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# 🌐 Lab 2 Notebook

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## Abstract

## Prelab

1. While looking at a gene on the genome browser, decide which track is best to use in order to see how well conserved a nucleotide sequence is between multiple species.
2. What is an E-value? What is an acceptable value?
3. Which tools should you use if you are given a protein sequence, composed of amino acids, and you want to find which species it belongs to?
4. Is there a track on the human genome browser, version hg19, used to find CRISPR/Cas9 target sites? If yes, give the name of the track and give a description of what it does in your own words.
5. Look up this amino acid sequence on Blastp. Give the protein name and species name of the top 5 searches. What do they have in common? Are any of these species' genomes on the UCSC genome browser? If so which one?

```
MEKFLFYLFLIGIAVRAQICPKRCVCQILSPNLATLCAKKGLLFVPPNIDRRTVELRLADNFVTNIKRKDFANMTSLVDLTLSRNTISFITPHAFADLRNL
RALHLNSNRLTKITNDMFSGLSNLHHLILNNNQLTLISSTAFDDVFALEELDLSYNNLETIPWDAVEKMVSLHTLSLDHNMIDNIPKGTFSHLHKMTRLDV
```

TSNKLQKLPPDPLFQRAQVLATSGIISPSTFALSFGGNPLHCNCELLWLRRLSREDDLETCASPALLTGRYFWSIPEEEFLCEPPLITRHTHEMRVLEGQR
ATLRCKARGDPEPAIHWISPEGKLISNATRSLVYDNGTLDILITTVKDTGAFTCIASNPAGEATQTVDLHIIKLPHLLNSTNHIHEPDPGSSDISTSTKSG
SNASSSNGDTKMSQDKIVVAEATSSTALLKFNFQRNIPGIRMFQIQYNGTYDDTLVYRMIPPTSKTFLVNNLASGT

## Lab results

1.
2.
3.

## Post lab

Now that you have familiarized yourself with these tools, write a short report on a gene of interest to you using the genome browser and BLAST. You must use information from at least 3 different tracks on the Genome browser, give any relevant information about the gene, and if it causes disease. Perform a BLAST search with at least 3 of the online tools.

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