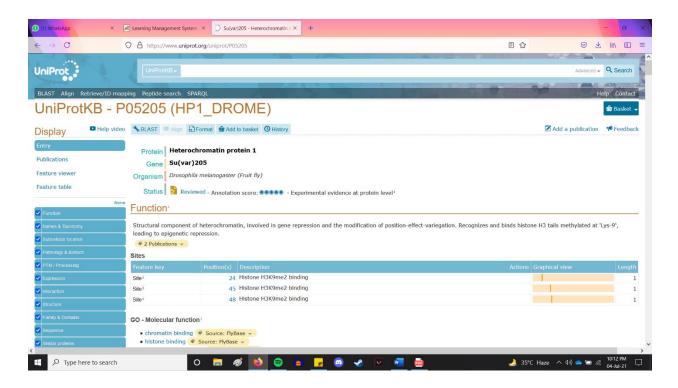
Hamza Akmal

24100232

Assignment 3

BIO 101

TA: AJ



Answer 1:

- a) 618 bp
- b) 5 exons, 4 introns

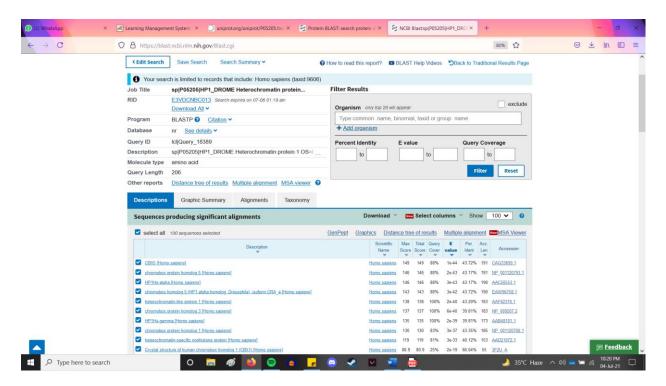
All orientations in 5' to 3'

- E1-CGC...TAG
- E2-TAT...AAG
- E3-GTG...GAG
- E4- GAG...CAG
- E5- CGC...TTC
- I1- GTG...TTC
- I2- GTG...CAG
- I3- GTA...TAG
- I4- GTA...AAG

- c) 2. 992 bp and 1109 bp
- d) It is a key structural part of heterochromatin and is pivotal in the repression of genes and modification of position-effect-variegation. It binds with the Histone H3 tail methylated at Lys9 and causes epigenetic repression.

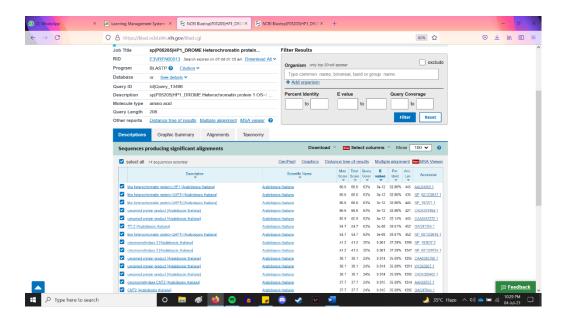
There are chromo 1 and Chromo 2 domains of length 59 present in it.

e) Homo Sapiens blast:



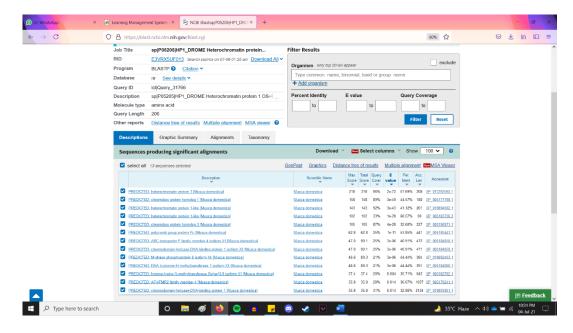
We have a high score, very low e-value and decently high query coverage for the top few hits which tells us that the match of the protein is not due to chance and that the sequences are alike.

Arabidopsis Thaliana Blast:



We have a low score and very low query coverage for the top few hits which tells us that the match of the protein is incomplete and we are probably not looking at the same sequence. There may be a lot of mutation in this protein sequence.

Musca Domestica:



There is a match with only 3-4 hits that have a high score, high query coverage and low e-value which tells us that the protein is possibly matching the sequences in those protein sequences to a greater degree. In the other hits, the protein has a very low score and even lesser query coverage which tells us that they are probably not similar proteins.

We used X-Ray crystallography to get the structure of this protein. Its assembly composition is heterodimer.

Answer 2:

a) HENRYCAVILL HARRYSTYLES 8-1057-10-1-2-3-2

ModBaseⁱ Search.

Score: 14

b) CHRISPRATT CHRISEVANS 98544-1-3401

Score: 31

Citations:

For Blast results:

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

For function and domain results:

"Specificity of the HP1 chromo domain for the methylated N-terminus of histone H3." Jacobs S.A., Taverna S.D., Zhang Y., Briggs S.D., Li J., Eissenberg J.C., Allis C.D., Khorasanizadeh S.

EMBO J. 20:5232-5241(2001) [PubMed] [Europe PMC] [Abstract]

Cited for: FUNCTION, MUTAGENESIS OF VAL-26.

"Structure of HP1 chromodomain bound to a lysine 9-methylated histone H3 tail." Jacobs S.A., Khorasanizadeh S.

Science 295:2080-2083(2002) [PubMed] [Europe PMC] [Abstract]

Cited for: X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 17-76, FUNCTION.

For protein structure:

https://www.ebi.ac.uk/pdbe/entry/pdb/1KNA