

Databases in molecular biology

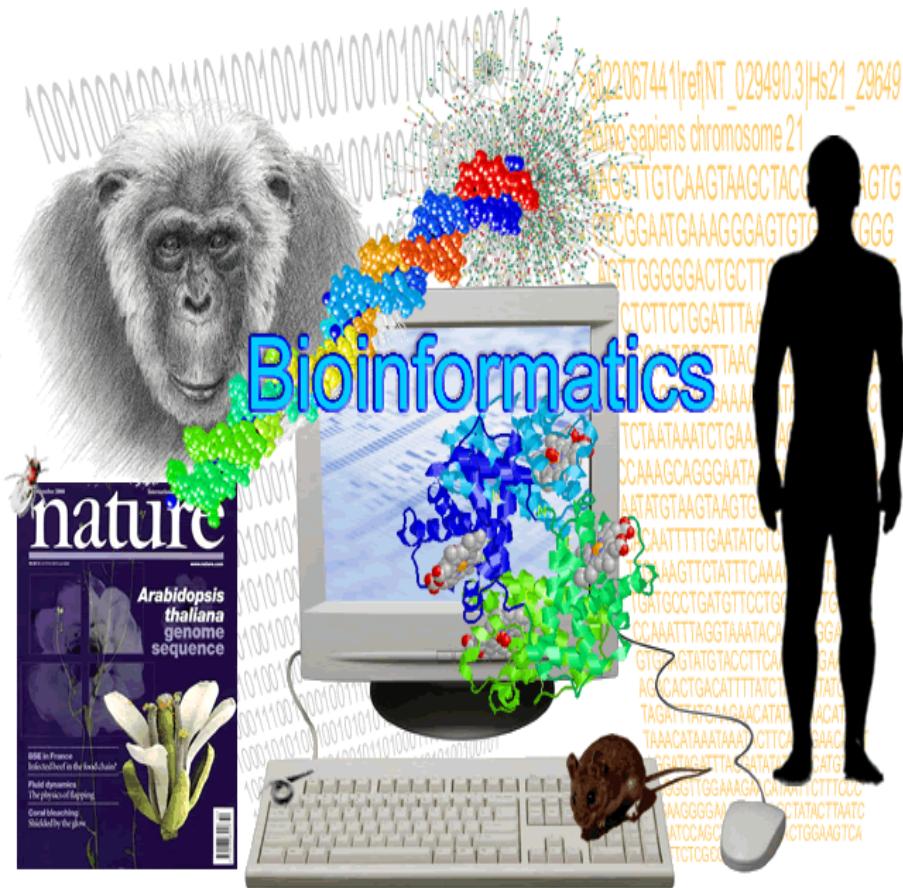
Bioinformatics Course UEB-VHIR
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Information in the omics era



- Massive quantities of information (not necessarily “big data”)
- Open-access
- For this information to be accessible it must be properly stored.
- Access to information
 - Must be fast
 - Must be flexible
- This has been made possible
 - Creating databases
 - Distributing them through the web

Biological Databases

- **Definition:** *libraries* of life sciences information, collected from scientific experiments, published literature, high-throughput experiment technology and computational analysis
- **What are they for?**
 - Storage of information
 - Data organization
 - Access information
 - Knowledge discovery
- There are many different general and specialized databases.
 - Large list published yearly in *NAR* : 1645 in 2022!
 - <https://www.oxfordjournals.org/nar/database/c/>
 - <https://academic.oup.com/nar/article/50/D1/D1/6495890>

Biological Databases

NAR Database Summary Paper Category List

[Nucleotide Sequence Databases](#)

[RNA sequence databases](#)

[Protein sequence databases](#)

[Structure Databases](#)

[Genomics Databases \(non-vertebrate\)](#)

[Metabolic and Signaling Pathways](#)

[Human and other Vertebrate Genomes](#)

[Human Genes and Diseases](#)

[Microarray Data and other Gene Expression Databases](#)

[Proteomics Resources](#)

[Other Molecular Biology Databases](#)

[Organelle databases](#)

[Plant databases](#)

[Immunological databases](#)

[Cell biology](#)

Nucleotide Databases

- [ASD](#)
- [ATD](#)
- [EMBL-Bank](#)
- [EMBL CDS](#)
- [Ensembl](#)
- [Genome Reviews](#)
- [IMGT/HLA](#)

Protein Databases

- [CSA](#)
- [GOA](#)
- [IntAct](#)
- [IntEnz](#)
- [InterPro](#)

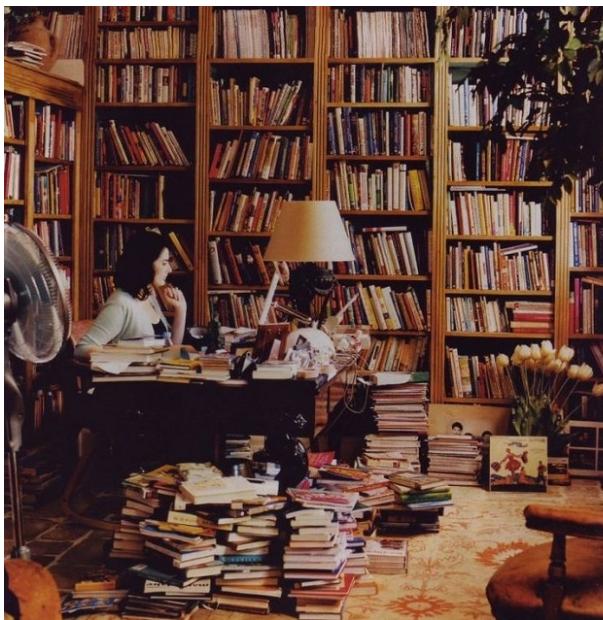
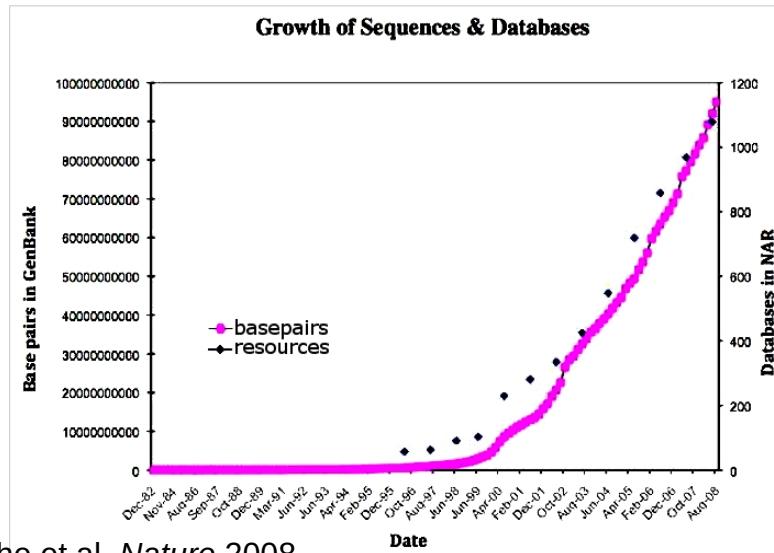
Microarray Databases

- [ArrayExpress](#)
- [MIAME](#)

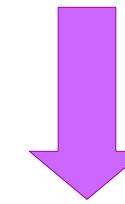
Literature Databases

- [MEDLINE](#)
- [OMIM](#)
- [Patent Abstracts](#)
- [more...](#)

Challenges



This large number of databases, though extremely useful, can lead to its own issues of redundancy and lack of integration.



- Structure/Integrate information
- Annotation and Curation
- Centralize data management

I. Structuring and Integrating the information

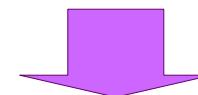
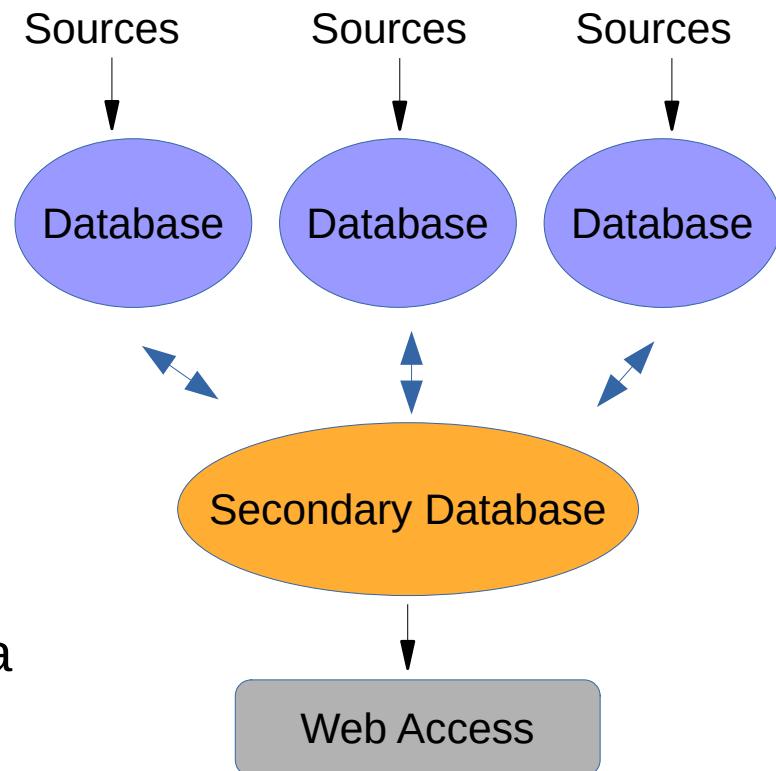
Integrating the information

- **Primary databases:**

- often hold only one type of specific data which is stored in their own archive.
- upload new data from experiments and update entries

- **Secondary databases:**

- use other databases as their source of information.
- often already process or analyze the data to get new results.



**Different formats and models
for structuring the data**

Integrating the information

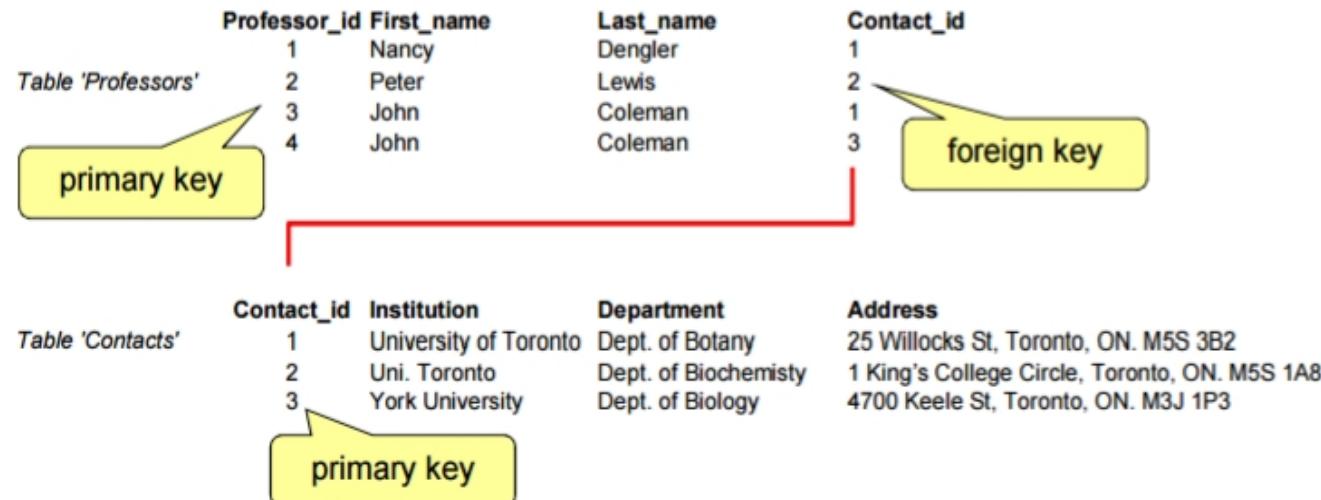
- The quality of the information in a database is closely related to its structure
- This aspect is also crucial for its efficiency and accessibility.
- There are many different types of file formats depending on the type of information they contain / source of data
- Most are based on the flat-file format (text file)

FASTA format (sequences)

Identifier	Description
sequence	>136435 Mus Musculus basic domain/leucine zipper transcription factor mRIIA, complete cds. gccccggccgcgtccccagacaaaaggcttggccggccggccggccggccgtgcgcctcgctccccgcctcccc cggttgcgcgtcttcgcggggggctttggctggcgcgtcccggccggccgaaagtttccccgcggcag cgccggctgagcctcgcttttagcgatggccggagctgagcatggggcaagagactgcccaccagccgct ggccatggagtacgtcaacgacttcgaccttctaagttcgacgtgaagaaggagccctggggcgccgga gcgtccggccggccatgcacacgcctgcagcctgctggctgggtcgccaccccgctcagcactccgt

Integrating the information

- Different models exist to relate/integrate the information (Relational, Hierarchical, Networks...).
- Most common model: Relational databases
 - flat-file format (text file)
 - Many tables linked to each other: cross-referencing through a key (common) field (unique identifier)



Integrating the information

- In many databases an entry can be identified in 2 (ore more!) different ways:
 - **Identifier** ("locus" in GenBank, "entry name" in UniProt): is a string of letters and digits. May change if the database curators decide that is no longer appropriate.
 - **Accession code (number)**: is a number (possibly with a few characters in front) that uniquely identifies an entry in its database. It is supposed to be stable.
 - **Versions and Gene Indices**: The same accession number may be associated with a different GI if a newer or corrected sequence is submitted. ([+info](#))

Example: human gene ADH6

GenBank

LOCUS	AH001409	2625 bp	DNA	linear	PRI	10-JUN-2016
DEFINITION	Homo sapiens alcohol dehydrogenase 6 (ADH6) gene, complete cds.					
ACCESSION	AH001409	M68895	M84402	M84403	M84404	M84405 M84406 M84407 M84408
						M84409
VERSION	AH001409.2					
KEYWORDS	.					
SOURCE	Homo sapiens (human)					

UniProt

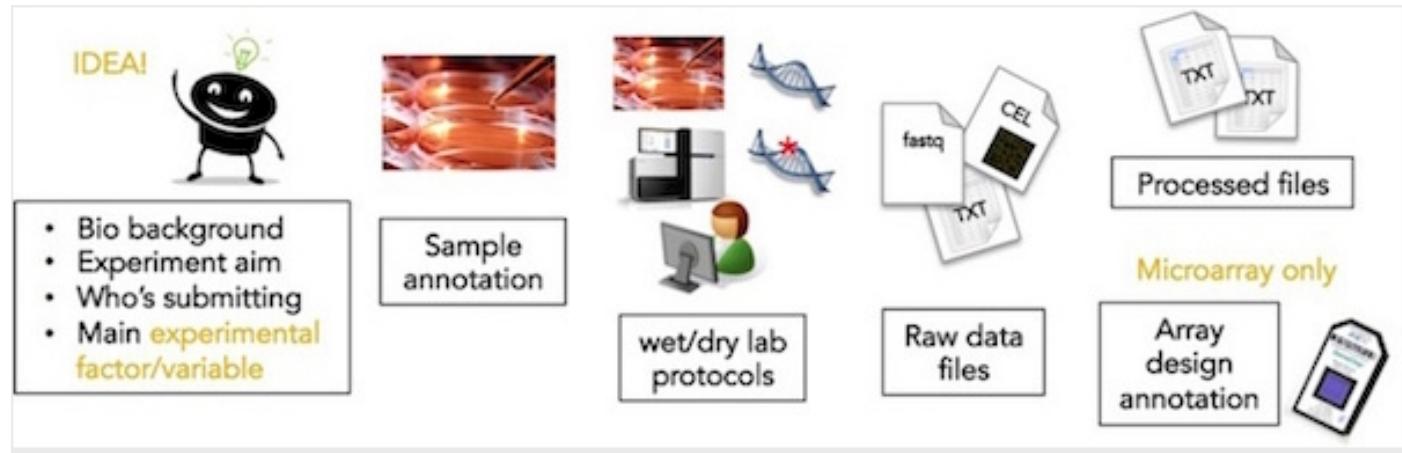
Entry	Entry name		Protein names		Gene names
P28332	ADH6_HUMAN		Alcohol dehydrogenase 6		ADH6

II. Data Annotation and Curation

Data Annotation

- Different levels of annotation
 - Data: annotation of sequences/genomes (chromosome position, gene function, ...)
 - Metadata: information for an experiment, identification of samples, ...
- Collaborative efforts to provide as much information about the data
- The **Minimum Information Standard** is a set of guidelines for reporting data

MIAME (Minimum Information About a Microarray Experiment)

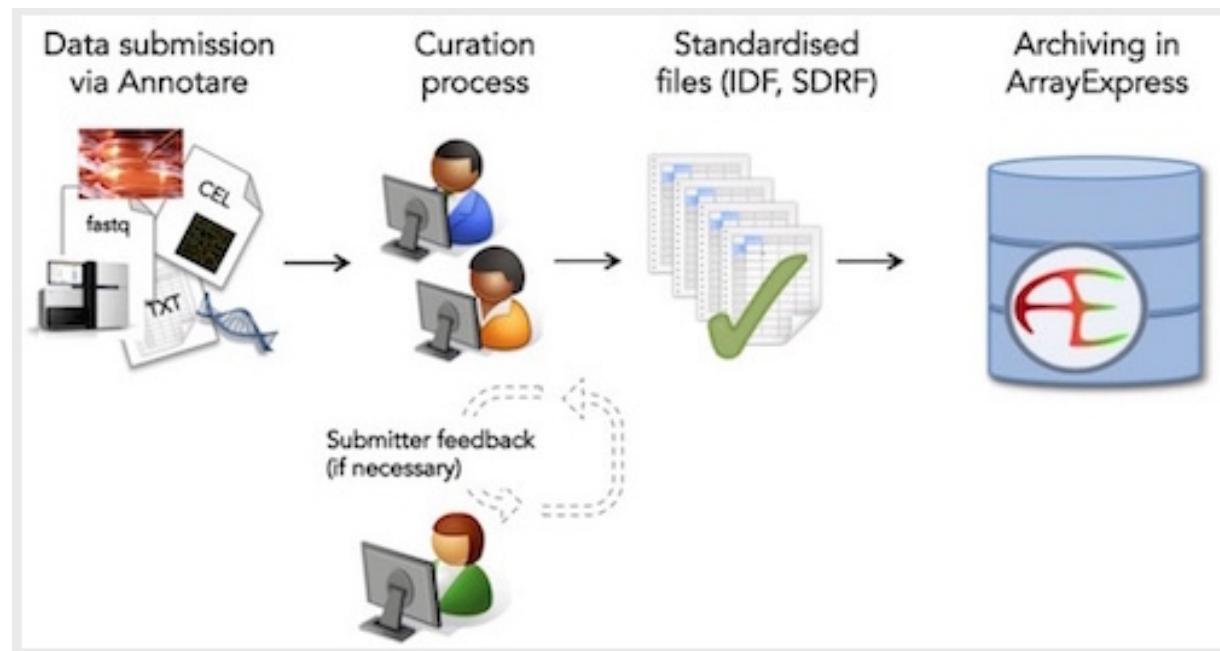


Source: <https://www.ebi.ac.uk/arrayexpress/submit/overview.html>

- Benefits:
 - Ensures the verification, interpretation and reproducibility of data
 - Facilitates the creation of structured databases and development of analysis

Data Curation

- It involves annotation, publication and presentation of the data such that the value of the data is maintained over time, and the data remains available for reuse and preservation.
- May be done by database experts or experts of the scientific community.

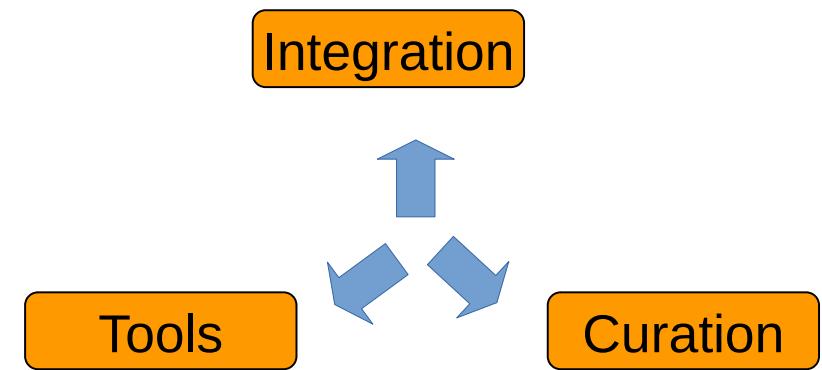


Source: <https://www.ebi.ac.uk/arrayexpress/submit/overview.html>

III. Centralizing data management

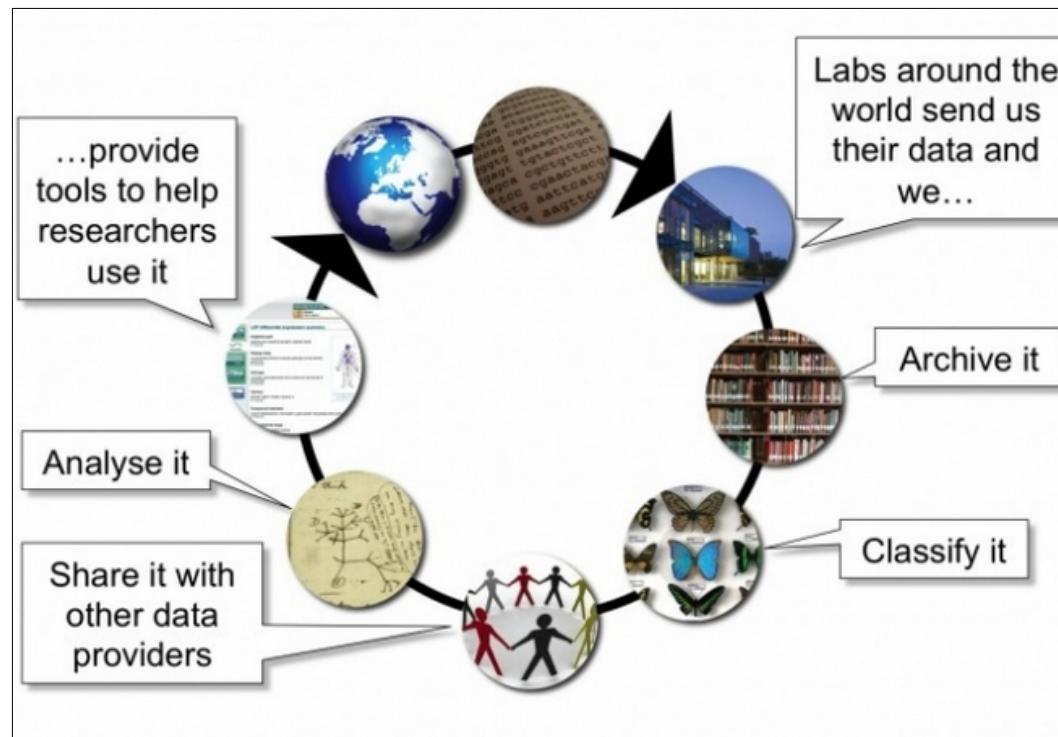
Centralizing data management

- General
 - **Resource providers**
- Subject-specific
 - **Collaborative projects**
 - **Multi-omics repositories**
 - **Genomic Browsers**



Resource providers

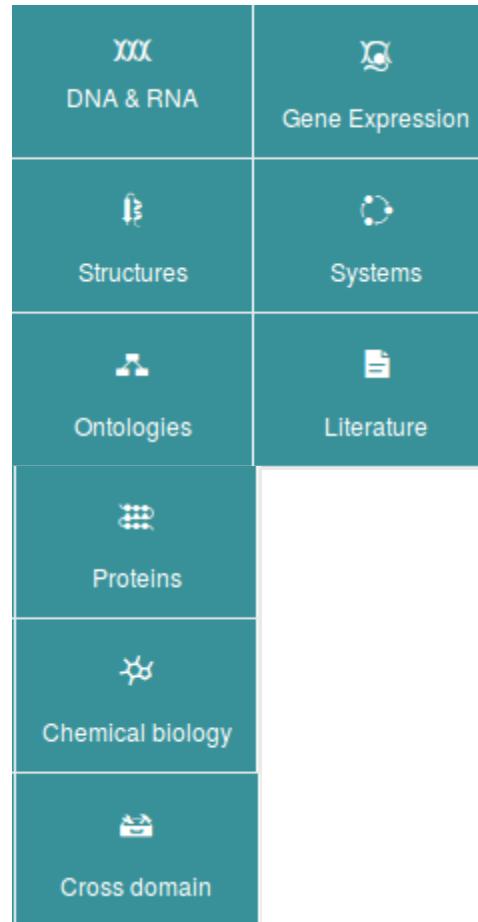
- Big organizations that act as *hubs* that provide transparent access to data sources.



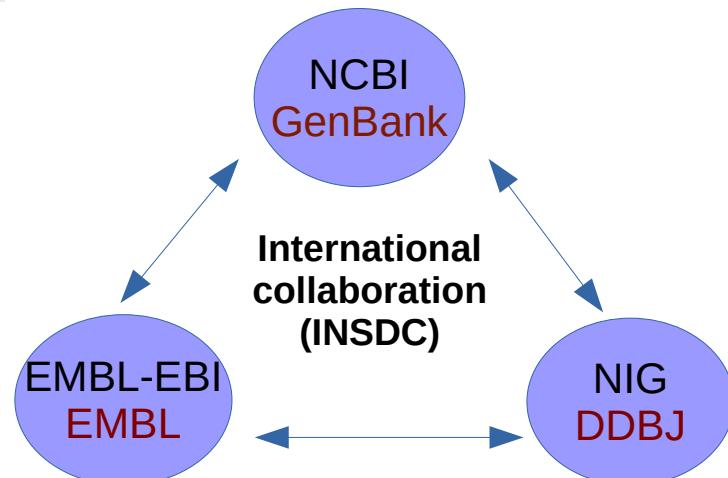
Resource providers



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



- Provide integrated access to databases
- Classification according to multiple criteria
- Primary databases may be common or specific
- Example: nucleotide DB are daily synchronized



Resource providers



[Amino Acid Explorer](#)

[Assembly Archive](#)

[Basic Local Alignment Search Tool \(BLAST\)](#)

[Batch Entrez](#)

[BioAssay Services](#)

[BLAST Link \(BLink\)](#)

[BLAST Microbial Genomes](#)

[BLAST RefSeqGene](#)

[CDTree](#)

[Cn3D](#)

[COBALT](#)

[Concise Microbial Protein BLAST](#)

[Conserved Domain Architecture Retrieval Tool \(CDART\)](#)

[Conserved Domain Search Service \(CD Search\)](#)

[Digital Differential Display \(DDD\)](#)

[Electronic PCR \(e-PCR\)](#)

[Frequency-weighted Link \(FLink\)](#)

Clustal Omega



Multiple sequence alignment of DNA or protein sequences. Clustal Omega replaces the older ClustalW alignment tools.

[Multiple sequence alignment](#)

InterProScan



InterProScan searches sequences against InterPro's predictive protein signatures.

[Protein feature detection](#) [Sequence motif recognition](#)

BLAST [protein]



Fast local similarity search tool for protein sequence databases.

[Sequence similarity search](#)

BLAST [nucleotide]



Fast local similarity search tool for nucleotide sequence databases.

[Sequence similarity search](#)

HMMER



Fast sensitive protein homology searches using profile hidden Markov models (HMMs) for querying against both sequence and HMM target databases.

[Sequence similarity search](#) [Protein function analysis](#)

- Provide a wide variety of data analysis tools that allow users to explore, manipulate, align, visualize and evaluate biological data.

Examples of Databases

Examples of Databases

Literature DB

- Contain different types of bibliographic information (articles, reviews, books, patents...). Not only peer-reviewed!
- PubMed (NCBI): references and abstracts on life and biomedical sciences
- Europe PMC (EBI-EMBL): a full-text literature database for life sciences
- ArXiv: repository of electronic pre-prints after moderation
- Patent databases (eg. EPO) can be accessed from EBI-search
- Biocatalogue: provides a curated catalog of life-sciences web services

Nature. Author manuscript; available in PMC 2014 Nov 7.
Published in final edited form as:
[Nature. 2013 Nov 7; 503\(7474\): 59–66.](#)
doi: [\[10.1038/nature12709\]](#)

PMCID: PMC3983910
NIHMSID: NIHMS524654
PMID: [24201279](#)

Cooperation between brain and islet in glucose homeostasis and diabetes

Michael W. Schwartz,¹ Randy J. Seeley,² Matthias H. Tschöp,³ Stephen C. Woods,⁴ Gregory J. Morton,¹ Martin G. Myers,⁵ and David D'Alessio²

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See other articles in PMC that [cite](#) the published article.

[Abstract](#) [Go to:](#)

Although a prominent role for the brain in glucose homeostasis was proposed by scientists in the nineteenth century, research throughout most of the twentieth century focused on evidence that the function of pancreatic islets is both necessary and sufficient to explain glucose homeostasis, and that diabetes results

Examples of Databases

Taxonomic DB

- Contain information about the classification of organisms, mainly from molecular data
- **Taxonomy DB**: curated classification and nomenclature for all of the organisms in the public sequence databases.
- This represents about 10% of described species



Examples of Databases

Nucleotide DB

- Contain DNA / RNA (coding or non-coding) sequences from all organisms
- Primary DB: GenBank (NCBI) / ENA (EMBL-EBI) / DDBJ (NIG)
- RefSeq** (NCBI) Project: maintains and curates a publicly available database of annotated genomic, transcript, and protein sequence records.
- Nucleotide**: collection from several DB (GenBank, RefSeq, TPA, PDB...)
- miRBase**: database of published miRNA sequences and annotation.

NCBI Resources How To

Nucleotide Nucleotide (brca1) AND "Homo sapiens"[organism:txid9606]
[Create alert](#) [Advanced](#)

[Learn more about upcoming changes to the Nucleotide, EST, and GSS databases.](#)

Species Animals (507) Summary ▾ 20 per page ▾ Sort by Default order ▾
 Molecule types mRNA (507) Customize ...
 ✓ RefSeq (507) Customize ...
 Sequence length Custom range...
 Release date Custom range...
 Revision date

Items: 1 to 20 of 507

1. Homo sapiens BRCA1, DNA repair associated (BRCA1), transcript variant 5, mRNA
 3,800 bp linear mRNA
 Accession: NM_007299.3 GI: 237681124
[Protein](#) [PubMed](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)

2. Homo sapiens BRCA1, DNA repair associated (BRCA1), transcript variant 1, mRNA
 7,224 bp linear mRNA
 Accession: NM_007299.3 GI: 237767282

miRBase

Home Search Browse Help Download Blog Submit hsa-mir-19a

Stem-loop sequence hsa-mir-19a

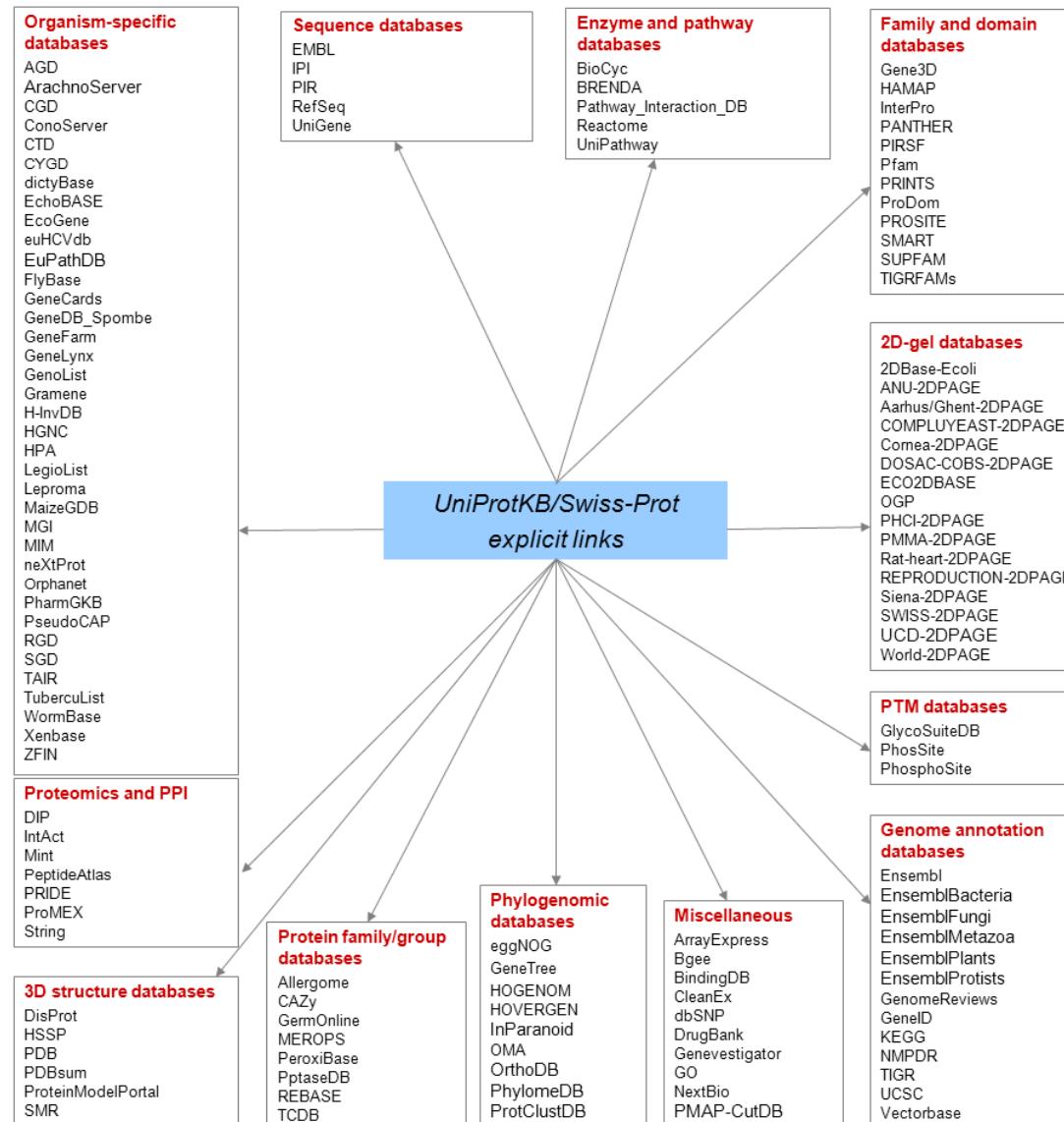
Accession	MI0000073 (change log)
Symbol	HGNC:MIR19A
Description	Homo sapiens miR-19a stem-loop
Gene family	MIPF0000011; mir-19
Literature search	 313 open access papers mention hsa-mir-19a (1573 sentences)
Stem-loop	<pre> u u -- --- ag 5' gcag cc cuguuuaguuuuggcauag uugcac uaca a 3' cguc gg gguagucaaaaacguaua aacgug augu g c u ua lug aa </pre> <p>Get sequence</p>

Examples of Databases

Protein DB

- Contain data from protein sequences, structures. Predicted / experimental.
- [Protein](#) (NCBI) / [UniProtKB](#): collection of protein **sequences** from several sources:
 - translations from annotated coding regions (GenBank, RefSeq.../TrEMBL)
 - Records from SwissProt, PIR, PRF, and PDB.
- [InterPro](#): integrates information from protein **family and domain** DB like Pfam, PROSITE, CDD, ...
- [PDB](#): contains **3D structural data** of large biological molecules (proteins, nucleic acids). Typically obtained by X-ray crystallography, NMR spectroscopy or cryo-electron microscopy.
- [IntAct](#): a curated DB of **molecular interactions**

Examples of Databases



Practicum

To warm up...

Querying databases to answer biological questions

- 1- Using [PubMed Advanced Search](#), look for a *review paper* published in *Nature* on *colorectal cancer* and authored by *David SS*
- 2- In the abstract, the authors mention a gene associated to the disease. Find a *well annotated mRNA* sequence for this gene using the [Nucleotide DB](#)
- 3- Look for MUTYH human protein in [UniProtKB](#)
 - Identify protein sequence, motifs and 3D structure
 - With which proteins interacts according to *IntAct DB*?

Practicum

1- Using PubMed Advanced Search, look for a *review* paper published in *Nature* on *colorectal cancer* and authored by *David SS*

Builder

All Fields dropdown: colorectal cancer Show index list

AND dropdown: Journal dropdown: Nature Show index list

AND dropdown: Publication Type dropdown: "review"[Publication Type] Show index list Hide index list

Search results (partial list):

- research support, nra, intramural (49210)
- research support, non u s govt (6930275)
- research support, u s govt, non p h s (790770)
- research support, u s govt, p h s (2460270)
- research support, u s government (2902642)
- retracted publication (6332)
- retraction of publication (6645)
- review (2456140) Previous 200 Next 200
- scientific integrity review (243)
- study characteristics (4803808)
- support of research (8501193)

Refresh index

AND dropdown: All Fields dropdown: Show index list

Search or Add to history

Practicum

2- In the abstract, the authors mention a gene associated to the disease. Find a *well annotated mRNA* sequence for this gene using the [Nucleotide DB](#)

Using filters

The screenshot shows the NCBI Nucleotide search interface. The search term "mutyh AND "Homo sapiens"[orgn:txid9606]" has been entered. The results page displays 20 items out of 38, filtered for mRNA in Homo sapiens. The first result is for "Homo sapiens mutY DNA glycosylase (MUTYH), transcript variant 13, mRNA". It includes details like accession NM_001350651.1, GI 1183596751, and links to Protein, PubMed, and Taxonomy. Below it is another entry for "Homo sapiens mutY DNA glycosylase (MUTYH), transcript variant 12, mRNA". A red bracket on the left groups the filter options under "Using filters".

Species: Summary ▾ 20 per page ▾ Sort by Default order ▾

Items: 1 to 20 of 38

Filters activated: mRNA, RefSeq. [Clear all](#)

[Homo sapiens mutY DNA glycosylase \(MUTYH\), transcript variant 13, mRNA](#)

1. 1,767 bp linear mRNA
Accession: NM_001350651.1 GI: 1183596751
[Protein](#) [PubMed](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)

[Homo sapiens mutY DNA glycosylase \(MUTYH\), transcript variant 12, mRNA](#)

2. 1,831 bp linear mRNA

Homo sapiens mutY DNA glycosylase (MUTYH), transcript

NCBI Reference Sequence: NM_001350651.1
[GenBank](#) [Graphics](#)

```
>NM_001350651.1 Homo sapiens mutY DNA glycosylase (MUTYH), transcript variant mRNA
CAGCCGGAGCCCGGTGATAACCGAACCTGTAGTCCTCGTGGCTAGTTCAAGCGGAAGGGAGCAGTC
TCTGAAGCTTGAGGAGCCTCTAGAACTATGAGCCGAGGCCCTCCCTCTCCAGAGGCCAGAGGCTT
AAGGCTACTCTGGGAAGCCGCTCACCGCTCGAGCTGCGGGAGCTGAAACTGCGCCATCGTCAGTGTG
GCGGCATGACACCGCTCGTCTCCGCTGAGTCGTCAGTGGGAGCATGAGGAAGGCCAGGAGCAGCCG
TGGGAAGTGGTACAGGAAGCAGGCCAGGAGCAGAGCATGCTAAAGAACAAACAGTC
GGCCAAGCCTTCTGCGCTGTAGAGACGTAGCTGAACTCACGCTTCCGAGGGAGCCTGCTAAGCTGG
ACGACCAAGAGAACCGGGACCTACCATGGAGAACGGCAGAGATGAGATGGACCTGGACAGGCCGGC
ATATGCTGAAGTGGCTACACTGAGGACCTGGCCAGTGCTTCCCTGGAGGAGGTGAATCAAACCTGGG
```

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3- Look for MUTYH human protein in UniProtKB

- Identify protein sequence, motifs and 3D structure
- With which proteins interacts according to IntAct DB?

UniProtKB - Q9UIF7 (MUTYH_HUMAN)

 Basket ▾

Display

 BLAST  Align  Format  Add to basket  History

 Feedback  Help video  Other tutorials and videos

Entry

Protein | Adenine DNA glycosylase

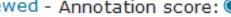
Publications

Gene | MUTYH

Feature viewer

Organism | Homo sapiens (Human)

Feature table

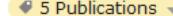
Status |  Reviewed - Annotation score:  - Experimental evidence at protein levelⁱ

None

Function

Functionⁱ

Names & Taxonomy

Involved in oxidative DNA damage repair. Initiates repair of A*oxoG to C*G by removing the inappropriately paired adenine base from the DNA backbone. Possesses both adenine and 2-OH-A DNA glycosylase activities.  5 Publications ▾

Subcellular location

Catalytic activityⁱ

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Interactionⁱ

Binary interactionsⁱ

With	Entry	#Exp.	IntAct	Notes
AGTRAP	Q6RW13	3	EBI-10321956, EBI-741181	

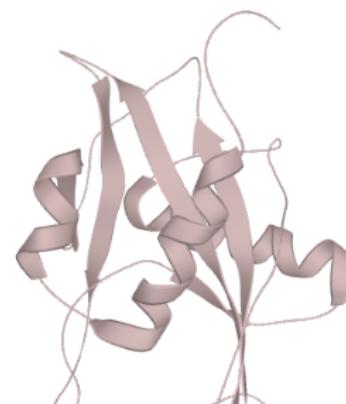
Protein-protein interaction databases

BioGrid ⁱ	110681, 11 interactors
DIP ⁱ	DIP-41972N
IntAct ⁱ	Q9UIF7, 15 interactors
MINT ⁱ	Q9UIF7
STRING ⁱ	9606.ENSP00000361170

Structureⁱ

Family and domain databases

CDD ⁱ	cd03431 DNA_Glycosylase_C, 1 hit cd00056 ENDO3c, 1 hit
Gene3D ⁱ	1.10.1670.10, 1 hit
InterPro ⁱ	View protein in InterPro IPR011257 DNA_glycosylase IPR004036 Endonuclease-III-like_CS2 IPR003651 Endonuclease3_FeS-loop_motif IPR004035 Endonuclease-III_FeS-bd_BS IPR003265 HhH-GPD_domain IPR000445 HhH_motif IPR023170 HTH_base_excis_C IPR029119 MutY_C IPR015797 NUDIX_hydrolase-like_dom_sf IPR000086 NUDIX_hydrolase_dom
Pfam ⁱ	View protein in Pfam PF00633 HHH, 1 hit PF00730 HhH-GPD, 1 hit PF14815 NUDIX_4, 1 hit
SMART ⁱ	View protein in SMART SM00478 ENDO3c, 1 hit SM00525 FES, 1 hit
SUPERFAMILY ⁱ	SSF48150 SSF48150, 1 hit SSF55811 SSF55811, 1 hit
PROSITE ⁱ	View protein in PROSITE PS00764 ENDONUCLEASE_III_1, 1 hit PS01155 ENDONUCLEASE_III_2, 1 hit PS51462 NUDIX, 1 hit



PDB Entry	Method	Resolution	Chain	Positions	Links
1X51	NMR		A	356-497	PDBe RCSB PDB PDBj PDBsum
3N5N	X-ray	2.30 Å	X/Y	76-362	PDBe RCSB PDB PDBj PDBsum

1 notificació

Examples of Databases

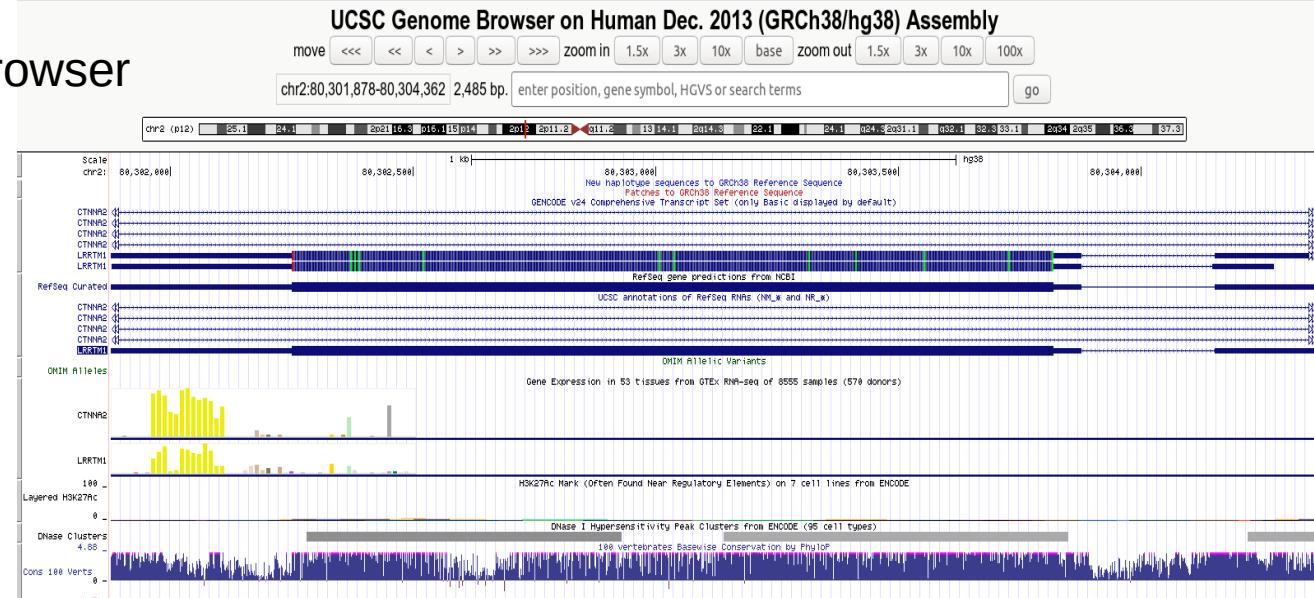
Genomic databases

- Organize information on genomes including sequences, maps, chromosomes, assemblies, and annotations
- Species-specific genome databases (eg. [Mouse Genome Informatics](#))
- Genome Browsers: provide tools for visualization and integrative genomic analysis

– NCBI [Genome Data Viewer](#)

– [UCSC Genome Browser](#)

– EBI's [Ensembl](#)



Examples of Databases

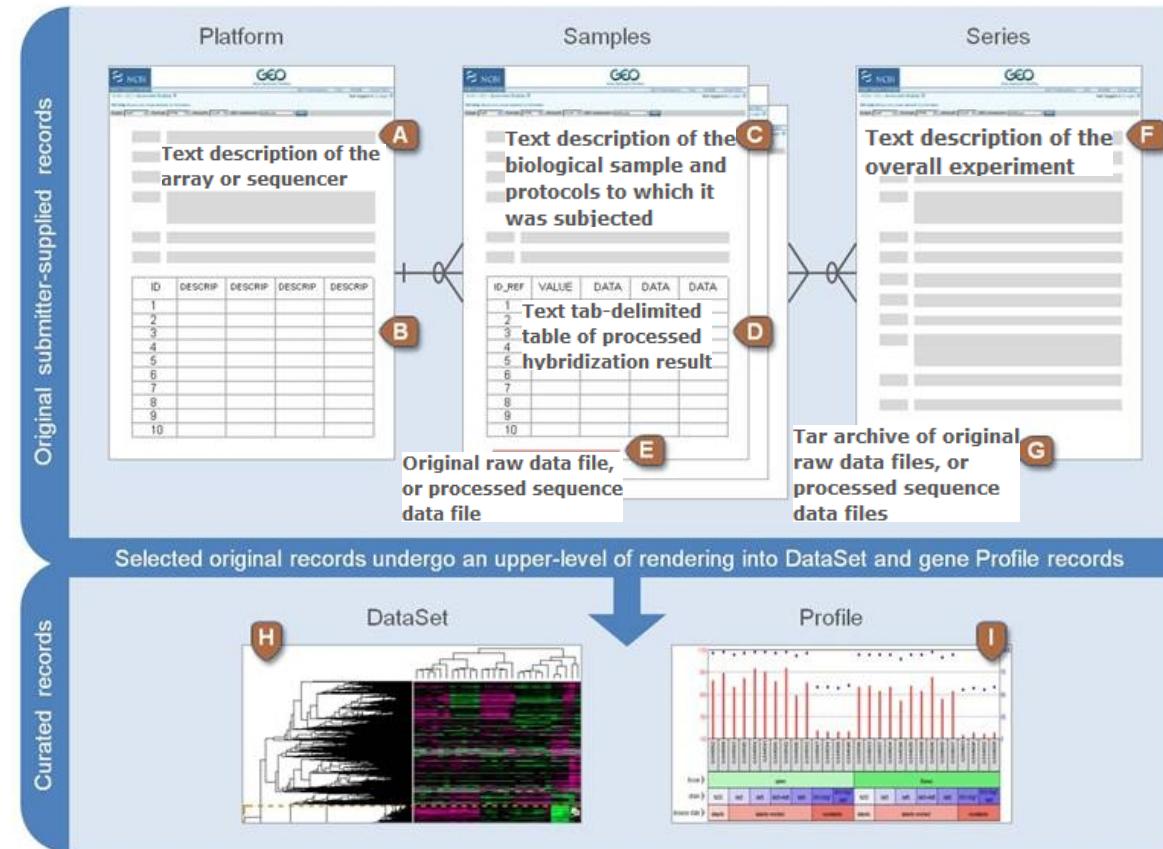
Gene Expression Databases

- Contain gene expression data derived from microarray, next-generation sequencing, and other forms of high-throughput functional genomics data submitted by the research community
- [Gene Expression Omnibus \(GEO\)](#) / [ArrayExpress \(EBI\)](#)
- [Sequence Read Archive \(SRA\)](#): stores raw sequencing data and alignment information from high-throughput sequencing platforms
- [GTEx](#)
- [Expression Atlas](#): provides gene expression results for different organisms, including metazoans and plants. Expression profiles of tissues from Human Protein Atlas, GTEx and FANTOM5, and of cancer cell lines from ENCODE, CCLE and Genentech projects can be explored.

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Retrieving data from GEO

- The **Gene Expression Omnibus (GEO)** is an international public repository that archives and freely distributes microarray, next-generation sequencing, and other forms of high-throughput functional genomics data submitted by the research community.
- Data organization:
 - Platform (GPLxxx)
 - Samples (GSMxxx)
 - Series (GSExxx)
 - Datasets (curated) (GSDxxx)
 - Profiles (curated)



See some examples

Practicum

Gene Expression Omnibus (GEO)

- Queries can be performed for datasets or gene expression profiles
 - **GEO Datasets**: stores original submitter-supplied study descriptions as well as curated gene expression DataSets.
 - **GEO Series (GSEXXX)**: original submitter-supplied record that summarizes a study
 - **GEO Datasets (GDSXXX)**: represents a collection of biologically- and statistically-comparable samples processed using the same platform.

Example with GDS browser:

DataSet	Title	Organism(s)	Platform	Series	Samples
GDS6248	Diet-induced obesity model: liver	<i>Mus musculus</i>	GPL6887	GSE39549	51
GDS6247	Diet-induced obesity model: white adipose tissue	<i>Mus musculus</i>	GPL6887	GSE39549	40
GDS6177	Acute alcohol consumption effect on whole blood (control...)	<i>Homo sapiens</i>	GPL570	GSE20489	25

Practicum

Retrieving data from GEO

Series GSE39549		Query DataSets for GSE39549
Status	Public on Mar 01, 2014	
Title	Time-course microarrays reveal early activation of the immune transcriptome and adipokine dysregulation leads to fibrosis in visceral adipose depots during diet-induced obesity	
Organism	Mus musculus	
Experiment type	Expression profiling by array	
Summary	Time-course analysis of adipocyte gene expression profiles response to high fat diet. The hypothesis tested in the present study was that in diet-induced obesity, early activation of TLR-mediated inflammatory signaling	
Overall design	Total RNA obtained from isolated epididymal and mesenteric adipose tissue of C57BL/6J mice fed normal diet or high fat diet for 2, 4, 8, 20 and 24 weeks	
Contributor(s)	Kwon E. Choi M	
Platforms (1)	GPL6887 Illumina MouseWG-6 v2.0 expression beadchip	
Samples (91) + More...	GSM971546 Mice fed Normal diet for 2weeks rep1 GSM971547 Mice fed Normal diet for 2weeks rep2 GSM971548 Mice fed Normal diet for 2weeks rep3	
Relations		
BioProject	PRJNA171109	
Analyze with GEO2R		

Study information

Platform used (data table with annotation of probes)

Samples

SOFT file can hold both data tables and descriptive information for multiple Platforms, Samples, and/or Series.

Series matrix with info for all samples and raw/processed data

Info on data files

Download family		Format
SOFT formatted family file(s)		SOFT 
MINiML formatted family file(s)		MINiML 
Series Matrix File(s)		TXT 
Supplementary file		
GSE39549_Matrix_non-normalized_EPI.txt.gz	8.4 Mb	(ftp)(http) TXT
GSE39549_Matrix_non-normalized_MES.txt.gz	2.9 Mb	(ftp)(http) TXT
GSE39549_RAW.tar	15.8 Mb	(http)(custom) TAR
<i>Raw data is available on Series record Processed data included within Sample table</i>		

Practicum

Retrieving data from GEO

Source name	Adipose tissue of mice
Organism	Mus musculus
Characteristics	strain: C57BL/6J treatment protocol: Normal diet time: 2 weeks age: 7 weeks tissue: epididymal adipose tissue
Treatment protocol	C57BL/6J mice were fed a high-fat diet (HFD) or normal diet (ND) and sacrificed at 5 time-points (2, 4, 8, 20 and 24 weeks) over 24 weeks.
Extracted molecule	total RNA
Extraction protocol	RNA was extracted with Trizol reagent, followed by clean-up and DNase I treatment with QIAGEN RNeasy mini kit in accordance with the prescribed protocol provided with the kit. Quality control was performed with Agilent Bioanalyzer.
Label	biotin
Label protocol	Biotinylated cRNA were prepared with the Ambion MessageAmp kit for Illumina arrays
Hybridization protocol	Standard Illumina hybridization protocol
Scan protocol	Standard Illumina scanning protocol
Description	Sample name: E2N1 replicate 1
Data processing	Raw data were extracted using the software provided by the manufacturer (Illumina BeadStudio v3.1.3 (Gene Expression Module v3.3.8). The data were normalised by quantile method using ArrayAssist®

Sample specifications
(identification, protocol, source...)

Data table header descriptions

ID_REF	VALUE
	normalized signal

Data table

ID_REF	VALUE
ILMN_2417611	7.1251793
ILMN_2762289	6.838682
ILMN_2896528	12.505199
ILMN_2721178	11.040463
ILMN_2458927	6.5777017

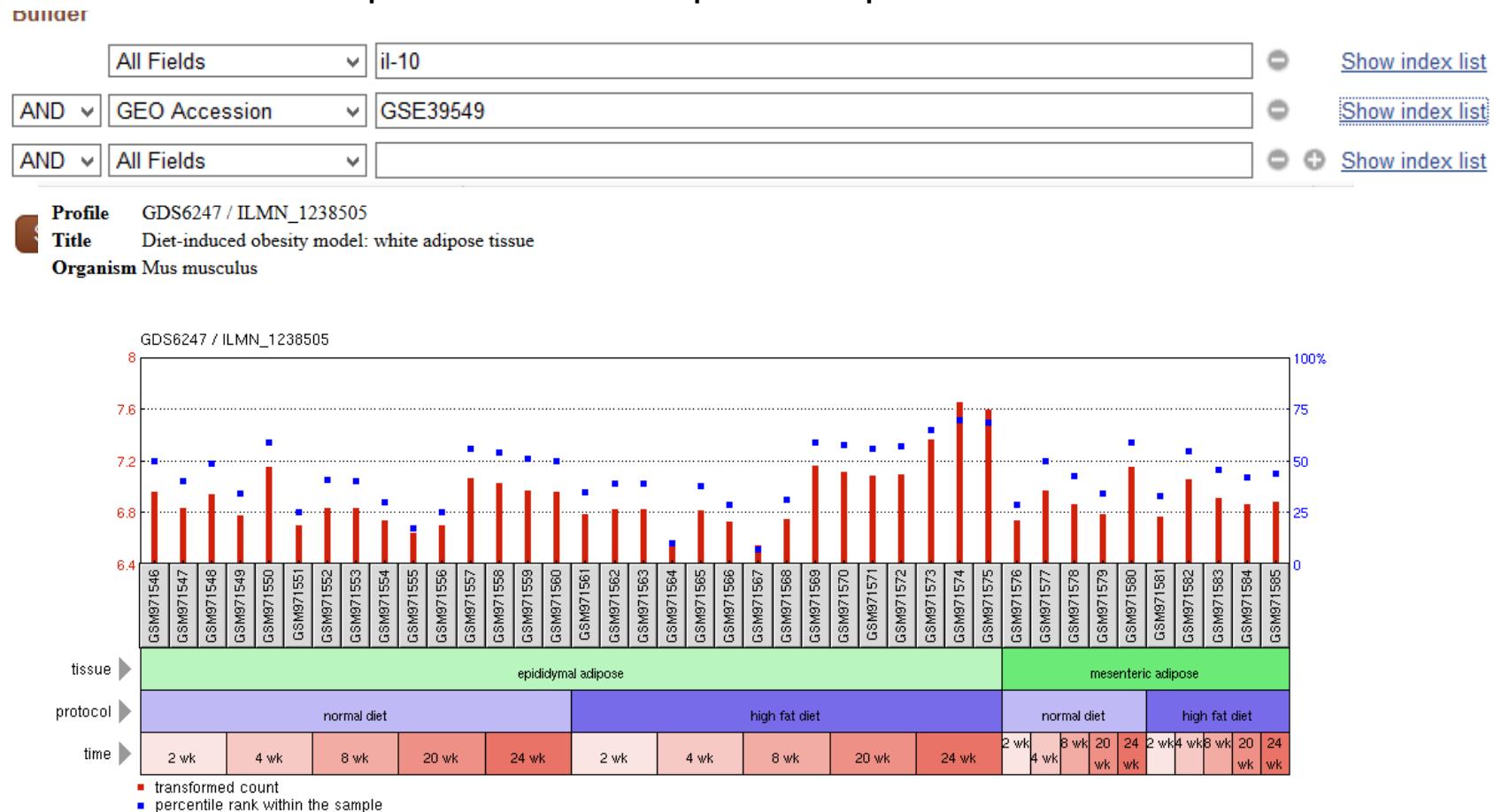
Data table with normalized expression values

Practicum

Retrieving data from GEO

- **GEO Profiles:** stores individual gene expression profiles from curated DataSets.

Example: search for expression profile of IL-10



Examples of Databases

- **Functional annotations**
 - [Gene Ontology](#) (GO): unify the representation of gene and gene product attributes across all species
 - [KEGG / Reactome](#): integrates genomic, chemical and systemic functional information
 - [Gene Cards](#)
- **Terapeutic targets**
 - [Therapeutic targets database](#)
 - [PharmGKB](#) : pharmacogenomics (impact of genetics on drug response)
- **Disease-related**
 - [DisGeNet](#): genes and variants associated to human diseases
 - [TCGA, COSMIC](#) (Cancer)

Examples of databases

- And many more that can be found in / accessed from:
 - Large list published yearly in [NAR](#)
 - Journal-recommended repositories for publication ([Nature](#))
 - Resource providers portals ([NCBI](#) / [EBI-EMBL](#))
 - Integrative projects (disease-specific / organism-specific)
 - Genome Browsers (genome-oriented)

Subject-specific repositories and collaborative projects

Subject-specific repositories

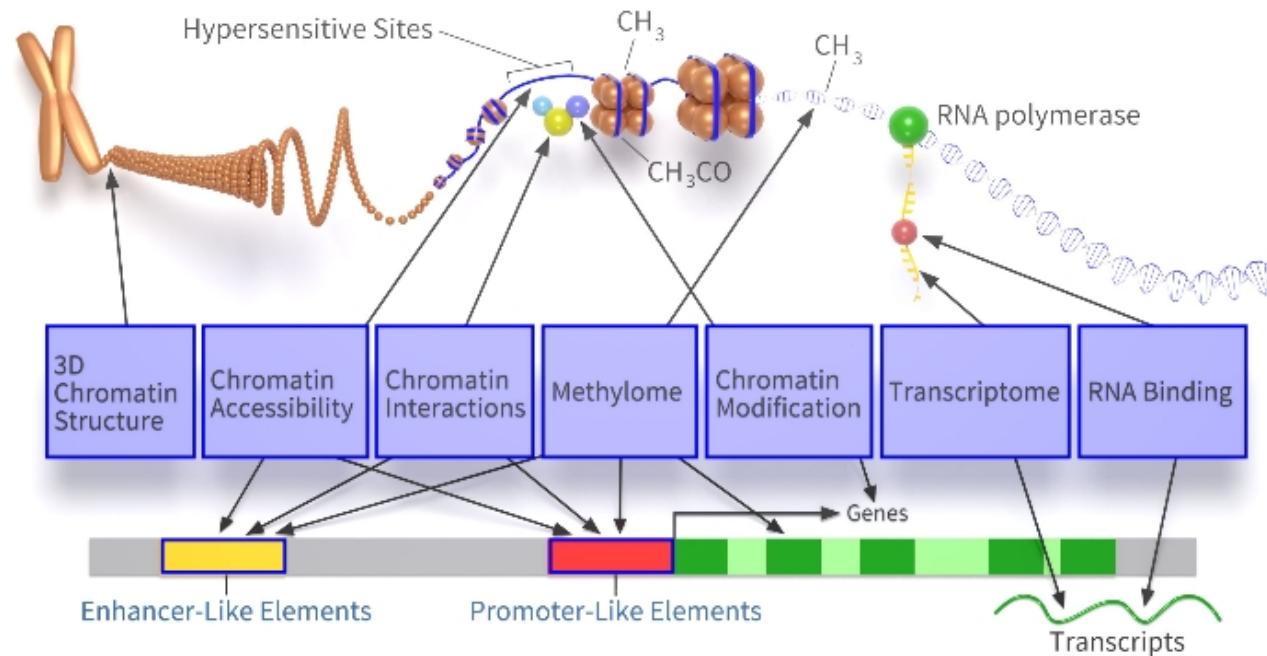
- Collective initiatives: summing efforts from different researchers from different sites of the world.
- **Integrate** different types of data (clinical, multi-omics,...) related to a **specific subject** (or sub-subject)
 - A disease
 - An organism
 - A biological question, tissue, ...
- Provide curated, standardized, **high-quality** datasets for public research
 - Raw and/or Processed data
- Provide specialized visualization and analysis tools through their web sites

Subject-specific repositories

ENCODE

<https://www.encodeproject.org/>

- The Encyclopedia of DNA Elements (ENCODE) Consortium is an ongoing international collaboration of research groups funded by the NHGRI.
- Intended as a follow-up to the Human Genome Project, it aims to identify all functional elements in the human genome (genes, transcripts, miRNA, regulatory elements, etc) employing a variety of assays and methods.

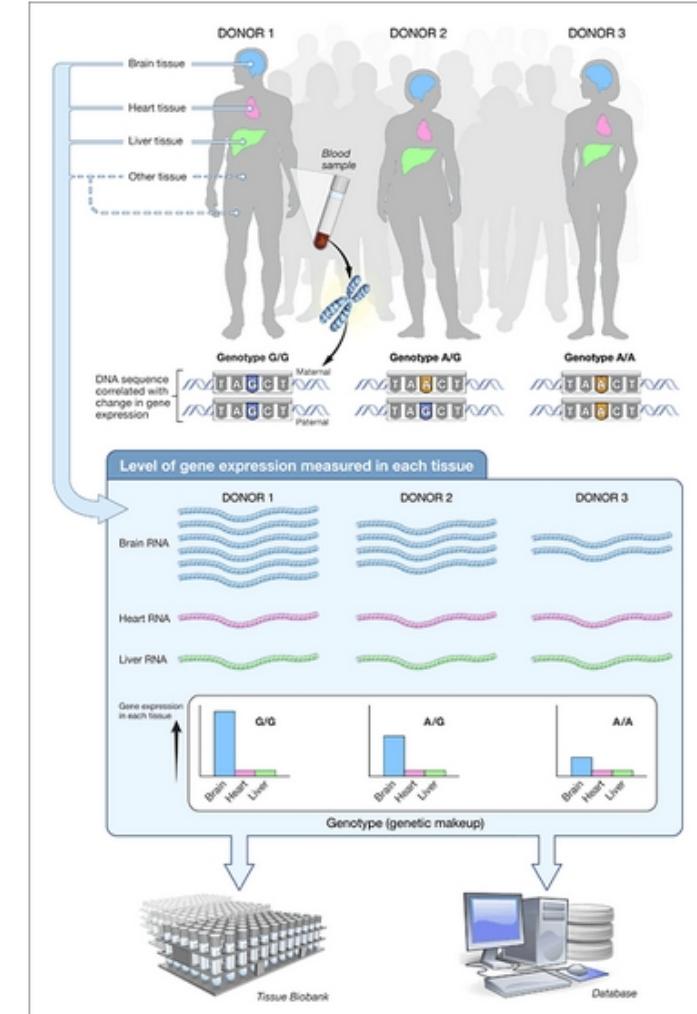
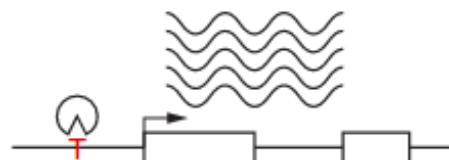


Subject-specific repositories

Genotype-Tissue Expression (GTEx) Project

<https://gtexportal.org/home/>

- Aims to provide the scientific community with a public resource to study tissue-specific gene expression and regulation and its relationship to genetic variation across individuals.
- On-going project
- Samples from 54 non-diseased tissues across nearly 1000 individuals who were also densely genotyped.
- Variations in gene expression that are highly correlated with genetic variation can be identified as expression quantitative trait loci, or eQTLs.

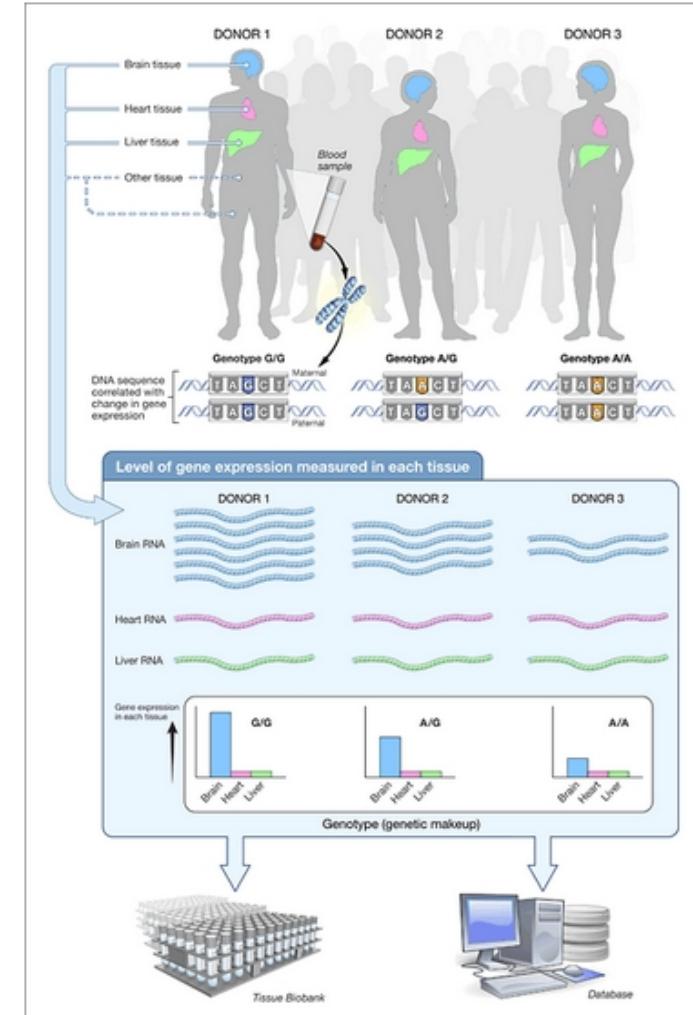


Subject-specific repositories

Genotype-Tissue Expression (GTEx) Project

<https://gtexportal.org/home/>

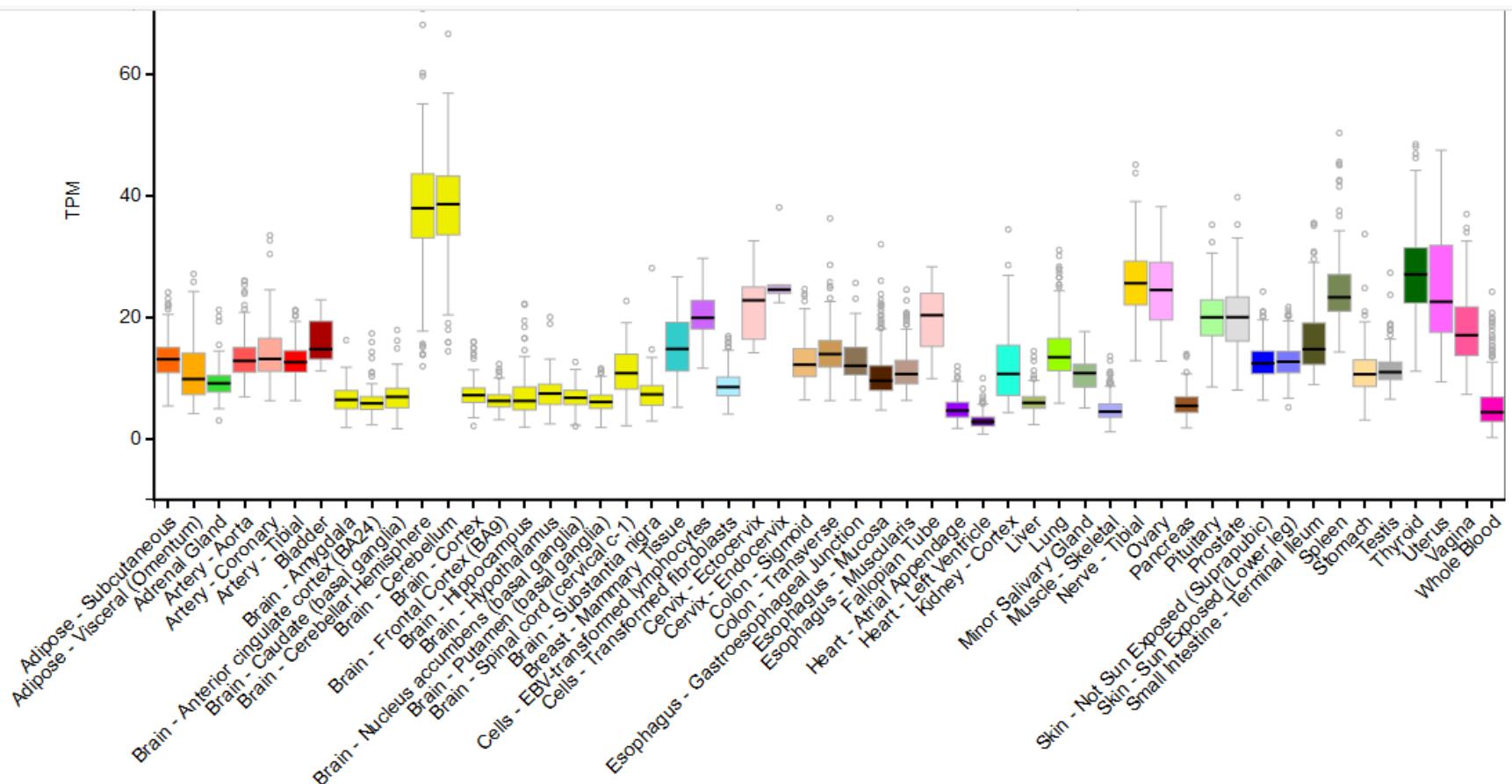
- Types of data provided:
 - Gene/transcript expression in tissues
 - variants associated to gene expression (eQTLs and sQTLs)
 - histology images
 - Patient/sample metadata
- Available datasets:
<https://www.gtexportal.org/home/datasets>
- Summary statistics:
<https://gtexportal.org/home/tissueSummaryPage>



Subject-specific repositories

Genotype-Tissue Expression (GTEx) Project

Example: Normal tissue expression profile of *mutyh* gene

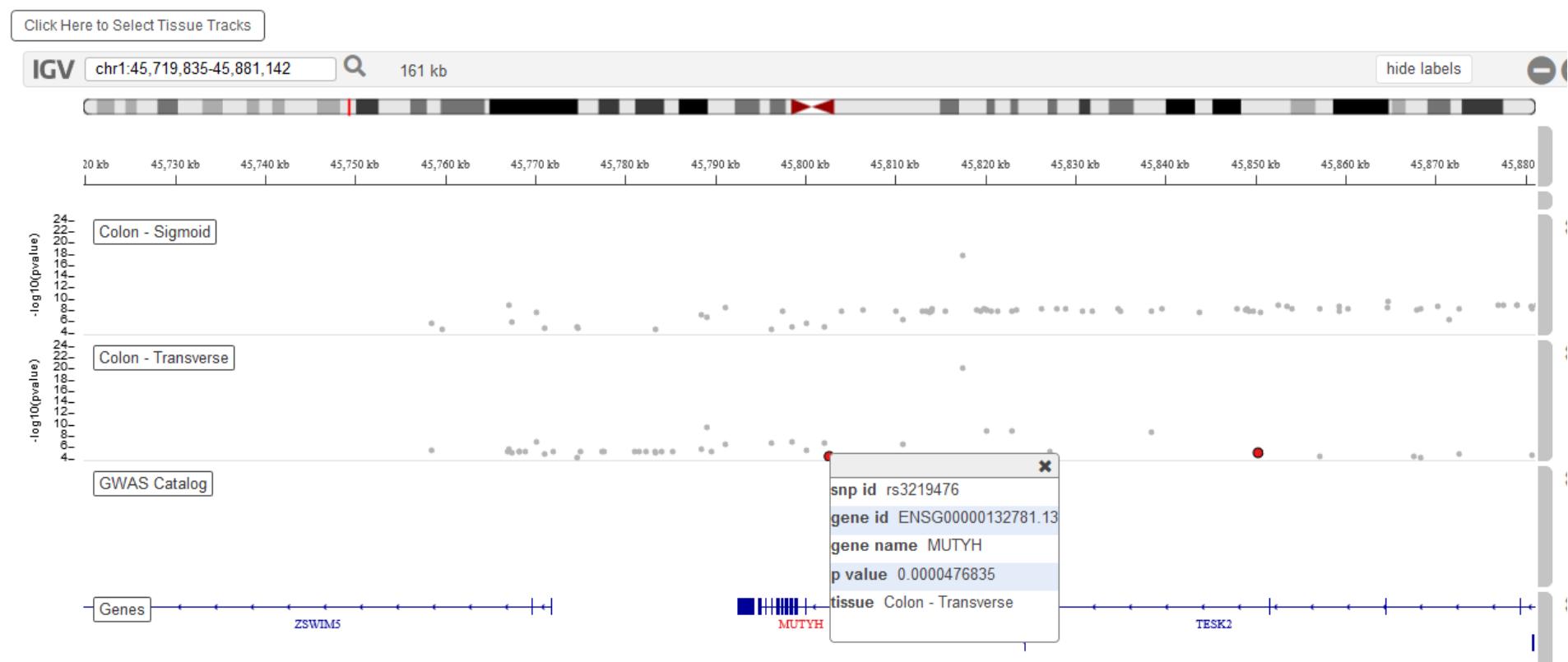


Subject-specific repositories

Genotype-Tissue Expression (GTEx) Project

Example: Looking for SNPs associated to changes in *mutyh* expression

GTEx IGV eQTL Browser



On the selected tissue eQTL tracks:

- Red dots are significant cis-eQTLs for the queried gene or SNP (at FDR<5%).
- Gray dots are significant cis-eQTLs for all other SNP-gene pairs within the genomic region.

Subject-specific repositories

Examples

- Disease-related multi-omics repositories (eg. cancer)

Table 1. List of multi-omics data repositories.

DATA REPOSITORY	WEB LINK	DISEASE	TYPES OF MULTI-OMICS DATA AVAILABLE
The Cancer Genome Atlas (TCGA)	https://cancergenome.nih.gov/	Cancer	RNA-Seq, DNA-Seq, miRNA-Seq, SNV, CNV, DNA methylation, and RPPA
Clinical Proteomic Tumor Analysis Consortium (CPTAC)	https://cptac-data-portal.georgetown.edu/cptacPublic/	Cancer	Proteomics data corresponding to TCGA cohorts
International Cancer Genomics Consortium (ICGC)	https://icgc.org/	Cancer	Whole genome sequencing, genomic variations data (somatic and germline mutation)
Cancer Cell Line Encyclopedia (CCLE)	https://portals.broadinstitute.org/ccle	Cancer cell line	Gene expression, copy number, and sequencing data; pharmacological profiles of 24 anticancer drugs
Molecular Taxonomy of Breast Cancer International Consortium (METABRIC)	http://molonc.bccrc.ca/aparicio-lab/research/metabric/	Breast cancer	Clinical traits, gene expression, SNP, and CNV
TARGET	https://ocg.cancer.gov/programs/target	Pediatric cancers	Gene expression, miRNA expression, copy number, and sequencing data
Omics Discovery Index	https://www.omicsdi.org	Consolidated data sets from 11 repositories in a uniform framework	Genomics, transcriptomics, proteomics, and metabolomics

Subject-specific repositories

The Cancer Genome Atlas (TCGA)

<https://cancergenome.nih.gov/>

- Collaboration between the National Cancer Institute (NCI) and the National Human Genome Research Institute (NHGRI) that has generated comprehensive, multi-dimensional maps of the key genomic changes in 33 types of cancer.
- High-quality tumor and matched normal samples from over 11,000 patients collected over 12 years (ended in 2015). The data collected includes:
 - Clinical information about participants
 - Metadata about the samples
 - Histopathology slide images from sample portions
 - Molecular information derived from the samples (e.g. mRNA/miRNA expression, protein expression, copy number, etc.)

Subject-specific repositories

The Cancer Genome Atlas (TCGA)

<https://cancergenome.nih.gov/>

- Data is available through the Genomic Data Commons (GDC) portal,
 - receives, processes, and distributes genomic, clinical, and biospecimen data from cancer research programs
 - Provides web-based analysis and visualization tools

The screenshot shows the GDC Data Portal homepage. At the top, there's a navigation bar with links for Home, Projects, Exploration, Analysis, Repository (which is highlighted), Quick Search, Manage Sets, Login, Cart (0), and GDC Apps. On the left, there's a sidebar with facets for 'File' (Simple Nucleotide Variation, Transcriptome Profiling, Biospecimen, Raw Sequencing Data, Copy Number Variation) and 'Data Category' (Primary Site, Project, Disease Type, Gender, Vital Status). The main area features several pie charts: one for Primary Site (various colors like blue, orange, green, purple), one for Project (mostly blue), one for Disease Type (various colors), one for Gender (blue and light blue), and one for Vital Status (blue, orange, yellow). Below these charts, it says 'Showing 1 - 20 of 33,096 cases'. At the bottom, there's a table for 'Available Files per Data Category' with columns for Seq, Exp, SNV, CNV, Meth, Clinical, and Bio. There are also buttons for Cart, Case ID, Project, Primary Site, Gender, Files, Biospecimen, Clinical, JSON, TSV, Save/Edit Case, and annotations.

Subject-specific repositories

The Cancer Genome Atlas (TCGA)

<https://cancergenome.nih.gov/>

Data in <https://portal.gdc.cancer.gov/>

- To take into account when downloading data from the GDC/TCGA:
 - Different procedures to process the data (workflows)
For documentation on procedures: <https://docs.gdc.cancer.gov/>
 - Two available sources to download GDC data:
 - GDC Legacy Archive: provides access to an unmodified copy of data that was previously stored in CGHub and in the TCGA Data Portal hosted by the TCGA Data Coordinating Center (DCC), in which uses as references GRCh37 (hg19) and GRCh36 (hg18).
 - GDC harmonized database: data available was harmonized against GRCh38 (hg38) using GDC Bioinformatics Pipelines which provides methods to the standardization of biospecimen and clinical data.

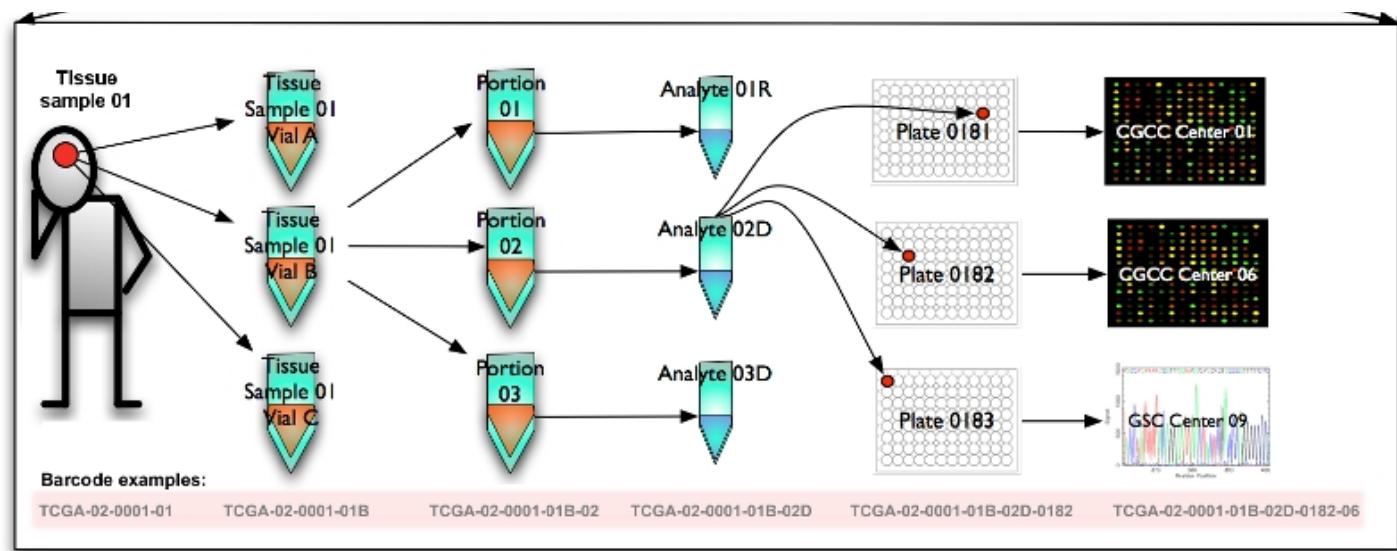
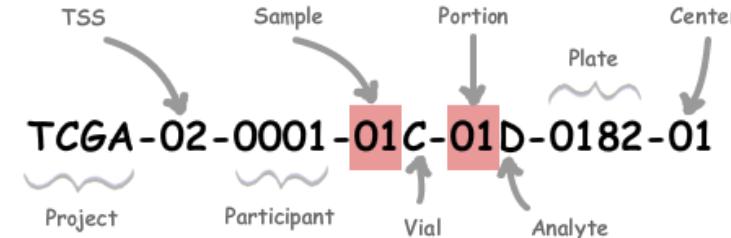
Subject-specific repositories

The Cancer Genome Atlas (TCGA)

<https://cancergenome.nih.gov/>

Data in <https://portal.gdc.cancer.gov/>

- To take into account when downloading data from the GDC/TCGA:
 - TCGA sample identification (barcode)



Subject-specific repositories

The Cancer Genome Atlas (TCGA)

NATIONAL CANCER INSTITUTE GDC Data Portal

Home Projects Exploration Analysis Repository Quick Search Manage Sets Login Cart 0 GDC Apps

e.g. TCGA-A5-A0G2, 432fe4a9-2...

Upload Case Set

Primary Site

- Ovary 163
- Breast 108
- Bronchus and lung 101
- Corpus uteri 64
- Skin 39

33 More...

Program

- TCGA 810

Project

- TCGA-OV 163
- TCGA-BRCA 108
- TCGA-UCEC 62

Cases (810) Genes (1) Mutations (124) OncoGrid

Primary Site Project Disease Type Gender Vital Status

Showing 1 - 20 of 810 cases

Available Files per Data Category

Case ID	Project	Primary Site	Gender	Files	Seq	Exp	SNV	CNV	Meth	Clinical	Bio	# Mutations	# Genes	Slides
TCGA-BK-A6W3	TCGA-UCEC	Corpus uteri	Female	56	4	5	16	4	1	10	16	1	1	2
TCGA-GN-A8LK	TCGA-SKCM	Skin	Male	51	4	5	16	4	1	7	14	1	1	2
TCGA-A5-A10F	TCGA-UCEC	Corpus uteri	Female	56	4	5	16	4	1	10	16	2	1	2
TCGA-L5-A8NM	TCGA-ESCA	Esophagus	Female	54	4	5	16	4	1	8	16	1	1	2
TCGA-BR-8591	TCGA-STAD	Stomach	Male	54	4	5	16	4	1	7	17	1	1	3
TCGA-II7-A9P7	TCGA-KIRP	Kidney	Male	52	4	5	16	4	1	8	14	1	1	2

Subject-specific repositories



Omics DI

Browse

Submit Data

Databases

API

Help ▾

Login

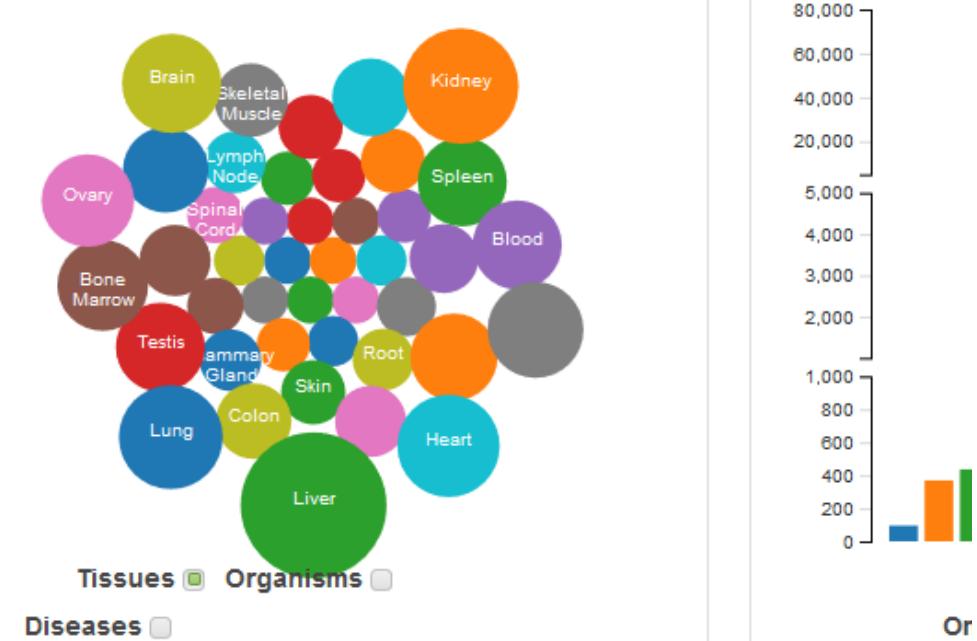
Organism, repository, gene, tissue, accession

Examples: Cancer, Homo sapiens, Orbitrap, Q9HAU5, Phospho, Hela, PXD001416

differentially further generated
potential pathways more derived known
extracted sequencing number
experiments expression
studies related overall tumor
revealed including sample
series novel analysis molecular
obtained regulation samples
important transcriptome patients
following through disease target
keywords mechanisms effects

Description Sample

Data



Subject-specific repositories

Examples

- Many other projects including
 - [1000 Genomes Project](#): the largest public catalogue of human variation and genotype data.
 - [Human Cell Atlas](#): aims to create comprehensive reference maps of all human cells
 - [NIH Roadmap Epigenomics Mapping Consortium](#): public resource of human epigenomic data

Subject-specific repositories

Examples



[About ▾](#) [Partners](#) [Related resources](#) [Bulk downloads](#) [Submit data](#)

[Viral Sequences](#) [Host Sequences](#) [Expression](#) [Proteins](#) [Biochemistry](#) [Literature](#)

Accelerating research through data sharing

- COVID-19 has put a spotlight on open science and open repositories to improve the discovery and access to research outputs.
- Many repositories initiatives arised to act as central hub for data management
- Challenges related to:
 - copyright, embargoes and licenses attached to resources
 - metadata and data curation
 - Infrastructure and connectivity

Subject-specific repositories

- Not all is human! Model organisms-based resources:

Organism	Scientific name	Database (link)
Baker's yeast	<i>Saccharomyces cerevisiae</i>	Saccharomyces Genome Database
Fission yeast	<i>Schizosaccharomyces pombe</i>	PomBase
Clawed frog	<i>Xenopus</i>	Xenbase
Fruitfly	<i>Drosophila melanogaster</i>	FlyBase
Mouse	<i>Mus musculus</i>	Mouse Genome Informatics
Nematode	<i>Caenorhabditis elegans</i>	WormBase
Rat	<i>Rattus norvegicus</i>	Rat Genome Database
Social amoeba	<i>Dictyostelium discoideum</i>	DictyBase
Thale cress	<i>Arabidopsis thaliana</i>	The Arabidopsis Information Resource
Maize	<i>Zea mays ssp. mays</i>	MaizeGDB
Zebrafish	<i>Danio rerio</i>	Zebrafish Information Network
Yeast	<i>Candida albicans</i>	CGD
Bacteria	<i>Escherichia coli</i>	EcoCyc

Tools for exploiting database information

Tools

- What are they for?
 - Search of information (eg. *Entrez*)
 - Finding/comparing sequences (eg. *BLAST*)
 - Data exploration and visualization (eg. *Genome Browsers*)
 - Manipulating and analyzing data
 - Make predictions
 - Knowledge discovery (data mining)
 - Downloading/Exporting data
- Can be accessed through
 - Web interface from resource providers, databases, projects or subject-specific repositories
 - Software (eg. *R*, *Cytoscape*)
 - Platforms (eg. *Galaxy*)

Tools



[Amino Acid Explorer](#)

[Assembly Archive](#)

[Basic Local Alignment Search Tool \(BLAST\)](#)

[Batch Entrez](#)

[BioAssay Services](#)

[BLAST Link \(BLink\)](#)

[BLAST Microbial Genomes](#)

[BLAST RefSeqGene](#)

[CDTree](#)

[Cn3D](#)

[COBALT](#)

[Concise Microbial Protein BLAST](#)

[Conserved Domain Architecture Retrieval Tool \(CDART\)](#)

[Conserved Domain Search Service \(CD Search\)](#)

[Digital Differential Display \(DDD\)](#)

[Electronic PCR \(e-PCR\)](#)

[Frequency-weighted Link \(FLink\)](#)

Clustal Omega



Multiple sequence alignment of DNA or protein sequences. Clustal Omega replaces the older ClustalW alignment tools.

[Multiple sequence alignment](#)

InterProScan



InterProScan searches sequences against InterPro's predictive protein signatures.

[Protein feature detection](#) [Sequence motif recognition](#)

BLAST [protein]



Fast local similarity search tool for protein sequence databases.

[Sequence similarity search](#)

BLAST [nucleotide]



Fast local similarity search tool for nucleotide sequence databases.

[Sequence similarity search](#)

HMMER



Fast sensitive protein homology searches using profile hidden Markov models (HMMs) for querying against both sequence and HMM target databases.

[Sequence similarity search](#) [Protein function analysis](#)

Tools

The Entrez Search and Retrieval System

- Text-based search and retrieval system used at NCBI for all of its major databases
- All databases indexed by Entrez can be searched via a single query string. This returns a unified results page, that shows the number of hits for the search in each of the databases, which are also links to actual search results for that particular database.
- Supports boolean operators (AND, OR, NOT, "", *)
- Use tags to limit parts of the search statement to particular fields.

```
term [field] OPERATOR term [field]
```

- Start with a general query and refine it progressively using Filters/Limits
- For individual databases, the Advanced Search and Limits pages assist greatly in the construction of complex queries.

Practicum

Example of database cross-search with Entrez

 **National Library of Medicine**
National Center for Biotechnology Information

COVID-19 is an emerging, rapidly evolving situation.
Get the latest public health information from CDC: <https://www.coronavirus.gov>.
Get the latest research from NIH: <https://www.nih.gov/coronavirus>.
Find NCBI SARS-CoV-2 literature, sequence, and clinical content: <https://www.ncbi.nlm.nih.gov/sars-cov-2/>.

Search NCBI colon cancer X **Search**

Results found in 31 databases

Literature	Genes	Proteins
Bookshelf 8,260	Gene 4,087	Conserved Domains 48
MeSH 26	GEO DataSets 12,615	Identical Protein Groups 3,244
NLM Catalog 654	GEO Profiles 779,994	Protein 10,835
PubMed 142,473	HomoloGene 14	Protein Clusters 2
PubMed Central 311,396	PopSet 5	Sparcle 297
		Structure 421

Tools



BLAST/BLAT | VEP | Tools | BioMart | Downloads | Help & Docs | Blog

Using this website

Annotation and prediction

Data access

API & software

About us



Help & Documentation

API & Software

Ensembl Tools

In this section

- [Ensembl Variant Effect Predictor](#)
 - [VEP web interface](#)
 - [VEP command line](#)
 - [Data formats](#)
 - [Variant Recoder](#)
 - [HaploSaurus](#)
 - [VEP FAQ](#)
- [Variant Simulator](#)
- [VCF to PED Converter](#)

Search documentation...

Go

Ensembl Tools

We provide a number of ready-made tools for processing both our data and yours. We routinely delete results from our servers after 10 days, so you will need to save the results indefinitely.

Processing your data

Name	Description	Online tool
Variant Effect Predictor 	Analyse your own variants and predict the functional consequences of known and unknown variants via our Variant Effect Predictor (VEP) tool.	
BLAST/BLAT	Search our genomes for your DNA or protein sequence.	
File Chameleon	Convert Ensembl files for use with other analysis tools	
Assembly Converter	Map (liftover) your data's coordinates to the current assembly.	
ID History Converter	Convert a set of Ensembl IDs from a previous release into their current equivalents.	
Linkage Disequilibrium Calculator	Calculate LD between variants using genotypes from a selected population.	
VCF to PED converter	Parse a vcf file to create a linkage pedigree file (ped) and a marker information file, which together may be loaded into ld visualization tools like Haplovview.	

Tools


[Home](#) [Install](#) [Help](#) [Developers](#) [About](#)

Search:

[Home](#) » BiocViews

All Packages

Bioconductor version 3.12 (Release)

Autocomplete biocViews search:

Software (1974)	
▶ AssayDomain	(791)
▶ BiologicalQuestion	(822)
▶ Infrastructure	(456)
▼ ResearchField (902)	
BiomedicalInformatics	(62)
CellBiology	(54)
Cheminformatics	(13)
ComparativeGenomics	(8)
Epigenetics	(63)
Epitranscriptomics	(1)
FunctionalGenomics	(53)
Genetics	(200)
ImmunoOncology	(447)
Lipidomics	(11)
MathematicalBiology	(8)
Metabolomics	(74)

Packages found under FunctionalGenomics:

Rank based on number of downloads: lower numbers are more frequently downloaded.

Show All entries

Search table:

Package	Maintainer	Title	Rank
limma	Gordon Smyth	Linear Models for Microarray Data	14
edgeR	Yunshun Chen, Gordon Smyth, Aaron Lun, Mark Robinson	Empirical Analysis of Digital Gene Expression Data in R	23
maftools	Anand Mayakonda	Summarize, Analyze and Visualize MAF Files	112
tximeta	Michael Love	Transcript Quantification Import with Automatic Metadata	162
DiffBind	Rory Stark	Differential Binding Analysis of ChIP-Seq Peak Data	165
annotatr	Raymond G. Cavalcante	Annotation of Genomic Regions to Genomic Annotations	274
variancePartition	Gabriel E. Hoffman	Quantify and interpret divers of variation in multilevel gene expression experiments	278

Tools

Galaxy Europe

Analyze Data Workflow Visualize ▾ Shared Data ▾ Help ▾ Login or Register  

Tools  

search tools

Get Data

Send Data

Collection Operations

GENERAL TEXT TOOLS

Text Manipulation

Filter and Sort

Join, Subtract and Group

GENOMIC FILE MANIPULATION

Convert Formats

FASTA/FASTQ

FASTQ Quality Control

Quality Control

SAM/BAM

BED

COVID-19 research!

Want to learn the best practices for the analysis of SARS-CoV-2 data using Galaxy? Visit the Galaxy SARS-CoV-2 portal at covid19.galaxyproject.org. We mirror **all public** SARS-CoV-2 data from ENA in a Galaxy data library for your convenience. The Galaxy community also created COVID-19 related trainings and we also maintain a [running document](#) with recent news. Our new preprint about [The landscape of SARS-CoV-2 RNA modifications](#) is out!

"Anyone, anywhere in the world should have free, unhindered access to not just my research, but to the research of every great and enquiring mind across the spectrum of human understanding." – Prof. Stephen Hawking

News

Nov 14, 2020  **UseGalaxy.eu Tool Updates for 2020-11-14**

Nov 7, 2020  **UseGalaxy.eu Tool Updates for 2020-11-07**

Nov 3, 2020  **November Galactic News!**

Oct 31, 2020  **UseGalaxy.eu Tool Updates for**

Events

Jan 25, 2021 - Jan 29, 2021   **2021 Galaxy Admin Training**

Dec 10, 2020   **Galaxy Developer Roundtable: Developer Training**

Dec 7, 2020 - Dec 10, 2020  **Hackathon sur les outils interactifs de Galaxy (GxIT)**

Dec 3, 2020   **DNA and DTA**

<https://usegalaxy.eu/>

Tools

Cytoscape App Store

Submit an App ▾ Search the App Store Sign In

All Apps

Newest Releases

Get Started with the App Store »

 **DKernel** 3.0+
DKernel uses Diffusion Kernel algorithm to propagate sub-

 **PathLinker** 3.0+
Reconstructs signaling pathways from protein interaction networks

 **XlinkCyNET** 3.0+
XlinkCyNET generates residue-to-residue connections provided by

 **IntAct App** 3.0+
BETA: Build molecular interaction networks from IntAct database.

 **MCODE** 3.0+
Clusters a given network based on topology to find densely

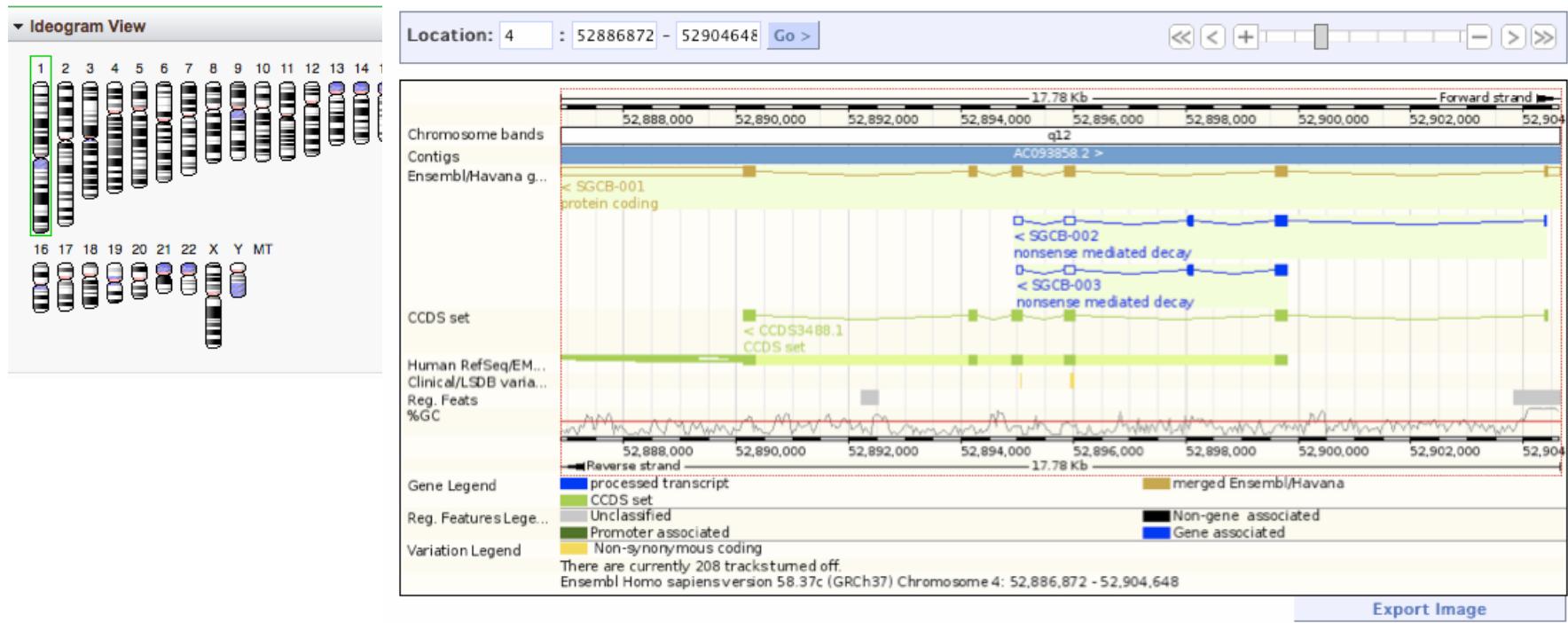
 **OmniPath** 3.0+
OmniPath: literature curated human signaling pathways

more newest releases »

Genome Browsers

Genome Browsers

- The advent of the Human Genome Project and subsequent projects to sequence genomes of other species and multiple individuals has driven the need for tools that can visualize vast amounts of genomics data.
- Genome Browsers bring together information from multiple resources, using the genome as a base for this annotation.
- Provide a graphic interface for visualization and integrative genomics analyses.



Genome Browsers

- A wealth of biological data can be viewed, downloaded and compared:
 - Genes
 - Genomic location
 - Gene model structures: exons, introns, UTRs
 - Transcripts: mRNA, splice variants, pseudogenes, non-coding RNA,...
 - Protein(s)
 - Links to other sources of information
 - Cytogenetic bands
 - Polymorphic markers
 - Genetic variation: SNPs, deletions/insertions, short tandem repeats,...
 - Repetitive sequences
 - Expressed Sequence Tags (ESTs)
 - cDNAs or mRNAs from related species
 - Regions of sequence homology

Genome Browsers

- Popular Genome Browsers:
 - NCBI [Genome Data Viewer](#)
 - EBI's [Ensembl](#)
 - UCSC Genome Browser

Genome Browsers

- Important concepts to be aware of:
 - Genome of reference
 - A reference genome (also known as a reference assembly) is a *digital* nucleic acid sequence database, assembled by scientists as a representative example of the set of genes in one idealized individual organism of a species.
 - Reference genomes are typically used as a guide on which new genomes are built, enabling them to be assembled much more quickly and cheaply than the initial Human Genome Project.
 - The reference provides a good approximation of the DNA of any single individual. But in regions with high allelic diversity the reference genome may differ significantly from other individuals
 - sets of *alternate loci* are assembled alongside the reference locus
 - There are reference genomes for multiple species of viruses, bacteria, fungus, plants, and animals.

Genome Browsers

- Important concepts to be aware of:
 - Genome of reference
 - The [Genome Reference Consortium](#) (GRC) is a collaborative effort between different institutes charged to maintain and improve reference genomes for human and some model organisms (mouse, zebrafish and chicken)
 - New assemblies are released every X years integrating improvements in sequence
 - closing gaps
 - fixing misrepresentations in the sequence
 - correcting sequences
 - The coordinates of your favorite gene in one assembly may not be the same as those in the next release of the assembly!
 - Always be aware of which version you are using
 - NCBI provides a [Genome Remapping Service](#)

Genome Browsers

- Important concepts to be aware of:

- Genome of reference

- To date, the major assembly releases for human, mouse, zebrafish, and chicken are GRCh38, GRCm38, GRCz11, and GRCg6a, respectively.

For human:

Release name	Date of release	Equivalent UCSC version
GRCh38	Dec 2013	hg38
GRCh37	Feb 2009	hg19
NCBI Build 36.1	Mar 2006	hg18
NCBI Build 35	May 2004	hg17
NCBI Build 34	Jul 2003	hg16

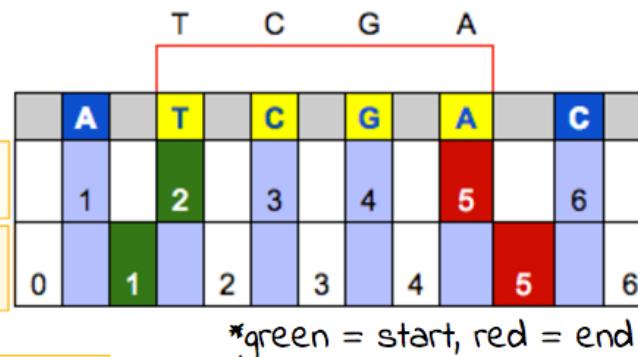
For mouse:

Release name	Date of release	Equivalent UCSC version
GRCm38	Dec 2011	mm10
NCBI Build 37	Jul 2007	mm9
NCBI Build 36	Feb 2006	mm8
NCBI Build 35	Aug 2005	mm7
NCBI Build 34	Mar 2005	mm6

- There are "minor" assembly updates in the form of genome *patches* which either correct errors in the assembly or add additional alternate loci *without changing chromosome coordinates*. (e.g. GRCh37.p1).
- The assembly **accession.version** is an unambiguous identifier for the assembly and should always be included in publications.

Genome Browsers

- Important concepts to be aware of:
 - Genome of reference (assembly version)
 - Genomic coordinate systems:
 - **base** coordinate system: the first nucleotide counts as position **1**
 - **interbase** coordinate system: the first nucleotide counts as position **0**
 - allows to represent features that occur between nucleotides (like a splice site)
 - simpler arithmetic for computing the length of features (length=end-start)
 - more rational conversion of coordinates from the + to the - strand



1-START, FULLY CLOSED (UCSC GB WEB)

0-START, HALF-OPEN (UCSC GB TABLES)

→ TCGA is 2-5 (both start and end included)

→ TCGA is 1-5 (start included, end excluded)

Genome Browsers

The “Position” format (referring to the “1-start, fully-closed” system as coordinates are “positioned” in the browser)

- Written as: chr1:12714000**1**-127140001
- No spaces.
- Includes punctuation: a colon after the chromosome, and a dash between the start and end coordinates.
- When in this format, the assumption is that the coordinate is 1-start, fully-closed.

The “BED” format (referring to the “0-start, half-open” system)

- Written as: chr1 12714000**0** 127140001
- Spaces between chromosome, start coordinate, and end coordinate.
- No punctuation.
- When in this format, the assumption is that the coordinates are 0-start, half-open.

Genome Browsers

- Important concepts to be aware of:
 - Genome of reference (assembly version)
 - Genomic coordinate systems:
 - Most genome annotation portals (e.g. NCBI or Ensembl), bioinformatics software (e.g. BLAST) and annotation file formats (e.g. GFF, BED) use the base coordinate system
 - The UCSC genome browser uses both systems:
 - the base coordinate system (1-based, fully-closed) is used in the UCSC genome browser display
 - the interbase coordinate (0-based, half-open) is used in their tools and file formats

Table 2. SNP coordinates in web browser (1-start) vs table (0-start)

rs782519173 (hg38)	Start	End
Positioned in web browser: 1-start, fully-closed	133255708	133255708
Stored in table: 0-start, half-open	133255707	133255708

Genome Browsers

- Popular Genome Browsers:
 - NCBI [Genome Data Viewer](#)
 - EBI's [Ensembl](#)
 - [UCSC Genome Browser](#)
 - [IGV](#) from Broad Institute
- Similar though may differ in:
 - Presentation
 - Species represented
 - Source of annotations / links to other resources
 - Tools

Genome Browsers

Ensembl

<https://www.ensembl.org/index.html>

- The project began in 1999, with the completion of the HGP, as a joint project between the EMBL-EBI and the Sanger Centre (now all moved to the EMBL-EBI).
- As of Ensembl release 106 (April 2022), more than 250 species are supported (mainly vertebrate species)
- Sister project: EnsemblGenomes for non-chordates
 - Since its establishment in 2009, the resource has grown rapidly and now contains over 1,400 eukaryotic and 44,000 prokaryotic genomes.
- Genome assemblies are retrieved from other institutes/consortia (eg. NCBI for human, mouse genomes)

Genome Browsers

Ensembl

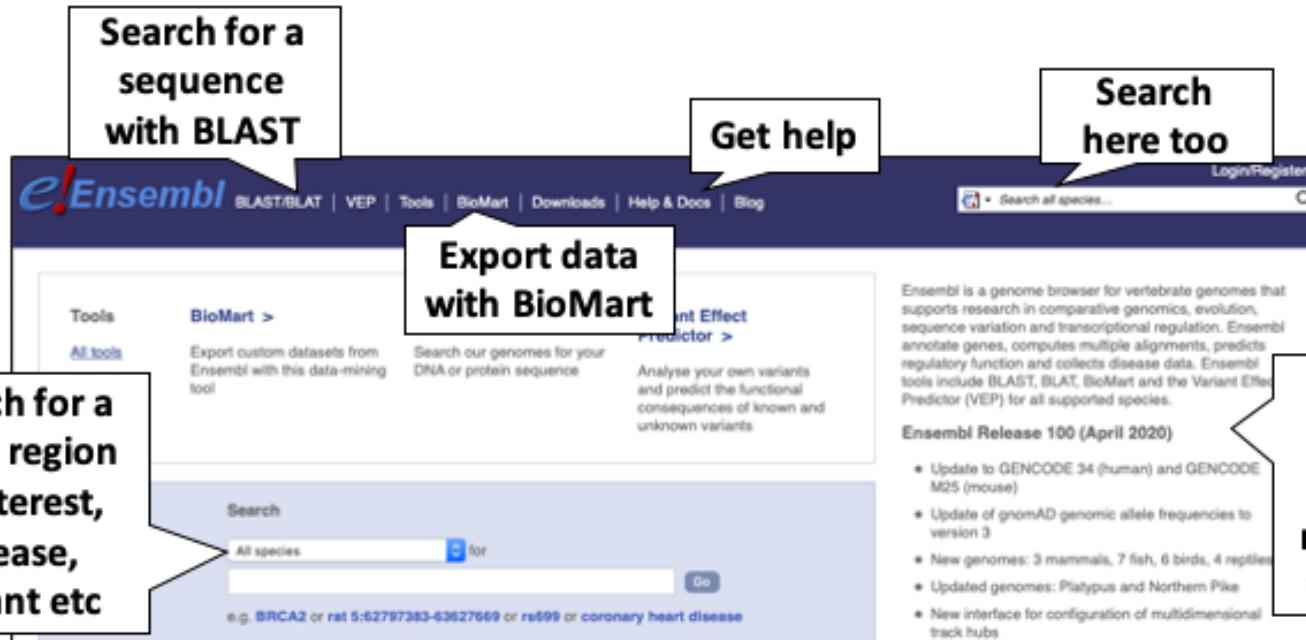
<https://www.ensembl.org/index.html>

- There are a number of ways to access Ensembl data:
 - From the website
 - Using BioMart tool to quickly obtain tables of gene information
 - Programmatically

Genome Browsers

Ensembl

<https://www.ensembl.org/index.html>



Search for a sequence with BLAST

Get help

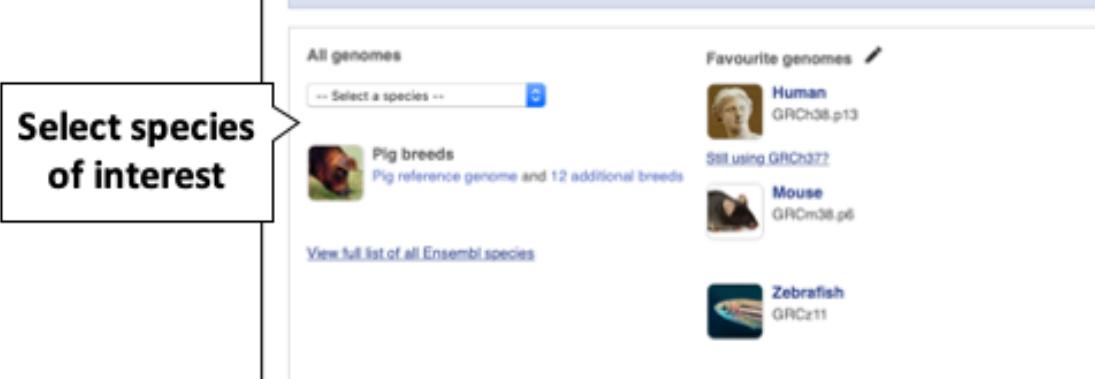
Search here too

Export data with BioMart

See the current release number and what's new

Select species of interest

The screenshot shows the Ensembl homepage with several search and analysis tools. On the left, there are boxes for searching sequences with BLAST and for selecting species of interest. In the center, there are sections for BioMart (data export), Variant Effect Predictor (variant analysis), and a general search bar. On the right, there is information about the current release (Release 100) and what's new, along with a 'Search here too' box.



Search for a gene, region of interest, disease, variant etc

Select species of interest

The screenshot shows a detailed view of the Ensembl genome browser. It features a search bar at the top where 'BRCA2' has been entered. Below the search bar, there are sections for 'All genomes' (with a dropdown menu for species selection) and 'Favourite genomes' (listing Human, Mouse, and Zebrafish). A sidebar on the left provides a 'View full list of all Ensembl species' link.

Ensembl is a genome browser for vertebrate genomes that supports research in comparative genomics, evolution, sequence variation and transcriptional regulation. Ensembl annotate genes, computes multiple alignments, predicts regulatory function and collects disease data. Ensembl tools include (BLAST, BLAT, BioMart and the Variant Effect Predictor (VEP) for all supported species.

Ensembl Release 100 (April 2020)

- Update to GENCODE 34 (human) and GENCODE M25 (mouse)
- Update of gnomAD genomic allele frequencies to version 3
- New genomes: 3 mammals, 7 fish, 6 birds, 4 reptiles
- Updated genomes: Platypus and Northern Pike
- New interface for configuration of multidimensional track hubs

[More release news](#) on our blog

Other news from our blog

- 29 May 2020: [Ensembl under lockdown – Part 3](#)
- 26 May 2020: [Normalising variants to standardise Ensembl VEP output](#)
- 21 May 2020: [Ensembl under lockdown – Part 2](#)

Genome Browsers

Ensembl

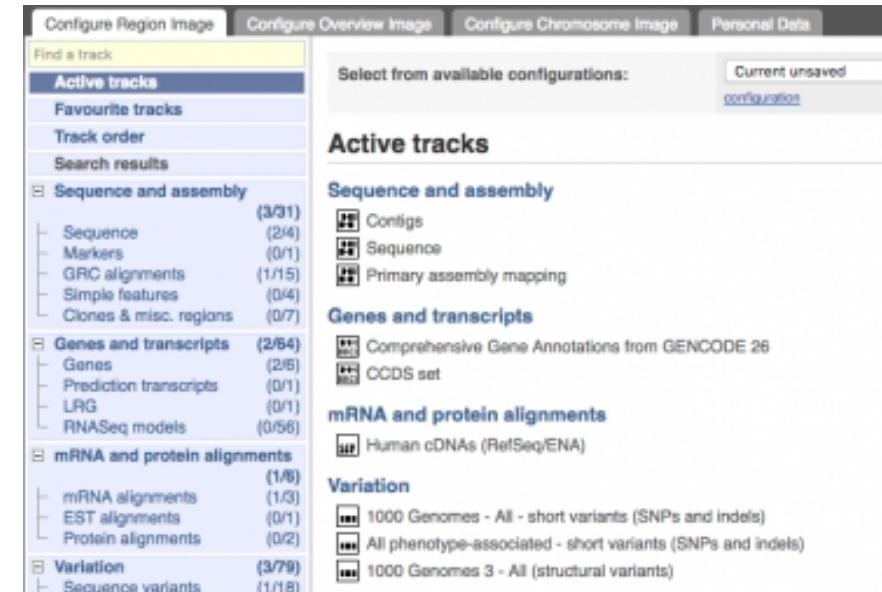
<https://www.ensembl.org/index.html>

- The navigation of the Ensembl website is organised into tabs, or main pages. The location, gene, transcript, variant and regulation tabs allow data browsing at that level.



The screenshot shows the Ensembl homepage for the Human genome (GRCh38.p13). At the top, there is a navigation bar with tabs for Location, Gene, Transcript, Variant, and Regulation. Below the navigation bar, there is a search bar with the query "BRCA2". The main content area displays information about the BRCA2 gene, including its location (13:32,315,086-32,400,266), gene ID (BRCA2), transcript ID (BRCA2-201), variant ID (rs55880202), and regulation ID (ENSR00000060894). There is also a "Jobs" button.

- The available annotations (tracks) to be displayed are configured through the 'Configure this page' button



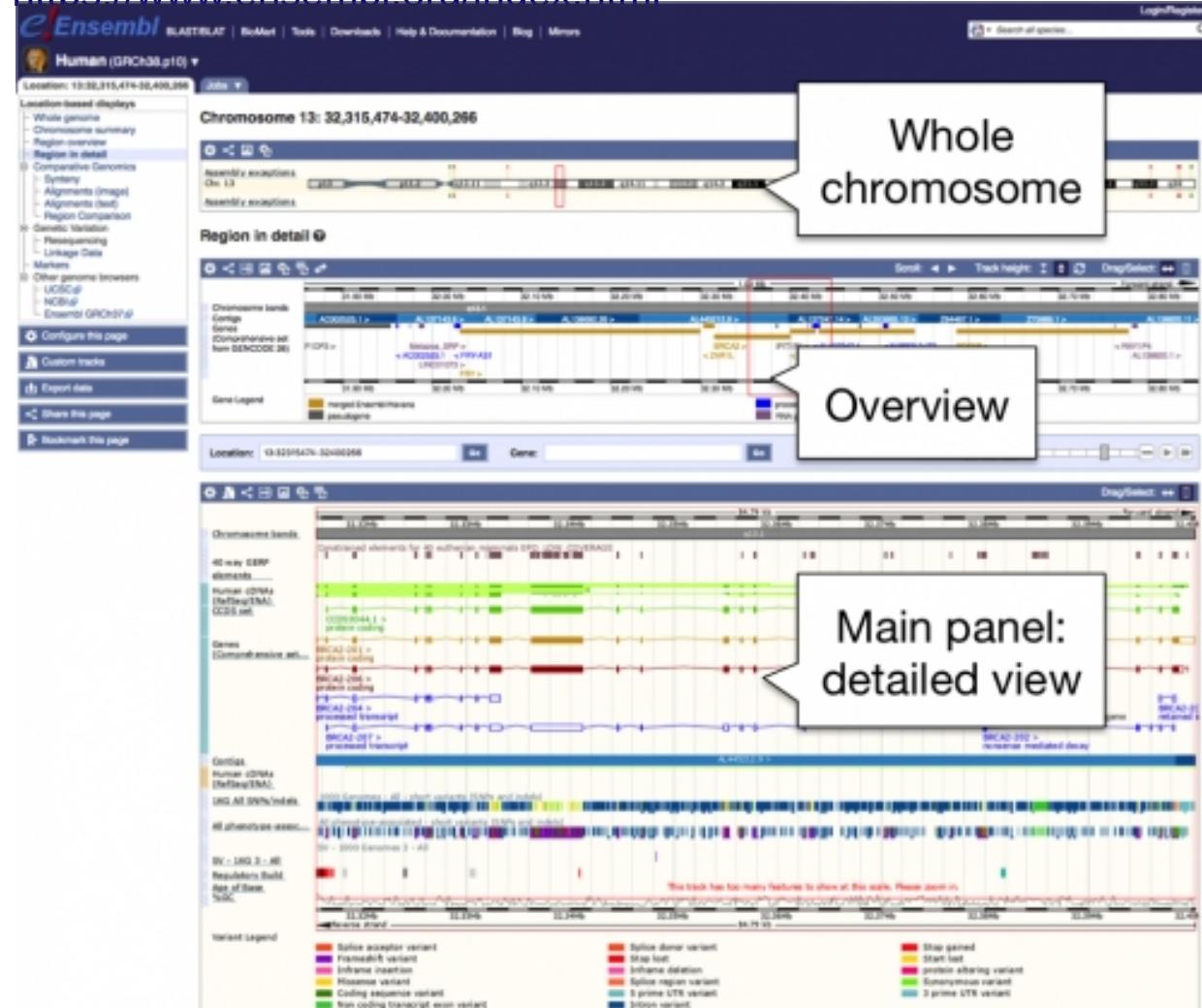
The screenshot shows the 'Configure this page' interface. At the top, there are four tabs: 'Configure Region Image', 'Configure Overview Image', 'Configure Chromosome Image', and 'Personal Data'. Below the tabs, there is a section titled 'Active tracks' with a list of selected configurations. To the right, there is a section titled 'Select from available configurations' with a link to 'Current unsaved configuration'. The 'Active tracks' section includes categories such as Sequence and assembly, Genes and transcripts, mRNA and protein alignments, and Variation, each with a list of available tracks and their counts.

Genome Browsers

- The location tab's main display is the 'region in detail', which shows a region of the genome up to 1 Mb long in a highly customisable view

Ensembl

<https://www.ensembl.org/index.html>

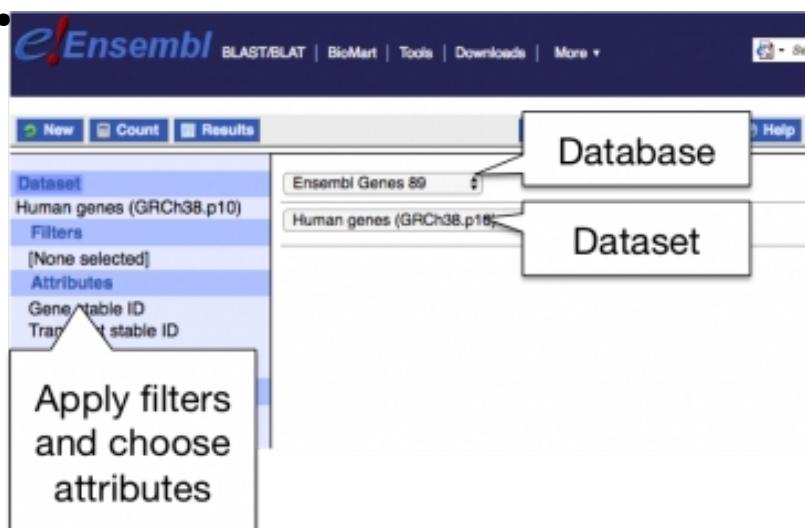


Genome Browsers

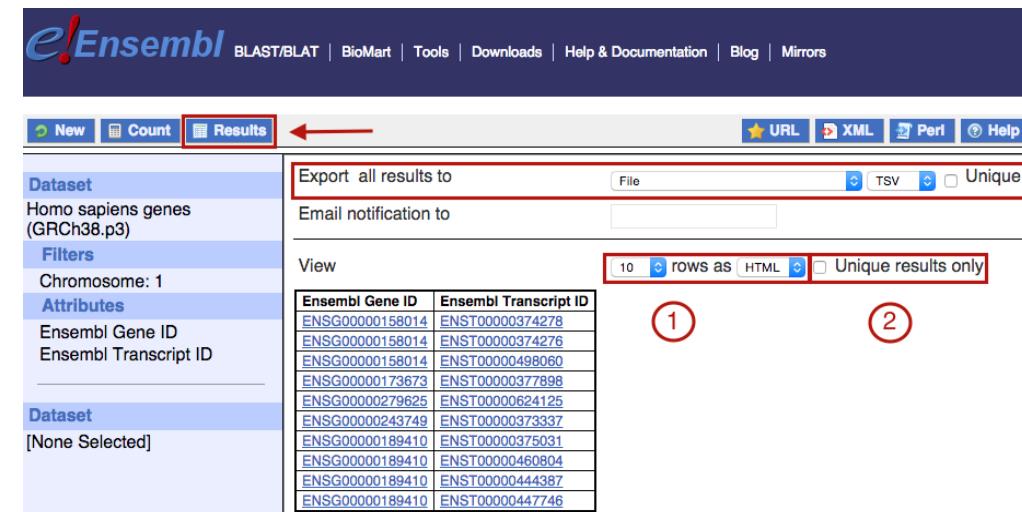
Ensembl

<https://www.ensembl.org/index.html>

- BioMart tool allows to:
 - Search and quickly generate tables of information.
 - Export data in different formats (FASTA, html, csv, tsv, xls ...)
 - ‘Translate’ one ID type into another (eg. an Ensembl gene ID to an NCBI RefSeqID)
 - Also in R! (see biomaRt Bioconductor's package)



The screenshot shows the Ensembl BioMart search interface. At the top, there are tabs for 'New', 'Count', and 'Results'. The 'Results' tab is highlighted. Below the tabs, there are two main sections: 'Database' and 'Dataset'. The 'Database' section contains a dropdown menu set to 'Ensembl Genes 89'. The 'Dataset' section contains a dropdown menu set to 'Human genes (GRCh38.p10)'. On the left side, there is a sidebar with sections for 'Dataset', 'Filters', 'Attributes', and 'Apply filters and choose attributes'. The 'Apply filters and choose attributes' section has a large callout box pointing to it.



The screenshot shows the Ensembl BioMart search interface with the 'Results' tab selected. The results table displays a list of Ensembl Gene IDs and their corresponding Ensembl Transcript IDs. Two annotations are present: a red arrow pointing to the 'Results' tab, and two red circles labeled '1' and '2' pointing to specific rows in the results table. The first row (1) is ENSG00000158014 and ENST00000374278. The second row (2) is ENSG00000158014 and ENST00000374276.

Ensembl Gene ID	Ensembl Transcript ID
ENSG00000158014	ENST00000374278
ENSG00000158014	ENST00000374276
ENSG00000158014	ENST00000498060
ENSG00000173673	ENST00000377898
ENSG00000279625	ENST00000624125
ENSG00000243749	ENST00000373337
ENSG00000189410	ENST00000375031
ENSG00000189410	ENST00000460804
ENSG00000189410	ENST00000444387
ENSG00000189410	ENST00000447746

Genome Browsers

Ensembl

- Other tools: <https://www.ensembl.org/index.html>



[**The Variant Effect Predictor**](#) is our most popular tool. Enter in transcript or genomic coordinates to determine the effect of sequence variation on transcripts and proteins. A [dbSNP](#) identifier will be given in the output, if there is a matching one.

[**The Assembly Converter**](#) allows coordinates from an older genome sequence to be updated to new coordinates (and vice-versa). As genomes are sequenced, the improved technology allows current genome sequence to be more accurate, containing fewer gaps and fewer mistakes. Using the most recent genome version or assembly is advised. Ensembl, the [UCSC genome browser](#), and [NCBI Genome Data Viewer](#) strive to show all annotation on the newest assembly possible, once the genome sequence is released to the public.

[**ID History converter**](#) displays IDs that are in the current version of Ensembl. Start with a list of old IDs, and see which ones are still used, and which ones have been ‘retired’, or changed into a different ID. Though Ensembl IDs are stable (a gene or transcript should always have the same ID), the ID can change if one gene is split into two, or two genes that were erroneously split in a previous release are fused together into one.

Genome Browsers

Ensembl

<https://www.ensembl.org/index.html>

- Resources for training:
 - Free Online EMBL course on using Ensembl genome browser
 - Free Online EMBL course on using EnsemblGenomes

Genome Browsers

UCSC Genome Browser

<https://genome.ucsc.edu/>

- Developed and maintained by the Genome Bioinformatics Group, within the UCSC Genomics Institute.
- It began as a resource for the distribution of the initial fruits of the Human Genome Project. Funded by the Howard Hughes Medical Institute and the NHGRI, the browser offered a graphical display of the first full-chromosome draft assembly of human genome sequence.
- In the ensuing years, the website has grown to include a broad collection of vertebrate and model organism assemblies and annotations, along with a large suite of tools for viewing, analyzing and downloading data.

Genome Browsers

UCSC Genome Browser

<https://genome.ucsc.edu/>

UNIVERSITY OF CALIFORNIA SANTA CRUZ Genomics Institute

UCSC Genome Browser

Home Genomes Genome Browser Tools Mirrors Downloads My Data Help About Us



Our tools

- **Genome Browser**
interactively visualize genomic data
- **BLAT**
rapidly align sequences to the genome
- **Table Browser**
download data from the Genome Browser database
- **Variant Annotation Integrator**
get functional effect predictions for variant calls
- **Data Integrator**
combine data sources from the Genome Browser database
- **Gene Sorter**
find genes that are similar by expression and other metrics
- **Genome Browser in a Box (GBiB)**
run the Genome Browser on your laptop or server
- **In-Silico PCR**
rapidly align PCR primer pairs to the genome
- **LiftOver**
convert genome coordinates between assemblies
- **Track Hubs**
import and view external data tracks

[More tools...](#)

Genome Browsers

UCSC Genome Browser

- Different search options:
a) By gene/transcript/protein name, symbol or ID: **LRRTM1**
b) By Chromosome number or region: **chr11:1038475-1075482**
c) By Keywords: kinase, receptor
d) By sequence (BLAT tool)
e) By track type (Track search)

Find Position

Human Assembly
Dec. 2013 (GRCh38/hg38)

Position/Search Term
Irrtm1
Current position: chr3:52,221,080-52,226,163

BLAT Search Genome

Genome: Search ALL Assembly: Query type: Sort output: Output type:

Human Dec. 2013 (GRCh38/hg38) BLAT's guess query,score hyperlink

submit I'm feeling lucky clear

Paste in a query sequence to find its location in the genome. Multiple sequences may be searched if separated by lines starting with '>' followed by the sequence name.

File Upload: Rather than pasting a sequence, you can choose to upload a text file containing the sequence.
Upload sequence: No file selected.

Genome Browsers

UCSC Genome Browser

<https://genome.ucsc.edu/>

- Multiple results depending on available annotations:
 - a)UCSC Genes
 - b)RefSeq Genes
 - c)Non-human RefSeq Genes: orthologs of the gene in other species
 - d)ENCODE Gencode
 - e)Human mRNA: annotated transcripts of the gene

[NRXN1 \(ENST00000404971.5\) at chr2:49920350-51032399](#) - Homo sapiens neurexin 1 (NRXN1), transcript variant alpha2,
[NRXN1 \(ENST00000625672.2\) at chr2:49918505-51028456](#) - Cell surface protein involved in cell-cell-interactions, e

NCBI RefSeq genes, curated subset (NM_*, NR_*, and YP_*)

[NM_178839.4 at chr2:80301878-80304362](#)

NCBI RefSeq genes, predicted subset (XM_* and XR_*)

[XM_017003986.1 at chr2:80302014-80304738](#)

[XM_017003987.1 at chr2:80302014-80304738](#)

RefSeq Genes

[LRRTM1 at chr2:80301878-80304362](#) - (NM_178839) leucine-rich repeat transmembrane neuronal protein 1 precursor

Non-Human RefSeq Genes

[LRRTM1 at chr2:80301917-80304282](#) - (NM_001257467) leucine-rich repeat transmembrane neuronal protein 1 precursor
[LRRTM1 at chr2:80302082-80304737](#) - (NM_001080304) leucine-rich repeat transmembrane neuronal protein 1 precursor
[LRRTM1 at chr2:80288477-80304427](#) - (NM_001133111) leucine-rich repeat transmembrane neuronal protein 1 precursor
[LRRTM1 at chr2:80288876-80304610](#) - (NM_001109374) leucine-rich repeat transmembrane neuronal protein 1 precursor
[Lrrtm1 at chr2:80301870-80304896](#) - (NM_028880) leucine-rich repeat transmembrane neuronal protein 1 precursor
[Lrrtm1 at chr2:80301870-80304896](#) - (NM_001362109) leucine-rich repeat transmembrane neuronal protein 1 precursor
[Lrrtm1 at chr2:80287776-80304896](#) - (NR_155300)
[Lrrtm1 at chr2:80287776-80304896](#) - (NR_155299)

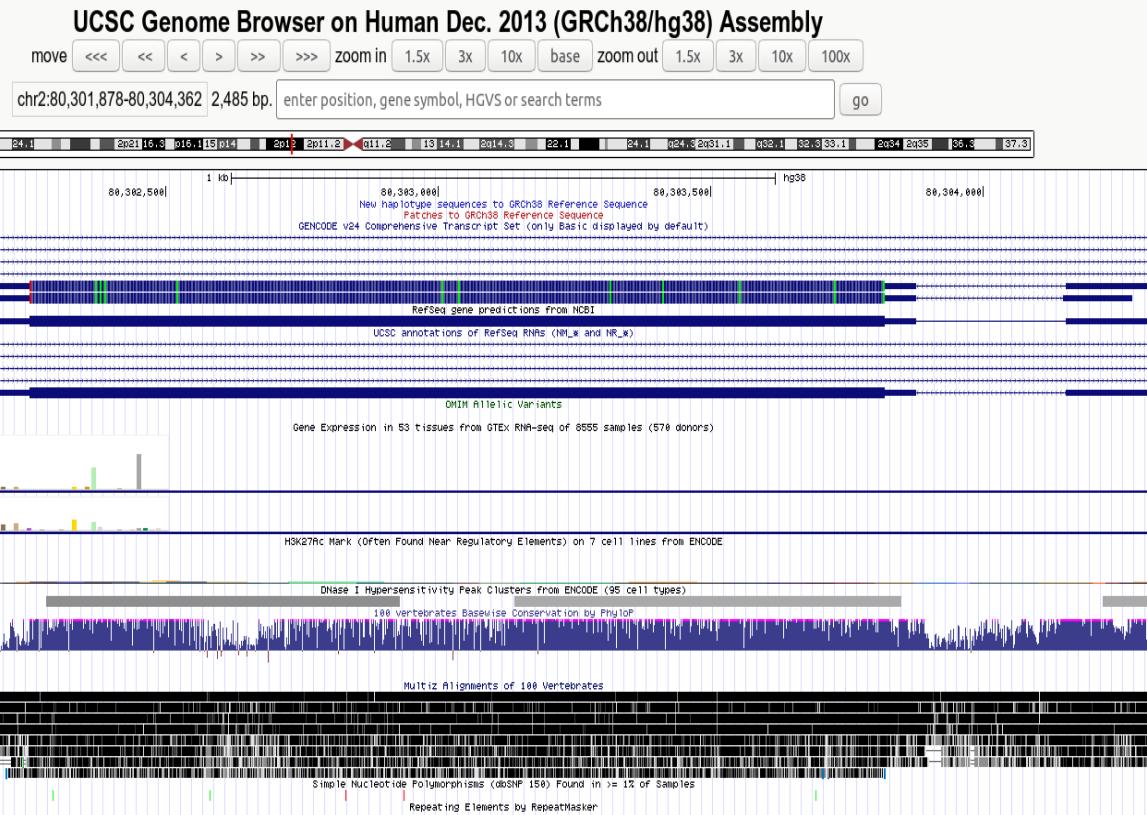
Basic Gene Annotation Set from GENCODE Version 28 (Ensembl 92)

[LRRTM1 at chr2:80301878-80304749](#)

[LRRTM1 at chr2:80301878-80304738](#)

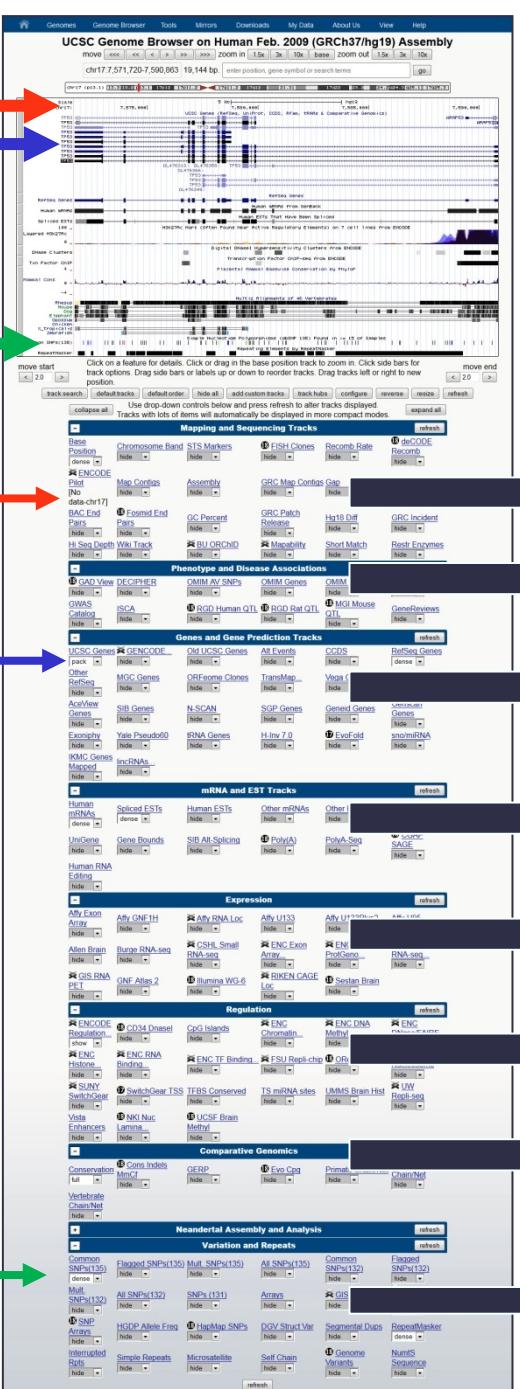
Genome Browsers

- Visualizing results: Genome Viewer and Tracks settings



- Genomic location is shown along with data annotations that link out to additional data and databases.

Tracks info and options



Genome Viewer

Tracks (data type)

Mapping and Sequencing Tracks

Phenotype and Disease Tracks

Genes and Gene Prediction Tracks
(including sno/miRNA data)

mRNA and EST Tracks

Expression *(such as microarray)*

Regulation *(including TFBS)*

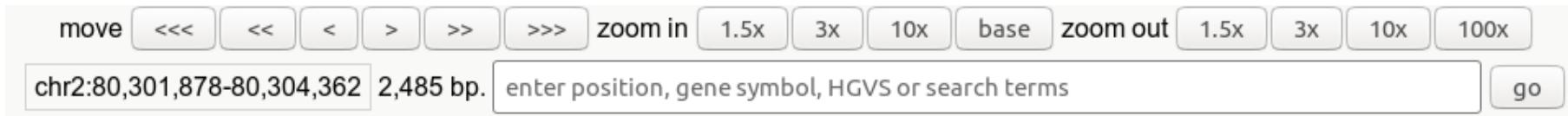
Comparative Genomics
As a group
Individual species

Variation and Repeats

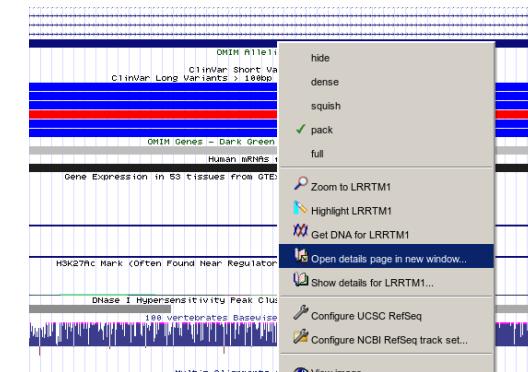
(including SNPs, copy number variation)

Genome Browsers

- Change your view or location with controls at the top



- Click on items to view details in new window or right click items to get details



- Change track display modes:
 - Tip: Hide all and then select specific tracks to visualize so you don't get lost

Source of information

Display modes:

- Hide=don't show
- Dense=features collapsed into a single line
- Squish, Pack, Full=features in different lines

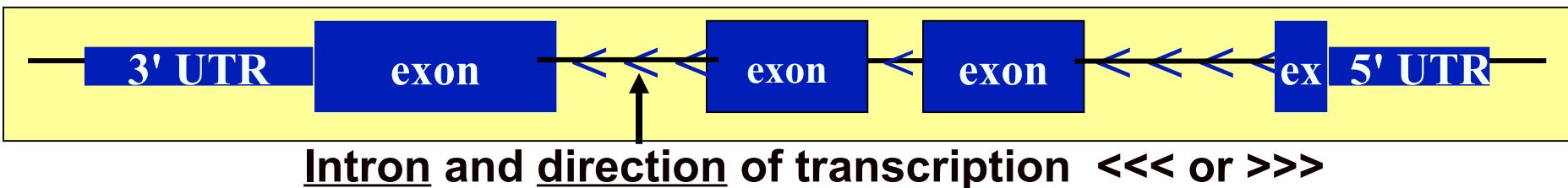
Refresh!

Genes and Gene Predictions

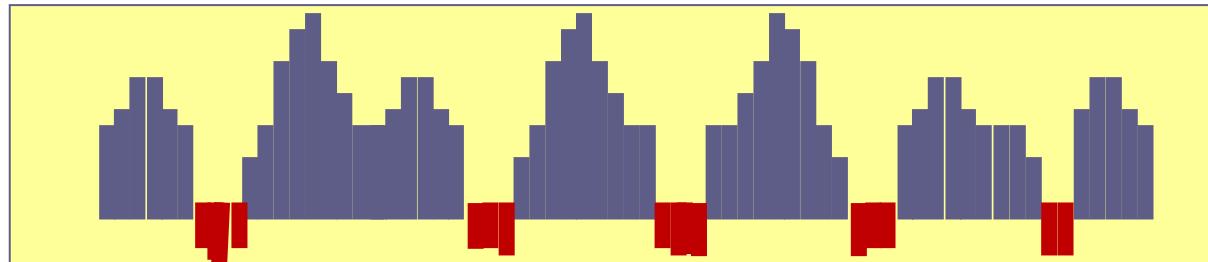
NCBI RefSeq	Other RefSeq	All GENCODE...
full	hide	hide
hide	Genscan Genes	19 IKMC Ger Mapped
Geneid Genes	hide	hide
dense	ORFeome Clones	hide
squish	Pfam in UCS	hide
Old UCSC Genes	UCSC Alt Events	UniProt
pack	hide	hide
full	TransMap...	hide
TransMap...	hide	hide

Genome Browsers

- Some visual clues:



Sequence conservation



height of a blue bar is increased likelihood of conservation,
red indicates a likelihood of faster-evolving regions

Alignment indications (Conservation pairs: “chain” or “net” style)

Alignments = boxes, Gaps = lines



Tick marks; a single location (STS, SNP)

Practicum

Retrieving information with the UCSC Genome Browser

<https://genome.ucsc.edu/>

1. What is the genomic localization of human *Irrtm1* gene?

-chromosome:

-position:

-strand:

2. Which genes are in the neighbourhood of this gene?

3. How many exons has the gene?

4. How many different transcripts do we know of this genomic region?

5. Can you find SNPs in this gene?

6. In which tissue is this gene mainly expressed?

7. Does the protein encoded by this gene have a transmembrane domain?

8. Has this gene an ortholog in mouse?

9. Use the CDS of human *Irrtm1* gene to localize this gene in mouse genome. (Use BLAT)

Practicum

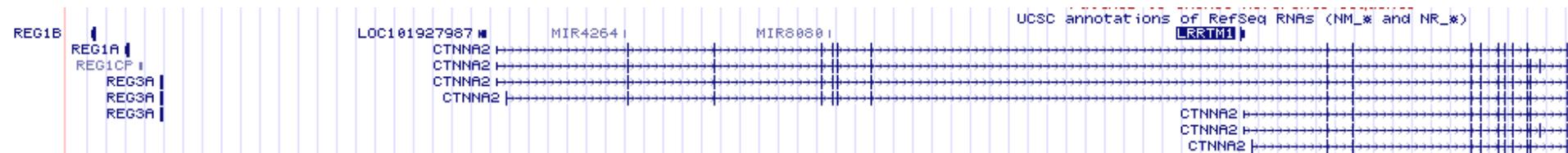
1. What is the genomic localization of human *Irrtm1* gene?

- Click on the gene to see the information

Position: [chr2:80301878-80304752](#)
Band: 2p12
Genomic Size: 2875
Strand: -
Gene Symbol: LRRTM1
CDS Start: complete
CDS End: complete

2. Which genes are in the neighborhood of this gene?

- Zoom out in genome viewer



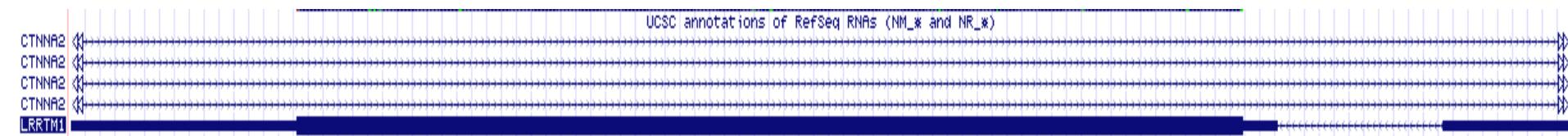
3. How many exons has the gene? 2

- Place the mouse on the gene
- Or: click on RefSeq link to open in NCBI-GenBank
- Or: TableBrowser

Practicum

4. How many different transcripts do we know of this genomic region? 5

- Use Genome Viewer or Table Browser for more detailed information



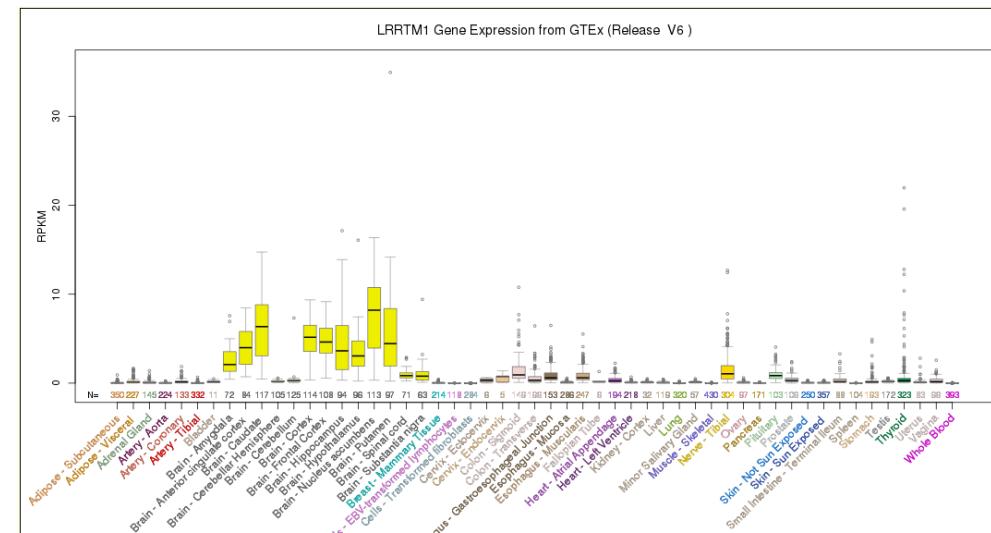
5. Can you find SNPs in this gene? yes

- Set display mode of track “Variation” > “SNPs” to ON



6. In which tissue is this gene mainly expressed? brain

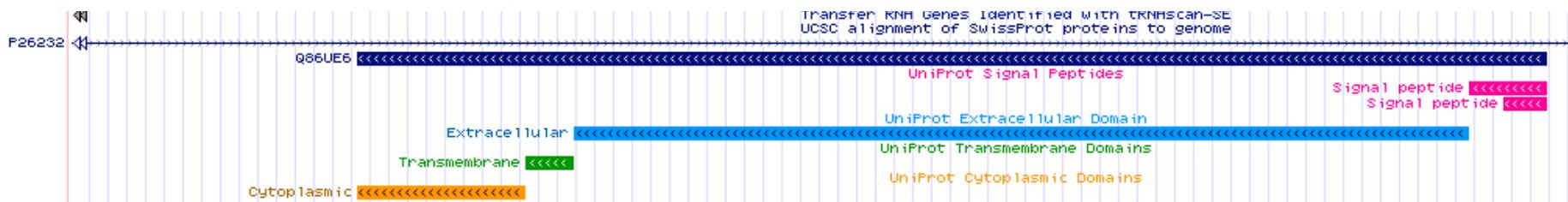
- Info in track “Expression” > “GTEx”



Practicum

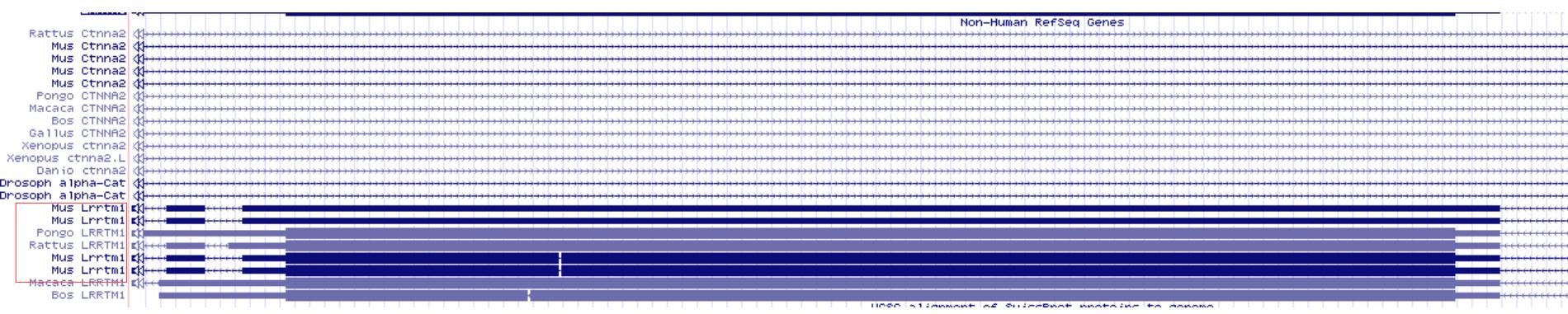
7. Does the protein encoded by this gene have a transmembrane domain?

- Set display mode of track “Gene and Gene Predictions” > “UniProt” to “pack”



8. Has this gene an ortholog in mouse? yes

- Set display mode of track “Gene and Gene Predictions” > “Other RefSeq” to “pack”



Practicum

9. Use the CDS of human *Irrtm1* gene to localize this gene in mouse genome.
 (Use BLAT)

- Get the CDS sequence of human gene:

Get Genomic Sequence Near Gene

Note: if you would prefer to get DNA for more than one feature of the

Sequence Retrieval Region Options:

- Promoter/Upstream by bases
- 5' UTR Exons
- CDS Exons
- 3' UTR Exons
- Introns
- Downstream by bases
- One FASTA record per gene.
- One FASTA record per region (exon, intron, etc.) with
- Split UTR and CDS parts of an exon into separate FASTA records

Note: if a feature is close to the beginning or end of a chromosome it

- Use BLAT to align this sequence on Mouse genome:

BLAT Search Genome

Genome: Search ALL

Assembly:

Query type:

Sort output:

Mouse

Dec. 2011 (GRCm38/mm10)

DNA

query,score

```

ATGGATTTCTCTGCTCGGTCTCTGCTATACTGGCTGCTGAGGGAGGC
CTCGGGGGTGGCTTGTGCTGCTGGGGGCTGCTTCAGATGCTGGCG
CCGCCCCCAGCGGGTGGCGAGCTGTGCCGTGCGAGGGGGCGCTGCTG
TACTCGGAGGGCCTCAACCTCACCGAGGCGCCAACACCTGTCCGGCT
GCTGGCTTGTCCCTGCCTACAAACAGCTCTCGAGCTGCCGCCGGCC
AGTTCACGGGTTAATGAGCTCACGGCTCTATCTGGATACAATCAC
ATCTGCTCGTGAGGGGACGCCCTTCAGAAACTGCCGAGTTAAGGA
ACTCACGCTGAGTCCAACCAGATACCCAACCTGCCAACACACCCTCC
GGCCATGCCAACCTGGCAGCGTGGACCTCTCGTACAACAAAGCTGAG
GGCTCGGCCGACCTCTCCACGGGCTGCCGAAGCTCACACGCTGCA
TATGCGGGCCAACGCCATTCCAGTTGTGCCGTGCGCATCTTCAGGACT
GCCGAGCTCAAGTTCTGACATGGATACAATCAGCTAAGAGCTG
GCCGCGCAACTTTGCCGGCTTAAAGCTACCGAGCTGCCACCTCGA
GCACAAAGCACTGGTCAAGGTGAACCTCGCCACTCCGCCCTCATCT
CCCTGCACTGCTCTGCCGGAGGAACAGGTGGCATTGGGGTACG

```

submit

I'm feeling lucky

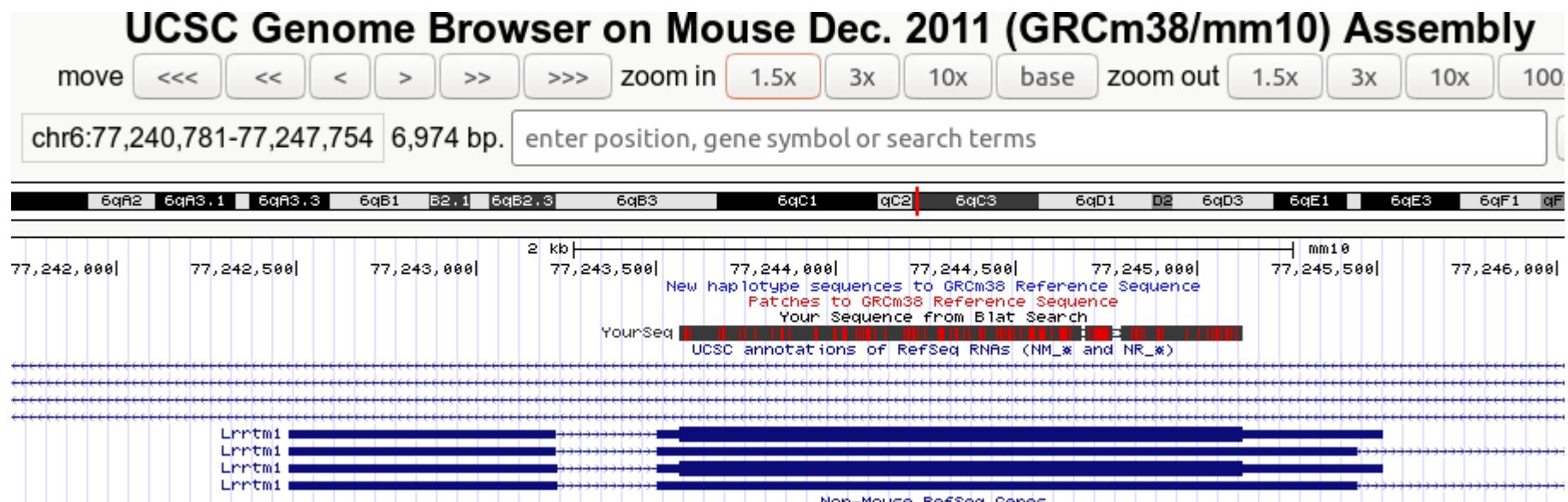
clear

Practicum

- Visualize entry with highest score

→

ACTIONS	QUERY	SCORE	START	END	QSIZE	IDENTITY	CHROM	STRAND	START	END	SPAN
browser details	YourSeq	1305	1	1569	1569	92.6%	chr6	+	77243562	77245130	1569
browser details	YourSeq	30	43	88	1569	94.2%	chr12	-	20883055	20883105	51
browser details	YourSeq	24	1304	1329	1569	96.2%	chr11	-	106320438	106320463	26
browser details	YourSeq	22	1399	1420	1569	100.0%	chr10	-	66129920	66129941	22
browser details	YourSeq	22	367	389	1569	100.0%	chr13	+	97550711	97550734	24
browser details	YourSeq	22	23	49	1569	92.4%	chr10	+	129969924	129969951	28
browser details	YourSeq	22	23	49	1569	92.4%	chr10	+	129978799	129978826	28
browser details	YourSeq	21	396	426	1569	83.9%	chr14	+	57525552	57525582	31
browser details	YourSeq	21	848	869	1569	100.0%	chr1	+	22046494	22046516	23

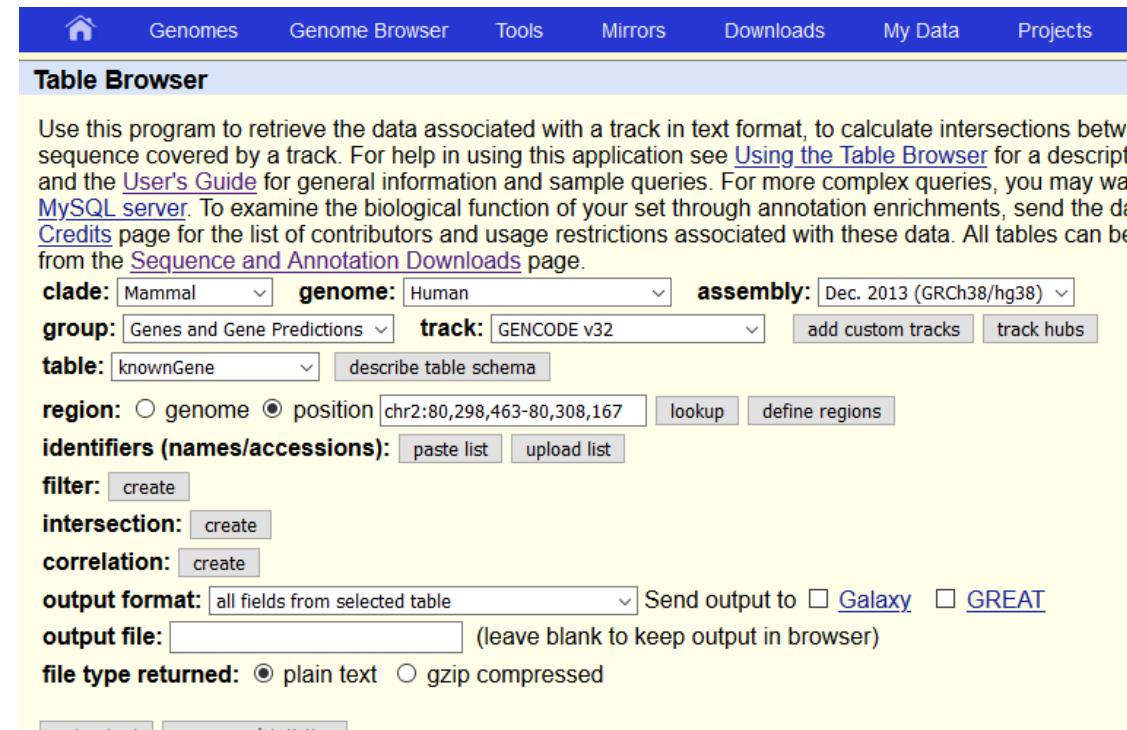


Genome Browsers

UCSC Genome Browser

<https://genome.ucsc.edu/>

- Table Browser tool allows to:
 - Search for genes and annotation
 - Combine queries on multiple tables or tracks
 - Display basic statistics over a dataset
 - Output to results table in convenient format
 - Retrieve sequences
 - Export to external resources



The screenshot shows the UCSC Table Browser interface. At the top, there is a navigation bar with links for Home, Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, and Projects. Below the navigation bar, the title "Table Browser" is displayed. The main content area contains a text block explaining the purpose of the browser, followed by a form for specifying search parameters. The form includes fields for clade (Mammal), genome (Human), assembly (Dec. 2013 (GRCh38/hg38)), group (Genes and Gene Predictions), track (GENCODE v32), table (knownGene), and various buttons for "add custom tracks", "track hubs", "lookup", "define regions", "paste list", "upload list", and "create". There are also sections for "filter", "intersection", "correlation", and "output format" (set to "all fields from selected table"). The bottom of the form includes buttons for "get output" and "summary/statistics". A note at the bottom states: "To reset all user cart settings (including custom tracks), [click here](#)".

Examples

Practicum

Retrieving information with the UCSC Genome Browser

<https://genome.ucsc.edu/>

10. Use the Table Browser to get the list of SNPs in your region

Table Browser

Use this program to retrieve the data associated with a track in text format, to calculate intersections between tracks, sequence covered by a track. For help in using this application see [Using the Table Browser](#) for a description of the c and the [User's Guide](#) for general information and sample queries. For more complex queries, you may want to use [G MySQL server](#). To examine the biological function of your set through annotation enrichments, send the data to [GRE Credits](#) page for the list of contributors and usage restrictions associated with these data. All tables can be download from the [Sequence and Annotation Downloads](#) page.

clade: Mammal genome: Human assembly: Dec. 2013 (GRCh38/hg38)

group: Variation track: dbSNP 153 add custom tracks track hubs

table: Common dbSNP(153) (dbSnp153Common) describe table schema

Note: Most dbSNP tables are huge. Trying to download them through the Table Browser usually leads to a timeout. Please see our [Data Access FAQ](#) on how to download dbSNP data.

region: genome position chr2:80,301,878-80,304,752 lookup define regions

identifiers (names/accessions):

filter:

subtrack merge:

intersection:

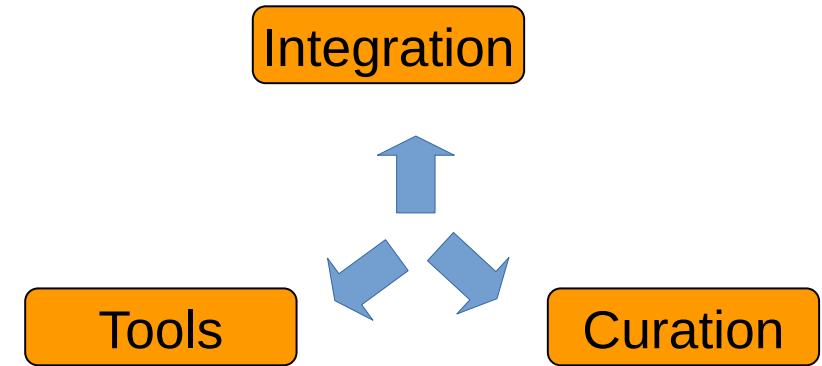
output format: Send output to Galaxy GREAT

Summary

- **Databases**
 - data collections
 - many types and diverse information
- **For information to be accessible / useful it must be**
 - Structured
 - Annotated
- **Resource Providers**
 - centers or organizations specialized in storing and maintaining databases
 - centralize data management

Summary

- General
 - **Resource providers**
- Subject-specific
 - **Collaborative projects**
 - **Multi-omics repositories**
- Bioinformatics tools for exploiting database information
 - **Queries and access to data**
 - **Genomic Browsers**



Final considerations

- Keeping informed about what you are seeing ensures correct interpretation of results
 - type of information (mRNA, gene, protein, SNP...)
 - source of information (curated, experimental, predicted, annotation, database)
 - specific tutorials: a good beginning
- Don't get overwhelmed: make specific queries, filter output
- When using data for drawing conclusions, appropriate controls may be used that make confidence of your search
 - scores of confidence
 - contrast information

