

genome.gov National Human Genome Research Institute

DIRECTOR'S REPORT

National Advisory Council for Human Genome Research

February 2012

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

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Proposed NHGRI Reorganization

Proposed NHGRI Reorganization



Times change and so, too, should institutions. For the National Human Genome Research Institute (NHGRI) at the National Institutes of Health (NIH), a natural time for change has arrived, and the Institute is proposing an internal reorganization to reflect our current and future genomics research portfolio and associated activities more appropriately.

In 1988, NIH created an office that eventually became NHGRI; at the time, the single charge to that office was to oversee NIH's contributions to the <u>Human Genome Project</u>. As such, the office started with a simple organization — a director's office and a team managing grants. Today, NHGRI manages dozens of named scientific projects and a research portfolio that is multifaceted and highly diverse. In aggregate, NHGRI's current

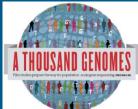
suite of responsibilities requires a more sophisticated management structure.

genome.gov/reorg

NHGRI @ ICHG/ASHG

- ELSI Concurrent Invited Session: "Emerging Ethical Issues in Large-Scale International Genomics Research Collaborations"
- 1000 Genomes Meeting & Tutorial





The 1000 Genomes Project Tutorial ICHG 2011 Montreal, Quebec, Canada October 13, 2011



Cell Commentary on Clinical Genomics





Genomics Reaches the Clinic: From Basic Discoveries to Clinical Impact

Teri A. Manolio¹ and Eric D. Green^{1,*} ¹National Human Genome Research Institute, National Institutes of Health, Bethesda, MD 20892, USA *Correspondence: egreen@nhgri.nih.gov DOI 10.1016/j.cell.2011.09.012

Today, more than ever, basic science research provides significant opportunities to advance our understanding about the genetic basis of human disease. Close interactions among laboratory, computational, and clinical research communities will be crucial to ensure that genomic discoveries advance medical science and, ultimately, improve human health.

Bettie Graham: Beyond Genomics







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NIH's National Center for Advancing Translational Sciences (NCATS)

NIH Launches National Center for

Advancing Translational Sciences

NCATS

National Center for Advancing Translational Sciences

NCATS News Frequently Asked Questions Related Links December 23, 2011

President Barack Obama has signed the Fiscal Year 2012 spending bill enabling the National Institutes of Health to establish the new National Center for Advancing Translational Sciences (NCATS). This action marks a major milestone in efforts to revolutionize the science of translation. NCATS provides our nation with an opportunity to forge a new paradigm for translational research that involves government, academia, industry, philanthropy, and patient advocacy groups. Through partnerships that capitalize upon our respective strengths, I believe we can work together to achieve our common goal: speeding the movement of scientific discoveries from the lab to patients.

Francis S. Collins, M.D., Ph.D. Director, National Institutes of Health





Relocation of Programs from the National Center for Research Resources



NCATS DPCPSI **NIBIB** NIGMS NIMHD NIDDK **NHLBI**

Proposed Merger of Institutes

Request for Information (RFI): Input into the Scientific Strategic Plan for the proposed National Institute of Substance Use and Addiction Disorders

Notice Number: NOT-OD-12-045

Key Dates Release Date: February 8, 2012 Response Date: May 11, 2012

Issued by National Institutes of Health (NIH)

Purpose

This Notice is a time-sensitive Request for Information (RFI) soliciting input into the Scientific Strategic Plan for the proposed new Institute with the working name of the National Institute of Substance Use and Addiction Disorders. This new Institute would result from the proposed reorganization of substance use, abuse, and addiction-related research at the NIH.





Target Validation Workshop



Joint NIH-Industry Target Validation Workshop

National Institutes of Health Building 31, C Wing, Conference Room 10 November 3–4, 2011



Executive Summary



NIH Plots Target Validation Initiative with Industry, Academia

October 20, 2011

NIH Plots Target Validation Initiative with Industry, Academia

By a GenomeWeb staff reporter

NEW YORK (GenomeWeb News) – The National Institutes of Health is planning to work with industry, government, and academia to create a collaborative precompetitive consortium focused on validating potential therapeutic targets using genomics, bioinformatics, and functional validation, according to NIH.

To kick off the initiative, NIH will hold a joint workshop on Nov. 3 and 4 with multiple partners from these sectors to explore the potential opportunities and challenges facing this type of initiative. The larger aim of the project is to develop faster and more accurate ways to realize the potential of translating new discoveries, identify promising targets, and predict which targets will be "biologically relevant and tractable," according to NIH.

Appropriations Update



Fiscal Year 2012 Appropriations Update



	Fiscal Year 2011	Fiscal Year 2012 President	Fiscal Year 2012 House	Fiscal Year 2012 Senate	Fiscal Year 2012 Enacted
NIH	\$30.7B	\$31.7B	\$31.7B	\$30.5B	\$30. B
NHGRI	\$511M	\$525M	\$525M	\$506M	\$513M (0.27%)

Fiscal Year 2013 Appropriations Update

Panel Fails to Reach Deal on Plan for Deficit Reduction



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Senator Rob Portman of Ohio, a Republican member of the deficit committee, speaking with reporters on Monday after panel members met on Capitol Hill.

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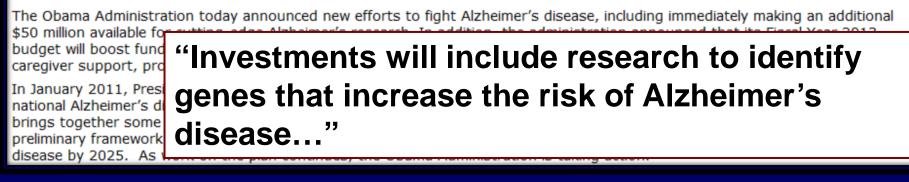


Alzheimer's Research Initiative

News Release

FOR IMMEDIATE RELEASE February 7, 2012 Contact: HHS Press Office (202) 690-6343

We can't wait: Administration announces new steps to fight Alzheimer's disease



The Washington Post

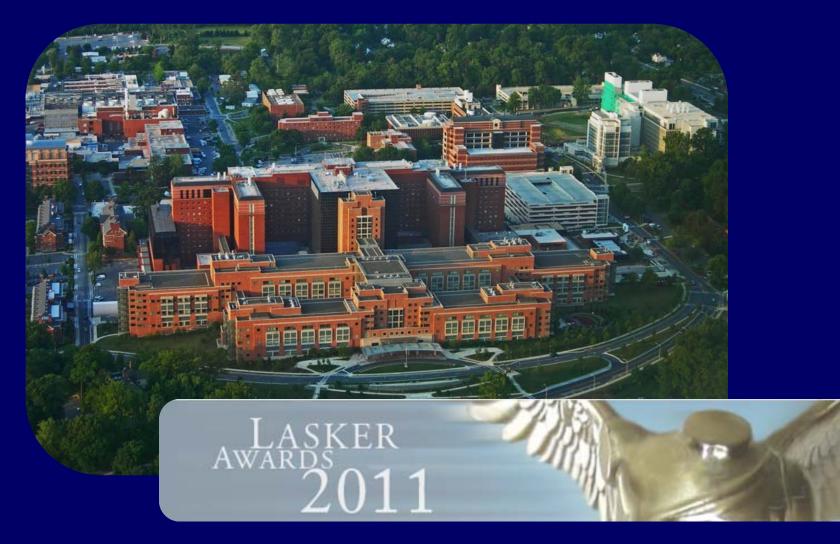
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Obama administration proposes raise for Alzheimer's research, some now and some next year

some next year

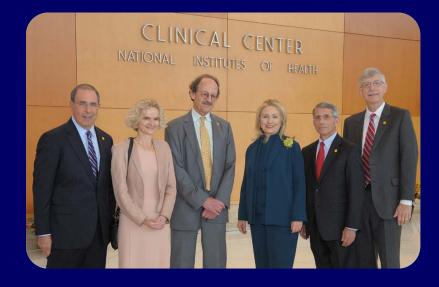
tor Alzheimer's research, some now and

NIH Clinical Center Receives Lasker-Bloomberg Public Service Award



Secretary of State Hillary Clinton Visits NIH





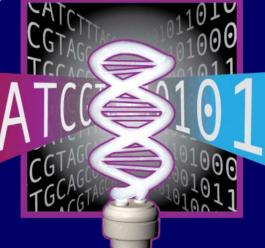


Advisory Committee to the NIH Director Working Group on Data and Informatics

 Working group to investigate the management, integration, and analysis of large biomedical datasets

 Called the NIH Data and Informatics Working Group

 Co-chaired by David DeMets and Larry Tabak



Request for Information: NIH Data and Informatics Working Group

- Scope of the issues
- Standards development
- Secondary use of data
- Data accessibility
- Incentives for data sharing
- Support needs



Submit comments by March 12, 2012

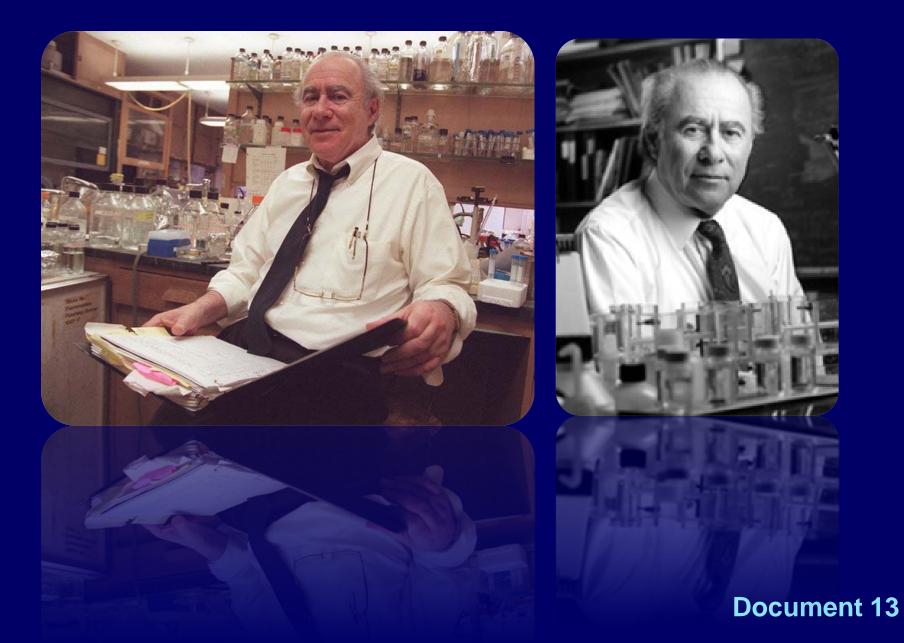
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Mourning the Loss of James Crow



Mourning the Loss of Norton Zinder



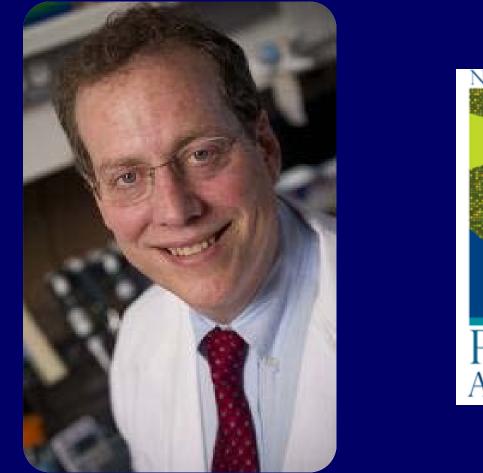
2011 ASHG Curt Stern Award





David Altshuler, M.D., Ph.D.

2011 NIH Director's Pioneer Award





Andrew Feinberg, M.D., M.P.H.

Best Graduate Student Presenter for Genetics at SACNAS National Conference



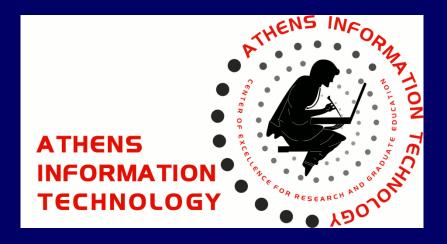


Devoted to Advancing Hispanics, Chicanos & Native Americans in Science

Keolu Fox, Ph.D.

2011 "Niki" Award Recipient





Manolis Kellis, Ph.D.

National Academy of Science Public Welfare Medal Recipient



Harold Shapiro, Ph.D.

Newly Elected ASHG Leadership



President Elect: Jeff Murray



Treasurer: Geoff Duyk

Board of Directors:



Vivian Cheung



Evan Eichler



Richard Gibbs

Elected to the Institute of Medicine 2011

- Martin Blaser
- Vivian Cheung
- Claire Fraser-Liggett
- Richard Gibbs
- David Relman



Elected to AAAS

- Andrew Feinberg
- Edward Marcotte
- Richard McCombie



Richard Myers

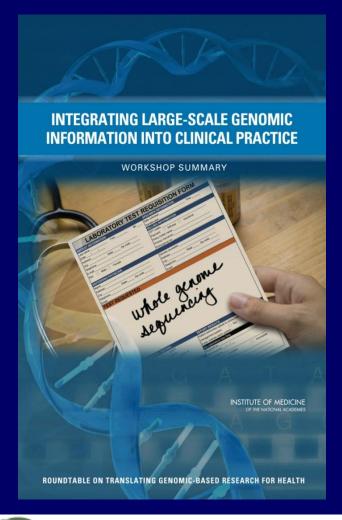
USPTO Study on Genetic Diagnostic Testing



Presidential Commission for the Study of Bioethical Issues Meeting: Whole-Genome Sequencing



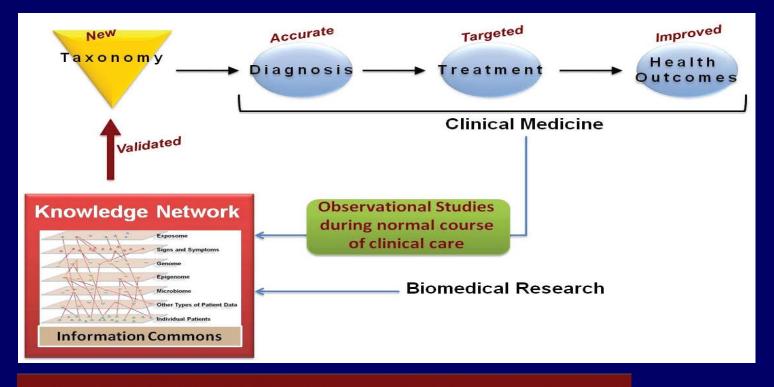
Institute of Medicine Report





National Academies Report

"Toward Precision Medicine: Building a Knowledge Network for Biomedical Research and a New Taxonomy of Disease"





Battelle Report on Genomic Clinical Testing Industry

The Economic and Functional Impacts of Genetic and Genomic Clinical Laboratory Testing in the United States

American College of Medical Genetics Changes Name to American College of Medical Genetics and Genomics



American College of Medical Genetics and Genomics Medical Genetics: Translating Genes Into Health®

Effective March 2012 at the ACMG Annual Clinical Genetics Meeting

NHGRI Genome Advance of the Month

Trauma regulates genes that predict survival

Septemb

By Jonat Science

October

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Science

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Dissecting the cause of the Black Death

Massively parallel sequencing:

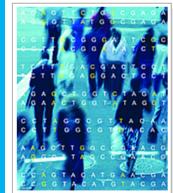
Taking an all-at-once approach to genetic testing in cancer

Comments 🖶



By Jor Population genomics: Answering questions from the microscopic to the geographic Sciend

Jonathan Max Gitlin Science Policy Analyst



The final Genome Advance of the Month for 2011 is actually a twofer, highlighting how population genomics can be used to answer questions in the diverse fields of vascular biology and anthropology. First up, from a multinational team of researchers lead by Dr. Christian Gieger in Germany, and Professor Willem Ouwehand and Dr. Nicole Soranzo in the United Kingdom, is a paper published in the journal *Nature*. The study takes advantage of genome-wide association study (GWAS) data previously collected in the course of other studies to uncover new genetic pathways that regulate how our bodies make platelets (the second most common blood cell after red blood cells).

Dr. Gieger and his colleagues began by using data gathered in 23 studies (from 48,666 participants of European descent) that had looked for genomic associations related to the number of platelets found in a patient's blood (their platelet count). They also looked at a

smaller subset of studies (13 cohorts, 18,600 participants) that included mean platelet volume as well as platelet count. This Casadei approach identified 68 areas (loci) of the human genome that were associated with platelet size and number, of which 52 had not previously been linked.

The team followed up this meta-analysis by examining the functions of these genomic loci in fruit flies and zebrafish, two model organisms widely used in genomics. This revealed a number of genes already known to be involved in blood cell regulation and formation, as well as 11 novel genes. Mutations in some of these genes had previously been implicated in Mendelian (rare) diseases and human cancers.







First Australian Aboriginal Genome Sequenced



Genome Of World's Oldest Woman Sequenced







Elaine Mardis, Ph.D.



"High-Tech Choir Master"







Eric Lander, Ph.D.

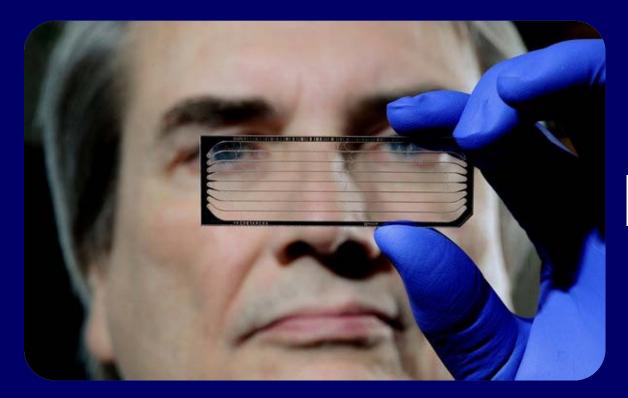
Che New York Eimes

"Power in Numbers"





"DNA Sequencing Caught in Deluge of Data"



The New York Times

Dick McCombie, Ph.D.



ENCODE

Genomics In The News...

NEWS IN FOCUS

NEWS IN FOCUS PROSPECTS International weekly journal of science New year, new science

Nature looks ahead to the key findings and events that may emerge in 2012.

LET'S TALK ABOUT EARTH

In June, scientists, politicians and campaigners of all stripes will flock to Rio de Janeiro, Brazil, for the United Nations' fourth Earth summit, devoted to sustainable development and the green economy. The conference - undoubtedly the major environmental meeting of 2012 — comes 20 years after the UN Framework Convention on Climate Change was signed at the first UN Earth summit, also in Rio.

THE SOURCE OF MARTIAN METHANE

NASA's car-sized rover, Curiosity, is set to arrive on Mars in August. The US\$2.5-billion craft will be lowered by an innovative

landing system — the 'sky crane' — into Gale crater, where it will study rock strata in a bid to unpick the red planets watery past. It will also sniff for methane in Mars's atmosphere, and could reveal whether the gas is being produced by geological processes - or by microbial martian life. Farther afield, NASA's Kepler mission surely ought to find a true extrasolar twin for Earth, with just the right size and orbit around a Sunlike star to be habitable.

ROBOTS, BRAINS OR GRAPHENE?

Six visionary research proposals will vie for huge grants from the European Commission's Future and Emerging Technologies Flagship scheme. The two winning projects, to be announced

in the latter half of the year, will each receive €1 billion (US\$1.3 billion) over the next decade. In the running are projects on graphene,

hypothesized to be massless, chargeless entities able to serve as their own antiparticles, which could be useful for forming stable bits in quantum computing. Experiments have suggested that in materials known as topological insulators, the collective motions of electrons create a quasiparticle that behaves like a Majorana.

DNA ENCYCLOPEDIA

Biologists know that much of what was once termed 'junk' DNA actually has a role. But which sequences are functional - and what do they do? The best answer so far will come with a major update from the US National Institutes



Will ICub and his robot friends win a €1-billion grant this year?

of Health's ENCODE (Encyclopedia of DNA Elements) project, which aims to identify all the functional elements in the human genome. patent protection, including the anticlotting Plavix (clopidogrel) and the antipsychotic Seroquel (quetiapine).

RAIDERS OF THE LOST LAKE

Within weeks, Russian researchers hope to finish drilling through Antarctica's ice sheet to reach Lake Vostok, a huge freshwater lake roughly 3,750 metres beneath the surface. It's a race against time: 10-50 metres of ice separate the team from its goal, which it must reach before the last aircraft of the season leaves in February. There'll be more drilling research in April, when Japan's Chikyu ship sets sail

to bore into the underwater fault that caused the magnitude-9.0 Tohoku # earthquake last year.

THE BIGGEST ARRAY

South Africa and Australia will find out by March which of them might host the \$2.1-billion Square Kilometre Array (SKA), which would be the world's largest radio telescope if it is built. The decision will be made by the SKA's programme development office in Man-

chester, UK. Meanwhile, the Atacama Large Millimeter/ STATES. Submillimeter Array in Chile's Atacama Desert should be 60% complete by the end of the year.

SPACEFLIGHT ADVANCES

In February, SpaceX of Hawthorne, California, hopes to be the first commercial firm to fly an unmanned cargo craft to the Interna-









U.S. NEWS | JANUARY 10, 2012 Soon, \$1,000 Will Map Your Genes



THE WALL STREET JOURNAL.

The goal, triggered in part by an initiative launched by the U.S. government's National Human Genome Research Institute in 2004, already has resulted in a

dramatic cost reduction in sequencing all three billion units of DNA, known as basepairs, that make up the human genetic code.





UC Davis police chief on leave after pepper spraying

UC Davis said early Monday in a news release that it was necessary to place police Chief Annette Spicuzza on administrative leave to restore trust and calm tensions.

By Jason Dearen, Associated Press / November 21, 2011



"Free speech is part of the DNA of this university, and non-violent protest has long been central to our history," UC President Mark G. Yudof said in a statement Sunday in response to the spraying of students sitting passively at UC Davis. "It is a value we must protect with vigilance."

What's in your car's DNA?

Our exclusive **Diagnostic Needs Analysis** can provide you the necessary information to prevent future problems down the road.

A quick analysis today can save costly repairs tomorrow. We'll diagnose the condition of your vital fluids and other components

motor oil

- belts and hoses
- transmission fluid
- brake fluid
- battery
 fuel system

- coolant
- and more!

I. General NHGRI Updates

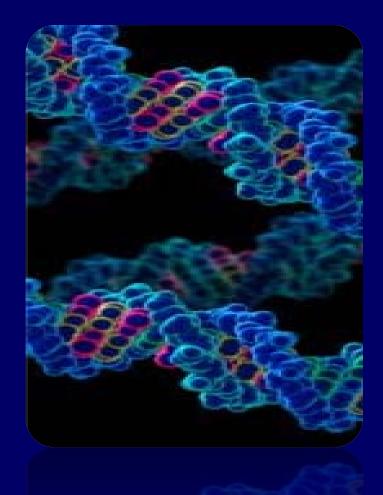
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Large-Scale Genome Sequencing Centers

 Baylor College of Medicine PI: Richard Gibbs \$21.3M in Year 1

Broad Institute
 PI: Eric Lander
 \$35.9M in Year 1

 Washington University PI: Richard Wilson \$28.4M in Year 1



Mendelian Disorders Genome Centers

 University of Washington (Coordination Center) Pls: Deborah Nickerson, Michael Bamshad, Mark Rieder, & Jay Shendure \$5.2M per year
 Yale University

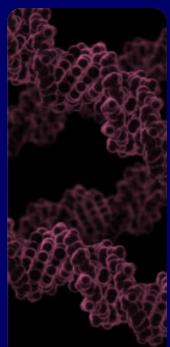
> Pls: Richard Lifton, Murat Gunel, Shrikant Mane, & Mark Gerstein

\$2.8M per year

 Baylor College of Medicine & Johns Hopkins University

> Pls: David Valle (Hopkins) & James Lupski (Baylor)

\$4M per year



Clinical Sequencing Exploratory Research Projects

Baylor College of Medicine

Pls: Sharon Plon & Will Parsons, \$1.8M per year (with NCI)

Brigham and Women's Hospital

PI: Robert Green, \$2.4M per year

- Children's Hosp. of Philadelphia
 Pls: Ian Krantz & Nancy B. Spinner, \$2.2M per year
- University of North Carolina
 PI: James Evans, \$1.6M per year
- University of Washington

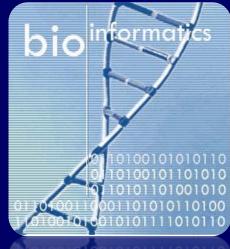
PI: Gail Jarvik, \$2.3M per year (with NCI)

Dana Farber Cancer Institute
 PIs: Levi Garraway & Pasi Janne, \$1.6M per year



Informatics Tools for High-Throughput Sequence Data Analysis Awards

- Broad Institute (\$1.0M in Year 1)
 PI: Mark DePristo
- Boston College & U. Michigan (\$1.0M in Year 1)
 Pls: Gabor Marth & Goncolo Abecasis
- Washington University (\$805K in Year 1)
 Pls: Li Ding & David Dooling
- Harvard (\$448K in Year 1)
 PI: Steven McCarroll
- Scripps Institute (\$382K in Year 1) PI: Ali Torkamani



University of Southern California (\$345K in Year 1)
 PIs: Ting Chen, Ewa Deelman, & James Knowles

Genome Sequencing Program: Comparative Genomics

A high-resolution map of human evolutionary constraint using 29 mammals

Kerstin Lindblad-Toh^{1,2}, Manuel Garber¹*, Or Zuk¹*, Michael F. Lin^{1,3}*, Brian J. Parker⁴*, Stefan Washietl³*, Pouya Kheradpour^{1,3}*, Jason Ernst^{1,3}*, Gregory Jordan⁵*, Evan Mauceli¹*, Lucas D. Ward^{1,3}*, Craig B. Lowe^{6,7,8}*, Alisha K. Holloway⁹*, Michele Clamp^{1,10}*, Sante Gnerre¹*, Jessica Alföldi¹, Kathryn Beal⁵, Jean Chang¹, Hiram Clawson⁶, James Cuff¹, Federica Di Palma¹, Stephen Fitzgerald⁵, Paul Flicek⁵, Mitchell Guttman¹, Melissa J. Hubisz¹², David B. Jaffe¹, Irwin Jungreis³, W. James Kent⁹, Dennis Kostka⁹, Marcia Lara¹, Andre L. Martins¹², Tim Massingham⁵, Ida Moltke⁴, Brian J. Raney⁶, Matthew D. Rasmussen³, Jim Robinson¹, Alexander Stark¹³, Albert J. Vilella⁵, Jiayu Wen⁴, Xiaohui Xie¹, Michael C. Zody¹, Broad Institute Sequencing Platform and Whole Genome Assembly Team[†], Kim C. Worley¹⁴, Christie L. Kovar¹⁴, Donna M. Muzny¹⁴, Richard A. Gibbs¹⁴, Baylor College of Medicine Human Genome Sequencing Center Sequencing Team[†], Wesley C. Warren¹⁵, Elaine R. Mardis¹⁵, George M. Weinstock^{14,15}, Richard K. Wilson¹⁵, Genome Institute at Washington University[†], Ewan Birney⁵, Elliott H. Margulies¹⁶, Javier Herrero⁵, Fric S. Lander¹ & Manolis Kellis^{1,3}

Nature (2011)





1st TCGA Scientific Symposium November 17 & 18, National Harbor

- 2-day symposium describing analyses of TCGA data
- Open to all
- 470 Attendees, representing 13 countries
- Co-chairs Lynda Chin (MD Anderson) & Elaine Mardis (WashU Genome Institute)
- 30 Talks (available on YouTube / Genome TV)
- 8 Hands-on sessions
- 159 Posters

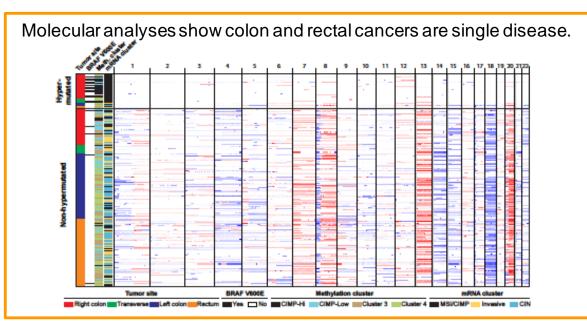
2nd Annual TCGA Symposium being planned for November 2012; American Asso. For Cancer Research (AACR) to co-sponsor





TCGA: by the numbers

- TCGA achieves goal of 5,000 specimens analyzed by end of 2011.
- 22 tumor projects underway
- Many cancers of greatest incidence nearing completion
 - Published: Glioblastoma, Ovarian
 - Submitted: Colorectal (see figure)
 - Expected 2012 publications: Breast, AML, Lung, Kidney



Glioblastoma □Ovarian Acute Myeloid Leukemia DColorectal Carcinoma □Breast Lung Squamous Cell Lung Adenocarcinoma □Renal Clear Cell Carcin. Renal papillary □Uterine (endometrial) Low grade glioma Gastric Carcinoma □Prostate □Bladder Cervical □Head and neck □Liver □Melanoma □Sarcoma Thyroid Lymphoma Pancreas

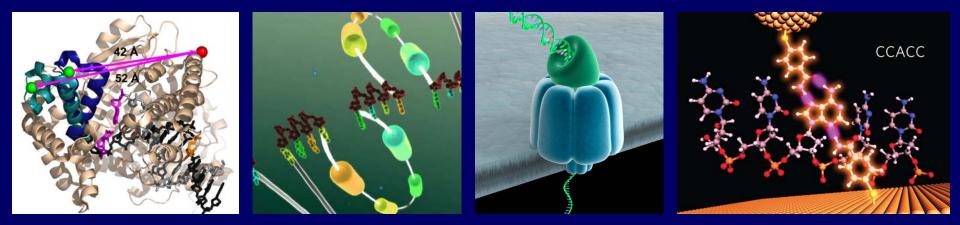
1000 Genomes

A Deep Catalog of Human Genetic Variation



- The Phase 1 paper is being written on 1094 samples from 14 populations, with 40 million SNP, indel, and deletion variants on integrated haplotypes
- The Phase 2 data set contains low-coverage and exome sequencing data on 1600 unrelated samples from 19 populations
- The Phase 3 sample collection from 7 more populations should be completed by April; all the sequencing should be completed by fall 2012, on 2500 unrelated individuals plus 161 trio kids
- Complete Genomics will deeply sequence 500 samples, including 161 trios

DNA Sequencing Technology Development



 Annual grantee meeting Grantees only: April 9-11 Public: April 11-12

 Presentation by Jeff Schloss later in Open Session



ENCODE & modENCODE



 Technology development RFA applications to be discussed in Closed Session

 Applications for the next production phase of ENCODE have been received and will be discussed at May 2012 Council meeting

modENCODE Symposium: June 20-21, 2012







 ENCODE analysis session at December GENEVA Steering Committee meeting launched new collaborations

- Integrated analysis papers:
 - ENCODE integrated manuscript under revision along with many companion papers
 - modENCODE comparison of fly, worm, and human
 - Mouse comparison of mouse and human

Return of Results Consortium

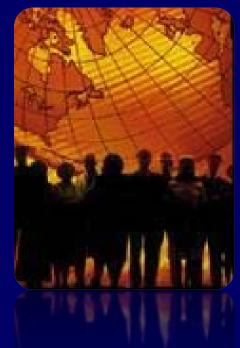
Components:

ELSI Return of Results RFAs (R01 and R21) ELSI investigators in the Clinical Sequencing Exploratory Research Projects (U01)

Related investigator-initiated projects

 Goal: Identify areas of possible consensus that can form basis for policy development

 Plans for sharing outcome measures and instruments underway



Centers of Excellence in Genomic Science (CEGS) & Diversity Action Plan (DAP)



 CEGS applications to be discussed in the Closed Session of this Council meeting

 Next receipt dates: CEGS: May 17, 2012 DAP: May 25, 2012

Characterizing and Displaying Genetic Variants for Clinical Action Workshop

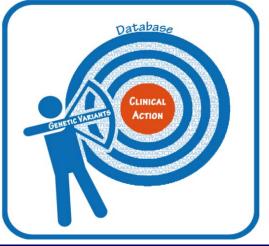
 Goal: Consider processes, databases, and other resources needed to:

Identify clinically relevant variants

Decide whether they are actionable and what the action should be

Provide for clinical use

- Video, presentations, and recommendations posted on genome.gov
- Concept Clearance presentation later today



Genomic Medicine II Meeting

- Second in series of four planned genomic medicine meetings
- Goals:



Develop ideas for multicenter collaborative pilot projects in genomic medicine
Learn of new projects ongoing at partner sites
Identify infrastructure needs and solutions to speed adoption of genomic medicine

- Video, presentations, and recommendations posted on genome.gov
- Concept Clearance presentation later today

I. General NHGRI Updates

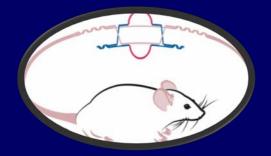
- II. General NIH Updates
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- VII. NHGRI Intramural Program

Molecular Libraries Program (MLP)

- MLP Screening & Chemistry Centers' midyear reports showed good progress toward milestones
- MLP Steering Committee meeting: Presentations on center-driven research projects
 Begin development of Molecular Libraries Biological Database



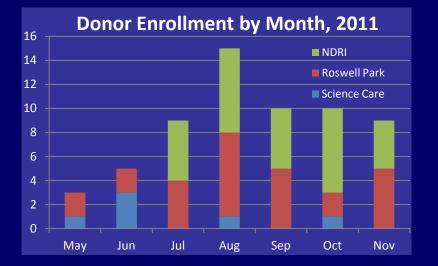
Knockout Mouse Projects



- KOMP Finale, KOMP2 Kickoff, and IMPC Launch Meeting: September 2011
- KOMP2 Awards for Knockout Mouse Production and Knockout Mouse Phenotyping
 - Baylor College of Medicine: Justice/Justice
 - The Jackson Laboratory: Donahue/Braun
 - UC Davis: Lloyd/Lloyd
- KOMP2 Award for Data Coordination Center and Database
 - European Bioinformatics Institute: Flicek

Genotype-Tissue Expression (GTEx)

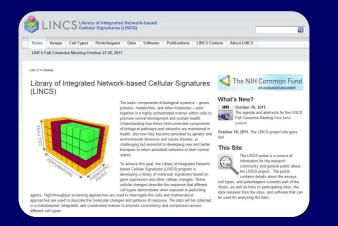
December 2011 meeting: Pilot roughly half completed



Enrolling 10 post-mortem donors/month (on target); RNA integrity very good

Proposal for scale up being developed

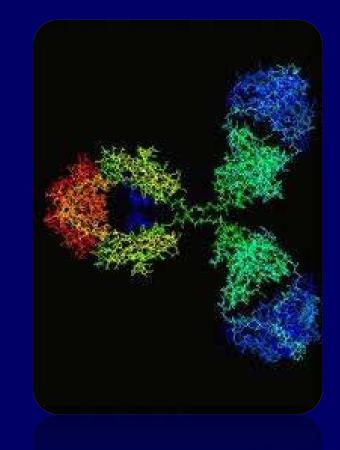
Library of Integrated Network-based Cellular Signatures (LINCS)



- Consortium meeting in October 2011
- LINCS program public web site now live
- Bridge funding proposal for Fiscal Year 2013
- Data release policy under development

Protein Capture Reagents Program

 Protein Capture Consortium meeting in December
 Working groups formed
 Development of public portal



 External Scientific Panel established for the program

Human Heredity and Health in Africa (H3Africa)

 Applications for four RFAs (centers, research projects, biorepositories, and bioinformatics network) received in December; excellent response

- Review of applications: March → May
- Biorepository RFA re-issued

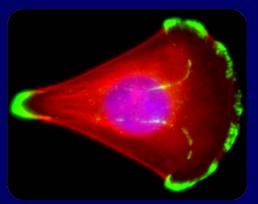
3

- Wellcome Trust application process proceeding well and on similar timeline
- Ethics and Genomics Research in Africa (EAGER-Africa) Meeting in November 2011

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Single Cell Analysis RFAs Issued



- Studies to Evaluate Cellular Heterogeneity using Transcriptional Profiling of Single Cells (U01)
- Exceptionally Innovative Tools and Technologies for Single Cell Analysis (R21)
- Accelerating the Integration and Translation of Technologies to Characterize Biological Processes at the Single Cell Level (R01)
- Applications were due in January

New Common Fund Initiative? 'Disruptive Proteomics Technologies'

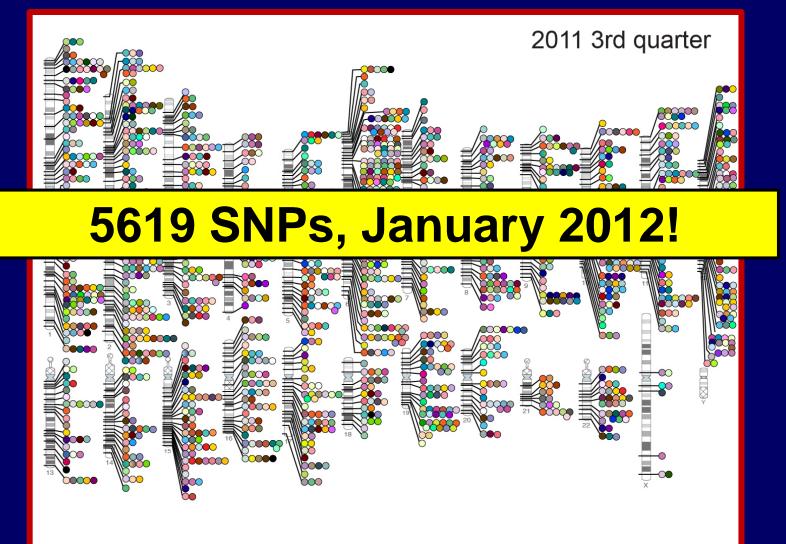
- Chosen for potential new Common Fund program starting in Fiscal Year 2013
 NIGMS and NHGRI as co-leads
- Strategic planning underway



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NHGRI Catalog of Published Genome-Wide Association Studies (GWAS)



GWAS Catalog: New Features

	S NCBI Resources	⊻ How To ♥	
	Gene	Gene	
		Limits Advanced	
	<u>Display Settings:</u> ⊙ Fu	Il Report Send to:	
First Autho	APOA5 apolipopro	tein A-V [Homo sapiens]	Risk Allele
Journal,	Gene ID: 116519, update		Frequency
			in Controls
	Summary		
	,		
Tan A	Official Symbol	APOA5 provided by <u>HGNC</u>	NR
December 30,	Official Full Name	apolipoprotein A-V provided by <u>HGNC</u>	
Hum Mol Gene	Primary source	HGNC:17288	NR
A genome-wid	Locus tag	UNQ411/PR0773	NR
association an	See related	Ensembl:ENSG00000110243; <u>HPRD:06966;</u> <u>MIM:606368;</u> <u>Vega:OTTHUMG00000046116</u>	
gene-environm	Gene type	protein coding	
interaction stu	RefSeq status	REVIEWED	
triglycerides le	Organism	<u>Homo sapiens</u> Eulermate: Materica: Chardete: Craniste: Vertebrate: Euteleasterii: Maranalia: Eutheria:	
healthy Chines	Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo	
population.	Also known as	RAP3; APOAV	
	Summary	The protein encoded by this gene is an apolipoprotein that plays an important role in regulating	
	,	the plasma triglyceride levels, a major risk factor for coronary artery disease. It is a component	
		of high density lipoprotein and is highly similar to a rat protein that is upregulated in response	
		to liver injury. Mutations in this gene have been associated with hypertriglyceridemia and	

healt popu

NEJM Genomic Medicine Series

Genomics, Health Care, and Society

Kathy L. Hudson, Ph.D.

Genomics and the Multifactorial Nature of Human Autoimmune Disease

Judy H. Cho, M.D., and Peter K. Gregersen, M.D.

Genomics of Cardiovascular Disease

Christopher J. O'Donnell, M.D., and Elizabeth G. Nabel, M.D.

ARDIOVASCULAR DISEASE IS THE LEADING CAUSE OF DEATH IN THE UNITED States. Considerable progress has been made in the past 50 years to define,

Genomics and Perinatal Care

Joann Bodurtha, M.D., M.P.H., and Jerome F. Strauss, III, M.D., Ph.D.

MONG BOTH PROSPECTIVE PARENTS AND PROVIDERS OF MEDICAL CARE, genetic and social concerns peak during the perinatal period. Advances in genomics and assisted reproductive technology have created new opportunities to detect genetic disorders and susceptibilities at multiple times during perinatal care and thus are relevant to these concerns. Emerging therapies for single-gene disorders may reshape these discussions.

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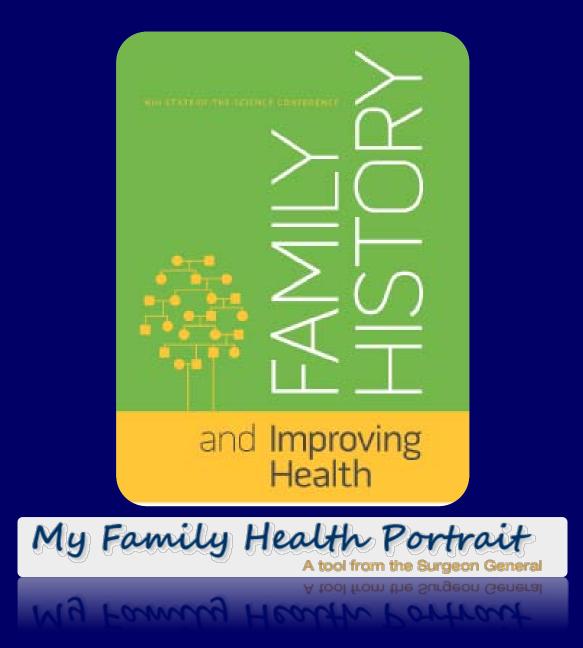
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U.S. Science and Engineering Festival



My Family Health Portrait



Genomic Medicine Lecture Series

Monthly seminars being held at Suburban Hospital in Bethesda



David Valle, M.D.



Larry Brody, Ph.D.

Genomic Opportunities for Studying Sickle Cell Disease Meeting: December 2011



Co-Chairs: Michael DeBaun, Richard Gibbs, and Julie Makani

Pharmacist Education Meeting



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Blue Ribbon Panel Review of NHGRI Intramural Research Program

- David Page, M.D. (Chair)
- Rick Myers, Ph.D. (NACHGR)
- Bruce Korf, M.D., Ph.D. (BSC)
- Wylie Burke, M.D., Ph.D
- Nancy Cox, Ph.D
- Bob Waterston, M.D., Ph.D
- Huda Zoghbi, M.D.

NHGRI Intramural Research Highlights



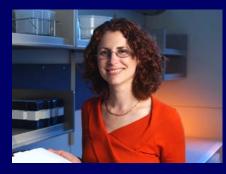
The NEW ENGLAND JOURNAL of MEDICINE

ORIGINAL ARTICLE

Cold Urticaria, Immunodeficiency, and Autoimmunity Related to *PLCG2* Deletions

Michael J. Ombrello, M.D., Elaine F. Remmers, Ph.D., Guangping Sun, M.D.,

Daniel L. Kastner, M.D., Ph.D., Matilda Katan, Ph.D., Hal M. Hoffman, M.D., and Joshua D. Milner, M.D.





NATURE GENETICS | LETTER

Exon capture analysis of G protein-coupled receptors identifies activating mutations in *GRM3* in melanoma Todd D Prickett, Xiaomu Wei, Isabel Cardenas-Navia, Jamie K Teer, Jimmy C Lin, Vijay Walia, Jared Gartner, Jiji Jiang, Praveen F Cherukuri, Alfredo Molinolo, Michael A Davies, Jeffrey E Gershenwald, Katherine Stemke-Hale, Steven A Rosenberg, Elliott H Margulies & Yardena Samuels



AJHG

Available online 2 February 2012

The Phenotype of a Germline Mutation in *PIGA*: The Gene Somatically Mutated in Paroxysmal Nocturnal Hemoglobinuria

Jennifer J. Johnston¹, Andrea L. Gropman², Julie C. Sapp¹, Jamie K. Teer¹, Jodie M. Martin², Cyndi F. Liu³, Xuan Yuan³, Zhaohui Ye³, Linzhao Cheng³, Robert A. Brodsky³, Leslie G. Biesecker^{1,4}, 🏜 🎬

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Ce

William Gahl Honored with Prestigious Service to America Medal









genome.gov National Human Genome Research Institute



Special Thanks!

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