

Protclass Program Guide

1. Install Protclass

- (1) Download the Protclass program from the link provided.
- (2) Download and Install the Java program: <https://java.com/en/download/>
- (3) Download and install ActivePerl program: <https://www.perl.org/get.html>
- (4) Copy the bio folder from “\Desktop\protclass\cgi-bin\functional_genomics” to the lib in the perl program folder: C:\Perl64\lib

2. Open Protclass

(1) Open a Command Prompt

On Windows7, go to: Start\All Programs\Accessories

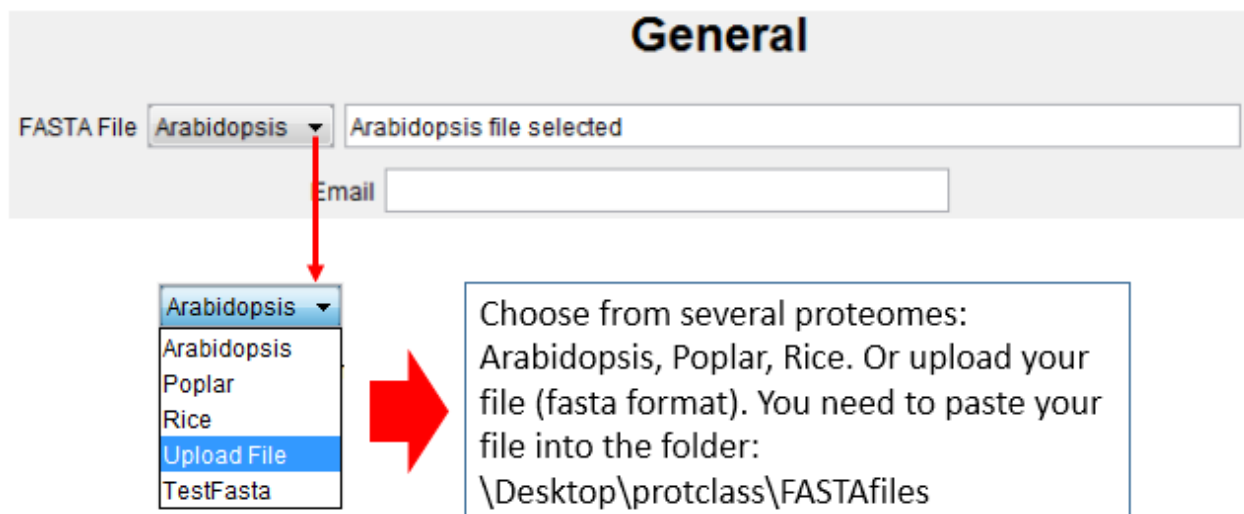
On Windows8, type “cmd” on windows UI and enter

(2) Change into the directory where the protclass_gui.class file is located

Type: cd Desktop\protclass\cgi-bin

(3) To open Protclass GUI, type: java protclass_gui

3. The Protclass GUI



BiasedAA

Include Test

Short

Long

Threshold

Window

Amino Acids

AgPeptide

Include Test

Short

Long

Threshold

Window

Amino Acids

Fasciclin

Include Test

H1 Motif

Search Length

AGP Region Motif

Extensin

Include Test

Pattern 0 Qty

Pattern 1 Qty

PRP

Include Test

Pattern 0 Qty

Pattern 1 Qty

SignalP

Include Test

Start

Search Length

Threshold

Search for biased amino acid composition. "Include Test" denotes if this test is to be performed (Yes) or not (No). "Short" and "Long" denotes the range of length of proteins to be included in the test. "Threshold" denotes the minimum percentage to pass the test. Default as 50%. "Window" denotes the length of sequence for calculation. "Amino Acids" denotes the types of biased amino acids.

Search for AgPeptide. Similar to the search for biased amino acid above, this test allows user to simultaneously search for short AG peptides and general AGPs.

Search for fasciclin AGPs. "H1 Motif" denotes a regular expression of known fasciclin AGP characteristic motif. "Search Length" denotes the maximum length for searching this motif. "AGP Region Motif" denotes the motif to be searched in the AGP domain of a protein.

Search for extensins. "Pattern 0" and "Pattern 1" denotes the motifs of extensin to be searched. "Qty" denotes the minimum number of occurrences to pass the test. Default values are displayed.

Search for proline-rich proteins. Similar to the search of extensins. Default values are displayed.

Search for the presence of signal peptide. This version of Protclass run each sequence through the SignalP 4.1 website. So just ignore the in-house parameters: "Start", "Search Length", and "Threshold".

GPI

Include Test

Min Philic Region

Max Philic Region

Min Phobic Region

Max Phobic Region

Omega Site Threshold

Hydrophobicity Threshold

BiasedPRP

Include Test

Short

Long

Threshold

Window

Amino Acids

Blast Analysis

Include Test

Threshold

Search for the presence of GPI anchor. This version of Protclass runs each protein sequence through big-PI plant predictor website. So these in-house parameters are not functional, except the “Include Test” option.

Search for biased PRPs. The parameters are the same as biased AGPs. Default values are displayed.

“Blast Analysis” takes each sequence to the NCBI blast website, blasts against Arabidopsis proteome, and returns the top five hits of Arabidopsis HRGPs.

After inputting all the parameters, click the “Submit” button to start running the program. Click “Reset” to all the values to default.

4. Obtain results

Once the “Submit” button is clicked, a folder will be created with several subfolders at the destination: \Desktop\protclass\cgi-bin with the time of starting the test as the folder name. Meanwhile, the program GUI will freeze until the program finishes running the test. Once finished, it creates two additional results files, a doc file that contains all the protein sequences that passed the test and a excel file that shows the results of test.

5. Contact information

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