

## LelantosGUI Tutorial

LelantosGUI has WuManber and SuffixArray implementations under Tools section. The settings of these algorithms are under Settings tab which is blocked until input sequence file and peptide query files are uploaded. In this tutorial, GUI usage is described step by step. To run the GUI application, JAVA should be installed and be available on the path. Double click on LelantosGUI.jar file and make sure WuManber.jar and Suffix\_array executables are in the same folder of GUI. Please use whole unzipped folder.

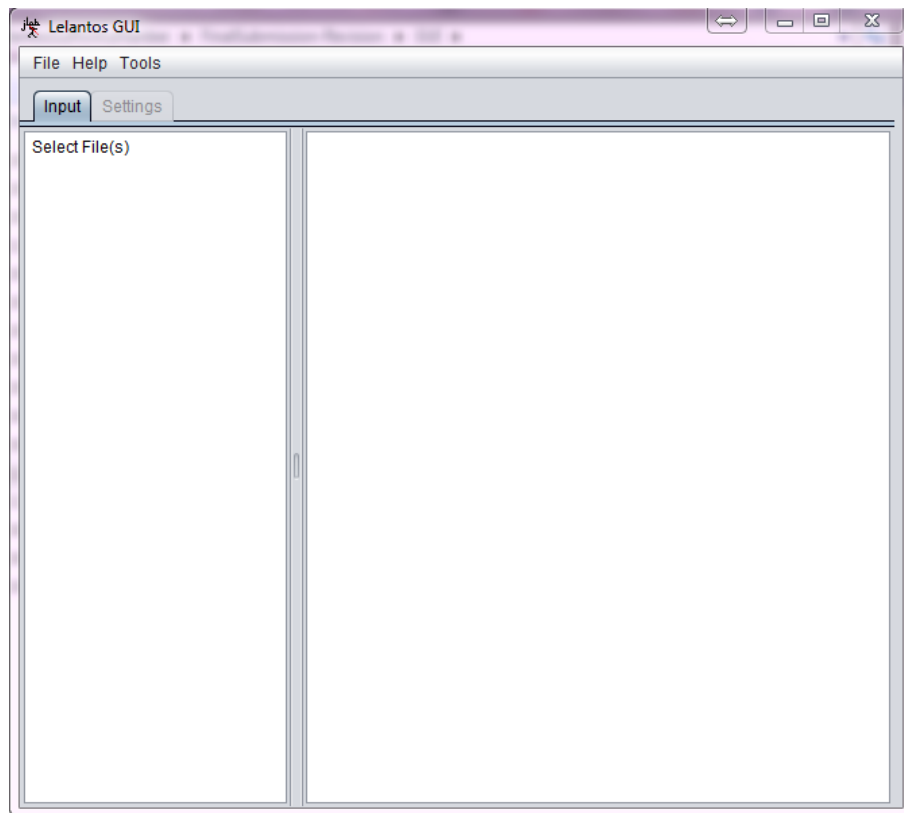


Figure 1: The general view of GUI

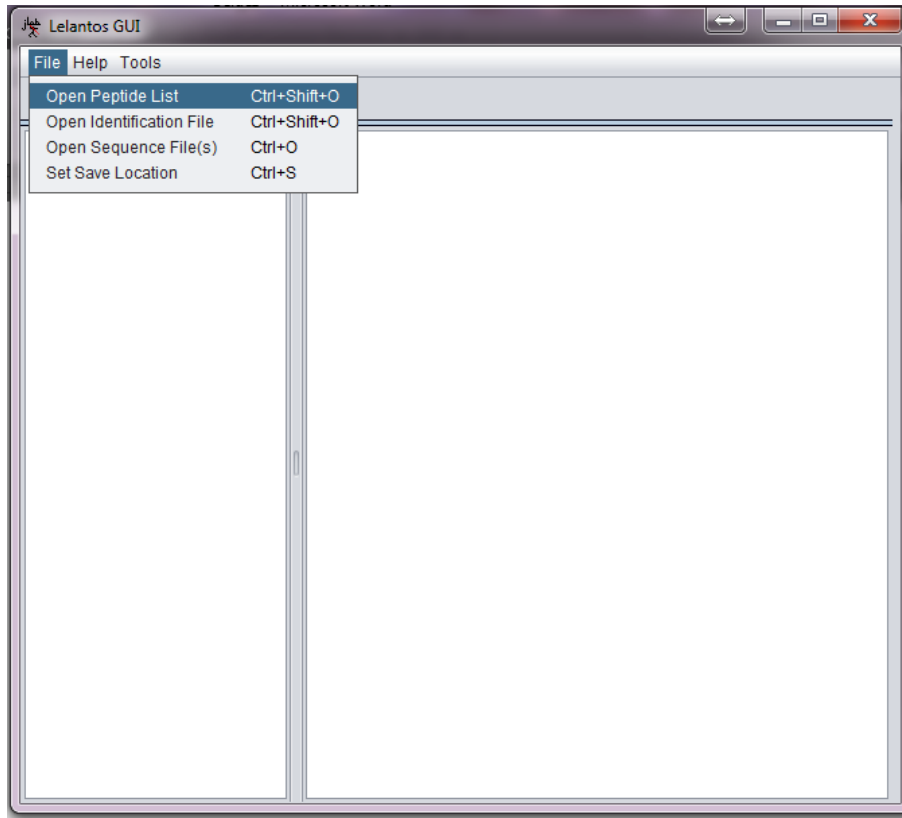


Figure 2: To upload peptide query sequences, either click on “Open Peptide List” which accepts peptide query file in FASTA format. Besides that peptide identification result file of a database search algorithm in mzid format can also be uploaded by clicking on “Open Identification File”.

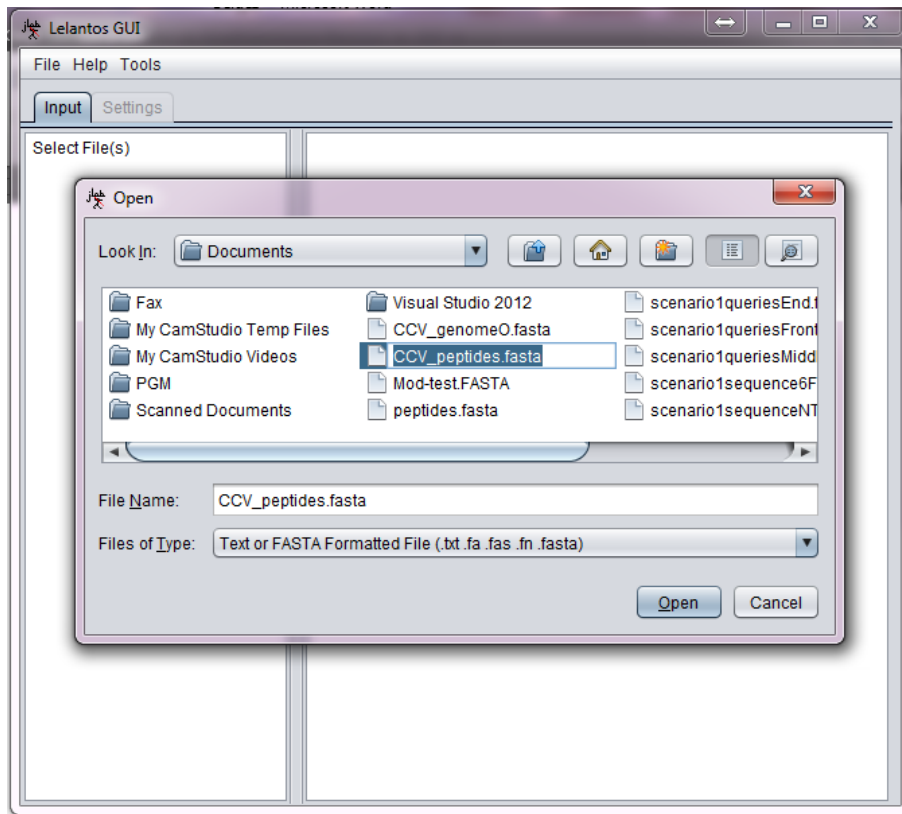


Figure 3: Valid FASTA file extensions are seen.

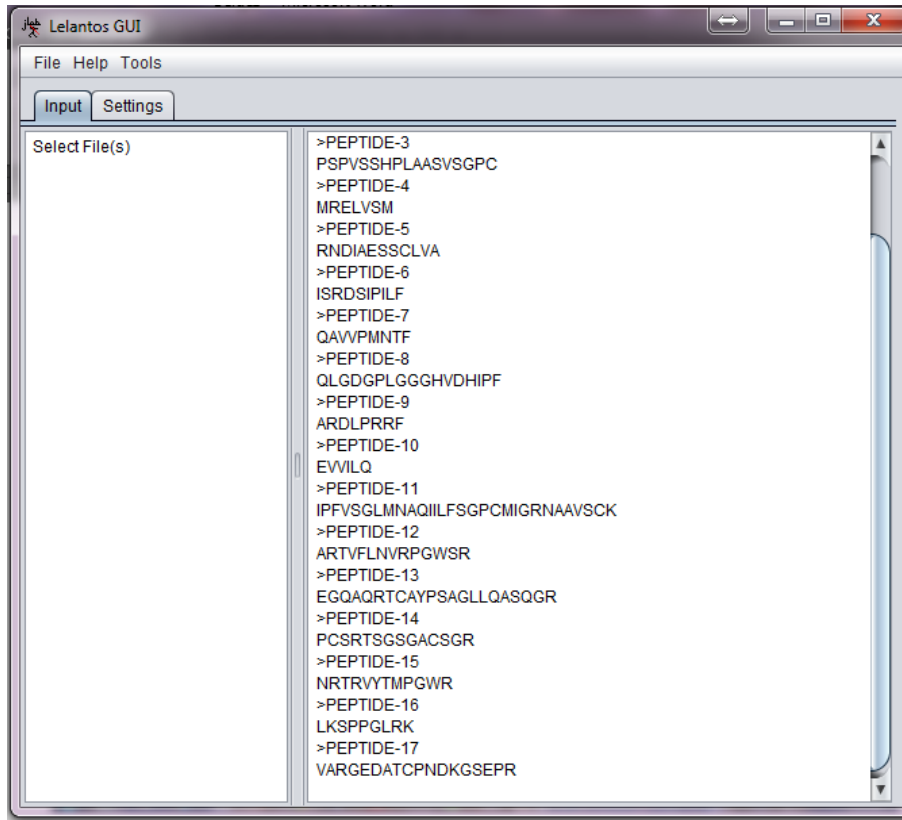


Figure 4. After peptide file is uploaded, sequences and identifiers are visible on right-panel.

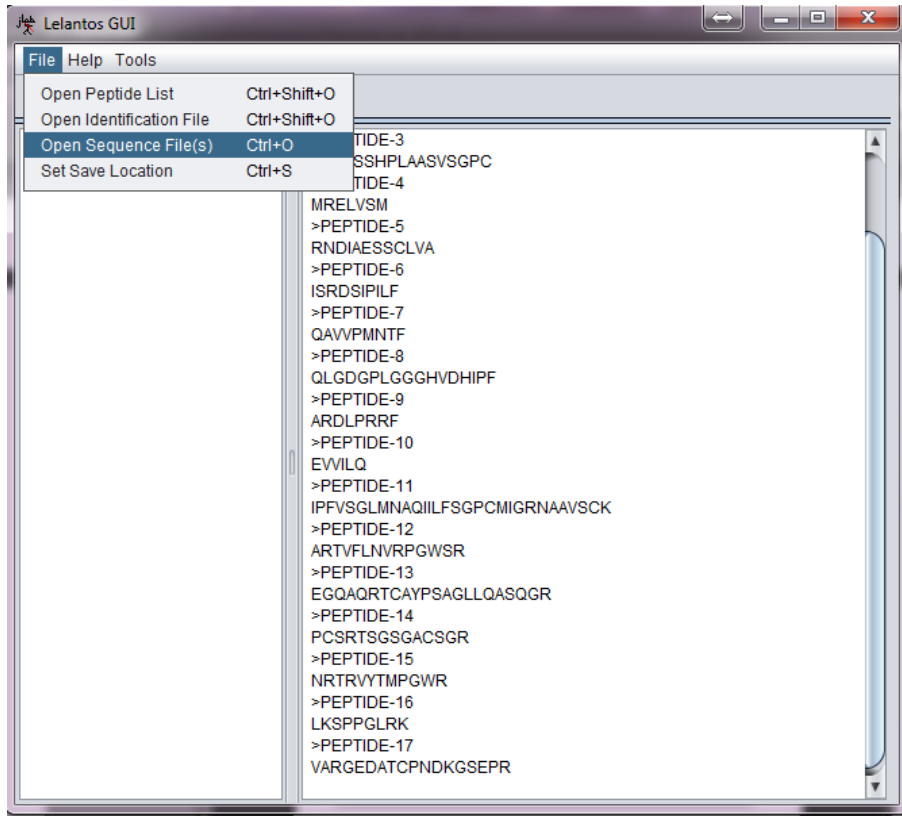


Figure 5: Peptide sequences are searched against sequence file. Sequence file can be either amino acid or nucleotide sequence. In order to upload sequence file, click on "Open Sequence File". The GUI allows upload of multiple sequence files.

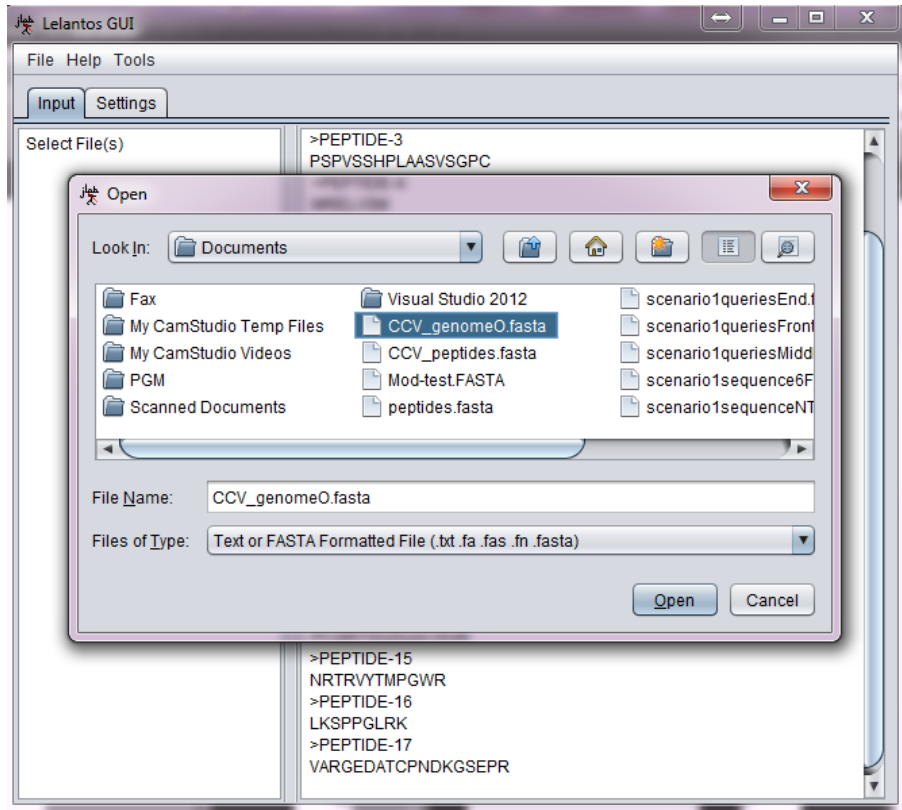


Figure 6: Here accepted file extensions are seen.

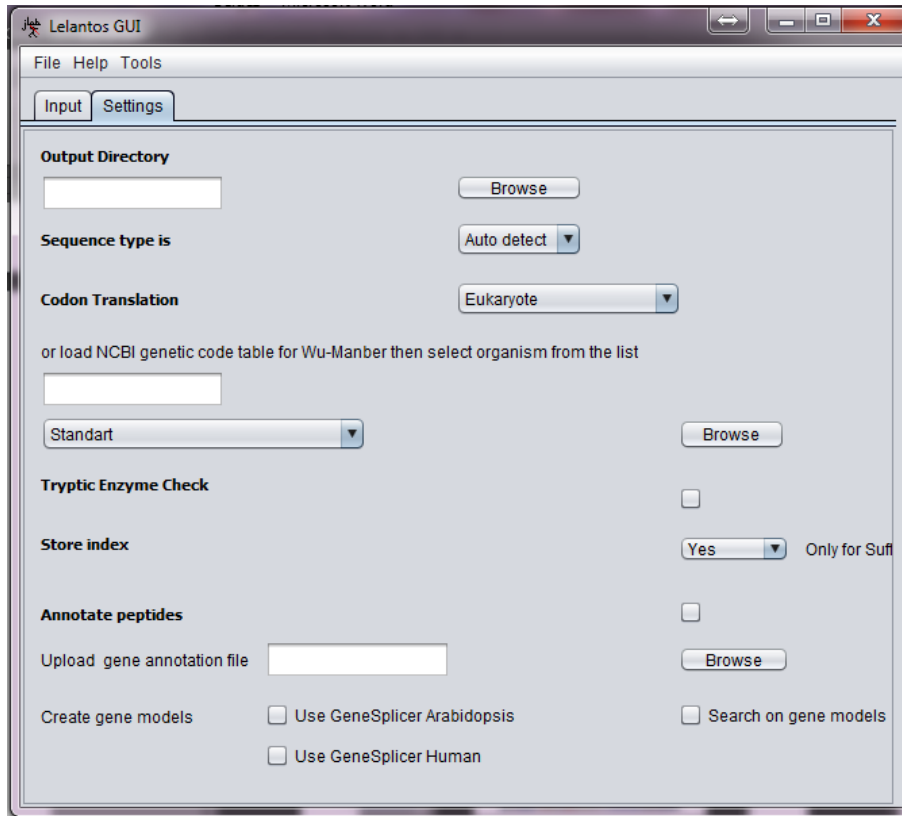


Figure 7: When peptide query file and sequence file are uploaded, settings tab will be visible. Output directory, sequence type, codon translation model and index file storage for only suffix tree are settings for search algorithms. In addition to that mapped peptides can be checked according to tryptic digestion rule.

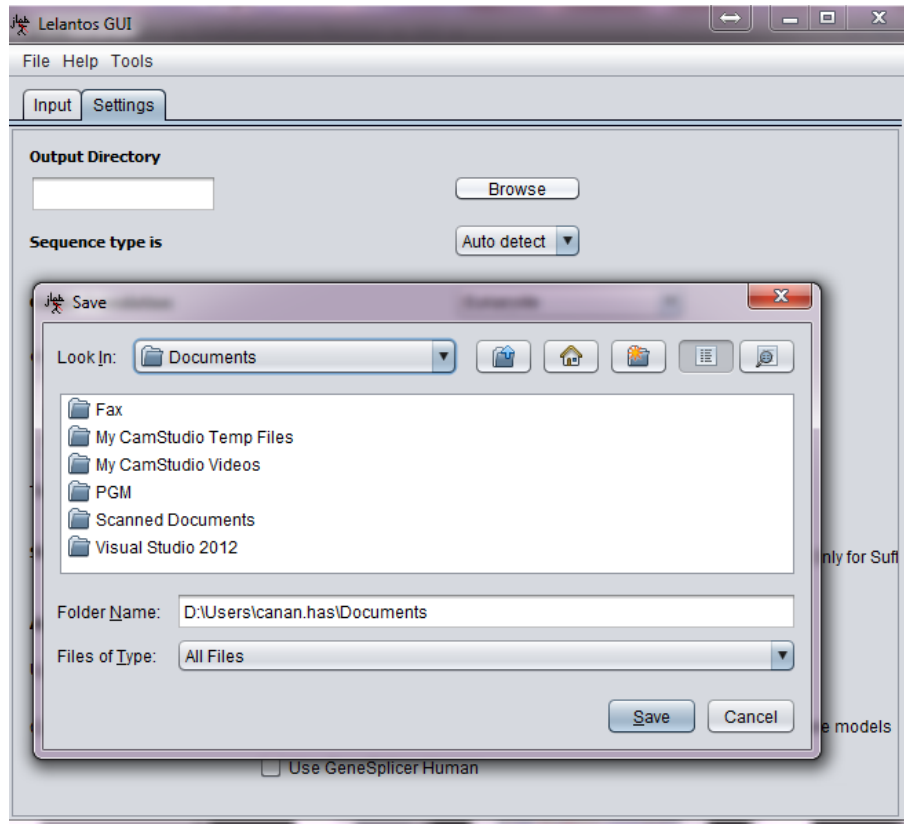


Figure 8: Result directory is selected. In GUI, result file name is given according to queried files. Output file is returned in *gff/gff3* format.



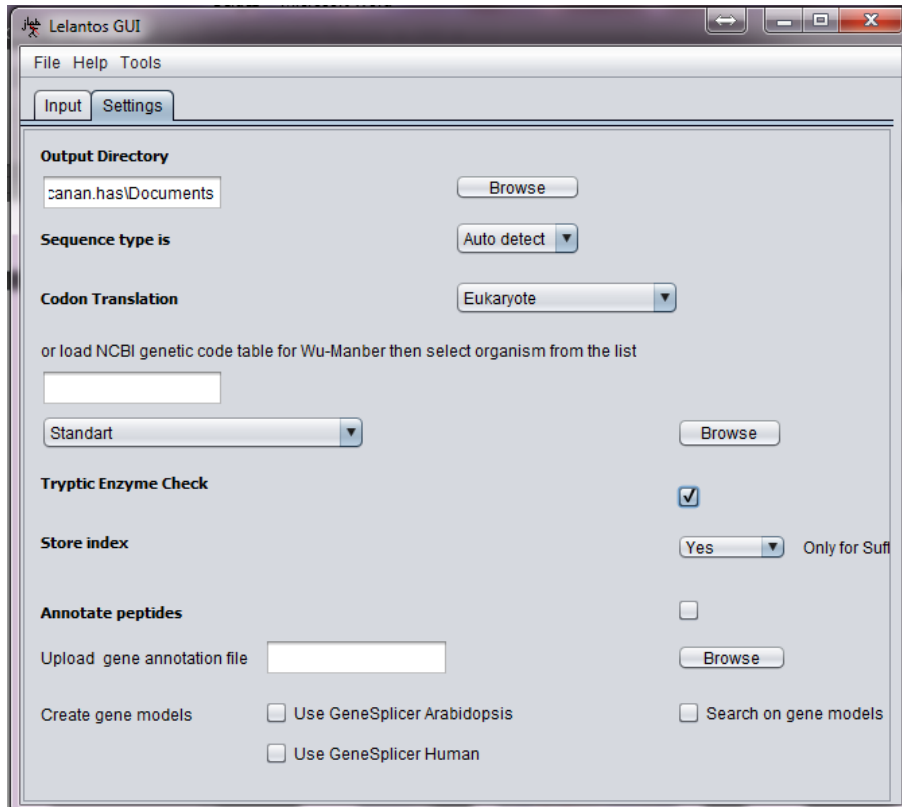


Figure 9: When Tryptic Enzyme Check box is clicked, peptides which are tryptic are written into a file called “Digested Peptides”. In case annotation will be done, annotation file in Ensembl GFF format must be uploaded. In case annotation will be assessed according to gene splicing event, GeneSplicer algorithm usage should be activated by clicking on suitable organism and “Search on gene models” box.

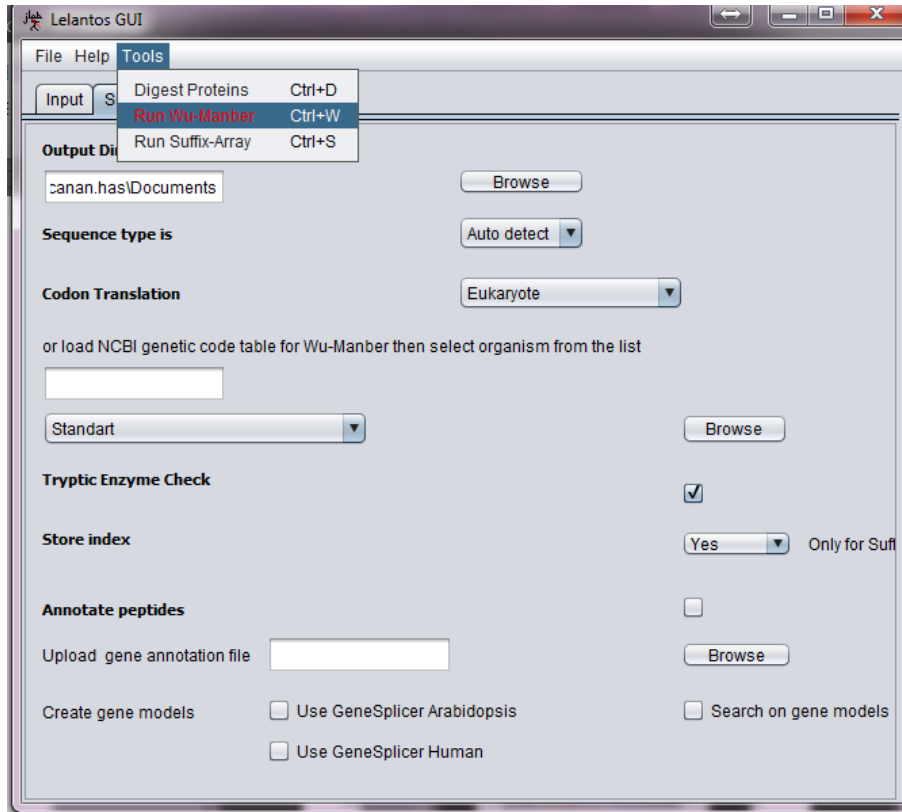


Figure 10: GUI suggests suitable algorithm according to size of sequence database file. Suitable algorithm is highlighted in red. However, other algorithm can also be used.

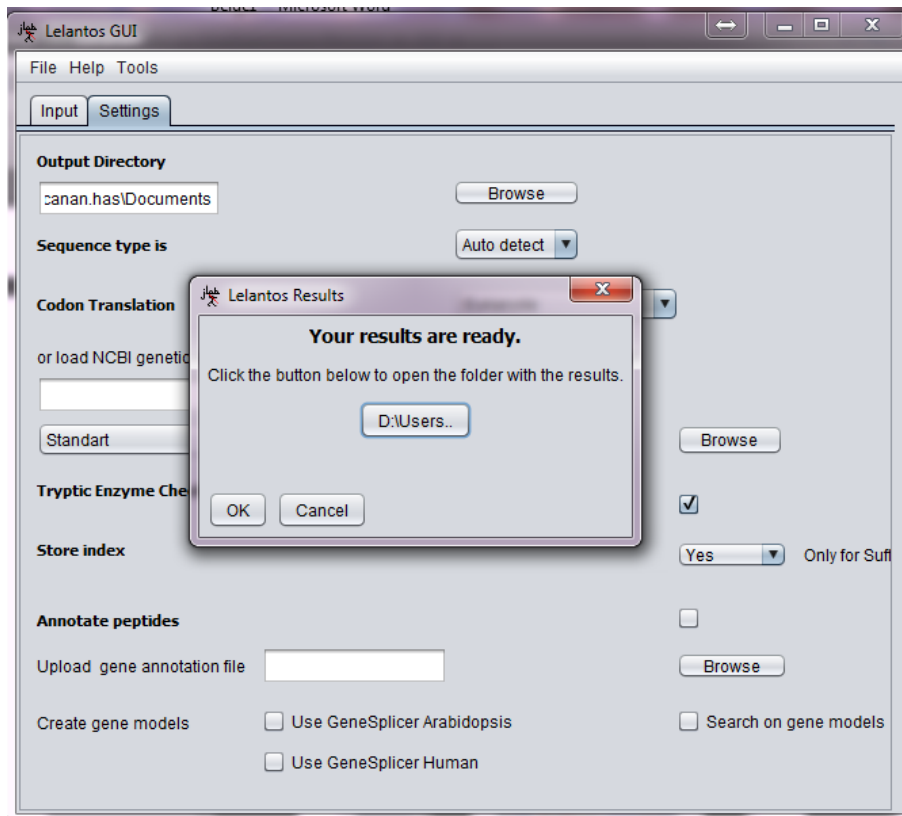


Figure 11: After finish of execution, a dialog box which directs users to result folder pops up.