2021-22

BIO F242
Introduction to Bioinformatics

Experiment - 6

Name : Suchismita Tripathy
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Gene Name : HUS1 Checkpoint Clamp Component (HUS1)
transcript variant X1
Organism : Theropithecus gelada
Accession Number : XM_025380797.1

28 March, 2022

1 Aim

To perform pairwise sequence alignment of Theropithecus gelada HUS1 Checkpoint Clamp Component (HUS1) transcript variant X1 gene and protein sequence using BLASTn and BLASTp to find out five closely related organisms (either Eukaryotes and Prokaryotes)

2 Materials Required

BLASTn, BLASTp, gene sequence of Theropithecus gelada HUS1 Checkpoint Clamp Component (HUS1) transcript variant X1

3 Procedure

1. Retrieve the genes and protein sequence in FASTA format from NCBI and ORF results respectively.

2. Open the web page of BLAST under NCBI.

3. Paste the appropriate sequence (Nucleotide for BLASTn and Protein for BLASTp) in a given space or upload your respective sequence for which you want to perform PSA.

4. Select appropriate parameters like word size, threshold value, output format, Gap open, and extension penalty in respective tools.

5. Take relevant screenshots of observations.

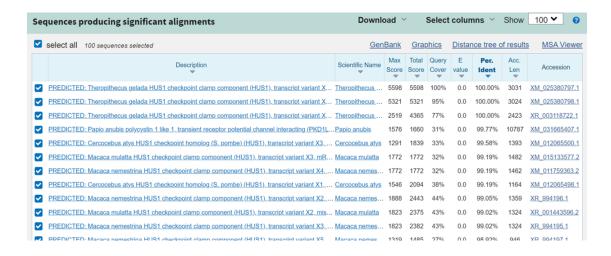6. Analyze the results.

4 Observations

4.1 BLASTn

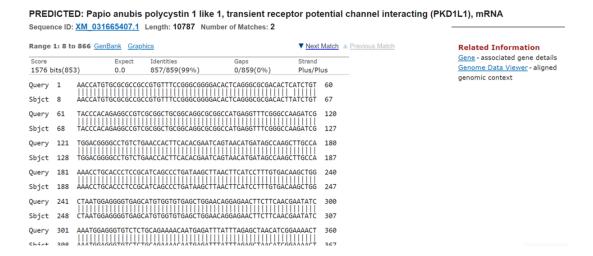Figure 1: Descriptions

Figure 2: Graphic Summary

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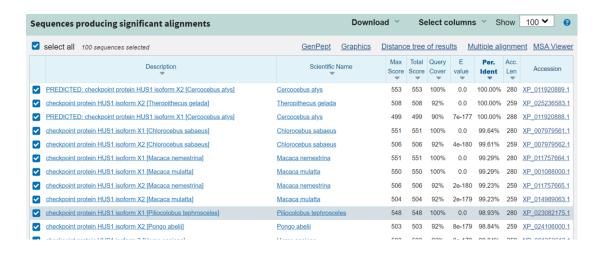Figure 3: Alignment with sequence showing highest similarity
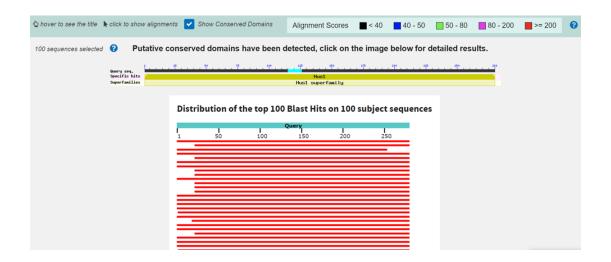
4.2 BLASTp

Figure 4: Descriptions

Figure 5: Graphic Summary

Figure 6: Alignment with sequence showing highest similarity

5 Inferences

5.1 BLASTn

The Pairwise Sequence Alignment (PSA) using BLASTn of Theropithecus gelada HUS1 Checkpoint Clamp Component (HUS1) transcript variant X1

nucleotide sequence shows maximum alignment with **Papio anubis having E-value 0 and percentage similarity of 99.77%**, respectively. The top five organisms that are showing maximum similarity with Theropithecus gelada HUS1 Checkpoint Clamp Component (HUS1) transcript variant X1 are:

1. **Papio anubis polycystin 1 like 1, transient receptor potential channel interacting (PKD1L1), mRNA** having E-value 0.0 and percentage similarity 99.77% respectively

2. **Cercocebus atys HUS1 checkpoint homolog (S. pombe) (HUS1), transcript variant X3, mRNA** having E-value 0.0 and percentage similarity 99.58% respectively

3. **Macaca mulatta HUS1 checkpoint clamp component (HUS1), transcript variant X3, mRNA** having E-value 0.0 and percentage similarity 99.19% respectively

4. **Macaca nemestrina HUS1 checkpoint clamp component (HUS1), transcript variant X4, mRNA** having E-value 0.0 and percentage similarity 99.19% respectively

5. **Cercocebus atys HUS1 checkpoint homolog (S. pombe) (HUS1), transcript variant X1, mRNA** having E-value 0.0 and percentage similarity 99.19% respectively

5.2   BLASTp

The Pairwise Sequence Alignment (PSA) using BLASTp of Theropithecus gelada HUS1 Checkpoint Clamp Component (HUS1) transcript variant X1 amino acid sequence shows maximum alignment with checkpoint protein HUS1 isoform X2 [Cercocebus atys] having E-value 0 and percentage similarity of 100%, respectively. The top five organisms that are showing maximum similarity with Theropithecus gelada HUS1 Checkpoint Clamp Component (HUS1) transcript variant X1 protein sequence are:

1. **checkpoint protein HUS1 isoform X2 [Cercocebus atys]** having E-value 0.0 and percentage similarity 100% respectively

2. **checkpoint protein HUS1 isoform X1 [Cercocebus atys]** having E-value 7e-177 and percentage similarity 100% respectively

3. **checkpoint protein HUS1 isoform X1 [Chlorocebus sabaeus]** having E-value 0.0 and percentage similarity 99.64% respectively

4. **checkpoint protein HUS1 isoform X2 [Chlorocebus sabaeus]** having E-value <u>4e-180</u> and percentage similarity <u>99.61%</u> respectively

5. **checkpoint protein HUS1 isoform X1 [Macaca nemestrina]** having E-value <u>0.0</u> and percentage similarity <u>99.29%</u> respectively