

# Genome Resources

Sequences | Variants | Interpretations

# RESOURCES FOR GENOMICS: UCSC GENOME BROWSER

- ▶ Originated from the Human Genome Project
- ▶ Most widely used general genome browser
- ▶ many default tracks
- ▶ many species
- ▶ customization with "BED" files

[genome.ucsc.edu](http://genome.ucsc.edu)

UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

chr1:11,102,837-11,267,747 164,911 bp. enter position, gene symbol, HGVS or search terms go

chr1 (p36.22) 1p31.1 1q12 1q41 q43q44

Scale 50 kb hg38 11,150,000 11,200,000 11,250,000

New haplotype sequences to GRCh38 Reference Sequence  
Patches to GRCh38 Reference Sequence

GENCODE v24 Comprehensive Transcript Set (only Basic displayed by default)  
MTOR MTOR-AS1 RNU6-537P ANGPTL7 RNU6-291P

RefSeq gene predictions from NCBI

OMIM Allelic Variants

Gene Expression in 53 tissues from GTEx RNA-seq of 8555 samples (570 donors)  
MTOR-AS1 RNU6-537P ANGPTL7 RNU6-291P RPL39P6

Layered H3K27Ac 100 0

DNase I Hypersensitivity Peak Clusters from ENCODE (95 cell types)

Cons 100 Verts 4.68 0

Multiz Alignments of 100 Vertebrates  
Rhesus Mouse Dog Elephant Chicken X\_tropicalis Zebrafish Lamprey

Common SNPs (150)  
Simple Nucleotide Polymorphisms (dbSNP 150) Found in >= 1% of Samples

Repeating Elements by RepeatMasker  
SINE LINE LTR DNA Simple Low Complexity Satellite RNA Other Unknown

move start < 2.0 > move end < 2.0 >

Click on a feature for details. Click or drag in the base position track to zoom in. Click side bars for track options. Drag side bars or labels up or down to reorder tracks. Drag tracks left or right to new position. Press "?" for keyboard shortcuts.

track search default tracks default order hide all add custom tracks track hubs configure multi-region reverse resize refresh

Use drop-down controls below and press refresh to alter tracks displayed.  
Tracks with lots of items will automatically be displayed in more compact modes.

collapse all expand all

# RESOURCES FOR GENOMICS: HUMAN GENOME RESOURCES AT NCBI

- ▶ Entry point for genome reference data
- ▶ Human genome assemblies
- ▶ Human variant collections (dbVar, ClinVar, dbSNP) for download

[www.ncbi.nlm.nih.gov/projects/genome/guide/human/](http://www.ncbi.nlm.nih.gov/projects/genome/guide/human/)

NIH U.S. National Library of Medicine NCBI National Center for Biotechnology Information Log in

## Human Genome Resources at NCBI

Download Browse View Learn

Search for Human Genes

Search

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y MT

Select a chromosome to access the [Genome Data Viewer](#)

### Download

	GRCh38	GRCh37
Reference Genome Sequence	<a href="#">Fasta</a>	<a href="#">Fasta</a>
RefSeq Reference Genome Annotation	<a href="#">gff3</a>	<a href="#">gff3</a>
RefSeq Transcripts	<a href="#">Fasta</a>	<a href="#">Fasta</a>
RefSeq Proteins	<a href="#">Fasta</a>	<a href="#">Fasta</a>
ClinVar	<a href="#">vcf</a>	<a href="#">vcf</a>
dbSNP	<a href="#">vcf</a>	<a href="#">vcf</a>
dbVar	<a href="#">vcf</a>	<a href="#">vcf</a>



# RESOURCES FOR GENOMICS: ENSEMBL

- ▶ Entry point for many genome data services and collections
- ▶ Downloads ("BioMart"), REST API

**Ensembl** BLAST/BLAT | VEP | Tools | BioMart | Downloads | Help & Docs | Blog Login/Register

Human (GRCh38.p14)

**Search Human (Homo sapiens)**

Search all categories Search... Go

e.g. [PPP2R2A](#) or [8:26291508-26372680](#) or [rs699](#) or [osteoarthritis](#)

**Genome assembly: GRCh38.p14 (GCA\_000001405.29)**

- More information and statistics
- Download DNA sequence (FASTA)
- Convert your data to GRCh38 coordinates
- Display your data in Ensembl

Other assemblies

GRCh37 Full Feb 2014 archive with BLAST, VEP and BioMart Go

**Comparative genomics**

What can I find? Homologues, gene trees, and whole genome alignments across multiple species.

- More about comparative analysis
- Download alignments (EMF)

**Regulation**

What can I find? DNA methylation, transcription factor binding sites, histone modifications, and regulatory features such as enhancers and repressors, and microarray annotations.

- More about the Ensembl regulatory build and microarray annotation
- Experimental data sources
- Download all regulatory features (GFF)

**Gene annotation**

What can I find? Protein-coding and non-coding genes, splice variants, cDNA and protein sequences, non-coding RNAs.

- More about this genebuild
- Download FASTA files for genes, cDNAs, ncRNA, proteins
- Download GTF or GFF3 files for genes, cDNAs, ncRNA, proteins
- Update your old Ensembl IDs

**Variation**

What can I find? Short sequence variants and longer structural variants; disease and other phenotypes

- More about variation in Ensembl
- Download all variants (GVF)
- Variant Effect Predictor **Ve!P**

[www.ensembl.org/Homo\\_sapiens/Info/Index](http://www.ensembl.org/Homo_sapiens/Info/Index)

**Where to find genome *variant* data ...**

# Reference Resources for Human Genome Variants

## NCBI:dbSNP



- single nucleotide polymorphisms (SNPs) and multiple small-scale variations
- including insertions/deletions, microsatellites, non-polymorphic variants

## NCBI:dbVAR



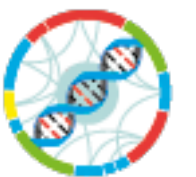
- genomic structural variation
- insertions, deletions, duplications, inversions, multinucleotide substitutions, mobile element insertions, translocations, complex chromosomal rearrangements

## NCBI:ClinVar



- aggregates information about genomic variation and its relationship to human health

## EMBL-EBI:EVA



- open-access database of all types of genetic variation data from all species

## Ensembl



- portal for many things genomic...

# RESOURCES FOR CANCER GENOMICS



**COSMIC v79, released 14-NOV-16**

COSMIC, the Catalogue Of Somatic Mutations In Cancer, is the world's largest and most comprehensive resource for exploring the impact of somatic mutations in human cancer.

Start using COSMIC by searching for a gene, cancer type, mutation, etc. below, or by browsing a region of the human genome using the map to the right.

eg: *Braf*, *COLO-829*, *Carcinoma*, *V600E*, *BRCA-UK*, *Campbell* **SEARCH**

## R Resources

Key COSMIC resources

- [Cell Lines Project](#)
- [COSMIC](#)
- [Whole Genomes](#)
- [Cancer Gene Census](#)
- [Drug Sensitivity](#)
- [Mutational Signatures](#)
- [GRCh37 Cancer Archive](#)

## T Tools

Additional tools to explore COSMIC

- [Cancer Browser](#)
- [Genome Browser](#)
- [GA4GH Beacon](#)
- [CONAN](#)

## C Expert Curation

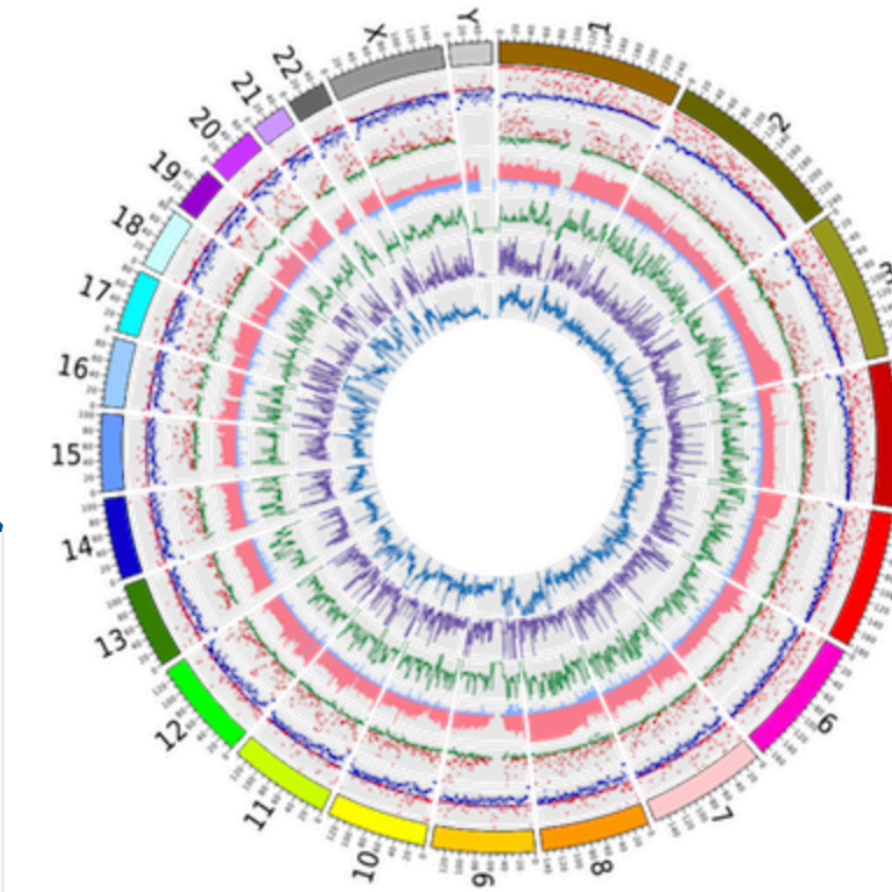
High quality curation by expert postdoctoral scientists

- [Drug Resistance](#)<sup>New</sup>
- [Cancer Gene Census](#)
- [Curated Genes](#)
- [Gene Fusions](#)
- [Genome-Wide Screens](#)

## D Data

Further details on using COSMIC's content

- [Downloads](#)
- [License](#)
- [Submission](#)
- [Genome Annotation](#)
- [Datasheets](#)
- [Help](#)
- [FAQ](#)



Browse the **genomic landscape** of cancer

## Cancer Gene Census Update

7 genes have been added to the [Cancer Gene Census](#) -

- [EPAS1](#) - Endothelial PAS domain protein 1.
- [PTPRT](#) - Protein tyrosine phosphatase, receptor type T.
- [PPM1D](#) - Protein phosphatase, Mg2+/Mn2+ dependent 1D.
- [BTK](#) - Bruton tyrosine kinase.
- [PREX2](#) - Phosphatidylinositol-3,4,5-trisphosphate dependent Rac exchange factor 2.
- [TP63](#) - Tumour protein p63.
- [QKI](#) - QKI, KH domain containing RNA binding.

For full details, see the [Datasheet](#).



## RESOURCES FOR GENOMICS: CLINGEN

- ▶ "The Genomic Variant WG brings together representatives from the Sequence and Structural Variant communities for focused discussions on resolving discrepancies in variant interpretation and creating consistent curation guidelines."
- ▶ Interpreted genome variants with disease association

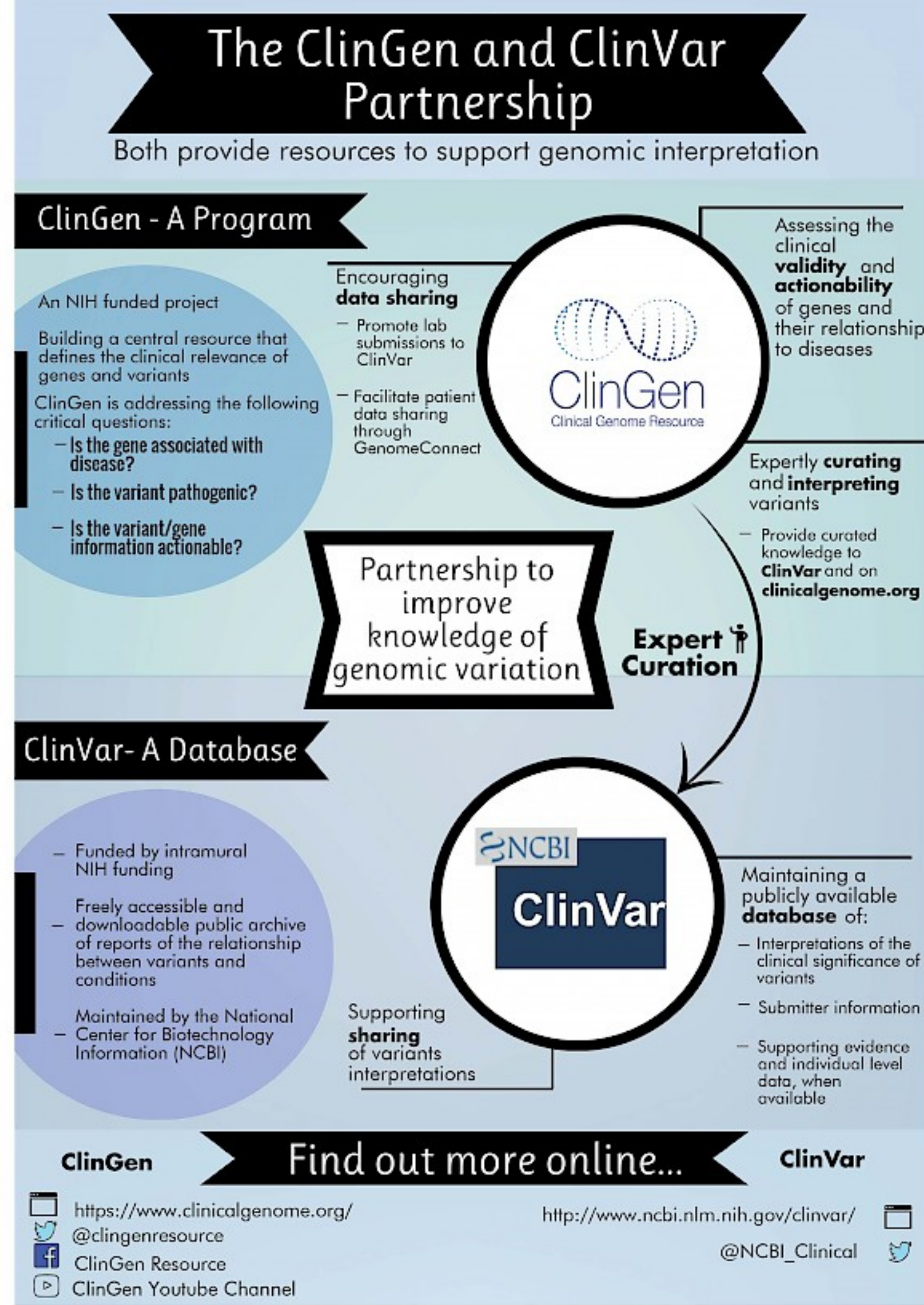
[clinicalgenome.org](http://clinicalgenome.org)

The screenshot shows the ClinGen website homepage. At the top left is the ClinGen logo (Clinical Genome Resource). To its right is a search bar with the text "Search our Knowledge Base for genes and diseases...". Below the search bar is a navigation menu with links for "About ClinGen", "Working Groups", "Resources", "GenomeConnect", "Share Your Data", and "Curation Activities". The main banner features a blue background with a blurred image of a lab. The text on the banner reads: "Defining the clinical relevance of genes & variants for precision medicine and research...". Below this text are three statistics: "1496 ClinGen Curated Genes", "31 Expert Groups", and "10446 Expert Reviewed Variants in ClinVar". To the right of these statistics is a search icon and the text "Knowledge Base Search". Below the banner is the slogan "Sharing Data. Building Knowledge. Improving Care." followed by a paragraph: "ClinGen is dedicated to building an authoritative central resource that defines the clinical relevance of genes and variants for use in precision medicine and research. Learn more about our organization and our ongoing efforts below." Below this paragraph are six icons in a 2x3 grid, each with a corresponding text label: "ClinGen-ClinVar Partnership", "How to share genomic & health data", "Learn about ClinGen curation activities", "GenomeConnect Patient Registry", "View ClinGen's Resources & Tools", and "Get Involved".



- ▶ ClinVar (an NCBI database/resource) is used as basis for curated variant <-> disease associations in ClinGen
- ▶ ClinGen - a funded project (application/funding limited)
- ▶ ClinVar - an internal NIH resource (dependent on political "goodwill")

[clinicalgenome.org](http://clinicalgenome.org)





# RESOURCES FOR CANCER GENOMICS

## CANCER GENOME ANATOMY PROJECT

### CGAP How To

#### Tools

#### CGAP Info

- Educational Resources
- Slide Tour
- Team Members
- References

#### CGAP Data

- Download

#### Quick Links:

- ICG
- NCI Home
- NCICB Home
- NCBI Home
- OCG

### Genes Chromosomes Tissues SAGE Genie RNAi Pathways

#### Cancer Genome Anatomy Project (CGAP)

The NCI's Cancer Genome Anatomy Project sought to determine the gene expression profiles of normal, precancer, and cancer cells, leading eventually to improved detection, diagnosis, and treatment for the patient. Resources generated by the CGAP initiative are available to the broad cancer community. Interconnected modules provide access to all CGAP data, bioinformatic analysis tools, and biological resources allowing the user to find "in silico" answers to biological questions in a fraction of the time it once took in the laboratory.

#### The CGAP Website

Interconnected modules provide access to all CGAP data, bioinformatic analysis tools, and biological resources allowing the user to find "in silico" answers to biological questions in a fraction of the time it once took in the laboratory.



#### Genes

Gene information, clone resources, SNP500Cancer, GAI, and transcriptome analysis.



#### Tissues

cDNA library information, methods, and EST-based gene expression analysis.



#### Pathways

Diagrams of biological pathways and protein complexes, with links to genetic resources for each known protein.



#### RNAi

RNA-interference constructs, targeted specifically against cancer relevant genes. New addition: Validated set of shRNAs.



#### Chromosomes

FISH-mapped BAC clones, SNP500Cancer, and the Mitelman database of chromosome aberrations.



#### SAGE Genie

Analysis of gene expression using long and short SAGE tag data for both human and mouse.



#### Tools

Direct access to all analytic and data mining tools developed for the project.

- Home
- Cancer Genome Projects
- Committees and Working Groups
- Policies and Guidelines
- Media

## ICGC Cancer Genome Projects

Committed projects to date: **89**

Sort by: Project

<b>Biliary Tract Cancer</b> Japan 🇯🇵	<b>Biliary Tract Cancer</b> Singapore 🇸🇬	<b>Bladder Cancer</b> China 🇨🇳
<b>Bladder Cancer</b> United States 🇺🇸	<b>Blood Cancer</b> China 🇨🇳	<b>Blood Cancer</b> Singapore 🇸🇬
<b>Blood Cancer</b> South Korea 🇰🇷	<b>Blood Cancer</b> United States 🇺🇸	<b>Blood Cancer</b> United States 🇺🇸
<b>Blood Cancer</b> United States 🇺🇸	<b>Blood Cancer</b> United States 🇺🇸	<b>Bone Cancer</b> France 🇫🇷
<b>Bone Cancer</b> United Kingdom 🇬🇧	<b>Bone Cancer</b> United States 🇺🇸	<b>Brain Cancer</b> Canada 🇨🇦
<b>Brain Cancer</b> China 🇨🇳	<b>Brain Cancer</b> United States 🇺🇸	<b>Brain Cancer</b> United States 🇺🇸
<b>Breast Cancer</b> China 🇨🇳	<b>Breast Cancer</b> European Union / United Kingdom 🇪🇺 🇬🇧	<b>Breast Cancer</b> France 🇫🇷
<b>Breast Cancer</b> Mexico 🇲🇽	<b>Breast Cancer</b> South Korea 🇰🇷	<b>Breast Cancer</b> South Korea 🇰🇷

**ICGC Goal:** To obtain a **comprehensive** description of **genomic, transcriptomic and epigenomic changes** in **50 different tumor types and/or subtypes** which are of clinical and societal importance across the globe.

[Read more »](#)

[Launch Data Portal »](#)

[Apply for Access to Controlled Data »](#)

#### Announcements

**23/August/2016** - The ICGC Data Coordination Center (DCC) is pleased to announce ICGC data portal data release 22 (<http://dcc.icgc.org>).

ICGC data release 22 in total comprises data from more than 16,000 cancer donors spanning 70 projects and 21 tumour sites.

**17/April/2016** - ICGCmed is pleased to announce the release of its white paper (<http://icgcmed.org>).

The International Cancer Genome Consortium for Medicine (ICGCmed) will link genomics data to clinical information, health and responses to therapies.

**18/November/2015** - The International Cancer Genome Consortium (ICGC) PanCancer dataset generated by the PanCancer Analysis of Whole Genomes (PCAWG) study is now available on Amazon Web Services (AWS), giving cancer researchers access to over 2,400 consistently analyzed genomes corresponding to over 1,100 unique ICGC donors (<https://icgc.org/icgc-in-the-cloud>).



# RESOURCES FOR GENOMICS - THEY MAY BREAK SOMETIMES ...

NCBI Resources How To Sign in to NCBI

**We are sorry, but the page you requested is no longer available.**

**NCBI's SKY-CGH site has been retired.**

The public data from this resource can be downloaded from our [FTP server](#) and will soon be available in the [dbVar database \(SKY-CGH\)](#).

You are here: NCBI > National Center for Biotechnology Information [Write to the Help Desk](#)

GETTING STARTED	RESOURCES	POPULAR	FEATURED	NCBI INFORMATION
<a href="#">NCBI Education</a>	<a href="#">Chemicals &amp; Bioassays</a>	<a href="#">PubMed</a>	<a href="#">Genetic Testing Registry</a>	<a href="#">About NCBI</a>
<a href="#">NCBI Help Manual</a>	<a href="#">Data &amp; Software</a>	<a href="#">Bookshelf</a>	<a href="#">PubMed Health</a>	<a href="#">Research at NCBI</a>
<a href="#">NCBI Handbook</a>	<a href="#">DNA &amp; RNA</a>	<a href="#">PubMed Central</a>	<a href="#">GenBank</a>	<a href="#">NCBI News</a>
<a href="#">Training &amp; Tutorials</a>	<a href="#">Domains &amp; Structures</a>	<a href="#">PubMed Health</a>	<a href="#">Reference Sequences</a>	<a href="#">NCBI FTP Site</a>
<a href="#">Submit Data</a>	<a href="#">Genes &amp; Expression</a>	<a href="#">BLAST</a>	<a href="#">Gene Expression Omnibus</a>	<a href="#">NCBI on Facebook</a>
	<a href="#">Genetics &amp; Medicine</a>	<a href="#">Nucleotide</a>	<a href="#">Map Viewer</a>	<a href="#">NCBI on Twitter</a>
	<a href="#">Genomes &amp; Maps</a>	<a href="#">Genome</a>	<a href="#">Human Genome</a>	<a href="#">NCBI on YouTube</a>
	<a href="#">Homology</a>	<a href="#">SNP</a>	<a href="#">Mouse Genome</a>	
	<a href="#">Literature</a>	<a href="#">Gene</a>	<a href="#">Influenza Virus</a>	
	<a href="#">Proteins</a>	<a href="#">Protein</a>	<a href="#">Primer-BLAST</a>	
	<a href="#">Sequence Analysis</a>	<a href="#">PubChem</a>	<a href="#">Sequence Read Archive</a>	
	<a href="#">Taxonomy</a>			
	<a href="#">Variation</a>			

National Center for Biotechnology Information, U.S. National Library of Medicine  
8600 Rockville Pike, Bethesda MD, 20894 USA  
[Policies and Guidelines](#) | [Contact](#)

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- [Genes](#)
- [Chromosomes](#)
- [Tissues](#)
- [SAGE Genie](#)
- [RNAi](#)
- [Pathways](#)
- [Tools](#)

## Cancer Genome Anatomy Project (CGAP)

The NCI's [Cancer Genome Anatomy Project](#) sought to determine the gene expression profiles of normal, precancer, and cancer cell diagnosis, and treatment for the patient. Resources generated by the CGAP initiative are available to the broad cancer community. data, bioinformatic analysis tools, and biological resources allowing the user to find "in silico" answers to biological questions in a

[Read more about CGAP](#) and access the many valuable resources.

- [CGCI](#)
- [Cancer Types](#)
- [Data Access](#)
- [Publications](#)
- [Resources](#)
- [Test](#)

## Cancer Genome Characterization Initiative (CGCI)

The [Cancer Genome Characterization \(CGC\) Initiative](#): Assessing the use of new genomics technologies to strategically characterize tumors. Groups involved with the CGCI Initiative make all of their data available through a publicly accessible database. Cancer C incorporates genomic characterization methods including exome and transcriptome analysis using second generation sequencing to leading to cancer.

[Read more about the CGC Initiative](#) and how the project is enabling the next generation of discovery through rapid data release an



Download Plugin:

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- [Accessibility](#)
- [Disclaimer](#)

A Service of the National Cancer Institute

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as of 2018-09-19



# VARIANT RESOURCES FOR CANCER GENOMICS

Resource name	Primary institute	Constituent Knowledge base	Cancer focused	Therapeutic evidence	Predisp. evidence	Diagnostic evidence	Prognostic evidence	Variant emphasis	URL
<b>Cancer Genome Interpreter (CGI)</b>	Institute for Research in Biomedicine, Barcelona, Spain	x	x	x				Somatic	<a href="https://www.cancergenomeinterpreter.org/home">https://www.cancergenomeinterpreter.org/home</a>
<b>Clinical Interpretation of Variants in Cancer (CIViC)</b>	Washington University School of Medicine (WashU)	x	x	x	x	x	x	All variants	<a href="http://www.civicdb.org">www.civicdb.org</a>
<b>JAX Clinical Knowledgebase (CKB)</b>	The Jackson Laboratory	x	x	x	x	x	x	Somatic	<a href="https://ckb.jax.org/">https://ckb.jax.org/</a>
<b>Molecular Match</b>	Molecular Match	x	x	x			x	Somatic	<a href="https://app.molecularmatch.com/">https://app.molecularmatch.com/</a>
<b>OncoKB</b>	Memorial Sloan Kettering Cancer Center	x	x	x				Somatic	<a href="http://oncokb.org/#/">http://oncokb.org/#/</a>
<b>Precision Medicine Knowledgebase (PMKB)</b>	Weill Cornell Medical College	x	x	x	x	x	x	Somatic	<a href="https://pmkb.weill.cornell.edu/">https://pmkb.weill.cornell.edu/</a>
<b>BRCA exchange</b>	GA4GH	x	x		x			Germline	<a href="http://brcaexchange.org/">http://brcaexchange.org/</a>
<b>Cancer Driver Log (CanDL)</b>	Ohio State University (OSU) / James Cancer Hospital		x	x				Somatic	<a href="https://candl.osu.edu/">https://candl.osu.edu/</a>
<b>Gene Drug Knowledge Database</b>	Synapse		x	x		x	x	Somatic	<a href="https://www.synapse.org/#!/Synapse:syn2370773/wiki/62707">https://www.synapse.org/#!/Synapse:syn2370773/wiki/62707</a>
<b>MatchMiner</b>	Dana-Farber Cancer Institute		x					Somatic	<a href="http://bcf.dfci.harvard.edu/knowledge-systems/">http://bcf.dfci.harvard.edu/knowledge-systems/</a>
<b>COSMIC Drug Resistance Curation</b>	Wellcome Trust Sanger Institute		x	x				Somatic	<a href="http://cancer.sanger.ac.uk/cosmic/drug_resistance">http://cancer.sanger.ac.uk/cosmic/drug_resistance</a>
<b>My Cancer Genome</b>	Vanderbilt University		x	x		x	x	Somatic	<a href="https://www.mycancergenome.org/">https://www.mycancergenome.org/</a>
<b>NCI Clinical Trials</b>	National Cancer Institute of the National Institutes of Health		x					Somatic	<a href="http://www.cancer.gov/about-cancer/treatment/clinical-trials">www.cancer.gov/about-cancer/treatment/clinical-trials</a>
<b>Personalized Cancer Therapy Database</b>	MD Anderson Cancer Center		x	x	x	x	x	Somatic	<a href="https://pct.mdanderson.org/#/home">https://pct.mdanderson.org/#/home</a>
<b>ClinGen Knowledge Base</b>	ClinGen				x			Germline	<a href="https://www.clinicalgenome.org/resources-tools/">https://www.clinicalgenome.org/resources-tools/</a>
<b>ClinVar</b>	National Center for Biotechnology Information			x	x			All variants	<a href="http://www.ncbi.nlm.nih.gov/clinvar/">http://www.ncbi.nlm.nih.gov/clinvar/</a>
<b>Pharmacogenomics Knowledgebase (PharmGKB)</b>	Stanford University			x				Germline	<a href="https://www.pharmgkb.org/">https://www.pharmgkb.org/</a>
<b>The Human Gene Mutation Database (HGMD)</b>	Institute of Medical Genetics in Cardiff				x			Germline	<a href="http://www.hgmd.cf.ac.uk">http://www.hgmd.cf.ac.uk</a>

Wagner et al. A harmonized meta-knowledgebase of clinical interpretations of cancer genomic variants. Nature Genetics (under review 2018)

# Beyond a Single Resource: Federation

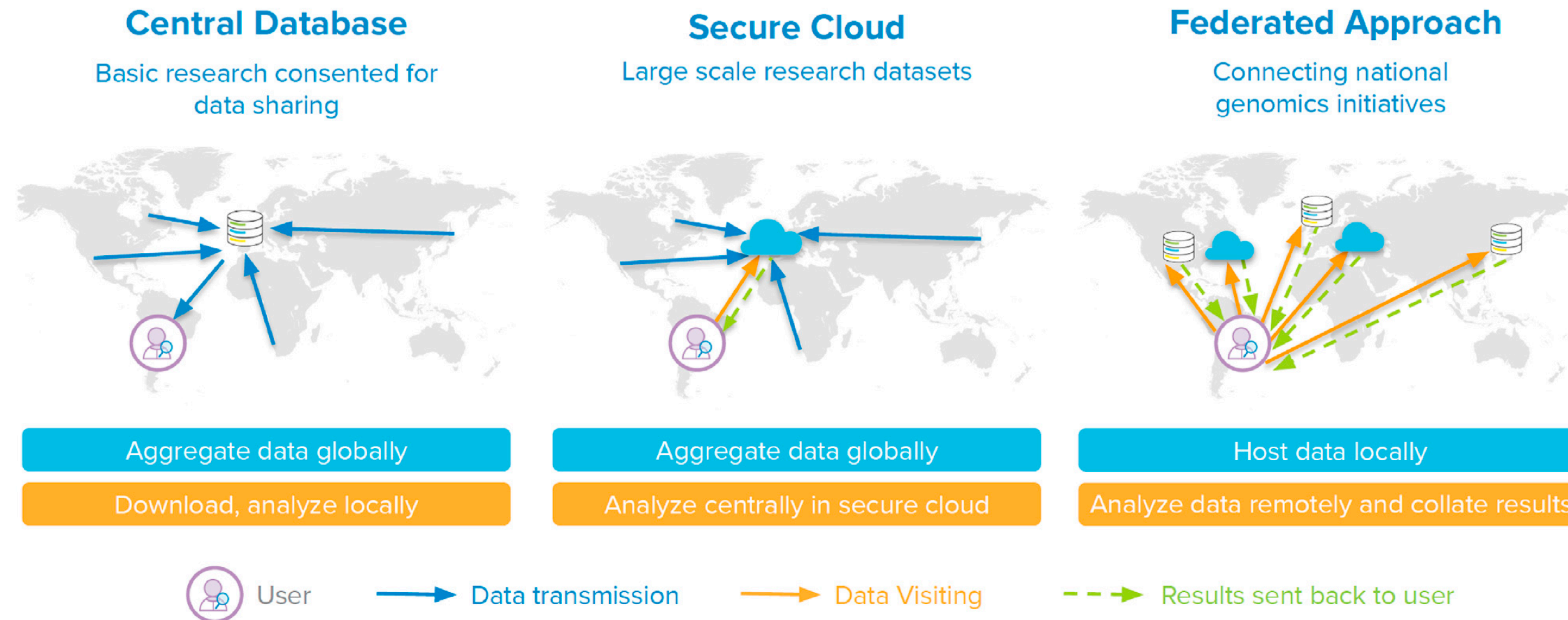
Cell Genomics

CellPress  
OPEN ACCESS

Commentary

**International federation of genomic medicine databases using GA4GH standards**

Adrian Thorogood,<sup>1,2,\*</sup> Heidi L. Rehm,<sup>3,4</sup> Peter Goodhand,<sup>5,6</sup> Angela J.H. Page,<sup>4,5</sup> Yann Joly,<sup>2</sup> Michael Baudis,<sup>7</sup> Jordi Rambla,<sup>8,9</sup> Arcadi Navarro,<sup>8,10,11,12</sup> Tommi H. Nyronen,<sup>13,14</sup> Mikael Linden,<sup>13,14</sup> Edward S. Dove,<sup>15</sup> Marc Fiume,<sup>16</sup> Michael Brudno,<sup>17</sup> Melissa S. Cline,<sup>18</sup> and Ewan Birney<sup>19</sup>



**Figure 1. Data sharing approaches: Central database, secure cloud, and federated**

Central database: Data from multiple sources are pooled in a central database. Researchers download copies of data and analyze them in their own computing environment.

Secure cloud: Data from multiple sources are pooled in a central cloud environment. Researchers remotely visit data and run their analyses in the cloud and download the result.

Federation: Data remain within locally controlled databases and computing environments, which may be cloud environments. Researchers remotely visit data, run their analyses at each site, and receive a local result, which can then be aggregated.

# Task: Exploring Genome Resources

- primary deposition databases
- interpreted databases (e.g. variant annotations...)
- suggestion: VICC paper (Wagner et al.)
  - Wagner et al (2020): A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer
- make some notes about different genome resources and their primary use
  - ➡ Don't think only "human" ヽ\_(ツ)\_/