

NAME: \_\_\_\_\_ PERIOD: \_\_\_\_\_ DATE: \_\_\_\_\_

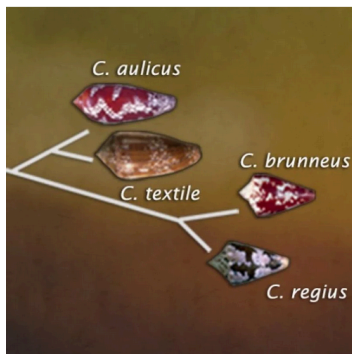
## Different Genes, Different Trees?

1. Navigate to

<https://www.biointeractive.org/classroom-resources/creating-phylogenetic-trees-dna-sequences>

# Creating Phylogenetic Trees from DNA Sequences

 Start Interactive



### Topic

Biochemistry & Molecular Biology

- DNA & RNA
- Biotechnology

### Evolution

- Phylogeny

### Resource Type

Interactive Media

- Click & Learn

### Level

High School — General


High School — AP/IB

College

### Used In

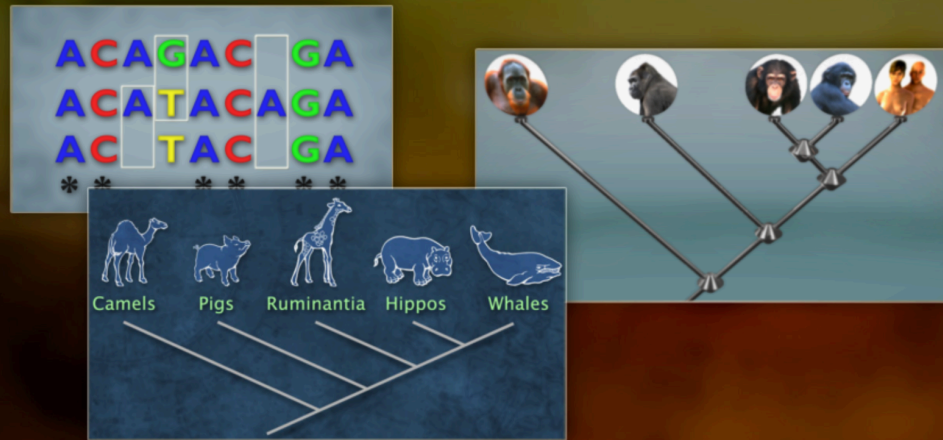
1 BioInteractive Playlists

### Saved By

 4 Members

and

Click on the green “Start Interactive” button in the top left of the page.



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Next

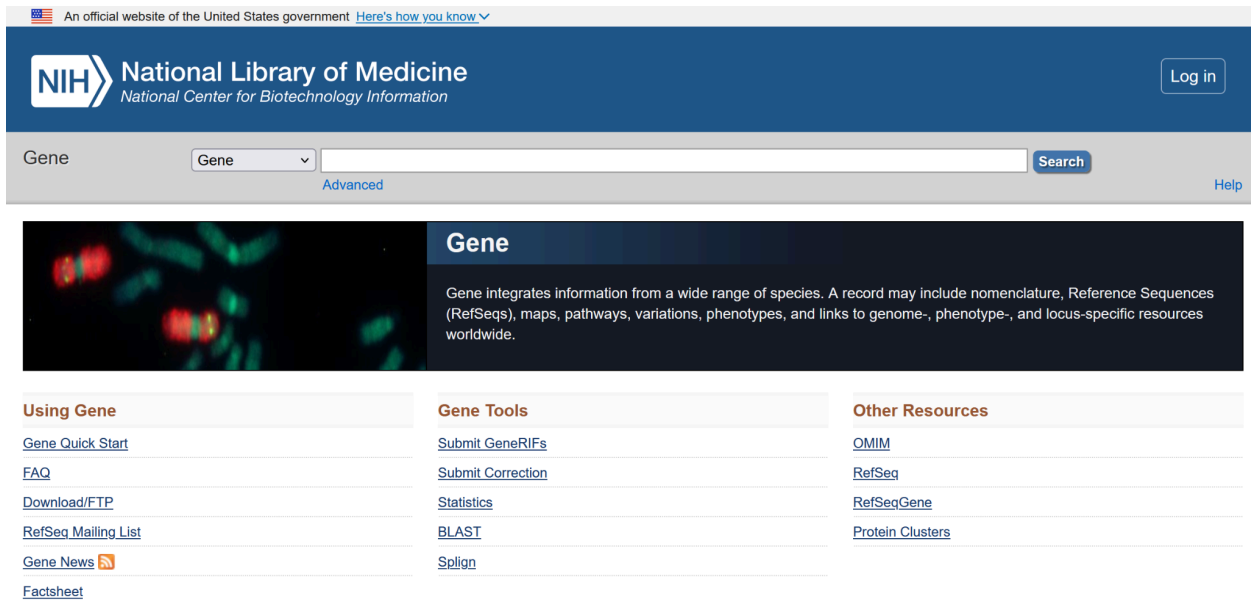
**Make sure to watch the videos on Slides 5, 6, 7, 10, 17, 18, 22, and 24.**

Now that you have been introduced to phylogenetic trees and cladograms, using molecular or morphological data, it is your turn to make some phylogenetic trees.

## Part 2:

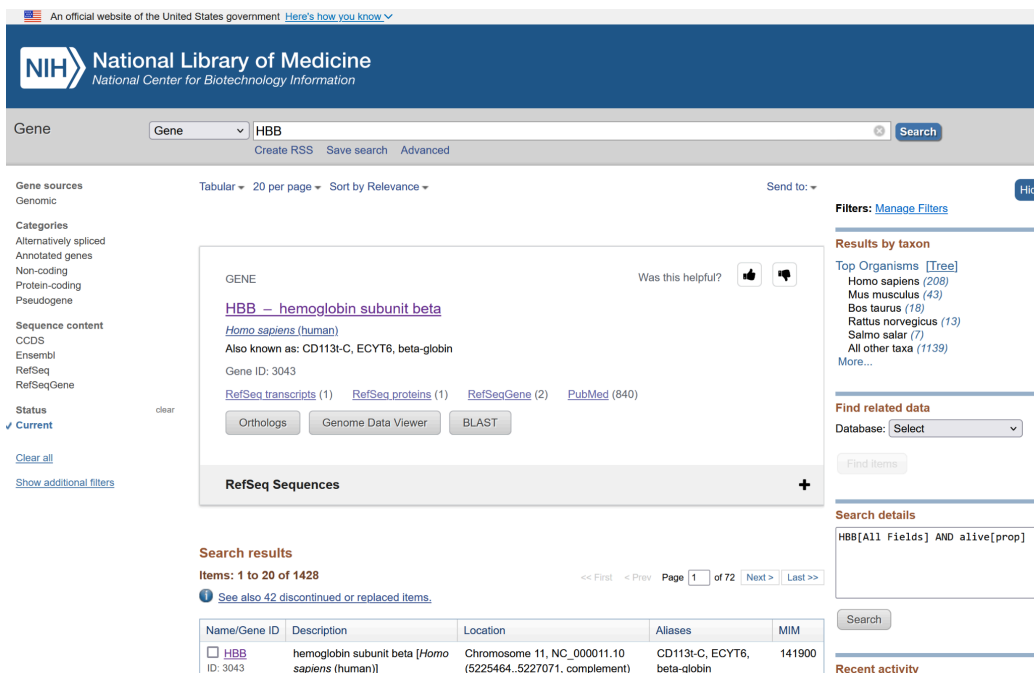
Phylogenetic trees can be made with little effort by utilizing NIH's NCBI (National Center for Biotechnology Information) Gene and COBALT tools.

1. Navigate to <https://www.ncbi.nlm.nih.gov/gene/>



The screenshot shows the NCBI Gene homepage. At the top, there's a header with the NIH logo and "National Library of Medicine National Center for Biotechnology Information". Below this is a search bar with the word "Gene" in a dropdown menu and a "Search" button. To the right of the search bar is a "Log in" button. Below the search bar is a section titled "Gene" with a description: "Gene integrates information from a wide range of species. A record may include nomenclature, Reference Sequences (RefSeqs), maps, pathways, variations, phenotypes, and links to genome-, phenotype-, and locus-specific resources worldwide." Below this are three columns of links: "Using Gene" (Gene Quick Start, FAQ, Download/FTP, RefSeq Mailing List, Gene News, Factsheet), "Gene Tools" (Submit GeneRIFs, Submit Correction, Statistics, BLAST, SnpIq), and "Other Resources" (OMIM, RefSeq, RefSeqGene, Protein Clusters).

2. Enter in the name of the gene your teacher provided. Here we will use the HBB gene (Hemoglobin Subunit Beta) gene. So type in HBB in Gene Search Bar at the top of the page.



The screenshot shows the NCBI Gene record for the HBB gene. The search bar at the top contains "HBB" and the "Search" button. Below the search bar is a section titled "Gene" with a description: "HBB – hemoglobin subunit beta Homo sapiens (human) Also known as: CD113t-C, ECT6, beta-globin". Below this are links to "RefSeq transcripts (1)", "RefSeq proteins (1)", "RefSeqGene (2)", and "PubMed (840)". Below these links are buttons for "Orthologs", "Genome Data Viewer", and "BLAST". Below the buttons is a section titled "RefSeq Sequences" with a "+" button. Below this is a section titled "Search results" with "Items: 1 to 20 of 1428". Below the search results is a table with the following data:

Name/Gene ID	Description	Location	Aliases	MIM
<input type="checkbox"/> HBB ID: 3043	hemoglobin subunit beta [ <i>Homo sapiens</i> (human)]	Chromosome 11, NC_000011.10 (5225464..5227071, complement)	CD113t-C, ECT6, beta-globin	141900

Below the table is a section titled "Recent activity".

Select the “HBB - hemoglobin subunit beta” link at the top.

On the page that is returned, you will click on the “**all**” link next to Orthologs

An official website of the United States government [Here's how you know](#)

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

Gene  [Advanced](#)

[Full Report](#) [Send to:](#)

**HBB hemoglobin subunit beta [ *Homo sapiens* (human) ]** [Download Datasets](#)

Gene ID: 3043, updated on 5-Aug-2024

**Summary**

**Official Symbol** HBB provided by [HGNC](#)  
**Official Full Name** hemoglobin subunit beta provided by [HGNC](#)  
**Primary source** [HGNC:HGNC:4827](#)  
**See related** [Ensembl:ENSG00000244734](#) [MIM:141900](#); [AllianceGenome:HGNC:4827](#)  
**Gene type** protein coding  
**RefSeq status** REVIEWED  
**Organism** [Homo sapiens](#)  
**Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo  
**Also known as** ECT6; CD113t-C; beta-globin  
**Summary** The alpha (HBA) and beta (HBB) loci determine the structure of the 2 types of polypeptide chains in adult hemoglobin, Hb A. The normal adult hemoglobin tetramer consists of two alpha chains and two beta chains. Mutant beta globin causes sickle cell anemia. Absence of beta chain causes beta-zero-thalassemia. Reduced amounts of detectable beta globin causes beta-plus-thalassemia. The order of the genes in the beta-globin cluster is 5'-epsilon -- gamma-G -- gamma-A -- delta -- beta--3'. [provided by RefSeq, Jul 2008]  
**Orthologs** [all](#)  
[NEW](#) Try the new [Gene table](#)  
Try the new [Transcript table](#)

**Genomic context**

The page that returns:

### HBB - hemoglobin subunit beta

The alpha (HBA) and beta (HBB) loci determine the structure of the 2 types of polypeptide chains in adult hemoglobin, Hb A. The normal adult hemoglobin tetramer consists of two alpha chains and two beta chains. Mutant beta globin causes sickle cell anemia. Absence of beta chain causes beta-zero-thalassemia. Reduced amounts of detectable beta globin causes beta-plus-thalassemia. The order of the genes in the beta-globin cluster is 5'-epsilon--gamma-G--gamma-A--delta--beta--3'. [provided by RefSeq, Jul 2008]

[Genes similar to HBB](#)

#### NCBI Orthologs [How was this calculated?](#)

0 items

16 genes for: placentals (*Eutheria*)

[Add to cart](#) [Protein alignment](#) [Download](#)

SEARCH THE TAXONOMY TREE

Enter taxonomic name

placentals

rabbits & hares

rodents

insectivores

flying lemurs

primates

armadillos and others

☐ 0 selected

Species	Gene	Architecture	aa	
<input type="checkbox"/> <i>Homo sapiens</i> human	<a href="#">HBB</a> hemoglobin subunit beta		147	
<input type="checkbox"/> <i>Macaca mulatta</i> Rhesus monkey	<a href="#">HBB</a> hemoglobin subunit beta		147	
<input type="checkbox"/> <i>Pongo abelii</i> Sumatran orangutan	<a href="#">HBB</a> hemoglobin subunit beta		147	

Select Homo sapiens, Rhesus Monkey, Sumatran orangutan, and Long-tailed chinchilla

Species	Gene	Architecture	aa	
<input checked="" type="checkbox"/> <i>Homo sapiens</i> human	<a href="#">HBB</a> hemoglobin subunit beta		147	
<input checked="" type="checkbox"/> <i>Macaca mulatta</i> Rhesus monkey	<a href="#">HBB</a> hemoglobin subunit beta		147	
<input checked="" type="checkbox"/> <i>Pongo abelii</i> Sumatran orangutan	<a href="#">HBB</a> hemoglobin subunit beta		147	
<input type="checkbox"/> <i>Choloepus didactylus</i> southern two-toed sloth	<a href="#">HBB</a> hemoglobin subunit beta		147	
<input checked="" type="checkbox"/> <i>Chinchilla lanigera</i> long-tailed chinchilla	<a href="#">Hbb</a> hemoglobin subunit beta		147	

Now click on the “Protein alignment” button in the center of the page.

16 genes for: placentals (*Eutheria*)

The screenshot shows the COBALT web interface. At the top, there are three buttons: "Add to cart", "Protein alignment" (which is highlighted with a dashed border and a callout arrow), and "Download". Below these buttons, there is a table with a "Species" column. The first row is checked and labeled "Homo sapiens human". A modal dialog titled "Protein alignment" is open, showing two radio button options: "one sequence per gene (4)" (which is selected) and "all sequences per gene (4)". At the bottom of the modal is a blue "Align" button. In the background, a table shows "4 selected" items.

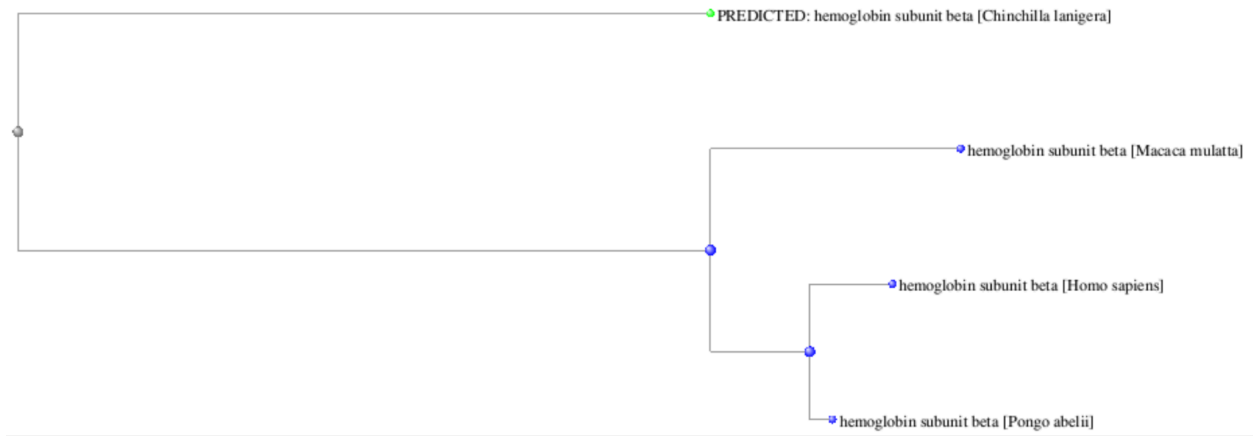
And click the “Align” blue button

The screenshot shows the COBALT web interface. The header includes the NIH logo and "U.S. National Library of Medicine" on the left, and the NCBI logo and "National Center for Biotechnology Information" on the right. The main heading is "COBALT" with the subtitle "Constraint-based Multiple Alignment Tool". Below this, a blue bar contains the text "COBALT computes a multiple protein sequence alignment using conserved domain and local sequence information". The "Enter Query Sequences" section has a text input field containing four protein accessions: NP\_000509.1, NP\_001157900.1, XP\_002822173.1, and XP\_005380133.1. There is a "Clear" link next to the input field. Below the input field, there is a section for "Or, upload FASTA file" with a "Browse..." button and the text "No file selected.". There is also a "Job Title" input field. At the bottom, there is a blue "Align" button and a checkbox labeled "Show results in a new window".

And click the “Align” blue button at the bottom.



Here is the phylogenetic tree for the species you selected based on the HBB genetic sequences in each organism.



Remember that

1. “*Macaca mulatta*” is the Rhesus monkey
2. “*Pongo abelii*” is the Sumatran orangutan
3. “*Chinchilla lanigera*” is the Long-tailed chinchilla



### **Discussion Questions**

1. Which 2 species are most related according to this tree?
2. Explain why you think that this tool (COBALT) inferred that these 2 species are most related.
3. Evaluate the tree produced by COBALT.
4. Indicate which branches you think are correct and which are incorrect?
5. Based on your understanding, use the space below to draw a phylogenetic tree that contains the correct placement of the species.