

A decorative banner with a light yellow background. On the left, there is a DNA microarray pattern of orange and white spots. On the right, there is a 3D molecular structure of a protein or DNA complex with yellow, red, and blue atoms.

# The Cancer Target Discovery and Development Network

**RFA CA-12-006**

**Pre-submission Meeting**

**April 24, 14:30 – 16:30**

**Bethesda, MD**

# Conference “dos and don’ts”

**The dial in number: 1-877-647-3411, PIN code: 6825846373**

**Url: <https://webmeeting.nih.gov/ca12-006/>**

- **DO identify yourself (name and institution) when asking a question**
- **DO keep your phone on mute to reduce background noise**
  - ❖ \*6 mutes the phone; if a phone is muted \*6 will “unmute”
- **DO NOT put the phone on hold since some Institutions have taped content, use mute instead**
  - ❖ FYI-should we hear music and/or advertisements, we will have to disconnect **ALL** the attendees and everyone will need to call back in (the only option possible since discussion is not possible with the background noise)

# Agenda

**14:30 – 14:45 p.m.    *CTD<sup>2</sup> Overview***

**Daniela S. Gerhard, Ph.D.**

**Director, Office of Cancer Genomics**

**14:45 – 15:00 p.m.    *Review Process***

**Dr. Marvin Salin**

**Special Review and Logistics Branch  
Division of Extramural Activities**

**15:00 – 15:15 p.m.    *Grant Administration***

**Mr. Michael S. Zarkin**

**Grants Management Specialist  
Office of Grants Administration**

**15:15 p.m. →**

**Q & A**

**<https://webmeeting.nih.gov/ca12-006/>**

# Examples of NIH Investment in Large Projects of Genomic Research

- **Therapeutically Applicable Research to Generate Effective Treatment (TARGET)**
- **The Cancer Genome Atlas (TCGA)**
- **Cancer Genome Anatomy Project/Cancer Genome Characterization Initiative (CGAP/CGCI)**
- **Genome-wide association studies (GWAS) of common and complex diseases and follow-up**
- **Others**

**Data generated is available to the research community**

# Molecular Characterization of Cancer is Essential but not Sufficient

- **Each tumor has hundreds to thousands genomic alterations**
  - ❖ Chromosomal changes: amplifications, deletions, translocations
  - ❖ Epigenetic changes
  - ❖ Mutations
  
- **Little is known about the cellular function of most genes, much less how sequence variants and mutations affect them**
  - ❖ Distinguishing initiating vs. driver vs. passenger mutations
    - ❑ Drivers are defined as genes involved in tumor maintenance
    - ❑ Evidence is accumulating that multiple subclones exist within a tumor and their frequency varies between patients
  - ❖ Genomic alterations result in cancer within specific context
    - ❑ Cell of origin
    - ❑ Other molecular alterations in genes that may have synergistic or antagonistic impact

# CTD<sup>2</sup>: A Bridge from Genomics to Therapeutics

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- **Mechanism of Support: U01 Cooperative Agreement**
  - ❖ Description: To support a discrete, specified, circumscribed project to be performed by the named investigator(s) in an area representing hers/his/their specific interest and competencies.
  - ❖ 6-8 applications may be funded in FY2013, for a period of up to 4 years
  - ❖ The new grantees will join the current CTD<sup>2</sup> Network  
<http://ocg.cancer.gov/programs/ctdd.asp>
- **Up to 2 applications from an Institution, except from those institutions which already have a CTD<sup>2</sup> member (list found on the web site listed above**
- **Use of de-identified human genome data: E4 exemption is required**
- **Data and Resource sharing plans are required**
  - ❖ The approach that was developed by the CTD<sup>2</sup> members is at  
<http://ctd2.nci.nih.gov/CTD2dataReleasePolicy.pdf>



- **The systematic identification of novel potential targets that may inspire future development of therapeutic applications**
  - ❖ The target candidates must be identified and characterized through exploration of the genomic and other molecular alterations
- **High throughput approaches to the identification of small molecules that can be used to study the biology of cancer types and targets**
- **As genomic data become available from TARGET, TCGA, CGCI, ICGC etc., they will be added**
  - ❖ **Be nimble, flexible and open to new opportunities**



# Concept Examples (from RFA)

- Identification of challenging, unconventional, or rarely addressed targets such as those involved in specific protein-protein interactions, specific protein-DNA interactions, regulatory RNA functions and others
- Prediction of mechanism(s) of resistance, primary or acquired, to therapy based on patients' genetic background and cancer-specific alterations
- Determination of the complex dependencies within each cancer type and the identification of combination of targets which could be exploited for therapeutic interventions
- Exploration of targets/target combinations suitable for possible synthetic lethality-based approaches, determination of the underlying mechanisms and/or identification of biologically modulators
- Development of probes, e.g., small molecules or micro RNAs (miRNAs), that modulate the targets (and their function) in the specific cell types, and the environment, in which the cancer(s) occur

# Important Dates

➤ **Letter of Intent to NCI**      **May 21, 2012**

❖ The PD, Daniela S. Gerhard Ph.D.

[gerhardd@mail.nih.gov](mailto:gerhardd@mail.nih.gov)

AND

❖ The SRO, Adriane Stoica Ph.D

[stoicaa2@mail.nih.gov](mailto:stoicaa2@mail.nih.gov)

➤ **Application due date**      **June 21, 2012**

➤ **Review**      **Early fall 2012**

➤ **Awards**      **April 2013**

# Questions?

Note: Slides and information from today's teleconference will be posted on the OCG web site: [ocg.cancer.gov](http://ocg.cancer.gov)

A decorative banner spanning the width of the slide. The left side shows a DNA microarray with a grid of orange spots. The right side shows a 3D ball-and-stick molecular model of a protein or DNA structure with yellow, red, and blue atoms.

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