**\*\* ABOUT \*\***

The custom protein query and blast tool offers an alignment and similarity analysis of a given e-coli protein from a database. The following tasks can be achieved by the tool:

* Perform a search for a specific polypeptide.
* Perform blast+ using the residue retrieved from the search.

Source code can be obtained here: http://bfx.eng.jhu.edu/mfaris1/class\_project/final\_project/

Demo with pre-uploaded files: http://bfx.eng.jhu.edu/mfaris1/class\_project/final\_project/search.html

**\*\* Requirements \*\***

1. Blast+ (Basic Local Alignment Search Tool)

* NCBI BLAST 2.6.0+ (Current)
* wget <ftp://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/LATEST/ncbi-blast-2.6.0+-x64-macosx.tar.gz>

1. Complete UniProtKB/Swiss-Prot data set in FASTA format.

* NCBI Database
* <ftp://ftp.uniprot.org/pub/databases/uniprot/current_release/knowledgebase/complete/uniprot_sprot.fasta.gz>

Manual for installation of the tools can be found at:

* Mac - http:// [www.ncbi.nlm.nih.gov/books/NBK52640/](http://www.ncbi.nlm.nih.gov/books/NBK52640/)
* Windows - http:// [www.ncbi.nlm.nih.gov/books/NBK52640/](http://www.ncbi.nlm.nih.gov/books/NBK52640/)

Recommended memory/cpu is 1gb.

**\*\* Detailed usage\***

1. Input the name of the product(polypeptide).
2. Click “Submit”
3. Copy and paste the protein sequence.
4. Click “blastp”

**\*\* Demo Data\*\***

1. Enter the name of the polypeptide such as “ligase”. The results will be displayed.
2. From the displayed output, copy the protein sequence.
3. Paste the sequence. (not functional)
4. Click blastp to look at the output.