Bioinformatics-I (BIF401)- HELP

Assignment No.01

Total Marks 15

Note: There are two questions. First one is theoretical and second one is practical. You are supposed to do your assignment by yourself. Any kind of plagiarism will be marked straight zero.

Question 1: What you have learnt in basics of Bioinformatics. Also enlist and discuss the tools software and methods you have studied till now. (7)

Question 2: Select a sequence of a candidate gene. You are required to find:

(8)

- 1. Full scientific name of the candidate gene.
- 2. Top 3 alignment result of the candidate gene with the complete information like accession number, Locus, Coding region etc.
- 3. Three more relevant ortholog.
- 4. Name of the tools and databases which you are using during this process.

Hint: (Orthologs are genes in different species that evolved from a common ancestral gene by speciation. Normally, orthologs retain the same function in the course of evolution)

Sample Assignment

1- Go to the NCBI database



Open NCBI



Select Protein database from here

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					Discovering associated data in PMC		

Enter the name of your candidate gene (a gene, which you want to work upon)



Enter it-> it will give you a list of all possible sequence datasets available related to the your gene (protein)



Open it and then you can see the full sequence with all desired information in the first line.



Click on the BLAST icon present at the top of right menu **OR** you can copy the sequence and open BLAST -> Protein to Protein (blastp) and past the sequence in input section.



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At the lower part of the page you will see a list of reference sequence of protein structure which our sequence has been mapped upon. Where at the right side different columns are giving the information about the identity, Query coverage and Accession ID etc

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Description	Max score	Total score	Query cover	E value	ldent	Accession
Chain A. Native Structure Of N-Acetylglutamate Synthase From Neisseria Gonorrhoeae	925	925	100%	0.0	100%	<u>2R8V A</u>
Chain A. Crystal Structure Of N-Acety/glutamate Synthase (Selenomet Substituted) From Neisseria Gonorrhoeae	909	909	99%	0.0	99%	<u>2R98 A</u>
Chain A. Crystal Structure Of C-Termianl Domain Of N-Acety/glutamate Synthase From Vibrio Parahaemolyticus	110	110	31%	1e-28	43%	<u>3E0K A</u>
Chain A. Acetylolutamate Kinase From Thermotoga Maritima Complexed With Its Inhibitor Arginine	108	108	58%	2e-26	30%	<u>2BTY A</u>
Chain A. The Complex Of Pii And Acetylojutamate Kinase From Synechococcus Elongatus Pcc7942	92.4	92.4	67%	2e-20	30%	<u>2JJ4 A</u>
Chain A. Arginine Feed-Back Inhibitable Acety/glutamate Kinase	86.7	86.7	59%	2e-18	26%	2BUF A
Chain A. N-acetylglutamate Kinase From Arabidoosis Thaliana In Complex With Pii From Chlamydomonas Reinhardtii	85.9	85.9	66%	3e-18	31%	<u>4USJ A</u>
Chain A, Structural Basis For The Regulation Of N-acetylglutamate Kinase By Pii In Arabidopsis Thaliana	73.9	73.9	61%	3e-14	27%	2RD5 A
Chain A, Crystal Structure Of Xcnags	62.4	62.4	70%	5e-10	27%	<u>386K A</u>
Chain A. Crystal Structure Of A Tetrameric Acety/glutamate Kinase From Saccharomyces Cerevisiae	55.8	55.8	59%	5e-08	24%	<u>3ZZI A</u>
Chain A. Crystal Structure Of The Amino Acid Kinase Domain From Saccharomyces Cerevisiae Acety/glutamate Kinase Complexed With Its Substrate N-Acety/glutamate	51.2	51.2	53%	1e-06	25%	<u>3ZZF A</u>
Chain A, Structure mmNAGS bound with L-arginine	47.8	47.8	71%	2e-05	27%	<u>4KZT A</u>
Chain A. Crystal Structure Of Mmnags In Space Group P3121 At 4.3 A Resolution	47.0	47.0	71%	3e-05	27%	<u>387Y A</u>
Chain A, Crystal Structure Of Native MmnagsK	47.0	47.0	71%	4e-05	27%	<u>386H A</u>
Chain A. Crystal structures of Seleno-substituted mutant mmNAGS in space group P212121	41.2	41.2	71%	0.002	26%	<u>386G A</u>
Chain A. The Crystal Structure Of Smu 665 From Streptococcus Mutans Ua159	38.1	38.1	63%	0.014	26%	<u>3L86 A</u>
Chain A. Crystal structure of the beta-glucosidase from Trichoderma harzianum	37.0	37.0	16%	0.053	44%	5BWF A
Chain A, E. coli LpoA N-terminal domain	35.8	35.8	12%	0.072	50%	<u>2MHK A</u>
Chain A. Crystal Structure Of Conjugated Polyketone Reductase C2 From Candida Parapsilosis	35.8	35.8	31%	0.096	31%	<u>3VXG_A</u>
Chain A. Structure of the plycoside hydrolase domain of PelA variant E218A from Pseudomonas aerupginosa	35.4	35.4	16%	0.11	46%	5TSY A
Chain A. Structure of the glycoside hydrolase domain of PelA from Pseudomonas aeruginosa	35.4	35.4	16%	0.12	46%	5TCB A
Chain C. Crystal Structure Of The Mot1 N-Terminal Domain In Complex With Tbp	34.7	34.7	7%			
Chain A. Small Molecule Inhibitors Of Ian	33.1	33.1	5%		Juesti	ions/con

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From here get the Complete information like accession number, Locus, Coding region etc. of the three references one by one and make a table.

Then go back to the first page where you found your first sequence from.



From the above page see the right top encircled area it will give you the information about the orthologs of the Human Gene.

Past the sequences of the same genes extracted from those three orthologs.

At the end enlist all the databases tools software which you will have used.