

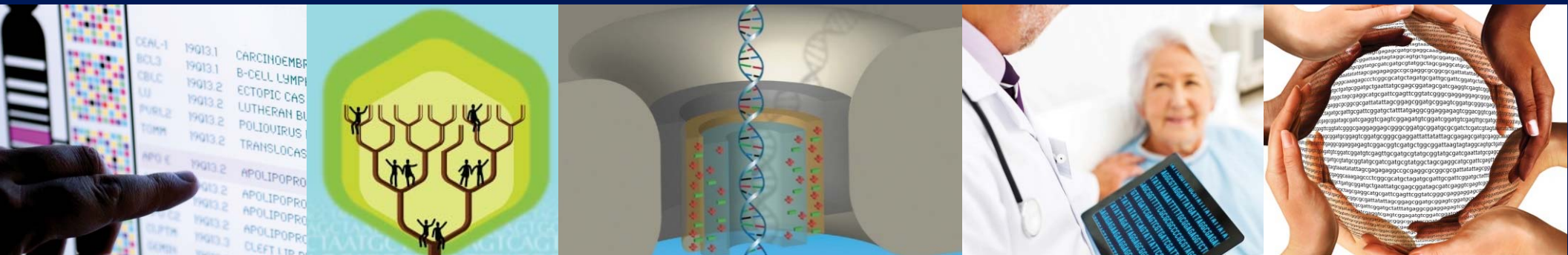


—
The **Forefront**
of **Genomics**
—

DIRECTOR'S REPORT

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

May 2018



Director's Report-Related Documents: May 2018

Director's Report



Director's Report



No.	Relevant Documents
1	Establishing a '2020 Vision for Genomics' Establishing a '2020 Vision for Genomics' Website News and Events Calendar Illumina Genomics Podcast
2	James Battey Departs as Director, National Institute on Deafness and Other Communication Disorders
3	Richard Nakamura Departs as Director, NIH Center for Scientific Review
4	Active Recruitment: NIH Chief Data Strategist and Director, Office of Data Science Strategy
5	New Director, U.S. Centers for Disease Control and Prevention

genome.gov/DirectorsReport

Document #



Open Session Presentations

- **NIH's Strategic Plan for Data Science**

Jon Lorsch

- **Concept Clearance: Center for ELSI Resources & Analysis**

Nicole Lockhart

- **Concept Clearance: Genomic Innovator Award**

Lisa Brooks

Open Session Presentations

- **Report on the NHGRI Intramural Research Program**
Dan Kastner
- **Report: Update on the NHGRI Genome Sequencing Program**
Adam Felsenfeld
Chris Wellington
- **Report: Update on the Undiagnosed Diseases Network**
Anastasia Wise

Director's Report Outline

- I. General NHGRI Updates
- II. General NIH Updates
- III. General Genomics Updates
- IV. NHGRI Extramural Research Program
- V. NIH Common Fund/Trans-NIH
- VI. NHGRI Division of Policy, Communications, and Education
- VII. NHGRI Intramural Research Program

Director's Report Outline

- I. General NHGRI Updates**
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Establishing a '2020 Vision for Genomics'



- 'Virtual' Town Hall – May 4, 2018
- Upcoming In-Person Town Halls
 - Seattle, WA – June 19, 2018
 - Palo Alto, CA – July 17, 2018
- News and Events Calendar
- Illumina Genomics Podcast

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James Battey Departs as Director, National Institute on Deafness and Other Communication Disorders



**James Battey,
M.D., Ph.D.**



**Judith Cooper,
Ph.D.**

Richard Nakamura Departs as Director, NIH Center for Scientific Review



**Richard Nakamura,
Ph.D.**



**Noni Byrnes,
Ph.D.**

Active Recruitment: NIH Chief Data Strategist and Director, Office of Data Science Strategy

U.S. Department of Health & Human Services

NIH National Institutes of Health
Turning Discovery Into Health

Search

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NIH Home > Jobs @ NIH > Executive Jobs

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- Scientific Fellowships/Trainees
- Veteran Employment
- Jobseekers with Disabilities
- Diversity at NIH
- Life at NIH

Vacancy Announcement

CHIEF DATA STRATEGIST AND DIRECTOR, OFFICE OF DATA SCIENCE STRATEGY

NIH Director

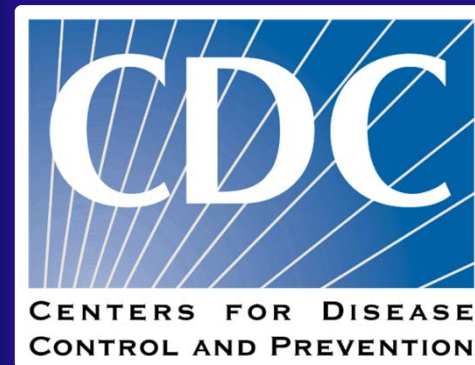
Position

The National Institutes of Health (NIH) is seeking exceptional executive candidates for the newly established position of Chief Data Strategist (CDS). The CDS will report directly to the NIH Director; s/he will serve as the principal advisor to the NIH Director and other NIH leadership in the broad domain of the large-scale platforms and technology/tools ecosystems that facilitate data science. The CDS will also serve as the Director of the newly formed Office of Data Science Strategy in the Division of Program Coordination, Planning, and Strategic Initiatives, Office of the Director (DPCPSI), NIH. In complementing existing NIH expertise and investments in computational biology, bioinformatics, biostatistics, information science, medical informatics, and quantitative biology, the CDS will: 1) provide leadership for a broad range of initiatives and projects that align with NIH's strategic plans; 2) catalyze the use of new platforms and methods to gain deeper insights from NIH's vast data resources; and 3) help mature competencies and capabilities of the biomedical research workforce—amongst NIH as well as our greater research ecosystem—to capitalize on new large-scale biomedical data and analytic tools.

New Director, U.S. Centers for Disease Control and Prevention



Robert Redfield, M.D.



Proposed Common Rule Implementation Delayed

The Common Rule, Updated

Jerry Menikoff, M.D., J.D., Julie Kaneshiro, M.A., and Ivor Pritchard, Ph.D.

DELATED

For the first time since it was issued in 1991, the Common Rule — the set of federal regulations for ethical conduct of human-subjects research — has been updated. Most of the requirements, many of which increase flexibility, will go into effect in 2018, which gives institutions a year to work toward implementation.

The public saw the beginnings of this effort in 2011, when the Department of Health

submitted, from a fairly wide swath of the public, including individuals, institutions, organizations, and societies. The comments, and influential reports including one from the National Academies of Sciences, Engineering, and Medicine,³ led to a long process of deliberation and discussion. The result is a final rule that differs significantly from what was initially proposed.

Most notably, the new rule does not adopt the proposal to

that implementing this proposal could significantly harm the ability to do important research, without producing any substantial off-setting benefits. The public response was particularly noteworthy, given that the premise behind the proposal was specifically tied to public sentiment: the NPRM had stated that continuing to allow research on unidentified biospecimens without consent would place “the publicly-funded research establishment in

- Proposes to delay Common Rule implementation to January 2019
- Asks for feedback about complying with burden-reducing provisions beginning in July 2018
- Open for comments until May 21, 2018

Proposed Bill: Advancing Access to Precision Medicine Act

115TH CONGRESS
2D SESSION

H. R. 5062

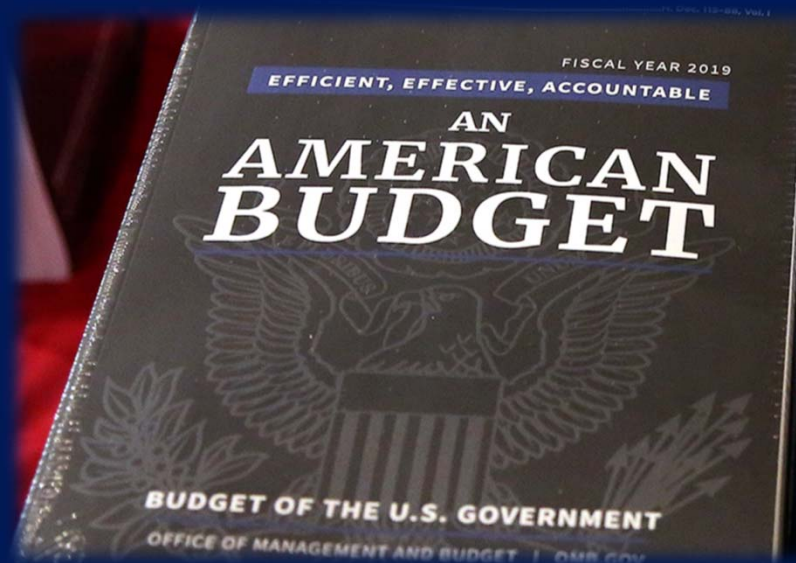
To provide for a study by the National Academy of Medicine on the use of genetic and genomic testing to improve health care, and for other purposes.

- H.R. 5062 introduced by Rep. Eric Swalwell (D-CA) in February
- Would charge the National Academy of Medicine to conduct a study on using genomics in medicine
- Would amend Medicaid to allow states to offer whole-genome sequencing for children with undiagnosed diseases

Fiscal Year 2018 Appropriations

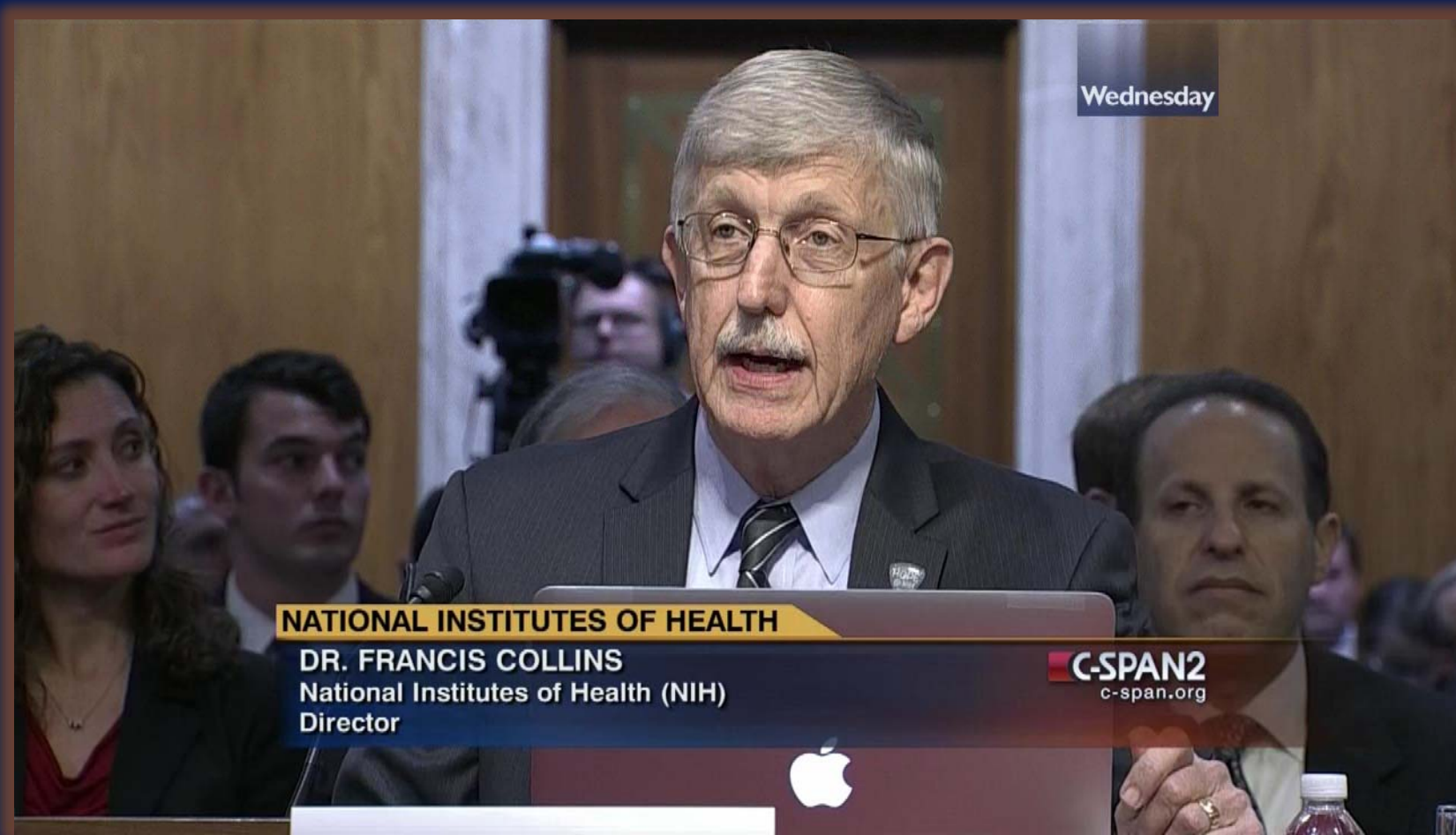
	Fiscal Year 2017 Budget	Fiscal Year 2018 Budget	Percent Increase
NIH	\$34.1 B	\$37.1 B	8.8%
NHGRI	\$528 M	\$556 M	5.4%

Fiscal Year 2019 Budget



- President's proposed Fiscal Year 2019 budget released in February
- Proposed ~8.1% reduction for NHGRI (over Fiscal Year 2018)
- Onward to Congress for consideration

Fiscal Year 2019 Budget



Wednesday

NATIONAL INSTITUTES OF HEALTH

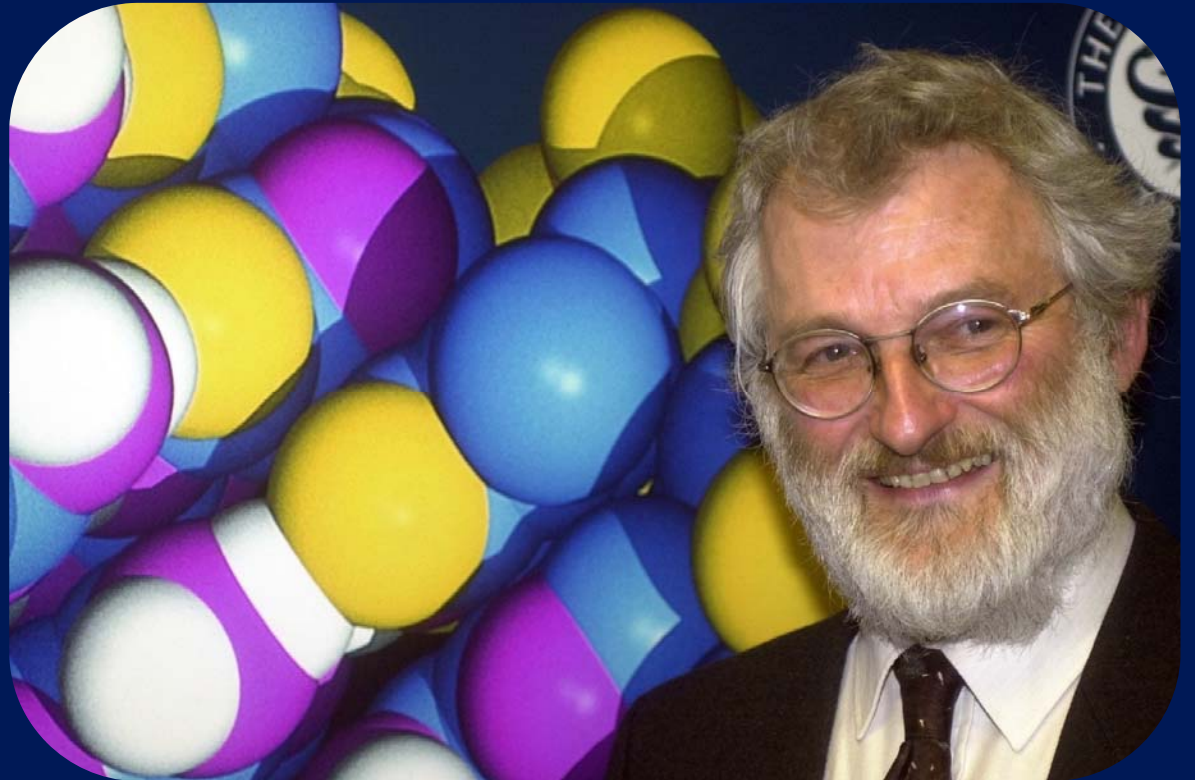
DR. FRANCIS COLLINS
National Institutes of Health (NIH)
Director

C-SPAN2
c-span.org

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Mourning the Loss of John Sulston



Mourning the Loss of Rep. Louise Slaughter



Rep. Louise Slaughter at Signing of GINA

AAAS Wachtel Cancer Research Award



Neville Sanjana, Ph.D.



Elected to National Academy of Sciences

Sarah Elgin

Michael Gottesman

Haig Kazazian

Stephen O'Brien

Simon Tavaré

Feng Zhang



**NATIONAL ACADEMY
OF SCIENCES**

New *Nature* Editor-in-Chief



Magdalena Skipper, Ph.D.



Genomes In The News...



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Genome Sequencing Program



Annual Consortium Meeting

- Research updates
- Sequencing progress
- Center goals & strategies
- Scientific talks
- Collaborations
- Opportunities to build common resources

Genome Sequencing Program

Centers for Common Disease Genomics

Disease Category	Sample Type	Samples Sequenced	Samples Projected
Cardiovascular	Genomes	34,089	47,298
	Exomes	21,129	56,172
Immune-Mediated	Genomes	9,013	12,424
	Exomes	1,435	19,715
Neuropsychiatric	Genomes	14,909	35,818
	Exomes	20,728	28,228
TOTAL		101,303	199,655

- Freeze 1:
20K WGSs
Nov 2017
- Freeze 2:
56K WGSs
Summer 2018

Genome Sequencing Program

Centers for Mendelian Genomics 

Finding the genes underlying human Mendelian conditions

Disease-Gene Associations

Tier 1 (Conservative) 2,197

Tier 2 (Suggestive) 1,000

Other Accomplishments

Tools and methods

Courses and training

463 publications

Key Collaborators

Knockout Mouse Project

Undiagnosed Disease Network

Matchmaker Exchange

Sample providers

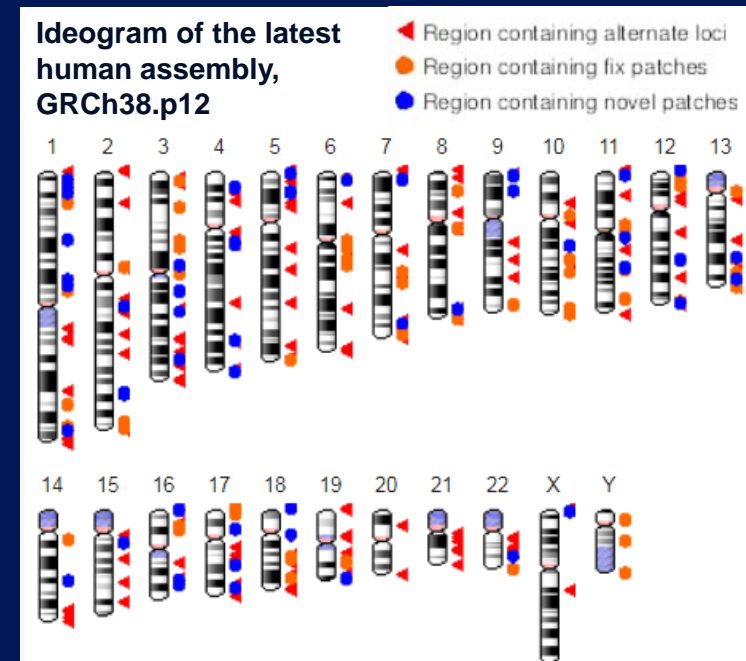
Patients and family members

Human Genome Reference Sequence Webinar

- Discussed future of NHGRI-funded components of the Genome Reference Consortium

- Topics included:

- How to represent reference genome
- How to include haplotype-resolved data
- What datasets are needed
- Bioinformatic tool development
- Education and outreach opportunities



THE CANCER GENOME ATLAS



CellPress

Sponsored by
i3 ORIGENE

Cell-of-Origin Patterns Oncogenic Processes Signaling Pathways Resources Events

Welcome to the Pan-Cancer Atlas

From The Cancer Genome Atlas (TCGA) consortium, a large-scale collaboration initiated and supported by the National Cancer Institute (NCI) and National Human Genome Research Institute (NHGRI).

From the analysis of over 11,000 tumors from 33 of the most prevalent forms of cancer, the Pan-Cancer Atlas provides a uniquely comprehensive, in-depth, and interconnected understanding of how, where, and why tumors arise in humans. As a singular and unified point of reference, the Pan-Cancer Atlas is an essential resource for the development of new treatments in the pursuit of precision medicine.

Cell Symposium – The TCGA Legacy: Multi-Omic Studies in Cancer

September 27-29, 2018
(Washington, DC)

Abstracts due June 15

Registration deadline August 10

Technology Development Program



- **Novel Nucleic Acid Sequencing Technology Development**
RFA-HG-18-001 (R01, also linked R21 and R43/44)
Next due date: June 27, 2018
- **Advanced Genomic Technology Development Meeting**
May 30 – June 1, Northeastern University (hosted by Meni Wanunu)



ENCyclopedia Of DNA Elements (ENCODE)

SCREEN: Search Candidate cis-Regulatory Elements by ENCODE

SCREEN

ccRE Search Results | Bed Upload | **SCN2A Gene Expression** | SCN2A RAMPAGE

SCN2A Gene Expression Profiles by RNA-seq

UCSC | GeneCards

Biosamples

TSV Search:

cell type	tissue
<input type="radio"/> A172	brain
<input type="radio"/> A549	lung
<input type="radio"/> A549 treated with dexamethasone	lung
<input type="radio"/> A549 treated with ethanol	lung
<input type="radio"/> A673	muscle
<input type="radio"/> ACC112	salivary glands
<input type="radio"/> adipocyte	adipose
<input type="radio"/> adipose derived mesenchymal stem cell	stem cell
<input type="radio"/> in vitro differentiated cells	
<input type="radio"/> adrenal gland female adult (51 years)	adrenal
<input type="radio"/> adrenal gland female fetal (108 days)	adrenal

Total: 622

Group by

Experiment | Tissue | Tissue Max

RNA type

Total RNA-seq | PolyA RNA-seq | any

TPM/FPKM | **Scale** | **Replicates**

TPM | Linear | Ind. | FPKM | Log2 | Avg.

Biosample Types

TSV

- cell line
- in vitro differentiated cells
- induced pluripotent stem cell line
- primary cell
- stem cell
- tissue

Cellular Compartments

TSV

- cell
- chromatin
- cytosol
- membrane
- nucleolus
- nucleoplasm
- nucleus

Tissue of origin

Download figure

brain	5.91 ENCS
spinal cord embryo	5.22 ENCSR699NLW spi
intestine	4.82 ENCSR969JYY germinal ma
kidney	2.49 ENCSR150JIX small intestine
stomach	1.99 ENCSR410DUZ left renal pelvis
gonad	1.54 ENCSR702IGQ stomach
connective tissue	1.38 ENCSR755LFM testis
lung	1 ENCSR192NBO fibroblast of breast
epithelium	0.76 ENCSR000COO AG04450
adrenal gland	0.56 ENCSR860HAA mammary epithelial cell
pancreas	0 ENCSR680AAZ adrenal gland
limb	0 ENCSR271DJ endocrine pancreas
liver	0 ENCSR547TNE muscle of arm
	0 ENCSR329MHM HepG2

© 2017 Weng Lab @UMass Med, ENCODE Data Analysis Center



ENCyclopedia Of DNA Elements (ENCODE)

Nucleic Acids Research

[← Previous Article](#)

[Next Article >](#)

[Art](#) **The ModERN Resource: Genome-Wide Binding Profiles**

for I Resource

Th Tran

Carri
Kriti

Williar
Hanee

Nuc
http
Pub

Samar
Robert

Jinrui
Valerie

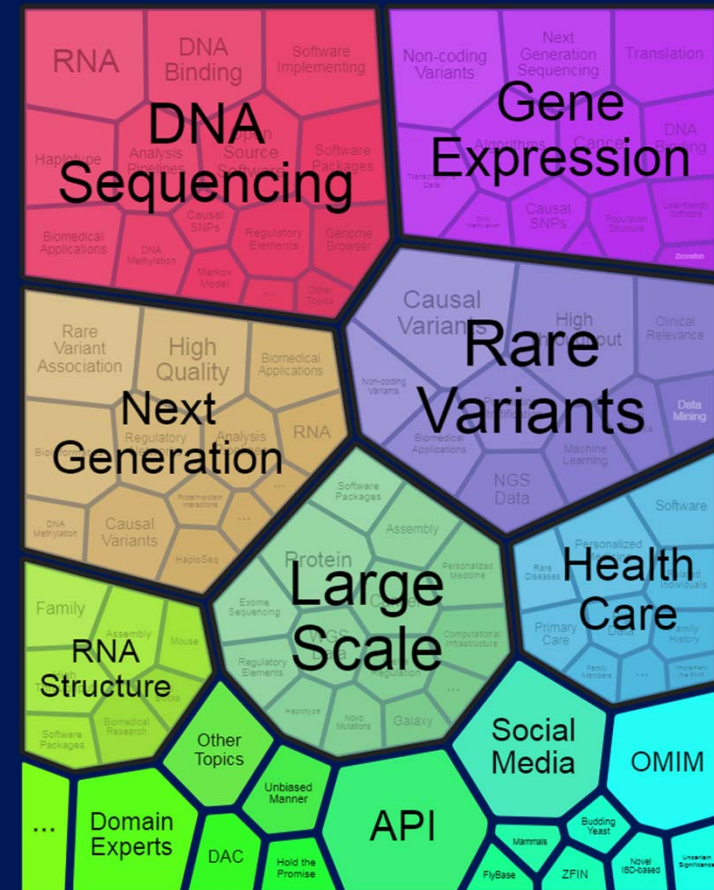
GENET

Impact of regulatory variation across human iPSCs and differentiated cells

Nicholas E. Banovich,^{1,7,8} Yang I. Li,^{2,7,9} Anil Raj,^{2,7} Michelle C. Ward,^{1,3} Peyton Greenside,⁴ Diego Calderon,⁴ Po Yuan Tung,^{1,3} Jonathan E. Burnett,¹ Marsha Myrthil,¹ Samantha M. Thomas,¹ Courtney K. Burrows,¹ Irene Gallego Romero,^{1,10} Bryan J. Pavlovic,¹ Anshul Kundaje,² Jonathan K. Pritchard,^{2,5,6} and Yoav Gilad^{1,3}

Computational Genomics and Data Science Program

- **Workshop in Fall 2016 yielded recommendations for next 3-5 years**
- **Release of Funding Opportunity Announcement in Summer 2018**
- **Innovative research efforts in computational genomics, data science, statistics, and bioinformatics**

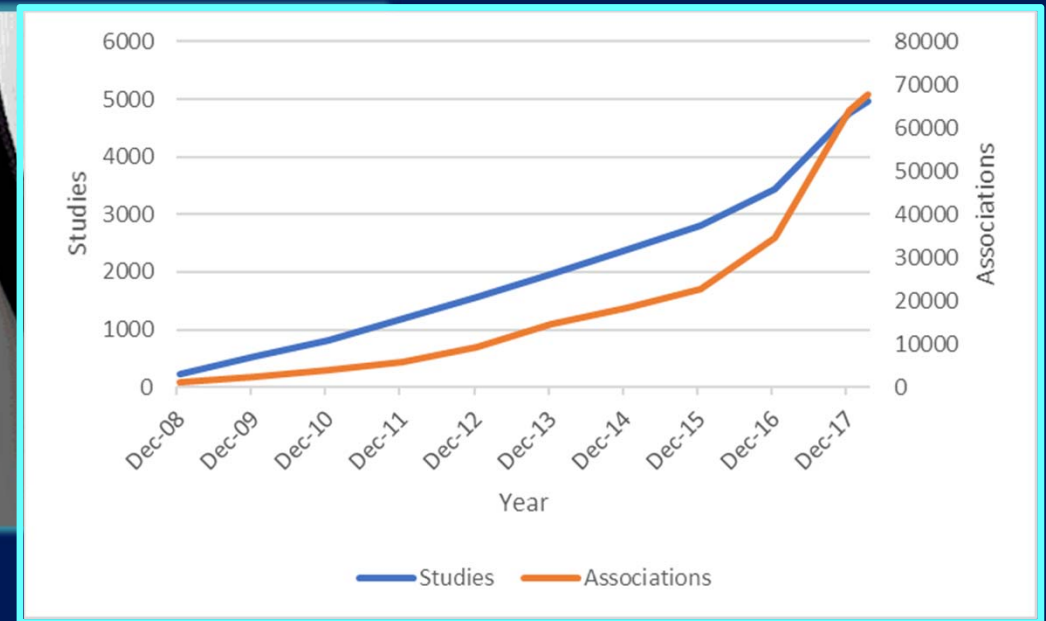
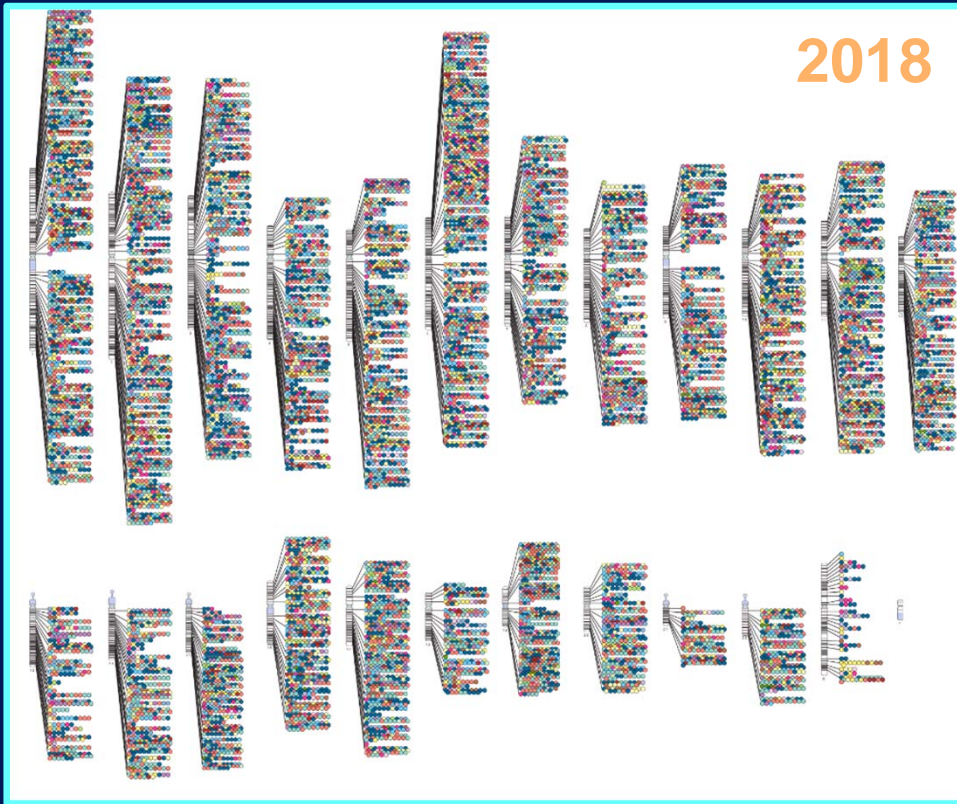


2nd Homomorphic Encryption Workshop




- Workshop to set community standards for broad use
- Homomorphic encryption allows analysis on encrypted data
- NHGRI providing SBIR support for secure, distributed GWAS
- MedCo, an i2b2 module for secure precision medicine

GWAS Catalog – 10th Anniversary



- 2018: 3,329 publications & 59,707 associations
- 3,118 citations of GWAS Catalog and associated papers

Clinical Genome Resource (ClinGen)



2018 | **ACMG Annual
Clinical Genetics Meeting**

APRIL 10-14 | EXHIBIT DATES: APRIL 11-13
CHARLOTTE CONVENTION CENTER | CHARLOTTE, NC

Clinical Genome Resource (ClinGen)

Gene Curation Coalition (GenCC)



Curating the Clinical Genome

23-25 May 2018

Wellcome Genome Campus, Hinxton, Cambridge, UK

Clinical Genome Resource (ClinGen)

Genetics in Medicine

Adaptation
classification
cardiomyopathy

Melissa A. Kelly, M
Steven M. H
Eden Haverfield
Kate Orland, MS
Kate Thomson,
Nicola
Christopher Se
Birgit Funke

Genetics in Medicine

Letter to the Editor

The ACMG,
for the inter

Leslie G Biesecker MD & Ste
Working Group



COLD SPRING HARBOR
Molecular Case Studies

COMMENTARY

Points to consider for sharing variant- level information from clinical genetic testing with ClinVar

Danielle R. Azzariti,^{1,6} Erin Rooney Riggs,^{2,6} Annie Niehaus,³
Laura Lyman Rodriguez,³ Erin M. Ramos,³ Brandi Kattman,⁴ Melissa J. Landrum,⁴
Christa L. Martin,^{2,6} and Heidi L. Rehm^{1,5,6}

Clinical Sequencing Evidence-Generating Research Program

2018

ACMG Annual
Clinical Genetics Meeting

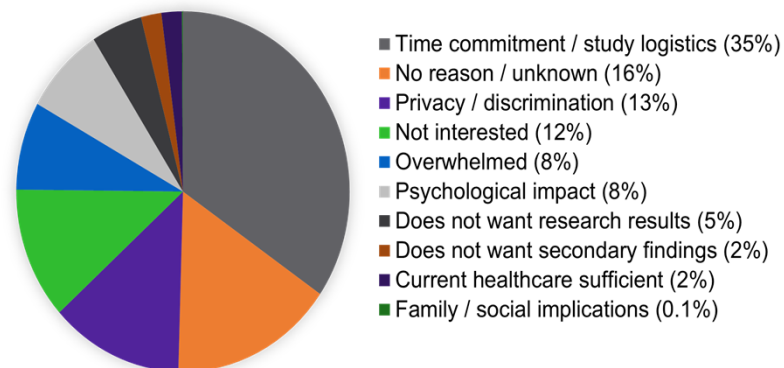
April 10–14 | Charlotte, NC

10 posters and presentations addressing: Secondary findings and complex genomic results; economic perspectives; sharing genomic results with family members

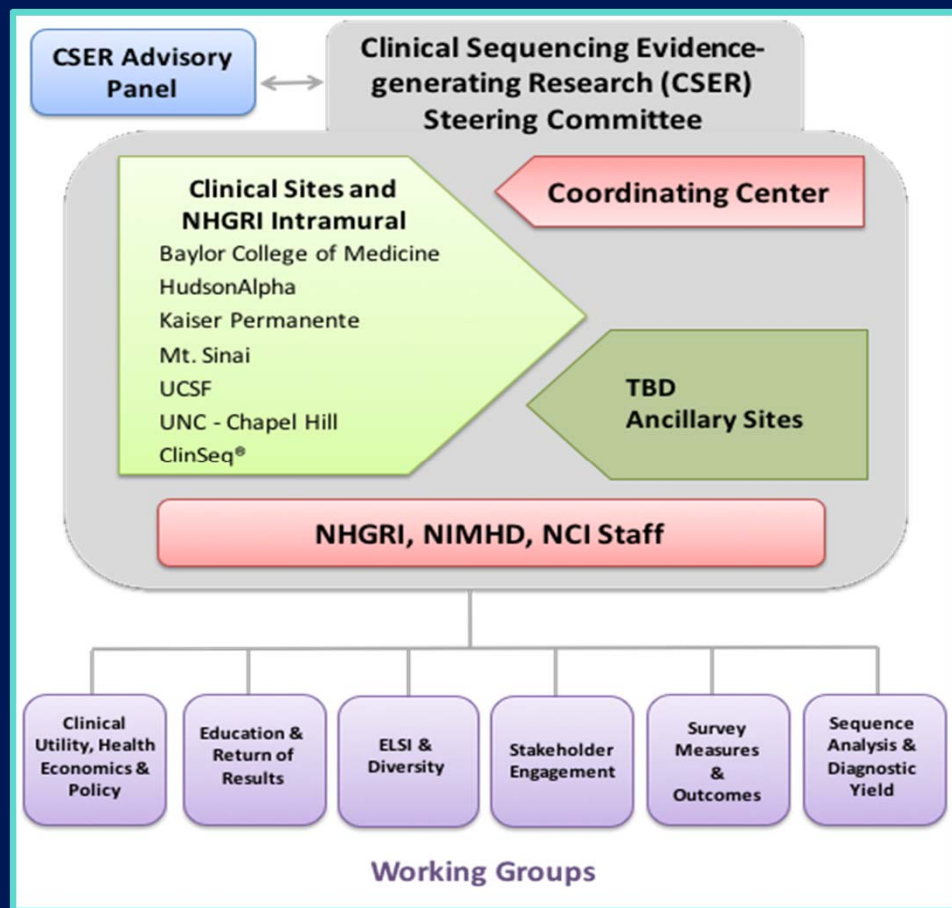
Why Patients Decline Genomic Sequencing Studies: Experiences from the CSER Consortium

PMID: 29497922

Laura M. Amendola¹ • Jill O. Robinson² • Ragan Hart¹ • Sawona Biswas^{3,4} • Kaitlyn Lee² • Barbara A. Bernhardt⁴ • Kelly East⁵ • Marian J. Gilmore⁶ • Tia L. Kauffman⁷ • Katie L. Lewis⁸ • Myra Roche⁹ • Sarah Scollon¹⁰ • Julia Wynn¹¹ • Carrie Blout¹²



Clinical Sequencing Evidence-Generating Research Program



Newborn Sequencing In Genomic Medicine and Public Health (NSIGHT)

Received: 31 July 2017 | Revised: 6 October 2017 | Accepted: 10 October 2017

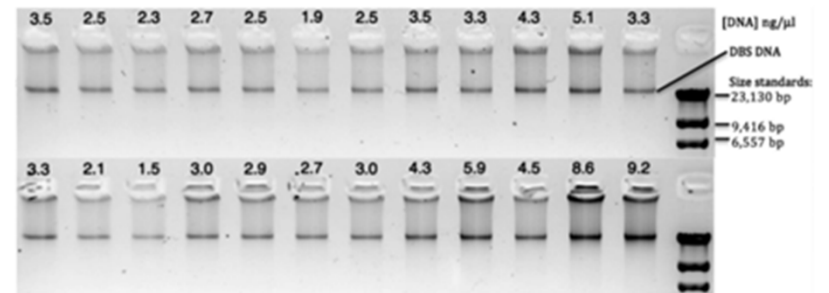
DOI: 10.1002/humu.23356

METHODS

Human Mutation
Variation, Informatics, and Disease

Whole exome and whole genome sequencing with dried blood spot DNA without whole genome amplification

Laia Bassaganyas^{1*} | George Freedman^{2*} | Dedeehya Vaka³ | Eunice Wan³ | Richard Lao³ | Flavia Chen³ | Mark Kvale³ | Robert J. Currier⁴ | Jennifer M. Puck^{2,3} | Pui-Yan Kwok^{1,3,5} 



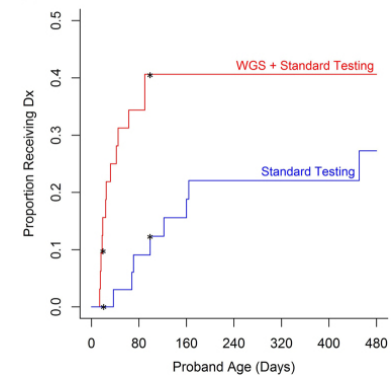
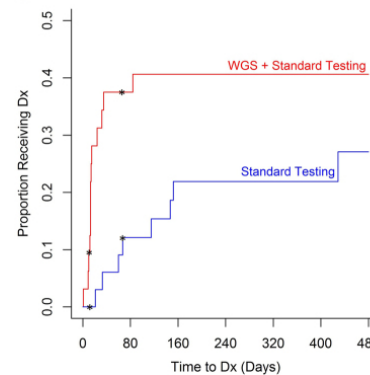
npj Genomic Medicine

www.nature.com/npjgenmed

ARTICLE OPEN

The NSIGHT1-randomized controlled trial: rapid whole-genome sequencing for accelerated etiologic diagnosis in critically ill infants

Josh E. Petrikin^{1,2,3}, Julie A. Cakici⁶, Michelle M. Clark⁴, Laurel K. Willig^{1,2,3}, Nathaly M. Sweeney^{4,5}, Emily G. Farrow^{1,2,3}, Carol J. Saunders^{1,3,6}, Isabelle Thiffault^{1,3,6}, Neil A. Miller¹, Lee Zellmer¹, Suzanne M. Herd¹, Anne M. Holmes², Serge Batalov⁴, Narayanan Veeraraghavan⁴, Laurie D. Smith^{1,3,7}, David P. Dimmock⁴, J. Steven Leeder^{2,3} and Stephen F. Kingsmore⁴



Missing Heritability Ten Years On Workshop

Workshop Conclusions:

- ❑ Using all associated SNPs explains much more heritability than genome-wide significant SNPs alone
- ❑ Increasing the proportion of heritability explained greatly improves reliability of prediction algorithms
- ❑ Expanding the study of African and other non-European populations is critically needed to enhance characterization of disease-associated genomic variants

International 100K+ Cohorts Summit

March 26-27, 2018 (Durham, NC)



Global Genomic
Medicine Collaborative

- **>50 very large cohorts from >30 countries (>25M participants)**
- **Conceived by Heads of International Research Organizations (HIROs) Group Leads – Jeremy Farrar and Francis Collins**
- **Agreed to develop searchable registry, common IT infrastructure, collaborative genome-sequencing and other –omics technologies**
- **Identifying other cohorts and developing collaborative efforts through G2MC and GA4GH**

Investigator-Initiated Genomic Medicine Research

Funding Opportunity Title	Investigator-Initiated Genomic Medicine Research (R01 Clinical Trial Optional)
Activity Code	R01 Research Project Grant
Announcement Type	New

	1 st	2 nd	3 rd	4 th	5 th	6 th
Receipt Dates	Jun 20, 2018	Oct 19, 2018	Jun 20, 2019	Oct 21, 2019	Jun 19, 2020	Oct 20, 2020

Activity Code	R21 Exploratory/Developmental Grant
Announcement Type	New
Related Notices	None
Funding Opportunity Announcement (FOA) Number	PAR-18-736

Ethical, Legal, & Social Implications (ELSI) Research Program

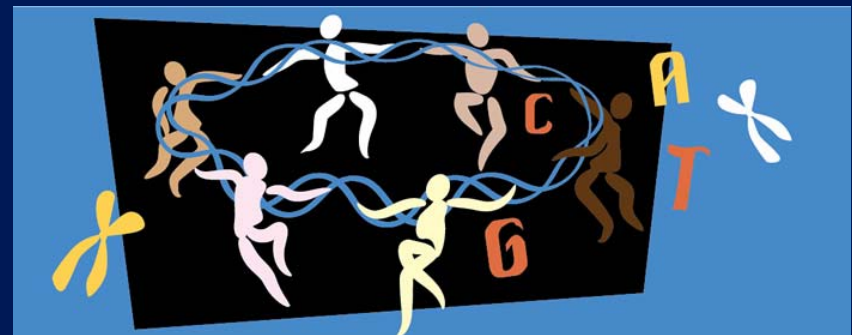
CEER Annual Meeting



Webinar:

Identifying Needs and Resources to Increase the Reach, Impact, and Transparency of ELSI Research

GSWG Annual Meeting



Training and Career Development

- **New ELSI T32 Program:**

University of Michigan

PI: Scott Roberts



- **New DAP Award:**

Duke University

PIs: Susanne Haga & Gregory Wray

Genomic Science and Medicine



Training and Career Development

2018 Meeting at UCLA



2019 Meeting in St. Louis (April)

NHGRI Extramural Research Highlights

Cell

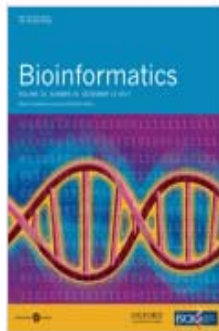
CellPress

Volume 172, Issue 3, 25 January 2018, Pages 491–499.e15

Article

Ultraconserved Enhancers Are Required for Normal Development

Diane E
Yupar S
Harring
Afzal 1,



Volume 33, Issue 24

15 December 2017

Article Contents

FIRE: functional inference of genetic variants that regulate gene expression

Nilah M Ioannidis ✉, Joe R Davis, Marianne K DeGorter, Nicholas B Larson, Shannon K McDonnell, Amy J French, Alexis J Battle, Trevor J Hastie, Stephen N Thibodeau, Stephen B Montgomery ... Show more

Author Notes

Bioinformatics, Volume 33, Issue 24, 15 December 2017, Pages 3895–3901,
<https://doi.org/10.1093/bioinformatics/btx534>

Published: 24 August 2017 **Article history** ▼

NHGRI Extramural Research Highlights



JAMIA
A SCHOLARLY JOURNAL OF INFORMATICS IN HEALTH AND BIOMEDICINE

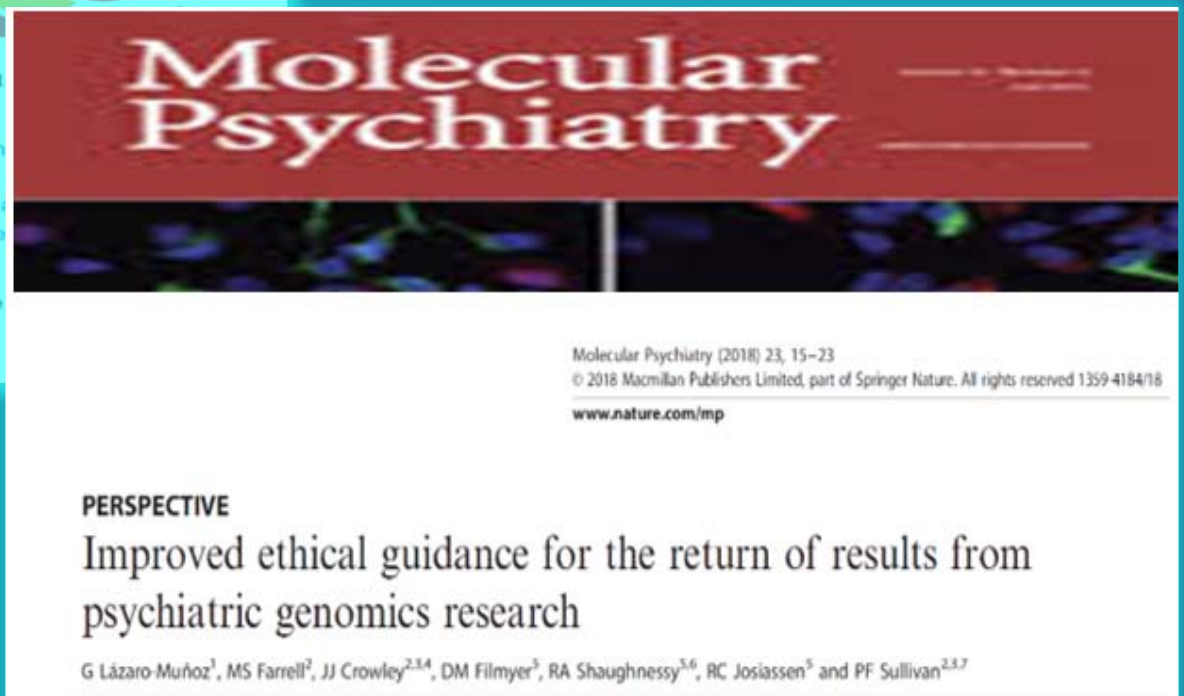
JULY 2017
Volume 24 Issue 4

Editor-in-Chief
Lucila Ohno-Machado

In this issue:
Automatic health record review to help prioritize gravity III Social Security disability applicants—p. 709
Shared decision-making

Addressing Beacon re-identification attacks: quantification and mitigation of privacy risks
Jean Louis Raisaro, Florian Tramèr, Zhanglong Ji, Diyue Bu, Yon Knox Carey, David Lloyd, Heidi Sofia, Dixie Baker, Paul Flicek, Suyash Shringarpure, Carlos Bustamante, Shuang Wang, Xiaoqi Lucila Ohno-Machado, Haixu Tang, XiaoFeng Wang, Jean-Pierre
Author Notes

Journal of the American Medical Informatics Association, Volume 2017, Pages 799–805, <https://doi.org/10.1093/jamia/ocw167>
Published: 20 February 2017 **Article history**



Molecular Psychiatry

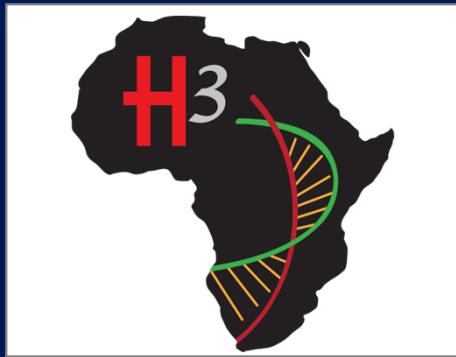
Molecular Psychiatry (2018) 23, 15–23
© 2018 Macmillan Publishers Limited, part of Springer Nature. All rights reserved 1359-4184/18
www.nature.com/mp

PERSPECTIVE
Improved ethical guidance for the return of results from psychiatric genomics research
G Lázaro-Muñoz¹, MS Farrell², JJ Crowley^{2,3,4}, DM Filmyer³, RA Shaughnessy^{3,6}, RC Josiassen⁵ and PF Sullivan^{2,3,7}

Director's Report Outline

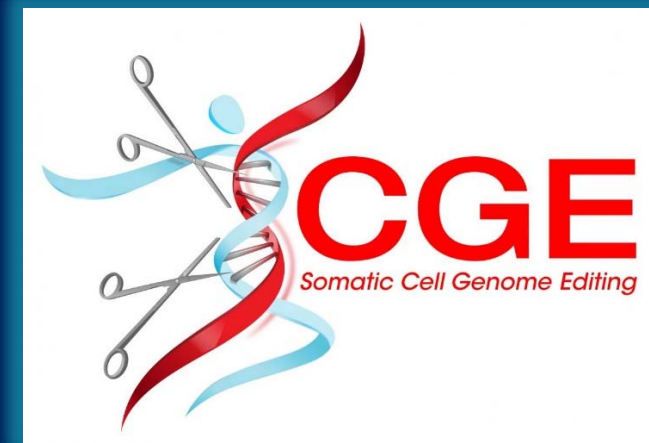
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Human Heredity and Health in Africa (H3Africa)



- **11th Consortium Meeting in March 2018 (Uganda)**
- **Recent publications**
- **Upcoming H3Africa ELSI research awards**

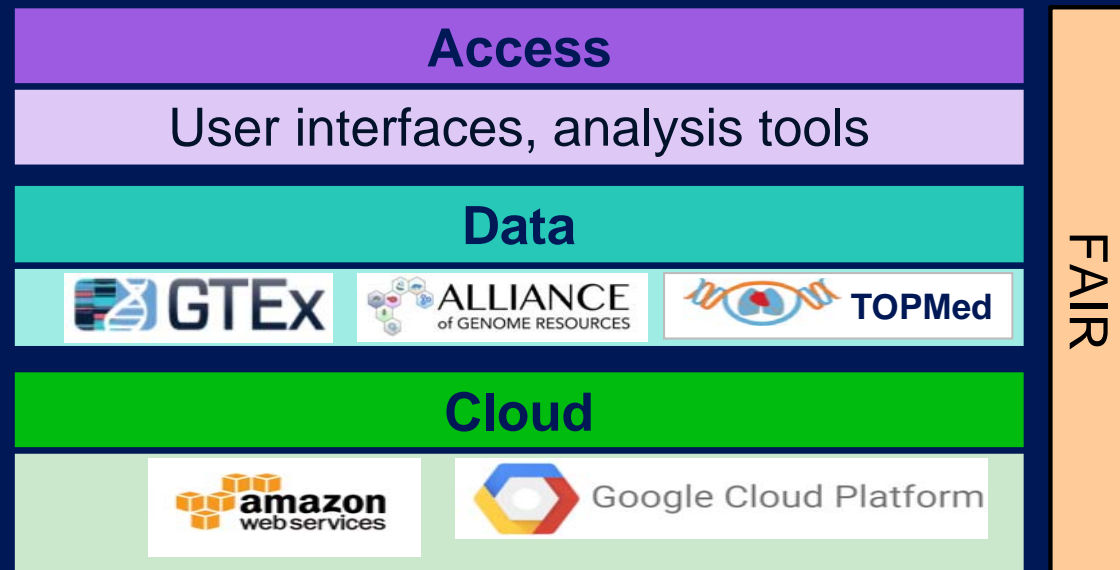
Somatic Cell Genome Editing



- Program aims to develop quality tools to perform effective and safe genome editing in human patients
- Applications received in response to 6 FOAs
- Kickoff meeting in December

NIH Data Commons Pilot Phase

- Pilot started in Sept 2017
- Initial Accomplishments:
 - Established governance
 - Developed project execution plan
 - Established processes for data access
- Implementation:
 - Stage I: April – Oct 2018
 - Stage II: Oct 2018 – Oct 2021



All of Us

RESEARCH PROGRAM

DAY 1 - MARCH 21st

8:30-11:25 **PLENARY 1: SETTING THE STAGE OPPORTUNITIES & NEEDS**

- WELCOME - Michelle Hamlet
- OPENING REMARKS: The VISION for PRECISION MEDICINE / PRECISION HEALTH - Francis Collins
- PROGRAM OVERVIEW - Eric Dishman
- KEYNOTE: BIG PICTURE SCIENTIFIC VISION - Gregory Simon
- KEYNOTE: PARTICIPANT PERSPECTIVE - Bray Patrick-Lake
- WORKSHOP GOALS and CHARGE and LOGISTICS - Gina S. Wei, Edward Ramos and Scott Wheeler

11:25-12:45 **LUNCH (ON YOUR OWN)**

12:45-3:00 **GROUND BREAKING DATA COLLECTION TECHNOLOGIES and METHODS**

OUTCOMES...

- GAIN NEW PERSPECTIVES on the DATA & RESEARCH OPPORTUNITIES the AoU PROGRAM COULD PRODUCE
- IDENTIFY BREAKTHROUGH DATA COLLECTION TECHNOLOGIES and METHODS for the AoU PROGRAM

3:00-3:20 **BREAK**

3:20-5:30 **THE BIG OPPORTUNITIES**

OUTCOMES...

- UNDERSTAND YOUR ROLE in DEFINING the FUTURE for AoU
- IDENTIFY the BIG OPPORTUNITIES RESEARCH QUESTIONS from WHICH USE CASES will be DEVELOPED

XCI - CROSS-CUTTING THEMES BREAK-OUT SESSION

HCI - HEALTH CONDITIONS BREAKOUT SESSION

Soon to be Issued Funding Announcement for All of Us Genome Centers (OT2)

Notice Number: NOT-PM-18-002

Key Dates

Release Date: March 16, 2018

Estimated Publication Date of Funding Announcement: May 2018

First Estimated Application Due Date: July 2018

Earliest Estimated Award Date: August 2018

Earliest Estimated Start Date: September 2018

Related Announcements

None

Issued by

National Institutes of Health (NIH)

Purpose

The National Institutes of Health intends to issue a funding announcement (FA) to solicit applications for large-scale Genome Centers to generate genomic data as part of the *All of Us* Research Program. The *All of Us* Research Program seeks to create one of the world's largest and most comprehensive precision medicine research platforms with a data

All of Us

RESEARCH PROGRAM

National Launch on May 6, 2018

Get Started - Sign Up

Here's a quick overview of what you'll need to do to join.



1 Create an Account

You will need to give an email address and password.



2 Fill in the Enrollment and Consent Forms

The process usually takes 18-30 minutes. If you leave the portal during the consent process, you will have to start again from the beginning.



3 Complete Surveys and More

Once you have given your consent, you will be asked to complete online health surveys. You may be asked to visit a partner center. There, you'll be asked to provide blood and urine samples and have your physical measurements taken. We may also ask you to share data from wearables or other personal devices.





Director's Report Outline

- I. General NHGRI Updates
- II. General NIH Updates
- III. General Genomics Updates
- IV. NHGRI Extramural Research Program
- V. NIH Common Fund/Trans-NIH
- VI. NHGRI Division of Policy, Communications, and Education**
- VII. NHGRI Intramural Research Program

National DNA Day 2018

National DNA DAY APRIL 25
15th Anniversary

"Ask Me Anything" (AMA) Series
On the reddit science community forum *"/r/Science"*
Featuring prominent geneticists from a range of research areas
April 20 & April 23-27, 2018

National DNA DAY APRIL 25
15th Anniversary


Louise M. Slaughter
National DNA Day Lecture

Bench to Bedside to Business
A Talk on Startups in Science

Olivier Noel, Ph.D.
DNAsimple Founder & CEO

April 25 | 4:00 p.m. - 5:30 p.m.
Lister Hill Auditorium (Building 38A)

Public Livestream at genome.gov/GenomeTVLive



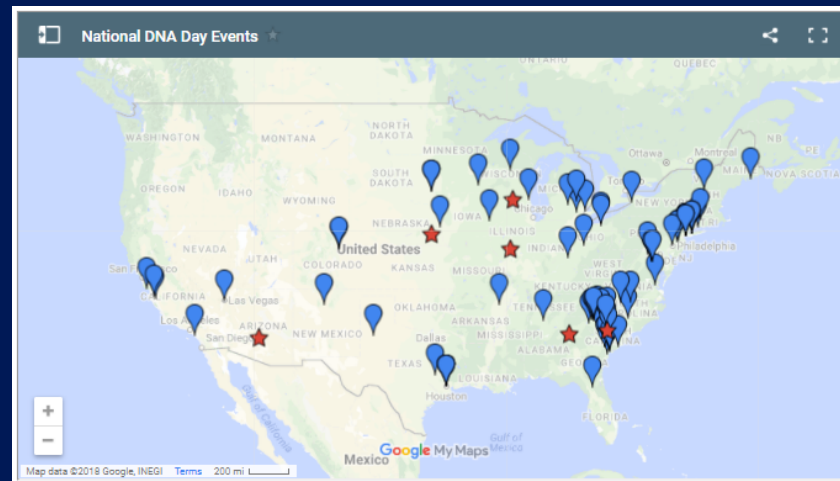
HOT (Human Origins Today) Topic:
Your Microbiome is a Part of this Microbial Planet



 **Lita Proctor, Ph.D.**
Program Director, Human Microbiome Project
Division of Genome Sciences
National Human Genome Research Institute
National Institutes of Health

National Museum of Natural History
Friday, April 27, 2018, 4:00 p.m. - 5:00 p.m.
FREE and open to the public



'15 for 15' Celebration

'15 for 15' Celebration

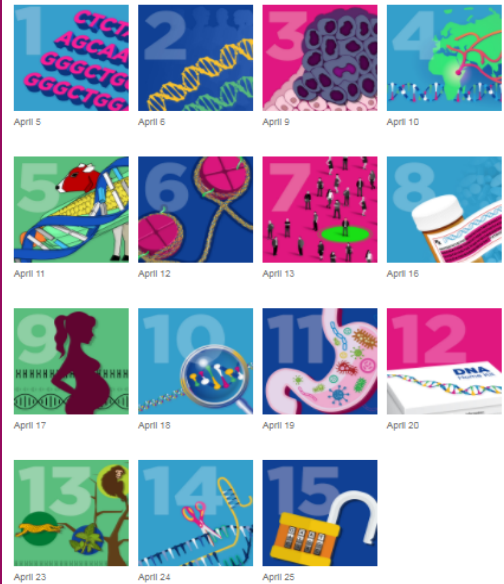
Fifteen ways genomics is now influencing our world



Whether you realize it or not, many parts of our daily lives are influenced by genomic information and genomic technologies. Genomics now provides a powerful lens for use in various areas - from medical decisions, to food safety, to ancestry.

April 22-18 will mark the 18th anniversary of the completion of the Human Genome Project. To commemorate this milestone and the genomic advances that have been made since 2003, the National Human Genome Research Institute (NHGRI) has launched the '15 for 15' Celebration - unveiling 15 ways that genomics has and will continue to transform our world.

We hope that you will join us on this journey and learn how genomics is influencing the world around you. Which genomic advance will you discover today?



DNA Sequencing

Reducing the cost of genome sequencing by a million-fold

April 5, 2018



Did you know ... that your genome contains about six billion individual building blocks - and that we can now read the order of all those building blocks in about a day and for about \$1000?

Leaps in technology since the Human Genome Project have enabled remarkable genomics-based advances in medicine, agriculture, forensics, and our understanding of evolution.

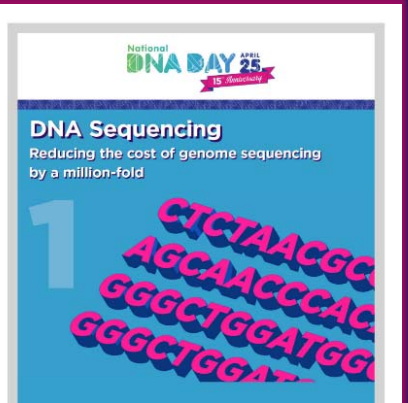
Our genome (that is, our DNA "blueprint") - and in fact the genomes of all life forms on earth - are made of four chemical "bases" strung together in varying orders. To study the exact order (or **sequence**) of someone's DNA, researchers follow three major steps: (1) purify and copy the DNA; (2) read the sequence; and (3) compare to other sequences.

First they use chemical methods to purify, then, for some methods, "**amplify**" the DNA in the sample - that means they copy small parts of the sample to reach high enough levels for measuring. The amplification step makes it possible to do DNA testing from very small starting amounts, like those in forensic samples or ancient bones. Then, **different methods** can be used to determine the order of each base in the DNA sample. Finally, they use computers to compare the sequence of the DNA to a reference sequence (for example, of the human genome), in order to see if there are any differences in the order of the bases.

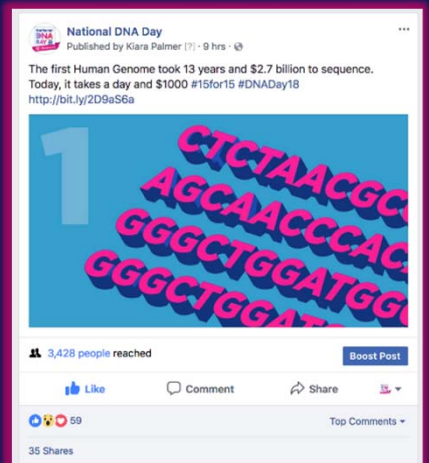
Technology Advances Since the Human Genome Project

The Human Genome Project opened the door to vast improvements in three major areas:

- The methods used to amplify and sequence DNA, including a million-fold reduction in the cost for sequencing a human genome.
- Continually improving the accuracy of the reference "**human genome sequences**" that everyone can use for comparing newly



Newsletter



Outreach Activities

NBC4 Health & Fitness Expo



USA Science & Engineering Festival

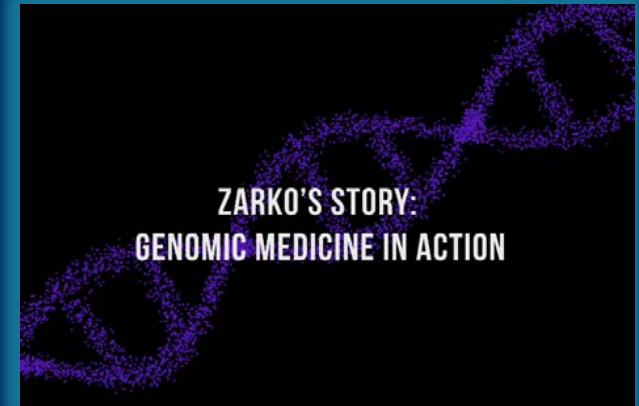


Genome: Unlocking Life's Code Exhibition

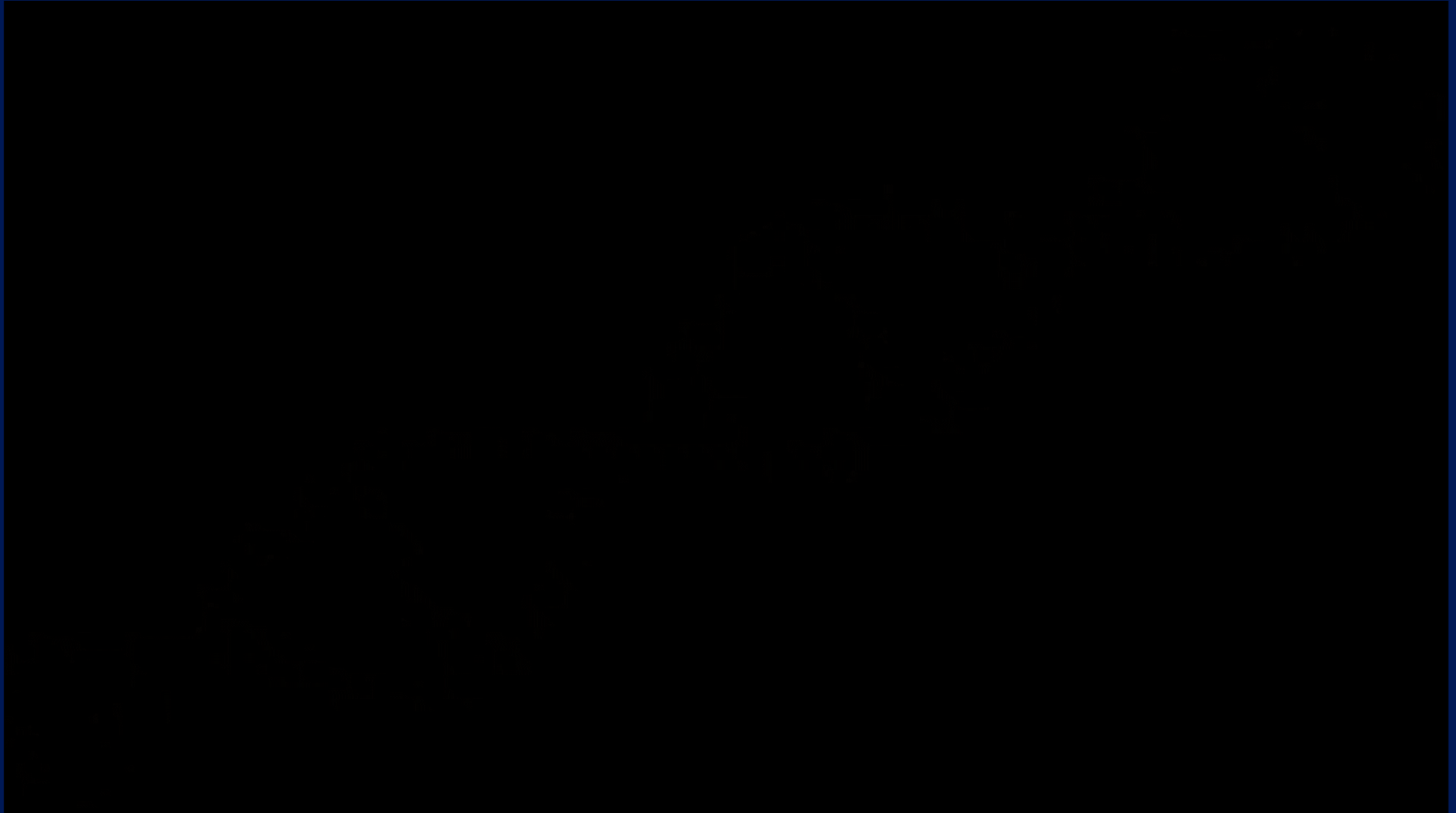


- June 23 to September 15, 2018
Rochester Art Center (Rochester, MN)
- Fall 2018
Orange County History Museum (Orlando, FL)

42 Degrees North Media: Educational Videos



42 Degrees North Media: Educational Videos



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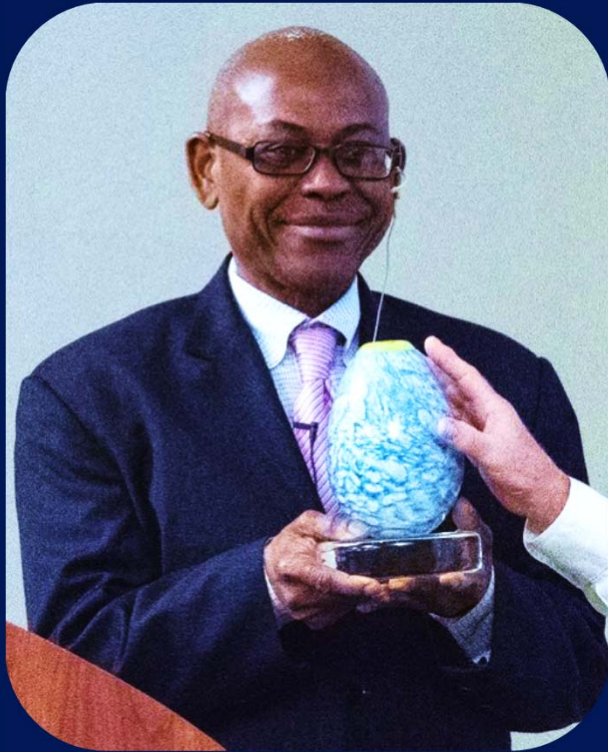
2018 Samuel J. Heyman Service to America Medals Finalist



Dan Kastner, M.D., Ph.D.



2018 HudsonAlpha Life Sciences Prize



Charles Rotimi, Ph.D.



NHGRI Intramural Research Highlights



AJHG

Whole-Genome-Sequence-Based Haplotypes Reveal Single Origin of the Sickle Allele during the Holocene Wet Phase



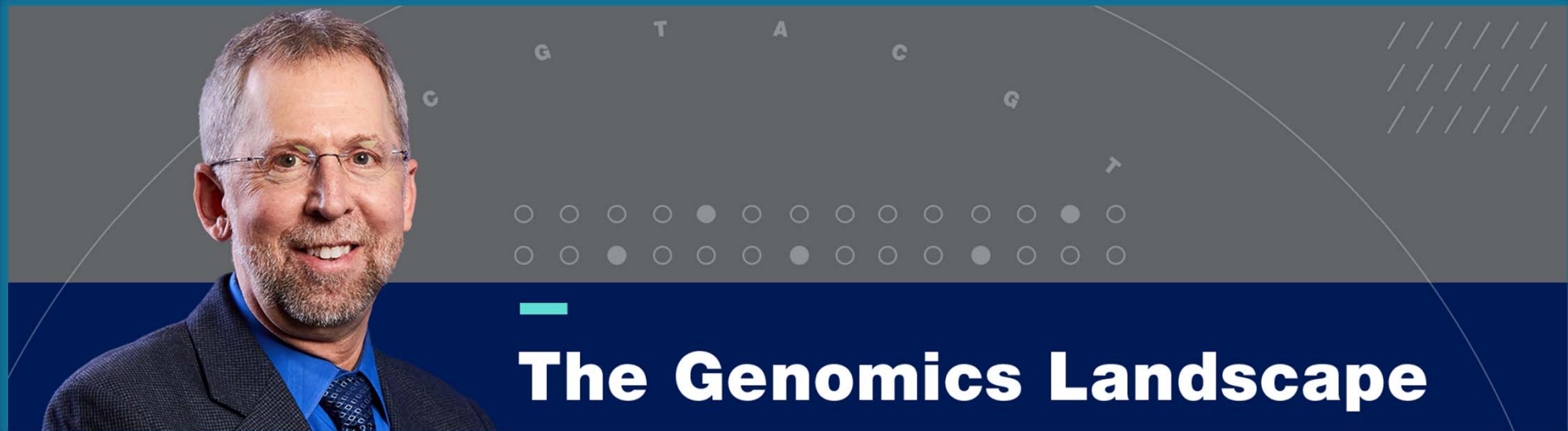
 **PLOS** | BIOLOGY

A direct link between MITF, innate immunity, and hair graying



Genomic Analysis of Hospital Plumbing Reveals Diverse Reservoir of Bacterial Plasmids Conferring Carbapenem Resistance

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