Introduction to BLAST using Human Leptin Answer Sheet

Name:

Faculty:

Course Name:

## Exercise Questions

1. Based on the information on this page, how does *leptin* control feeding?

2. According to these search results, on which chromosome is the *leptin* gene located?

3. How do you know that the leptin gene is on the + strand of the chromosome it’s located on?

4. The picture depicts two annotated transcripts (XM\_005250340.5 and NM\_000230.3). What is the difference between the RefSeq record that begins with the XM\_ prefix and the record that begins with the NM\_ prefix? Both mRNA records have 4 green boxes, 2 light green in color (1 on each end) and 2 dark green. What do you think each of those boxes refers to?

5. Why do you think you want the protein sequence as opposed to the nucleotide sequence?

6. What is the relationship between V and M that warranted a + designation?

7. What is the percent identity and percent positives (aka percent similarity) of the *Bubalus bubalis* leptin sequence compared to the human sequence?

8. How many hits came out of this search? Are all of them significant matches? Does the BLAST result support the hypothesis that chimps have a homolog of the human *leptin* gene?

9. Did you obtain matches from this search? Are they significant matches? How do you know? Does this data support your hypothesis about the presence of a leptin homolog in chimps?

## Summative Questions

1. List three types of information that one can access using NCBI databases

2. What is difference between percent identity and percent similarity in the output of a BLAST search?

3. In your own words, state how the output of a BLAST search can support the hypothesis that two organisms contain homologs of the same gene?