

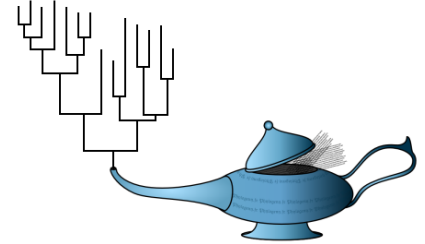
# RESOURCE #2: Using the Website Phylogeny.fr

[www.phylogeny.fr](http://www.phylogeny.fr)

1) **What is Phylogeny.fr?** A free, simple-to-use web service dedicated to reconstructing and analyzing phylogenetic relationships with molecular sequences.

2) **How do I use Phylogeny.fr?**

a) For our purposes, you will be using the “One Click” option of phylogenetic analysis.



→ Scroll down below the genie lamp and select “One Click”

## Phylogeny analysis

### “One Click”

Paste your set of sequences and let the software make decisions on your behalf (Each step is optimized for your data).

### “Advanced”

Manually set parameters for the various steps.

### “A la Carte”

Create your own phylogeny workflow using more programs available.

b) You may title your work, “**Phylogenetic Tree w/Molecular Data**” in the analysis box here:

1. Overview    2. Data & Settings

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Name of the analysis (optional):

c) The file you created that contains the DNA sequences for Hemoglobin alpha is known as a FASTA file. You will now use this FASTA file to build a phylogenetic tree.

→ **Copy all of the data in your FASTA file, starting with the > symbol and scientific name of your first species, and ending with the last nucleotide of your last species.**

→ **Paste all of the data in the box and click SUBMIT.**

Upload your set of sequences in FASTA, EMBL or NEXUS format from a file:  
 No file chosen  
Or paste it here (load example of sequences):

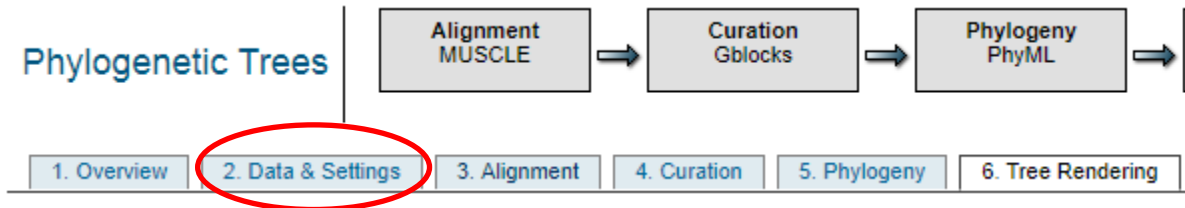
d) Wait patiently. Each nucleotide essentially represents a character (like in the matrix of the aliens) and the program runs an algorithm to determine the maximum likelihood tree.

e) Draw the phylogenetic tree in **TREE BOX B**.

# Where does the Discovery Species fit in?

See your student guide and **RESOURCE #2** for further details.

Go back to your existing Phylogeny.fr window and click **Data & Settings**



f) In the box, underneath the last DNA Sequence, skip a space and add a > and the name of the discovery species.

For example: > Hedgehog *Erinaceus europaeus*

g) Using Resource #1, **SEARCH** the DNA sequence for Hemoglobin alpha of the discovery species, and then **PASTE** the DNA sequence underneath the last species in your original list.

```
CCAACCCATCGCCAGCCC TCCGACAGCGAGCAGCCAAATGAGATGAAATAAAACTGTGTGLATTGTGCTCCAG
>Hedgehog Erinaceus europaeus
TGAGTCCCAGCACTTCTGATCCAACAGAGACTCAGAAAGAACTCACCATGGTGTCTGCAACTGACAAG
GCCAACGTCAAGACTTTCTGGGGCAAGCTCGGCGGCCATGGCGGGCAGTATGGCGGGCAGGCTCTGGACA
GAATGTTCCAGGCCACCCACCAAGACCTACTTCCCCCACTTCGACCTGAACCCGGGCTCCGCTCA
GGTCAAAGGCCATGGCAAGAAGGTGGCAGATGCTCTGACCACTGCTGTGAACAACCTGGACGACGTTCCA
GGAGCCCTGTCTGCCCTGAGCGACCTGCACGCGCACAAGCTGCGTGTGGACCCCGTCAACTTCAAGCTCC
TGAGCCACTGTCTGCTGGTGACCCCTGGCCCTCCACCACCCTGCAGACTTCACCCCGCGGTGCACGCCTC
CCTGGACAAGTTCCTGGCTACAGTGGCCACTGTGCTGACCTCCAAGTACCGTTAAGCCACAGCCTGTCCA
GTCCCTGTCTGCAGGGCGTCCCCAACCTCTCAATAAAGTCTGATGGGCAGCA
```

Clear

h) Click **SUBMIT** and view the altered phylogenetic tree.

i) Copy the tree into the box for **TREE C** and answer the Analysis Questions.