Name:

Date:

Group:

BLAST: Access to biomedical and genomic information

BLAST stands for "Basic Local Alignment Search Tool". It is a web based program to find regions of similarities between sequences. The program compares nucleotide or protein sequences to sequence databases--genetic information already uploaded to the web. The goal of the program is to calculate statistical significance of matches between any given nucleotide sequence that we feed into it, and the sequences mapped and stored into BLAST's databases:

"BLAST can be used to infer functional and evolutionary relationships between sequences as well as help identify members of gene families."

This lab will be done in groups of 2 to 3 members, one computer per group.

Instructions:

1. Type "BLAST' on the Google search bar
2. Click the first link that appears.
3. Click on the link that says "Human." (This is your database for all the genomic information that has been uploaded to BLAST). Open the page on a new tab. Keep this page open for later use.
4. On a second tab, access the following address: www.uniprot.org/uniprot/P29794 (This address takes you to a database that has has genetic information that corresponds to proteins).
5. In the "query box", right at the top of the uniprot page, type the scientific name of any organism you wish to compare its protein sequence to the human BLAST database.
6. Your query will result in a list of genetic information that codes for proteins. You will access any link on the column labeled as "Entry":

Entry
H2RA81
K7BRX1
Q30934
Q28797
H2R0Y5
K7BTX4
V9GZE7
V9GZJ7
Q5D7J1

Once you've accessed the "Entry" link, click the "fasta" box, one of the orange boxes displayed like this: text xml rdf/xml gff fasta. Copy the protein sequence (Each letter stands for an amino acid sequence. Important: Copy ONLY the capitalized letters).

Now, with the amino acid sequence properly copied, you can access the page opened in step 3.

In this step you will do the actual research using the logarithms that will tell you wether the amino acid sequence you found has any alignment (simillarities) with human amino acid sequences stored on this database.

- Paste the copied sequence where it says "Enter query sequence". (Notice that there are a series of tabs above the query box. For this query you need to be on the "blastp" tab).
- Go to the bottom of the page and click BLAST. Wait for your teacher's instructions.