

**Opportunity Title:** Identifying Hazardous Nuclear Reactor Emissions Via Microbial Reactomes

**Opportunity Reference Code:** IC-16-03

**Organization** Office of the Director of National Intelligence (ODNI)

**Reference Code** IC-16-03

**How to Apply** **Create and release your Profile on Zintellect** – Postdoctoral applicants must create an account and complete a profile in the on-line application system. **Please note: your resume/CV may not exceed 2 pages.**

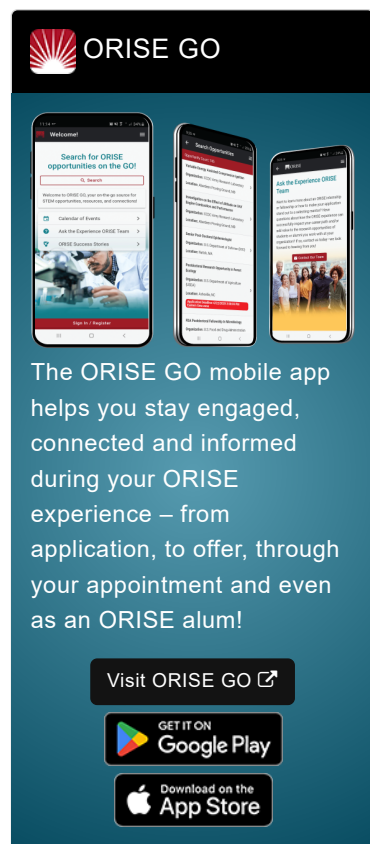
**Complete your application** – Enter the rest of the information required for the IC Postdoc Program Research Opportunity. The application itself contains detailed instructions for each one of these components: availability, citizenship, transcripts, dissertation abstract, publication and presentation plan, and information about your Research Advisor co-applicant.

**Application Deadline** 4/15/2016 6:00:00 PM Eastern Time Zone

**Description** Throughout the world, nuclear reactors are increasingly used as a source of clean and inexpensive energy. While there are many benefits to this energy source, threats from chemical and heavy metal emissions, as well as slow, small scale leakage exist. While catastrophic failure is likely to be immediately detected, these lower levels of emission may not be noticed for longer periods between regular testing. In addition low level long term exposures below regulatory limits may not be reported, causing long term preventable health hazards. Radiation testing and leak detection involve costly equipment and methods that can fail.


Microorganisms could potentially provide a sensitive system for persistent surveillance and measurement of nuclear emissions from power plants. Microbial organisms in soil that has been contaminated by nuclear activity show characteristic and potentially temporally measurable genotypic and phenotypic alterations, including changes in gene expression, morphology, protein isoforms and protein modification. Over time, the species composition of the microbial community changes as the surviving microbes increase resistance against ionizing radiation and heavy metal exposure. These immediate and temporal changes, collectively called the nuclear emissions resistance profile, could potentially be exploited to create an endogenous, measurable and persistent signature of hazardous emissions from nuclear reactors.


While there is an extensive body of research categorizing long-term speciation changes in microbial populations near nuclear reactors, little work has been done to characterize the immediate and near term molecular changes in soil bacteria in response to nuclear reactor specific emissions. Improving our understanding of these changes could increase our ability to use soil samples for environmental testing. A multi-omic approach that analyses changes at transcriptional, translational and post-translational levels could assist in developing profiles specific for nuclear emissions. Additionally, recognizing and measuring these changes could allow us to detect leaks and changes in emissions at an earlier point in time, minimizing long term hazards to the human population in the area and




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saving some of the cost needed to successfully perform extensive environmental remediation

**Example Approaches**

This research should identify and measure molecular resistance changes in response to nuclear reactor emissions in the complete soil microbiome, rather than narrowing to species specific changes. As many microbes use similar means to protect themselves from damaging radiation and heavy metal contamination, bioinformatic and protein predictive techniques that that identify and characterize ubiquitous but specific changes within multiple soil biomes should be prioritized. Approaches that utilize multi-omic analysis to create great profile specificity are welcomed.

This research could include:

- Identification of gene expression changes via microarray screening and metagenomic approaches using multiplexed primers that capture the same gene expression change in multiple soil species
- Proteomic screening to identify measurable changes in protein expression, protein cleavage and activation as well as protein isoforms as preservation mechanisms against nuclear reactor emissions
- Morphological changes in color or colony formation that may occur as a result of increased gene expression, such as increase in radiation-protective melanin production.
- Gene expression changes that are indicative of speciation changes in microbial community composition in response to environmental challenges over middle to long term exposure to emissions.

**Eligibility Requirements**

- **Citizenship:** U.S. Citizen Only
- **Degree:** Doctoral Degree.
- **Discipline(s):**
  - **Business** ([11](#) 👁)
  - **Chemistry and Materials Sciences** ([12](#) 👁)
  - **Communications and Graphics Design** ([6](#) 👁)
  - **Computer, Information, and Data Sciences** ([16](#) 👁)
  - **Earth and Geosciences** ([21](#) 👁)
  - **Engineering** ([27](#) 👁)
  - **Environmental and Marine Sciences** ([14](#) 👁)
  - **Life Health and Medical Sciences** ([45](#) 👁)
  - **Mathematics and Statistics** ([10](#) 👁)
  - **Other Non-Science & Engineering** ([13](#) 👁)
  - **Physics** ([16](#) 👁)
  - **Science & Engineering-related** ([1](#) 👁)
  - **Social and Behavioral Sciences** ([28](#) 👁)