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1. The initial PSI-BLAST and BLAST output were identical. This is because PSI-BLAST’s first iteration is actually a BLAST search. PSI-BLAST then uses the results of the first iteration to build scoring matrices for each position in the protein, using this matrix on the next iteration.
2. It took seven iterations completely eliminate new sequences from appearing in the PSI-BLAST results. As the scoring matrix changes with each iteration, the context/family of the protein becomes more relevant in the search. The probability of a particular protein substitution differs with each protein family. The iterative PSI-BLAST search takes this into account.
3. For this particular protein sequence, the PSI-BLAST results with the default parameters versus the results with wordsize = 2 and E = 0.001 were identical. This is probably because BLAST was able to find very close matches. Out all the sequences found to be matches, the lowest Identity was 84%. Therefore, all of the results have a very, very low E value to begin with.