TEXAS TECH UNIVERSITY
HEALTH SCIENCES CENTER

Through the Looking Glass: Genetic Information Resources for You, Health Care Professionals, and Researchers

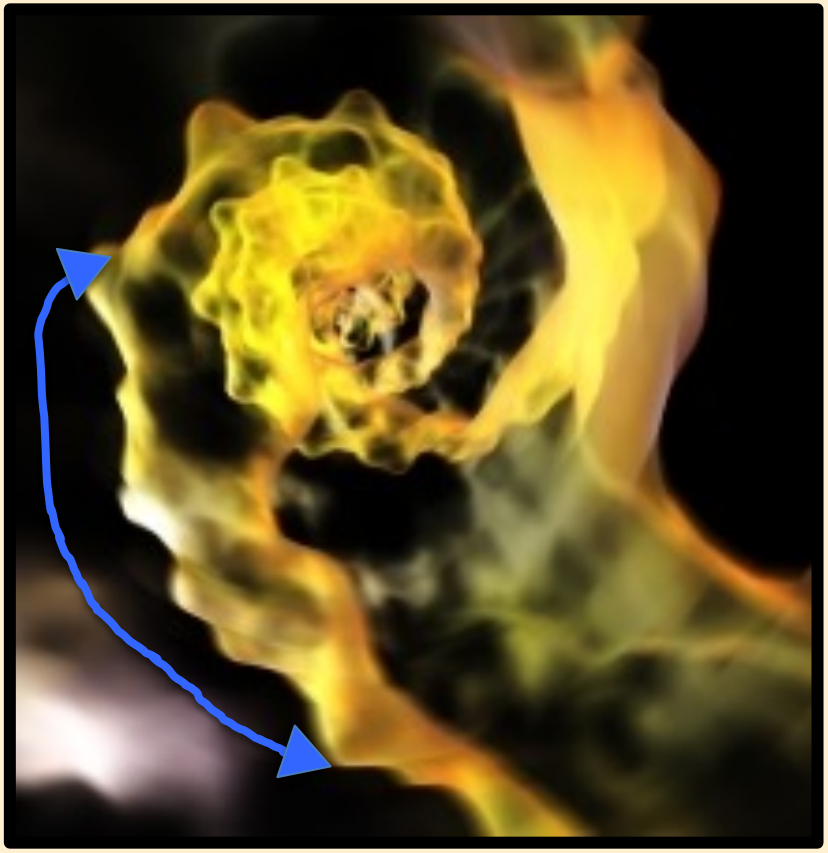
Texas Tech Universities Health Sciences Center Libraries – Peggy Edwards, AMLS

Let’s go on a journey…

using x-ray crystallographic diffraction!

Retrieved January 5, 2015 from http://www.neurtrons.ornl.gov

What is it?



Spiral IV – X-ray crystallographic data was used from real DNA molecules to paint a unique portrait of the double helix. The image omits the chemical bonds that crisscross the center of the molecule, so that the structural features of the helix, such as the major and minor grooves, can be seen more easily.

Credit: Kenneth Eward, BioGrafx Scientific & Medical Images, Ovid Michigan

Retrieved January 5, 2015 from http://www.nsf.gov/news/mmg/mmg_disp.jsp?med_id=70960

Who are they?

J. Craig Venter, Ph.D.
founder Celera Genomics,
The Institute for Genomic Research, &
J. Craig Venter Institute

Retrieved January 5, 2015 from http://www.nsf.gov

Francis Collins, M.D.
director (in the year 2000) of
National Center for Human
Genome Research

Retrieved January 5, 2015 from http://www.nih.gov

The Human Genome Project

Identified and mapped all genes in human genome

Largest international collaborative effort ever

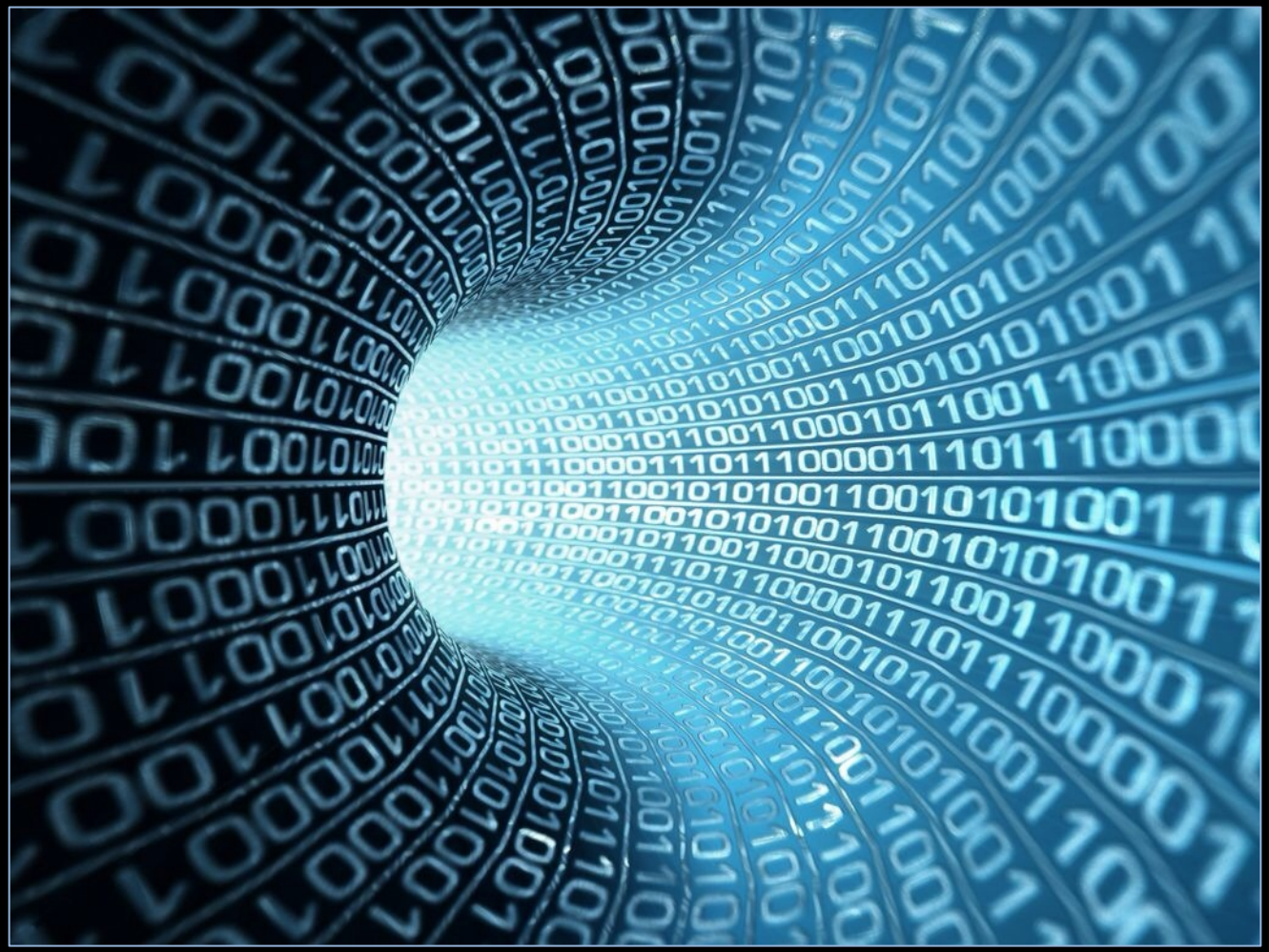
Dr. Collins directed
NIH's public project

Dr. Venter directed
Celera's private project

Completed in February 2001

Retrieved January 5, 2015 from http://www.genome.gov

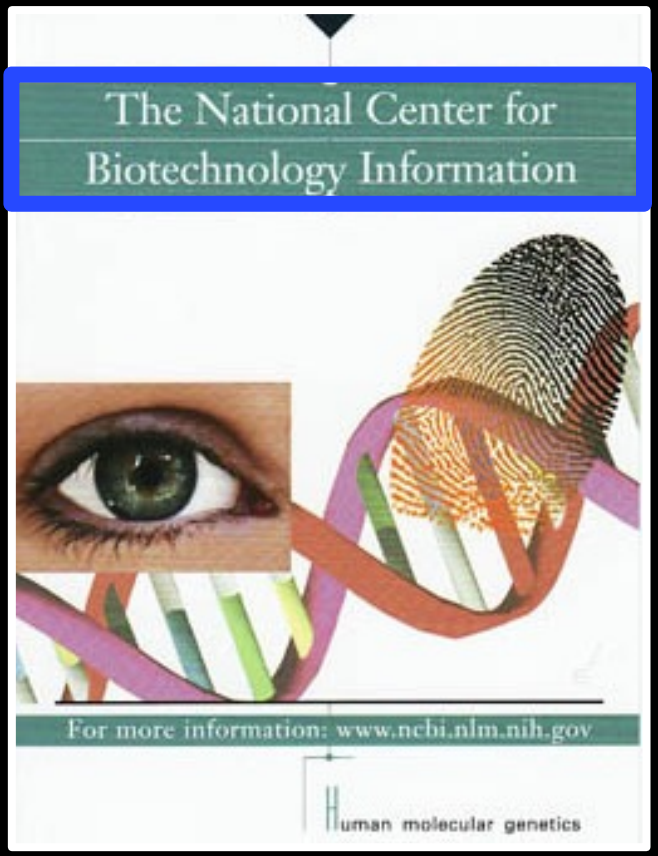
Genetics Research Produces Big Data!!

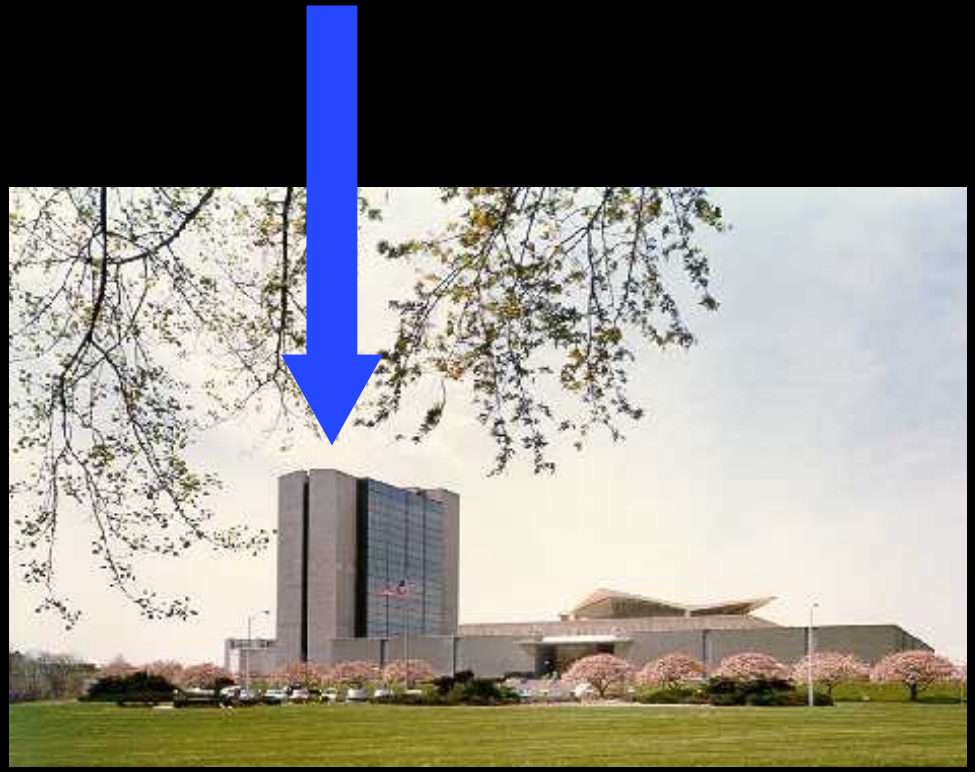


Retrieved January 5, 2015 from http://www.ndep.nv.gov

NCBI's Databases are Freely Available for Anyone!

Produced by





at the National Library of Medicine

at the National Institutes of Health

Retrieved January 5, 2015 from http://ncbi.gov

Retrieved January 5, 2015 from http://www.nlm.nih.gov

But I'm Not a Scientist or a Doctor or …

Why is this important to me???

http://www.research.archives.gov

Angelina Jolie

Breast Cancer

www.loc.gov

Abraham Lincoln

Marfan's Syndrome

Genetic predispositions or inherited diseases!

http://www.directorsblog.nih.gov

Sam Berns

Progeria

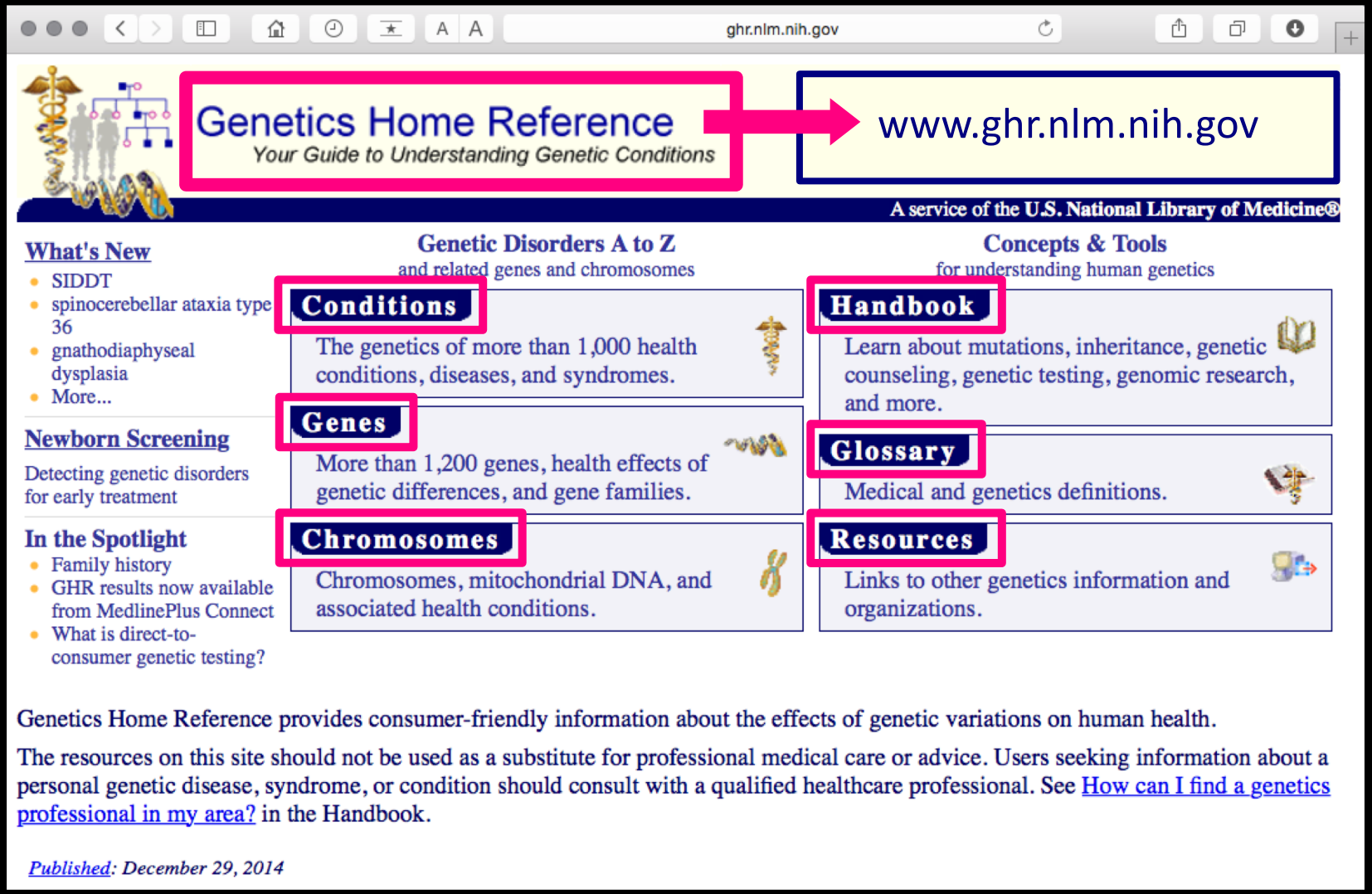
http://www.blogs.america.gov

Sonia Sotomayor

Type 1 Diabetes

All images retrieved January, 2015

Free Genetic Information Resources for Everyone!



What is Progeria?

Sam Berns

ghr.nlm.nih.gov

Genetics Home Reference
Your Guide to Understanding Genetic Conditions

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Conditions >

Hutchinson-Gilford progeria syndrome

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- Related Gene(s)
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MedlinePlus
Health information

Genetic and Rare Diseases Information Center
Information about genetic conditions and rare diseases

Additional NIH Resources
National Institutes of Health

Educational resources
Information pages

Patient support
For patients and families

Gene Reviews
Clinical summary

Genetic Testing Registry
Genetic testing

ClinicalTrials.gov
Research studies

PubMed
Recent literature

OMIM
Genetic disorder catalog

External link disclaimer

On this page: Description | Genetic changes | Inheritance | Diagnosis | Additional information | Other names | Glossary definitions

Reviewed July 2007

What is Hutchinson-Gilford progeria syndrome?

Hutchinson-Gilford progeria syndrome is a genetic condition characterized by the dramatic, rapid appearance of aging beginning in childhood. Affected children typically look normal at birth and in early infancy, but then grow more slowly than other children and do not gain weight at the expected rate (failure to thrive). They develop a characteristic facial appearance including prominent eyes, a thin nose with a beaked tip, thin lips, a small chin, and protruding ears. Hutchinson-Gilford progeria syndrome also causes hair loss (alopecia), aged-looking skin, joint abnormalities, and a loss of fat under the skin (subcutaneous fat). This condition does not disrupt intellectual development or the development of motor skills such as sitting, standing, and walking.

People with Hutchinson-Gilford progeria syndrome experience severe hardening of the arteries (arteriosclerosis) beginning in childhood. This condition greatly increases the chances of having a heart attack or stroke at a young age. These serious complications can worsen over time and are life-threatening for affected individuals.

How common is Hutchinson-Gilford progeria syndrome?

This condition is very rare; it is reported to occur in 1 in 4 million newborns worldwide. More than 130 cases have been reported in the scientific literature since the condition was first described in 1886.

What genes are related to Hutchinson-Gilford progeria syndrome?

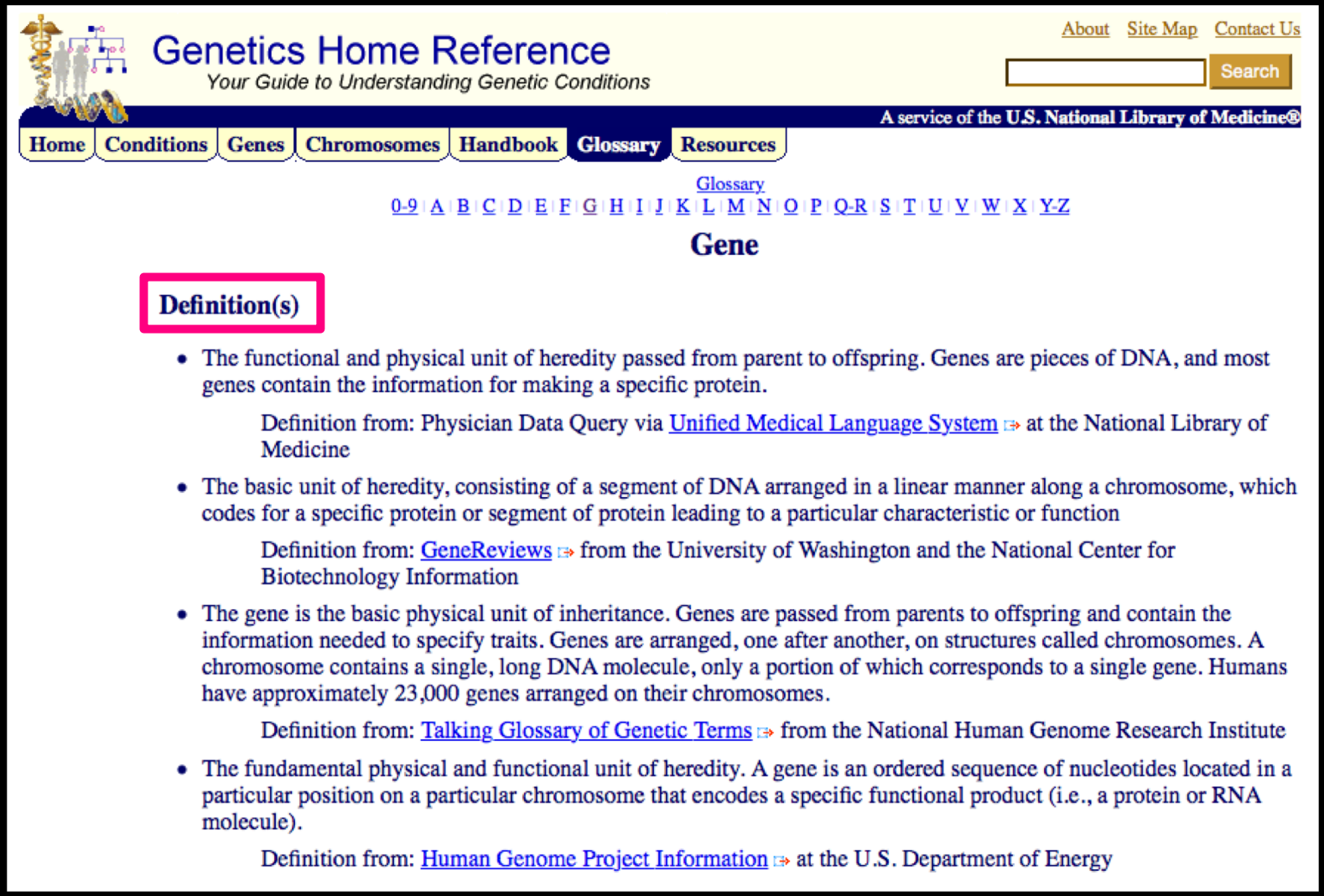
Mutations in the *LMNA* gene cause Hutchinson-Gilford progeria syndrome.

The *LMNA* gene provides instructions for making a protein called lamin A. This protein plays an important role in determining the shape of the nucleus within cells. It is an essential scaffolding (supporting) component of the nuclear envelope, which is the membrane that surrounds the nucleus. Mutations that cause Hutchinson-Gilford progeria syndrome result in the production of an abnormal version of the lamin A protein. The altered protein makes the nuclear envelope unstable and progressively damages the nucleus, making cells more likely to die prematurely. Researchers are working to determine how these changes lead to the characteristic features of Hutchinson-Gilford progeria syndrome.

Read more about the *LMNA* gene.

Retrieved January, 2015 from http://www.directorsblog.nih.gov

What is a gene?



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Your Guide to Understanding Genetic Conditions

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Glossary

0-9 | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q-R | S | T | U | V | W | X | Y-Z

Gene

Definition(s)

- The functional and physical unit of heredity passed from parent to offspring. Genes are pieces of DNA, and most genes contain the information for making a specific protein.

  Definition from: Physician Data Query via Unified Medical Language System at the National Library of Medicine

- The basic unit of heredity, consisting of a segment of DNA arranged in a linear manner along a chromosome, which codes for a specific protein or segment of protein leading to a particular characteristic or function

  Definition from: GeneReviews from the University of Washington and the National Center for Biotechnology Information

- The gene is the basic physical unit of inheritance. Genes are passed from parents to offspring and contain the information needed to specify traits. Genes are arranged, one after another, on structures called chromosomes. A chromosome contains a single, long DNA molecule, only a portion of which corresponds to a single gene. Humans have approximately 23,000 genes arranged on their chromosomes.

  Definition from: Talking Glossary of Genetic Terms from the National Human Genome Research Institute

- The fundamental physical and functional unit of heredity. A gene is an ordered sequence of nucleotides located in a particular position on a particular chromosome that encodes a specific functional product (i.e., a protein or RNA molecule).

  Definition from: Human Genome Project Information at the U.S. Department of Energy

My Doctor says I have a BRCA2 gene variant -

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Genes > ***BRCA2***

Print version

- Related Condition(s)
- References
- Quick links to this topic

Educational resources
Information pages

Gene Reviews
Clinical summary

Genetic Testing Registry
Genetic testing

On this page: Name | Normal function | Gene families | Genetic changes | Gene location | Additional information | Other names | About genes | Glossary definitions

Reviewed August 2007

What is the official name of the *BRCA2* gene?

The official name of this gene is "breast cancer 2, early onset."

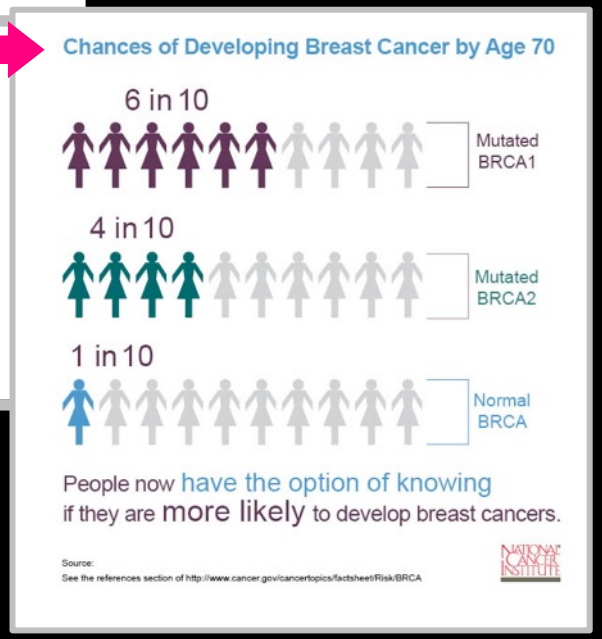
BRCA2 is the gene's official symbol. The *BRCA2* gene is also known by other names, listed below.

Read more about gene names and symbols on the About page.

How are changes in the *BRCA2* gene related to health conditions?

breast cancer - increased risk from variations of the *BRCA2* gene

Researchers have identified more than 800 mutations in the *BRCA2* gene, many of which are associated with an increased risk of breast cancer. Many *BRCA2* mutations insert or delete a small number of DNA building blocks (nucleotides) in the gene. Most of these genetic changes disrupt protein production from one copy of the gene in each cell, resulting in an abnormally small, nonfunctional version of the BRCA2 protein. Researchers believe that the defective BRCA2 protein is unable to help repair damaged DNA or fix mutations that occur in other genes. As these defects accumulate, they can allow cells to grow and divide uncontrollably and form a tumor.



Which chromosome is related to Down Syndrome?

Down syndrome

Down syndrome is a chromosomal condition that is associated with intellectual disability, a characteristic facial appearance, and weak muscle tone (hypotonia) in infancy. This condition is most often caused by trisomy 21. Trisomy 21 means that each cell in the body has three copies of chromosome 21 instead of the usual two copies.

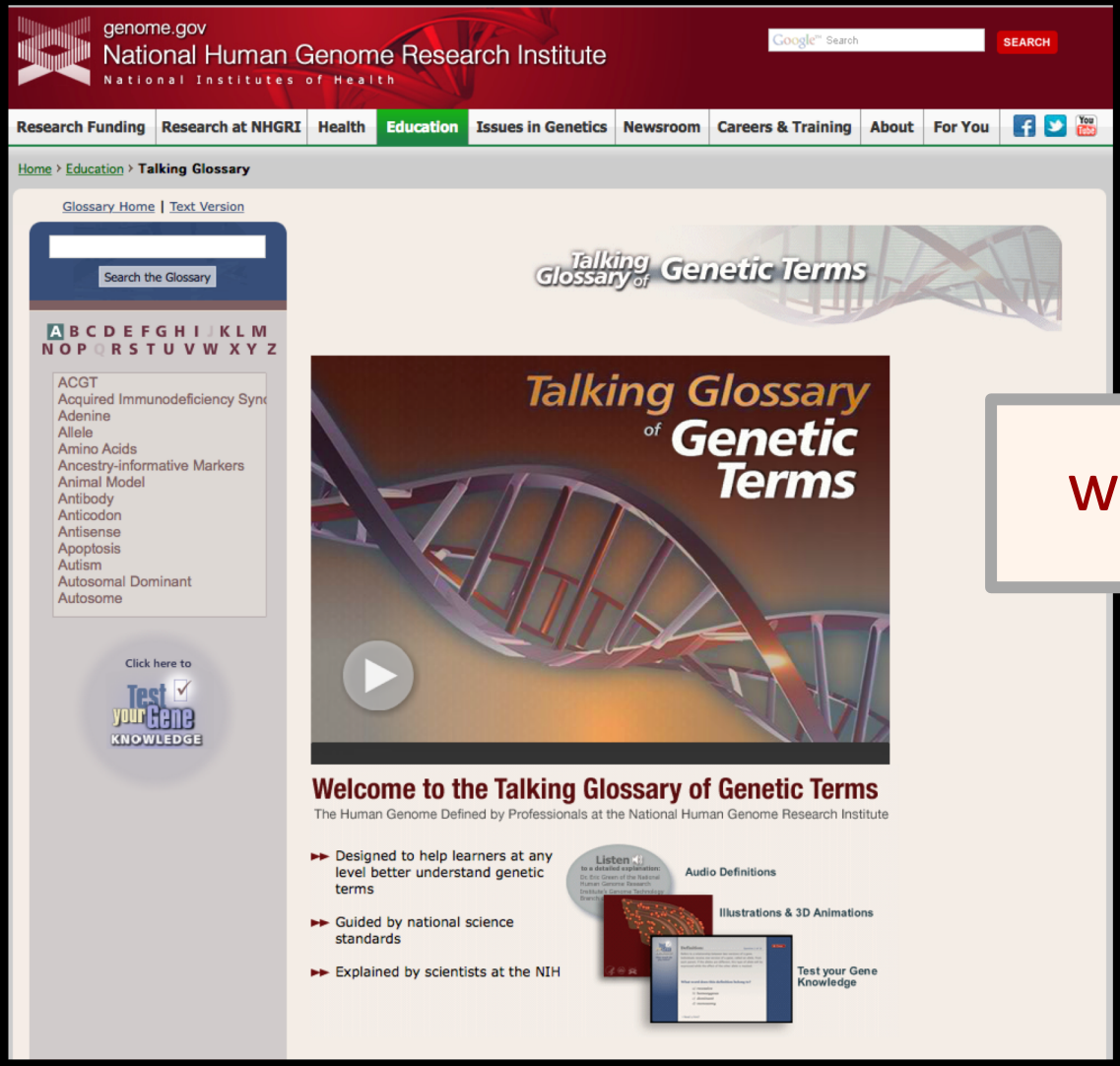
Less commonly, Down syndrome occurs when part of chromosome 21 becomes attached (translocated) to another chromosome during the formation of reproductive cells (eggs and sperm) or very early in fetal development. Affected people have two copies of chromosome 21 plus extra material from chromosome 21 attached to another chromosome, resulting in three copies of genetic material from chromosome 21. Affected individuals with this genetic change are said to have translocation Down syndrome.

In a very small percentage of cases, Down syndrome results from an extra copy of chromosome 21 in only some of the body's cells. In these people, the condition is called mosaic Down syndrome.

Researchers believe that having extra copies of genes on chromosome 21 disrupts the course of normal development, causing the characteristic features of Down syndrome and the increased risk of health problems associated with this condition.

Retrieved January 5, 2015 from http://nichd.nih.gov

Talking Glossary of Genetic Terms



www.genome.gov

Talking Glossary of Genetic Terms

Search the Glossary

A B C D E F G H I J K L
N O P Q R S T U V W X

Deletion
Diabetes (Diabetes Mellitus)
Diploid
DNA (Deoxyribonucleic Acid)
DNA Fingerprinting
DNA Replication
DNA Sequencing
Dominant
Double Helix
Down Syndrome (Trisomy 21
Duplication

Deletion

Pronunciation

Deletion is a type of mutation involving the loss of genetic material. It can be small, involving a single missing DNA base pair, or large, involving a piece of a chromosome.

Listen
Maximilian Muenke, M.D. defines Deletion

Profile | Illustration

Maximilian Muenke, M.D.

Chief and Senior Investigator, Medical Genetics Branch; Head, Human Development Section; Director, Medical Genetics Residency and Fellowship Training Programs and Combined Pediatrics and Medical Genetics Residency Training Program

Dr. Muenke's research program seeks to improve knowledge about the formation of the central nervous system and to elucidate the origin of developmental disabilities and mental retardation. Specifically, his laboratory investigates birth defects that affect normal embryonic development and lead to neurological impairment. His two major areas of focus are holoprosencephaly (HPE) and attention deficit hyperactivity disorder (ADHD). Holoprosencephaly is a common birth defect characterized by the failure of the brain to divide properly into left and right hemispheres during early development. Children born with HPE show various degrees of developmental disabilities and mental retardation.

Send this term to a friend | How to cite this term for research papers

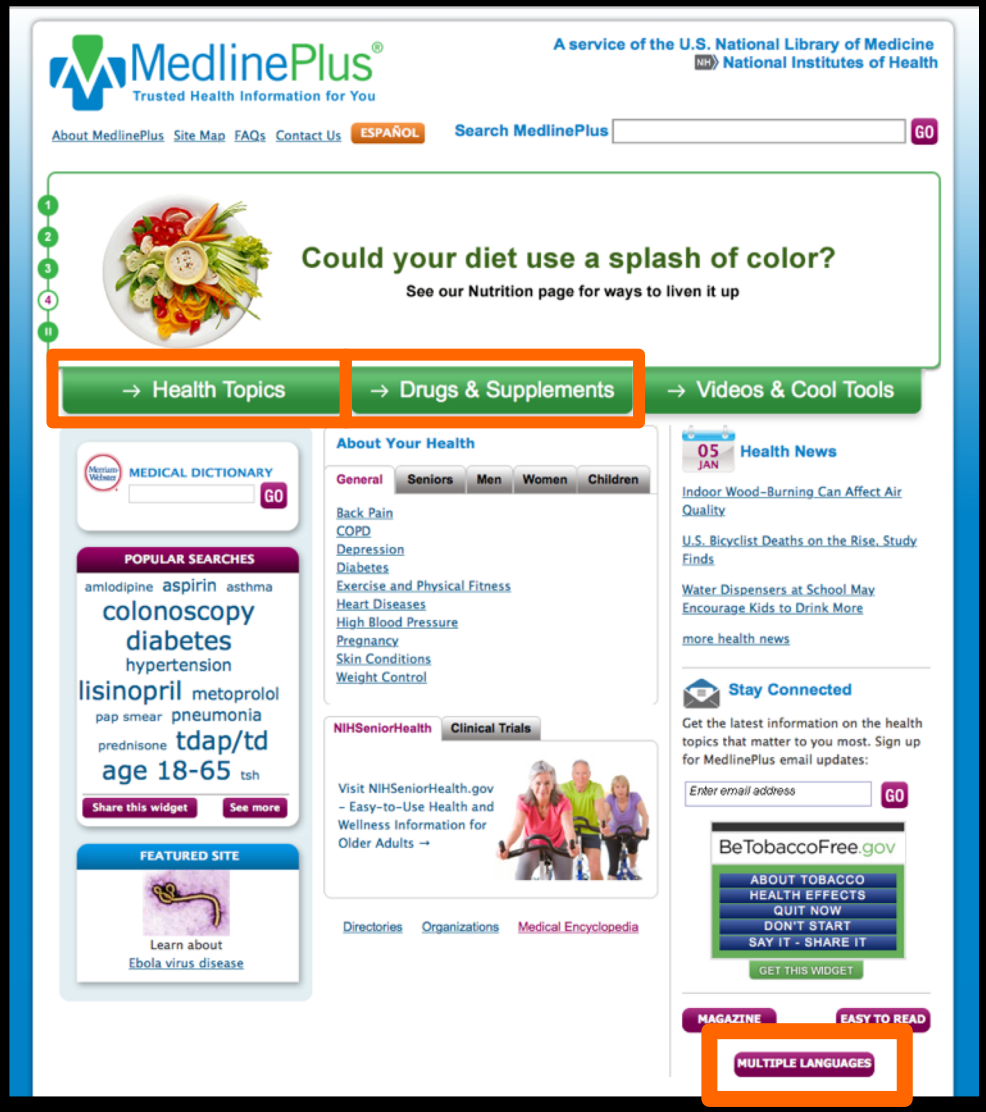
Related Terms

- Base Pair
- Chromosome
- DNA (Deoxyribonucleic Acid)
- Gene
- Mutation

Illustrations

- Download PDF
- Download PPT

I want to know more about health …



www.MedlinePlus.gov

from National Library of Medicine at N.I.H.

free, reliable information

easy to understand

links to more resources

many different languages

I’m a Clinician or a Nurse or a Therapist…

Why is this important to me???

Web-Based Resources for Clinical Bioinformatics

Anthony M. Joshua and Paul C. Boutros

Methods in Molecular Medicine. 2008; 141:309-29

PMID: 18453097

In the post-Human Genome Project era, awareness of the resources available through the internet is essential to both molecular biologists and clinicians.

… (it) is important to understand the principles upon which hypotheses are generated, experiments are based and conclusions reached.

… (knowing about) resources often facilitates their use and adoption

Have you had a lot of flu patients?

Centers for Disease Control and Prevention
CDC 24/7: Saving Lives, Protecting People™

Influenza (Flu)

Recommend Tweet Share

The most recent FluView report for the 2014-2015 flu season shows that flu season in the United States has begun and about half the country is experiencing high levels of flu activity. Reports of flu illnesses, hospitalizations and deaths are elevated. Activity is expected to continue for several weeks, especially in parts of the country that have not yet seen significant activity.

Retrieved January 5, 2015 from http://www.nih.gov

Data from NIAID Influenza Genome Sequencing Project and GenBank

data essential to identification of the genetic determinants of influenza pathogenicity

tools for flu sequence analysis

DNA & clinical data related to human Major Histocompatibility Complex

MHC:
array of genes that play a central role in

susceptibility to infectious diseases

the success of organ transplants

Retrieved January 5, 2015 from http://www.iipdigital.usembassy.gov and www.health.wyo.gov

National Human Genome Research Institute

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

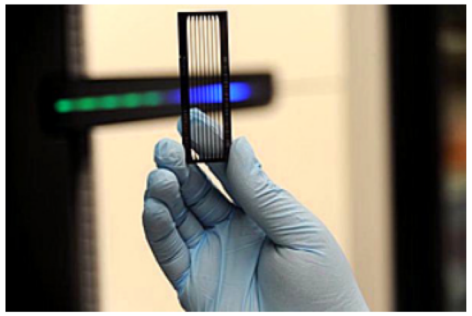
Research Funding | Research at NHGRI | Health | Education | Issues in Genetics | Newsroom | Caree

Home › Research Funding › Research Funding Divisions › Division of Genome Sciences › **Genome Technology Program**

Division of Genome Sciences

- Centers of Excellence in Genomic Science
- Division Staff
- ENCODE Project
- Functional Analysis Program
- Genetic Variation Program
- Genome Informatics and
- **Genome Technology Program**
- Program (GSP)

Genome Technology Program



- Overview
- Related Information
- Reports
- Policies
- Funding Opportunities
- Advanced Sequencing Technology Awards new
- Features
- Publications and Patents
- Staff

See Also:

- Grants Home
- Applying for an NHGRI Grant
- Grants Policies and Guidelines
- Funded Grants and Grant History
- NHGRI/NIH Active Grants
- NHGRI Funding Opportunities E-Mail List

Grants!

Genome Technology Program Overview

The Genome Technology program supports research to develop new
low-cost determination of DNA sequence, SNP genotyping (Genetic
defined) experiments (Functional Analysis Program). Priorities inclu
efficiency and decrease cost while maintaining or improving data qu
to achieve orders-of-magnitude improvement. Integration of proces

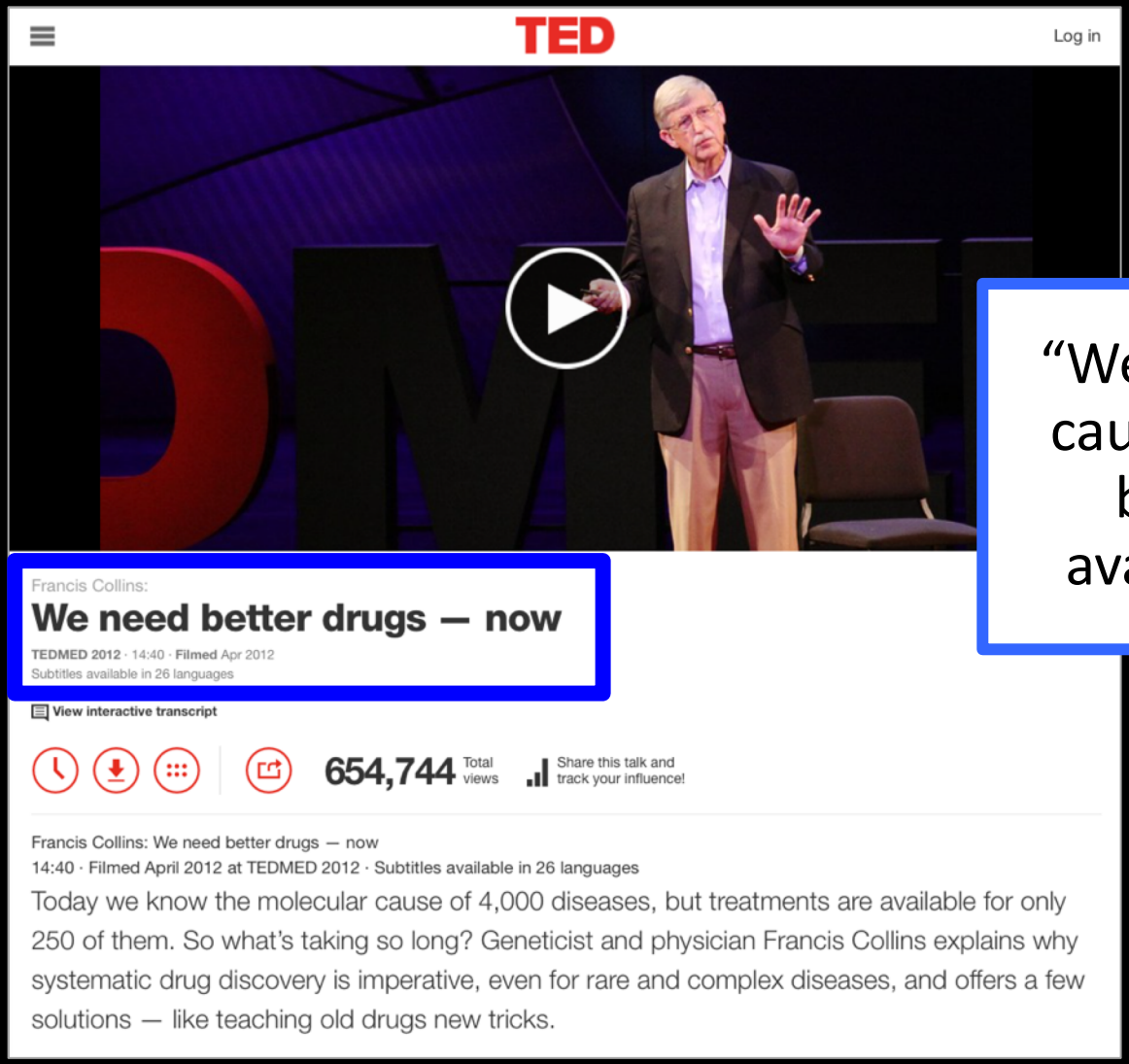
The program also supports and coordinates transfer of technology fr
multidisciplinary programs that closely integrate research projects a

The National Human Genome Research Institute (NHGRI) participate
bioengineering research. The development of integrated concepts ar
research, methods and approaches. NHGRI supports bioengineering
program announcements and requests for application, and through
announcements, such as the Bioengineering Research Grants (BRG)
and other Funding Opportunities that are listed below.

NHGRI GOAL:

Sequencing a genome for only $1,000.00!

NIH Director: Francis Collins, M.D.



"We know the molecular cause of 4,000 diseases, but treatments are available for only 250."

Retrieved January 5, 2015 from http://www.ted.com

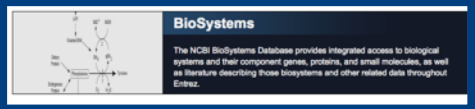
I'm a Research Scientist…

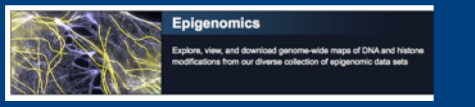
What do the NCBI Genetics Databases include???

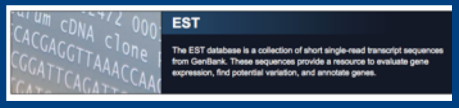
Growing Collection of Publicly Available Databases

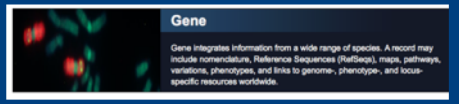
www.ncbi.nlm.nih.gov

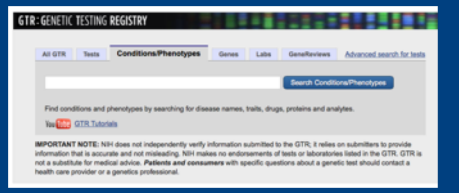
NCBI's Molecular Biology Databases

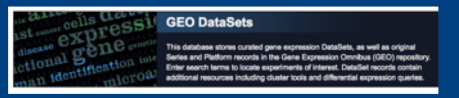


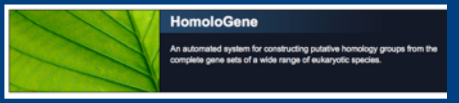


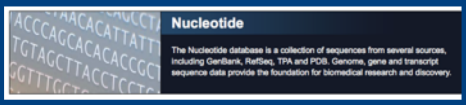


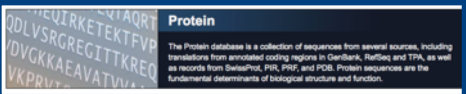


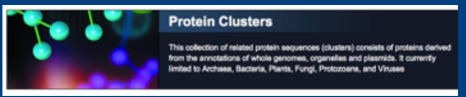


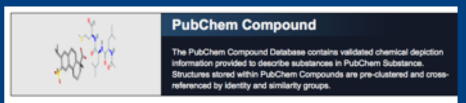


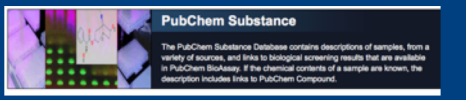


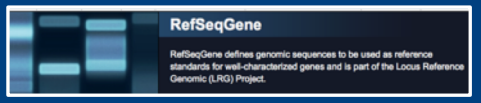


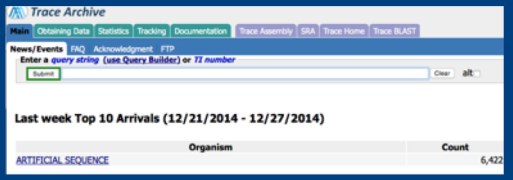


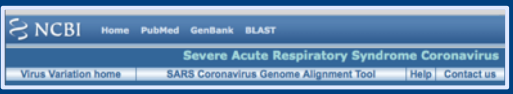


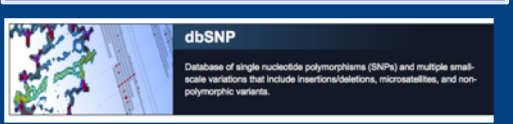




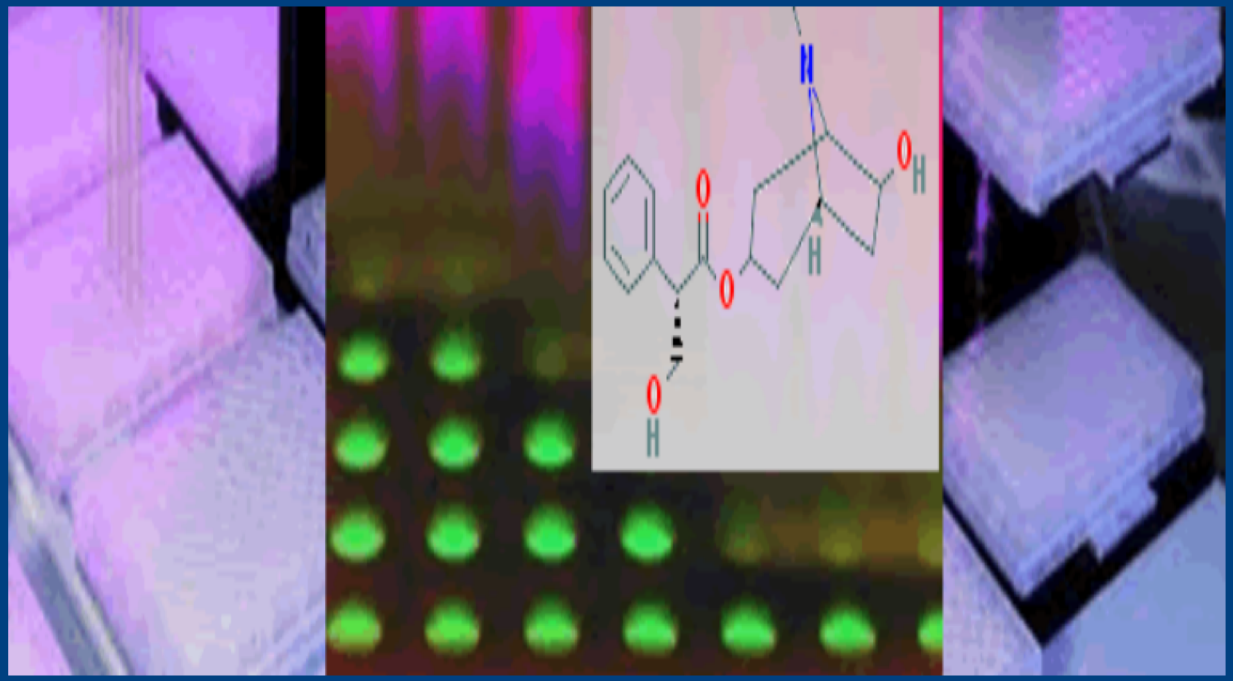


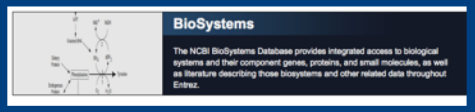


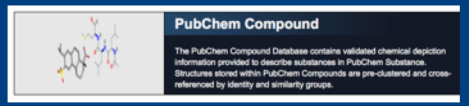


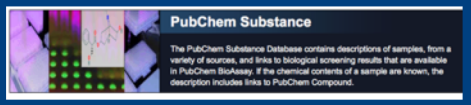


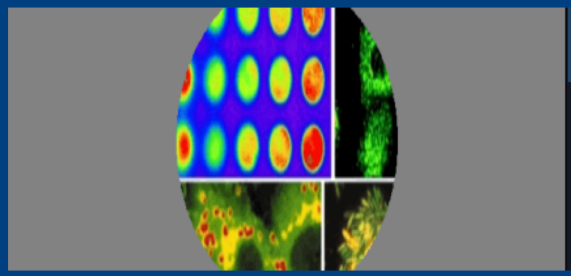
Chemical and Bioassays







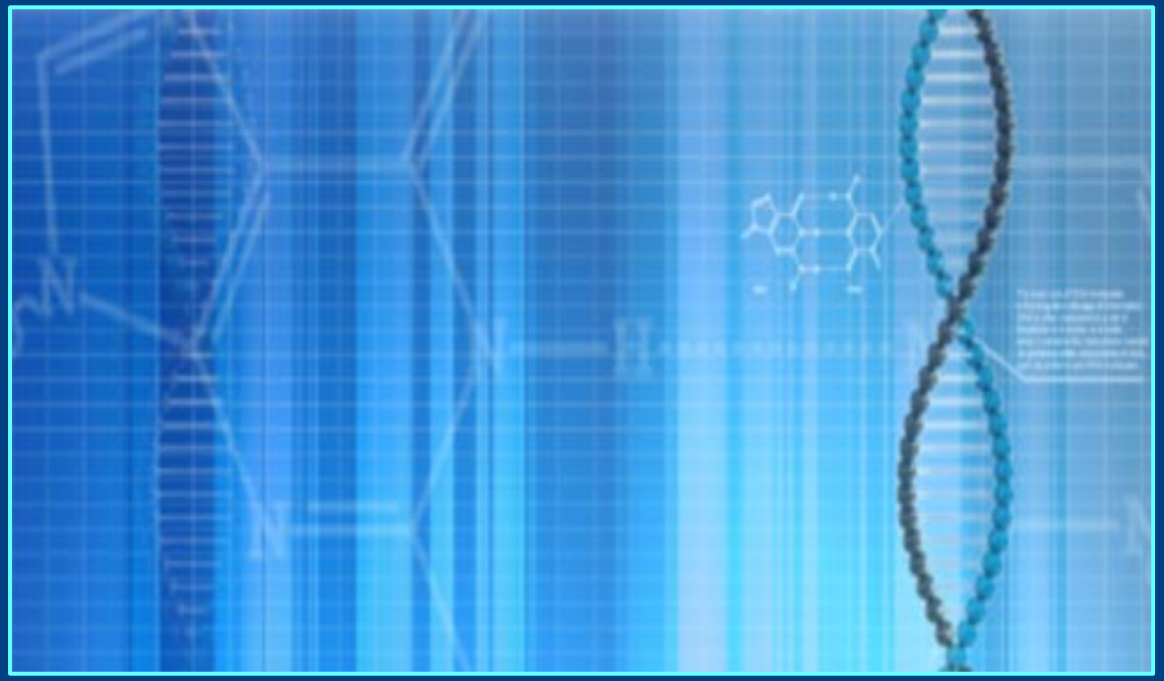




PubChem BioAssay

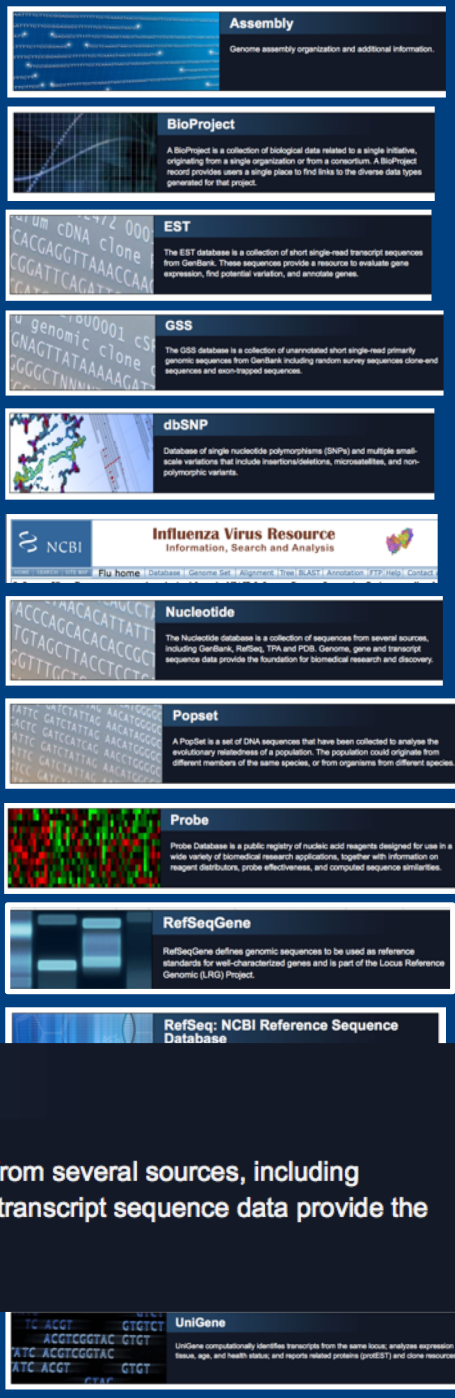
The PubChem BioAssay Database contains bioactivity screens of chemical substances described in PubChem Substance. It provides searchable descriptions of each bioassay, including descriptions of the conditions and readouts specific to that screening procedure.

DNA and RNA

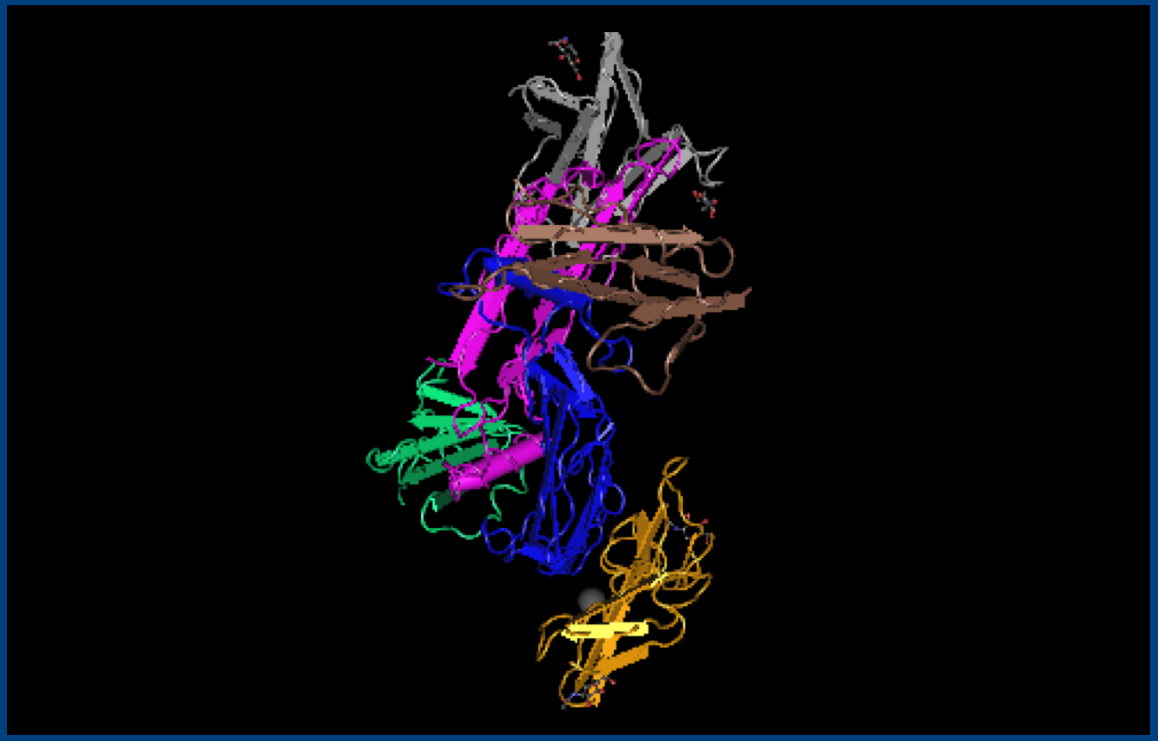


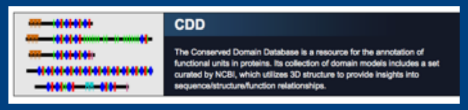
Nucleotide

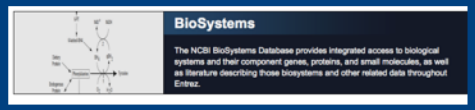
The Nucleotide database is a collection of sequences from several sources, including GenBank, RefSeq, TPA and PDB. Genome, gene and transcript sequence data provide the foundation for biomedical research and discovery.

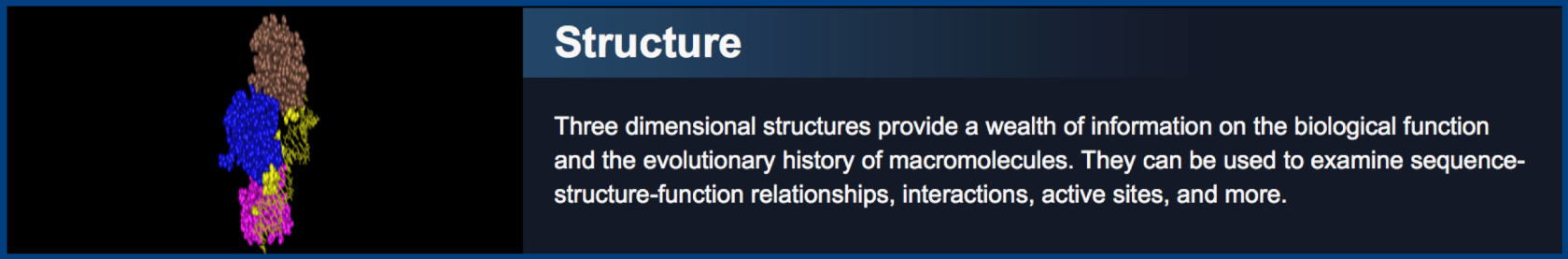


Domains and Structures

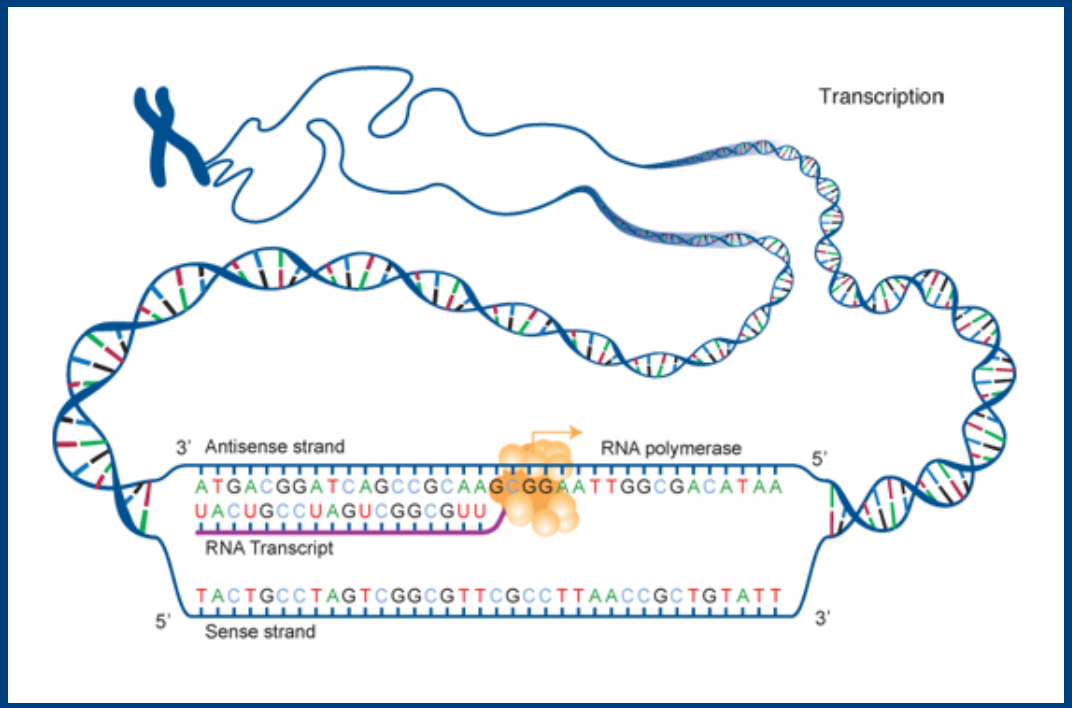


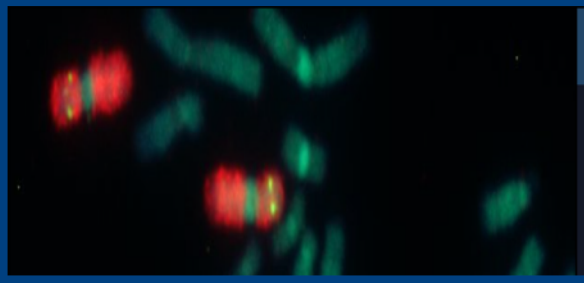






Genes and Expression

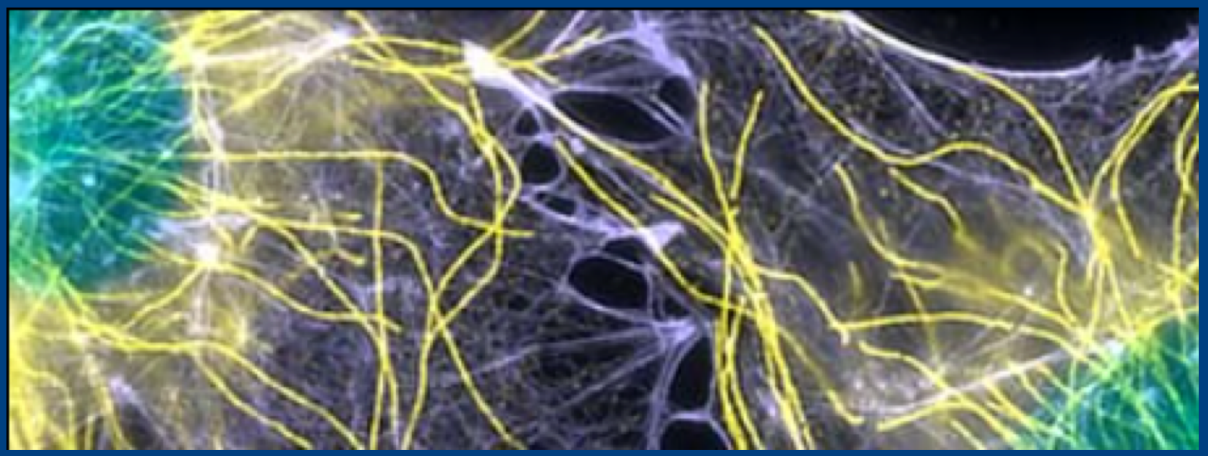




Gene

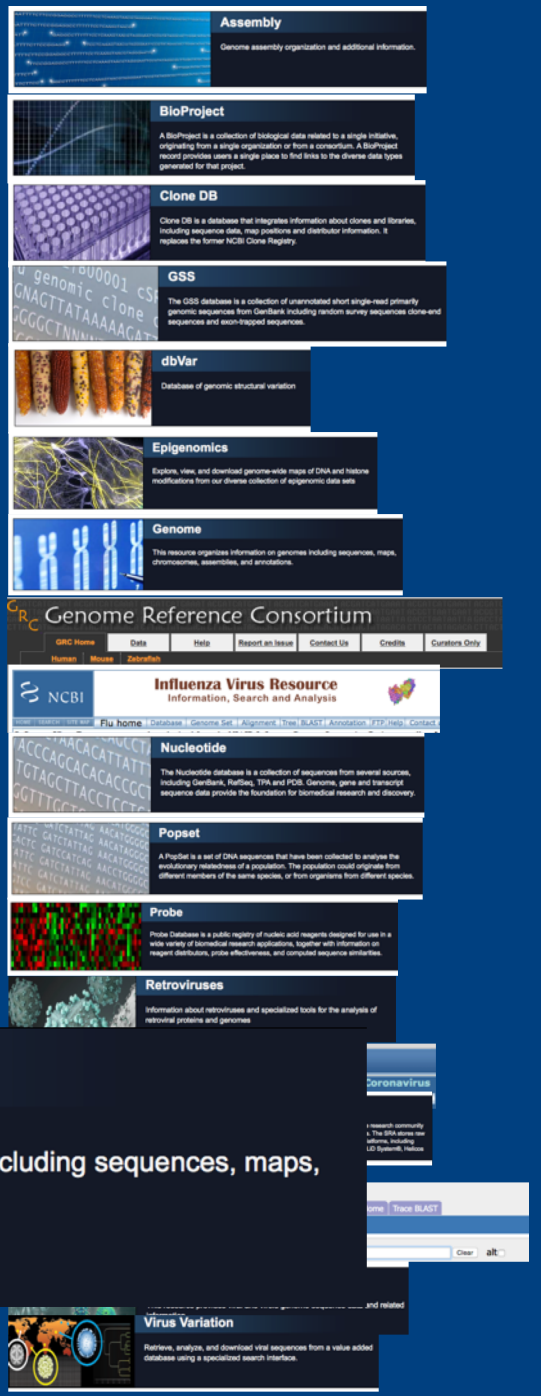
Gene integrates information from a wide range of species. A record may include nomenclature, Reference Sequences (RefSeqs), maps, pathways, variations, phenotypes, and links to genome-, phenotype-, and locus-specific resources worldwide.

Genomes and Maps

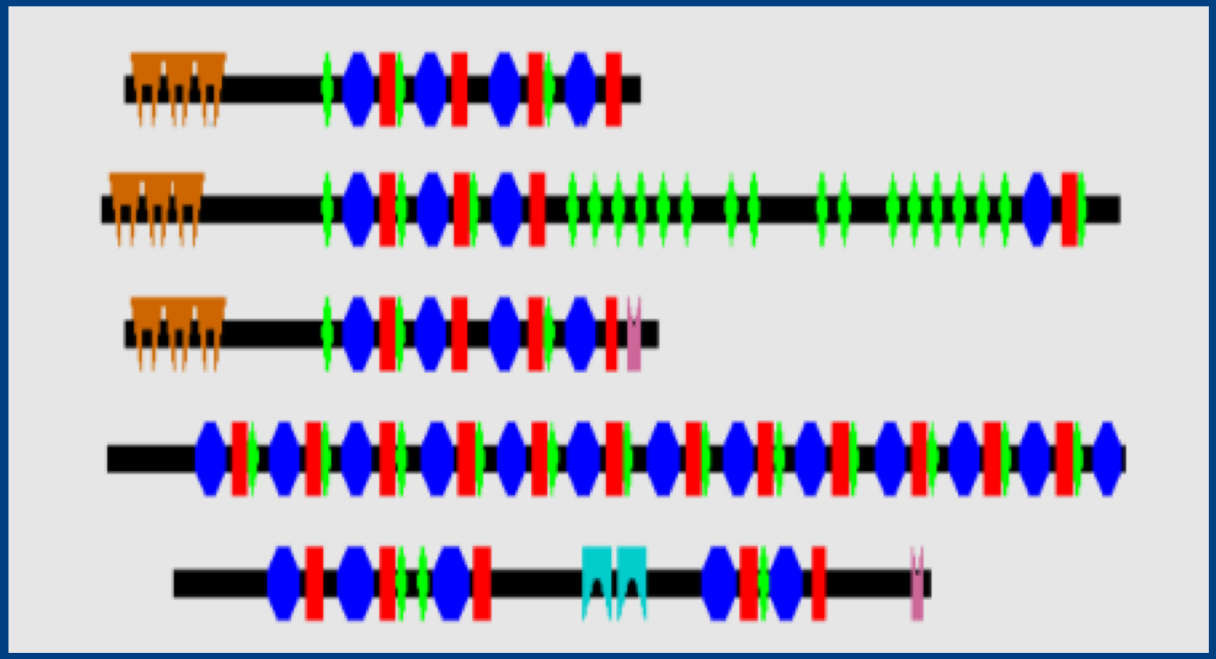


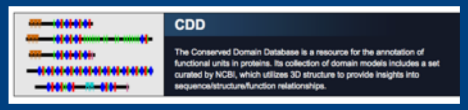
Genome

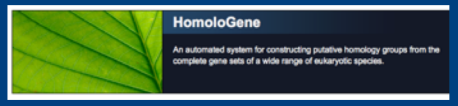
This resource organizes information on genomes including sequences, maps, chromosomes, assemblies, and annotations.



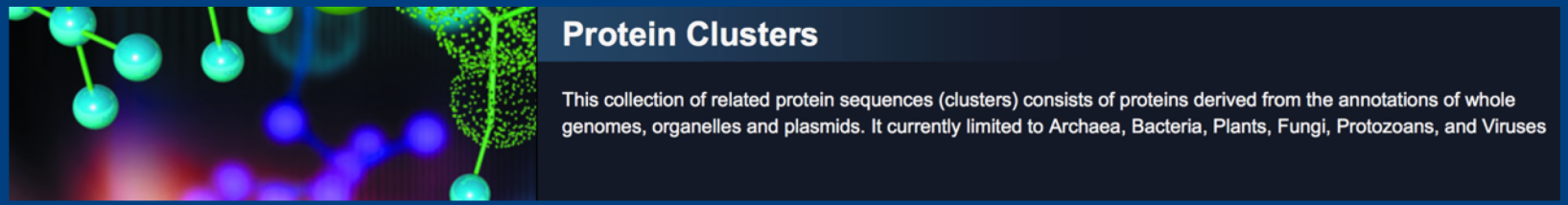
Homology




CDD
The Conserved Domain Database is a resource for the annotation of functional units in proteins. Its collection of domain models includes a set curated by NCBI, which utilizes 3D structure to provide insights into sequence/structure/function relationships.


HomoloGene
An automated system for constructing putative homology groups from the complete gene sets of a wide range of eukaryotic species.


Protein Clusters
This collection of related protein sequences (clusters) consists of proteins derived from the annotations of whole genomes, organelles and plasmids. It currently limited to Archaea, Bacteria, Plants, Fungi, Protozoans, and Viruses


Protein Clusters
This collection of related protein sequences (clusters) consists of proteins derived from the annotations of whole genomes, organelles and plasmids. It currently limited to Archaea, Bacteria, Plants, Fungi, Protozoans, and Viruses

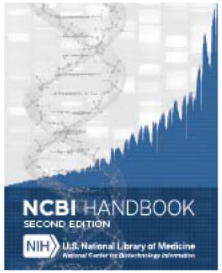
Literature

PubMed

PubMed comprises more than 24 million citations for biomedical literature from MEDLINE, life science journals, and online books. Citations may include links to full-text content from PubMed Central and publisher web sites.

PMC

PubMed Central® (PMC) is a free full-text archive of biomedical and life sciences journal literature at the U.S. National Institutes of Health's National Library of Medicine (NIH/NLM).



The NCBI Handbook, 2nd edition

Bethesda (MD): National Center for Biotechnology Information (US); 2013-.

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Edited by Roberta A Pagon, Editor-in-chief, Margaret P Adam, Holly H Ardinger, Thomas D Bird, Cynthia R Dolan, Chin-To Fong, Richard JH Smith, and Karen Stephens.

Seattle (WA): University of Washington, Seattle; 1993-2014.
ISSN: 2372-0697

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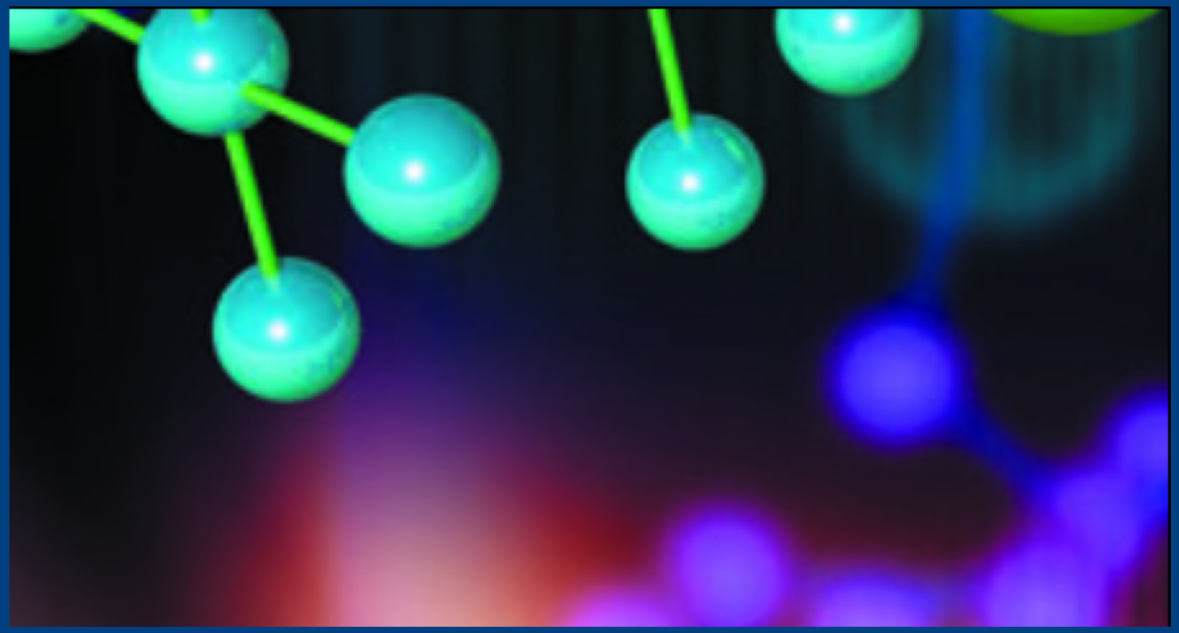
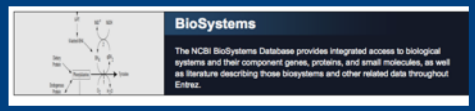
Proteins

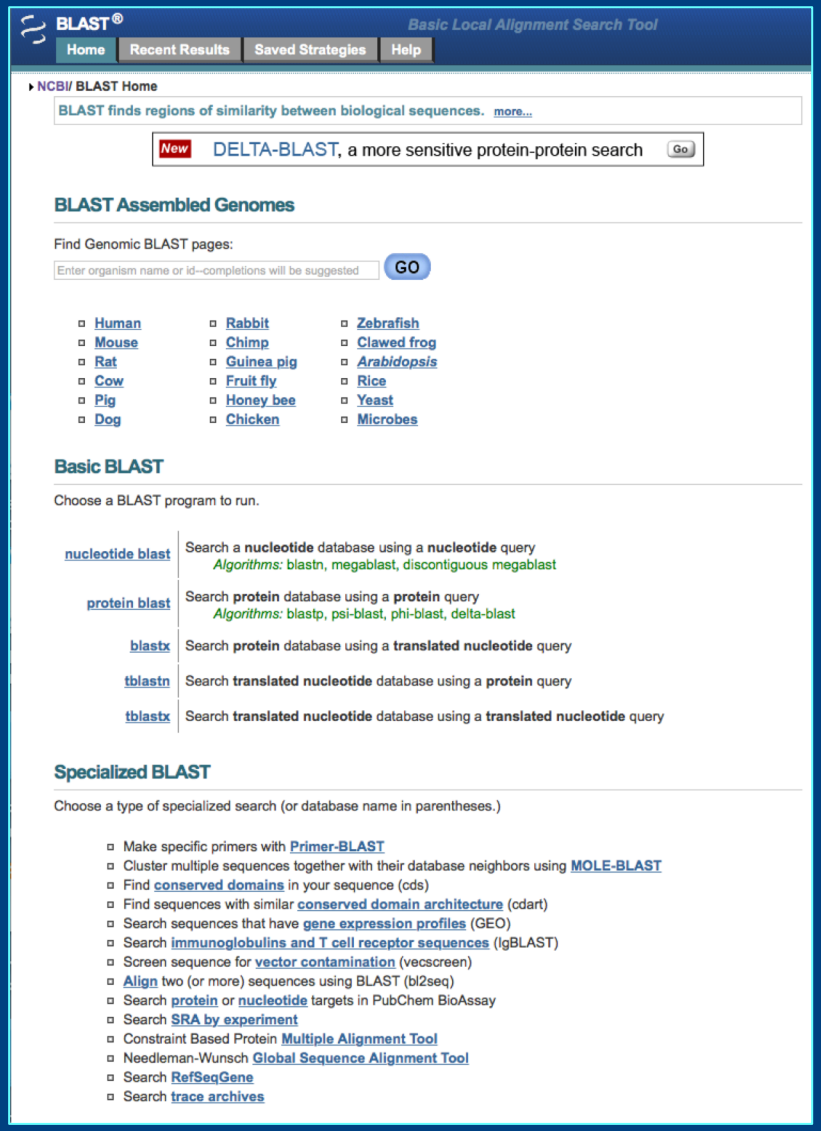




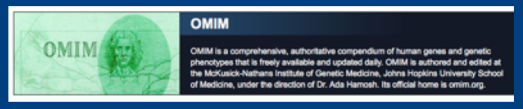
Protein

The Protein database is a collection of sequences from several sources, including translations from annotated coding regions in GenBank, RefSeq and TPA, as well as records from SwissProt, PIR, PRF, and PDB. Protein sequences are the fundamental determinants of biological structure and function.

Sequence Analysis



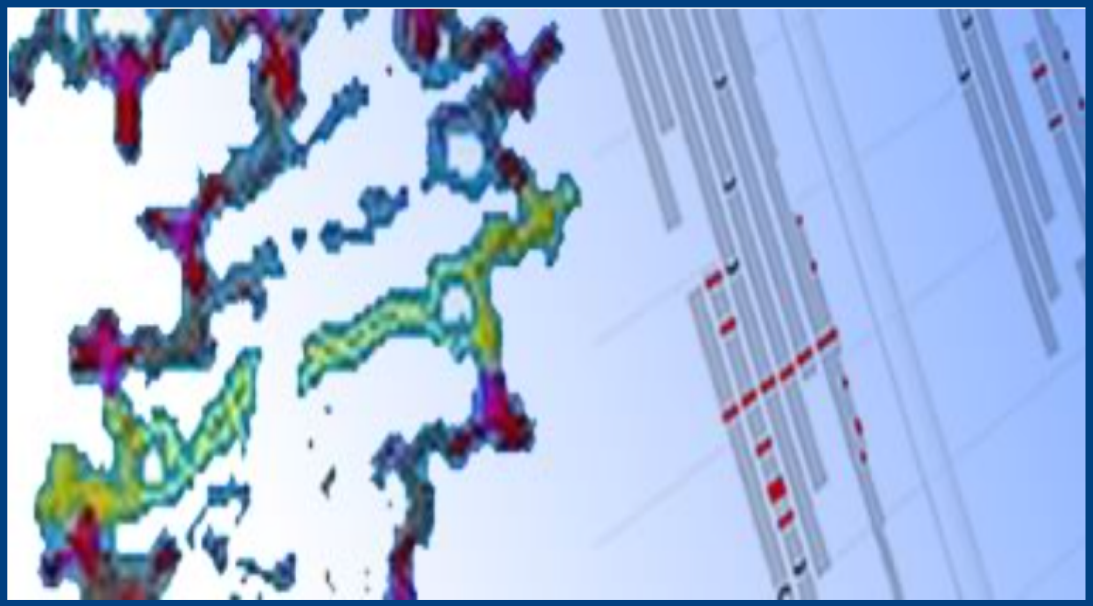
Taxonomy

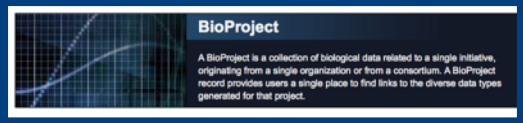


OMIM

OMIM is a comprehensive, authoritative compendium of human genes and genetic phenotypes that is freely available and updated daily. OMIM is authored and edited at the McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University School of Medicine, under the direction of Dr. Ada Hamosh. Its official home is omim.org.

Variation




BioProject
A BioProject is a collection of biological data related to a single initiative, originating from a single organization or from a consortium. A BioProject record provides users a single place to find links to the diverse data types generated for that project.


ACTGATGGTATGGGGCCAAGAGATATATCT
CAGGTACGGCTGTCATCACTTAGACCTCAC
CAGGGCTGGGCATAAAAGTCAGGGCAGAGC
CCATGGTGCATCTGACTCCTGAGGAGAAGT
GCAGGTTGGTATCAAGGTTACAAGACAGGT
GGCACTGACTCTCTCTGCCTATTGGTCTAT
ClinVar
ClinVar aggregates information about sequence variation and its relationship to human health.


NCBI
dbMHC Home
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External Links
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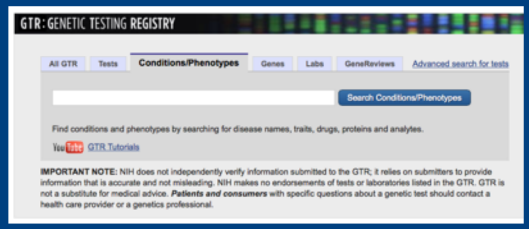
dbSNP
Database of single nucleotide polymorphisms (SNPs) and multiple small-scale variations that include insertions/deletions, microsatellites, and non-polymorphic variants.


GTR: GENETIC TESTING REGISTRY
All GTR
Tests
Conditions/Phenotypes
Genes
Labs
GeneReviews
Advanced search for tests
Search Conditions/Phenotypes
Find conditions and phenotypes by searching for disease names, traits, drugs, proteins and analytes.
GTR Tutorials
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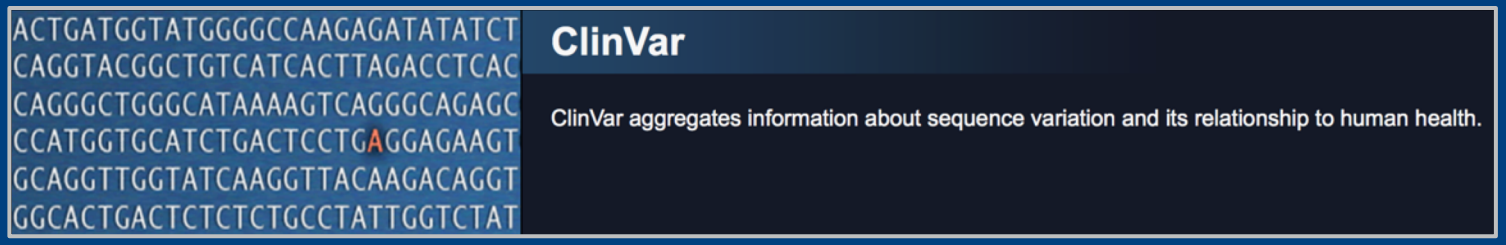
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CCATGGTGCATCTGACTCCTGAGGAGAAGT
GCAGGTTGGTATCAAGGTTACAAGACAGGT
GGCACTGACTCTCTCTGCCTATTGGTCTAT
ClinVar
ClinVar aggregates information about sequence variation and its relationship to human health.

More Information

Database resources of the National Center for Biotechnology Information

Nucleic Acids Research. 2010 Jan;38(Database issue):D13-D25

PMID: 19910364

Eric W. Sayers[1,*], Tanya Barrett[1], Dennis A. Benson[1], Evan Bolton[1], Stephen H. Bryant[1], Kathi Canese[1], Vyacheslav Chetvernin[1], Deanna M. Church[1], Michael DiCuccio[1], Scott Federhen[1], Michael Feolo[1], Ian M. Fingerman[1], Lewis Y. Geer[1], Wolfgang Helmberg[2], Yuri Kapustin[1], Sergey Krasnov[1], David Landsman[1], David J. Lipman[1], Zhiyong Lu[1], Thomas L. Madden[1], Tom Madej[1], Donna R. Maglott[1], Aron Marchler-Bauer[1], Vadim Miller[1], Ilene Karsch-Mizrachi[1], James Ostell[1], Anna Panchenko[1], Lon Phan[1], Kim D. Pruitt[1], Gregory D. Schuler[1], Edwin Sequeira[1], Stephen T. Sherry[1], Martin Shumway[1], Karl Sirotkin[1], Douglas Slotta[1], Alexandre Souvorov[1], Grigory Starchenko[1], Tatiana A. Tatusova[1], Lukas Wagner[1], Yanli Wang[1], W. John Wilbur[1], Eugene Yaschenko[1] and Jian Ye[1]

[1]National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Building 38A, 8600 Rockville Pike, Bethesda, MD 20894, USA and [2]University Clinic of Blood Group Serology and Transfusion Medicine, Medical University of Graz, Auenbruggerplatz 3, A-8036 Graz, Austria

Received September 30, 2011; Revised and Accepted November 14, 2011

ABSTRACT

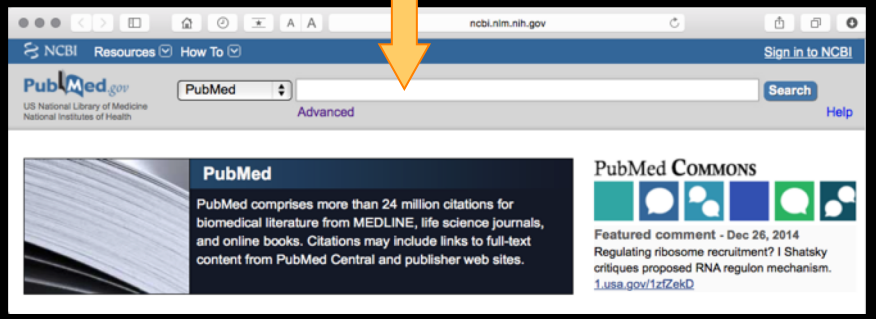
In addition to maintaining the GenBank® nucleic acid sequence database, the National Center for Biotechnology Information (NCBI) provides analysis and retrieval resources for the data in GenBank and other biological data made available through the NCBI Website. NCBI resources include Entrez, the Entrez Programming Utilities, MyNCBI, PubMed, PubMed Central (PMC), Gene, the NCBI Taxonomy Browser, BLAST, BLAST Link (BLink), Primer-BLAST, COBALT, Splign, RefSeq, UniGene, HomoloGene, ProtEST, dbMHC, dbSNP, dbVar, Epigenomics, Genome and related tools, the Map Viewer, Model Maker, Evidence Viewer, Trace Archive, Sequence Read Archive, BioProject, BioSample, Retroviral Genotyping Tools, HIV-1/Human Protein Interaction Database, Gene Expression Omnibus (GEO), Probe, Online Mendelian Inheritance in Animals (OMIA), the Molecular Modeling Database (MMDB), the Conserved Domain Database (CDD), the Conserved Domain Architecture Retrieval Tool (CDART), Biosystems, Protein Clusters and the PubChem suite of small molecule databases. Augmenting many of the Web applications are custom implementations of the BLAST program optimized to search specialized data sets. All of these resources can be accessed through the NCBI home page at www.ncbi.nlm.nih.gov.

INTRODUCTION

The National Center for Biotechnology Information (NCBI) at the National Institutes of Health was created in 1988 to develop information systems for molecular biology. In addition to maintaining the GenBank® (1) nucleic acid sequence database, which receives data through the international collaboration with DDBJ and EMBL-Bank as well as from the scientific community, NCBI provides data retrieval systems and computational resources for the analysis of GenBank data and many other kinds of biological data. For the purposes of this article, after a summary of recent developments and an introduction to the Entrez system, the NCBI suite of resources is grouped into 10 broad categories based on those in the NCBI guide. All resources discussed are available from the NCBI guide at www.ncbi.nlm.nih.gov and can also be located using the *Site Search* database. In most

*To whom correspondence should be addressed. Tel: 301 496 2475; Fax: 301 480 9241; Email: sayers@ncbi.nlm.nih.gov

PMID: 19910364



How do I learn to search the NCBI Genetics Databases???

ncbi.nlm.nih.gov

NCBI Resources How To Sign in to NCBI

NCBI
National Center for Biotechnology Information

All Databases Search

- NCBI Home
- Resource List (A-Z)
- All Resources
- Chemicals & Bioassays
- Data & Software
- DNA & RNA
- Domains & Structures
- Genes & Expression
- Genetics & Medicine
- Genomes & Maps
- Homology
- Literature
- Proteins
- Sequence Analysis
- Taxonomy
- Training & Tutorials
- Variation

Welcome to NCBI

The National Center for Biotechnology Information advances science and health by providing access to biomedical and genomic information.

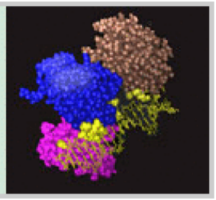
About the NCBI | Mission | Organization | Research | NCBI News

Get Started

- Tools: Analyze data using NCBI software
- Downloads: Get NCBI data or software
- How Tos: Learn how to accomplish specific tasks at NCBI
- Submissions: Submit data to GenBank or other NCBI databases

3D Structures

Explore three-dimensional structures of proteins, DNA, and RNA molecules. Examine sequence-structure relationships, active sites, molecular interactions, biological activities of bound chemicals, and associated biosystems.



II 1 2 3 4 5 6 7 8

www.ncbi.nlm.nih.gov

Popular Resources

PubMed
Bookshelf
PubMed Central
PubMed Health
BLAST
Nucleotide
Genome
SNP
Gene
Protein
PubChem

NCBI Announcements

NCBI staff will attend International Plant and Animal Genome Conference XXIII
Jan 5, 2015

Next week, NCBI staff will present

NCBI webinar A Submitter's Guide to GenBank, Part 2 on January 7th
Dec 31, 2014

On January 7th, NCBI will present the

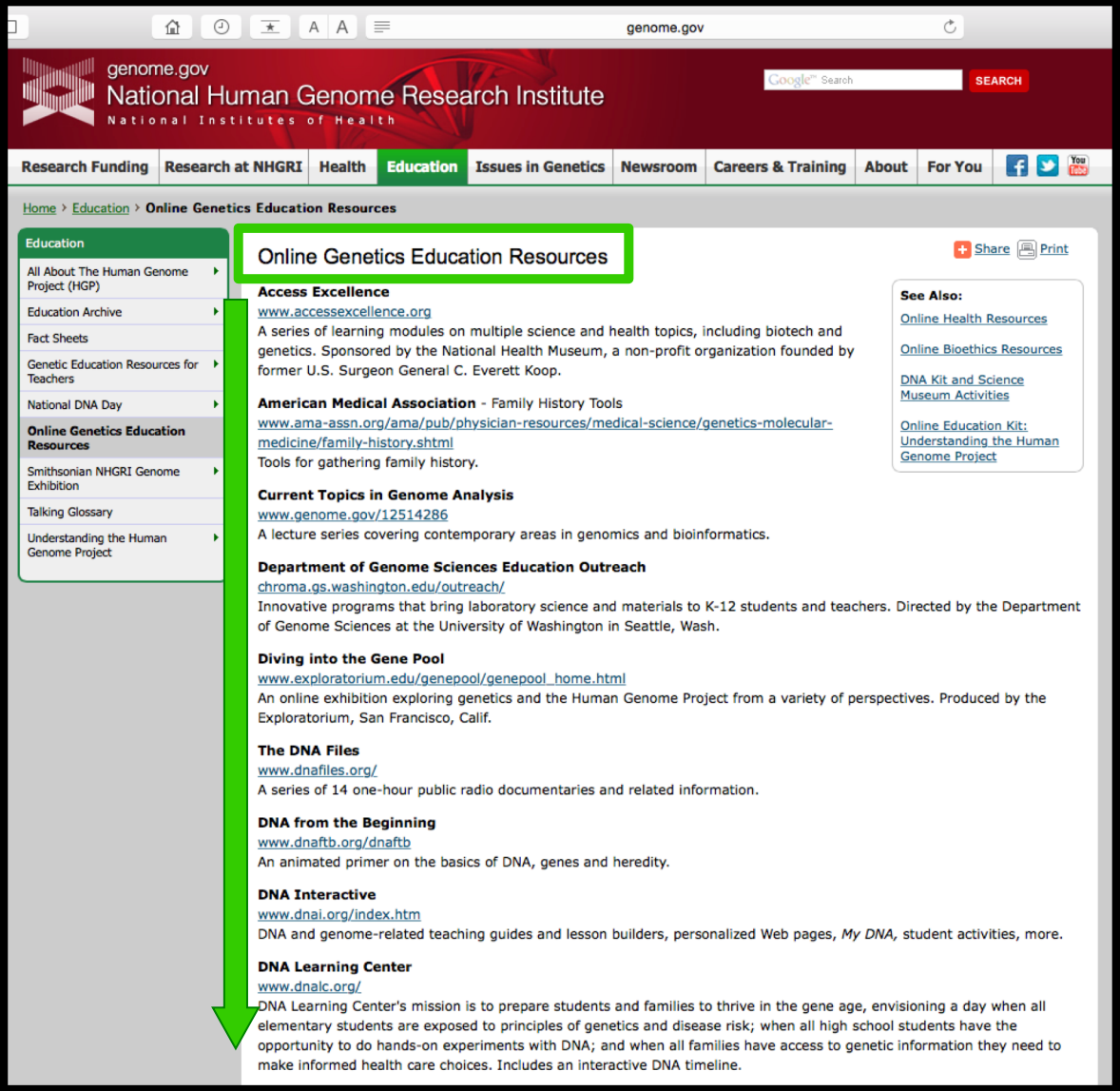
GenBank release 205.0 is now available via FTP
Dec 16, 2014

Release 205.0 (12/12/2014) has

More...

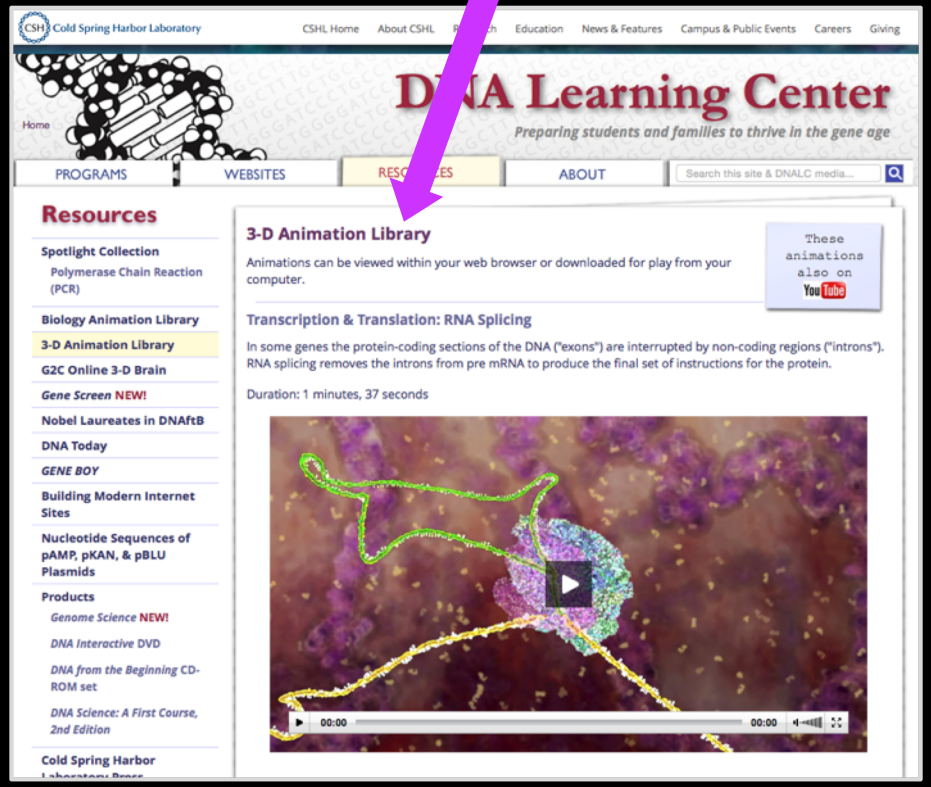
What are some websites where I can learn more about genetics?

www.genome.gov



www.dnalc.org

includes



The Future of Medicine

diagnosis and treatment based on your genome!

Retrieved January 5, 2015 from http://www.genome.gov

We live in the age of information.

Retrieved January 5, 2015 from http://www.energy.gov

http://www.research.archives.gov

http://www.iipdigital.usembassy.gov

http://www.in.go
v

http://www.nihrecord.nih.gov

http://www.directorsblog.nih.gov

http://www.blogs.america.gov

http://www.nichd.nih.gov

http://www.ncbi.nlm.nih.gov

All images retrieved January, 2015

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The End