-assisted coding with code review.

Learning Objectives: Under the guidance of a mentor, you will:

- Learn how viral evolution influences the reliability of PCR-based diagnostics for avian influenza and other rapidly changing pathogens while developing computational primer-design and optimization approaches for multiplex PCR assays.
- Develop skills in machine learning, molecular-data analysis, and structural biology by modeling primer–template mismatches, studying influenza protein adaptation to mammalian receptors, and using tools such as AlphaFold-based protein modeling, glycan-aware docking, and molecular-dynamics simulations.
- Gain experience validating computational predictions with laboratory-generated diagnostic data from federal animal-health research partners while building an understanding of influenza virology, molecular diagnostics, viral host adaptation, and zoonotic-

disease surveillance.
- Strengthen programming and research-computing skills in Python, with opportunities to learn Rust, collaborative software development, code review, AI-assisted coding practices, and the development of reproducible open-source research tools and datasets.
- Build interdisciplinary research, scientific communication, and professional skills through collaboration across biology, virology, bioinformatics, machine learning, and structural modeling, as well as through conference presentations and first-author publication opportunities.

Mentor(s): The mentor for this opportunity is Adam Rivers (adam.rivers@usda.gov). Dr. Adam Rivers is a coauthor of QIIME 2, a widely used bioinformatics platform, and developer of tools including ITSxpress, Guidemaker, Branchwater, and Tamipami. The lab builds open, reproducible software that other scientists adopt. If you have questions about the nature of the research, please contact the mentor.

Anticipated Appointment Start Date: January 2027. Start date is flexible and will depend on a variety of factors.

Appointment Length: The appointment will be for two years.

Level of Participation: The appointment is full time.

Citizenship Requirements: This opportunity is available to U.S. citizens only.

ORISE Information: This program, administered by ORAU through its contract with the U.S. Department of Energy (DOE) to manage the Oak Ridge Institute for Science and Education (ORISE), was established through an interagency agreement between DOE and ARS. Participants do not become employees of USDA, ARS, DOE or the program administrator, and there are no employment-related benefits. Proof of health insurance is required for participation in this program. Health insurance can be obtained through ORISE.

Questions: Please visit our Program Website. After reading, if you have additional questions about the application process, please email ORISE.ARS.HQPostdoc@orau.org and include the reference code for this opportunity.

Qualifications The qualified candidate should be currently pursuing or have received a doctoral degree in the one of the relevant fields (biology, molecular biology, bioinformatics, computational biology, machine learning, biophysics, or a related field). Degree must have been received within the past four years, or anticipated to be received by 1/30/2027.

Highly desired:

- A strong biology/molecular background and the motivation to build real skill in machine learning and computational methods (we'll train you),

or;

- A strong computational/ML background and interest in learning the virology and molecular biology (we'll train you on that side).

Preferred skills:

- Experience with PCR/qPCR assay design, primer design, or molecular diagnostics
- Familiarity with protein structure prediction tools (AlphaFold, ESMFold) or molecular dynamics packages (OpenMM, GROMACS, AMBER force fields)
- Hands-on deep learning experience (PyTorch or TensorFlow), even outside biological data
- Proficiency in Python and scripting ; willingness to pick up Rust as the lab transitions
- Experience with reproducible-research tooling: git, workflow managers like Nextflow, containerization, slurm
- Background in virology, influenza biology, microbiology or animal/agricultural disease systems
- A track record of first-author publication or open-source software contribution
- Comfortable researching across a disciplinary boundary, either explaining computational methods to biologists or biological context to computational collaborator

Stipend $74,677.00 – $74,678.00 Yearly

Point of Contact Janeen

Eligibility Requirements

- **Citizenship:** U.S. Citizen Only
- **Degree:** Doctoral Degree received within the last 48 months or anticipated to be received by 1/30/2027 12:00:00 AM.
- **Discipline(s):**
  - **Chemistry and Materials Sciences** (12 👁)
  - **Computer, Information, and Data Sciences** (17 👁)
  - **Earth and Geosciences** (21 👁)
  - **Engineering** (29 👁)
  - **Environmental and Marine Sciences** (14 👁)
  - **Life Health and Medical Sciences** (51 👁)
  - **Mathematics and Statistics** (11 👁)
  - **Physics** (16 👁)
  - **Science & Engineering-related** (1 👁)
- **Veteran Status:** Veterans Preference, degree received within the last 120 month(s).