#### 2021-22

# BIO F242 Introduction to Bioinformatics

# Experiment - 4

Name: Suchismita Tripathy ID: 2019A7PS0554P

Gene Name : HUS1 Checkpoint Clamp Component (HUS1)

 $transcript\ variant\ X1$ 

Organism : Theropithecus gelada Accession Number :  $XM_025380797.1$ 

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### 1 Aim

To predict the number of Open Reading Frames (ORF) present in your gene sequence along with maximum length of ORF and its protein sequence in all possible frames using ORF Finder.

# 2 Materials Required

ORF Finder, gene sequence of Theropithecus gelada HUS1 Checkpoint Clamp Component (HUS1) transcript variant X1

#### 3 Procedure

- 1. Open the home page of NCBI and retrieve the Theropithecus gelada HUS1 Checkpoint Clamp Component (HUS1) transcript variant X1 gene sequence in Fasta format having "Accession No" (XM\_025380797.1).
- 2. Open the home page of ORF Finder (https://www.ncbi.nlm.nih.gov/orffinder/)
- 3. Select the parameters such as like ORF length, genetic code, type of start codon and nested ORFs etc.
- 4. Take appropriate screenshots of observations.
- 5. Analyze the results.

### 4 Observations

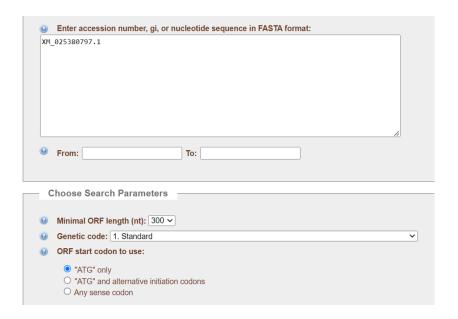


Figure 1: ORF Finder Input Screenshot

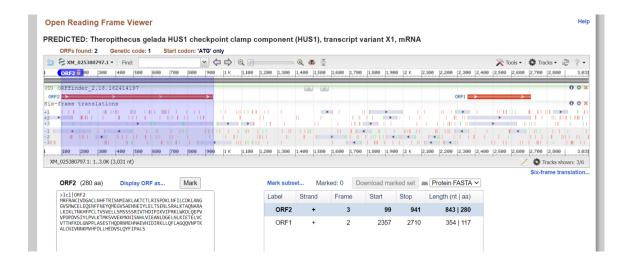


Figure 2: ORF Finder Output Screenshot 1/3

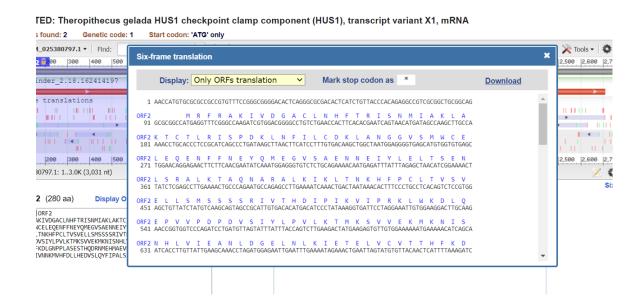


Figure 3: ORF Finder Output Screenshot 2/3



Figure 4: ORF Finder Output Screenshot 3/3

# 5 Inferences

The given gene sequence of Theropithecus gelada HUS1 Checkpoint Clamp Component (HUS1) transcript variant X1 consists of :

2 Number of ORFs

The ORF that has Maximum Length ORF2

The length of ORF that has Maximum Length 843

The location of START Codon in Maximum Length of ORF 99

The location of STOP Codon in Maximum Length of ORF 941

The Direction of STRAND in Maximum Length of ORF +

The Length of Amino Acid encoded by BIGGEST ORF 280 amino acids