

# Eastern Mediterranean University

## Faculty of Arts and Sciences

### Molecular Biology and Genetics

#### BIOL312 - Practical 4

1- Match up the following BLAST search programs with their correct descriptions:

- |          |  |
|----------|--|
| -BLASTP  | (a) Nucleotide query against a nucleotide sequence database              |
| -BLASTN  | (b) Protein query against a translated nucleotide sequence database      |
| -BLASTX  | (c) Translated nucleotide query against a protein database               |
| -TBLASTN | (d) Protein query against a protein database                             |
| -TBLASTX | (e) Translated nucleotide query against a translated nucleotide database |

2- Find the paralogous protein of BAA00361.1 . Explain and define your answer with reasons. Explain the steps (including which BLAST programme) you performed.

3- Identify the unknown protein by using below amino acid sequence. Give information about best match. How is the distance tree of first three hits? Have a printscreen of the distance tree.

MNRRDFIKNTAIASAASVAGLSVPSSMLGAQEEDWKWDKAVCRFCGTGCGIMIARKDGKIVATKGDPAAP  
VNRGLNCIKGYFNAKIMYGEDRLVMPLLRMNEKGEFDKKGKFQQVSWQRAFDEMEKQFKKAYNELGVTGI  
GIFGSGQYTIQEGYAALKLAKAGFRTNNIDPNARHCMASAVVGMQTFGVDEPSGCYDDIELTDITITWG  
ANMAEMHPILWSRVSDRKLNSLDKVKVNLSTFSNRTSNIADIEIIFKPNTDLAIWNYIAREIVYNHPEA  
MDMKFIKDHCVFATGYADIGYGMRRNPNHPKFESEKDTVEKENVITLDDEEATSLSYLGVKAGDKFEMK  
HQGVADKNWEISFDEFKGLAPYTTYARVAKGDDNESLEDFKKKLQELANLYIEKNRNVVSWFTMGFN  
QHTRGSWVNEQAYMVHFLGKQAKPGSGAFSLTGQPSACGTAREVGTFSHRLPADMVVANPKHREISEKI  
WKVPAKTINPKPGSPYLNIMRDLEDGKIKFAWVQVNNPWQNTANANHWIAAAREMDNFIVVSDCYPGISA  
KVADLILPSAMIYEKYGAYGNAERRTQHWKQQLPVGAAASDTWQILEFAKRFKLKEVWKEQKVDNKLTL  
PSVLEEKAMGYSEDDTLFDVLFANKEAKSFNPNDIAIKGFDNTDVKGDERKIQGS DGKEFTGYGFFVQK  
YLWEEYRKFGGLGHGHDLADFDTYHKVRGLRWPVVGKETQWRFNTKFDYYAKKAAPNSDFAFYGFDFNKML  
TNGDLIAPKDEKEHSIKNKAKIFFRPFMKAPERPSKEYPFWLATGRVLEHWHSGTMTMRPELYRAVPEA  
LCYMSEKDGEKLGDLVWVESRRGKVKARVDMRGRNKPPVGLVYVPWFDENVYINKVTLDATCPLSK  
QTDFFKCAVKIYKA

4- By using the following cDNA sequence in *Homo sapiens*, search for the other DNA sequences to find one that encodes the same or similar protein. Which basic BLAST program you should use? What is the accession number of the possible match? Interpret the alignment result.

```
ATGACTTCTACCTGGTGATGCCCTTCAT
GCAGACGGATCTGCAGAAGATCATGGGGATGGAGTTCAGTGAGGAGAAGATCCAGTACCTGGTGTATCAG
ATGCTCAAAGGCCTTAAGTACATCCACTCTGCTGGGGTCGTGCACAGGGACCTGAAGCCAGGCAACCTGG
CTGTGAATGAGGACTGTGAACTGAAGATT
```

5- Is there a `creatine kinase B-type (*Homo sapiens* – NP\_001814.2)` ortholog represented in a genomic DNA database? Give details about your answer. Eg: Accession number, similarity percentage, expected value etc..

**Submission Deadline: 14.04.2020 - @23:59**