BIOINFORMATICS LAB – AP BIOLOGY

Bioinformatics is the science of collecting and analyzing complex biological data. Bioinformatics combines computer science, statistics and biology to allow scientists to do many things:

- Build phylogenetic trees
- Study mutations found in human cancers
- Investigate where genes are expressed (transcribed and translated) in an organism
- Examine interactions between genes
- Analyze circadian rhythms in expression of genes

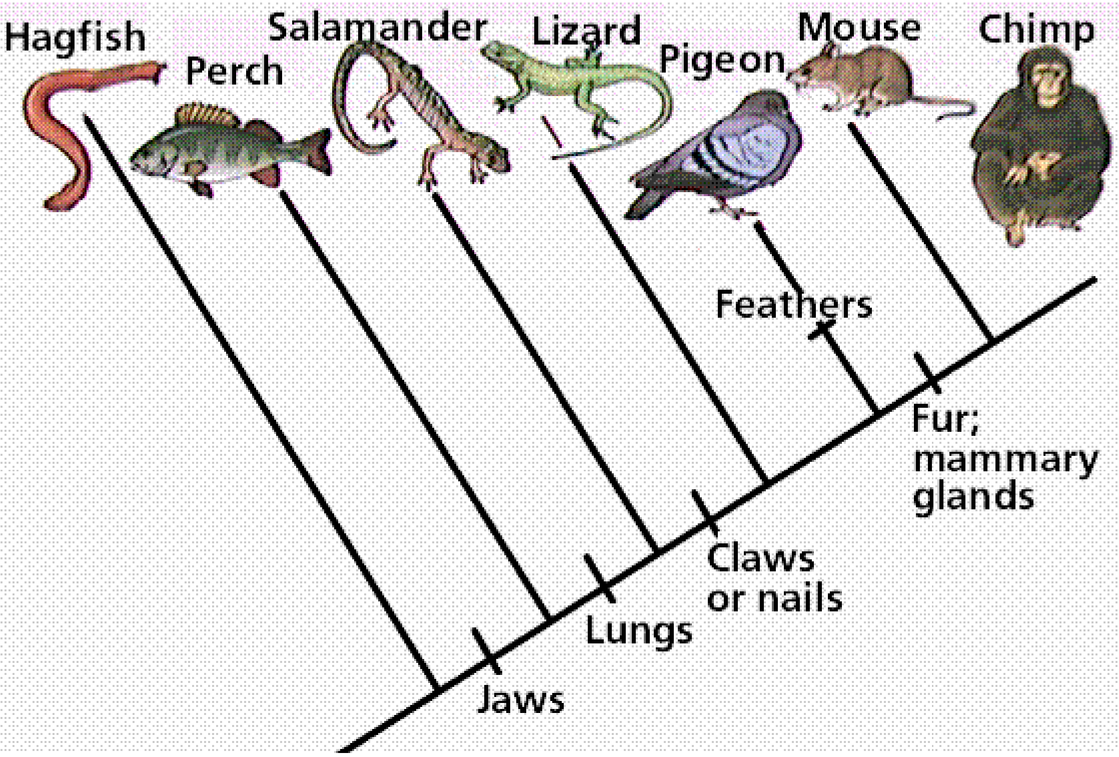
And much, much more.

We will start by using DNA sequences isolated from a fossil to propose placement of that fossil on a phylogenetic tree, then we will explore some of the other free resources available online to do bioinformatics.

BLAST – Basic Local Alignment Search Tool

One of the ways to determine the degree of relatedness between organisms is to compare their DNA sequences. The more recently organisms shared a common ancestor, the more closely related they will be, and they will have a greater homology (similarity) in their DNA sequences. In bioinformatics, a **sequence alignment** is a way of arranging the **sequences** of **DNA**, RNA, or protein to identify regions of similarity. BLAST compares the sequence you are interested in (the "query" sequence) to the millions of known DNA sequences available, looking for the greatest degree of homology. Looking at these homologous sequences (called "hits") can be useful in determining the function of a gene (if a gene is involved in glycolysis in mice, it is very likely that the human version of that gene is also involved in glycolysis) or how closely related two species are (the more DNA in common, the more closely related). You will be using BLAST to propose a possible placement of a fossil on a cladogram (aka phylogenetic tree).

Here is an example of a simple cladogram:

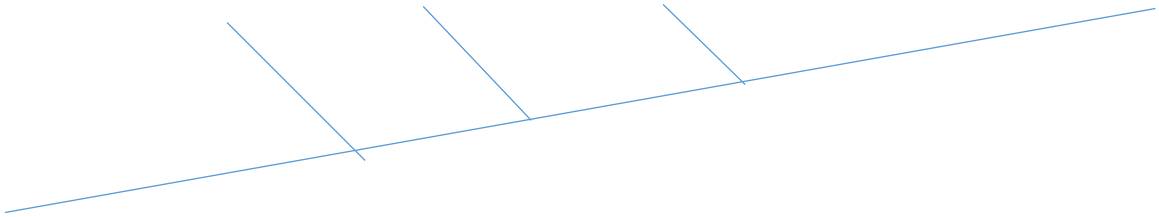


This cladogram includes synapomorphies, shared derived characteristics.   From the cladogram, we can say that all of the organisms except the hagfish have the derived characteristic of jaws, while only mice and chimps share the derived characteristics of fur and mammary glands.

While the previous cladogram could tell us about the characteristics that organisms share, we can also use shared characteristics to construct cladograms. Below is a table showing some of the characteristics of major plant groups:

Physical Characteristics of Major Plant Groups			
Plant Group	**Vascular Tissue**	**Flowers**	**Seeds**
Mosses	0	0	0
Conifers	+	0	+
Angiosperms	+	+	+
Ferns	+	0	0

The more shared characteristics two organisms have, the more closely related they are. Using the data above, propose an arrangement of mosses, conifers, angiosperms and ferns on the cladogram below.

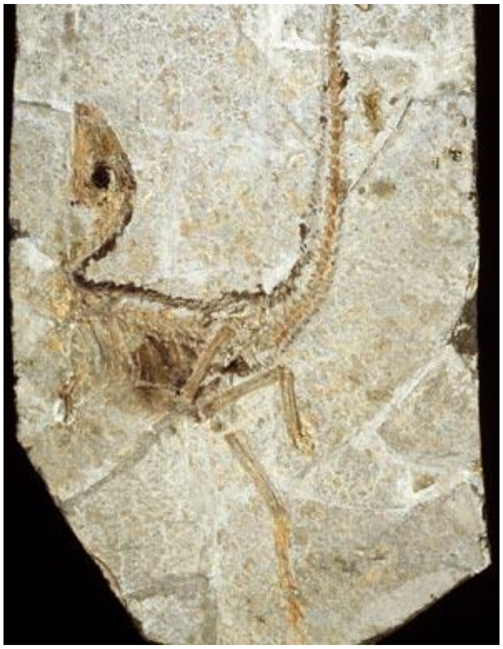


GAPDH (glyceraldehydes 3-phosphate dehydrogenase) is an enzyme that catalyzes the sixth step in glycolysis, an important reaction that produces molecules used in cellular respiration. The following data table shows the percentage similarity of this gene and the protein it expresses in humans versus other species. For example, according to the table, the GAPDH gene in chimpanzees is 99.6% identical to the gene found in humans, while the primary sequence of the corresponding protein is identical.

Percentage Similarity of the GADPH gene and protein with *Homo sapiens*		
Organism	**Gene Percentage Similarity with Homo sapiens**	**Protein Percentage Similarity with Homo sapiens**
Pan troglodytes	99.6	100
Canis lupus familiaris	91.3	95.2
Drosophila melanogaster	72.4	76.7
Caenorhabditis elegans	68.2	74.3

Based on the data, which species is most closely related to humans? Least closely?
Why are the percentage similarities higher for the proteins than the genes?

The Liaoning Province in northeastern China is a rich source of dinosaur fossils. In the 1990s, scientists found the following fossil:

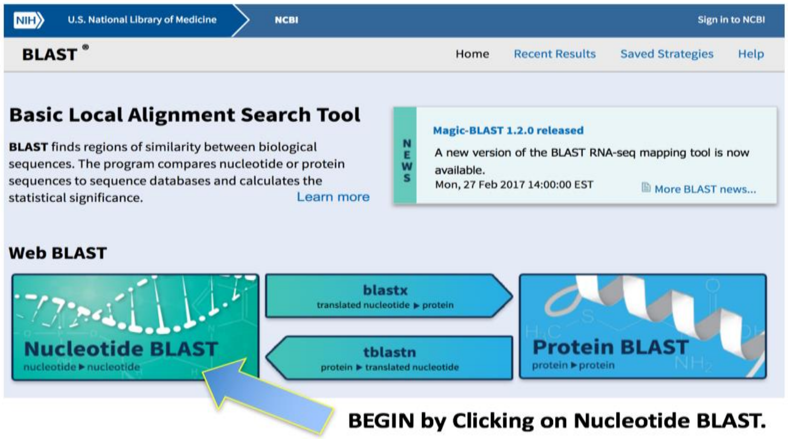


Based on the morphology (shape) of the fossil in the picture, make a hypothesis as to where the organism in the fossil should be placed on the cladogram below. (Draw a line labeled “fossil specimen” on the cladogram). In Darwin’s day, scientists had to rely on the morphology of the fossil and information gleaned from the surrounding rock layers when classifying a fossil Now, with the advent of biotechnology, scientists can sometimes isolate intact DNA from fossils, sequence the DNA, and use this information to refine the fossil’s classification.

Scientists were able to isolate and sequence DNA from this fossil. Your job is to take the fossil DNA sequences (found on the class webpage), run them through the BLAST tool, and use your results to propose a placement of that fossil on a cladogram.

PART ONE

1. Go to the BLAST homepage (https://blast.ncbi.nlm.nih.gov/Blast.cgi). Click on the Nucleotide Blast box.



Basic Local Alignment Search Tool

BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance. Learn more

NEWS

Magic-BLAST 1.2.0 released

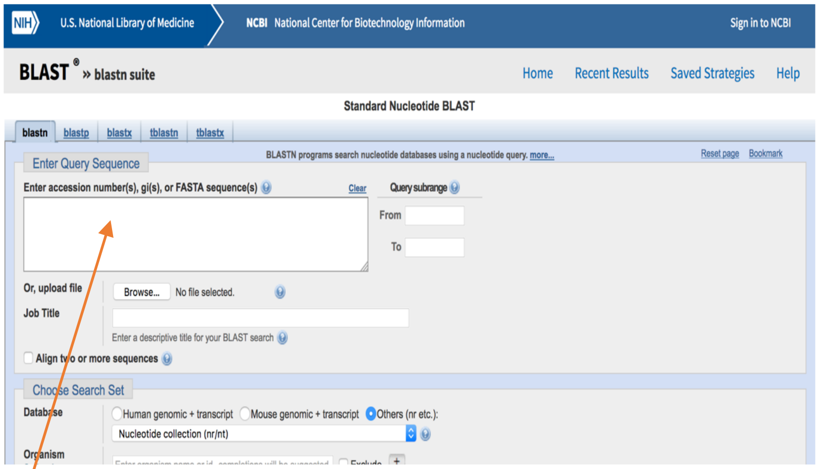
A new version of the BLAST RNA-seq mapping tool is now available.

Mon, 27 Feb 2017 14:00:00 EST

More BLAST news...

BEGIN by Clicking on Nucleotide BLAST.

2. Your screen should look something like this:



Standard Nucleotide BLAST

BLASTN programs search nucleotide databases using a nucleotide query. more...

Enter accession number(s), gi(s), or FASTA sequence(s)

Or, upload file: Browse... No file selected.

Job Title

Enter a descriptive title for your BLAST search

□ Align two or more sequences

Database: ○ Human genomic + transcript ○ Mouse genomic + transcript ● Others (nr etc.):

Nucleotide collection (nr/nt)

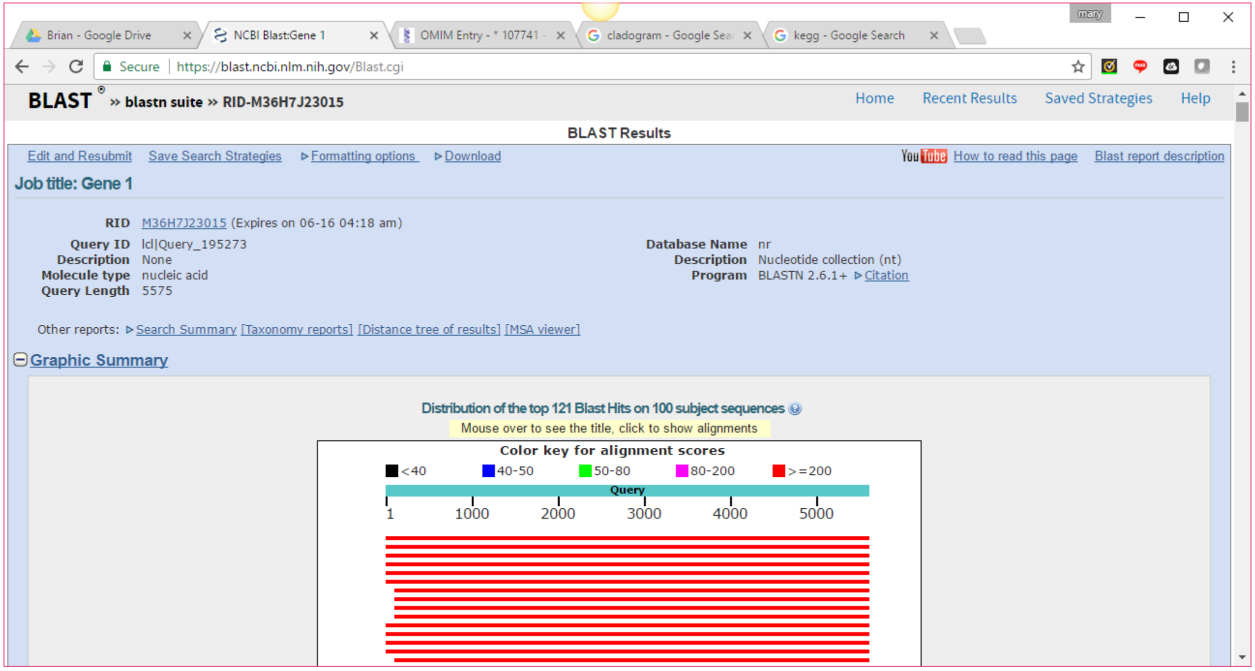
Organism

Enter organism name or id - completions will be suggested □ Exclude

Query box   In the query box, copy and paste your first DNA sequence.

3. For “Job Title” enter “Gene 1” or “Gene 2” or etc…..
4. For “Database” use the pull down menu to choose “Nucleotide Collection.” Leave “Organism” black since we want to search all organisms.
5. Under “Program Selection” optimize for “highly similar sequences.”
6. Click the “BLAST” button at the bottom of the screen, then ***be patient***! Depending on the speed of your internet connection and how busy the server is, it may take a few minutes to see your results.

Your results will look something like this:



Job title: Gene 1

RID M36H7J23015 (Expires on 06-16 04:18 am)

Query ID lcl|Query_195273
Description None
Molecule type nucleic acid
Query Length 5575

Database Name nr
Description Nucleotide collection (nt)
Program BLASTN 2.6.1+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [MSA viewer]

⊖Graphic Summary
Distribution of the top 121 Blast Hits on 100 subject sequences
Mouse over to see the title, click to show alignments
Color key for alignment scores
■<40
🟦40-50
🟩50-80
🟪80-200
🟥>=200
Query
1
1000
2000
3000
4000
5000

Here is some of the information this screen is telling you:

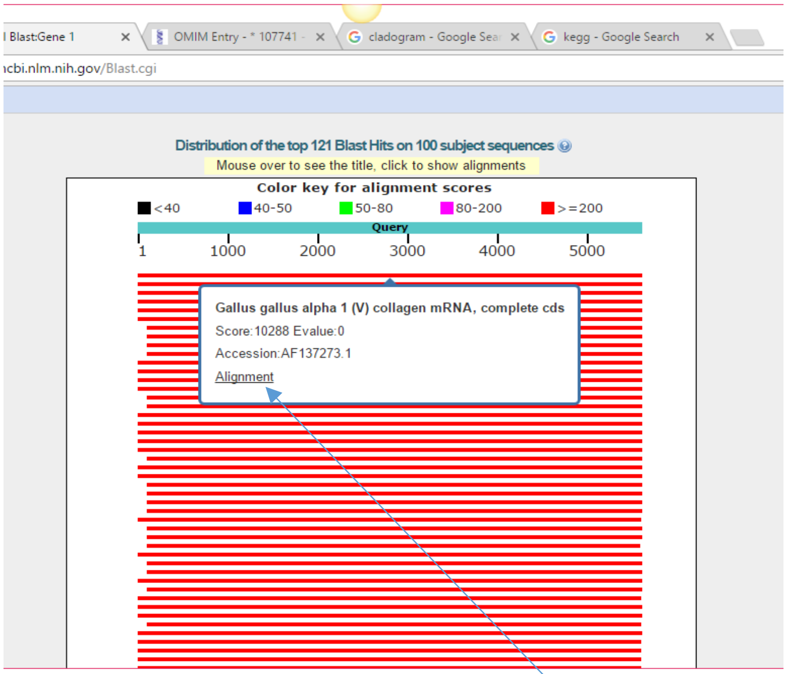
Query ID: this is a unique search identifier that indexes your specific search

Molecule type: nucleic acid (since we were looking at DNA)

Query length: 5575 (the number of nucleotides in your query sequence – gene 1 in this example)

7. Now look at the colored bars. Red indicates a strong match with a high level of homology. Each bar represents a “hit,” or a sequence that the BLAST program found in the database that has a high level of homology with your query sequence. The bars are arranged in order with the strongest hit (with the highest degree of homology) on top. Click on the strongest hit (top red bar)

You should see something like this:



Distribution of the top 121 Blast Hits on 100 subject sequences

Mouse over to see the title, click to show alignments

Color key for alignment scores

■	🟦	🟩	🟪	🟥
<40	40-50	50-80	80-200	>=200

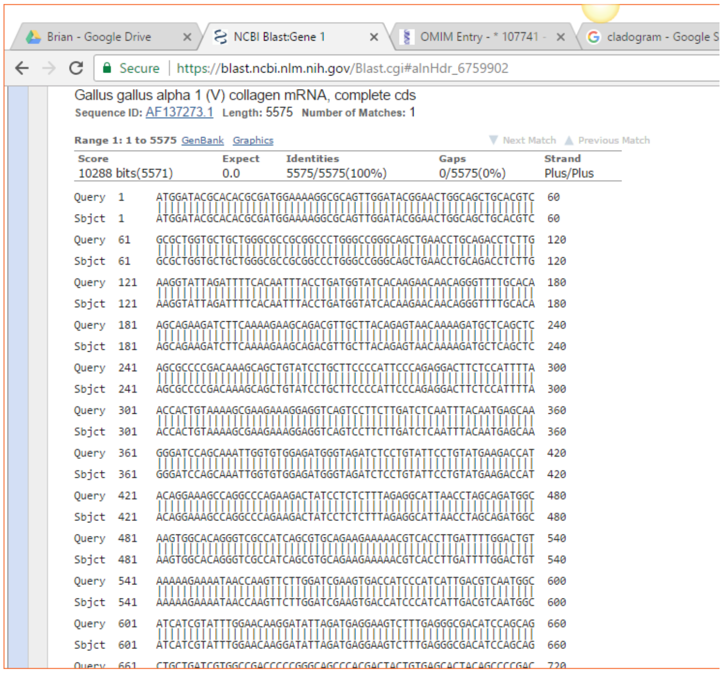
Gallus gallus alpha 1 (V) collagen mRNA, complete cds

Score:10288 Evalue:0

Accession:AF137273.1

Alignment

8. The white box tells you that this sequence came from the organism *Gallus gallus* (google it if you don't know what organism that is) and the DNA sequence in that organism codes for the protein collagen. Now click on the word "Alignment" in the white box



Gallus gallus alpha 1 (V) collagen mRNA, complete cds

Sequence ID: AF137273.1 Length: 5575 Number of Matches: 1

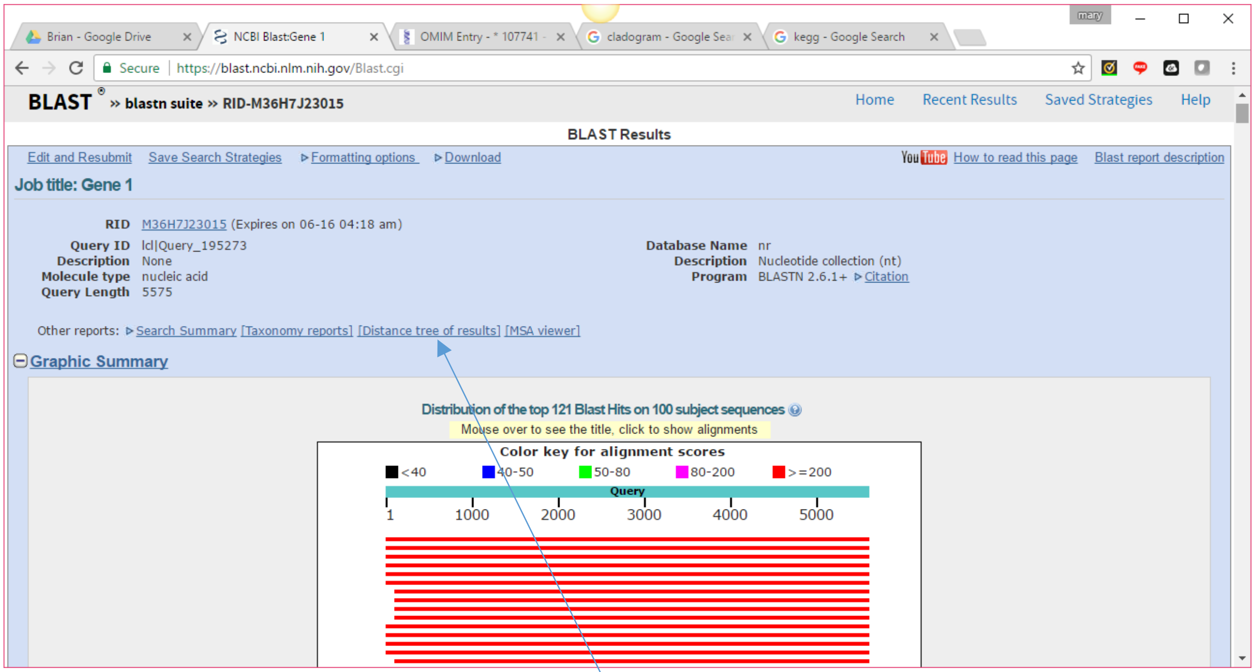
Range 1: 1 to 5575 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
10288 bits(5571)	0.0	5575/5575(100%)	0/5575(0%)	Plus/Plus

```
Query  1    ATGGATACGCACACGCGATGGAAAAGGCGCAGTTGGATACGGAACTGGCAGCTGCACGTC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ATGGATACGCACACGCGATGGAAAAGGCGCAGTTGGATACGGAACTGGCAGCTGCACGTC  60

Query  61   GCGCTGGTGCTGCTGGGCGCCGCGGCCCTGGGCCGGGCAGCTGAACCTGCAGACCTCTTG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GCGCTGGTGCTGCTGGGCGCCGCGGCCCTGGGCCGGGCAGCTGAACCTGCAGACCTCTTG  120

Query  121  AAGGTATTAGATTTTCACAATTTACCTGATGGTATCACAAGAACAACAGGGTTTTGCACA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AAGGTATTAGATTTTCACAATTTACCTGATGGTATCACAAGAACAACAGGGTTTTGCACA  180

Query  181  AGCAGAAGATCTTCAAAAGAAGCAGACGTTGCTTACAGAGTAACAAAAGATGCTCAGCTC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AGCAGAAGATCTTCAAAAGAAGCAGACGTTGCTTACAGAGTAACAAAAGATGCTCAGCTC  240

Query  241  AGCGCCCCGACAAAGCAGCTGTATCCTGCTTCCCCATTCCCAGAGGACTTCTCCATTTTA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AGCGCCCCGACAAAGCAGCTGTATCCTGCTTCCCCATTCCCAGAGGACTTCTCCATTTTA  300

Query  301  ACCACTGTAAAAGCGAAGAAAGGAGGTCAGTCCTTCTTGATCTCAATTTACAATGAGCAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ACCACTGTAAAAGCGAAGAAAGGAGGTCAGTCCTTCTTGATCTCAATTTACAATGAGCAA  360

Query  361  GGGATCCAGCAAATTGGTGTGGAGATGGGTAGATCTCCTGTATTCCTGTATGAAGACCAT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GGGATCCAGCAAATTGGTGTGGAGATGGGTAGATCTCCTGTATTCCTGTATGAAGACCAT  420

Query  421  ACAGGAAAGCCAGGCCCAGAAGACTATCCTCTCTTTAGAGGCATTAACCTAGCAGATGGC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  ACAGGAAAGCCAGGCCCAGAAGACTATCCTCTCTTTAGAGGCATTAACCTAGCAGATGGC  480

Query  481  AAGTGGCACAGGGTCGCCATCAGCGTGCAGAAGAAAAACGTCACCTTGATTTTGGACTGT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AAGTGGCACAGGGTCGCCATCAGCGTGCAGAAGAAAAACGTCACCTTGATTTTGGACTGT  540

Query  541  AAAAAGAAAATAACCAAGTTCTTGGATCGAAGTGACCATCCCATCATTGACGTCAATGGC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AAAAAGAAAATAACCAAGTTCTTGGATCGAAGTGACCATCCCATCATTGACGTCAATGGC  600

Query  601  ATCATCGTATTTGGAACAAGGATATTAGATGAGGAAGTCTTTGAGGGCGACATCCAGCAG  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  ATCATCGTATTTGGAACAAGGATATTAGATGAGGAAGTCTTTGAGGGCGACATCCAGCAG  660

Query  661  CTGCTGATCGTGGCCGACCCCCGGGCAGCCCACGACTACTGTGAGCACTACAGCCCCGAC  720
```

9. This is NOT a double stranded sequence of DNA. How do you know this?

The query line shows the DNA sequence you copied into BLAST. The Sbjct line show the aligned DNA sequence that BLAST found in the database. Each vertical line represents a match between the query and subject sequences. Score tells you how strong the homology is, anything over 200 is considered a strong match. Record the score in your notes. Now use the back arrow to return to the screen with the red bars.



BLAST® » blastn suite » RID-M36H7J23015

BLAST Results

Job title: Gene 1

RID	M36H7J23015 (Expires on 06-16 04:18 am)		
Query ID	lcl|Query_195273	Database Name	nr
Description	None	Description	Nucleotide collection (nt)
Molecule type	nucleic acid	Program	BLASTN 2.6.1+ ▷ Citation
Query Length	5575		

Other reports: ▷ Search Summary [Taxonomy reports] [Distance tree of results] [MSA viewer]

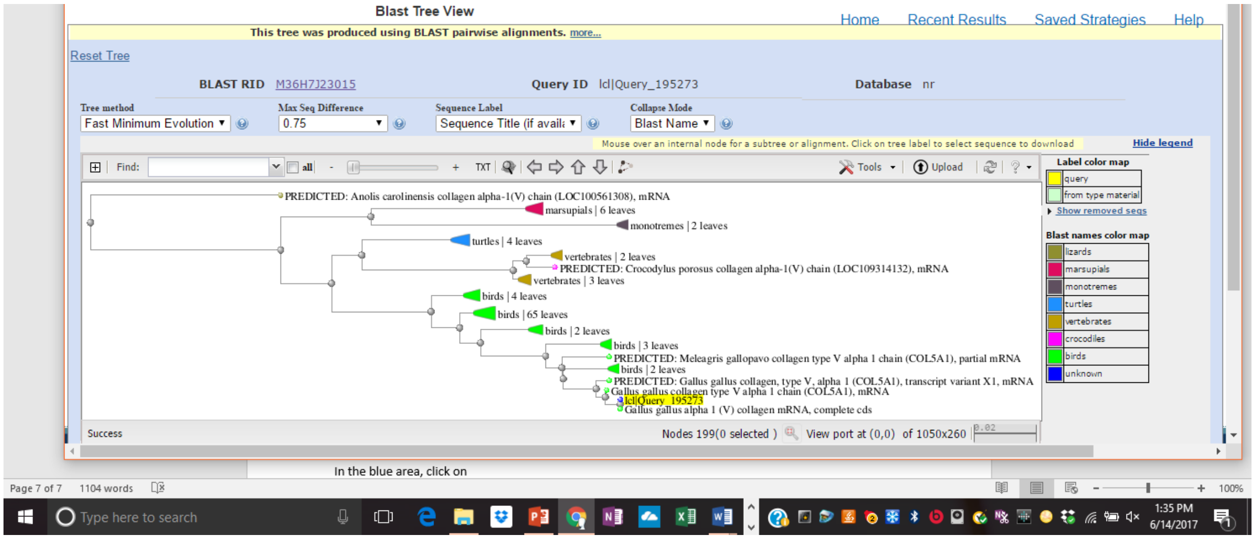
Graphic Summary

Distribution of the top 121 Blast Hits on 100 subject sequences

Mouse over to see the title, click to show alignments

Color key for alignment scores

10. In the blue area, click on "distance tree of results." This will create for you a proposed cladogram with your query sequence highlighted in yellow and placed on the cladogram.



Blast Tree View

This tree was produced using BLAST pairwise alignments. more...

Reset Tree

BLAST RID M36H7J23015 Query ID lcl|Query_195273 Database nr

Tree method: Fast Minimum Evolution

Max Seq Difference: 0.75

Sequence Label: Sequence Title (if availa

Collapse Mode: Blast Name

Mouse over an internal node for a subtree or alignment. Click on tree label to select sequence to download

Success

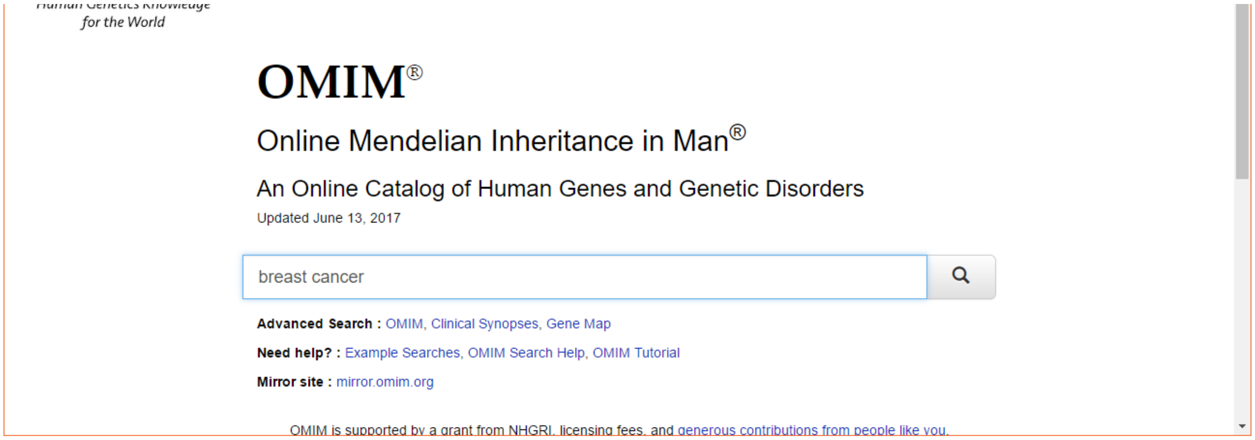
Nodes 199(0 selected) View port at (0,0) of 1050x260

11. Based on the identity of the species *Gallus gallus* and the distance tree of results, do you want to revise your initial placement of the fossil on the cladogram? Why or why not?

Repeat steps #1-11 for the remaining gene sequences obtained from the fossil. Where do you think the fossil should be placed on the initial cladogram and why?

PART TWO – ONLINE MENDELIAN INHERITANCE IN MAN (OMIM)

1. Google "OMIM" or click on this link https://www.omim.org/



Human Genetics Knowledge
for the World

OMIM®

Online Mendelian Inheritance in Man®

An Online Catalog of Human Genes and Genetic Disorders

Updated June 13, 2017

Advanced Search : OMIM, Clinical Synopses, Gene Map

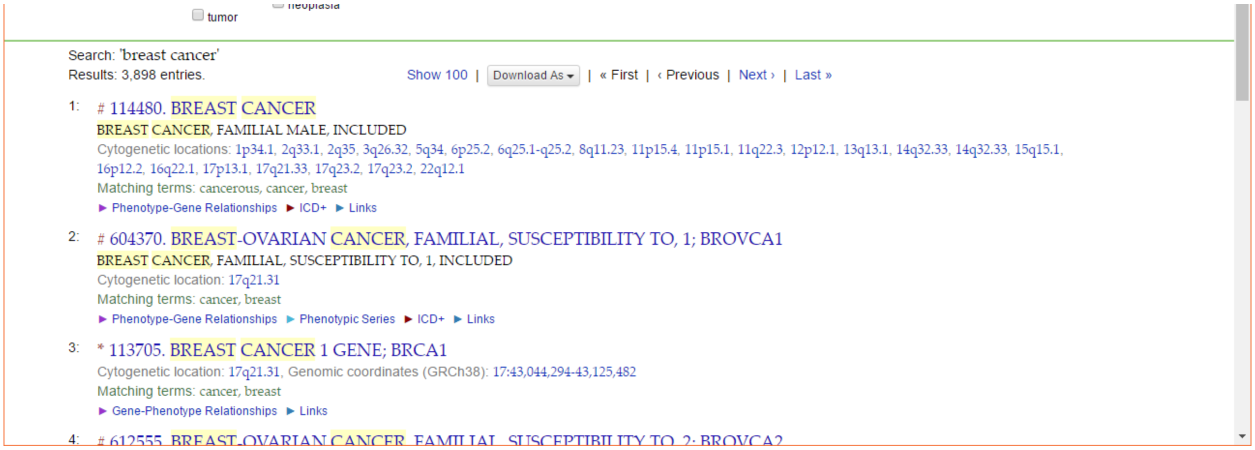
Need help? : Example Searches, OMIM Search Help, OMIM Tutorial

Mirror site : mirror.omim.org

OMIM is supported by a grant from NHGRI, licensing fees, and generous contributions from people like you.

In the search box enter the name of a disease or gene you are interested in. I'm using breast cancer

Here is what you might see:



Search: 'breast cancer'
Results: 3,898 entries.

Show 100 | Download As ▾ | « First | ‹ Previous | Next › | Last »

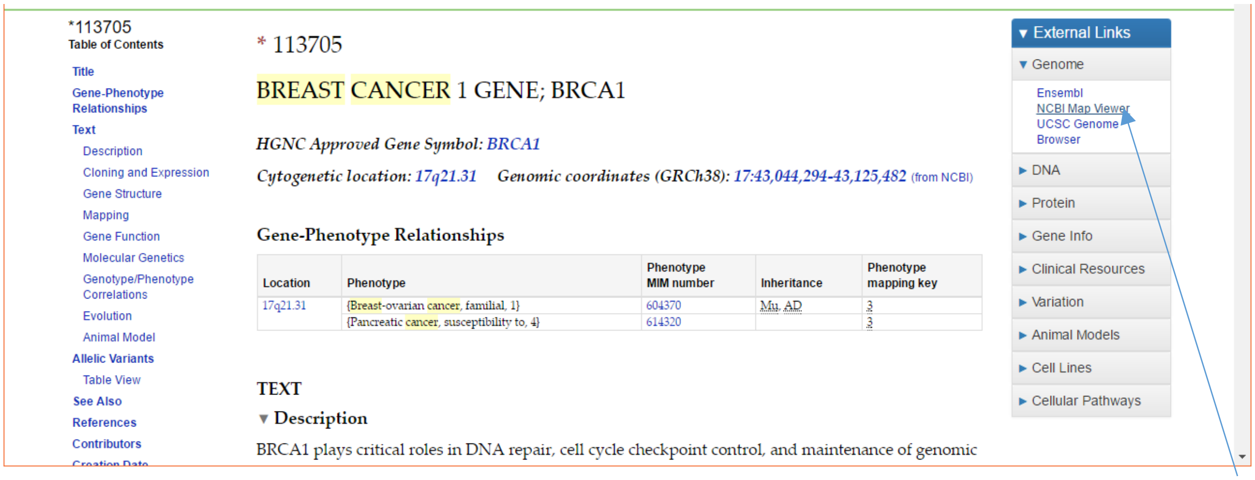
1: # 114480. BREAST CANCER
BREAST CANCER, FAMILIAL MALE, INCLUDED
Cytogenetic locations: 1p34.1, 2q33.1, 2q35, 3q26.32, 5q34, 6p25.2, 6q25.1-q25.2, 8q11.23, 11p15.4, 11p15.1, 11q22.3, 12p12.1, 13q13.1, 14q32.33, 14q32.33, 15q15.1, 16p12.2, 16q22.1, 17p13.1, 17q21.33, 17q23.2, 17q23.2, 22q12.1
Matching terms: cancerous, cancer, breast
▶ Phenotype-Gene Relationships ▶ ICD+ ▶ Links

2: # 604370. BREAST-OVARIAN CANCER, FAMILIAL, SUSCEPTIBILITY TO, 1; BROVCA1
BREAST CANCER, FAMILIAL, SUSCEPTIBILITY TO, 1, INCLUDED
Cytogenetic location: 17q21.31
Matching terms: cancer, breast
▶ Phenotype-Gene Relationships ▶ Phenotypic Series ▶ ICD+ ▶ Links

3: * 113705. BREAST CANCER 1 GENE; BRCA1
Cytogenetic location: 17q21.31, Genomic coordinates (GRCh38): 17:43,044,294-43,125,482
Matching terms: cancer, breast
▶ Gene-Phenotype Relationships ▶ Links

4: # 612555. BREAST-OVARIAN CANCER, FAMILIAL, SUSCEPTIBILITY TO, 2; BROVCA2

Note that the third result is for one of the most well know breast cancer genes, BRCA1. Click on one of your search results to find more information about your gene. I clicked on BRCA1 and saw this:



*113705
Table of Contents

* 113705

BREAST CANCER 1 GENE; BRCA1

HGNC Approved Gene Symbol: BRCA1

Cytogenetic location: 17q21.31 *Genomic coordinates (GRCh38): 17:43,044,294-43,125,482* (from NCBI)

Gene-Phenotype Relationships

Location	Phenotype	Phenotype MIM number	Inheritance	Phenotype mapping key
17q21.31	{Breast-ovarian cancer, familial, 1}	604370	Mu, AD	3
	{Pancreatic cancer, susceptibility to, 4}	614320		3

TEXT

▼ Description

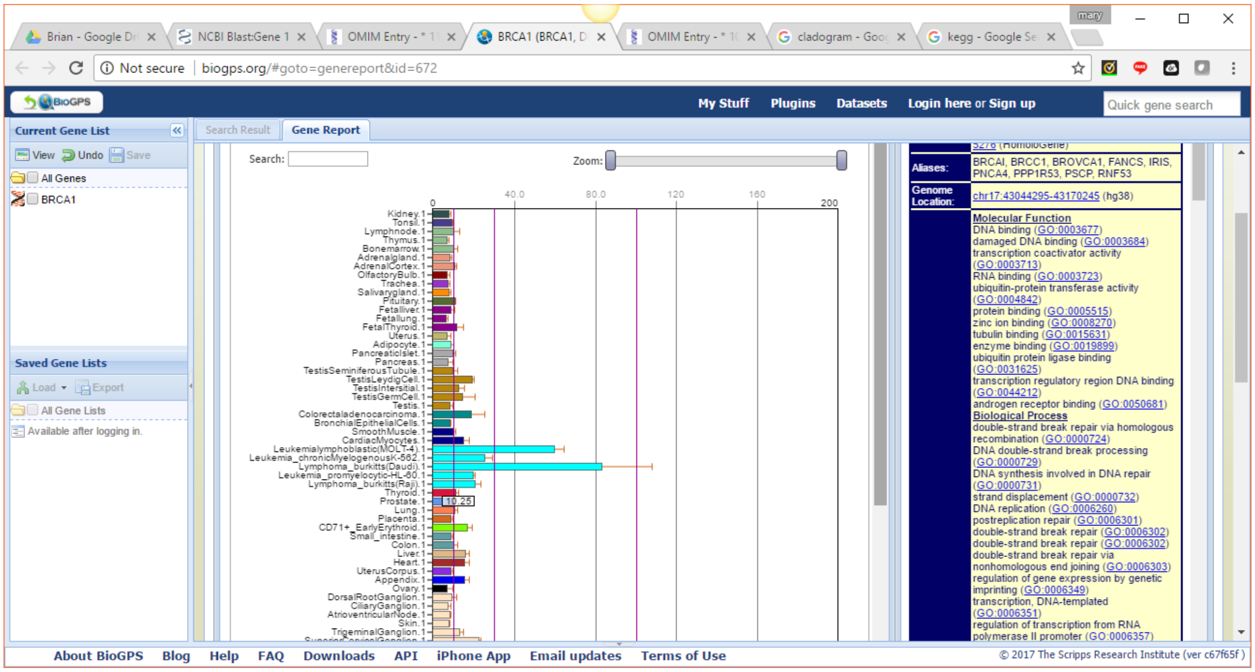
BRCA1 plays critical roles in DNA repair, cell cycle checkpoint control, and maintenance of genomic

On the left hand side of the screen in blue, you can find a wealth of information about the gene, such as its structure and function.

2. On the right hand side of the screen, click on “genome” and then NCBI Map viewer to see what chromosome(s) the gene resides on. Record the location of your gene.

PART THREE – BioGPS – Bio Gene Portal System

3. On the right hand side of the screen, click on “Gene Info” and then “BioGPS.” This will open a new window that will show you in which tissues your gene of interest is most expressed in (highest levels of mRNA). If there is little difference in the expression of your gene among different tissues, it is probably necessary in most, if not all, cells and is called a “housekeeping gene.” You can use the slider to zoom in and out. Record where your gene is most strongly expressed.



5276 (HomoloGene)

Aliases: BRCAI, BRCC1, BROVCA1, FANCS, IRIS, PNCA4, PPP1R53, PSCP, RNF53

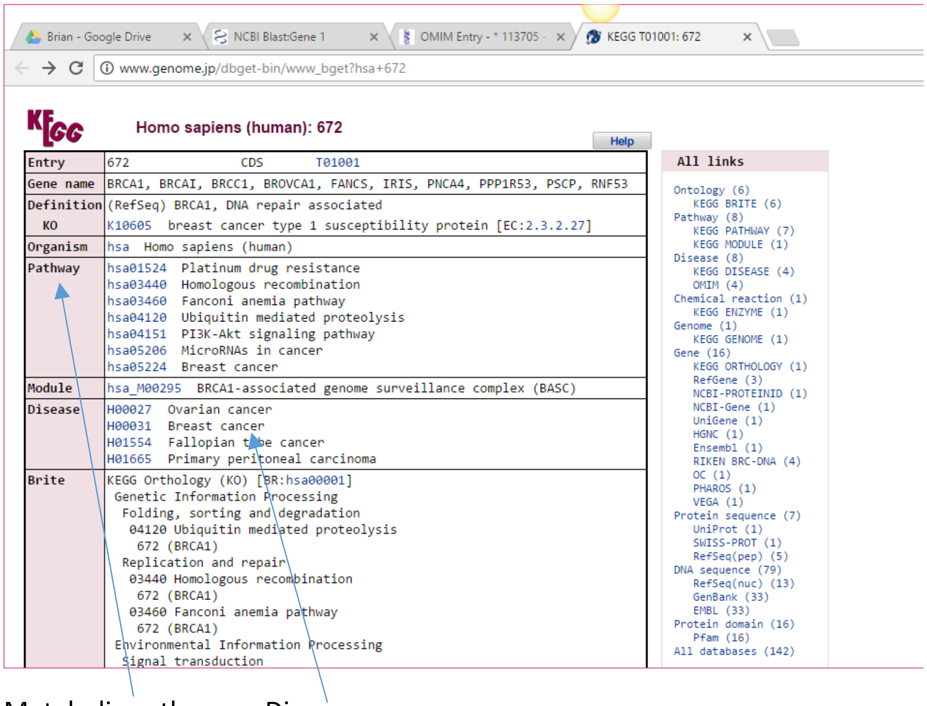
Genome Location: chr17:43044295-43170245 (hg38)

Molecular Function
DNA binding (GO:0003677)
damaged DNA binding (GO:0003684)
transcription coactivator activity (GO:0003713)
RNA binding (GO:0003723)
ubiquitin-protein transferase activity (GO:0004842)
protein binding (GO:0005515)
zinc ion binding (GO:0008270)
tubulin binding (GO:0015631)
enzyme binding (GO:0019899)
ubiquitin protein ligase binding (GO:0031625)
transcription regulatory region DNA binding (GO:0044212)
androgen receptor binding (GO:0050681)

Biological Process
double-strand break repair via homologous recombination (GO:0000724)
DNA double-strand break processing (GO:0000729)
DNA synthesis involved in DNA repair (GO:0000731)
strand displacement (GO:0000732)
DNA replication (GO:0006260)
postreplication repair (GO:0006301)
double-strand break repair (GO:0006302)
double-strand break repair (GO:0006302)
double-strand break repair via nonhomologous end joining (GO:0006303)
regulation of gene expression by genetic imprinting (GO:0006349)
transcription, DNA-templated (GO:0006351)
regulation of transcription from RNA polymerase II promoter (GO:0006357)

PART FOUR – KEGG – KYOTO ENCYCLOPEDIA OF GENES AND GENOMES

4. On the right side of the screen, click on “KEGG” This will give you information on the metabolic pathways the gene is part of, diseases related to this gene, the structure of the gene, the amino acid sequence of the protein coded for by the gene, and the nucleotide sequence of the gene.



Homo sapiens (human): 672

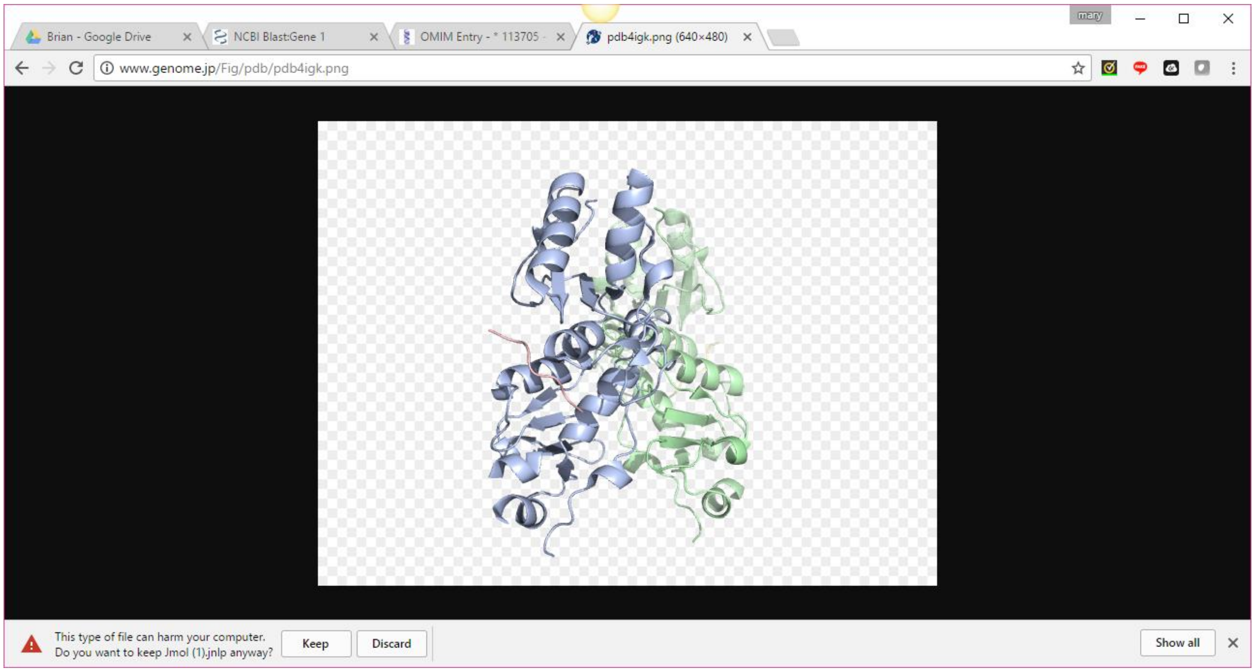
Entry	672 CDS T01001
Gene name	BRCA1, BRCAI, BRCC1, BROVCA1, FANCS, IRIS, PNCA4, PPP1R53, PSCP, RNF53
Definition	(RefSeq) BRCA1, DNA repair associated
KO	K10605 breast cancer type 1 susceptibility protein [EC:2.3.2.27]
Organism	hsa Homo sapiens (human)
Pathway	hsa01524 Platinum drug resistance hsa03440 Homologous recombination hsa03460 Fanconi anemia pathway hsa04120 Ubiquitin mediated proteolysis hsa04151 PI3K-Akt signaling pathway hsa05206 MicroRNAs in cancer hsa05224 Breast cancer
Module	hsa_M00295 BRCA1-associated genome surveillance complex (BASC)
Disease	H00027 Ovarian cancer H00031 Breast cancer H01554 Fallopian tube cancer H01665 Primary peritoneal carcinoma
Brite	KEGG Orthology (KO) [BR:hsa00001] Genetic Information Processing Folding, sorting and degradation 04120 Ubiquitin mediated proteolysis 672 (BRCA1) Replication and repair 03440 Homologous recombination 672 (BRCA1) 03460 Fanconi anemia pathway 672 (BRCA1) Environmental Information Processing Signal transduction

All links

```
Ontology (6)
   KEGG BRITE (6)
Pathway (8)
   KEGG PATHWAY (7)
   KEGG MODULE (1)
Disease (8)
   KEGG DISEASE (4)
   OMIM (4)
Chemical reaction (1)
   KEGG ENZYME (1)
Genome (1)
   KEGG GENOME (1)
Gene (16)
   KEGG ORTHOLOGY (1)
   RefGene (3)
   NCBI-PROTEINID (1)
   NCBI-Gene (1)
   UniGene (1)
   HGNC (1)
   Ensembl (1)
   RIKEN BRC-DNA (4)
   OC (1)
   PHAROS (1)
   VEGA (1)
Protein sequence (7)
   UniProt (1)
   SWISS-PROT (1)
   RefSeq(pep) (5)
DNA sequence (79)
   RefSeq(nuc) (13)
   GenBank (33)
   EMBL (33)
Protein domain (16)
   Pfam (16)
All databases (142)
```

Metabolic pathways   Diseases

Scroll down to structure and click on "JMOL" to see the 3D structure of the protein coded for by the gene.



This type of file can harm your computer.
Do you want to keep Jmol (1).jnlp anyway?

Estimate from the picture how many alpha helices and beta sheets are present in the protein.

PART FIVE – CIRCADB – CIRCADIAN RHYTHMS

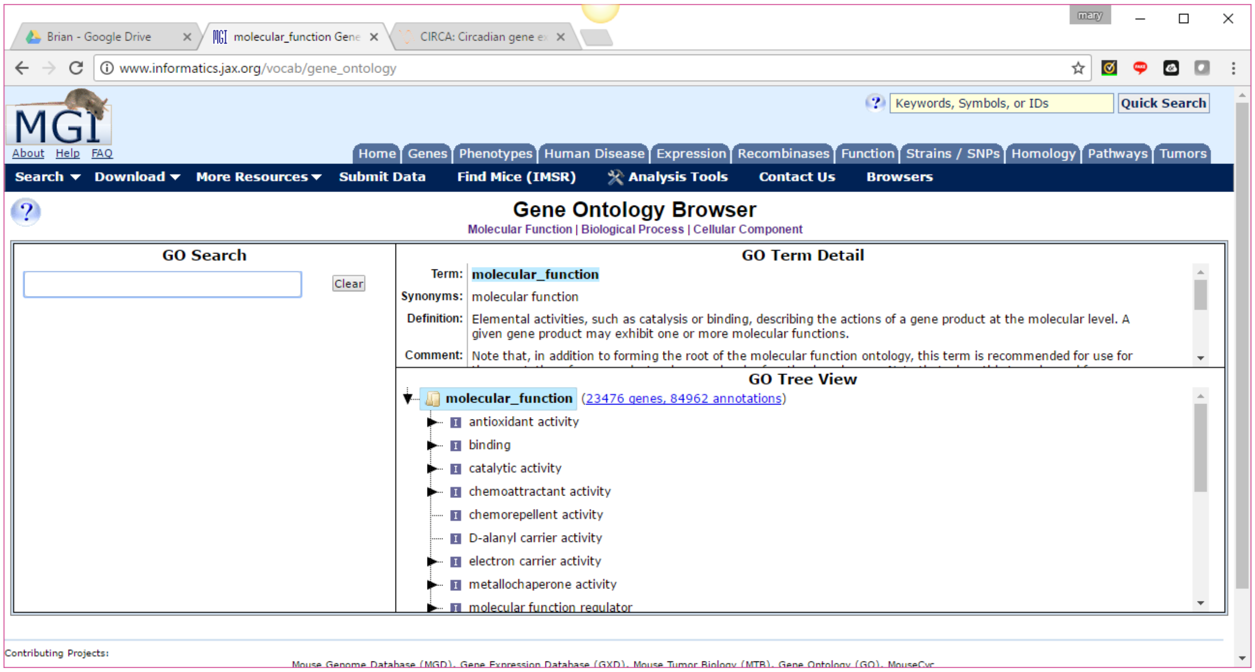
1. Go to http://circadb.hogeneschlab.org/

2. Enter the name of your gene

3. Examine the results and determine if the expression of your gene of interest is subject to circadian rhythms.

PART SIX – MGI – Mouse Genome Informatics

4. Go to http://www.informatics.jax.org/vocab/gene_ontology



Gene Ontology Browser

Molecular Function | Biological Process | Cellular Component

GO Search

GO Term Detail

Term: molecular_function

Synonyms: molecular function

Definition: Elemental activities, such as catalysis or binding, describing the actions of a gene product at the molecular level. A given gene product may exhibit one or more molecular functions.

Comment: Note that, in addition to forming the root of the molecular function ontology, this term is recommended for use for

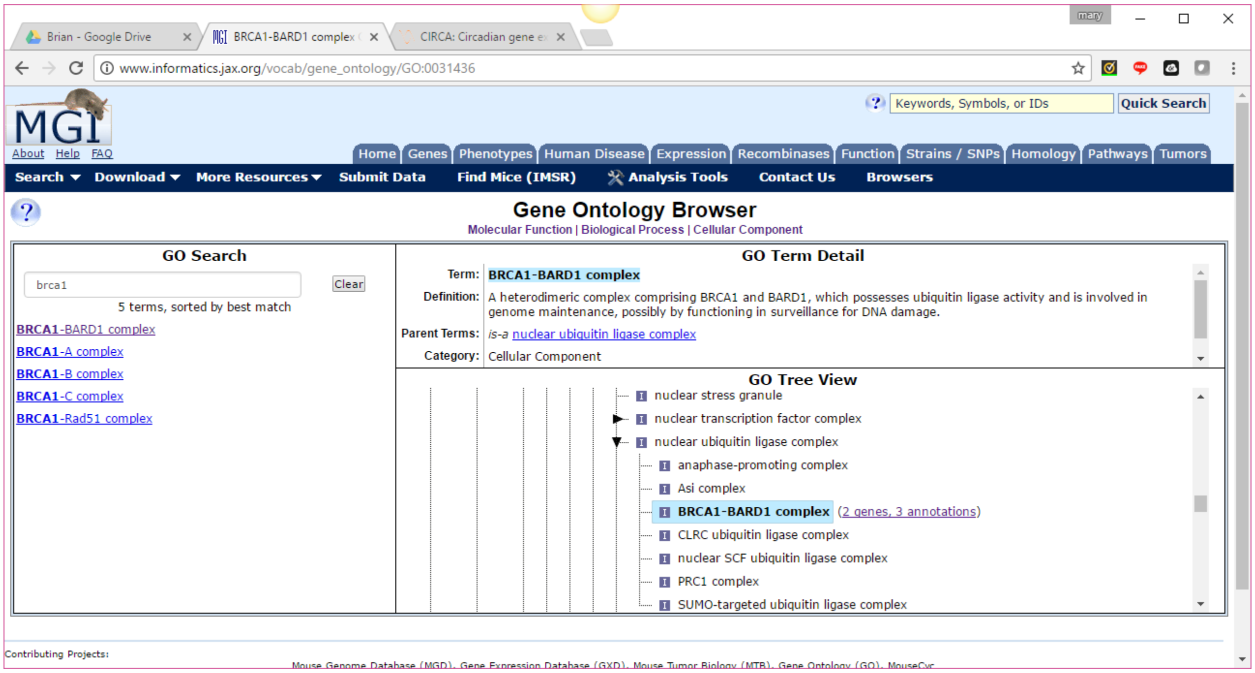
GO Tree View

- molecular_function (23476 genes, 84962 annotations)
  - antioxidant activity
  - binding
  - catalytic activity
  - chemoattractant activity
  - chemorepellent activity
  - D-alanyl carrier activity
  - electron carrier activity
  - metallochaperone activity
  - molecular function regulator

Contributing Projects:

Mouse Genome Database (MGD), Gene Expression Database (GXD), Mouse Tumor Biology (MTB), Gene Ontology (GO), MouseCyc

5. In the search box enter the name of your gene.
6. This screen should give you some ideas as to the function of your gene



Brian - Google Drive
BRCA1-BARD1 complex
CIRCA: Circadian gene ex
mary
www.informatics.jax.org/vocab/gene_ontology/GO:0031436
MGI
About Help FAQ
Keywords, Symbols, or IDs
Quick Search
Home Genes Phenotypes Human Disease Expression Recombinases Function Strains / SNPs Homology Pathways Tumors
Search ▾ Download ▾ More Resources ▾ Submit Data Find Mice (IMSR) Analysis Tools Contact Us Browsers

Gene Ontology Browser

Molecular Function | Biological Process | Cellular Component

GO Search

brca1 | Clear

5 terms, sorted by best match

- **BRCA1**-BARD1 complex
- **BRCA1**-A complex
- **BRCA1**-B complex
- **BRCA1**-C complex
- **BRCA1**-Rad51 complex

GO Term Detail

Term:	**BRCA1-BARD1 complex**
Definition:	A heterodimeric complex comprising BRCA1 and BARD1, which possesses ubiquitin ligase activity and is involved in genome maintenance, possibly by functioning in surveillance for DNA damage.
Parent Terms:	*is-a* nuclear ubiquitin ligase complex
Category:	Cellular Component

GO Tree View

```
I nuclear stress granule
► I nuclear transcription factor complex
▼ I nuclear ubiquitin ligase complex
    I anaphase-promoting complex
    I Asi complex
    I BRCA1-BARD1 complex (2 genes, 3 annotations)
    I CLRC ubiquitin ligase complex
    I nuclear SCF ubiquitin ligase complex
    I PRC1 complex
    I SUMO-targeted ubiquitin ligase complex
```

Contributing Projects:

Mouse Genome Database (MGD), Gene Expression Database (GXD), Mouse Tumor Biology (MTB), Gene Ontology (GO), MouseCyc