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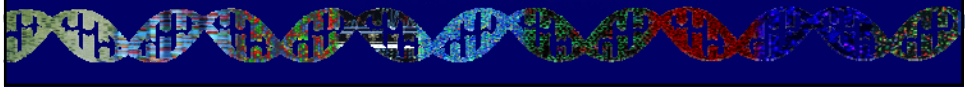
National Human Genome Research Institute
National Institutes of Health

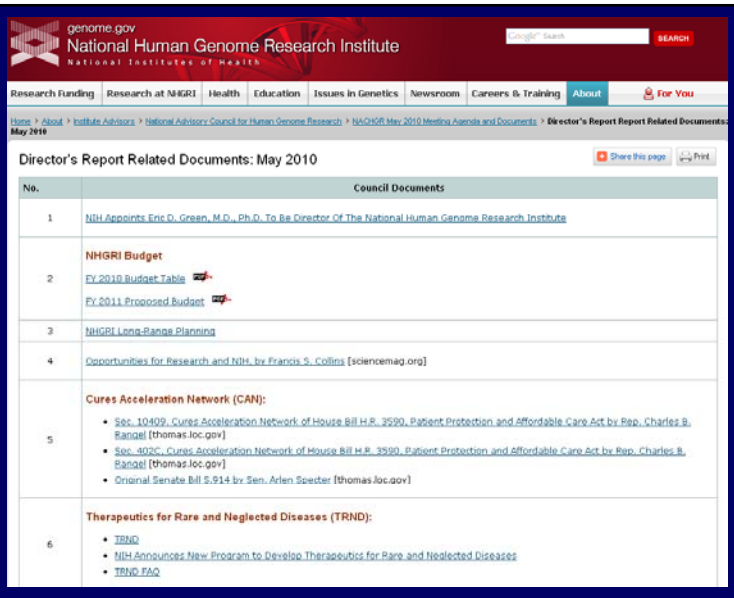
DIRECTOR'S REPORT

National Advisory Council for Human Genome Research

May 2010

Eric Green, M.D., Ph.D.
Director, NHGRI





genome.gov/DirectorsReport

Document #

genome.gov/Director

Document 1

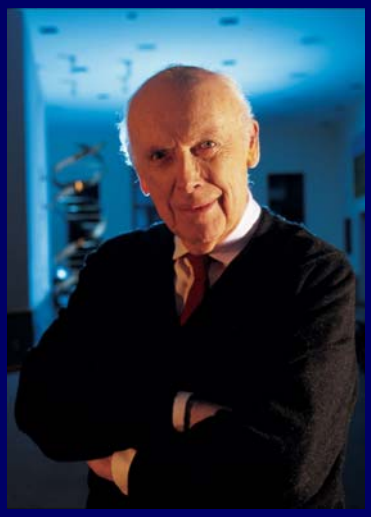
Thanks!

Eric Green, M.D., Ph.D.
Director, NHGRI

Eric Green, M.D., Ph.D.
Director, NHGRI

Previous NCHGR/NHGRI Directors

James Watson



1989-1992

Francis Collins

1993-2008

I. General NHGRI Updates

II. General NIH Updates

III. Genomics Updates

IV. NHGRI Extramural Program

V. NIH Common Fund Programs

VI. NHGRI Office of the Director

VII. NHGRI Intramural Program

Eric Green, M.D., Ph.D.
Director, NHGRI

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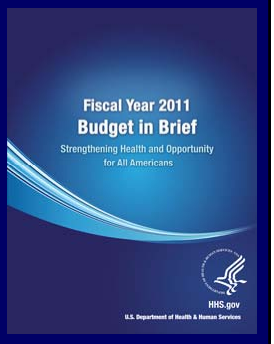
NHGRI Appointments/Recruitments

- **Appointed:**
  - Eric Green, NHGRI Director
  - Mark Guyer, Acting Deputy Director
  - Ellen Rolfes, Deputy Executive Officer
  - Ann Fitzpatrick, Budget Officer
- **Recruitments:**
  - Scientific Director (Active)
  - Deputy Director (Pending)
  - ELSI 'Director' (Pending)
- **On 'Detail' to the Office of the Director:**
  - Kris Wetterstrand
  - Rudy Pozzatti

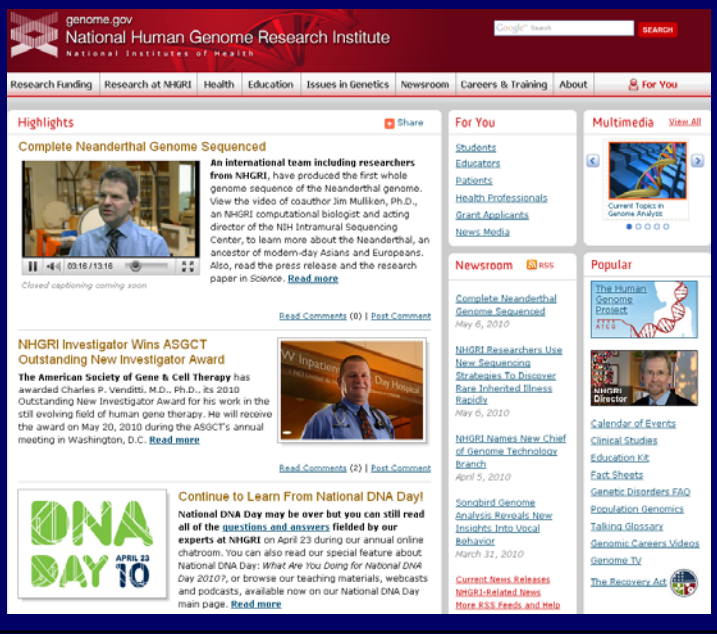
NIH & NHGRI Appropriations Update

- **FY2010**
  - NHGRI: $516M (2.7% increase)
  - NIH: $31B (2.3% increase)
- **FY2011 (President's Budget)**
  - NHGRI: $534M (3.5% increase)
  - NIH: $32B (3.2% increase)



Document 2

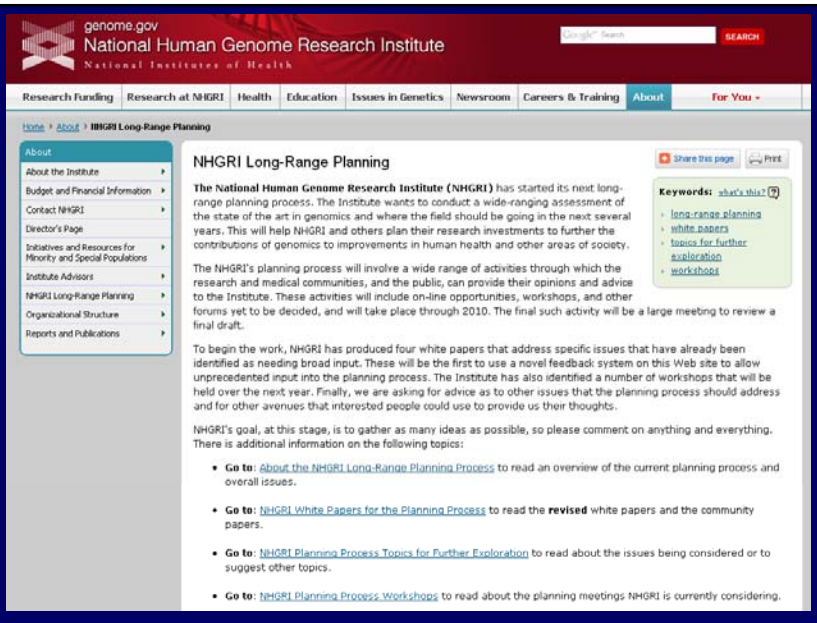
Electronic 'Facelift' for genome.gov



2010 @ NHGRI

- Eric Green's 'Rookie Year' as Director
- 13th Anniversary of 'Institute Status' (January)
- 10th Anniversary of Completion of Draft Human Genome Sequence (June)
- 20th Anniversary of Start of Human Genome Project (October)
- Completion of New Strategic Plan for Genomics (December)

NHGRI Strategic Planning Process



genome.gov/Planning

Document 3

NHGRI Strategic Planning Process

White Papers and Web-based Feedback

Applying Genomics to Clinical Problems: Diagnostics, Preventive Medicine, and Pharmacogenomics

Applying Genomics to Clinical Problems: Therapeutics

A Vision for the Future of Genomics: Education and Community Engagement

The Future of Genome Sequencing

NHGRI Strategic Planning Process

April 2008	Planning Process Kick-Off Meeting
May 2008	ELSI Assessment Panel Report and "Decade of ELSI" Meeting
Sept. 2008	Social and Behavioral Research in Genomics Workshop
Sept. 2008	Health Disparities, Race, and Genomics Summit
Feb. 2009	The Dark Matter of Genomic Associations with Complex Diseases Workshop
March 2009	The Future of Sequencing Workshop
July 2009	Internal Review of Comments Received Regarding Web-posted White Papers
Oct. 2009	Genomics of Gene Regulation Workshop
Feb. 2010	Council Input

NHGRI Strategic Planning Process

March 2010	Cloud Computing Workshop
April 2010	Informatics Planning Workshop
May/June 2010	Develop Draft Plan
July 2010	Airlie Center 'Finale' Meeting
August 2010	Refine/Revise Plan
Sept. 2010	Council Endorsement of Plan
Oct. 2010	Finalize and Submit Plan for Publication
Dec. 2010	Publication of Strategic Plan
Dec. 17 2010	NIH Symposium Commemorating New Strategic Plan and 20th Anniversary of HGP Start

Vivien Bonazzi

We Are Here

'Finale Meeting': July 6-8, 2010

Airlie Meeting: Remote Video Access & Blog

* Those who could not attend in person
* ~100 Genomics/Genetics Trainees

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Five Major Opportunities for NIH


POLICYFORUM

RESEARCH AGENDA

Opportunities for Research and NIH

Francis S. Collins

The promise of fundamental advances in diagnosis, prevention, and treatment of disease has never been greater.

The mission of the National Institutes of Health (NIH) is science in pursuit of fundamental knowledge about the nature and behavior of living systems and the application of that knowledge to extend healthy life and to reduce the burdens of illness and disability. The power of the molecular approach to health and disease has steadily gained momentum over the past several decades and is now poised to catalyze a revolution in medicine. The foundation of success in biomedical research has always been, and no doubt will continue to be, the creative insights of individual investigators. But increasingly those investigators are working in teams, accelerated by interdisciplinary approaches and empowered by open access to tools, databases, and technologies, to a careful balance in needed between investigator-initiated projects and large-scale community resource programs. For both individual and large-scale efforts, it is appropriate to identify areas of particular promise. Here are five such areas that are ripe for major advances that could reap substantial downstream benefits.

High Throughput Technologies

In the past, most biomedical basic science projects required investigators to limit their scope to a single aspect of cell biology or physiology. The revolution now sweeping the field is the ability to be comprehensive—for example, to define all of the genes of the human or a model organism, all of the human proteins and their structures, all of the common variations in the genome, all of the major pathways for signal transduction in the cell, all of the patterns of gene expression in the brain, all of the steps involved in early development, or all of the components of the immune system. Further development of technologies in areas such as DNA sequencing, imaging, nanotechnology, proteomics, metabolomics, small-molecule screening, and RNA interference are ripe for aggressive investment. Furthermore, these technologies will spur the production of massive and complex data sets and will require major investments in computational biology.

As one example, the Cancer Genome Atlas (1) is now poised to derive comprehensive information about the genetic underpinnings of 20 major tumor types. This information will likely force a complete revision of diagnostic categories in cancer and will usher in an era where abnormal pathways in specific tumors will be matched with the known targets of existing therapeutics. Another example is the opportunity to understand how interactions between ourselves and the microbes that live on us and in us (the "microbiome") can influence health and disease (2).

Translational Medicine

Critics have complained in the past that NIH is too slow to translate basic discoveries into new diagnostic and treatment advances in the clinic. Some of that criticism may have been deserved, but often the pathway from molecular insight to therapeutic benefit was just not discernible. For many disorders, that is now changing. Three major factors have contributed to this: (i) the discovery of the fundamental basis of hundreds of diseases has advanced dramatically, (ii) with support from the NIH Roadmap, academic investigators supported by NIH now have access to resources to enable them to convert fundamental observations into assays that can be used to screen hundreds of thousands of candidates for drug development, (iii) public-private partnerships are being more widely embraced in the drug-development pipeline to enable biotech and pharmaceutical companies to pick up promising compounds that have been effectively "de-risked" by academic investigators and to bring them to clinical trials and U.S. Food and Drug Administration (FDA) approval.

As one example, the NIH Therapeutics for Rare and Neglected Diseases (TRND) (3) program will allow certain promising compounds to be taken through the preclinical phase by NIH, in an open environment where the world's experts on the disease can be involved. Furthermore, as information about common diseases increases, many are being resolved into distinct molecular subsets, and so the TRND model will be even more widely applicable.

The first human protocol (for spinal cord injury) involving human embryonic stem cells (hESCs) was approved by the FDA in 2009, and the opening up of federal support for hESC research will bring many investigators into this field. The capability of transforming human skin fibroblasts and other cells into induced pluripotent stem cells (iPSCs) opens up a powerful strategy for therapeutic replacement of damaged or abnormal tissue without the risk of transplant rejection (4–6). Although much work remains to be done to investigate possible risks, the iPSC approach stands as one of the most breathtaking advances of the last several years, and every effort should be made to pursue the basic and therapeutic implications with maximum speed.

Benefiting Health Care Reform

U.S. expenditures on health care now represent 17% of our Gross Domestic Product, are continuing to grow, and are excessive as a percentage of per capita gross income com-

26 1 JANUARY 2010 VOL 327 SCIENCE www.sciencemag.org

Science (2010)

Document 4

Five Major Opportunities for NIH


POLICYFORUM

RESEARCH AGENDA

Opportunities for Research and NIH

The promise of fundamental advances in diagnosis, prevention, and treatment of disease has never been greater.

Francis S. Collins

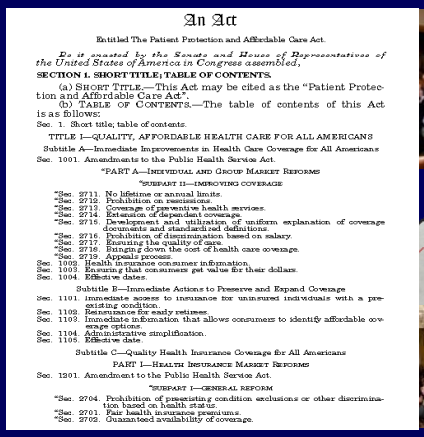
Science (2010)

- High-Throughput Technologies
- Translational Medicine
- Benefiting Health Care Reform
- Focusing More on Global Health
- Reinvigorating and Empowering the Biomedical Research Community

Opportunity #2: Translating Basic Science Discoveries into New and Better Treatments

Cures Acceleration Network (CAN) in the Health Care Reform Act

Patient Protection and Affordable Care Act
(Public Law 111-148)



An Act

Entitled The Patient Protection and Affordable Care Act.

Be it enacted by the Senate and House of Representatives of the United States of America in Congress assembled,

SECTION 1. SHORT TITLE; TABLE OF CONTENTS.

(a) SHORT TITLE.—This Act may be cited as the "Patient Protection and Affordable Care Act".

(b) TABLE OF CONTENTS.—The table of contents of this Act is as follows:

Sec. 1. Short title; table of contents.

TITLE I—QUALITY, AFFORDABLE HEALTH CARE FOR ALL AMERICANS

Subtitle A—Immediate Improvements in Health Care Coverage for All Americans

Sec. 1001. Amendments to the Public Health Service Act.

"PART A—INDIVIDUAL AND GROUP MARKET REFORMS

"SUBPART II—IMPROVING COVERAGE

"Sec. 2711. No lifetime or annual limits.
"Sec. 2712. Prohibition on rescissions.
"Sec. 2713. Coverage of preventive health services.
"Sec. 2714. Extension of dependent coverage.
"Sec. 2715. Development and utilization of uniform explanation of coverage documents and standardized definitions.
"Sec. 2716. Prohibition of discrimination based on salary.
"Sec. 2717. Ensuring the quality of care.
"Sec. 2718. Bringing down the cost of health care coverage.
"Sec. 2719. Appeals process.
Sec. 1002. Health insurance consumer information.
Sec. 1003. Ensuring that consumers get value for their dollars.
Sec. 1004. Effective dates.

Subtitle B—Immediate Actions to Preserve and Expand Coverage

Sec. 1101. Immediate access to insurance for uninsured individuals with a preexisting condition.
Sec. 1102. Reinsurance for early retirees.
Sec. 1103. Immediate information that allows consumers to identify affordable coverage options.
Sec. 1104. Administrative simplification.
Sec. 1105. Effective date.

Subtitle C—Quality Health Insurance Coverage for All Americans

PART I—HEALTH INSURANCE MARKET REFORMS

Sec. 1201. Amendment to the Public Health Service Act.

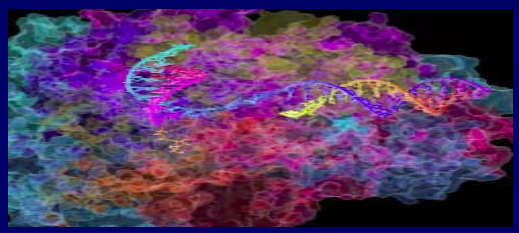
"SUBPART I—GENERAL REFORM

"Sec. 2704. Prohibition of preexisting condition exclusions or other discrimination based on health status.
"Sec. 2701. Fair health insurance premiums.
"Sec. 2702. Guaranteed availability of coverage.

Tasks the NIH with playing a key role in the development of "high need cures"

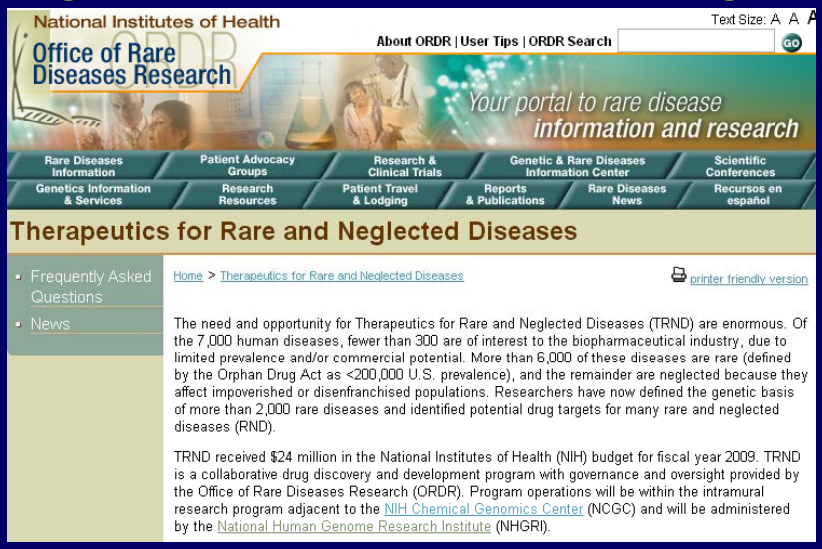
Cures Acceleration Network (CAN)

- **Goal: Advance development of new treatments and cures by reducing barriers between laboratory discoveries and clinical trials**
- **Within the NIH Office of the Director**
- **Authorized budget for FY2010: $500M**
- **Provides flexible funding and new award mechanisms (e.g., DARPA-like)**
- **'No-Year' funds**



Document 5

Therapeutics for Rare and Neglected Diseases (TRND) Program



Document 6

Therapeutics for Rare and Neglected Diseases (TRND) Program

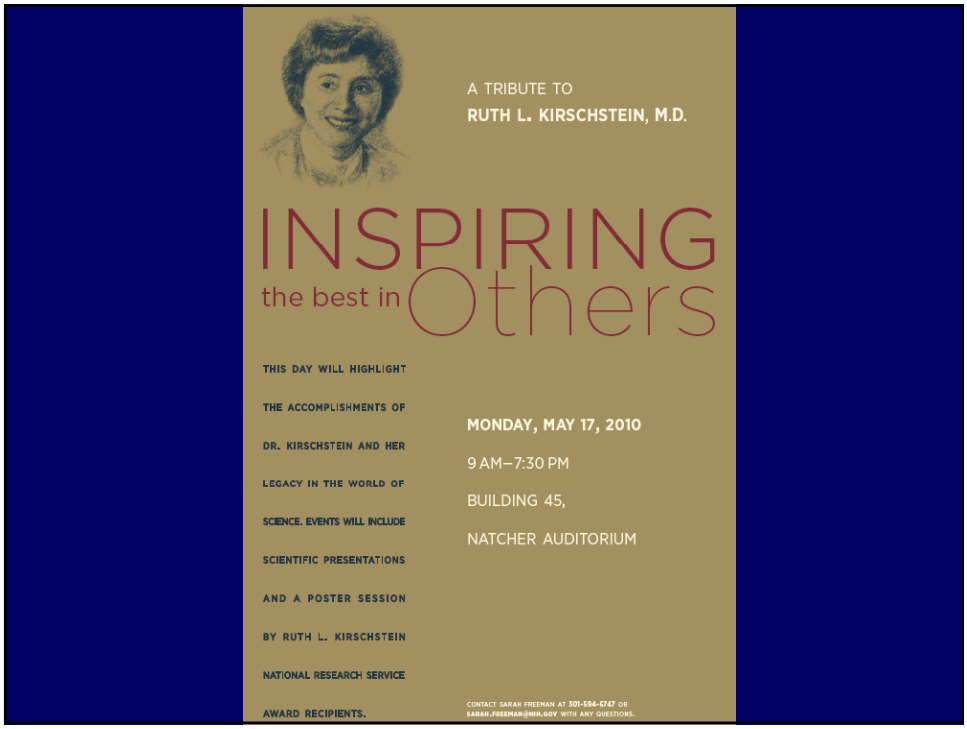
- $25M in FY2010; Likely to $50M in FY2011
- Develop candidate drugs for rare and neglected diseases not addressed by private sector
  - Starting point: probes/leads
  - Endpoint: IND/Phase I-II licensable to biotech/pharma/foundation
  - 25% effort for improving preclinical drug development processes
- Three ongoing pilot projects
  - Schistosomiasis
  - Niemann-Pick Type C
  - Hereditary Inclusion Body Myopathy
- Laboratory space, outsourcing contracts, & hiring ongoing
- Expect solicitation of proposals in FY2011

Eric Green, M.D., Ph.D.
Director, NHGRI

Major NIH Recruitments

- **Active Recruitments:**
  - NICHD Director
  - NIH Division of Program Coordination, Planning, and Strategic Initiatives (DPCPSI) Director
  - NIH Deputy Director for Extramural Research
  - NHLBI Director
  - Associate Director for Budget (closes June 1, 2010)
- **'Any Minute Now' Appointment:**
  - NCI Director
- **Pending Recruitment/Appointment:**
  - NIH Deputy Director

NIH Says Goodbye to Dr. Ruth Kirschstein


A TRIBUTE TO
RUTH L. KIRSCHSTEIN, M.D.
INSPIRING
the best in Others
THIS DAY WILL HIGHLIGHT
THE ACCOMPLISHMENTS OF
DR. KIRSCHSTEIN AND HER
LEGACY IN THE WORLD OF
SCIENCE. EVENTS WILL INCLUDE
SCIENTIFIC PRESENTATIONS
AND A POSTER SESSION
BY RUTH L. KIRSCHSTEIN
NATIONAL RESEARCH SERVICE
AWARD RECIPIENTS.
MONDAY, MAY 17, 2010
9 AM–7:30 PM
BUILDING 45,
NATCHER AUDITORIUM
CONTACT SARAH FREEMAN AT 301-594-6747 OR
SARAH.FREEMAN@NIH.GOV WITH ANY QUESTIONS.


CBS News.com
CBS Evening News
The Early Show
48 Hours Mystery
60 Minutes
CBSNEWS
LIVE CLOSING ARGUMENTS IN TRIAL OF CONFESSED ABC
ROEDER
Home Video CBS Evening News Videos
Where America Stands: Cancer
Add a comment
Share:
Cancer claims more than 500,000 American lives annually. In the "Where America Stands" series, Katie Couric reports on how the latest research is trying to move beyond chemotherapy to more targeted therapies.

New U.S. Surgeon General

- Dr. Regina Benjamin
- Rural family physician from Louisiana
- MacArthur Genius Award recipient

President Obama Visits NIH

Document 7

I. General NHGRI Updates

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New Members of the Institute of Medicine

INSTITUTE OF MEDICINE
OF THE NATIONAL ACADEMIES

- **NHGRI Grantees**
  - Zac Kohane
  - Russ Altman
  - Pat Brown
- **NHGRI Advisors**
  - Larry Green (BSC)
  - Alex Joyner (BSC)
- **NIH Institute Directors**
  - Story Landis (NINDS)
  - Griff Rodgers (NIDDK)

Document 8

New Members of the National Academy of Sciences

- NHGRI Grantees
  - Trudy MacKay
  - Kevin Struhl
- NHGRI Friend
  - Daniel Kastner (NIAMS)

Document 9

2009 ASHG Curt Stern Award

- Drs. Jim Kent and David Haussler received the 2009 Curt Stern Award
- Given for outstanding achievements in the field of human genetics during the past decade

Genetics Society of America Award

- Dr. Bill Gelbart given the George W. Beadle Award for outstanding contributions to the community of genetics researchers
- The award is for FlyBase, the central digital repository for the *Drosophila* genome

GSA Genetics Society of America
Discover. Understand. Inform.

FlyBase

2009 Presidential Medal of Science

Drs. Francis Collins and Craig Venter

Document 10

10th Annual Albany Medical Center Prize

Drs. David Botstein, Francis Collins and Eric Lander

Document 11

2010 American Society for Microbiology Promega Biotechnology Research Award

- Award honors outstanding contributions to the application of biotechnology through fundamental microbiological research and development
- Dr. Maynard Olson

Scripps Genomic Medicine Award

- Award is presented at the 2010 *Future of Genomic Medicine Conference* to researchers who have an "extraordinary impact on genomic medicine"
- Dr. Elaine Mardis

Forbes Article – A First: Diagnosis by DNA

Health

A First: Diagnosis By DNA

Matthew Herper, 02.23.10, 06:00 AM EST

In a big leap for medicine, gene sequencing helps doctors treat a sick infant.

© Eric Millette for Forbes

Yale's Richard Lifton is making it cheaper to decipher a person's entire genetic code.

Document 12

Eric Green, M.D., Ph.D.
Director, NHGRI

NHGRI's Teri Manolio Earns Presidential Rank Award

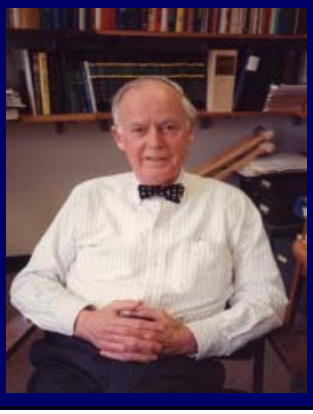
- Presidential Rank Award for Meritorious Service Award honors high-performing senior career employees for "sustained extraordinary accomplishment"
- Executives are nominated by their agency heads, evaluated by citizen panels, and designated by the President
- Evaluation criteria focus on and results

Mourning the Loss of Leena Peltonin

- Head of Human Genetics at the Wellcome Trust Sanger Institute
- Passed away at age 57 on March 11, 2010 at her home in Finland after a long and courageous battle with cancer.

Mourning the Loss of Barton Childs

- Legendary geneticist and teacher, as well as Professor Emeritus of pediatrics at the Johns Hopkins University School of Medicine
- Passed away at age 93 on February 18, 2010 after a short illness

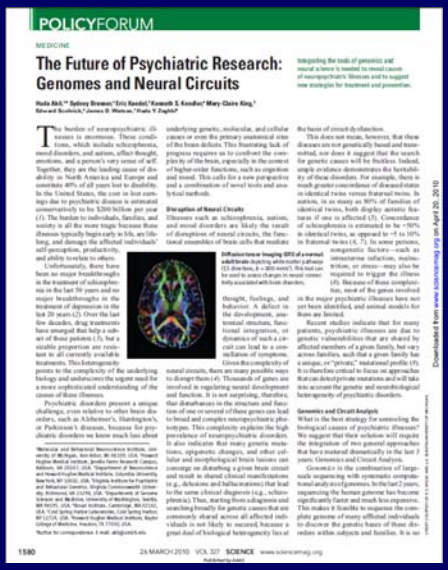


Archon X Prize in Genomics

- $10M prize to sequence 100 human genomes in <10 days and at $10K per genome
- NHGRI participating in many discussions
- NHGRI consulted on cost accounting and quality issues

Document 13

Science Policy Forum – *The Future of Psychiatric Research*



POLICYFORUM

MEDICINE

The Future of Psychiatric Research: Genomes and Neural Circuits

Integrating the tools of genomics and neural science is needed to reveal causes of neuropsychiatric illnesses and to suggest new strategies for treatment and prevention.

Hoda Akil,* Sydney Brenner,* Eric Kandel,* Kenneth S. Kendler,* Mary-Claire King,* Edward Scolnick,* James D. Watson,* Huda Y. Zoghbi*

The burden of neuropsychiatric illnesses is enormous. These conditions, which include schizophrenia, mood disorders, and autism, affect thought, emotions, and a person's very sense of self. Together, they are the leading cause of disability in North America and Europe and constitute 40% of all years lost to disability. In the United States, the cost in lost earnings due to psychiatric disease is estimated conservatively to be $200 billion per year (1). The burden to individuals, families, and society is all the more tragic because these illnesses typically begin early in life, are lifelong, and damage the affected individuals' self-perception, productivity, and ability to relate to others.

Unfortunately, there have been no major breakthroughs in the treatment of schizophrenia in the last 50 years and no major breakthroughs in the treatment of depression in the last 20 years (2). Over the last few decades, drug treatments have emerged that help a subset of those patients (3), but a sizable proportion are resistant to all currently available treatments. This heterogeneity points to the complexity of the underlying biology and underscores the urgent need for a more sophisticated understanding of the causes of these illnesses.

Psychiatric disorders present a unique challenge, even relative to other brain disorders, such as Alzheimer's, Huntington's, or Parkinson's diseases, because for psychiatric disorders we know much less about the basis of circuit dysfunction.

This does not mean, however, that these diseases are not genetically based and transmitted, nor does it suggest that the search for genetic causes will be fruitless. Indeed, ample evidence demonstrates the heritability of these disorders. For example, there is much greater concordance of diseased states in identical twins versus fraternal twins. In autism, in as many as 90% of families of identical twins, both display autistic features if one is affected (5). Concordance of schizophrenia is estimated to be ~50% in identical twins, as opposed to ~5 to 10% in fraternal twins (4, 7). In some persons, nongenetic factors—such as intrauterine infection, malnutrition, or stress—may also be required to trigger the illness (4). Because of these complexities, most of the genes involved in the major psychiatric illnesses have not yet been identified, and animal models for them are limited.

Recent studies indicate that for many patients, psychiatric illnesses are due to genetic vulnerabilities that are shared by affected members of a given family, but vary across families, such that a given family has a unique, or "private," mutational profile (8). It is therefore critical to focus on approaches that can detect private mutations and will take into account the genetic and neurobiological heterogeneity of psychiatric disorders.

Genomics and Circuit Analysis

What is the best strategy for unraveling the biological causes of psychiatric illnesses? We suggest that their solution will require the integration of two general approaches that have matured dramatically in the last 3 years: Genomics and Circuit Analysis.

Genomics is the combination of large-scale sequencing with systematic computational analysis of genomes. In the last 2 years, sequencing the human genome has become significantly faster and much less expensive. This makes it feasible to sequence the complete genome of many afflicted individuals to discover the genetic bases of these disorders within subjects and families. It is not

Document 14

Advances in Genome Biology and Technology Meeting

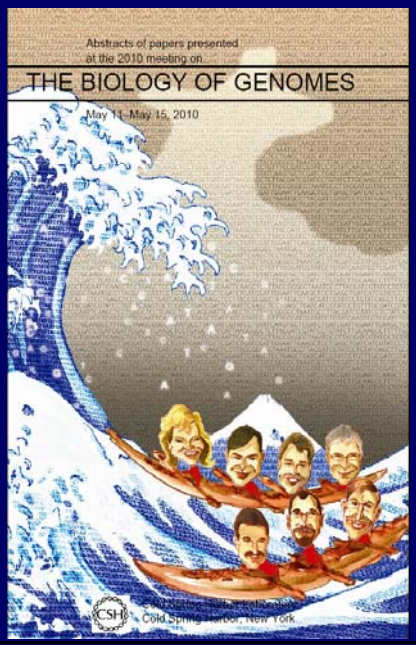
AGBT | Advances in Genome Biology and Technology

February 24-27, 2010

Introduction of several high-throughput sequencing platforms and partnerships

Helicos Introduces New Sequencing Kits to Enhance Versatility of the HeliScope(TM) Single Molecule Sequencer

CSHL Biology of Genomes Meeting



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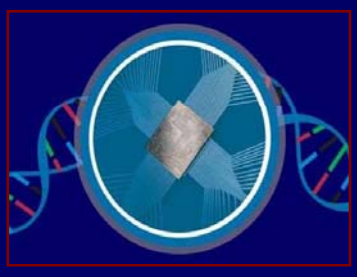
Large-Scale Sequencing Program

Concept Clearance:	Adam Felsenfeld
1000 Genomes:	Lisa Brooks
TCGA:	Brad Ozenberger
Human Genome Reference Consortium:	Deanna Church (NCBI)

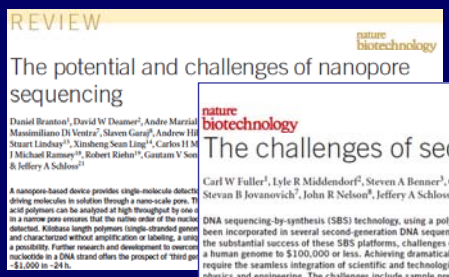
DNA Sequencing Technologies

Various Notable Developments in the Deployment of Next-Generation DNA Sequencing Technologies…



DNA Sequencing Technologies

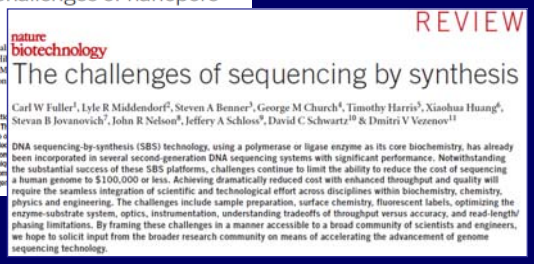
- Review articles published by grantee collaborative effort


REVIEW

nature biotechnology

The potential and challenges of nanopore sequencing

2008


nature biotechnology

REVIEW

The challenges of sequencing by synthesis

Carl W Fuller[1], Lyle R Middendorf[2], Steven A Benner[3], George M Church[4], Timothy Harris[5], Xiaohua Huang[6], Stevan B Jovanovich[7], John R Nelson[8], Jeffery A Schloss[9], David C Schwartz[10] & Dmitri V Vezenov[11]

DNA sequencing-by-synthesis (SBS) technology, using a polymerase or ligase enzyme as its core biochemistry, has already been incorporated in several second-generation DNA sequencing systems with significant performance. Notwithstanding the substantial success of these SBS platforms, challenges continue to limit the ability to reduce the cost of sequencing a human genome to $100,000 or less. Achieving dramatically reduced cost with enhanced throughput and quality will require the seamless integration of scientific and technological effort across disciplines within biochemistry, chemistry, physics and engineering. The challenges include sample preparation, surface chemistry, fluorescent labels, optimizing the enzyme-substrate system, optics, instrumentation, understanding tradeoffs of throughput versus accuracy, and read-length/phasing limitations. By framing these challenges in a manner accessible to a broad community of scientists and engineers, we hope to solicit input from the broader research community on means of accelerating the advancement of genome sequencing technology.

2009

- Annual grantee meeting held in March 2010, including 1-day public meeting

Document 15

Complete Genomics

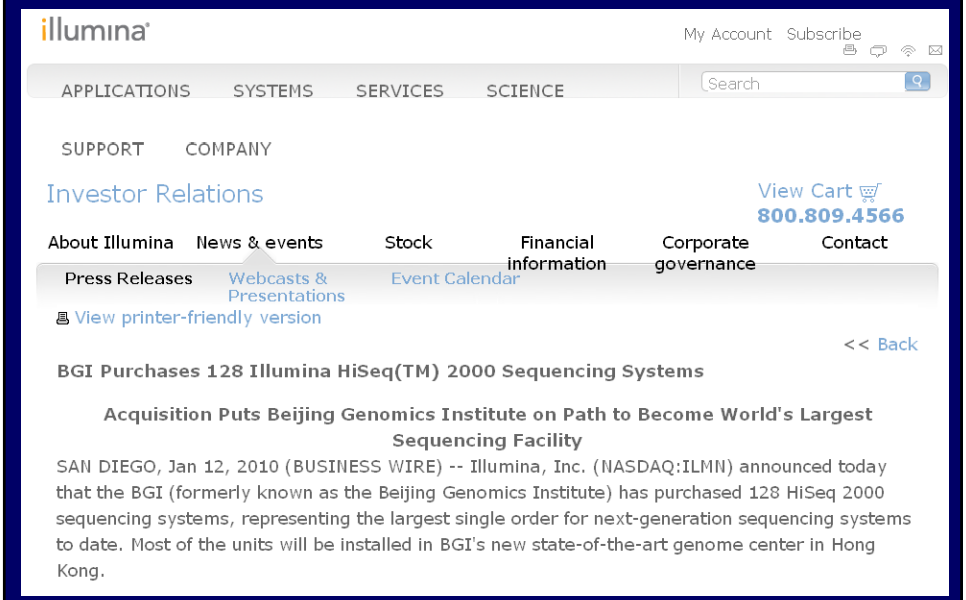

Human Genome Sequencing Using Unchained Base Reads on Self-Assembling DNA Nanoarrays

Science (2009)

Document 16

Illumina

Illumina and BGI



Illumina and BGI

NEWS FEATURE

THE SEQUENCE FACTORY

The bold ambitions of one institute could make China the world leader in genome sequencing. **David Cyranoski** asks if its science will survive the industrial ramp-up.

In 2006, Li Yingrui left Peking University for the BGI, China's premier genome-sequencing institute. Now, freckled and fresh-faced at 23 years old, he bustles at the way a senior BGI colleague characterized his college career — saying Li was wasting time playing video games and sleeping during class. "I didn't sleep in lectures," Li says. "I just didn't go."

He runs a team of 120 bioinformaticians, most no older than himself. His love of games has served him well when deciphering the flood of data spilling out of the BGI's sequencers every day. But "science is more satisfying" than video games, he says. "There's more passion."

The people at the BGI — which stopped officially using the name Beijing Genomics Institute in 2007 after moving its headquarters to Shenzhen — brim with passion, and an ambition so naked that it unsettles some. In the past few years the institute has leapt to the forefront of genome sequencing with a bevy of papers in top-tier journals. Some recent achievements include the genomes of the cucumber[1], the giant panda[2], the first complete sequence of an ancient human[3] and, in this issue of Nature[4], the genomes of more than 1,000 species of gut bacteria, compiled from 577 billion base pairs of sequence data.

The mission, BGI staff say with an almost rehearsed uniformity, is to prove that genomics matters to ordinary people. "The whole institute feels this huge responsibility," says Wang Jun, executive director of the BGI and a professor at the University of Copenhagen. The strategy is to sequence — well, pretty much anything that the BGI or its expanding list of collaborators wants to sequence. It has launched projects to tackle 10,000 microbial genomes and those of 1,000 plants and animals as part of an effort to create a genomic tree of life covering the major evolutionary branches. Important species, such as rice, will be sequenced 100 times over, and for humans there seems no limit to the number the institute would like sequenced.

To fulfil that mission, the BGI is transforming itself into a genomics factory, producing cheap, high-quality sequence with an army of young bioinformaticians and a growing arsenal of expensive equipment. In January, the BGI announced the purchase of 128 of the world's newest, fastest sequencers, the Hiseq 2000 from Illumina, each of which can produce 25 billion base pairs of sequence in a day. When all are running at full tilt, the BGI could theoretically sequence more than 10,000 human genomes in a year. This puts it on track to surpass the entire sequencing output of the United States, says David Wheeler, director of the Molecular Biology Computational Resource at Baylor College of Medicine in Houston, Texas. "It is clear there is a new map of the genomics world," he says.

The change that the BGI has reduced science to brute mechanization does little to ruffle feathers in Shenzhen. Wang himself quips that the BGI brings little intellectual capital into projects. "We are the muscle, we have no brain." But such comments belie a quiet confidence, in everyone from the BGI's seasoned management to its youngest recruits, that they can make an impact not just to the balance of sequencing power but also in biology, medicine and agriculture. This will be a challenge given the significant losses taken out to expand capacity. Torn between scientific and financial goals, even its founder can't seem to decide whether the BGI is a business or a non-profit research institute. Genome scientists around the world are watching to see how it will strike a balance. Edison Liu, director of the Genome Institute of Singapore and head of the Human Genome Organization warns: "If they are just a sequence-for-money operation, they will not be remembered."

Getting far from the emperor

China was late to the genomics frenzy of the 1990s that led to the sequencing of the human genome. The fact that the country didn't miss out altogether is thanks largely to the BGI's determined, charismatic and sometimes abrasive leader Yang Huanming ('Henry'). As the human genome project was nearing completion, Yang and a small group of sequencing advocates tried to get China involved. They found support from the Chinese Academy of Sciences (CAS), which secured a building and a start-up fund of 1 million renminbi (US$150,000). Wang announced the establishment of the BGI on 9 September 1999, at nine seconds past the ninth minute of the ninth hour. Few accounts portend more longevity in Chinese numerology, says Wang. That November, the government issued a grant of 3 million renminbi, of which the BGI got the lion's share, to support the sequencing of 1% of the human

"In Shenzhen, the mountains are high and the emperor is far away."

Life Technologies

Life Technologies and Ignite Institute

Broad-Mexico Collaboration

Washington U.-St. Jude Collaboration

Washington University in St. Louis

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Washington University, St. Jude team to unravel genetic basis of childhood cancers

Largest research project to date aimed at understanding the genetic origins of pediatric cancers

January 25, 2010

By Caroline Arbanas

Forward | Facebook this | Tweet this | Share more

Washington University School of Medicine in St. Louis and St. Jude Children's Research Hospital have announced an unprecedented effort to identify the genetic changes that give rise to some of the world's deadliest childhood cancers. The team has joined forces to decode the genomes of more than 600 childhood cancer patients, who have contributed tumor

COURTESY PHOTO

(Left to right) Francis Collins, M.D., Ph.D., director of the National Institutes of Health, Larry J. Shapiro, M.D., executive vice chancellor for medical affairs and dean of Washington University School of

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Mammalian Gene Collection (MGC)

Mammalian
Gene
Collection

Resource

The completion of the Mammalian Gene Collection (MGC)

The MGC Project Team[1]

Since its start, the Mammalian Gene Collection (MGC) has sought to provide at least one full-protein-coding sequence cDNA clone for every human and mouse gene with a RefSeq transcript, and at least 6200 rat genes. The MGC cloning effort initially relied on random expressed sequence tag screening of cDNA libraries. Here, we summarize our recent progress using directed RT-PCR cloning and DNA synthesis. The MGC now contains clones with the entire protein-coding sequence for 92% of human and 89% of mouse genes with curated RefSeq (NM-accession) transcripts, and for 97% of human and 96% of mouse genes with curated RefSeq transcripts that have one or more PubMed publications, in addition to clones for more than 6300 rat genes. These high-quality MGC clones and their sequences are accessible without restriction to researchers worldwide.

Genome Research (2009)

Document 17

Songbird Genome Sequence

- >800 genes appear to play a role in the male zebra finch's ability to learn songs from his father
- Song behavior engages complex gene regulatory networks within the brain of the songbird, networks that rely on parts of the genome once considered 'junk'

The genome of a songbird

Wesley C. Warren[1], David F. Clayton[2], Hans Ellegren[3], Arthur P. Arnold[4], LaDeana W. Hillier[1], Axel Künstner[5], Steve Searle[5], Simon White[5], Albert J. Vilella[6], Susan Fairley[5], Andreas Heger[7], Lesheng Kong[7], Chris P. Ponting[7], Erich D. Jarvis[8], Claudio V. Mello[9], Pat Minx[1], Peter Lovell[9], Tarciso A. F. Velho[9], Margaret Ferris[2], Christopher N. Balakrishnan[2], Saurabh Sinha[2], Charles Blatti[2], Sarah E. London[2], Yun Li[2], Ya-Chi Lin[2], Julia George[2], Jonathan Sweedler[2], Bruce Southey[2], Preethi Gunaratne[10], Michael Watson[11], Kiwoong Nam[3], Niclas Backström[3], Linnea Smeds[3], Benoit Nabholz[3], Yuichiro Itoh[4], Osceola Whitney[8], Andreas R. Pfenning[8], Jason Howard[8], Martin Völker[11], Bejamin M. Skinner[12], Darren K. Griffin[12], Liang Ye[1], William M. McLaren[6], Paul Flicek[6], Victor Quesada[13], Gloria Velasco[13], Carlos Lopez-Otin[13], Xose S. Puente[13], Tsviya Olender[14], Doron Lancet[14], Arian F. A. Smit[15], Robert Hubley[15], Miriam K. Konkel[16], Jerilyn A. Walker[16], Mark A. Batzer[16], Wanjun Gu[17], David D. Pollock[17], Lin Chen[18], Ze Cheng[18], Evan E. Eichler[18], Jessica Stapley[18], Jon Slate[19], Robert Ekblom[19], Tim Birkhead[19], Terry Burke[19], David Burt[20], Constance Scharff[21], Iris Adam[21], Hugues Richard[22], Marc Sultan[22], Alexey Soldatov[22], Hans Lehrach[22], Scott V. Edwards[23], Shiaw-Pyng Yang[24], XiaoChing Li[25], Tina Graves[1], Lucinda Fulton[1], Joanne Nelson[1], Asif Chinwalla[1], Shunfeng Hou[1], Elaine R. Mardis[1] & Richard K. Wilson[1]

Nature (2010)

Document 18

Genome 10K

GENOME 10K©

(David Haussler, Stephen O'Brien, & Oliver Ryder)

- Organize communities to coordinate and provide DNA samples from 10,000 species representing all extant vertebrate groups
- Ultimately to sequence >10K vertebrate genomes to address questions in genome evolution, comparative annotation, and conservation biology

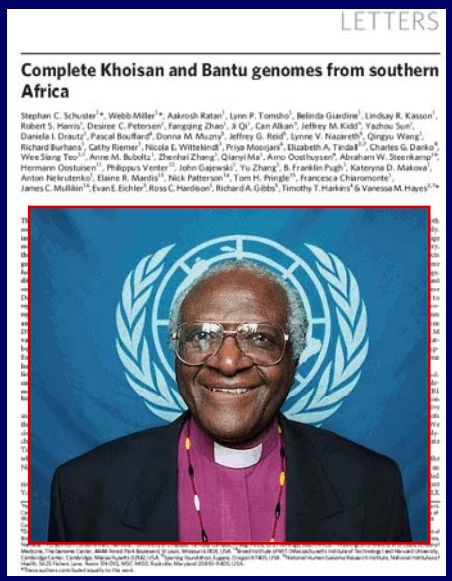
Genome 10K: A Proposal to Obtain Whole-Genome Sequence for 10 000 Vertebrate Species

GENOME 10K COMMUNITY OF SCIENTISTS*

J. Heredity (2009)

Document 19

Personal Genomes: Recent Additions



Nature (2010)

Document 20

Personal Genomes: Recent Additions

The NEW ENGLAND JOURNAL of MEDICINE

ORIGINAL ARTICLE

Whole-Genome Sequencing in a Patient with Charcot–Marie–Tooth Neuropathy

James R. Lupski, M.D., Ph.D., Jeffrey G. Reid, Ph.D., Claudia Gonzaga-Jauregui, B.S., David Rio Deiros, B.S., David C.Y. Chen, M.Sc., Lynne Nazareth, Ph.D., Matthew Bainbridge, M.Sc., Huyen Dinh, B.S., Chyn Jing, M.Sc., David A. Wheeler, Ph.D., Amy L. McGuire, J.D., Ph.D., Feng Zhang, Ph.D., Pawel Stankiewicz, M.D., Ph.D., John J. Halperin, M.D., Chengyong Yang, Ph.D., Curtis Gehman, Ph.D., Danwei Guo, M.Sc., Rola K. Irikat, B.S., Warren Tom, B.S., Nick J. Fantin, B.S., Donna M. Muzny, M.Sc., and Richard A. Gibbs, Ph.D.

ABSTRACT

BACKGROUND

Whole-genome sequencing may revolutionize medical diagnostics through rapid identification of alleles that cause disease. However, even in cases with simple patterns of inheritance and unambiguous diagnoses, the relationship between disease phenotypes and their corresponding genetic changes can be complicated. Comprehensive diagnostic assays must therefore identify all possible DNA changes in each haplotype and determine which are responsible for the underlying disorder. The high number of rare, heterogeneous mutations present in all humans and the paucity of known functional variants in more than 90% of annotated genes make this challenge particularly difficult. Thus, the identification of the molecular basis of a genetic disease by means of whole-genome sequencing has remained elusive. We therefore aimed to assess the usefulness of human whole-genome sequencing for genetic diagnosis in a patient with Charcot–Marie–Tooth disease.

NEJM (2010)

Document 21

Personal Genomes: Recent Additions

illumina

Illumina and Glenn Close Announce the First Full Coverage DNA Sequencing of a Named Female

SAN DIEGO, Mar 11, 2010 (BUSINESS WIRE) -- Illumina, Inc. (NASDAQ:ILMN) today announced that it has sequenced the DNA of American actress Glenn Close, the first publicly named female to have her DNA sequenced to full coverage. The service was completed in Illumina's CLIA certified and CAP accredited laboratory utilizing Illumina's Genome Analyzer technology and following the established process shown at http://www.everygenome.com/. Ms. Close's DNA was sequenced to an average depth greater than 30 fold, providing information on SNP variation and allowing for the analysis of other structural characteristics of the genome such as insertions, deletions and rearrangements. Specifically, over 95% of the known genome was reported, including over 12 million genotype calls on previously documented SNPs. In addition, 379,000 SNPs previously not reported in any public database were found.

"We are very excited to work with Glenn Close to produce the first named female sequence," said Jay Flatley, president and CEO of Illumina. "We are entering a new era in genomic health where information from an individual's genome will increasingly inform lifestyle decisions and ultimately assist with health management. Ms. Close has been active in health issues, and her participation helps bring attention to the potential benefits of individuals gaining access to their genetic information. With this information, physicians will be able to make better healthcare decisions for their patients in the future."

Glenn Close joins a small group of individuals who have had their genomes sequenced. "There is bipolar disorder and schizophrenia in my family, illnesses that, like other medical conditions, are thought to have genetic underpinnings," said Ms. Close. "As human sequencing becomes increasingly routine, my hope is that researchers will unravel the genetic aspects of mental illnesses to bring greater awareness about the diseases, de-stigmatize them and pave the way for more effective treatments."

REUTERS

Glenn Close has genes mapped

Thu, Mar 11 2010

By Julie Steenhuysen

CHICAGO (Reuters) - Archbishop Desmond Tutu has done it. So has genome pioneer Craig Venter.

And now American film actress Glenn Close has joined a handful of celebrities to have their genome sequenced in the name of science.

Close, who stars in the FX television series "Damages" and is known for movie roles including "Fatal Attraction" and "Dangerous Liaisons," said the offer was too good to pass up.

Document 22

Personal Genomes: Recent Additions

Clinical assessment incorporating a personal genome

Euan A Ashley, Atul J Butte, Matthew T Wheeler, Rong Chen, Teri E Klein, Frederick E Dewey, Joel T Dudley, Kelly E Ormond, Aleksandra Pavlovic, Alexander A Morgan, Dmitry Pushkarev, Norma F Neff, Louanne Hudgins, Li Gong, Laura M Hodges, Dorit S Berlin, Caroline F Thorn, Katrin Sangkuhl, Joan M Hebert, Mark Woon, Hersh Sagreiya, Ryan Whaley, Joshua W Knowles, Michael F Chou, Joseph V Thakuria, Abraham M Rosenbaum, Alexander Wait Zaranek, George M Church, Henry T Greely, Stephen R Quake, Russ B Altman

***Lancet* (2010)**

Document 23

Personal Genomes: Recent Additions

Genome, epigenome and RNA sequences of monozygotic twins discordant for multiple sclerosis

Sergio E. Baranzini[1], Joann Mudge[2], Jennifer C. van Velkinburgh[2], Pouya Khankhanian[1], Irina Khrebtukova[3], Neil A. Miller[2], Lu Zhang[3], Andrew D. Farmer[2], Callum J. Bell[2], Ryan W. Kim[2], Gregory D. May[2], Jimmy E. Woodward[2], Stacy J. Caillier[1], Joseph P. McElroy[1], Refujia Gomez[1], Marcelo J. Pando[4], Leonda E. Clendenen[2], Elena E. Ganusova[2], Faye D. Schilkey[2], Thiruvarangan Ramaraj[2], Omar A. Khan[5], Jim J. Huntley[3], Shujun Luo[3], Pui-yan Kwok[6,7], Thomas D. Wu[8], Gary P. Schroth[3], Jorge R. Oksenberg[1,7], Stephen L. Hauser[1,7] & Stephen F. Kingsmore[2]

***Nature* (2010)**

Document 24

(Im)Personal Genomes: Recent Additions

A Draft Sequence of the Neandertal Genome

Richard E. Green,[1*†‡] Johannes Krause,[1†§] Adrian W. Briggs,[1†§] Tomislav Maricic,[1†§] Udo Stenzel,[1†§] Martin Kircher,[1†§] Nick Patterson,[2†§] Heng Li,[2†] Weiwei Zhai,[3†‖] Markus Hsi-Yang Fritz,[4†] Nancy F. Hansen,[5†] Eric Y. Durand,[3†] Anna-Sapfo Malaspinas,[3†] Jeffrey D. Jensen,[6†] Tomas Marques-Bonet,[7,13†] Can Alkan,[7†] Kay Prüfer,[1†] Matthias Meyer,[1†] Hernán A. Burbano,[1†] Jeffrey M. Good,[1,8†] Rigo Schultz,[1] Ayinuer Aximu-Petri,[1] Anne Butthof,[1] Barbara Höber,[1] Barbara Höffner,[1] Madlen Siegemund,[1] Antje Weihmann,[1] Chad Nusbaum,[2] Eric S. Lander,[2] Carsten Russ,[2] Nathaniel Novod,[2] Jason Affourtit,[9] Michael Egholm,[9] Christine Verna,[21] Pavao Rudan,[10] Dejana Brajkovic,[11] Željko Kucan,[10] Ivan Gušic,[10] Vladimir B. Doronichev,[12] Liubov V. Golovanova,[12] Carles Lalueza-Fox,[13] Marco de la Rasilla,[14] Javier Fortea,[14¶] Antonio Rosas,[15] Ralf W. Schmitz,[16,17] Philip L. F. Johnson,[18†] Evan E. Eichler,[7†] Daniel Falush,[19†] Ewan Birney,[4†] James C. Mullikin,[5†] Montgomery Slatkin,[3†] Rasmus Nielsen,[3†] Janet Kelso,[1†] Michael Lachmann,[1†] David Reich,[2,20*†] Svante Pääbo[1*†]

Science (2010)

Document 25

Computation/Bioinformatics

Meeting Reports: Vivien Bonazzi

1. Cloud Computing
2. Informatics and Analysis Planning

Joint NCBI-NHGRI Meetings

NCBI
National Center for Biotechnology Information

ENCODE & modENCODE: General

ENCODE

mod ENCODE

- ENCODE and modENCODE Consortia joint annual meeting in March 2010 (>200 participants)
- In April 2010, both Consortia evaluated in 'mid-course review'
- Recommendations from 'mid-course review' to be discussed in closed session

ENCODE & modENCODE: Publications

- Two recent *Science* papers
- modENCODE is writing fly and worm integrated analysis papers
- ENCODE preparing 'ENCODE 101' paper to describe how to access/use ENCODE data
- Analysis Workshop planned for July 2010 will focus on ENCODE integrative analysis paper

Document 26

Knockout Mouse Project (KOMP)

Goal: production of 8500 null mutants by Oct. 2011

- International Knockout Mouse Consortium (IKMC)
- Mutate all protein-coding genes in mouse embryonic stem cells
- Funded by NIH, EU, Wellcome Trust, Canada, Texas Enterprise Fund

KOMP Repository
Knock Out Mouse Project 1-888-KOMP-MICE

OppNet

OPPNET Basic Behavioral & Social Science Opportunity Network

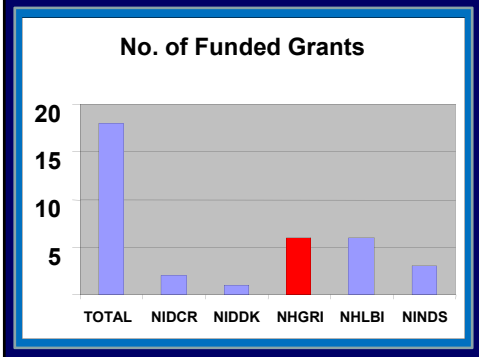
- 2010: $10 million in ARRA funding for competitive supplements and K18 awards
- Areas for 2011-2014 Funding (~$30M/year):
  - Social Gradients
  - Sleep/Circadian Rhythms
  - Stress
  - Health Behavior
  - Social Environment
  - Capacity Building
- Future funding from base appropriations proportional to total appropriation

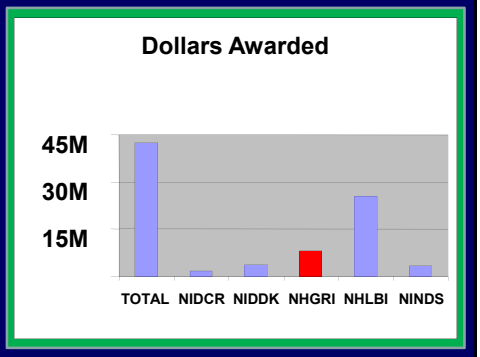
Document 27

Dissemination of Genomics

NIH ARRA Funding: Medical Sequencing

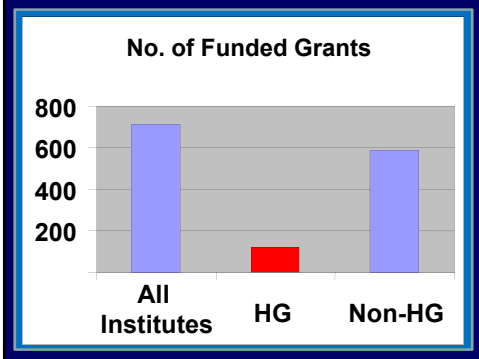
(NHGRI Study Section)

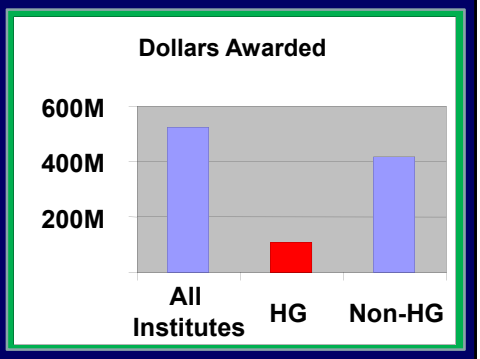




NIH ARRA Funding: 'Human Genome'

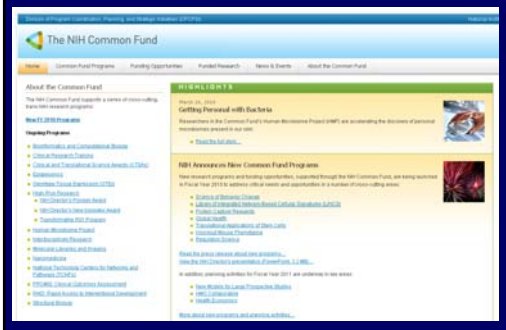
(Database Query)





I. General NHGRI Updates
II. General NIH Updates
III. Genomics Updates
IV. NHGRI Extramural Program
V. NIH Common Fund Programs
VI. NHGRI Office of the Director
VII. NHGRI Intramural Program

The NIH Common Fund



nihroadmap.nih.gov

Common Fund Programs, April, 2010

Molecular Libraries Program (MLP) – The MLP is an integrated set of initiatives, the goal of which is to provide academic researchers high throughput screening (HTS) and chemistry resources to find and develop small molecules that can serve as chemical probes for research. The initiative consists of three main components: a large, shared collection of small molecules, a network of screening and chemistry centers, and a public database of all assay results. Launched in FY2004; FY2010 - $113,252,000

Technology Centers for Networks and Pathways (TCNPs) – The TCNPs develop technologies to measure the dynamics of protein interactions, modifications, translocation, expression, and activity, with temporal, spatial, and quantitative resolution. Launched in FY 2004; FY2010 - $10,940,000

Structural Biology of Membrane Proteins - The Structural Biology of Membrane Proteins Roadmap Program is developing novel approaches for the production and stabilization of membrane proteins so that their structures may be determined at high resolution. Launched in FY2004; FY2010 - $8,038,000

National Centers for Biomedical Computing (NCBCs) – The NCBCs develop computational tools that are intended to catalyze research in basic and clinical science. The centers create innovative software programs and other tools that arm the biomedical community with the methods needed to integrate, analyze, model, simulate, and share data relevant to human health and disease. Launched in FY2004; FY2010 - $25,597,000

High Risk/High Reward Research (HRHR) Program – The HRHR Program is intended to support scientists of exceptional creativity who propose highly innovative approaches to major contemporary challenges in biomedical research. By bringing their unique perspectives and abilities to bear on key research questions, these visionary scientists may develop seminal theories or technologies that will propel fields forward and speed the translation of research into improved health. Launched in FY2004; FY2010 – $170,464,000

Document 28

Molecular Libraries Program

Progress Update

Pilot Phase (2004 to mid-2008)	191 HTS Projects
Production Phase (2008 to 2010)	169 HTS Projects

Total Probes Discovered: 153

Document 29

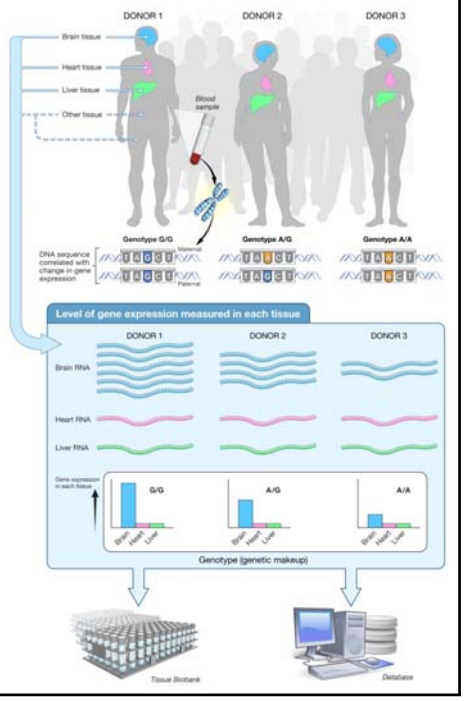
Molecular Libraries Program

Future Program Milestones

- Year 2 Performance-Based Funding
- Mid-Course Review: August 2010

GTEx
Genotype-Tissue Expression

- 2.5-year pilot
- Goal: Collect multiple tissues (n≥30) from 160 deceased donors for eQTL analyses
- Laboratory and Tissue Collection Sites (awards ~June 2010)
- RNA-Seq on 1000 samples and arrays on a subset
- If successful, will scale to 1000 donors in Years 3-5



Human Microbiome Project (HMP)

Reference Genome Sequences: 329 strains complete, 1151 in pipelines

Sequencing of Samples (300 subjects, 14-18 samples/subject):

Expect HMP sequences can be accepted @ NCBI by May 24th

- 16S rDNA data of 6800 samples; freeze May 1st
- WGS data of 564-580 samples; freeze July 1st

Publications from Centers (4):

Four manuscripts in preparation

- Sample collection (protocol, consent, etc)
- Benchmarking of samples
- Results from first 41 donors
- Milestone publication: broad analysis of sequencing results

Demonstration Projects (15):

- Pilot studies of microbiome and disease correlations
- June 2-3 Review: transition from UH2 to UH3

Human microbiome research network meeting:

- Inviting non-HMP human microbiome researchers
- Aug. 31-Sept. 2 (St. Louis)

Document 30


New Opportunities for the Common Fund
New Programs for 2010
Library of Integrated Network-based Cellular Signatures (LINCS)
Protein Capture Reagents
Global Health
Translational Applications of Stem Cells
Mouse Phenotyping
Science of Behavior Change
Regulatory Science
Considerations for 2011
Health Economics
HMO Collaboratory
New Models for Large Prospective Studies


New Opportunities for the Common Fund
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Science of Behavior Change
Regulatory Science
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Health Economics
HMO Collaboratory
New Models for Large Prospective Studies

Common Fund Budget FY10-FY14 (in thousands)

Program	FY10	FY11	FY12	FY13	FY14
LINCS	3,000	10,000	10,000		
Mouse Phenotyping (KOMP2)	500	11,000	11,000	11,000	11,000
Science of Behavior Change	4,060	4,290	4,300	4,545	4,560
Global Health	3,747	8,000	8,000	8,000	8,000
Protein Capture	1,500	8,000	8,000	7,000	2,000
Regulatory Science	2,000	2,000	2,000		
NIH iPS Cell Center	3,000	6,000	10,000	15,000	18,000
TOTAL New Programs	**17,807**	**49,290**	**53,300**	**45,545**	**43,560**
TOTAL Existing Programs	**523,088**	**489,755**	**403,089**	**335,657**	**270,934**
CF Appropriation	**544,109**	**561,629**	**561,629**	**561,629**	**561,629**
Funds Remaining for New Programs	**3,214**	**22,584**	**105,240**	**180,427**	**247,135**

Knockout Mouse Phenotyping Program: KOMP^2

International Knockout Mouse Consortium (IKMC)

KOMP^2 --- Knockout Mouse Phenotyping Program

- **Standardized, broad phenotyping of 8,500 KO mice derived from IKMC ES cells**
- **Comprehensive definition of *in vivo* function of mammalian genes and identification of new models of disease**
- **Coordinated with other international activities**

FY10: Oct 2009 Planning Meeting, April 2010 Phenotyping Workshop
FY10: Continued Planning ($500K)
FY11-FY15: Pilot to create cost-efficient phenotyping pipeline --
2,500 mutants in 5years ($11M/yr Common Fund+ $11M/yr IC match)

Program Leaders: James Battey (NIDCD) & Eric Green (NHGRI)

Library of Integrated Network-based Cellular Signatures (LINCS)

Establishing the feasibility of the approach and creating the first installment of a reference collection

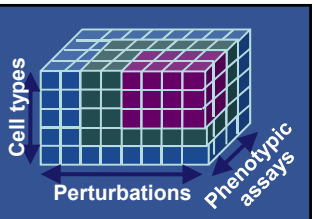
The Connectivity Map: Using Gene-Expression Signatures to Connect Small Molecules, Genes, and Disease

Justin Lamb,[1*] Emily D. Crawford,[1†] David Peck,[1] Joshua W. Modell,[1] Irene C. Blat,[1] Matthew J. Wrobel,[1] Jim Lerner,[1] Jean-Philippe Brunet,[1] Aravind Subramanian,[1] Kenneth N. Ross,[1] Michael Reich,[1] Haley Hieronymus,[1,2] Guo Wei,[1,2] Scott A. Armstrong,[2,3] Stephen J. Haggarty,[1,4] Paul A. Clemons,[1] Ru Wei,[1] Steven A. Carr,[1] Eric S. Lander,[1,5,6] Todd R. Golub[1,2,3,5,7*]

To pursue a systematic approach to the discovery of functional connections among diseases, genetic perturbation, and drug action, we have created the first installment of a reference collection of gene-expression profiles from cultured human cells treated with bioactive small molecules, together with pattern-matching software to mine these data. We demonstrate that this "Connectivity Map" resource can be used to find connections among small molecules sharing a mechanism of action, chemicals and physiological processes, and diseases and drugs. These results indicate the feasibility of the approach and suggest the value of a large-scale community Connectivity Map project.

***Science* (2006)**

LINCS Program



Planning Workshop: Fall 2008

Program Goals: Facilitate a mechanistic understanding of disease in support of drug and biomarker development

- Create a library of perturbation-induced molecular and cellular signatures of cellular responses to genetic variation, environmental exposures and clinical phenotypes
- Establish common standards and best practices
- Develop new technologies/tools for generating and analyzing cellular signatures

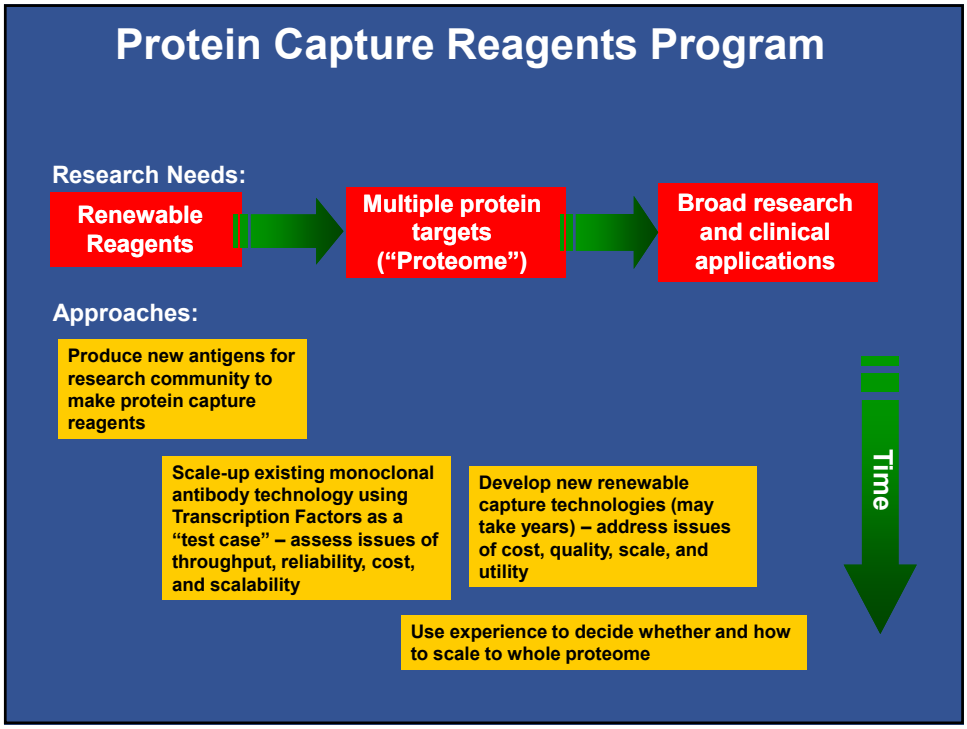
Phase 1:

- RFA-RM-10-003: Large Scale Production of Perturbation-Induced Cellular Signatures
- RFA-RM-10-004: New Laboratory-based Technology Development
- RFA-RM-10-005: Computational Tool Development and Integrative Data Analyses

Budget FY2010 - FY2012: $3M in FY2010, $10M in FY2011 and FY2012

Phase 2: Scale-up of LINCS pending Phase 1 evaluation

Program Leaders:
Alan Michelson (NHLBI) &
Mark Guyer (NHGRI)



Protein Capture Reagents Program

	FY10	FY11	FY12	FY13	FY14	FY15	TOTAL
Antigen Production	1.0	1.0	1.0				3.0
mAbs for Transcription Factors		2.0	2.0	2.0	2.0	2.0	10.0
Planning Phase for Pilot (Workshops)	0.5						0.5
New Reagent Tech Development & Piloting		5.0	5.0	5.0			15.0
TOTAL	1.5M	8.0M	8.0M	7.0M	2.0M	2.0M	28.5M

Program Leaders: Jeremy Berg (NIGMS), Eric Green (NHGRI), & James Battey (NIDCD)

Research Programs in Global Health

RFA-TW-10-008: Medical Education Partnership Initiative in Sub-Saharan Africa ($3M/yr, FY10-FY15) – Initiative focused on PEPFAR goals (funding from OGAC, HRSA, OAR, FIC)

- **Goal:** Common Fund to expand scope to include non-communicable diseases and health priorities beyond HIV/AIDS

Program Leader: Roger Glass (FIC)

Common Disease in Africa Project (CDAP):

- Partnership w/ African Society of Human Genetics, NIH, and Wellcome Trust
- Developed from *Frontiers Meeting* and other venues since 2009
- **Goal:** Develop research African capacity and network to study genetic and environmental factors of common diseases

Planned Activities:

- International conference in Cape Town, SA; workshop in Bamako, Mali; and conference in Nairobi, Kenya to discuss strategies, design, and training
- **Budget:** $746,517 (FY10), $5M/yr (FY11-FY15) – Matching funds by Wellcome Trust
- **Program Leader:** Eric Green (NHGRI)

NIH iPS Cell Center

Create a world-class Center of Excellence in iPS cell technology

Timeline:

FY10 Hire a Center Director and renovate space, select diseases (intramural or extramural collaboration) for pilot studies ($3M)

FY11 Hire staff, optimize generation of iPS cells from normals and patient cohorts, investigate differentiation strategies, develop iPS biobank, and initiate NCGC screens ($6M)

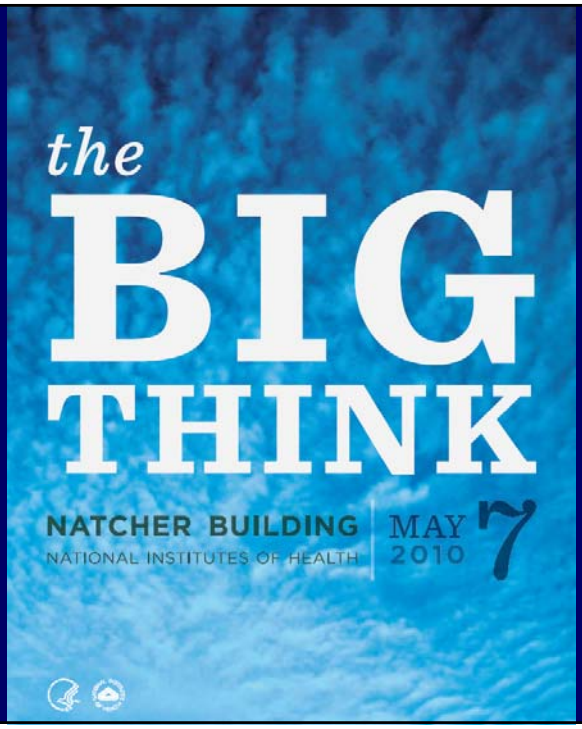
FY12 Use genetic and small molecule approaches to correct iPS cell disease phenotypes and initiate preclinical, pilot studies to assess feasibility of iPS approaches in selected disease disorders ($10M)

FY13-14 Scale-up production and generation of GMP-grade iPS cells and selection of candidate disorders for focus of therapeutic intervention ($15M in FY13, $18M in FY14)

Program Leaders: Michael Gottesman (OIR), Stephen Katz (NIAMS), & Story Landis (NINDS)

Common Fund Budget FY10-FY14 (in thousands)

Program	FY10	FY11	FY12	FY13	FY14
LINCS	3,000	10,000	10,000		
Mouse Phenotyping (KOMP2)	500	11,000	11,000	11,000	11,000
Science of Behavior Change	4,060	4,290	4,300	4,545	4,560
Global Health	3,747	8,000	8,000	8,000	8,000
Protein Capture	1,500	8,000	8,000	7,000	2,000
Regulatory Science	2,000	2,000	2,000		
NIH iPS Cell Center	3,000	6,000	10,000	15,000	18,000
TOTAL New Programs	**17,807**	**49,290**	**53,300**	**45,545**	**43,560**
TOTAL Existing Programs	**523,088**	**489,755**	**403,089**	**335,657**	**270,934**
CF Appropriation	**544,109**	**561,629**	**561,629**	**561,629**	**561,629**
Funds Remaining for New Programs	**3,214**	**22,584**	**105,240**	**180,427**	**247,135**



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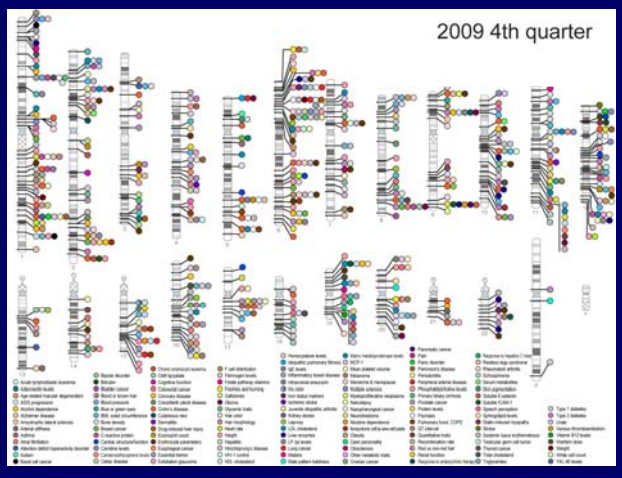
VII. NHGRI Intramural Program

Office of Population Genomics

NHGRI GWAS catalog now includes over 540 publications and 2600 SNP-trait associations



genome.gov/gwastudies

Document 31

The *eMERGE* Network

electronic Medical Records & Genomics

A consortium of biorepositories linked to electronic medical records data for conducting genomic studies

Anonymization of electronic medical records for validating genome-wide association studies

Grigorios Loukides[1], Aris Gkoulalas-Divanis, and Bradley Malin

***PNAS* (2010)**

PheWAS: Demonstrating the feasibility of a phenome-wide scan to discover gene-disease associations

Joshua C. Denny, MD, MS[1,2*], Marylyn D. Ritchie, PhD[3], Melissa Basford, MBA[1] Jill Pulley, MBA[1,2], Lisa Bastarache, MS[1], Kristin Brown-Gentry, MS[3], Deede Wang, BS[2], Dan R. Masys, MD[1], Dan M. Roden, MD[2], and Dana C. Crawford, PhD[3]

***Bioinformatics* (2010)**

Robust Replication of Genotype-Phenotype Associations across Multiple Diseases in an Electronic Medical Record

Marylyn D. Ritchie,[2,7,9] Joshua C. Denny,[5,6,9] Dana C. Crawford,[2,7] Andrea H. Ramirez,[6] Justin B. Weiner,[6] Jill M. Pulley,[3] Melissa A. Basford,[1,3] Kristin Brown-Gentry,[2] Jeffrey R. Balser,[3,4,8] Daniel R. Masys,[5] Jonathan L. Haines,[2,7] and Dan M. Roden[1,6,8,*]

***AJHG* (2010)**

Document 32

www.phenxtoolkit.org

Document 33

Office of Population Genomics Programs

- Presentations by Teri Manolio on:

  New Models for Large Prospective Studies

  Concept Clearance-- eMERGE

DNA Day (April 23, 2010)

- Ambassadors visited the NIH Children's Inn on two occasions in April to do hands on activity with patients, siblings, and parents
- ~20 Ambassadors visited ~25 schools in DC, MD, and VA throughout March, April, and May
- NHGRI chatroom was held on April 23 from 8am until 6pm EDT, with >70 experts answering ~1400 questions

Document 34

Genomics Career Website

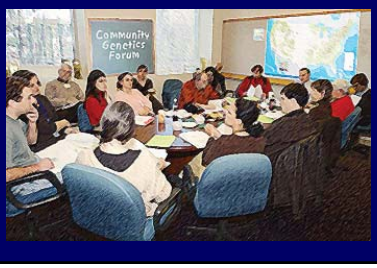
- Showcases interactive videos of genomic professionals
- >50 genomic careers can be explored in the areas of genome science, medicine, genetic counseling, ethics, law, and others
- Includes interviews with leading professionals and tours of genomic facilities in

genome.gov/GenomicCareers

Document 35

2010 Community Genetics Forum

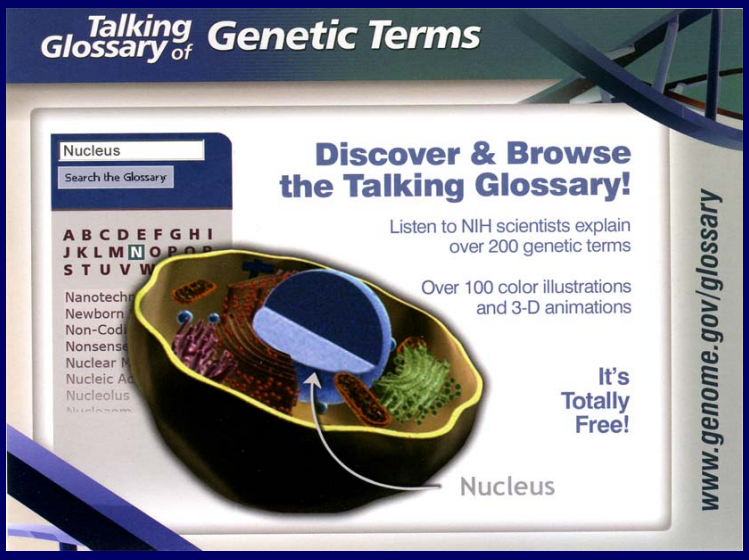
- May 1, 2010 in Salt Lake City, Utah
- 500 attendees from diverse communities (African American, Chinese American, Tongan, African Refuge, Native American, Hispanic American)
- NHGRI staff attended to lend expertise on Forum topics (heart disease, cancer, diabetes)



Gene Patenting

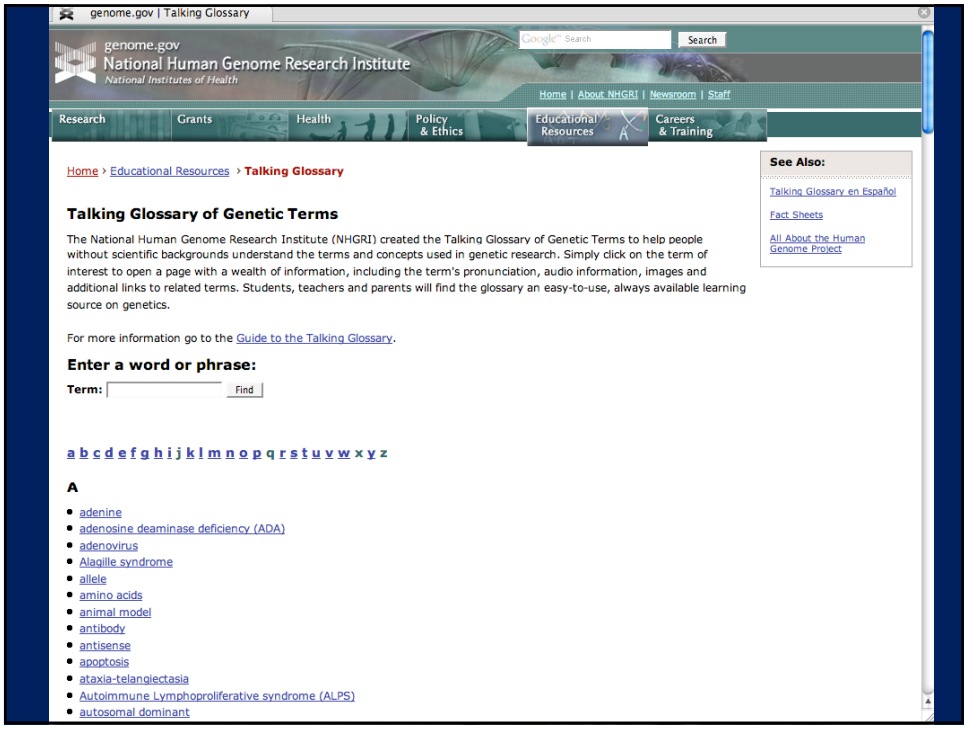
- Update on gene patenting by Council Members Contreras and Ossorio
- Two major developments:
  1. SACGHS issued report on gene patents and licensing practices
  2. Recent ruling in "Myriad" case invalidated claims in BRCA1 and BRCA2 patents

Revamped NHGRI Talking Glossary



genome.gov/glossary

Document 36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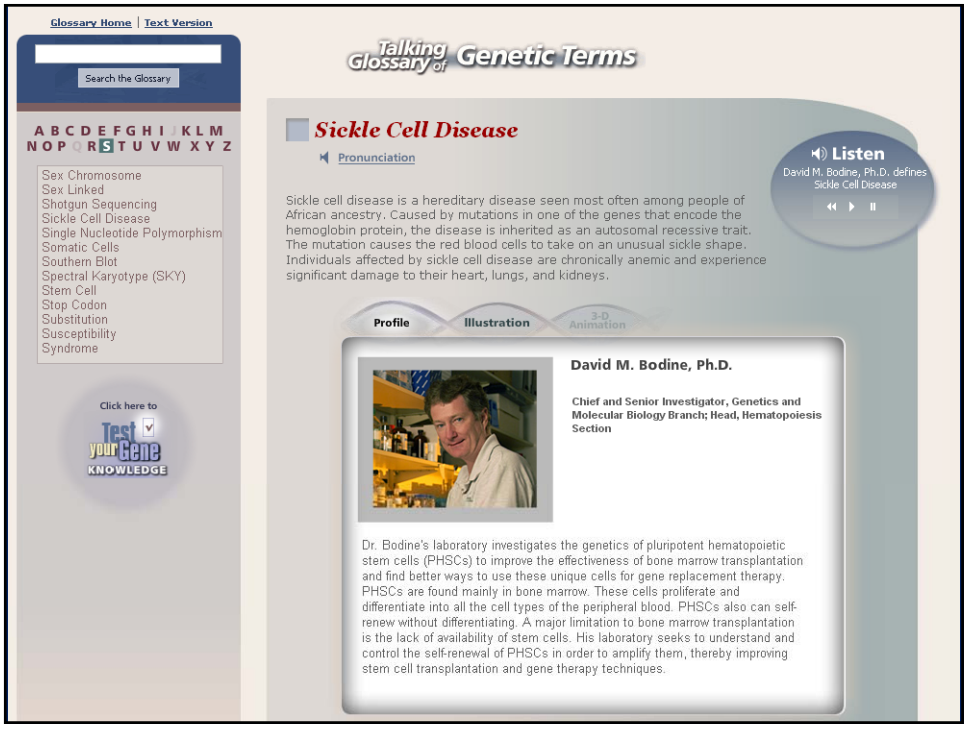
Fact Sheets
All About the Human Genome Project
Talking Glossary of Genetic Terms
The National Human Genome Research Institute (NHGRI) created the Talking Glossary of Genetic Terms to help people without scientific backgrounds understand the terms and concepts used in genetic research. Simply click on the term of interest to open a page with a wealth of information, including the term's pronunciation, audio information, images and additional links to related terms. Students, teachers and parents will find the glossary an easy-to-use, always available learning source on genetics.
For more information go to the Guide to the Talking Glossary.
Enter a word or phrase:
Term:
Find
a b c d e f g h i j k l m n o p q r s t u v w x y z
A
adenine
adenosine deaminase deficiency (ADA)
adenovirus
Alagille syndrome
allele
amino acids
animal model
antibody
antisense
apoptosis
ataxia-telangiectasia
Autoimmune Lymphoproliferative syndrome (ALPS)
autosomal dominant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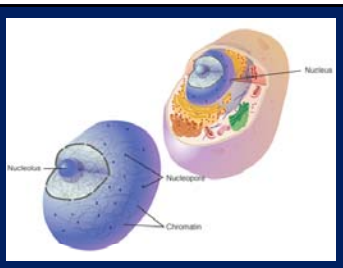
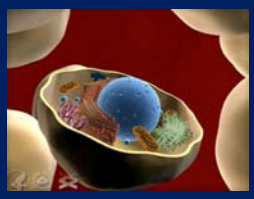
A B C D E F G H I J K L M
N O P Q R S T U V W X Y Z
Sex Chromosome
Sex Linked
Shotgun Sequencing
Sickle Cell Disease
Single Nucleotide Polymorphism
Somatic Cells
Southern Blot
Spectral Karyotype (SKY)
Stem Cell
Stop Codon
Substitution
Susceptibility
Syndrome
Click here to
Test your Gene KNOWLEDGE
Talking Glossary of Genetic Terms
Sickle Cell Disease
Pronunciation
Listen
David M. Bodine, Ph.D. defines Sickle Cell Disease
Sickle cell disease is a hereditary disease seen most often among people of African ancestry. Caused by mutations in one of the genes that encode the hemoglobin protein, the disease is inherited as an autosomal recessive trait. The mutation causes the red blood cells to take on an unusual sickle shape. Individuals affected by sickle cell disease are chronically anemic and experience significant damage to their heart, lungs, and kidneys.
Profile
Illustration
3-D Animation
David M. Bodine, Ph.D.
Chief and Senior Investigator, Genetics and Molecular Biology Branch; Head, Hematopoiesis Section
Dr. Bodine's laboratory investigates the genetics of pluripotent hematopoietic stem cells (PHSCs) to improve the effectiveness of bone marrow transplantation and find better ways to use these unique cells for gene replacement therapy. PHSCs are found mainly in bone marrow. These cells proliferate and differentiate into all the cell types of the peripheral blood. PHSCs also can self-renew without differentiating. A major limitation to bone marrow transplantation is the lack of availability of stem cells. His laboratory seeks to understand and control the self-renewal of PHSCs in order to amplify them, thereby improving stem cell transplantation and gene therapy techniques.



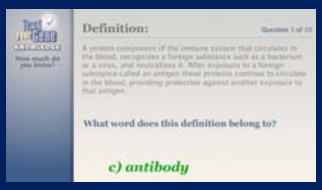
Illustrations:

- Color illustrations
- Scientist and educator vetted
- Available as downloads in PDF and PPT files
- Basic and advanced versions
- Over 100 (increasing to 150)
- Same illustrator for all files



3D Animations:

- 23 unique 3-D animations viewable online
- Contextual, not narrated
- Available to teachers in larger versions



Test Your Gene Knowledge Quiz:

- 85 random terms
- Sounds/sound muting
- Printable certificate with grade/name
- "In the Classroom" & "In the Media" versions

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New NHGRI Deputy Clinical Director

Cynthia Tifft, M.D., Ph.D.

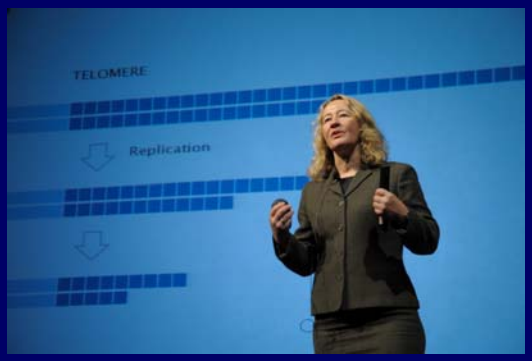
Associate Investigator, Medical Genetics Branch
Director of Pediatrics, Undiagnosed Diseases Program

- Expert in cell biology and storage disorders
- Former Chief, Div. Genetics and Metabolism, CNMC
- Scientific Advisory Committee, National Tay-Sachs and Allied Diseases Association

Document 37

Nobel Prize Winner Gives Trent Lecture

Carol Greider, Ph.D.



2009 Jeffrey M. Trent Lectureship in Cancer Research:
Telomerase and the Consequences of Telomere Dysfunction

Document 38

Undiagnosed Diseases Program (UDP)

rarediseases.info.nih.gov

Media Coverage of the UDP

Document 39

Dr. Charles Venditti Wins ASGCT New Investigator Award

- American Society of Gene and Cell Therapy (ASGCT) selected Dr. Venditti as recipient of its 2010 Outstanding New Investigator Award
- His recent studies suggest a path forward for gene therapies to treat organic acidemias

Document 40

Dr. Fabio Candotti Elected to ASGCT Board

- Dr. Candotti was elected to the Board of Directors of the American Society of Gene and Cell Therapy (ASGCT)
- A leading gene therapy researcher within the NHGRI Intramural Program

Dr. Larry Brody Appointed Chief of Genome Technology Branch

- Genome Technology Branch (GTB) is the largest of the 7 NHGRI Intramural Branches
- Dr. Brody also serves as Chief Scientific Officer of the Center for Inherited Diseases Research (CIDR)

Document 41

Recent NHGRI Intramural Research 'Headlines'

Ellen Sidransky
(Parkinson's disease)

Les Biesecker
(X-linked cleft palate)

Francis Collins
(Diabetes)

Joan Bailey-Wilson
(Lung cancer)

Max Muenke
(ADHD)

Bill Pavan
(Microcephaly)

Document 42