

We are going to explore the HIV genome.

- Go to NCBI at: <u>http://www.ncbi.nlm.nih.gov/projects/gorf</u>. We are going to use "ORF finder" to locate the opening reading frames of HIV.
- Get the Homo sapiens genomic sequence "hiv_sequence.txt" from www.cs.sjsu.edu/faculty/khuri/Rabat_2013
- Paste the sequence in the ORF window at NCBI.
- Hit the "OrfFind" button.

On the resulting page from NCBI:

• Change the sensitivity from 100 to 300 and click on "Redraw".

1) How many ORFs are reported by the ORF finder with sensitivity 300? _____.

2) Write down the exact start and end points for each predicted ORF.

| Frame | Starting Position | End Position | Length |
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3) Note that by clicking on the bars that represent the individual ORFs, we get the sequence of that reading frame including its translation.

- Click on the longest ORF. Keep "blastp" under "Program" in the new page.
- Choose "swissprot" under "Databases" and click on "BLAST".
- Accept all the default values from the new page and click on "View report".

Examine the result and identify the name of the gene.

• Label the appropriate ORF in the diagram with the name of the gene you found. In other words, write the name of the ORF (gene) on the following diagram.

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4) Repeat the process described in part 3 with all the ORFs (genes) that are on the positive strand.

5) What organism does the "hiv_sequence.txt" most probably come from? Why?

6) Consult the second page of the hands-on exercise.

The original source is at: http://hiv-web.lanl.gov/content/immunology/pdf/2000/intro/GenomeMaps.pdf

The diagram has 3 genomes.

Based on your findings above, which genome (HIV-1, HIV-2, SIV) are you working with?

7) In parts 1 thru 4 you found some ORFs that encode genes. Are they all in "Genome Maps"? _____

8) Which genes did you miss? In other words, which genes are in "Genome Maps" and not in the diagram you completed in parts 3 and 4? Just name the 2 or 3 large genes you missed.

9) Explain how you can find the genes (ORFs) you missed.

10) Name two genes on the positive strand that overlap.