

Using Databases to Obtain Real Amino Acid Sequence Data to Compare Various Fish Species and Create Evolutionary Trees

Products of the Lab to be turned in:

1. Print out of FASTA sequences for myosin heavy chain for the different species
2. Print out of the computer generated cladogram (actual names of species displayed, not accession number) based on myosin heavy chain
3. Print out of FASTA sequences for actin for the different species
4. Print out of the computer generated cladogram (actual names of species displayed, not accession number) based on actin
5. Focus questions on lab handout answered.

When finished with the list above, start the further exploration section.

What protein are you researching?

What gene, disease, or biological process is it related to?