National Human Genome Research Institute

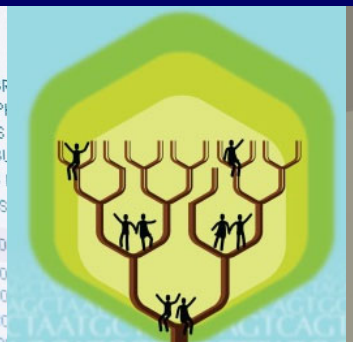
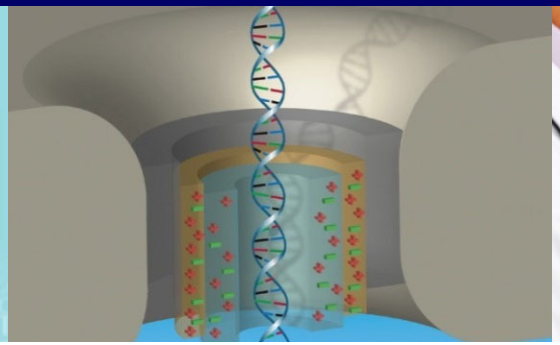
The Forefront of Genomics®

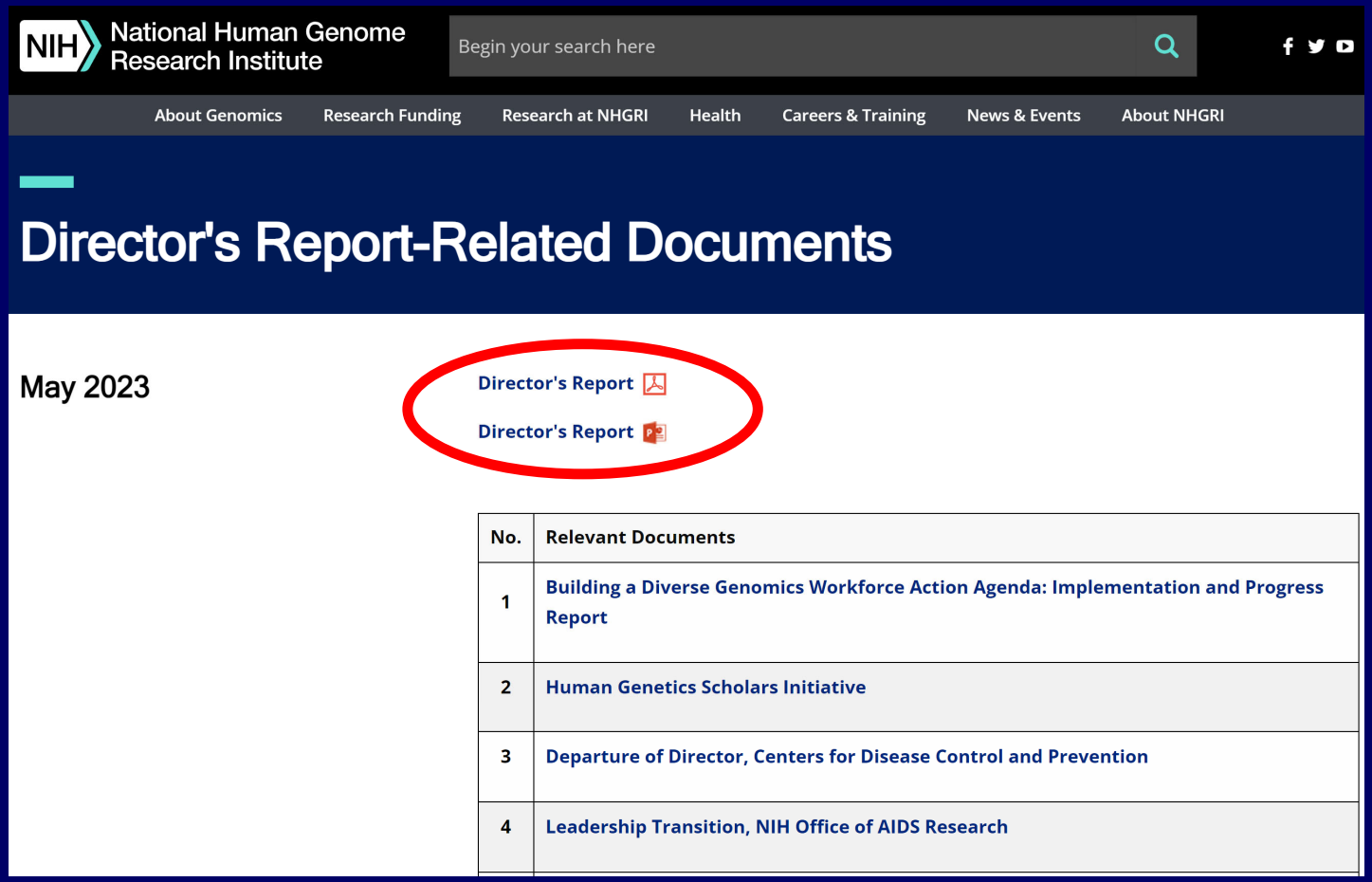
DIRECTOR'S REPORT

Eric Green, M.D., Ph.D.

Director, NHGRI

May 2023



genome.gov/DirectorsReport

Document #

Open Session Agenda

Presentations:

NHGRI Intramural Research Program Report
Charles Rotimi

NHGRI Intramural Research Program Blue Ribbon Panel Report
Gail Jarvik & Lynn Jorde

NASEM Report on the Use of Race, Ethnicity, and Ancestry as Population Descriptors
Aravinda Chakravarti & Charmaine Royal

Open Session Agenda

Presentation:

Update on the H3Africa Program
Jennifer Troyer

Concept Clearances:

Genomic-Enabled Learning Health Systems
Robb Rowley

Developing Novel Theory and Methods for Understanding the Genetic Architecture of Complex Traits
Alexander Arguello

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 Communications, Policy, and Education

VII. NHGRI Intramural Research Program

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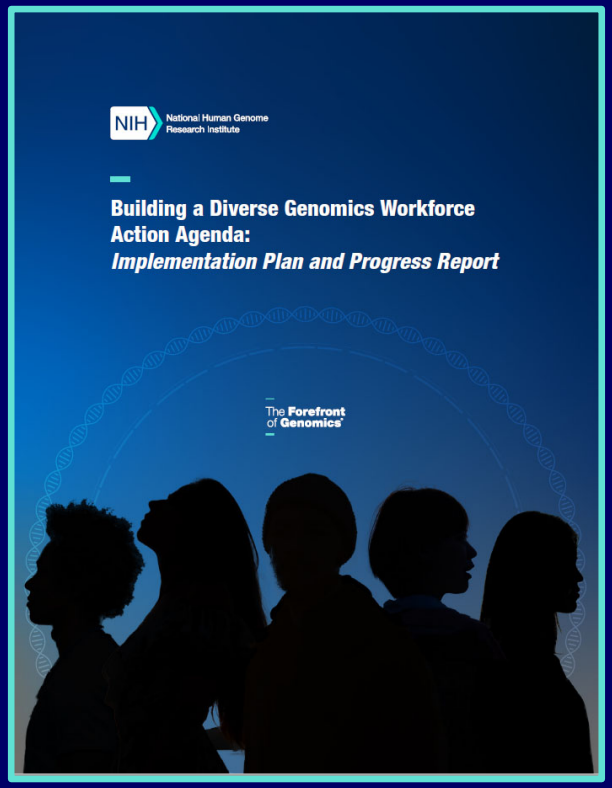
Building a Diverse Genomics Workforce Action Agenda: Implementation and Progress Report

- Details programs, projects, initiatives, and engagements that have been enacted since release of Action Agenda in 2021
- Diversifying the genomics workforce cannot be achieved without support from the scientific community



Document 1

Human Genetics Scholars Initiative

- >20 predoctoral, postdoctoral, and early-career scholars visited NHGRI
- Discussed research funding and career development opportunities
- NHGRI has supported this initiative since 2019

Document 2

NHGRI Leadership: Director's Working Group

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Departure of Director, Centers for Disease Control and Prevention

Rochelle Walensky, M.D., M.P.H.

CDC
CENTERS FOR DISEASE CONTROL AND PREVENTION

Document 3

Leadership Transition, NIH Office of AIDS Research

Maureen Goodenow, Ph.D.

Bill Kapogiannis, M.D.

Document 4

New Director, NIH Tribal Health Research Office

Karina Walters, Ph.D., M.S.W.

NIH TRIBAL HEALTH RESEARCH

Departure of Senior Advisor, NIH Office of the Director

Carrie Wolinetz, Ph.D.

National Institutes of Health

Document 6

NIH-Wide Strategic Plan for Diversity, Equity, Inclusion, and Accessibility (DEIA)

- Fiscal Years 2023-2027
- NIH's role as a people-centered organization
- Encourages enhancing DEIA in operations, workforce, and research
- Crosscutting themes promoting transparency, communication, and engagement; fostering sustainable change; and harnessing data
- Roadmap for NIH-supported institutions

Document 7

Recommendations for Improving National Research Service Award (NRSA) Fellowship Review

Recommendations for Improving NRSA Fellowship Review

Read the Request for Information on Recommendations for Improving NRSA Fellowship Review and Submit Comments

Submit Comments Online

Synopsis of Issue

NIH is recommending changes to the peer review of Ruth L. Kirschstein National Research Service Award (NRSA) fellowship applications by restructuring the review criteria and modifying some sections of the PHS Fellowship Supplemental Form that are specific to NRSAs. The goal of

RFI open through June 23, 2023

Request for Information (RFI) on Recommendations for Improving NRSA Fellowship Review

Notice Number:
NOT-OD-23-110

Key Dates

Release Date:
April 24, 2023

Response Date:
June 23, 2023

Fiscal Year 2024 Appropriations

	FY2022 ($)	FY2023 ($)	FY2024 PB ($)	Increase ($)	Increase (%)
NIH	$46.178 billion *	$49.178 billion *	$51.098 billion *	$1.92 billion	3.9%
NHGRI	$636 million	$661 million	$661 million	$0	0%

* Includes appropriations for both NIH and ARPA-H

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Mourning the Loss of Paul Berg

Document 10

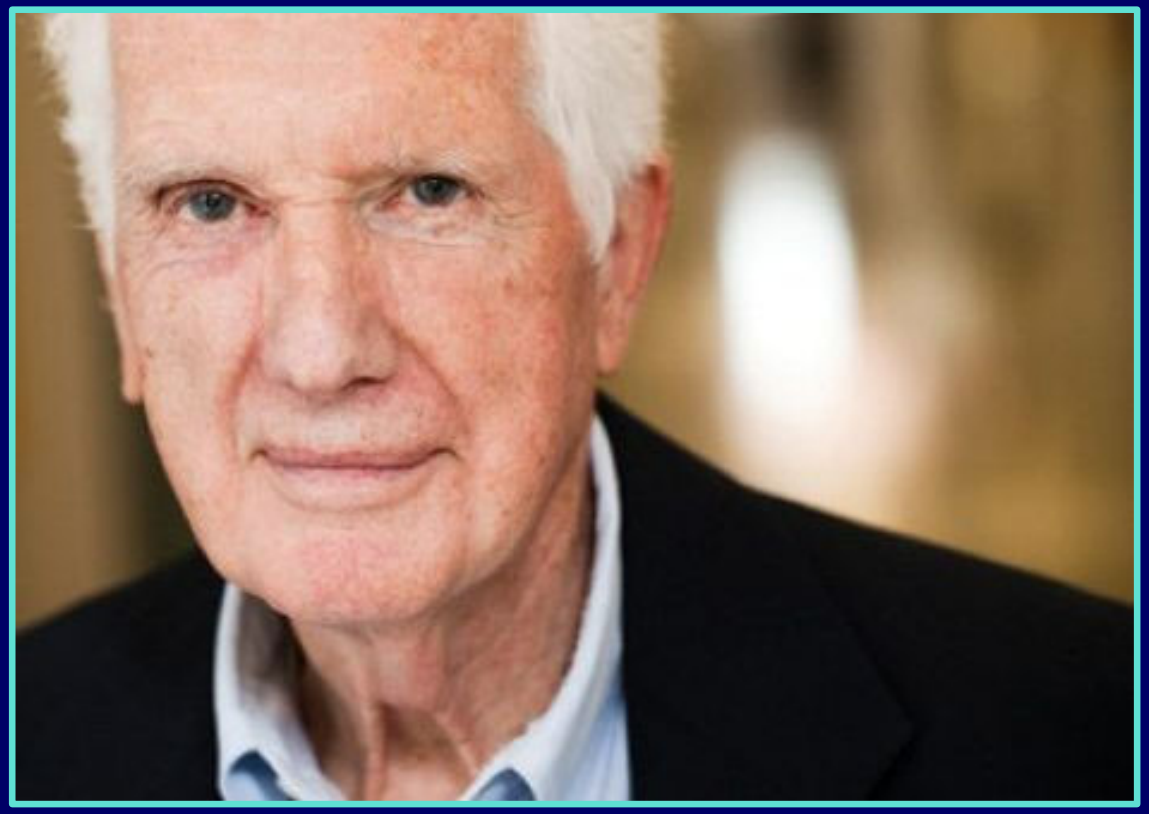
Mourning the Loss of Casey Brown

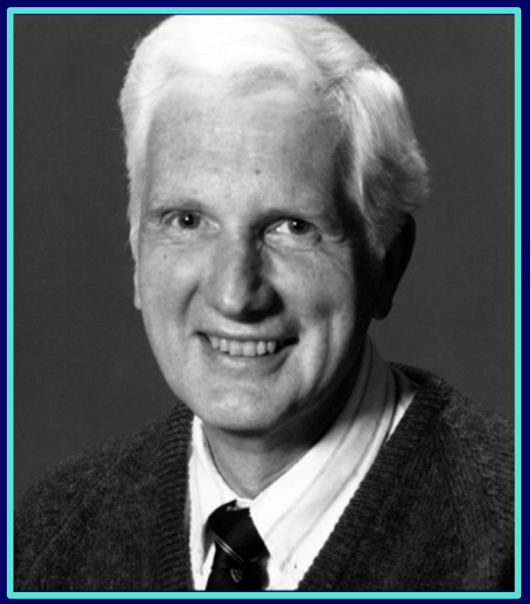
Document 11

Mourning the Loss of Janet Sinsheimer

Document 12

Mourning the Loss of Charles Scriver





Document 13

New Director, Wellcome Sanger Institute

Matt Hurles, Ph.D.

wellcome sanger institute

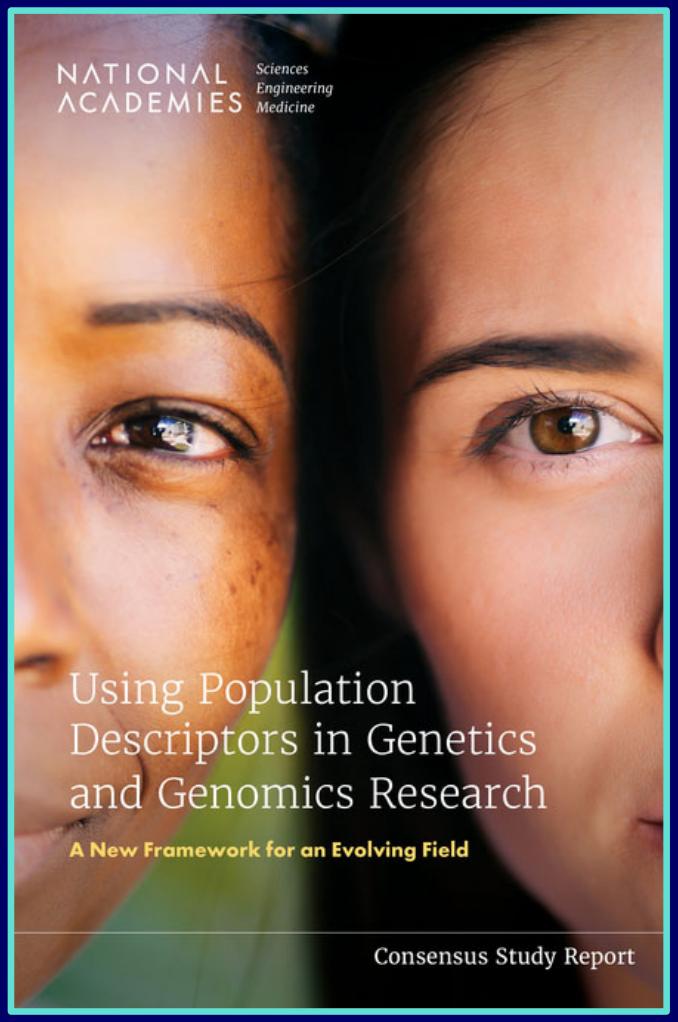
Elected to National Academy of Sciences

NATIONAL ACADEMY OF SCIENCES

Spyros Artavanis-Tsakonas
Claire Fraser
Jo Handelsman
Daphne Koller
Leonid Kruglyak
Xihong Lin
John O'Shea
Anna Marie Pyle
Richard Roberts
Yosef Shiloh
Alice Ting
Anne Yoder
Phil Zamore
Kenneth Zaret

Document 15

NASEM Population Descriptors Report



- 14 NIH institutes, centers, and offices were co-sponsors
- NHGRI served as task co-leader with *All of Us* Research Program
- Past and current uses of population descriptors
- Proposes guiding principles and a new framework for the field
- Aravinda Chakravarti and Charmaine Royal will present later

Document 16

NASEM Study: Toward Sequencing and Mapping RNA Modifications

- **Public workshop held in March**
- **Facilitate additional community brainstorming and problem-solving**

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Human Genome Reference Program (HGRP)

- Collection of high-quality reference human genome sequences
- Includes sequences from 47 people
- Four papers recently published

Document 18

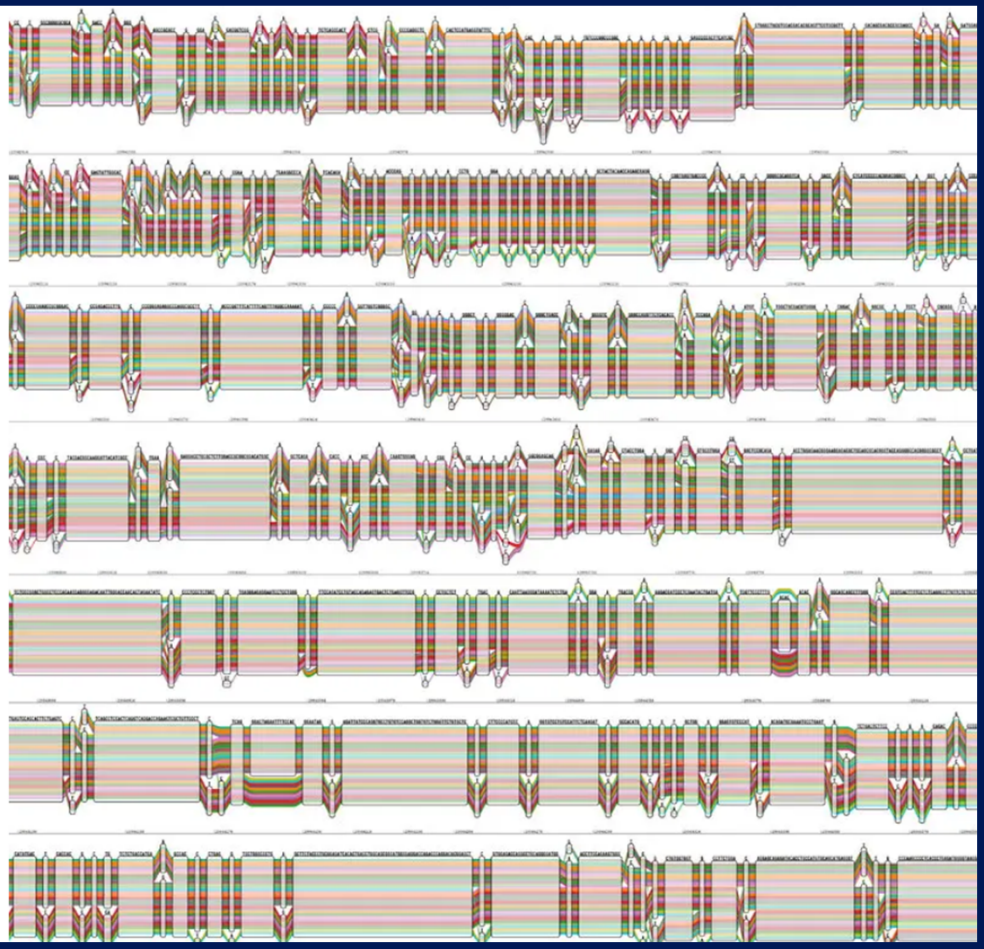
Human Genome Reference Program (HGRP)

The New York Times

Account

Scientists Unveil a More Diverse Human Genome

The "pangenome," which collated genetic sequences from 47 people of diverse ethnic backgrounds, could greatly expand the reach of personalized medicine.



Document 18

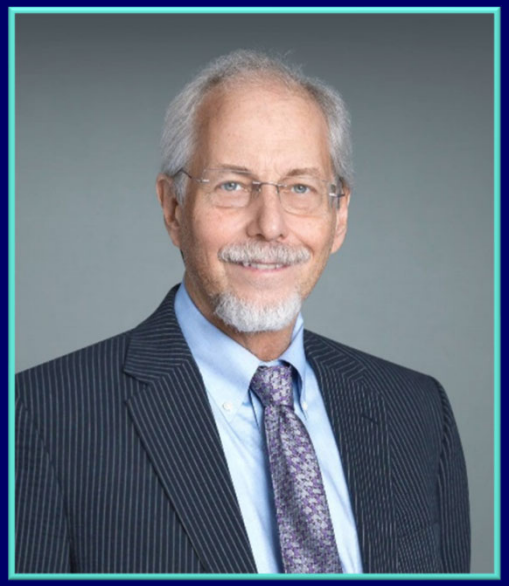
Zoonomia Project

- Special issue in *Science*
- >150 researchers using comparative genomics to understand >240 species
- NHGRI-funded genome sequencing and analysis projects

Comparative genomics of Balto, a famous historic dog, captures lost diversity of 1920s sled dogs

KATHERINE L. MOON , HEATHER J. HUSON , [...], AND BETH SHAPIRO +8 authors Authors Info &

Centers of Excellence in Genomic Science (CEGS)



Jef Boeke , Ph.D.

NYU Langone Health

PAR-23-098 CEGS Reissued

Next Receipt Dates: June 23, 2023; June 21, 2024

Molecular Phenotypes of Null Alleles in Cells (MorPhiC)

- **Data Production Reseach & Development Centers**

The Jackson Laboratory
PI: Paul Robson

Memorial Sloan Kettering Cancer Center
PI: Danwei Huangfu

Northwestern University
PI: Mazhar Adli

UCSF University of California San Francisco
PI: Luke Gilbert

- **Data Resource & Administrative Coordinating Center**

UNIVERSITY OF MIAMI
PI: Stephan Schürer

- **Data Analysis & Validation Centers**

May 2023 Council

- **In-person meeting took place in January/February 2023**

Document 21

Developmental Genotype-Tissue Expression (dGTEx)

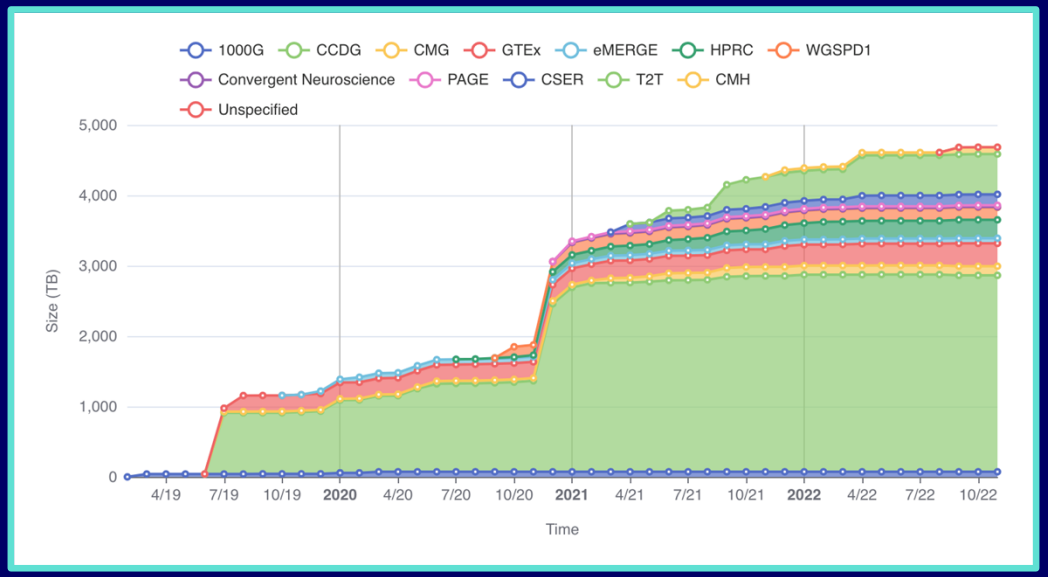
Data Integration and Statistical Analysis Methods (DISAM) (U01 Clinical Trial Not Allowed)

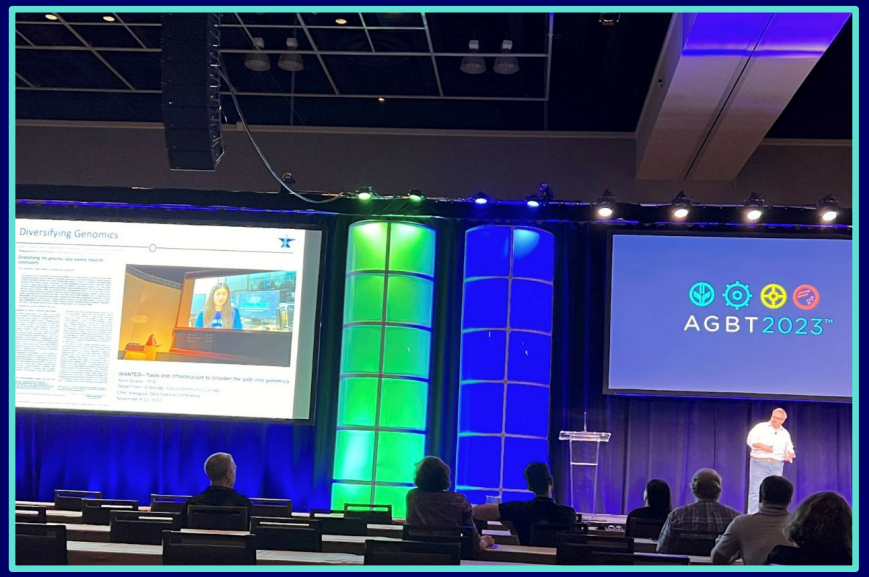
U01 Research Project – Cooperative Agreements

New Funding Opportunity Announcement:

- RFA-HG-23-005 Data Integration and Statistical Analysis Methods
- Develop methods for analyses of data from human and non-human primate dGTEx efforts
- Applications due Nov. 20, 2023

NHGRI Analysis, Visualization, and Informatics Lab-space (AnVIL)





- Over 600,000 genomes and five petabytes of data
- AnVIL presented at AGBT Meeting in February 2023

Computational Genomics and Data Science (CGDS) Program

Genomic Community Resources

- **NHGRI Genomic Community Resources PAR-23-124**

  Due dates in 2023: May 25 and September 25

- **Trans-NIH Notice of Intent to Publish**

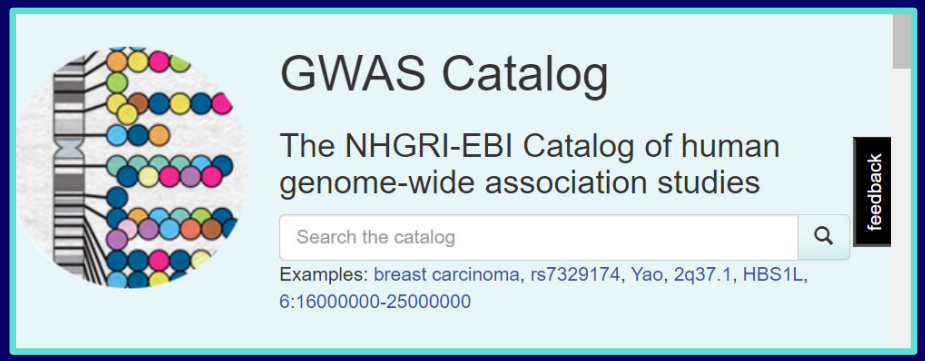
  Established Data Repositories and Knowledgebases
  NOT-OD-23-099

  Early-stage Data Repositories and Knowledgebases
  NOT-OD-23-093

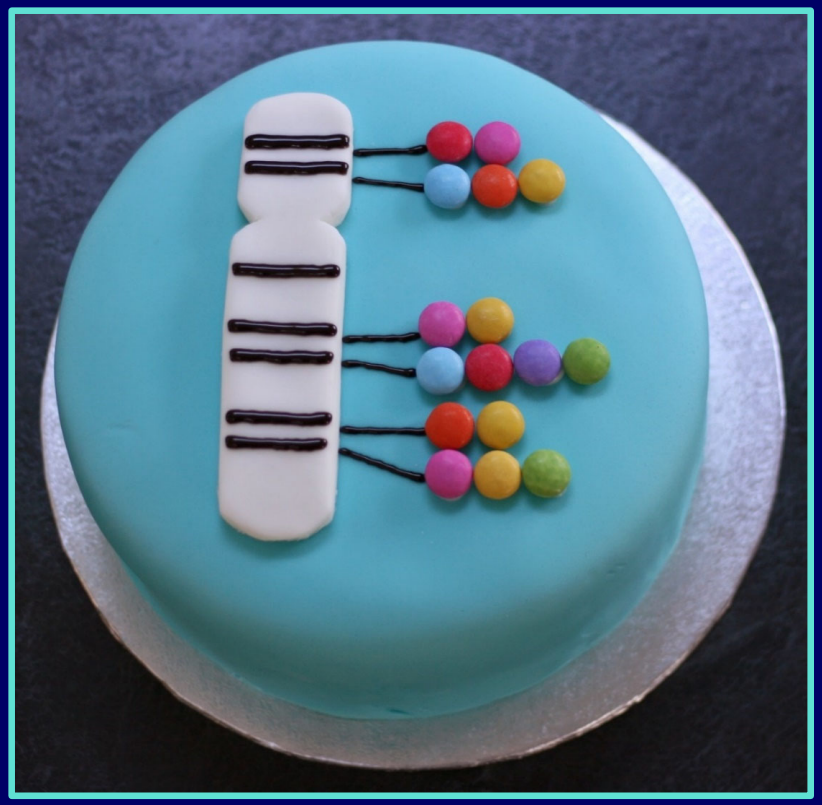
  Earliest estimated application due date: Fall 2023

Genome-Wide Association Studies (GWAS) Catalog

15th Anniversary



- **>515,000 curated associations from >6300 publications**
- **>60,000 user-submitted summary statistics**
- **>5,800 citations of the GWAS Catalog and associated papers**



Credit: Jackie MacArthur

eMERGE network
ELECTRONIC MEDICAL RECORDS AND GENOMICS

Genome-informed risk assessment (GIRA)

- ❑ PRS
- ❑ Monogenic risk
- ❑ Family health history
- ❑ Clinical covariates

eMERGE has returned 753 results & 156 high-risk results

eMERGE network

ELECTRONIC MEDICAL RECORDS AND GENOMICS

Marker paper published January 2023

ARTICLE

Returning integrated genomic risk and clinical recommendations: The eMERGE study

ARTICLE INFO

Article history:
Received 26 July 2022
Received in revised form
16 December 2022
Accepted 21 December 2022
Available online 6 January 2023

Keywords:
Common variants
Family history
Genotyping
Monogenic risks
Polygenic risk scores

ABSTRACT

Purpose: Assessing the risk of common, complex diseases requires consideration of clinical risk factors as well as monogenic and polygenic risks, which in turn may be reflected in family history. Returning risks to individuals and providers may influence preventive care or use of prophylactic therapies for those individuals at high genetic risk.
Methods: To enable integrated genetic risk assessment, the eMERGE (electronic MEdical Records and GEnomics) network is enrolling 25,000 diverse individuals in a prospective cohort study across 10 sites. The network developed methods to return cross-ancestry polygenic risk scores, monogenic risks, family history, and clinical risk assessments via a genome-informed risk assessment (GIRA) report and will assess uptake of care recommendations after return of results.
Results: GIRAs include summary care recommendations for 11 conditions, education pages, and clinical laboratory reports. The return of high-risk GIRA to individuals and providers includes guidelines for care and lifestyle recommendations. Assembling the GIRA required infrastructure and workflows for ingesting and presenting content from multiple sources. Recruitment began in February 2022.
Conclusion: Return of a novel report for communicating monogenic, polygenic, and family history-based risk factors will inform the benefits of integrated genetic risk assessment for routine health care.

Document 26

Clinical Sequencing Evidence-Generating Research Program (CSER)

- **CSER at ACMG 2023: 10 oral presentations & 9 posters**

Differences in genes implicated in disease comparing prenatal to pediatric patients (Sparks et al.)

Development and validation of new CSER-wide outcome measure to assess the impact of genomic sequencing on children and adults (Smith et al.)

Prenatal exome sequencing in an underrepresented population (Norton et al.)

cser
Clinical Sequencing Evidence-Generating Research

Clinical Sequencing Evidence-Generating Research Program (CSER)

Lessons Learned and Challenges

Research during the COVID-19 pandemic

> Am J Med Genet A. 2023 Feb;191(2):391-399. doi: 10.1002/ajmg.a.63033. Epub 2022 Nov 7.

Conducting clinical genomics research during the COVID-19 pandemic: Lessons learned from the CSER consortium experience

Stephanie A Kraft [1 2], Heidi Russell [3], Jeannette T Bensen [4], Katherine E Bonini [5], Jill O Robinson [6], Nuriye Sahin-Hodoglugil [7], Kathleen Renna [8 9], Lucia A Hindorff [8], Dave Kaufman [9], Carol R Horowitz [10], Margaret Waltz [11], Jamilyn M Zepp [12], Sara J Knight [13]

Designing and implementing research in underrepresented populations

> Contemp Clin Trials. 2023 Feb;125:107063. doi: 10.1016/j.cct.2022.107063. Epub 2022 Dec 22.

Lessons learned while starting multi-institutional genetics research in diverse populations: A report from the Clinical Sequencing Evidence-Generating Research (CSER) consortium

Heidi Russell [1], Hadley Stevens Smith [2], Jeannette T Bensen [3], Priyanka Murali [4], Bart S Ferket [5], Candice Finnila [6], Lucia A Hindorff [7], Nuriye Sahin-Hodoglugil [8]

Clinical Genome Resource (ClinGen)

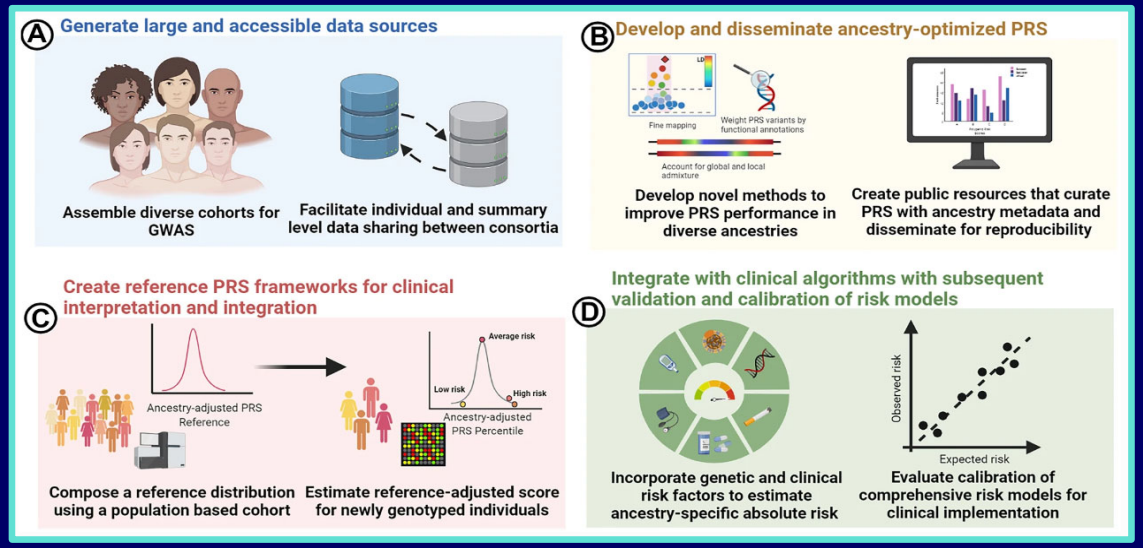
International Collaborations

H3Africa Workshop Participation

Variant Curation Interface Workshop, India 2022

Polygenic RIsk MEthods in Diverse Populations (PRIMED) Consortium

PRIMED consortium



- PRIMED publications (~32)
- Methods Review Working Group → Methods Development Working Group
- Joint meeting with eMERGE

emerge network
ELECTRONIC MEDICAL RECORDS AND GENOMICS

Document 29

Global Genomic Medicine Consortium (G2MC)

7th International Conference

- Campus Biotech in Geneva
- *Genomic Medicine for Everyone*
- Themes:
  - Implementation of Genomic Medicine
  - Collaboration
  - Diversity, Equity, & Inclusion (DEI) in Genomics
- Registration now open

Advancing Genomic Medicine Research (AGMR)

Notice of Intent to Publish a Notice of Funding Opportunity for Advancing Genomic Medicine Research (R01/ R21 Clinical Trial Optional)

Notice Numbers: NOT-HG-23-034, NOT-HG-23-035

Topics funded:

- Undiagnosed diseases
- EHR integrated tools
- Evidence for clinical & economic value
- Newborn screening
- Promoting access for underserved populations

Technology Development Program

Virtual Outreach Series

- Direct RNA Sequencing & Base Modifications
- Single-Molecule Protein Sequencing
- Advances in Single-Cell Analysis
- Genome-Scale Regulatory Mechanisms

All events are free, virtual, and open to the public

Registration is required

Small Business Program

Transition Grant Opportunity

- Funding for early-career academic scientists interested in transitioning to entrepreneurship while supporting technology transfer
- Unique fast-track mechanism:
  Phase I STTR → Phase II SBIR
- Mentorship required and entrepreneurship training provided
- Partnership with NCI, NIBIB, and NIDA
- Applications due August 21, 2023

SBIR · STTR
America's Seed Fund

Training and Career Development Program

- 8th Annual Training Meeting
- Hosted by Duke University and held in Salt Lake City
- 300 in-person attendees and 50 virtual attendees

Genomics Workforce Diversity Programs

Notices of Funding Opportunities

- **PAR-23-123: Entry-Level Modules (ELM) for Training the Genomics Research Workforce**

  Receipt date: June 1

- **PAR-23-137: NIH Science Education Partnership Award (SEPA)**

  Receipt date: July 14

Extramural Investigator-Initiated Highlights

Multi-ancestry transcriptome-wide association analyses yield insights into tobacco use biology and drug repurposing

Fang Chen, Xing
Khunsriraksakul,
Allison E. Ashley
Bis, John Blange
Chuang, Adolfo

A *cis*-regulatory lexicon of DNA motif combinations mediating cell-type-specific gene regulation

Laura K.H. Donoh
Poornima H. Neel
and Paul A. Khava

"Extremely slow and capricious": A qualitative exploration of genetic researcher priorities in selecting shared data resources

M. Grace Trinidad[1], Kerry A. Ryan[2], Chris D. Krenz[2], J. Scott Roberts[2,3], Amy L. McGuire[4], Raymond De Vries[1,2,5], Brian J. Zikmund-Fisher[2,3], Sharon Kardia[6], Erica Marsh[5], Jane Forman[7], Madison Kent[8], David Wilborn[9], Kayte Spector-Bagdady[2,5,*]

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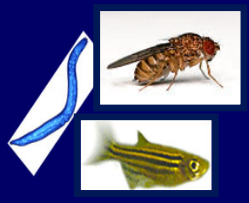
Undiagnosed Diseases Network

Solving Medical Mysteries Through Team Science

Applications: 6354 → **Accepted: 2535**

Clinical Evaluations: 2159

Sequencing: 2180



Model Organisms: 301

Metabolomics: 312

Diagnosed: 679

Data Sharing

Manuscripts published: **210**

Variant interpretations submitted to ClinVar: **647**

Records shared across Matchmaker Exchange: **1991**

Undiagnosed Diseases Network

- **Transition from NIH Common Fund support to Trans-NIH support**

  Led by NINDS and supported by 16 NIH institutes and centers:

  NCATS, NCCIH, NCI, NEI, NHGRI, NHLBI, NIA, NIAID, NIAMS, NICHD, NIDCD, NIDCR, NIDDK, NIEHS, NIGMS, NLM

- **Vision: evolve into a larger, self-sustained network to provide expert diagnostic services for undiagnosed patients and to foster scientific discovery**

- **Data Management Coordinating Center (Fiscal Year 2023-2027)**

  Awarded to Harvard Medical School (PI: Kohane)

- **Diagnostic Centers of Excellence**

Bridge to Artificial Intelligence (Bridge2AI)

- **Four Centers:**
  - Functional genomics
  - Voice as a biomarker of disease
  - AI/ML in acute care
  - Human health restoration after disease
- **Bridge Center for cross-program coordination and dissemination**
- **First Bridge2AI in-person consortium meeting in April**

Somatic Mosaicism Across Human Tissues (SMaHT)

Tissue Procurement Center

Data Analysis Center

Organizational Center

Genome Characterization Centers

Baylor College of Medicine
Broad Institute
New York Genome Center
Seattle Children's Hospital
Washington University

Tools and Technology Development Awards

All of Us
RESEARCH PROGRAM

- Release of nearly 250,000 whole-genome sequences
- 45% of data from people who identify as a member of a group underrepresented in medical research

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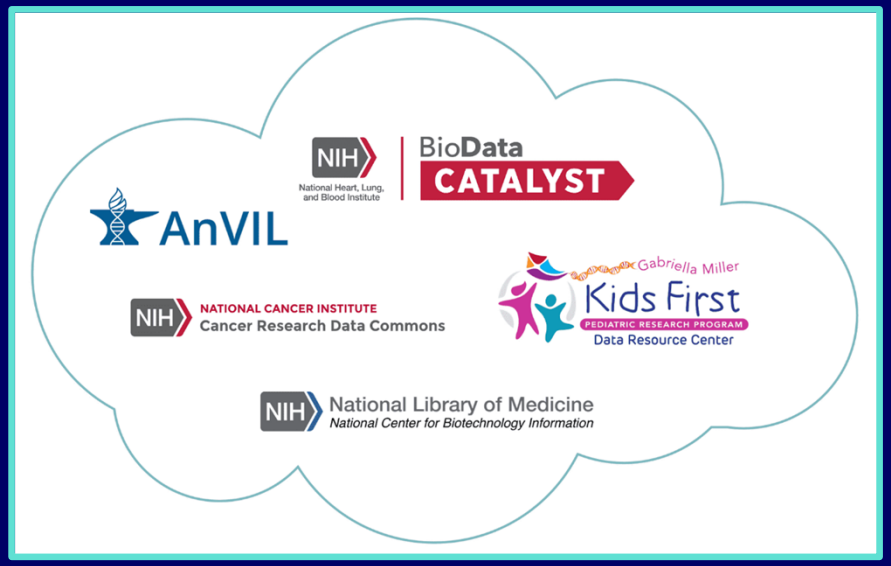
NIH Cloud Platform Interoperability (NCPI)



- Establish a trans-NIH, cloud-based, federated data ecosystem
- NCPI Administrative Coordinating Center
- Solicitations for interoperability projects

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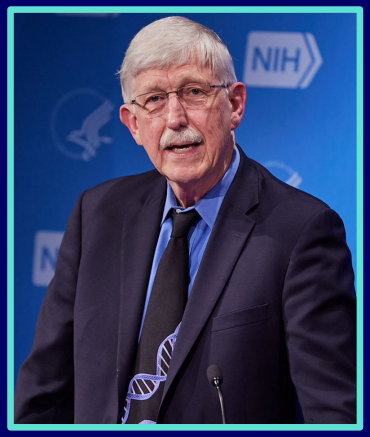
2023 Genomics Anniversaries



Document 42

New NHGRI Videos on GenomeTV/YouTube

Purifying Strawberry DNA

Sequencing a Genome

Document 44

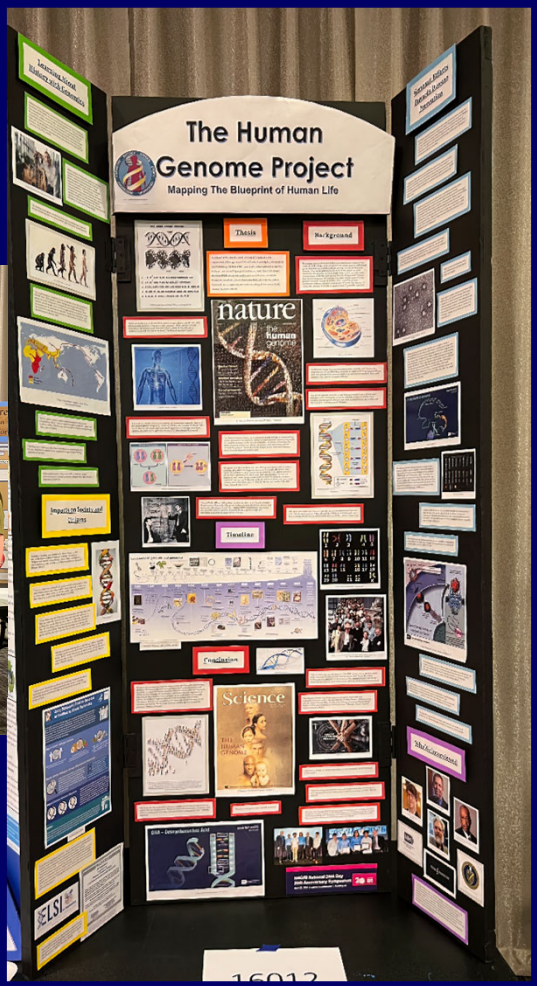
Human Genome Project 'G5' Virtual Reunion

Document 45

Genome: Unlocking Life's Code Exhibition Pieces Now on Display at NIH

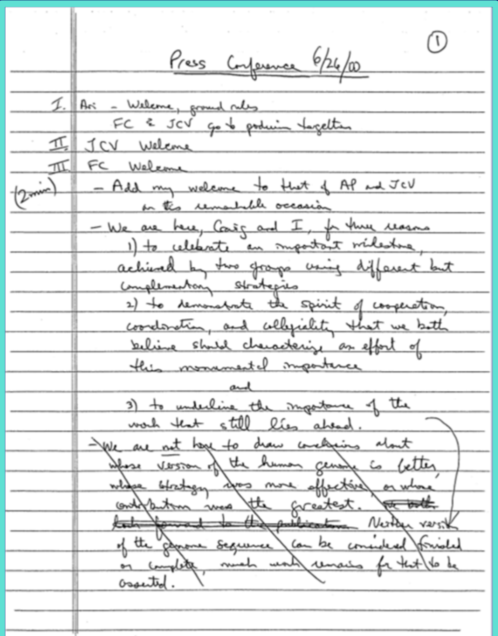
- Opened in 2013, traveled to 12 U.S. states and Canada
- Attracted millions of visitors over the last 10 years
- Five pieces of the exhibition now on display at NIH

Genomics Featured in National History Day



NHGRI History of Genomics Program

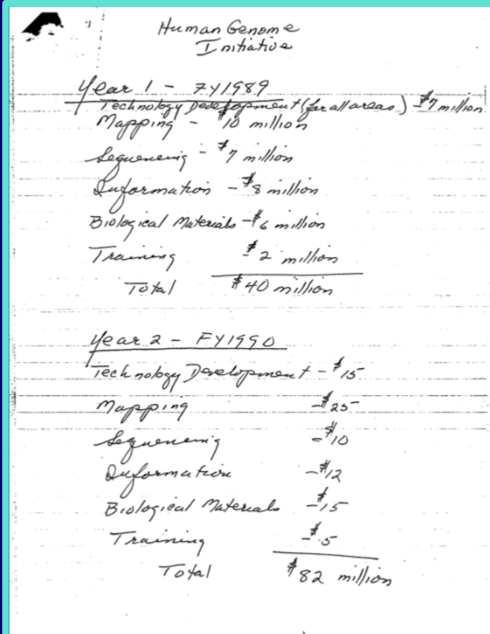
Archive Highlight



①

Press Conference 6/26/00

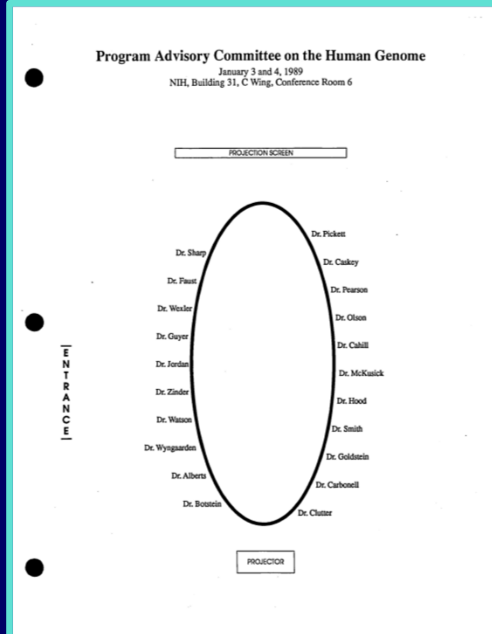
I. Ari – Welcome, ground rules
FC & JCV go to podium together
II. JCV Welcome
III. FC Welcome
(2 min) – Add my welcome to that of AP and JCV on this remarkable occasion
– We are here, Craig and I, for three reasons
1) to celebrate an important milestone, achieved by two groups using different but complementary strategies
2) to demonstrate the spirit of cooperation, coordination, and collegiality that we both believe should characterize an effort of this monumental importance
and
3) to underline the importance of the work that still lies ahead.
– We are not here to draw conclusions about whose version of the human genome is better, whose strategy was more effective, or whose contribution was the greatest. ~~We both look forward to the publications~~ Neither version of the genome sequence can be considered finished or complete, much work remains for that to be asserted.



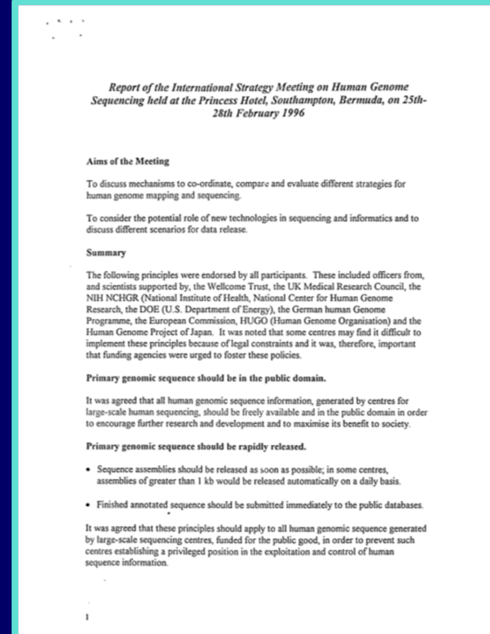
Human Genome Initiative

Year 1 – FY1989
Technology Development (for all areas) $7 million
Mapping – 10 million
Sequencing – $7 million
Informatics – $8 million
Biological Materials – $6 million
Training $2 million
Total $40 million

Year 2 – FY1990
Technology Development – $15
Mapping $25
Sequencing – $10
Informatics – $12
Biological Materials – $15
Training – $5
Total $82 million



Program Advisory Committee on the Human Genome
January 3 and 4, 1989
NIH, Building 31, C Wing, Conference Room 6



Report of the International Strategy Meeting on Human Genome Sequencing held at the Princess Hotel, Southampton, Bermuda, on 25th-28th February 1996

Aims of the Meeting

To discuss mechanisms to co-ordinate, compare and evaluate different strategies for human genome mapping and sequencing.

To consider the potential role of new technologies in sequencing and informatics and to discuss different scenarios for data release.

Summary

The following principles were endorsed by all participants. These included officers from, and scientists supported by, the Wellcome Trust, the UK Medical Research Council, the NIH NCHGR (National Institute of Health, National Center for Human Genome Research, the DOE (U.S. Department of Energy), the German human Genome Programme, the European Commission, HUGO (Human Genome Organisation) and the Human Genome Project of Japan. It was noted that some centres may find it difficult to implement these principles because of legal constraints and it was, therefore, important that funding agencies were urged to foster these policies.

Primary genomic sequence should be in the public domain.

It was agreed that all human genomic sequence information, generated by centres for large-scale human sequencing, should be freely available and in the public domain in order to encourage further research and development and to maximise its benefit to society.

Primary genomic sequence should be rapidly released.

- Sequence assemblies should be released as soon as possible; in some centres, assemblies of greater than 1 kb would be released automatically on a daily basis.
- Finished annotated sequence should be submitted immediately to the public databases.

It was agreed that these principles should apply to all human genomic sequence generated by large-scale sequencing centres, funded for the public good, in order to prevent such centres establishing a privileged position in the exploitation and control of human sequence information.

1

Inter-Society Committee for Practitioner Education in Coordinating Genomics (ISCC-PEG)

ISCC-PEG 12th Annual Meeting

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New Chief, Education and Community Involvement Branch

Beth Tuck, M.A.

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 Communications, Policy, and Education

VII. NHGRI Intramural Research Program

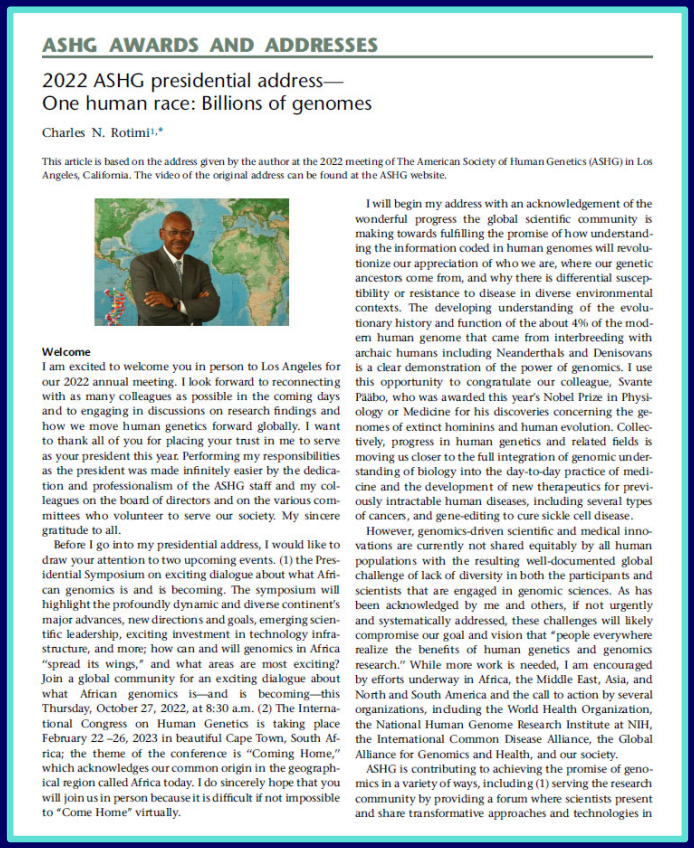
Samuel J. Heyman Service to America Medal Finalists

PARTNERSHIP FOR PUBLIC SERVICE

SAMUEL J. HEYMAN SERVICE TO AMERICA MEDALS

American Society of Human Genetics

2022 Presidential Address



ASHG AWARDS AND ADDRESSES

2022 ASHG presidential address—
One human race: Billions of genomes

Charles N. Rotimi[1,*]

This article is based on the address given by the author at the 2022 meeting of The American Society of Human Genetics (ASHG) in Los Angeles, California. The video of the original address can be found at the ASHG website.

Welcome

I am excited to welcome you in person to Los Angeles for our 2022 annual meeting. I look forward to reconnecting with as many colleagues as possible in the coming days and to engaging in discussions on research findings and how we move human genetics forward globally. I want to thank all of you for placing your trust in me to serve as your president this year. Performing my responsibilities as the president was made infinitely easier by the dedication and professionalism of the ASHG staff and my colleagues on the board of directors and on the various committees who volunteer to serve our society. My sincere gratitude to all.

Before I go into my presidential address, I would like to draw your attention to two upcoming events. (1) the Presidential Symposium on exciting dialogue about what African genomics is and is becoming. The symposium will highlight the profoundly dynamic and diverse continent's major advances, new directions and goals, emerging scientific leadership, exciting investment in technology infrastructure, and more; how can and will genomics in Africa "spread its wings," and what areas are most exciting? Join a global community for an exciting dialogue about what African genomics is—and is becoming—this Thursday, October 27, 2022, at 8:30 a.m. (2) The International Congress on Human Genetics is taking place February 22 –26, 2023 in beautiful Cape Town, South Africa; the theme of the conference is "Coming Home," which acknowledges our common origin in the geographical region called Africa today. I do sincerely hope that you will join us in person because it is difficult if not impossible to "Come Home" virtually.

I will begin my address with an acknowledgement of the wonderful progress the global scientific community is making towards fulfilling the promise of how understanding the information coded in human genomes will revolutionize our appreciation of who we are, where our genetic ancestors come from, and why there is differential susceptibility or resistance to disease in diverse environmental contexts. The developing understanding of the evolutionary history and function of the about 4% of the modern human genome that came from interbreeding with archaic humans including Neanderthals and Denisovans is a clear demonstration of the power of genomics. I use this opportunity to congratulate our colleague, Svante Pääbo, who was awarded this year's Nobel Prize in Physiology or Medicine for his discoveries concerning the genomes of extinct hominins and human evolution. Collectively, progress in human genetics and related fields is moving us closer to the full integration of genomic understanding of biology into the day-to-day practice of medicine and the development of new therapeutics for previously intractable human diseases, including several types of cancers, and gene-editing to cure sickle cell disease.

However, genomics-driven scientific and medical innovations are currently not shared equitably by all human populations with the resulting well-documented global challenge of lack of diversity in both the participants and scientists that are engaged in genomic sciences. As has been acknowledged by me and others, if not urgently and systematically addressed, these challenges will likely compromise our goal and vision that "people everywhere realize the benefits of human genetics and genomics research." While more work is needed, I am encouraged by efforts underway in Africa, the Middle East, Asia, and North and South America and the call to action by several organizations, including the World Health Organization, the National Human Genome Research Institute at NIH, the International Common Disease Alliance, the Global Alliance for Genomics and Health, and our society.

ASHG is contributing to achieving the promise of genomics in a variety of ways, including (1) serving the research community by providing a forum where scientists present and share transformative approaches and technologies in

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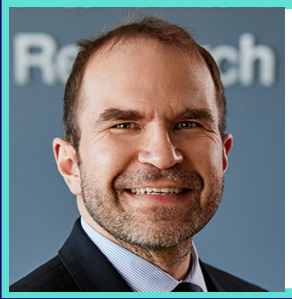
NHGRI Intramural Research Highlights

Biological Psychiatry

The impact of Mmu17 non-Hsa21 orthologous genes in the Ts65Dn mouse model of Down syndrome: the "gold standard" refuted

ScienceAdvances

The dogs of Chernobyl: Demographic insights into populations inhabiting the nuclear exclusion zone



nature biotechnology

Telomere-to-telomere assembly of diploid chromosomes with Verkko

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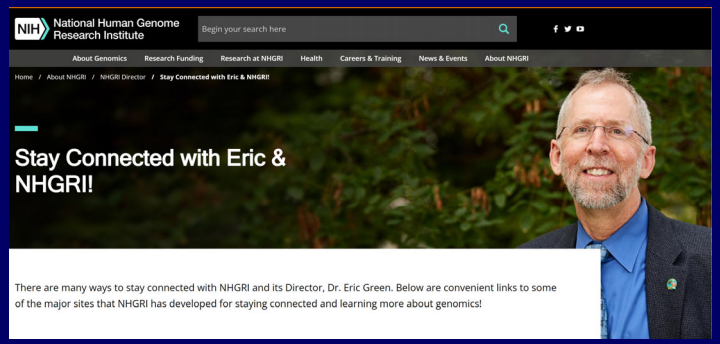
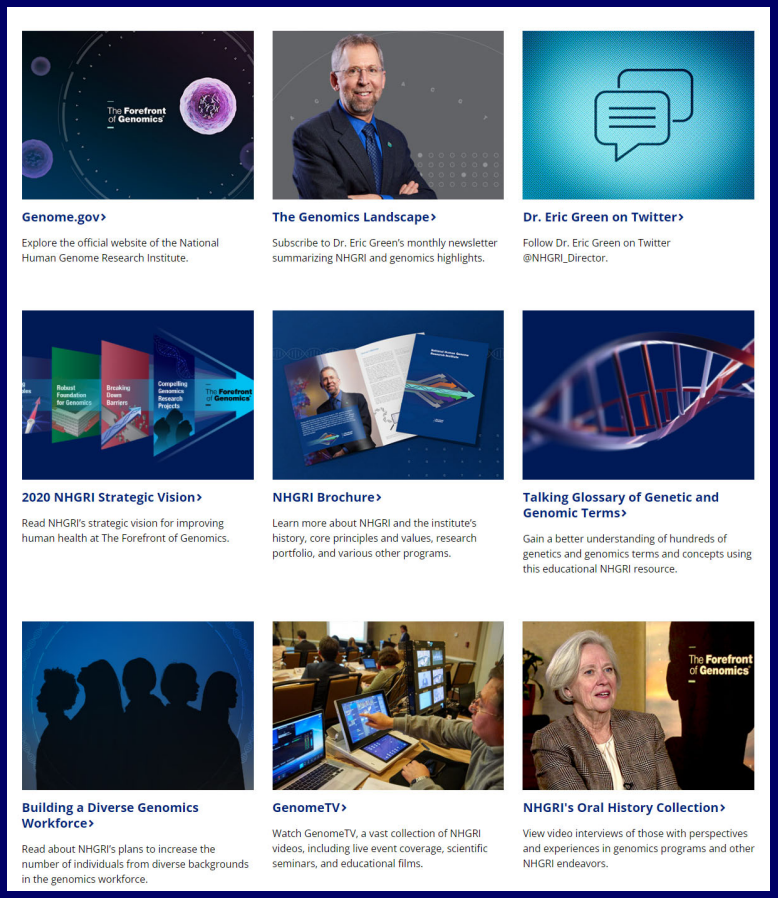
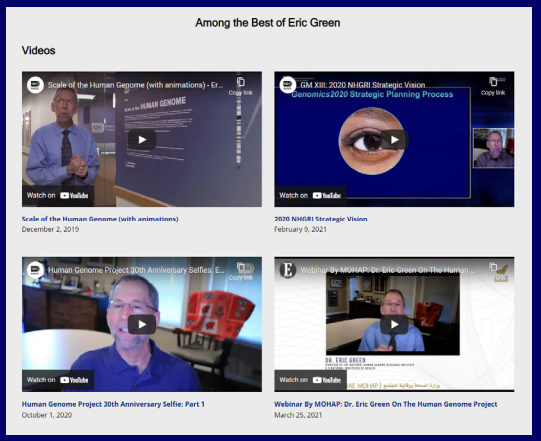
‘One-Stop-Shop’ to Stay Connected

genome.gov/stayconnected







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National Human Genome Research Institute

Thanks!

Special Thanks!


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of Genomics®