**Lab sheet#3**

**Practicing ENSEMBL**

**Objective:**

* To know how to brows different data in ENSEMBL.

**Using ENSEMBL genome browser, search for the human *TAC1* gene to answer the following questions:**

1. What is the ENSEMBL identifier of the gene?
2. What is the full name of this gene?
3. On which chromosome is this gene located? And show the graphical position of the gene on the chromosome (region in details).
4. Is the gene transcribed from the forward or from the reverse strand of the genome assembly?
5. How many transcripts (splice variants) has ENSEMBL annotated for it?
6. Which transcript has a CCDS record associated with it?
7. Show how each variant differ from the other by showing the transcript diagram.
8. What is the function of TAC1?
9. Are there any diseases associated with variants in this gene?
10. Retrieve the TAC1 gene sequence.
11. Find two SNPs associated with the gene.
12. What is the longest transcript, and how long is the protein it encodes? Retrieve the amino acid sequence.
13. How many exons does it have?
14. Are any of the exons completely or partially translated?
15. Retrieve the sequence of the transcript.
16. Is it possible to monitor the expression of TAC1-201 using the Illumina microarray?

**Exercise:**

**3**

**Search for the human *HBB* gene:**

* On which chromosome is this gene located?
* How many transcripts has ENSEMBL annotated for it?
* How many completely translated exons does HBB-206 have?
* Retrieve the sequence of HBB-206 transcript.
* Find two diseases associated with HBB gene variants in human.