BIOL 264, Fall 2006
Grading for Lab Report #2

Introduction:

Stronger papers clearly identified the assigned sequence, providing some background information on the evolutionary issues within the gene family and the biochemical role of the protein. Strong papers made good use of outside sources and cited them appropriately.

Weaker papers dealt only superficially with the evolution and function of the protein, or they inappropriately emphasized function when subsequent data and discussion did not address functional issues. These papers made weak or superficial use of literature associated with identified sequences, and these sources of information may not have been cited.

Results and Discussion:

Stronger papers included attractive, well labeled figures that were readable and informative.

Weaker papers had cryptic abbreviations and/or poorly written legends.

Stronger papers translated the cDNA sequence in the proper frame and included the 5' and 3' untranslated regions. Nucleotides were accurately numbered.

Weaker papers did not properly identify the open reading frame.

Stronger papers included a phylogenetic tree that made sense. The sequences included in the tree were carefully chosen to demonstrate a point about the evolution of the protein family. The outgroup was logically chosen, and the rationale for the choice was included in the text. Alleles or splice variants of the same gene were not included.

Weaker papers showed phylogenetic trees that were haphazardly constructed. Software output was accepted without critical consideration or revision. The outgroup was not carefully chosen. Including only the closest matches from the BLAST search resulted in using polymorphisms and splice variants rather than true gene homologs.

Stronger papers correctly identified broad themes in observations about the tree topology, timing and effect of gene duplications, etc.. Surprises and discrepancies were pointed out and alternative explanations discussed in light of available data.

Weaker papers included only superficial discussion of the tree topology and gene duplication during evolution of the protein family. Surprising or confounding results were only superficially mentioned, if at all, and potential explanations were not offered.

Stronger papers supported claims about the relationship between gene number and potential functional roles with statements from the literature.

Weaker papers glossed over functional implications and made no use of relevant literature.

General considerations:

Stronger papers were well written. They exhibited a logical flow of ideas, included well organized paragraphs with strong topic sentences, and utilized stylistically strong sentences, avoiding unpleasant repetition in language use.

Weaker papers were haphazardly organized and written. They contained grammatical, spelling, and typographical errors. Lack of editing was evident.