BIF401-Bioinformatics

Assignment 2,Spring 2023

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Inbox for LMS activities on Paid Basis

Due Date July 17

یہ صرف ایک نمونہ حل ہے۔

ہر طالب علم کو انسانوں کا مختلف پروٹین چننا ہوگا اور پھر یہ تمام عمل شروع سے آخر تک کرنا ہوگا۔

اگر آپ یہ استعمال کرتے ہیں، تو آپ کو نمبر نہیں ملیں گے کیونکہ ہر طالب علم کو مختلف پروٹین چن کر اس طریقہ کار کے مطابق کام کرنا ہوگا۔

Step 1: Selecting a Protein Sequence

1. Go to the NCBI database at https://www.ncbi.nlm.nih.gov/.
2. In the search bar, type the name of the protein you're interested in. For example, let's say we're interested in the protein "Hemoglobin, alpha 1". Type that into the search bar and hit enter.
3. Click on the first result under the "Protein" category.
4. On this page, you will find the information you need: the sequence is displayed under the "SEQUENCE" section, the accession number is listed at the top of the page, the sequence length is displayed next to the sequence, and the function of the protein is usually described in the "General protein information" section.

a) **Protein Selected**

Hemoglobin Alpha 1

b) Accession :

AAB59408

c)Query Sequence :

```
>AAB59408.1 hemoglobin alpha 1 [Homo sapiens]
MVLSPADKTNVKAAWGKVGAHAGEYGAEALERMFLSFPTTKTYFPHFDLSHGSAQVKGHGKKVADALTNA
VAHVDDMPNALSALSDLHAHKLRVDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVSTVLTSK
YR
```

d)Sequence Length :

142

e)Functions of Selected Protein (Hemoglobin Alpha1)

1. Oxygen Binding: Hemoglobin Alpha 1 combines with three other subunits (two Beta and two Alpha) to form a functional hemoglobin molecule. It binds and carries oxygen from the lungs to tissues throughout the body, ensuring an adequate oxygen supply for cellular respiration.

2. Carbon Dioxide Transport: Hemoglobin Alpha 1 also assists in carrying carbon dioxide, a waste product of cellular metabolism, from the tissues back to the lungs, where it is exhaled.

3. pH Regulation: Hemoglobin Alpha 1 helps maintain the pH balance in the blood by binding to hydrogen ions (H+). This buffering capacity helps prevent significant changes in blood pH, contributing to overall physiological homeostasis.

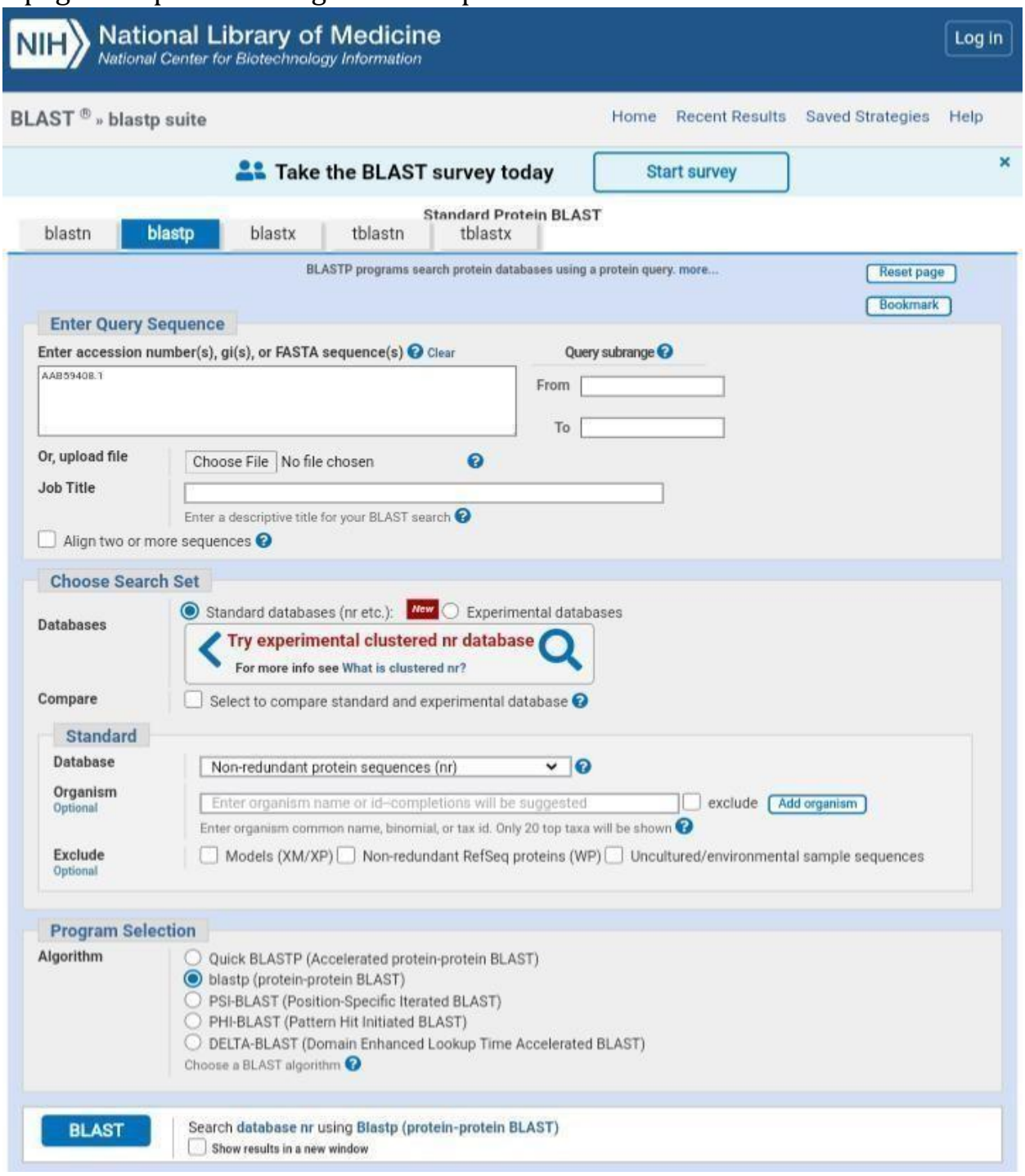
4. Allosteric Regulation: Hemoglobin Alpha 1 participates in allosteric interactions with other hemoglobin subunits, affecting its affinity for oxygen. This allows hemoglobin to adapt to varying oxygen concentrations, facilitating efficient oxygen loading and unloading in different tissues.

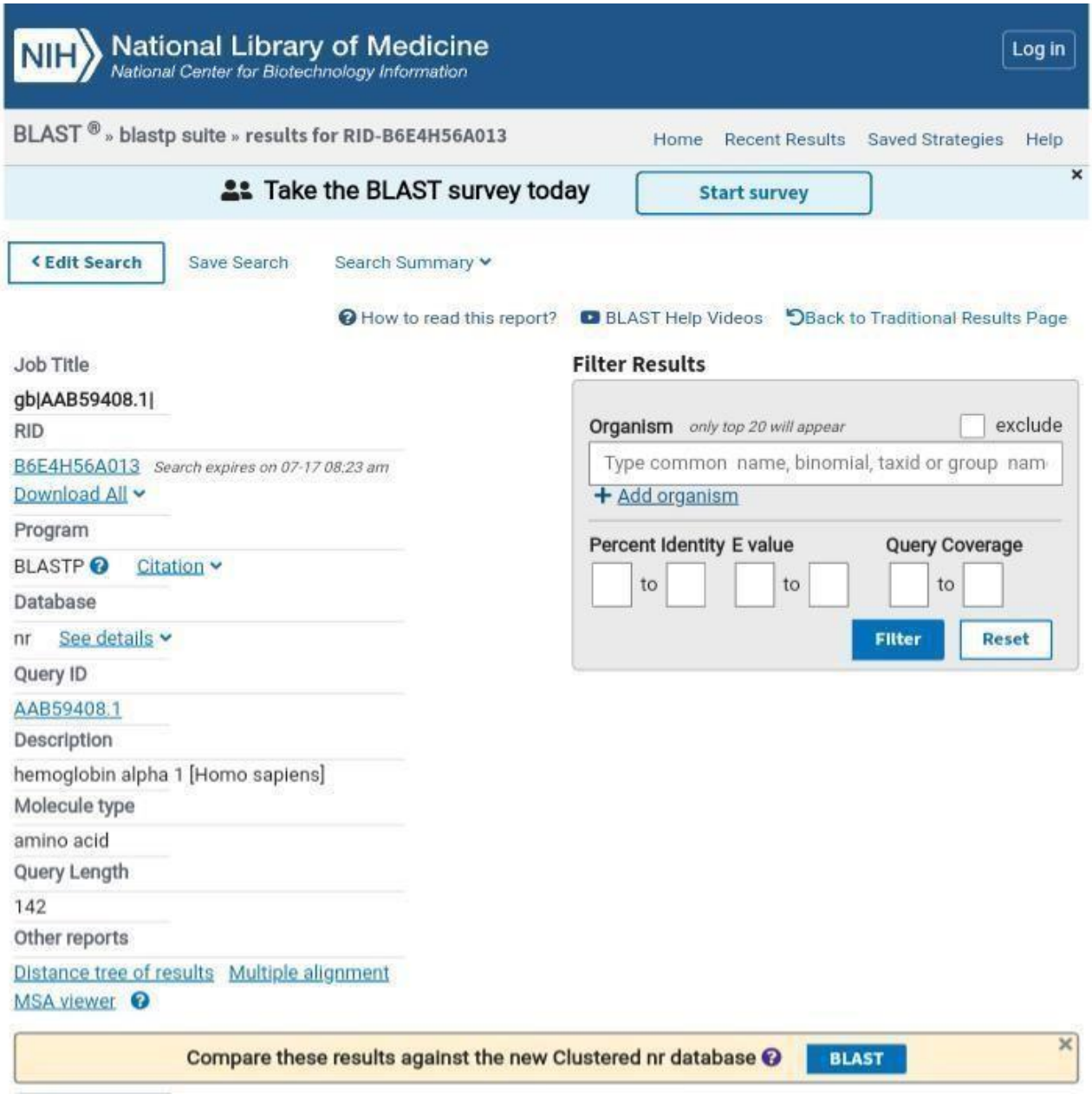
5. Genetic Disorders: Mutations in the Hemoglobin Alpha 1 gene can result in hemoglobinopathies, such as alpha-thalassemia or Hb Bart's hydrops fetalis syndrome, which affect the production or structure of hemoglobin, leading to various health complications.

Step 2: Performing a BLAST Search

1. Go to the BLAST server at NCBI: https://blast.ncbi.nlm.nih.gov/Blast.cgi.
2. Select "Protein BLAST".
3. Paste the protein sequence you obtained in Step 1 into the "Enter Query Sequence" box.
4. Click the "BLAST" button at the bottom of the page.

5. Wait for the results to load. Once they do, you can take a screenshot of the page to capture the alignment output.





Step 3: Multiple Sequence Alignment with ClustalW

1. Go to the ClustalW web interface at https://www.genome.jp/toolsbin/clustalw.

2. Paste the protein sequences of the same gene from 5 different species into the box. You can obtain these sequences from the NCBI database, just like you did in Step 1.

3. Select "Phylip" as the output format.

4. Click the "Run" button.

5. Once the results load, you can capture them for your document.

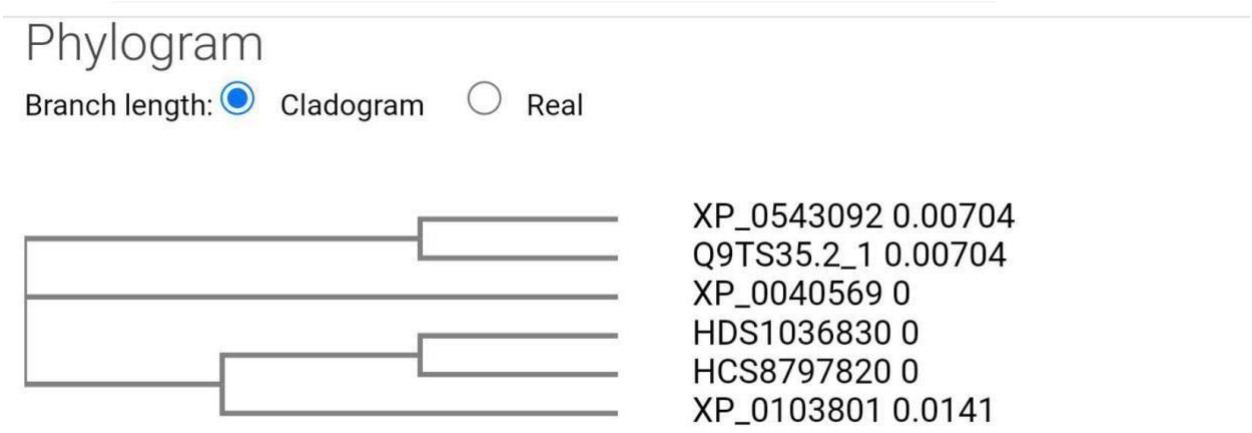
clustalw.phy

```
     6    142
XP_0543092 MVLSPADKTN VKTAWGKVGA HAGDYGAEAL ERMFLSFPTT KTYFPHFDLS
Q9TS35.2_1 MVLSPADKTN VKAAWGKVGA HAGDYGAEAL ERMFLSFPTT KTYFPHFDLS
XP_0040569 MVLSPADKTN VKAAWGKVGA HAGDYGAEAL ERMFLSFPTT KTYFPHFDLS
HDS1036830 MVLSPADKTN VKAAWGKVGA HAGEYGAEAL ERMFLSFPTT KTYFPHFDLS
HCS8797820 MVLSPADKTN VKAAWGKVGA HAGEYGAEAL ERMFLSFPTT KTYFPHFDLS  XP_0103801
MVLSPADKTN VKAAWGKVGG HGGEYGAEAL ERMFLSFPTT KTYFPHFDLS
HGSAQVKGHG KKVADALTNA VAHVDDMPNA LSALSDLHAH KLRVDPVNFK
           HGSAQVKGHG KKVADALTNA VAHVDDMPNA LSALSDLHAH KLRVDPVNFK
           HGSAQVKGHG KKVADALTNA VAHVDDMPNA LSALSDLHAH KLRVDPVNFK
           HGSAQVKGHG KKVADALTNA VAHVDDMPNA LSALSDLHAH KLRVDPVNFK
           HGSAQVKGHG KKVADALTNA VAHVDDMPNA LSALSDLHAH KLRVDPVNFK
HGSAQVKGHG KKVADALTNA VAHVDDMPNA LSALSDLHAH KLRVDPVNFK


           LLSHCLLVTL AAHLPAEFTP AVHASLDKFL ASVSTVLTSK YR
           LLSHCLLVTL AAHHPAEFTP AVHASLDKFL ASVSTVLTSK YR
           LLSHCLLVTL AAHLPAEFTP AVHASLDKFL ASVSTVLTSK YR
           LLSHCLLVTL AAHLPAEFTP AVHASLDKFL ASVSTVLTSK --
           LLSHCLLVTL AAHLPAEFTP AVHASLDKFL ASVSTVLTSK --
           LLSHCLLVTL AAHLPAEFTP AVHASLDKFL ASVSTVLTSK YR
```

Step 4: Creating a Phylogenetic Tree with EBI – Simple Phylogeny

1. Go to the EBI Simple Phylogeny tool at https://www.ebi.ac.uk/Tools/phylogeny/simple_phylogeny/.
2. Paste the multiple sequence alignment results you obtained in Step 3 into the box.
3. Click the "Submit" button.
4. Once the results load, you can capture the phylogenetic tree for your document.




```
(
(
XP_0543092:0.00704,
Q9TS35.2_1:0.00704) :0.00000,
XP_0040569:0.00000,
(
(
HDS1036830:0.00000,
HCS8797820:0.00000)  :0.00018,
XP_0103801:0.01410)
:0.00702);
```

Remember to clearly indicate a match in your BLAST results that represents a gene/protein sequence homologous to your query protein. You can do this by highlighting the match in your screenshot or mentioning it in your document.