

9/10/04
BCH 258
York Lectures
BLAST/VAST Problem Set

DUE TO VINCENT BY Friday September 24, 2004

- 1) Obtain the cDNA for human and *drosophila* (fruit fly) bisphosphate nucleotidase (BPNT1). The accession numbers are NP_006076 and CG7789-PA, respectively. Print the nucleotide and protein sequences.
- 2) Using the nucleotide and protein sequences, determine the chromosomal localization and the intron/EXON structure of the Human and Fly genes. Draw a scale model of each genome structure listing exons by box and introns as lines. At the beginning and end of each exon, number the nucleotide (bottom of drawing) and amino acid sequences (top side of box). Please do not print out the nucleotide sequence!!
- 3) Search the fly and human databases for proteins with sequence homology to BPNT. Hint: there are only about 7 distinct relatives. List each new protein and its function if known (please do not just print out the blast as many genes are entered multiple times). Draw an evolutionary tree of the protein family for both humans and flies..
- 4) Obtain the PDB file for rat BPNT (1JP4.pdb). Using the VAST comparison website, determine if there are any structurally related proteins to the rat BPNT? Select 3 or 4 representative relatives (ie different enzymes) and 1) make a table of related pdb files; 2) list the RMS deviation of each structure as compared to 1JP4 (include the number of residues that are conserved versus the total) and 3) print the sequence alignment outputted by the CE program (which is based on the structural alignment). How did this alignment compare to the BLAST alignment obtained in problem #3? Download the 1JP4 structure, print out a ribbon diagram of the structure and map the conserved regions (from the alignment) onto this structure. For each conserved sequence element classify it as a loop, turn or helix or strand.