To produce several global alignments for comparison, T-COFFEE and COBALT were used. Although not included as an option in the Edgar paper, I chose to use COLBALT because of personal familiarity. T-COFFEE was chosen because it is one of the more accurate multiple sequence aligners for under 100 sequences for proteins of under 10,000 residue length. For both tools, regions of low percent identity caused differential alignment. The globally aligning multiple sequence tools produced a different output from BLAST due to model fit. BLAST fits every sequence to one model, the query sequence, while global aligners fit multiple sequences to each-other. Based on the very similar output from the two global aligners, T-COFFEE may be the better option due to its user friendly interface with color coding sequence differentiation. T-COFFEE also produces helpful alignment scores, an option not produced by COBALT. However, it may be useful to use a hybridized approach. COBALT produces useful output regarding to location of a particular sequence’s alignment while T-COFFEE does not. Both T-COFFEE and COBALT found near perfect alignment between the 10 sequences for 250 residues. Within this 250 residue alignment, all but one sequence exhibited an identical deletion of 10 residues. Throughout the rest of the alignment of the sequences there was a high degree of variation. Based on the results of the multiple sequence alignments, the highly conserved areas between the sequences are most likely influenced by selective pressure and any mutation is deleterious. The areas of high variation are most likely under far less selective pressure, indicated by their high degree of variability. Overall, it is very likely that these 10 sequences are orthologues of the human COL1A1 protein.