

Return to the BLAST home page (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>). Return to the Protein BLAST search to identify the polypeptide which you have been analyzing. (You may use either sequence.). Copy and paste the sequence into the “Enter Query Sequence box. Be sure that the box “Align two or more sequences” is **NOT** checked. Choose “Quick BLASTP” under the Program Selection. Click the “Blast” button at the bottom.

26. WHAT GENE ENCODES FOR THE POLYPEPTIDE YOU WERE ANALYZING? FGFR3 fibroblast growth factor receptor 3

Click on “Description”, then choose “Gene” under “Related Information” to answer the following two questions.

27. WHAT IS THE FUNCTION OF THIS PROTEIN? Click on “Description” and then “Gene” under “Related Information” to the right to get this information. The extracellular portion of the protein interacts with fibroblast growth factors, setting in motion a cascade of downstream signals, ultimately influencing mitogenesis and differentiation. This particular family member binds acidic and basic fibroblast growth hormone and plays a role in bone development and maintenance.

28. WHAT HUMAN DISEASE IS CAUSED BY A MUTATION IN THIS GENE? Again, this information can be gained by clicking on “Description” and then “Gene” under “Related Information” to the right to get this information. craniosynostosis and multiple types of skeletal dysplasia

29. WHAT IS THE CONNECTION AMONG THE FOLLOWING: NIH, NLM, NCBI, and HHS? (What do the abbreviations stand for? Who oversees what?) The National Institutes of Health (NIH), a division of the U.S. Department of Health and Human Services (HHS), oversees the National Library of Medicine (NLM). Within NLM, the National Center for Biotechnology Information (NCBI) is responsible for providing access to biomedical and genomic information through various databases and tools.

30. WHAT WAS ONE POSITIVE THING AND ONE NEGATIVE THING YOU ENCOUNTERED WHILE DOING THIS ASSIGNMENT? One positive thing is that I got to experience how to look up genomic data and compare different sequences. I did not encounter anything negative during the assignment.