



## **NCI Guidelines for ARRA Research and Research Infrastructure Grand Opportunities: Identifying Potential Viral Signatures in Large Scale Studies of Germline and Somatic Changes in Cancer Genomes Pilot Program**

**Title: Recovery Act Limited Competition for NIH Grants: Research and Research Infrastructure “Grand Opportunities” (RC2)**

**Announcement Number:** [RFA-OD-09-004](#)

**Release Date:** April 30, 2009

**Receipt Date:** May 29, 2009

The National Cancer Institute (NCI) is participating in the Research and Research Infrastructure Grand Opportunities (GO) Program ([RFA-OD-09-004](#); RC2 grant), which has been issued by the NIH to support research on high impact ideas that lend themselves to short-term, non-renewable funding, and may lay the foundation for new fields of investigation. Through its participation on this and other related funding initiatives, the NCI is committed to fulfilling the goals of the American Recovery and Reinvestment Act (ARRA) to help stimulate the economy through support of biomedical and behavioral research. Additional information the Recovery Act and related NIH opportunities is available through the [Office of Extramural Research](#).

### **Areas of Scientific Priority:**

Over the past several years, the increasing association of cancer with the presence of viruses (and other infectious agents) suggests that using current molecular virology technologies to explore cancer as compared with normal genomes may provide new clues to the origin/causation of certain cancers. Historically, both DNA and RNA viruses have been demonstrated to be causative or contributory agents in a number of cancers ranging from cervical (HPVs) and liver cancers (hepatitis viruses) to hematological malignancies (HTLV viruses). As part of its participation on Recovery Act Limited Competition for NIH Grants: Research and Research Infrastructure “Grand Opportunities” (RC2), the NCI has significant interest in utilizing recent advances in large scale genome characterization and expertise along with technologies in molecular virology to begin exploration of characterized cancer genomes from specific cancer types and subtypes for the presence of viral-associated signatures.

Recent progress in the large scale identification of germ line genomic alterations through genome wide association studies (GWAS) and the characterization of



genome changes including mutations through The Cancer Genome Atlas (TCGA) provides a range of unique opportunities to also examine these genomes for the presence of viral information. These large-scale genome characterization efforts are identifying specific SNPs (WGA studies) in well characterized cohorts; and multi-dimensional genomic changes (copy number, expression, epigenomics changes and mutations) – along with clinical information and outcomes data from treated patients through TCGA. These data are being made broadly available through patient-privacy protected public databases.

NCI is interested in attracting specialized network(s) of molecular virologists or comparable resource(s) to perform targeted high through-put viral screening on selected tumors that have been characterized for genomic alterations. This will require collaboration with existing consortia (TCGA) and cohorts (WGA studies) for sample availability. It is anticipated that applicants will have depth in molecular virology techniques and technologies - well beyond routine screens for known oncogenic viruses - along with significant experience in interpretation of resulting data. The recommended focus areas include, but are not limited to, the following:

- Networks of investigators with demonstrated expertise and capabilities in molecular virology to conduct high quality screening of selected well characterized tumor and normal samples from GWAS studies and/or TCGA tumors that have been characterized for somatic genomic alterations – including mutations. Screens should include viral signatures/partial signatures beyond the normal range of cancer-related DNA and RNA viruses.
- Innovative/new experimental approaches (molecular virology, imaging, etc.) that will enable identification of DNA and/or RNA signatures in selected well characterized tumor and normal samples from GWAS or TCGA studies of specific cancers.
- Innovative Bioinformatics/computations approaches/methods that facilitate the identification of viral signatures from existing data bases (CN, expression, epigenomic and/or sequence data) or data deriving from molecular virology methods/technologies.

### **Funding Priorities:**

Overall, NCI expects to make awards for a period of up to 2 years to pilot the concept of exploring samples/data from high throughput genome characterization programs such as TCGA and GWAS for the presence of viral information. NCI may devote up to \$3 million for this pilot program – with number of networks dependent on the breadth of overall capabilities in molecular virology and innovative approaches that could inform a more robust effort to screen cancer genomes for presence of viral information.

**The budget cap for each award proposal is \$1M in total costs per year.**



## Application Guidelines:

Applications for NCI funds supporting the scientific areas listed above **MUST** follow the guidelines listed in RFA-OD-09-004.

### Key Dates ([RFA-OD-09-004](#)):

Letter of Intent Receipt Date:	May 8, 2009
<b>Application Receipt Date:</b>	<b>May 29, 2009</b>
Peer Review Date:	June/July 2009
Council Review Date:	August 2009
Earliest Anticipated Start Date:	September 30, 2009
Expiration Date:	May 28, 2009

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