

pharmaceuticals dispensed by each program. DSS/HRSA will continue to compile summary reports that are distributed back to grantees and State ADAPs on a quarterly basis. HRSA, the Department of Health and Human

Services and the Office of Management and Budget also utilize these summary reports. The data collected are used to guide program planning, formulate budget recommendations, and monitor State ADAPs, especially monitoring the

balance between an individual State ADAP's available resources against the client demand for medications. The burden estimates are as follows:

HRSA form	Number of respondents	Responses per respondent	Total responses	Hours per responses	Total burden hours
Title II ADAP Grantees (Clients and Expenditures)	54	12	648	0.75	486
Title II ADAP Grantees (Pricing)	54	4	216	0.75	162
Total	54	16	864	0.75	648

Send comments to Susan G. Queen, HRSA Reports Clearance Officer, Room 14-33, Parklawn Building, 5600 Fishers Lane, Rockville, MD 20857. Written comments should be received on or before August 28, 2000.

Dated: June 21, 2000.

Jane Harrison,

Director, Division of Policy Review and Coordination.

[FR Doc. 00-16257 Filed 6-27-00; 8:45 am]

BILLING CODE 4160-15-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.

High-Speed Interlaced Spin Echo Magnetic Resonance Imaging

Jeff Duyn (CC)

DHHS Reference No. E-171-99/0 filed 30 Dec 1999

Licensing Contact: Carol Salata; 301/496-7735 ext. 232; e-mail: cs253n@nih.gov

Spin-echo acquisition in magnetic resonance imaging (MRI) facilitates the observation of anatomical abnormalities in pathologies such as brain tumors, stroke and multiple sclerosis. It can also be applied in conjunction with perfusion techniques for the investigation of function, based on susceptibility contrast agents as well as blood oxygen level dependent (BOLD) contrast. Improving the efficiency of spin echo MRI is the subject of the current invention. It provides a method of reducing scan time in multi-slice spin-echo MRI through effective use of the echo delay time between radio frequency (RF) excitation and reception. This technique has been evaluated in examples of brain scans and has indications that a substantial increase in scan speed can be achieved without loss in image signal-to-noise ratio or contrast.

Laparoscopic Sac Holder Assembly

McClellan M. Walther, Frank Harrington (NCI)

Serial No. 09/368,824 filed 05 Aug 1999

Licensing Contact: John Peter Kim; 301/496-7056 ext. 264; e-mail: jk141n@nih.gov

The present application describes a device and method for accessing and retrieving tissue from a body cavity through minimally invasive endoscopic procedures. Specifically, the present invention consists of a sac holding device, having a rotatable hinge joining bowed leaf elements. The bowed leaf elements form a loop which is adapted to open and close the sac by rotation of the bowed leaf elements. With this laparoscopic device, one can easily contain materials that have been

targeted for removal from body cavities. Pieces of infected or cancerous tissue and body fluids are easily contained and can be removed without the danger of collateral contamination.

Novel Diagnostic Standards for Virus Detection and Quantification

Richard Y. Wang and James W. Shih (CC)

DHHS Reference Nos. E-228-98/0 filed 20 Apr 1999 and E-228-98/1 filed 20 Apr 2000

Licensing Contact: John Peter Kim; 301/496-7056 ext. 264; e-mail: jk141n@nih.gov

The gene amplification is a tool for the detection of trace amounts of nucleic acids and the clinical applications of this technique in diagnosis of human diseases have been widely demonstrated. There are numerous steps from sample preparation to final product analysis for gene amplification-based molecular diagnosis of clinical specimens. Small variations in each step among different samples can have profound impacts on the final results.

There is a need for stable and well-calibrated internal standards to enable to monitor every step of the amplification process, e.g., sample preparation, gene amplification, and amplicon detection. The subject invention is directed to internal standards as recombinant viral particles. The particles contain modified target sequence and multiple targets can also be packaged. Particles containing RNA target sequence of human hepatitis C virus (HCV) were constructed as example. Thus, this approach in making internal standards has commercial potential in molecular testing for clinical diagnosis, blood screening, and process validation.

Dated: June 15, 2000.

Jack Spiegel,

Director, Division of Technology Development and Transfer, Office of Technology Transfer, National Institutes of Health.

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BILLING CODE 4140-01-P

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Gene Profiling Arrays

Ena Wang, Lance Miller, Francesco Marincola (NCI)

DHHS Reference No. E-086-00/0 filed 28 Mar 2000

Licensing Contact: Richard Rodriguez; 301/496-7056 ext. 287; e-mail: rr154z@nih.gov

The invention(s) embodied in this application, provides for ordered arrays of mixtures of nucleic acid molecules, which reflect the gene expression profile of one or more specimens, such as different cell types or tissues. In particular embodiments, complete mRNA mixtures (*i.e.* gene transcripts) or cDNA representatives from specimens are individually arrayed on a substrate. Such mixtures of nucleic acids can be derived from any specimen source, including animal, plant and/or microbial cells and can be assembled in any collection desired. The collections

can, for instance, include nucleic acid mixtures from different cell types, different phenotypes, cells grown under different conditions, cells of different ages or developmental stages, and so forth. The nucleic acid arrays are provided in both macro- and micro-formats and are suitable for measuring the relative abundance of particular gene transcripts across a collection of complex nucleic acid mixtures.

Techniques are also disclosed for producing high-fidelity, amplified mixtures of nucleic acid molecules using a combination of RNA (sense or anti-sense) amplification and template-switching synthesis. Amplified mixtures produced using this method can, for instance, be applied to the disclosed arrays. The disclosed arrays allow high throughput analysis of differential gene expression in a specimen, such as a tumor, or a variety of specimens, such as a variety of tumors, and is suitable for automated preparation and analysis.

The Isolation of a New Gene, TRAG, Associated with TGF- β

Snorri S. Thorgeirsson, Sean R. Sanders (NCI)

DHHS Ref. No. E-047-00/0 filed 07 Mar 2000 and 60/187,848 filed 08 Mar 2000

Licensing Contact: Susan S. Rucker; 301/406-7056 ext. 245; e-mail: sr156v@nih.gov

A new gene has been isolated from a cell line resistant to a protein, TGF- β , which can block the proliferation of cancer cells. This resistance endows the cell with cancer forming abilities. The protein encoded by the newly-discovered TRAG gene has been found at much higher levels in these cancer-forming cells than their non-cancerous ancestors. In addition, the TRAG protein is greatly elevated in many other rodent and human cancer cell lines and in primary mouse liver tumors, but not in surrounding non-tumorous tissue. This indicates a strong association between TRAG and cancer-forming potential. TRAG may be involved in the mechanism by which normal cells become cancerous. The TRAG gene could provide an excellent target for cancer or gene therapy. Abrogation of TRAG protein production using anti-sense oligonucleotides or antibodies could conceivably prevent, reduce, or destroy certain types of tumors.

Identification of a Novel Domain in the Tumor Necrosis Factor Receptor Ligand Family that Mediates Pre-Ligand Receptor Assembly and Function

MJ Lenardo, FK Chan, R Siegel (all of NIAID)

Serial No. 60/181,909 filed 11 Feb 2000

Licensing Contact: Susan S. Rucker; 301/496-7056 ext. 245; e-mail: sr156v@nih.gov

This application discloses the identification of a functional domain, which is essential for signaling involving receptors of the Tumor Necrosis Factor Superfamily (TNFR's) including TNFR-1 (p60), TNFR-2 (p80), Fas, TRAIL-R, LT β R, CD40, CD30, CD27, HVEM, OX40 and DR4. The functional domain, denoted the Pre-Ligand Assembly Domain (PLAD), can be isolated as functional polypeptides which can be useful in inhibiting the first step in TNFR mediated signaling, ligand-independent assembly of members of the TNFR Superfamily. The ability to inhibit TNFR signaling suggests that these PLAD polypeptides may be useful in developing new therapeutic molecules or as therapeutic molecules themselves for modulation of immune responses, apoptosis, and inflammation.

In addition to being available for license, the investigators who have developed this technology are also willing to consider entering into a CRADA relationship with companies interested in commercial development of this technology.

Transition Metal Complexes of N,N',N''-trialkyl-cis,cis-1,3,5-triaminocyclohexane and Related Compositions and Methods

Martin W Brechbiel, Roy P. Planalp, Kim A. Deal (NCI)

DHHS Reference No. E-072-99/0 filed 10 Aug 1999

Licensing Specialist: Girish C. Barua; 301/496-7735 ext. 263; gb18t@nih.gov

The invention is directed to copper complexes of N,N',N''-trimethyl-cis,cis-1,3,5-triaminocyclohexane and N,N',N''-triethyl-cis,cis-1,3,5-triaminocyclohexane as well as methods of producing and using said complexes. These complexes are capable of cleaving DNA and RNA *in vitro* and could be used for the treatment of cancer or other disease states that are characterized by abnormal cellular proliferation. The complexes could also be used as delivery agents or as imaging-tracers. These complexes offer advantages over previously described cleaving methodologies, *e.g.*, oxidative or transesterification protocols. The disclosed copper-complexes act via hydrolytic reactions. These advantages could offer significant benefits over related therapeutic approaches to the aforementioned abnormal conditions.