*Respondents:* 1,630. *Estimated Number of Responses Per Respondent:* 1. *Average Burden Hours Per Response:* 0.1. *Estimated Total Annual Burden Hours Requested:* 163.

The annualized cost to respondents is estimated at:

| Type of respondents | Estimated number of respondents | Estimated number of responses per respondent | Average burden hours per response | Estimated total annual burden hours requested |
|---|---|---|---|---|
| Guest Researcher | 400 | 1 | 0.1 | 40 |
| Special Volunteer | 1230 | 1 | 0.1 | 123 |
| Total | 1630 | 1 | 0.1 | 163 |

There are no Capital Costs, Operating Costs, and/or Maintenance Costs to report.

*Request for Comments:* Written comments and/or suggestions from the public and affected agencies are invited on one or more of the following points: (1) Whether the proposed collection of information is necessary for the proper performance of the agency, including whether the information will have practical utility; (2) The accuracy of the agency's estimate of the proposed collection of information, including the validity of the methodology and assumptions used; (3) Ways to enhance the quality, utility, and the clarity of information to be collected; and (4) Ways to minimize the burden of the collection of information on those who are to respond, including the use of appropriate automated, electronic, mechanical, or other technological collection techniques or other forms of information technology.

*For Further Information:* To request more information on the proposed project or to obtain a copy of the data collection plans and instruments, contact: Ms. Yetta L. Patterson, Personnel Management Specialist, Office of Human Resource Management, OD, NIH Building 31, Room 1C39, 31 Center Drive MSC 2272, Bethesda, MD 20892–2272.

*Comments Due Date:* Comments regarding this information collection are best assured of having their full effect if received within 60-days of the date of this publication and/or suggestions regarding the items contained in this notice, especially regarding the estimated public burden and associated response time, should be directed to the: Office of Management and Budget, Office of Regulatory Affairs, New Executive Office Building, Room 10235, Washington, D.C. 20503, Attention: Desk Officer for NIH. To request more information on the proposed project or to obtain a copy of the data collection plans and instruments, contact: Ms. Yetta L. Patterson, Personnel Management Specialist, Office of Human Resource Management, OD, NIH, Building 31, Room 1C39, 31 Center Drive MSC 2272, Bethesda, MD 20892–2272.

Dated: February 3, 1999.

**Stephen C. Benowitz,**

*Director of Human Resources.*

[FR Doc. 99–3236 Filed 2–9–99; 8:45 am]

**BILLING CODE 4140–01–M**

## DEPARTMENT OF HEALTH AND HUMAN SERVICES

### National Institutes of Health

### National Institute of Environmental Health Sciences: Opportunity for a Cooperative Research and Development Agreement (CRADA) for Development of Technology and Application Testing of Toxicological cDNA Microarrays

**AGENCY:** National Institute of Environmental Health Sciences, National Institutes of Health, PHS, DHHS.

**ACTION:** Notice.

**SUMMARY:** The National Institutes of Health (NIH) seeks an agreement with a company(s) which can pursue the development of technology and application testing of toxicological cDNA microarrays for analysis of exposed human and mouse biological samples. The National Institute of Environmental Health Sciences (NIEHS) is in the first phases of developing and testing this technology for application to human toxicology. A CRADA for the co-development of technology or testing of this new toxicology assay will be granted to the awardee(s).

**DATES:** Capability statements must be received by NIH on or before April 12, 1999.

**ADDRESSES:** Proposals and questions about this opportunity may be addressed to Dr. J. Carl Barrett, Scientific Director, NIEHS, Mail Drop C2–15, P.O. Box 12233, Research Triangle Park, NC 27709; Telephone (919) 541–2992; Fax (919) 541–7784; E-mail BARRETT@NIEHS.NIH.GOV

**SUPPLEMENTARY INFORMATION:** cDNA microarrays are tools that can be used to analyze changes in genome-wide patterns of gene expression. This technology may potentially revolutionize the way toxicological problems are investigated. The main challenges facing investigators in environmental health research is to assess exposures and identify hazards. Defining the mechanisms of action of environmental agents can greatly assist in hazard identification, species extrapolation, and risk assessment. Given that exposures to different classes of toxicants result in distinct patterns of altered gene expression, microarray technology can be utilized to categorize and classify these effects. In defined model systems, treatment with known agents, such as polycyclic aromatic hydrocarbons, dioxin-like compounds, peroxisome proliferators, oxidant stress, or estrogenic chemicals may provide a gene expression signature on a microarray which represents the cellular response to these agents. These same systems can then be treated with unknown, suspect agents to determine if one or more of these standard signatures is elicited. This approach will also help elucidate an agent's mechanism of action and may also be used to detect changes in exposed human populations, information essential for the risk assessment process. cDNA microarrays could also be used to potentially determine cross-talk between combinations of agents (i.e. dioxin and estrogen). Microarray technology could in the long run, provide a relatively inexpensive, quick way to screen for potential bio-reactive agents.

We are in the process of establishing cDNA microarray technology at the NIEHS. Currently, we are developing custom DNA chips that are human cDNA clone subarrays oriented toward the expression of genes involved in responses to toxic insult. These include xenobiotic metabolizing enzymes, cell

cycle components, oncogenes, tumor suppressor genes, DNA repair genes, estrogen-responsive genes, oxidative stress genes, and genes known to be involved in apoptotic cell death. This technology is in developmental stages at NIEHS, and we are interested in establishing relationships with CRADA partners to further our efforts on technology development and application toward toxicology research.

NIEHS seeks partnerships for collaboration in the development of arrayed cDNA libraries from various tissue sources, the development of toxicology models to test/validate the use of microarray technology in toxicology testing, and the development of bioinformatics support involving pattern recognition and classification.

**Roles of NIEHS**

1. Provide project coordination for overall project development and testing.
2. Establish various classes of toxicology gene expression arrays and subarrays based on existing data from toxicology studies or specific cDNA libraries.
3. To manufacture DNA chips from provided DNA sets and arrayed libraries, label and hybridize RNA probes to the expression arrays, and scan data and analyze and compile results.
4. To validate methods and expression array patterns using probes generated from established toxicology exposure models that have been developed by NIEHS or CRADA partner(s).

**Role of the CRADA Partner(s)**

1. Provide cDNA libraries from rodent and human sources that may be compatible for use to generate targets for use in synthesis of gene chips. May include custom cDNA library isolation from a variety of species and tissue sources.
2. Provide clone arrays from cDNA libraries from rodent and human sources, including arrays from custom, tissue-specific cDNA libraries. Also includes the sequence validation of arrayed clones.
3. Provide RNAs from traditional toxicology assays/models for use in validation testing of the use of microarray in toxicological identification/exposure assessment.
4. Provide bioinformatics/database support to subarray development and compilation and analysis of data, including pattern recognition from expression analyses experiments.

Selection criteria for choosing the CRADA partner(s) will include, but will not be limited to, the following:

1. Experience in the generation of high quality cDNA libraries, including custom and subtractive libraries. Ability to array cDNA libraries and provide resources to sequence-validate library clones.
2. Experience in toxicology testing models and ability to provide high quality and quantity RNA from these models.
3. Experience in database management and the development of software for the analysis of pattern recognition. May also include plasmid purification and PCR amplification of DNA from existing sub-arrayed library sets.

Dated: February 1, 1999.

**Jack Spiegel,**

*Director, Division of Technology Development and Transfer, Office of Technology Transfer.*

[FR Doc. 99–3237 Filed 2–9–99; 8:45 am]

**BILLING CODE 4140–01–M**

## DEPARTMENT OF HEALTH AND HUMAN SERVICES

### National Institutes of Health

### Government-Owned Inventions; Availability for Licensing

**AGENCY:** National Institutes of Health, Public Health Service, DHHS.

**ACTION:** Notice.

**SUMMARY:** The inventions listed below are owned by agencies of the U.S. Government and are available for licensing in the U.S. in accordance with 35 U.S.C. 207 to achieve expeditious commercialization of results of federally-funded research and development. Foreign patent applications are filed on selected inventions to extend market coverage for companies and may also be available for licensing.

**ADDRESSES:** Licensing information and copies of the U.S. patent applications listed below may be obtained by writing to the indicated licensing contact at the Office of Technology Transfer, National Institutes of Health, 6011 Executive Boulevard, Suite 325, Rockville, Maryland 20852–3804; telephone: 301/496–7057; fax: 301/402–0220. A signed Confidential Disclosure Agreement will be required to receive copies of the patent applications.

**A Method Of Using A $\beta_2$-Adrenergic Receptor Agonist That Selectively Activates $G_s$ Proteins In The Treatment Of Cardiovascular Disease**

Rui-Ping Xiao, Edward G Lakatta, Heping Cheng (NIA)
Serial No. 60/102,475 filed 30 Sep 98
*Licensing Contact:* Charles Maynard; 301/406–7735 ext. 243; *e-mail:* cm251n@nih.gov

This technology relates to a method of using $\beta_2$-adrenergic receptor agonist that selectively activates $G_s$ proteins in the treatment of cardiovascular disease. In particular, this invention relates to a method of using fenoterol to activate selectively $G_s$ proteins in the treatment of acute heart failure, chronic heart failure and aging heart. In the heart, β-adrenergic receptor (βAR) stimulation provides the primary regulatory mechanism on cardiac function. There are at least two βAR subtypes, namely $\beta_1$AR and $\beta_2$AR, that exist in the myocardium, although $\beta_1$AR predominates. While $\beta_1$AR couples to stimulatory G proteins ($G_s$), $\beta_2$AR elicits bifurcated signaling pathways mediated by $G_s$ and $G_i$, resulting in functionally opposing effects on cardiac function. In failing and aged hearts, the overall response to βAR stimulation is markedly diminished due to the down-regulation of $\beta_1$AR and an up-regulation of $G_i$ proteins.

This invention is predicated on the surprising and unexpected discovery that a $\beta_2$AR agonist can selectively activate $G_s$ proteins, and is further predicated on the discovery that selective activation of $G_s$ proteins by a $\beta_2$AR agonist can revive βAR contractile support in failing hearts.

An object of the present invention is to provide ligands (agonists and antagonists), and methods for the selective activation and inactivation of a subset of signaling pathways coupled to any given receptor of any cell or tissue type. It is another object of the present invention to provide ligands and methods for the selective activation and inactivation of a subset of signaling pathways involving G proteins. In particular, $G_s$ and $G_i$ proteins coupled to a cardiovascular receptor such as $\beta_2$ AR for the treatment of cardiovascular disease.

**Aminohydroxylated Adenine Derivatives**

KB Sharpless, DM Jerina, KR Dress, LJ Goossen, AS Pilcher, H Kroth, AR Ramesha (NIDDK)
Serial No. 60/091,900 filed 07 Jul 98
*Licensing Contact:* Charles Maynard; 301/496–7735 ext. 243; *e-mail:* cm251n@nih.gov

The invention herein describes a process for the addition of adenine and its derivatives to olefins to produce cis-vicinal aminoalcohols. The adenine moiety is contained in numerous drugs as well as plant growth regulators. In addition, adducts of purine bases in