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National Human Genome Research Institute

National Institutes of Health

DIRECTOR'S REPORT

National Advisory Council
for Human Genome Research

September 2012

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





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National Human Genome Research Institute

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Home > About > Institute Advisors > National Advisory Council for Human Genome Research > Director's Report Related Documents: September 2012

Director's Report Related Documents: September 2012

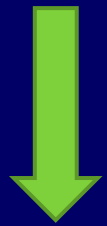
[Director's Report](#) PDF

[Director's Report](#) PDF

No.	Documents
1	NHGRI Reorganization
2	Smithsonian Genome Exhibition Update
3	2012 Pro Bono Humanum Award [prnewswire.com]
4	Augmenting the NIH Message [public.cq.com]
5	Editorial from the NIH Director PDF [sciencemag.org]
6	Maria Freire: New President of the Foundation for NIH [fnih.org]
7	NIGMS Director Search [jobs.nih.gov]
	Advisory Committee to the NIH Director Working Group Reports
8	<ul style="list-style-type: none">Working Group on Data and Informatics Report PDF [acd.od.nih.gov]Working Group on Biomedical Workforce Report PDF [acd.od.nih.gov]Working Group on Diversity in the Biomedical Research Workforce Report PDF [acd.od.nih.gov]

genome.gov/DirectorsReport

Document #



Open Session Presentations

- **Genomic Medicine Working Group Update**
 - **Rex Chisholm and Teri Manolio**

- **Meeting Reports:**
 1. **Workshop on “Establishing a Central Resource of Data from Genome Sequencing Projects”**
 - **Lisa Brooks**

 2. **Workshop on “Sequencing in Cohort Studies and Large Sample Collections”**
 - **Teri Manolio**

 3. **Workshop on “Integrating Functional Data for Connecting Genotype to Phenotype”**
 - **Adam Felsenfeld**

Open Session Presentations

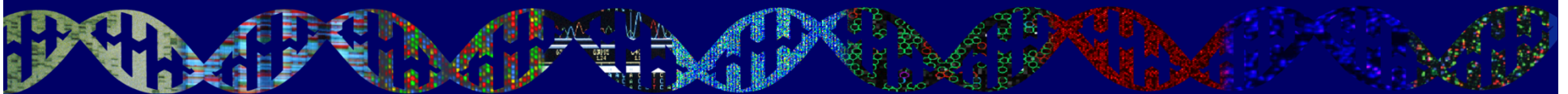
- **Project Update: GWAS Catalog**
 - **Lucia Hindorff**
- **NHGRI and the NIH Common Fund**
 - **Mark Guyer**
- **Concept Clearance: “Family History Implementation in the Challenging Setting of Routine Clinical Care”**
 - **Anastasia Wise**

Open Session Presentations

NHGRI Intramural Research Program:

- **Update from the NHGRI Scientific Director**
 - **Dan Kastner**
- **Report from the Blue Ribbon Panel Review**
 - **Rick Myers and David Page**

- 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**



I. General NHGRI Updates

II. General NIH Updates

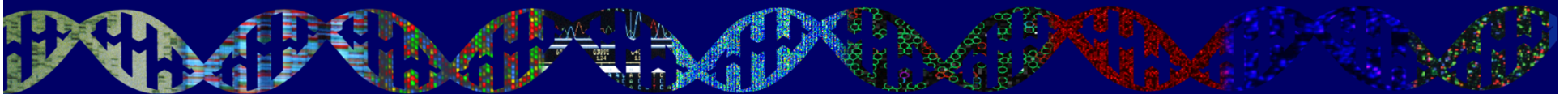
III. Genomics Updates

IV. NHGRI Extramural Program

V. NIH Common Fund Programs

VI. NHGRI Office of the Director

VII. NHGRI Intramural Program



NHGRI Reorganization



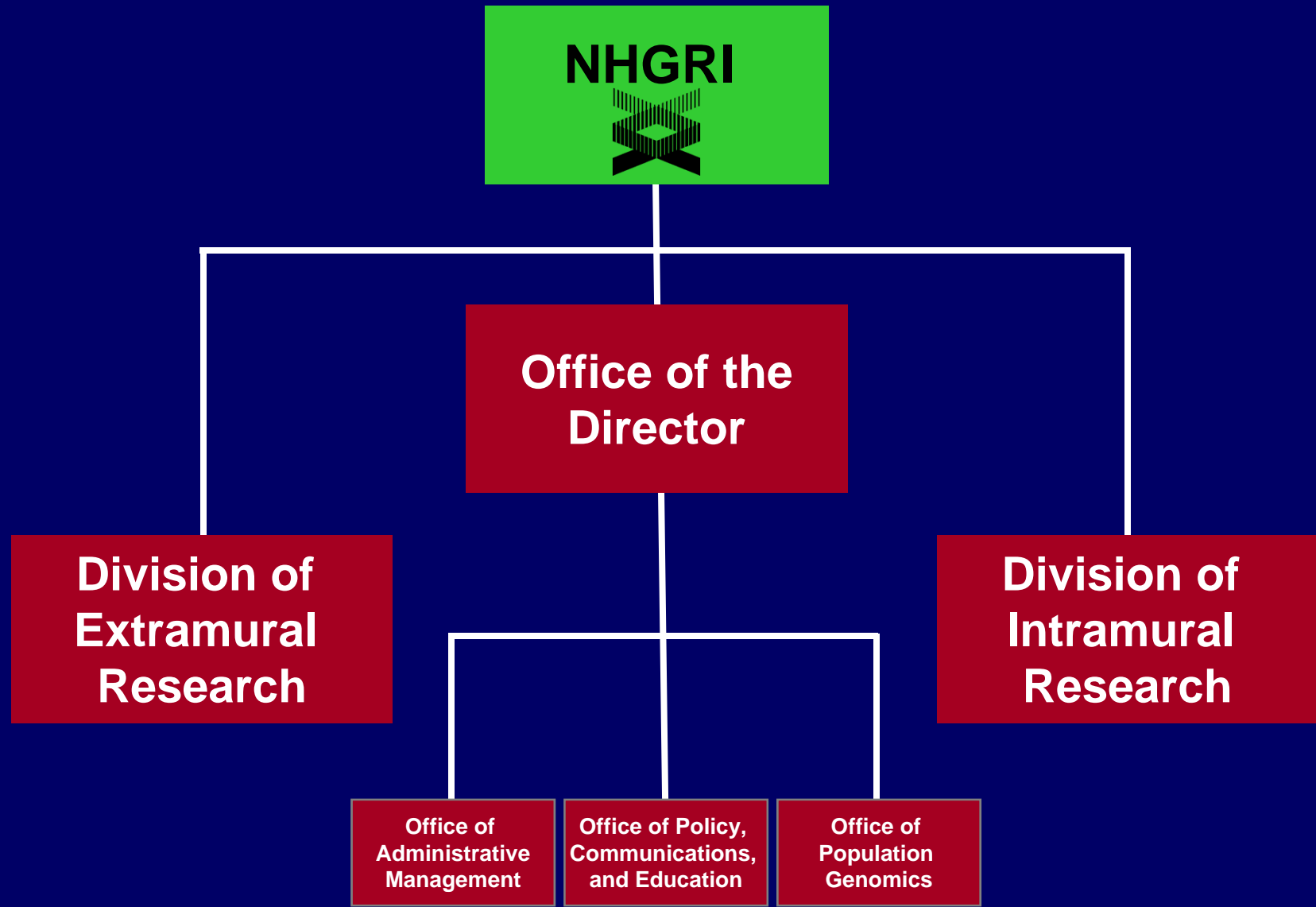
Announcing Today:

***Proposed reorganization of NHGRI
has been approved and will be
implemented on October 1, 2012***

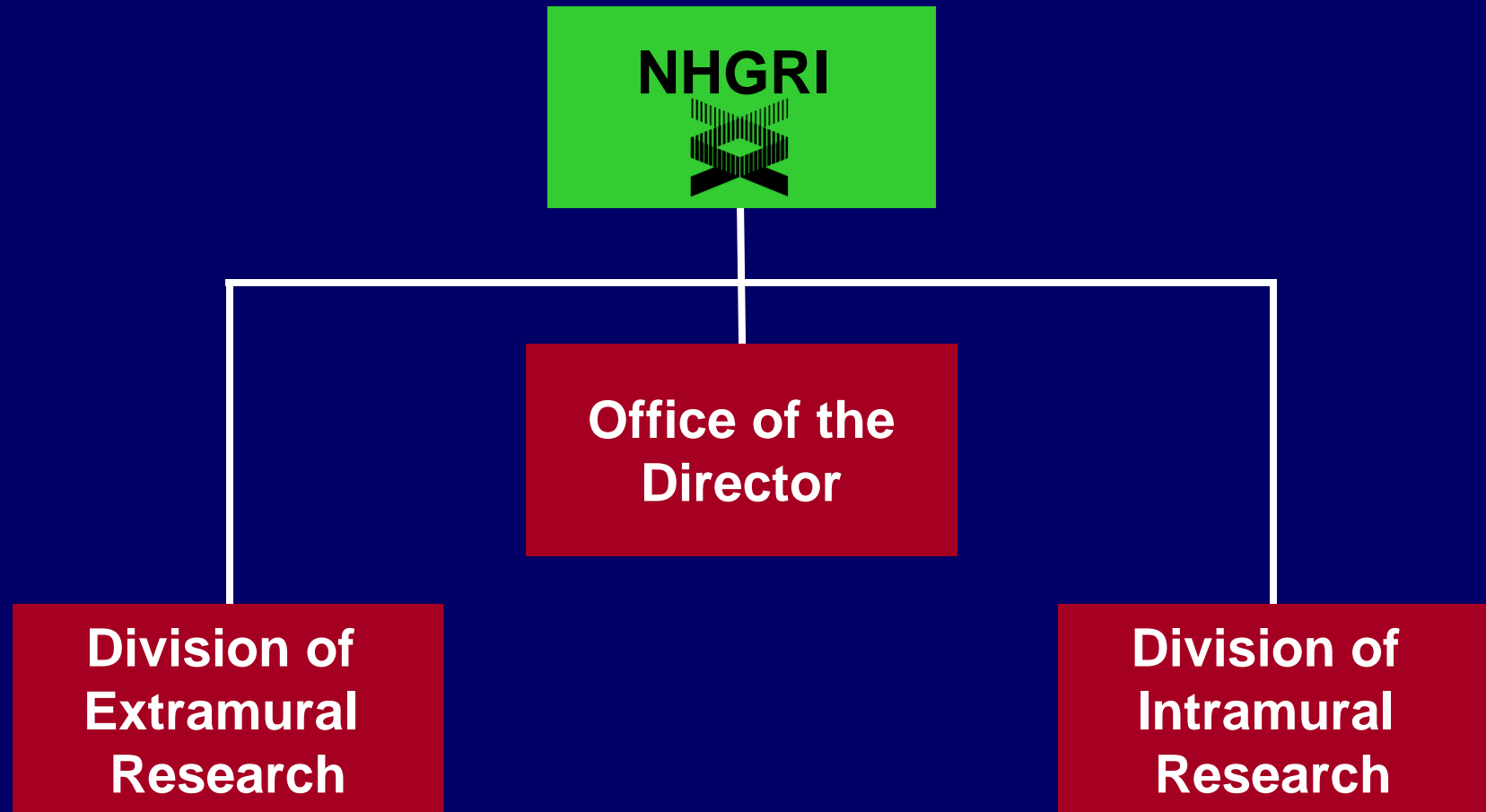
See genome.gov/reorg

Document 1

Current NHGRI Organizational Structure



Current NHGRI Organizational Structure

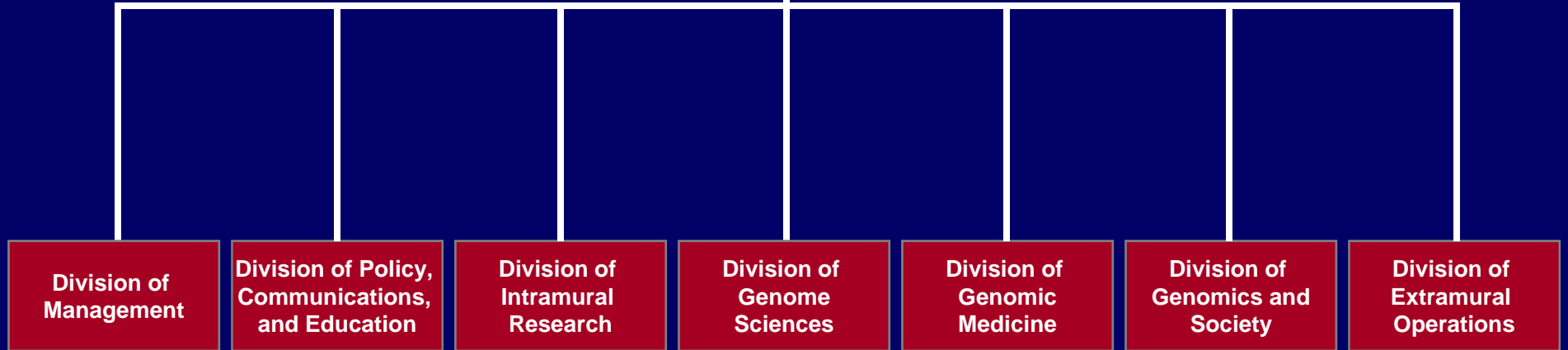


**Major
Changes**

**Minor
Changes**

**No
Changes**

New NHGRI Organizational Structure



From the Office of the Director

Extramural Research Program

Steps to NHGRI Reorganization

- Followed guidance in NIH Reform Act of 2006
- Two public meetings:
 - Webinar on Jan. 18, 2012
 - NACHGR Meeting on Feb. 13, 2012
- Reorganization package submitted: February, 2012
- Final approval: June, 2012
- Announcement of reorganization: Sept. 10, 2012
- Implementation of reorganization: Oct. 1, 2012



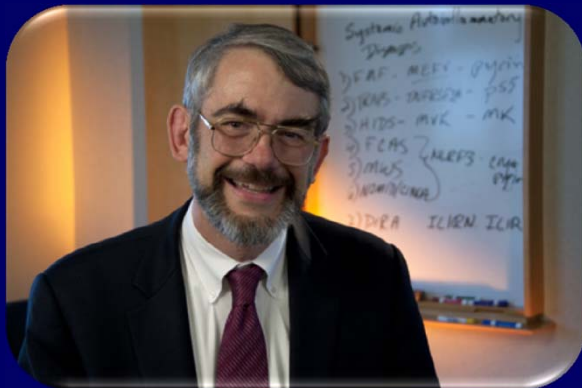
Division Leadership



Janis Mullaney, B.S., M.B.A.
Director
Division of Management

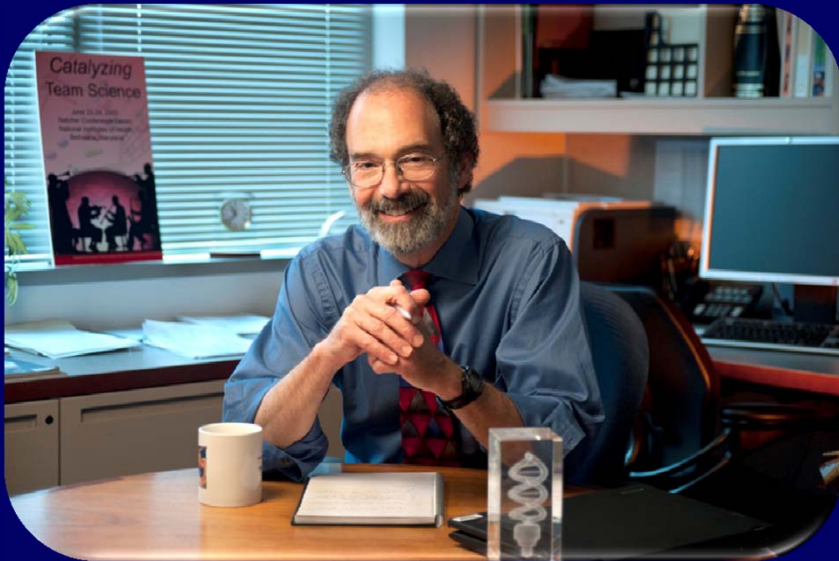


Laura Lyman Rodriguez, Ph.D.
Director
**Division of Policy, Communications,
and Education**



Dan Kastner, M.D., Ph.D.
Director
Division of Intramural Research

Leadership: Division of Genome Sciences



Jeff Schloss, Ph.D.
Director



Peter Good, Ph.D.
Deputy Director

Leadership: Division of Genomic Medicine



**Teri Manolio, M.D., Ph.D.
Director**



**Brad Ozenberger, Ph.D.
Deputy Director**

Leadership: Division of Extramural Operations



Bettie Graham, Ph.D.
Director



Rudy Pozzatti, Ph.D.
Deputy Director

Leadership: Division of Genomics and Society

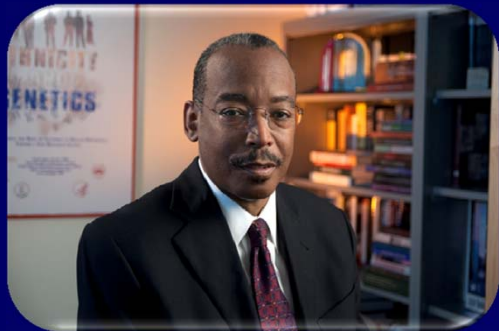


**Mark Guyer, Ph.D.
Acting Director**

Senior Advisor Appointments



Jane Peterson, Ph.D.
Senior Advisor to the
NHGRI Office of the Director

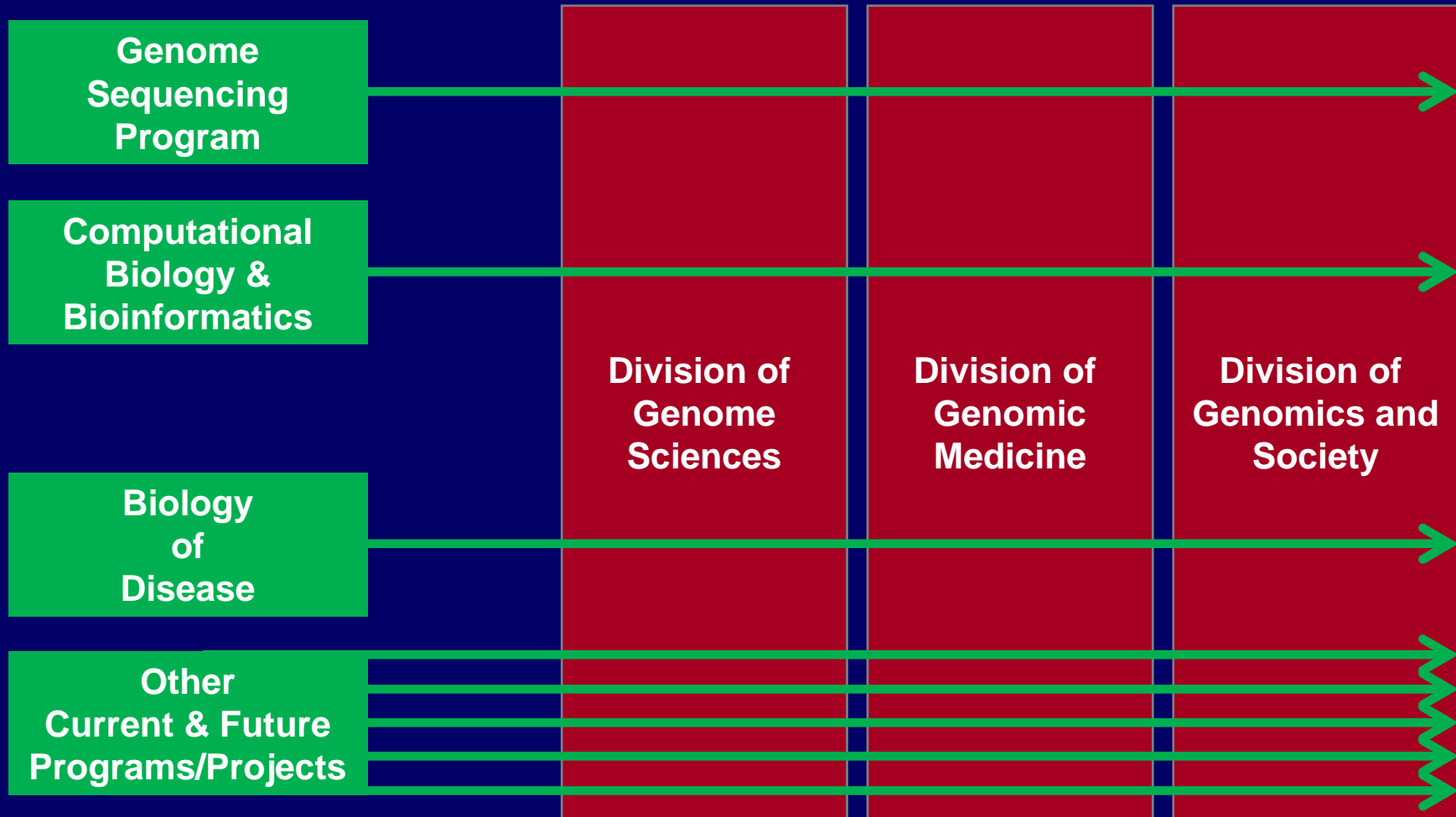


Vence Bonham, J.D.
Senior Advisor to the
NHGRI Director on
Genomics and Health Disparities

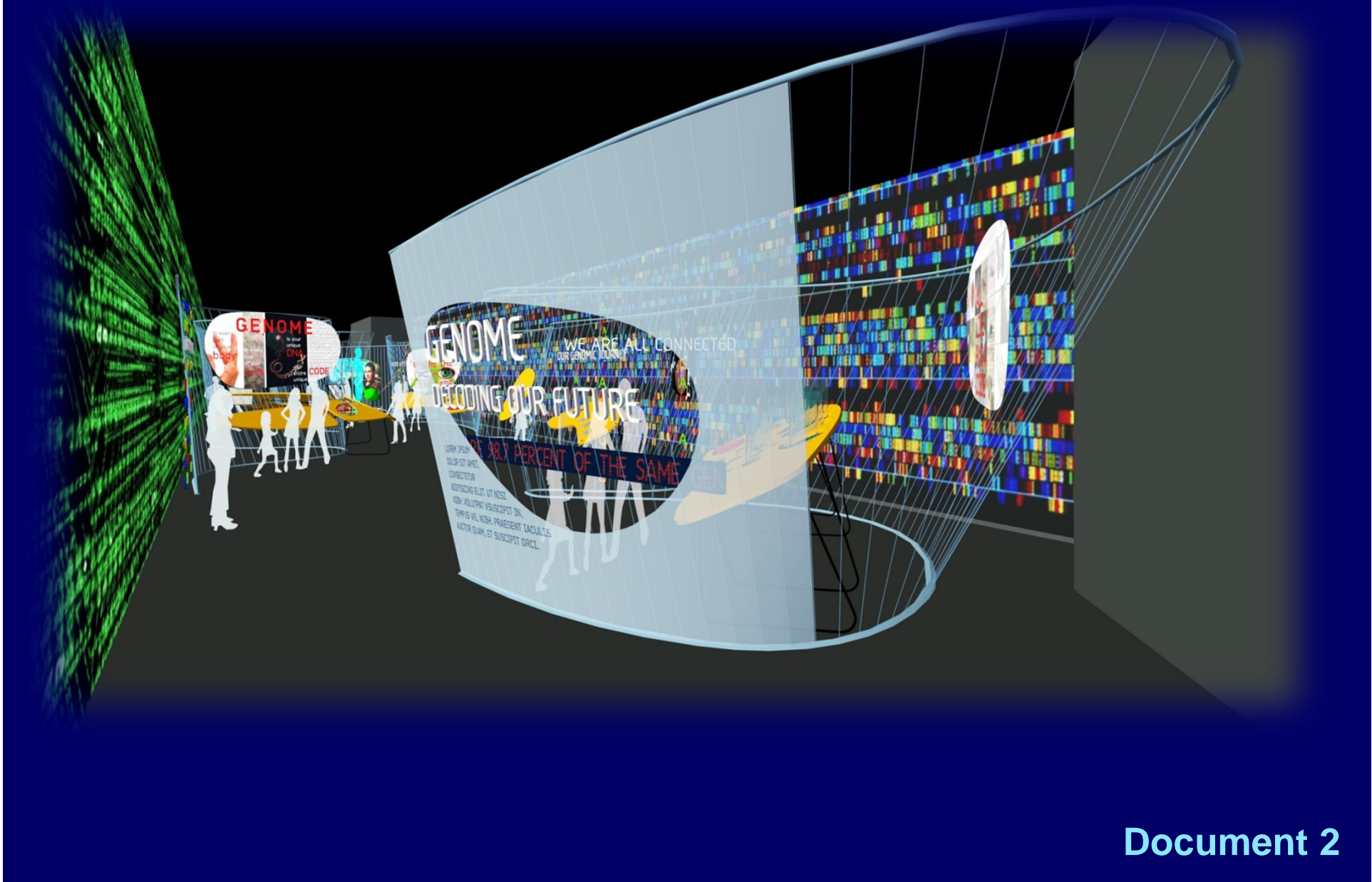


Karen Rothenberg, J.D., M.P.A.
Senior Advisor to the
NHGRI Director on
Genomics and Society

Program/Project Oversight and Execution



Smithsonian Genome Exhibition Update



NHGRI Staff Retirement



Elizabeth Thomson, DNSc, RN, CGC, FAAN

New ASHG/NHGRI Policy Fellow



Laura Koontz, Ph.D.

Eric Green 'Down Under'



I. General NHGRI Updates

II. General NIH Updates

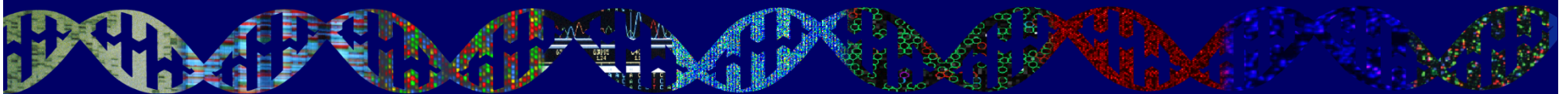
III. Genomics Updates

IV. NHGRI Extramural Program

V. NIH Common Fund Programs

VI. NHGRI Office of the Director

VII. NHGRI Intramural Program



2012 Pro Bono Humanum Award



PRIX GALIEN USA
NEW YORK *2012*
OCTOBER 16TH, 2012

Francis Collins, M.D., Ph.D.

Augmenting the NIH Message



“Increasingly, he’s describing NIH not just as a powerful force in the war against disease... but also an incubator of new jobs and new products”

Editorial from the NIH Director



Francis S. Collins is director of the U.S.

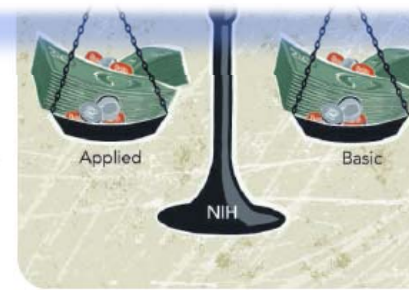
NIH Basics

"WHEN EVERYBODY GETS TO ONE SIDE OF THE BOAT, IT USUALLY TIPS OVER." THAT SAYING MAY have originated on Wall Street, but it also stands as a warning to those charting the future of

EDITORIAL

“Americans need to know that today’s basic research is the engine that powers tomorrow’s therapeutic discoveries.”

in basic research (HIV treatment as prevention). Basic research also accounts for most of the 135 Nobel Prizes won by NIH-supported scientists, including the 2011 awards to Bruce Beutler and Jules Hoffmann for their discoveries about innate immunity, and the late Ralph Steinman for adaptive immunity. Likewise, current NIH grantee Arthur Horwich and past grantee F. Ulrich Hartl captured 2011 Lasker awards for landmark explorations of the cell’s protein-folding machinery. Their work, which provided insights on protein misfolding in neurodegenerative disease, is among countless examples of basic research, including that with model organisms,* giving rise to medical advances.



New President of the Foundation for NIH



Maria Freire, Ph.D.

New Director of the NIH Office of Research on Women's Health (ORWH)



Janine Clayton, M.D.

NIGMS Director Search

NIGMS Feedback Loop Blog

A catalyst for interaction with the scientific community



Search for NIGMS Director Resumes



Posted by [Story Landis](#)  on **Wednesday, Aug 1, 2012 11:10 AM EDT**
[Post a Comment](#) | [View Comments \(7\)](#)

The search for the next director of NIGMS has officially restarted. If you want to play a leading role in shaping the future of biomedical research, see the just-issued [vacancy announcement](#) for details on how to apply. If you know of others who might be interested in this position, please share this information with them.

The NIGMS director is the Institute's "chief visionary," setting goals, priorities and policies. He or she oversees a budget of \$2.4 billion, which funds basic research in cell biology, biophysics, genetics, developmental biology, pharmacology, physiology, biological chemistry, biomedical technology, bioinformatics, computational biology, and selected behavioral and clinical areas. NIGMS also supports a significant amount of research training and has programs designed to develop and increase the diversity of the biomedical and behavioral research workforce.

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Data and Informatics Working Group



National Institutes of Health

Data and Informatics Working Group

Draft Report to
The Advisory Committee to the Director

June 15, 2012

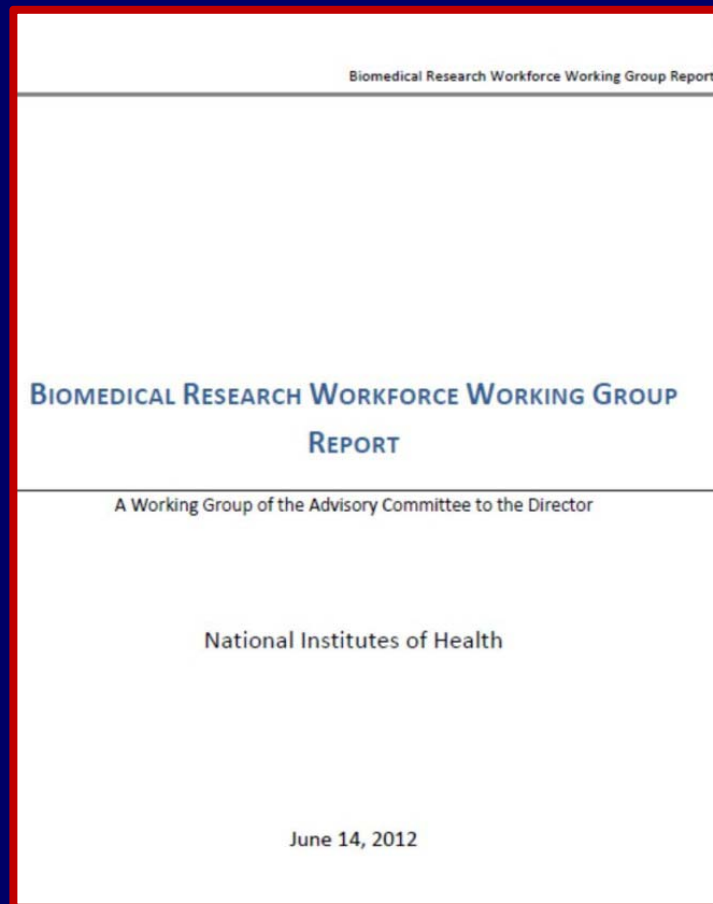
ADVISORY COMMITTEE TO THE DIRECTOR

Advisory Committee to
the Director

Working Group on Data and Informatics

Document 8

Biomedical Research Workforce Working Group



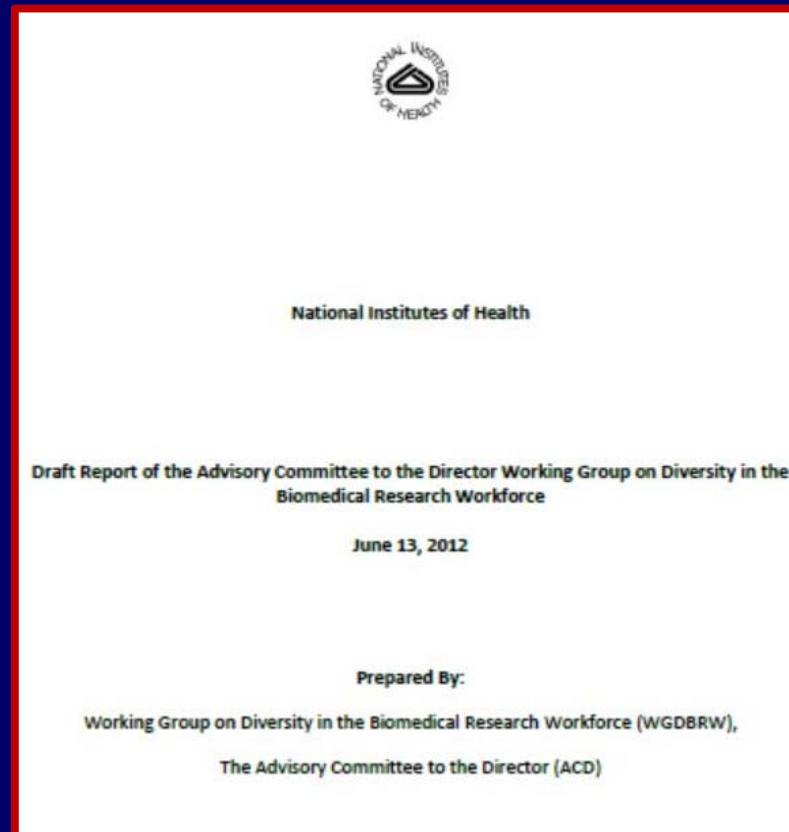
ADVISORY COMMITTEE TO THE DIRECTOR

Advisory Committee to
the Director

Biomedical Workforce Task Force

Document 8

Working Group on Diversity in the Biomedical Research Workforce



ADVISORY COMMITTEE TO THE DIRECTOR

Advisory Committee to
the Director

Charter

Working Group on Diversity in the
Biomedical Research Workforce

Document 8

Courts Give NIH hESC Funding the 'All Clear'



Drs. Sherley and Deisher



Secretary Sebelius

NIH Fiscal Year 2013 Appropriation

- Continuing Resolution (CR) agreement will keep the government running through March
- Regular appropriations process will not be completed until the next Congress

	Actual FY2012	President FY2013	House FY2013	Senate FY2013
NIH	\$30.7 B	\$30.7 B	\$30.6 B	\$30.7 B
NHGRI	\$513 M	\$511 M (-0.29%)	\$512 M	\$513 M

House Energy & Commerce Subcommittee on Health: NIH Oversight Hearing



- Hearing entitled “*The National Institutes of Health - A Review of Its Reforms, Priorities, and Progress*”
- Reviewed the implementation of the 2006 NIH Reform Act, progress of NCATS, and the determination of NIH funding and research priorities

I. General NHGRI Updates

II. General NIH Updates

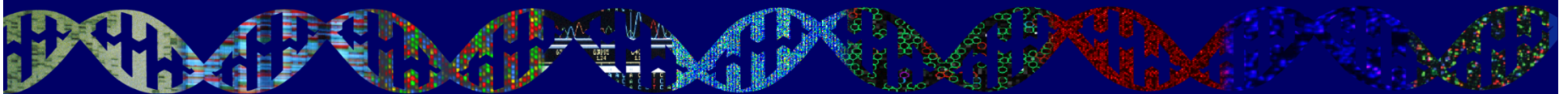
III. Genomics Updates

IV. NHGRI Extramural Program

V. NIH Common Fund Programs

VI. NHGRI Office of the Director

VII. NHGRI Intramural Program



2012 Lemelson-MIT Prize



LEMELSON-MIT
Celebrating innovation, inspiring youth

Steve Quake, D.Phil.

Document 11

Amy McGuire Named Center Director



Amy McGuire, J.D., Ph.D.

Joann Boughman Leaving ASHG



Joann Boughman, Ph.D.

Presidential Commission for the Study of Bioethical Issues

DEPARTMENT OF HEALTH AND HUMAN SERVICES

Public Meeting of the Presidential Commission for the Study of Bioethical Issues

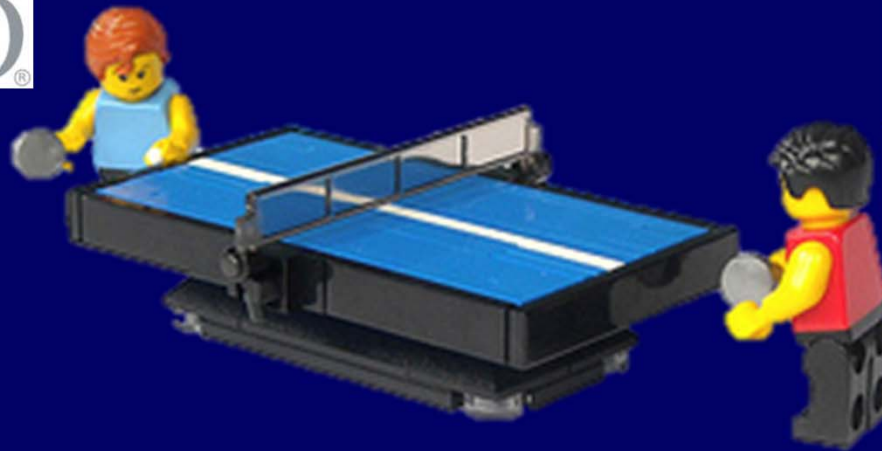
AGENCY: Department of Health and Human Services, Office of the Assistant Secretary for Health, Presidential Commission for the Study of Bioethical Issues.

ACTION: Notice of meeting.

SUMMARY: The Presidential Commission for the Study of Bioethical Issues will conduct its tenth meeting in August. At



Biotech Patents and the Courts



NHGRI Genome Advance of the Month

Uncovering the Archeological Landscape of Cancer Genomes

By Roseanne F. Zhao, Ph.D.
Intramural Fellow

Researchers view DNA through 3D lens

By Andrea H. Ramirez, M.D., M.S.
Clinical Fellow, NHGRI

The Human Microbiome Project: Extending the definition of what constitutes a human

By Joy Yang
Post-baccalaureate Fellow

A Genetic Fountain of Youth?

By Danielle Daee, Ph.D.
Intramural Postdoctoral Fellow, NHGRI



As we age our hair turns gray, our skin wrinkles and our muscles lose their tone. Some turn to surgical remedies to combat these less-than-glamorous side effects of aging. Beyond surgical reversal, scientists have worked diligently to understand the fundamental mechanisms of aging, knowing that a clearer understanding may reveal ways to slow the aging process.

Genetically speaking, a person remains virtually unchanged through the course of his or her life. In contrast, a person's physical appearance changes dramatically throughout the years. If a person's genes are largely unchanged, what accounts for these striking physical differences?

This month's Genome Advance of the Month compares newborns and centenarians to see if [epigenetic](#) changes, or alterations in the signals on the genes rather than the genes themselves, could be associated with aging.

There are thousands of genes in the human genome, but by turning on and off a specific combination of genes, a cell can develop into a heart, skin, or the other diverse tissues of the human body. To allow the right combination of genes to be expressed for a particular cell, proteins mark genes with flags, or epigenetic changes, that tell the cell to turn the gene on or off. One type of flag, methylation, occurs in large repetitive "CG" sequences called CpG islands.

Genomics in the News...



Science on  **NBCNEWS.com**

A smart bunch of scientists unpeel banana's genome

Achievement opens way for a better fruit more resistant to parasites and other stresses

NewScientist

Health

Exome sequencing gets to the root of rare diseases

nature

International weekly journal of science

Genome study highlights risk factor for multiple sclerosis

Discovery of genetic variant could help to improve clinical trials of potential therapies.

Genomics in the News...



The New York Times



The New York Times

Health

Genetic Gamble

New Approaches to Fighting Cancer

PART ONE
A Race to Leukemia's
Source

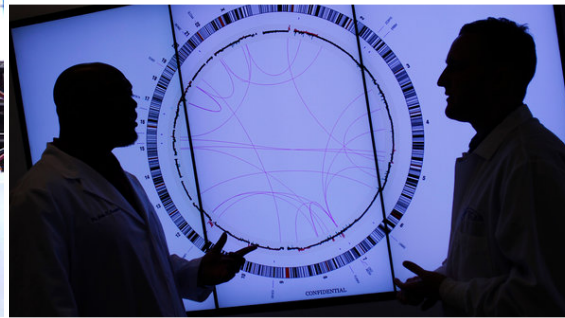
PART TWO
Promise and Heartbreak

PART THREE
What a Tumor Holds in
Store

In Treatment for Leukemia, Glimpses of the Future



A New Treatment's Tantalizing Promise Brings Heartbreaking Ups and Downs



A Life-Death Predictor Adds to a Cancer's Strain



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

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NHGRI Genome Sequencing Program

- **Large-Scale Genome Sequencing and Analysis Centers**
- **Centers for Mendelian Genomics**
- **Clinical Sequencing Exploratory Research Projects**
- **Informatics Tools for High-Throughput Sequence Data Analysis**
- **Meeting involving all components: October 2012**



Large-Scale Genome Sequencing and Analysis Centers

- Alzheimer's disease genome sequencing project in late planning stages
- Most recent quarter: 57 Tb produced
- Papers published or in press:

Cancer

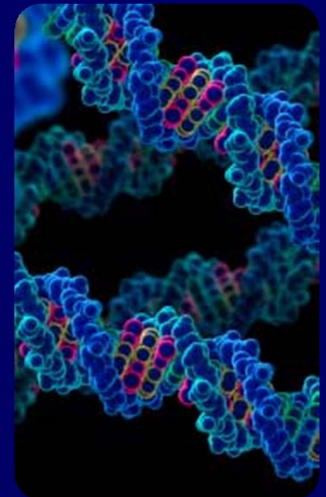
Autism

Rare diseases

Microbiome

Clinical

Methods/Reference



- Ongoing projects: cancer, complex disease, rare diseases and comparative sequencing



TCGA Papers:

- **Colorectal Carcinoma**
Nature 487:330-337, 2012
- **Lung Squamous Cell Carcinoma**
Nature, published on-line (September 9, 2012)
- **Breast Carcinoma (in press)**
- **Kidney Clear Cell Carcinoma (in preparation)**
- **Acute Myeloid Leukemia (in preparation)**

ARTICLE

doi:10.1038/nature11252

**Comprehensive molecular characterization
of human colon and rectal cancer**

The Cancer Genome Atlas Network*

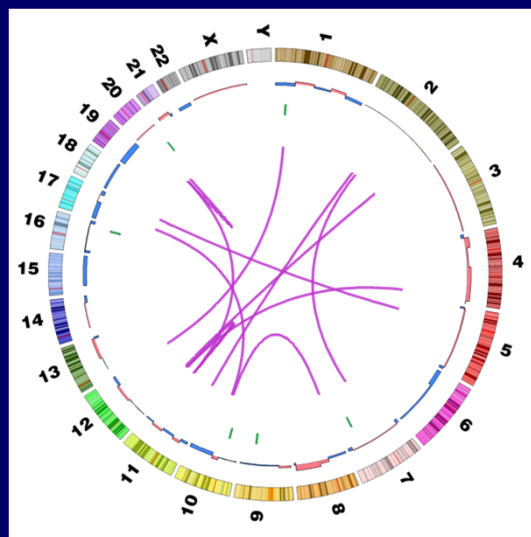
THE CANCER GENOME ATLAS



2nd Annual TCGA Scientific Symposium

November 27-28, 2012

Crystal City, VA

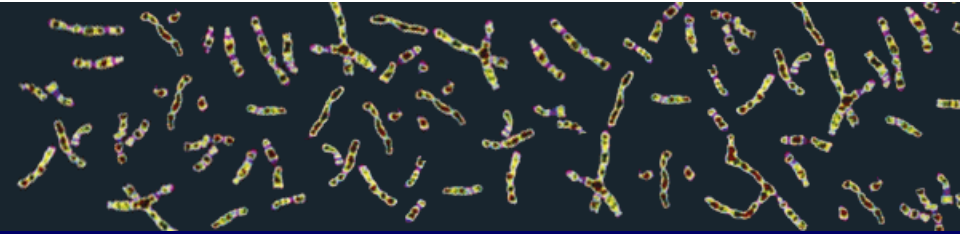


Co-Chairs: Matthew Meyerson & Ilya Shmulevich

Document 19

1000 Genomes

A Deep Catalog of Human Genetic Variation



- **Now working on methods development**
- **All 2500 samples (25 populations) should be sequenced by December and analyzed next year**
- **The Phase 1 paper on variation in 1092 samples (14 populations) will be published by November**



- **>100 Mendelian diseases selected; sequencing ongoing**
- **A number of disease genes identified**
- ***AJMG* Commentary:**
 - The Centers for Mendelian Genomics: a new large-scale initiative to identify the genes underlying rare Mendelian conditions. *Am J Med Genet* (2012)**
- **Joint sample solicitation group now receiving samples**
- **Educational program on Mendelian genomics at 2012 ASHG Meeting**

Clinical Sequencing Exploratory Research (CSER) Projects

- **Strong response to the reissued RFA (HG-12-009)**
- **Applications to be discussed at the February Council meeting**
- **NCI and NIDA have tentatively agreed to support awards relevant to their missions**
- **Also received applications for a Coordination Center**



Informatics 'iSeqTools' Network



NHGRI awards funding to develop tools for genome sequence analyses

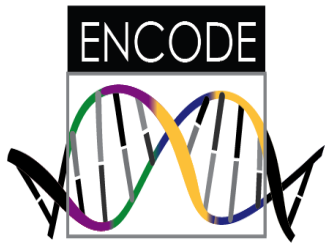
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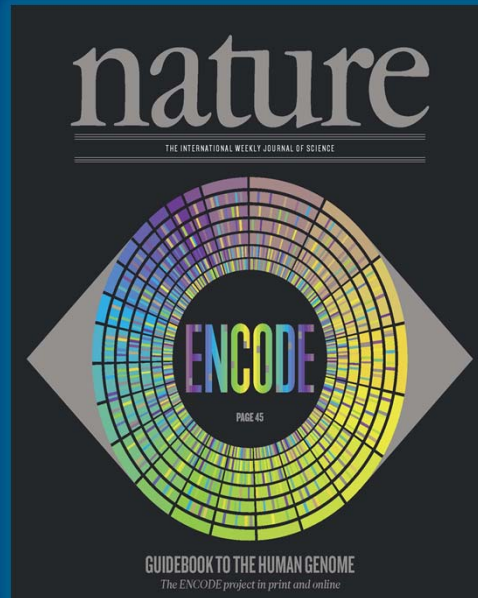
The goal of sequencing a human genome for \$1000 is well within reach, but that's just the beginning of the story. Once a genome is sequenced, researchers are left with the formidable challenge of analyzing and interpreting its embedded code — a complex task that requires sophisticated data analysis tools.

With increasingly dropping DNA sequencing costs, more and more researchers are generating large amounts of genome sequence data. With such data in hand, researchers then need to use many data analysis tools to detect genetic patterns underlying various common diseases, to diagnose diseases and to individualize treatments.

As one component of its new [Genome Sequencing Program](#) announced in December 2011, the National Human Genome Research Institute (NHGRI) has awarded six researchers approximately \$4 million in fiscal year (FY) 2012 to create robust, well-documented and well-supported computer software programs for analyzing genome sequence data that can be readily adopted outside of large genome sequencing centers. Many sequence analysis tools have been developed and are publically available, but their use is often limited by the lack of experts who can install and use the tools.



ENCODE



ARTICLE

An integrated encyclopedia of DNA elements in the human genome

The ENCODE Project Consortium*

The human genome encodes the blueprint of life, but the function of the vast majority of its nearly three billion bases is unknown. The Encyclopedia of DNA Elements (ENCODE) project has systematically mapped regions of transcripts, transcription factor association, chromatin structure and histone modification. These data enabled us to assign biochemical functions for 80% of the genome, in particular outside the well-studied protein-coding regions. Many discovered candidate regulatory elements are physically associated with one another and with expressed genes, providing new insights into the mechanisms of gene regulation. The newly identified elements also show a statistical correspondence to regions variants linked to human disease, and can thereby guide the interpretation of this variation. Overall, the project provides new insights into the organization and regulation of our genes and genome, and is an expansive resource of functional annotations for biomedical research.

The human genome sequence provides the underlying code for human biology. Despite intensive study, especially in identifying protein-coding genes, our understanding of the genome is far from complete, particularly with regard to non-coding RNAs, alternatively spliced transcripts and regulatory sequences. Systematic analysis of transcripts and regulatory information are essential for the identification of genes and regulatory regions, and are an important resource for the study of human biology and disease. Such analyses can also provide complementary views of the organization and variability of genes and regulatory information across cellular contexts, species and individuals.

The Encyclopedia of DNA Elements (ENCODE) project aims to delineate all functional elements encoded in the human genome¹. Operationally, we define a functional element as a discrete genome segment that encodes a defined product (for example, protein or non-coding RNA) or displays a reproducible biochemical signature (for example, protein binding, or a specific chromatin structure). Comparative genomic studies suggest that 3–4% of bases are under purifying (negative) selection^{2,3}, and therefore are functional, although other analyses have suggested much higher estimates^{4–6}. In a pilot phase covering 1% of the genome, the ENCODE project annotated 60% of mammalian evolutionarily constrained bases, but also identified many additional putative functional elements without evidence of constraint⁷. The advent of more powerful DNA sequencing technologies now enables whole-genome and more precise analysis with a broad repertoire of functional assays.

Here we describe the production and initial analysis of LocusZoom data sets designed to annotate functional elements in the entire human genome. We integrate results from diverse experiments within cell types, and experimental tracking of different cell types, and all ENCODE data with other resources, such as candidate regions from genome-wide association studies (GWAS) and evolutionarily conserved regions. Together, these efforts reveal important features about the organization and function of the human genome, summarized below.

*The vast majority (90.4%) of the human genome participates in at least one biochemical RNA and/or chromatin-associated event in at least one cell type. Much of the genome lies close to a regulatory event.

90% of the genome lies within 1 kilobase (kb) of a DNA-protein interaction (as assessed by bound ChIP-seq motifs or DNase I footprinting), and 69% is within 1.7 kb of at least one of the biochemical events measured by ENCODE.

Private-specific elements as well as elements without detectable mammalian constraint show aggregate evidence of negative selection, thus, some of them are expected to be functional.

Classification of the genome with seven chromatin states in a mean total set of 399,124 regions with enhancer-like features and 70,202 regions with promoter-like features, as well as hundreds of thousands of other regions. High-resolution analyses further subdivide the genome into thousands of associations with distinct functional properties.

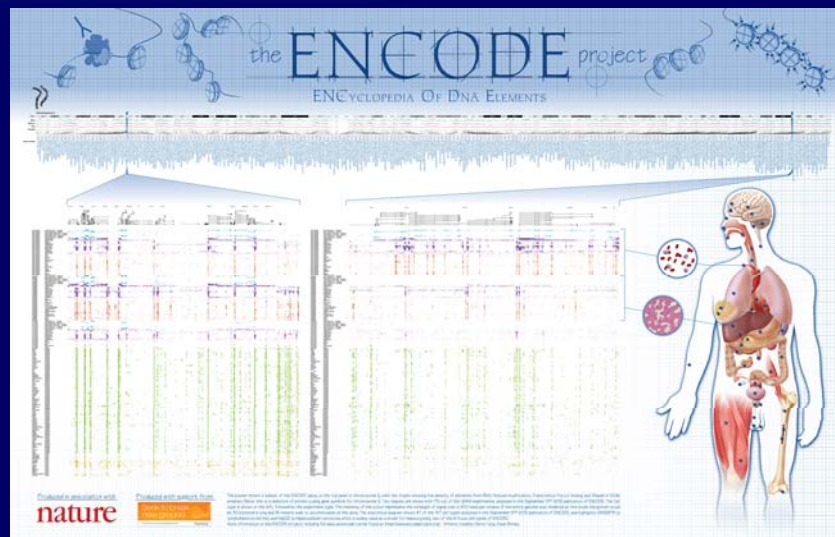
It is possible to correlate quantitatively RNA-seq production and processing with both chromatin marks and transcription factor binding at promoters, indicating that promoter functionality can explain most of the variation in RNA expression.

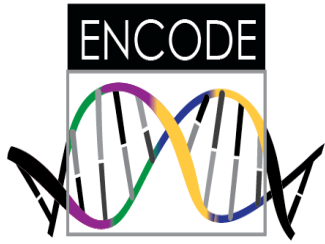
Many non-coding variants in individual genome sequences lie in ENCODE-annotated functional regions; this number is at least as large as that for the protein-coding genes.

Single nucleotide polymorphisms (SNPs) associated with disease by GWAS are enriched within non-coding functional elements, with a majority residing in or near ENCODE-defined regions that are outside of protein-coding genes. In many cases, the disease phenotypes can be associated with a specific cell type or transcription factor.

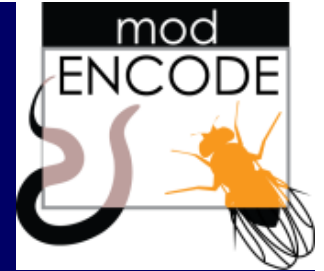
ENCODE data production and initial analyses

Since 2007, ENCODE has developed methods and performed a large number of sequence-based studies to map functional elements across the human genome⁷. The elements mapped (and approaches used) include RNA-based regions (RNA-seq, CAGE, RNA-FET and manual annotation), protein-binding regions (mass spectrometry), transcription factor binding sites (ChIP-seq and DNase-seq), chromatin structure (DNase-seq, FAIRE-seq, histone ChIP-seq and HiChIP-seq), and DNA methylation sites (BS-seq) (Supp. 1: Data methods and observations, Supplementary Table 1, section P, details production statistics). To compare and integrate results across different laboratories, data production efforts focused on two selected





ENCODE



'Junk DNA' concept debunked by new analysis of human genome

The Washington Post Politics Opinions

Health & Science

Researchers: 'Junk' DNA plays major role in disease

By Dan Vergano, USA TODAY

Comment

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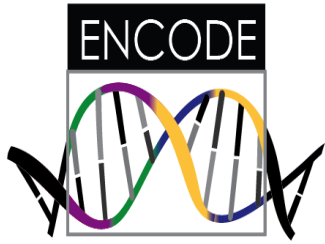
DNA project interprets 'book of life'

The New York Times



September 5, 2012

Far From Junk, 'DNA Dark Matter' Plays Crucial Role



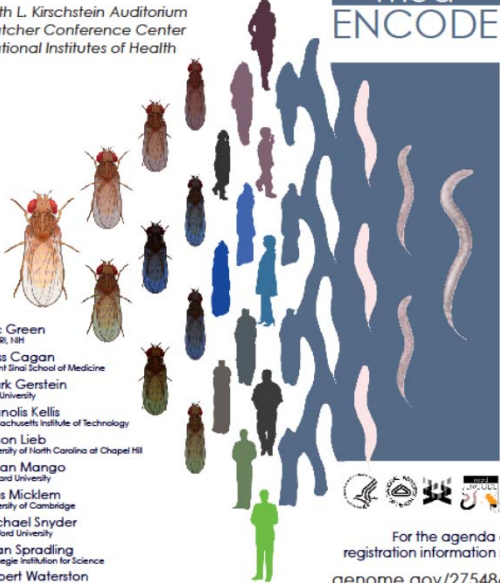

modENCODE & ENCODE



- **modENCODE Symposium in June 2012**
- **Next round of ENCODE grants to be funded by the end of September**

Genomics of model organisms
and human biology:
Insights from the modENCODE Project
model organism ENCYclopedia Of DNA Elements

June 20-21, 2012
Ruth L. Kirschstein Auditorium
Natcher Conference Center
National Institutes of Health



Eric Green
NIH, NHGRI

Ross Cagan
Mount Sinai School of Medicine

Mark Gerstein
Yale University

Manolis Kellis
Massachusetts Institute of Technology

Jason Lieb
University of North Carolina at Chapel Hill

Susan Mango
Harvard University

Gos Micklem
University of Cambridge

Michael Snyder
Stanford University

Allan Spradling
Carnegie Institution for Science

Robert Waterston
University of Washington

For the agenda and
registration information see:
genome.gov/27548680

Sign Language Interpreters will be provided. Individuals with disabilities who need reasonable accommodation to participate in this event should contact Jeannine Mjoseth, NHGRI, mjoseth@mail.nih.gov, 301-594-1043 or the Federal Relay (1-800-877-8339).

Centers of Excellence in ELSI Research (CEER) Program

- New CEER applications received in July; to be discussed at February Council meeting
- 8th Annual CEER Investigators Meeting in October



Genomic Medicine RFAs

- **Genomic Medicine Pilot Demonstration Projects (U01)**

Receipt Date: July 19, 2012

- **Population Architecture Using Genomics and Epidemiology (PAGE), Phase II (U01)**

Receipt Date: October 18, 2012

- **Clinically Relevant Genetic Variants Resource: A Unified Approach for Identifying Genetic Variants for Clinical Use (U01)**

Receipt Date: October 23, 2012

- **Genomic Sequencing and Newborn Screening Disorders (U19)**

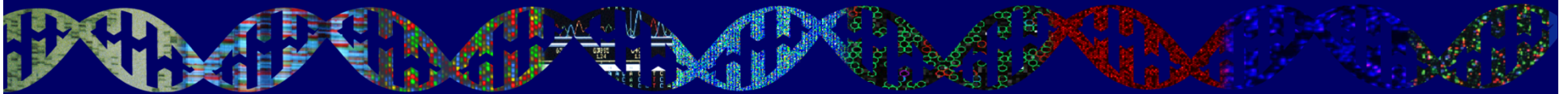
Receipt Date: November 19, 2012

Upcoming Meetings

- CEGS Annual Grantee Meeting (October)
- ENCODE and the Common Fund Epigenomics Program Joint Tutorial at ASHG (November)



- 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



Molecular Libraries Program (MLP)

- MLP beginning 5th Year of Production Phase
- Start of 'ramp down' in funding
- Network reduced to five centers
- Comprehensive & chemistry centers remain
- BioAssay Research Database (BARD)
- MLP ends after Year 6



Human Microbiome Project (HMP)

Nature: 2 Consortium papers

PloS Collection: 18 associated papers



HMP Press Coverage



4 Wires

13 Dailies

5 International outlets

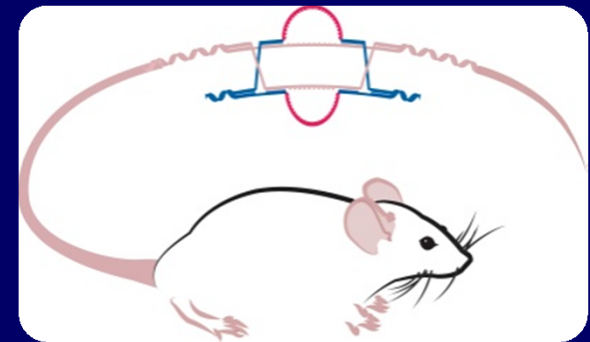
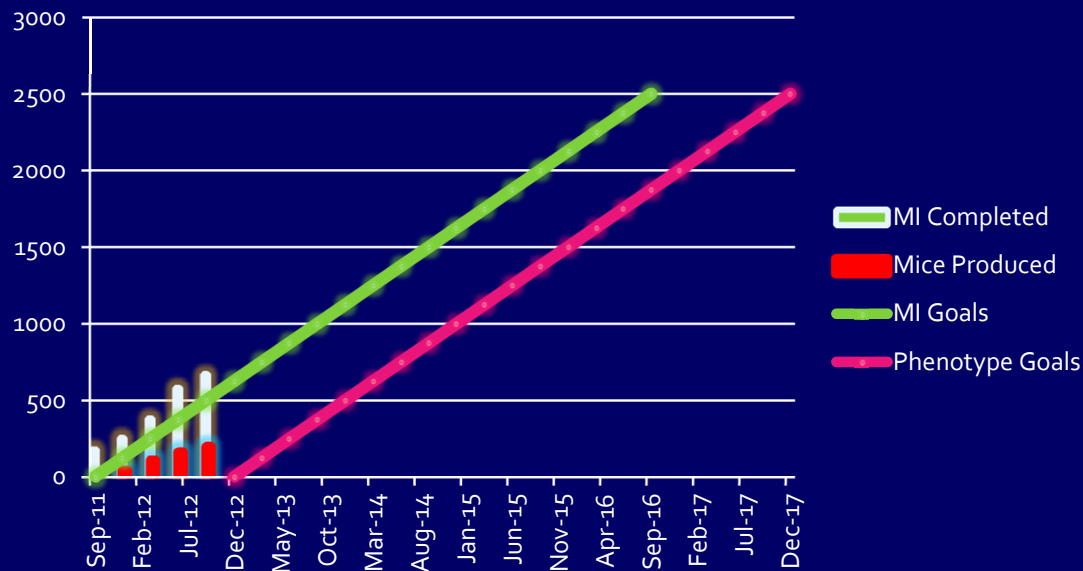
8 Science publications

2 Business magazines

1 PBS NewsHour

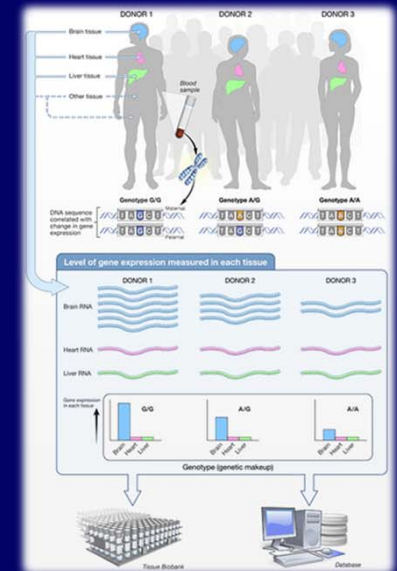
Knockout Mouse Phenotyping Project (KOMP²)

In 5 years, make and phenotype 2,500 live mouse strains from knockout ES cells



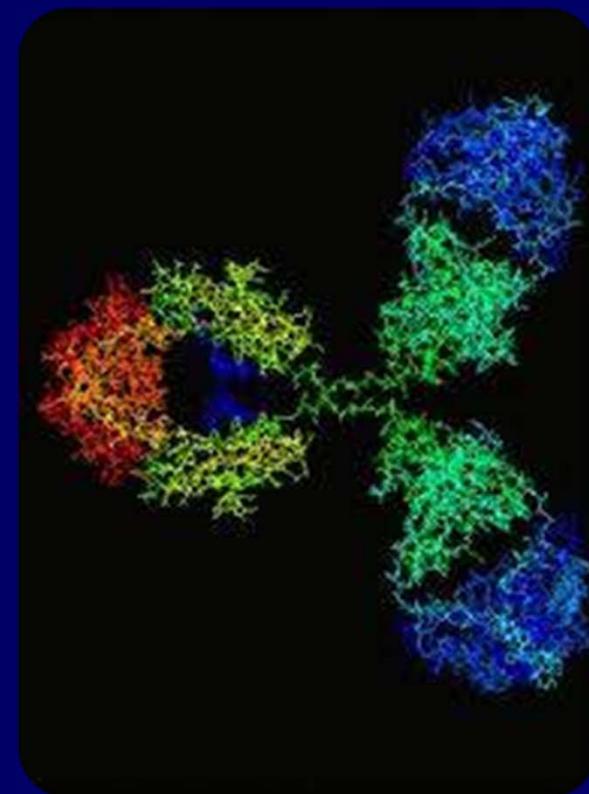
Genotype-Tissue Expression (GTEx)

- Scale-up approved
- Ultimate resource of:
 - 900 post-mortem donors
 - Fully genotyped
 - RNA-Seq (>20,000 samples, 30 organs)
- Quarterly dbGaP data releases
- ELSI study of donor families



Protein Capture Reagents Program

- **External Scientific Panel meeting in July 2012**
- **\$500K supplement request for antigen center approved**
- **Production Centers site visits in February 2013**
- **Website seeking input on human transcription factor priority list**





H3Africa

Human Heredity and Health in Africa



- **NIH and Wellcome Trust (WT) H3Africa awards released in August 2012**
- **Inaugural Meeting of the H3Africa Consortium to be held in Ethiopia in October 2012**
 - **Official press announcement of NIH & WT awards**
 - **Presentations by NIH & WT grantees**
 - **Discussion of H3Africa policies (e.g., data release, resource sharing, and consent)**
 - **Discussion of implementing H3ABioNet (the H3Africa bioinformatics network) and the H3Africa biorepositories**



H3Africa

Human Heredity and Health in Africa



- **Independent Expert Committee (Barry Bloom and Kay Davies, Co-Chairs)**
- **New FOA for the H3Africa ELSI Program released in June 2012**
- **Re-issued FOAs for H3Africa Collaborative Centers, Research Projects, and Biorepositories in August 2012**

NIH Director's Award: H3Africa Program Staff Recipients



Undiagnosed Diseases Program (UDP)



- To assist patients with unknown disorders reach an accurate diagnosis
- To discover new diseases that provide insight into human physiology and genetics
- ~500 patients to date; definitive diagnoses in 39
- 16 new human genetic disorders identified

UDP: A New Common Fund Program

- **Expansion to a national UDP Network**
- **Network of ~6 Extramural sites**
- **Improved data storage, access, and analysis**
- **Training and fellowship programs for rare disease diagnostics**
- **Next steps:**
 - Request for Information (RFI) – Sept. 18, 2012**
 - Investigator Webinar – September 2012**
 - Public Webinar – October 2012**

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GENOMICS in Medicine Lecture Series

First Friday of each month, 8-9 AM

Suburban Hospital Auditorium

November 2: Max Muenke, NHGRI
*Genetics and Genomics of Attention
Deficit Hyperactivity Disorder*

Invited Speakers: November 2012 through February 2013

Max Muenke, NHGRI
Ellen Sidransky, NHGRI
Kenneth Fishbeck, NINDS
William Figg Sr., NCI



JOHNS HOPKINS
M E D I C I N E



National
Human Genome
Research Institute



SUBURBAN HOSPITAL
JOHNS HOPKINS MEDICINE

2012 Summer Workshop in Genomics



- Participants included 28 biology and nursing school faculty and 12 pre-doctoral students
- Lectures given by researchers and staff from across NHGRI

Advancing Pharmacist Education with G2C2



- Built on the November, 2011 meeting
- Commitment to using NHGRI's G2C2 tool
- Commitment to evaluating and revising current competencies for genomics education

Assessing the Economics of Genomic Medicine



INSTITUTE OF MEDICINE
OF THE NATIONAL ACADEMIES

- **July 2012 Meeting**
- **Explored economics of integrating whole-genome sequencing in clinical care**
- **Identified needs include:**
 - Formal methods for valuing ‘personal utility’**
 - Scalable economics evaluation methods for large numbers of variants/genes**
 - More robust outcomes research for modeling economic scenarios**

Genomic Nursing State of Science: Establishing Future Research Directions



- Meeting convened to get input
- Nursing research recommendations posted for comment

NHGRI Digital Media Database

genome.gov
National Human Genome Research Institute
National Institutes of Health

Google™ Search SEARCH

Research Funding Research at NHGRI Health Education Issues in Genetics **Newsroom** Careers & Training About For You

Home > Newsroom > Media Resources > Digital Media Database

Digital Media Database

Google™ Search Digital Media Database Search DMD Search Tips

Welcome to the genome.gov Digital Media Database (DMD). This easily searchable database contains downloadable high-resolution photographs, graphics and video files related to the field of genomic research and the activities of the National Human Genome Research Institute. These public domain images may be freely used, although we suggest you read more about our copyright rules under the [About DMD](#) page.

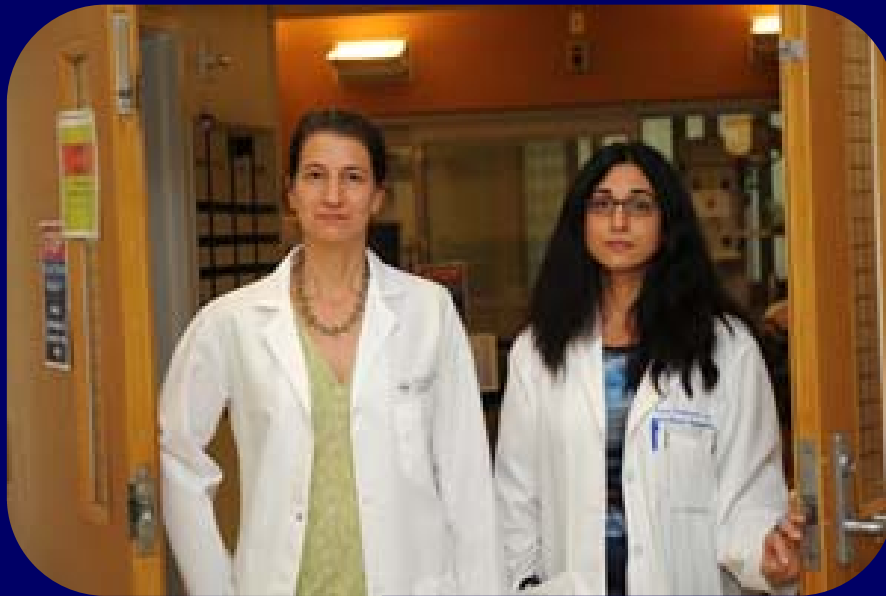
Digital media included in this collection represents more than two decades of research activities by the institute, including photos of the animals sequenced to help understand the human genome to the people and technologies used in genomic research. NHGRI hopes you will find this resource useful.

- People
- Events
- Lab/Technology
- Plants
- Animals
- Microorganisms
- Graphics
- Videos

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Tracking a 'Super Bug' in NIH Clinical Center



Science AAAS.ORG | FEEDBACK | HELP | LIBRARIANS Science Translational Medicine

▶ **Science Translational Medicine** Integrating Medicine and Science

RESEARCH ARTICLE

NOSOCOMIAL INFECTION

Tracking a Hospital Outbreak of Carbapenem-Resistant *Klebsiella pneumoniae* with Whole-Genome Sequencing



NHGRI Intramural Research Highlights



AJHG The American Journal
of Human Genetics

ASHG The American Society of Human Genetics
discover • educate • advocate

**Secondary Variants in Individuals Undergoing Exome Sequencing:
Screening of 572 Individuals Identifies High-Penetrance Mutations
in Cancer-Susceptibility Genes**

Immunity

Volume 36, Issue 6, 29 June 2012, Pages 1003–1016

Article

**Positive and Negative Signaling through SLAM Receptors
Regulate Synapse Organization and Thresholds of Cytolysis**

**Cell
PRESS**



BRAIN

A JOURNAL OF NEUROLOGY

**The neurobiology of glucocerebrosidase-
associated parkinsonism: a positron emission
tomography study of dopamine synthesis and
regional cerebral blood flow**

NIH Undiagnosed Diseases Program (UDP) on 60 Minutes



**Dr. Camilo Toro explains a 'Hard Case' to
CBS correspondent Lara Logan**

Document 40



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Special Thanks!





NATIONAL HUMAN GENOME RESEARCH INSTITUTE



*Advancing human health
through genomics research*