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BIO 294 Genetics

April 22, 2024

**Genome Assignment**

**Chromosome Maps:**

1. Chromosome 3
2. 1900 genes
3. 200 million base pairs
4. MLH1 colon cancer gene
5. The MLH1 genes are homologous to enzymes in the DNA mismatch repair pathway. This gene provides instructions for making proteins that function in DNA repair.

**Introduction to Nucleotide BLAST:**

1. Homo sapiens CFTR (CFTR) gene, partial cds
2. The encoded protein functions as a chloride channel and controls ion and water secretion and absorption in epithelial cells.
3. Mutations of this gene cause cystic fibrosis.
4. Chromosome 7
5. Gorilla gorilla gorilla
6. lowland gorilla
7. No, this does not surprise me because the human species and gorilla species are closely related and have similar genetic characteristics.
8. Question 13 parts
   1. Nomascus leucogenys
   2. White-cheeked gibbon
   3. No there were no gaps (0%)
9. Genetic sequence alignment accounts for genetic mutations that have occurred due to insertions or deletions in a genetic sequence.
10. NM\_145556 is a gene that functions in protein coding. Is responsible for enabling RNA polymerase II cis-regulatory region sequence-specific DNA binding activity and pre-mRNA intronic binding activity.
11. NM\_013444 is a gene that functions in protein coding. This gene is specifically responsible for encoding ubiquitin-like protein (ubiquilin).
12. NM\_001010850 is a gene involved in protein coding. This gene is responsible for encoding a multifunctional protein component of the heterogeneous nuclear ribonucleoprotein (hnRNP) complex.
13. KJ174530 is a gene involved in protein coding. This gene functions in encoding a specific protein that binds copper and zinc ions and destroys free superoxide radicals in the body.
14. Lou Gherigs disease
15. Genbank is a genetic sequence database, which includes an annotated collection of all public DNA sequences.

**Introduction to Protein BLAST:**

1. cDNA (copy/complementary DNA) is synthetic DNA that is complementary to the mRNA transcribed from the gene. cDNA is synthesized by reverse transcription of a RNA molecule.
2. Beta-globin (Homo sapiens)
3. No, I do not see any noticeable differences between the two amino acid sequences other than their lengths differing by one.
4. Only difference I observed was the length. Sequence 1 length was 805 and sequence 2 length was 806.
5. No, there were no gaps in the sequence alignment (0%).
6. FGFR3
7. This gene functions in protein coding. It is responsible for encoding FGFR3.
8. Mutations of this gene can cause craniosynostosis and multiple types of skeletal dysplasia.
9. NIH: National Institutes of Health - is overseen by the U.S. department of health and human services.

NLM: National Library of Medicine - is overseen by the U.S. federal government and is an institute within the NIH.

NCBI: National Center for Biotechnology Information - is a branch of the NIH and is overseen by the federal government.

HHS: U.S. Department of Human and Health Services - is an executive branch department of the federal government which is overseen by the federal government.

NIH, NLM, NCBI, and HHS are all overseen by the federal government. NLM and NCBI are branches or institutes of the NIH, which is directly overseen by the HHS.

1. One positive thing I encountered while completing this assignment was becoming more familiar with the internet-based genes and diseases website. One negative I experienced while completing this assignment was that the website could be very slow and difficult to load in an effective manner.

**Works Cited**

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