

Chemistry 428

Lab 4

BLAST

You will be given 2 sequences (via email) and you will determine what each sequence is from and give specifics on the organism it is from.

BLAST is a program by NCBI. BLAST uses a basic algorithm that can be implemented in DNA sequence database searches. The BLAST option that we will be using is blastn it compares a nucleotide sequence against a nucleotide sequence database.

First go to <http://www.ncbi.nlm.nih.gov/BLAST/>. Then under Nucleotide click on Nucleotide-nucleotide BLAST (blastn).

In the search box put in your sequence.

For options choose:

database - nr

limit by entrez query - All organisms

Choose filter – Low complexity

Expect – 10

Word Size – 11

Then click on BLAST! You will be given a request ID write this down and report it in your lab report and book. The results will be ready in about a minute. At this point you may click on Format!.

Then under the sequences producing significant alignments report the first 3 results along with their score (bits) and E values. Use the first result to determine what organism the sequence is from.

Your lab report will consist of a brief intro (i.e. you used nucleotide-nucleotide BLAST on this sequence), request ID for each, first three results for each and information of the most likely organism that the sequence came from for each (a few paragraphs on the organism).