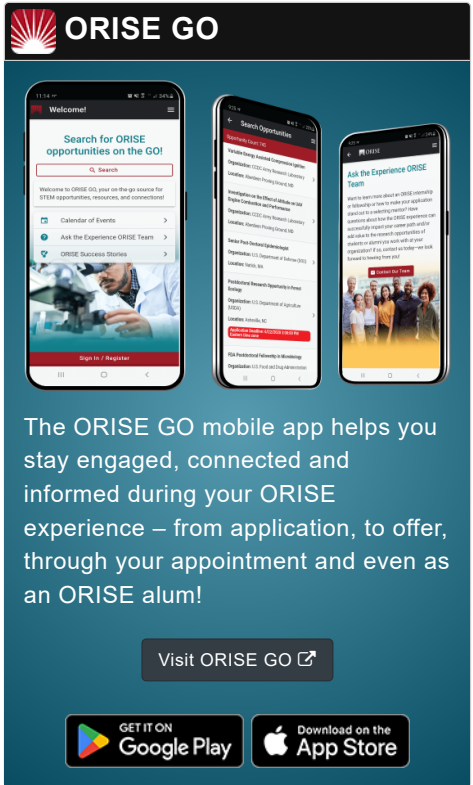


Opportunity Title: Post-Bachelor's Research Appointment in Influenza

Opportunity Reference Code: ARS-VPRU-2016-0020-06



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Organization U.S. Department of Agriculture (USDA)

Reference Code ARS-VPRU-2016-0020-06

How to Apply A complete application package 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. Selected candidate must provide proof of completion of the degree before the appointment can start. Proof must be sent to ORISE directly from the academic institution including graduation date and degree awarded. All transcripts must be in English or include an official English translation. Click [here](#) for detailed information about acceptable transcripts.
- A current resume/CV
- Two references – While two references are requested, applications will be considered without reference information. It is preferred that a complete application package contains a minimum of one reference.

If you have questions, send an email to USDA-ARS@oraui.org. Please include the reference code for this opportunity in your email.

Description A post-bachelor's research opportunity is available with the U.S. Department of Agriculture (USDA) Agricultural Research Service (ARS) Virus and Prion Research Unit (VPRU) National Animal Disease Center in Ames, IA.

The incumbent's overall responsibility is characterization of the genetic evolution of influenza A viruses (IAV) in swine; and to collect, analyze, and maintain physical and electronic data in support of the Intervention Strategies to Control Influenza A Virus (IAV) Infection in Swine project plan. The incumbent will participate as a team member with the scientist and other laboratory staff in all phases of the research process and will assume technical and operational responsibility for specific phases of the research.

Specific goals are to quantify genetic evolution of IAV from swine and define the global relatedness of swine influenza viruses through computational analyses with IAV sequences in the context of contemporary and historical isolates for determination of phylogenetic relationships, interspecies transmission, epidemiologic patterns, and antigenic drift or shift. The incumbent will use databases for efficient management and analysis of swine IAV sequence data.

The position is within the Virus and Prion Research Unit.

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Scientists in this unit maintain a comprehensive IAV research program including investigation of virulence mechanisms, vaccinology, immunology, and virus evolution.

The appointment is full-time for 1 year and may be renewed based upon recommendation of the ARS and availability of funding. The selected applicant will receive a stipend as support for their living and other expenses during this appointment. Stipend rates are determined by ARS officials, and are based on the applicant's academic and professional background. The participant must show proof of health and medical insurance. Health insurance can be obtained through ORISE. The participant will not enter into an employee/employer relationship with ORISE, ORAU, USDA, ARS, or any other office or agency. Instead, the participant will be affiliated with ORISE for the administration of the appointment through the ORISE appointment letter and Terms of Appointment.

While participants will not enter into an employment relationship with ARS, this position requires a pre-appointment check and a full background investigation.

This opportunity is available to U.S. citizens only.



For more information about the ARS Research Participation Program, please visit the [Program Website](#).

Qualifications To be eligible, applicants must have received a B.S. degree with an emphasis on the disciplines of genetics, evolution, and/or molecular biology and have additional knowledge of research and research techniques. Knowledge of molecular epidemiology, statistical inference methods, virology, and/or genetics are preferred.

The incumbent must be skilled in the analysis of molecular sequence data using maximum likelihood and Bayesian phylogenetic methods (e.g., BEAST), the use of scripting languages (e.g. Python and R), and biologic databases and other bioinformatic tools.

The successful candidate must also possess good record keeping, the ability to troubleshoot problems, improve or develop new procedures, the ability to locate and interpret peer-reviewed publications, and good interpersonal skills to work in a team environment. Skilled use of common computer software is required and skill with science-specific software is preferred.

**Eligibility
Requirements**

- **Citizenship:** U.S. Citizen Only
- **Degree:** Bachelor's Degree.
- **Discipline(s):**
 - **Communications and Graphics Design** (1 )
 - **Computer, Information, and Data Sciences** (3 )

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- **Life Health and Medical Sciences** (7 )