ProteoAnnotator user guide

1- Download the latest version from: http://www.proteoannotator.org/?q=installation
2- Extract the zip file. Example, extract ProteoAnnotator-1.0.zip
3- Download the test files from: http://www.proteoannotator.org/?q=installation
4- Extract the zip file. Example, extract the ProteoAnnotator_test_files.zip
5- Change the directory to the extracted ProteoAnnotator-1.0.zip.
6- Run the following command:

```
java -Xmx10G -jar mzidentml-lib-1.6.10-SNAPSHOT.jar ProteoAnnotator -inputGFF
PATH_TO_ProteoAnnotator_test_files\canonical_gene_model\ToxoDB-10.0_TgondiiME49.gff -
spectrum_files PATH_TO_ProteoAnnotator_test_files\mgf\Orbitap-1DE\combined.mgf -
outputFolder PATH_TO_ProteoAnnotator_test_files\output_results -inputPredicted
"PATH_TO_ProteoAnnotator_test_files\non_canonical_gene_model\augustus\augustus.gff;PAT
H_TO_ProteoAnnotator_test_files\non_canonical_gene_model\augustus\augustus.aa##PATH_TO
_ProteoAnnotator_test_files\non_canonical_gene_model\glimmer\Toxo-Glimmer-ME49.gff" -
prefix orbitap-1DE toxo10  -compress false -searchParameters
"PATH_TO_ProteoAnnotator_test_files\search.txt" -peptideThreshValue 0.01 -
proteinThreshValue 0.01 –enableMsgf true
```

IMPORTANT: Replace `PATH_TO_ProteoAnnotator_test_files` with the actual path to the unzipped ProteoAnnotator_test_files folder.

Example (change it to match your folder structures):

```
java -Xmx10G -jar mzidentml-lib-1.6.10-SNAPSHOT.jar ProteoAnnotator -inputGFF
C:\ProteoAnnotator_test_files\canonical_gene_model\ToxoDB-10.0_TgondiiME49.gff -
spectrum_files C:\ProteoAnnotator_test_files\mgf\Orbitap-1DE\combined.mgf -
outputFolder C:\ProteoAnnotator_test_files\output_results -inputPredicted
"C:\ProteoAnnotator_test_files\non_canonical_gene_model\augustus\augustus.gff;C:\Prote
oAnnotator_test_files\non_canonical_gene_model\augustus\augustus.aa##C:\ProteoAnnotato
r_test_files\non_canonical_gene_model\glimmer\Toxo-Glimmer-ME49.gff" -prefix orbitap-
1DE_toxo10_  -compress false -searchParameters
"C:\ProteoAnnotator_test_files\search.txt" -peptideThreshValue 0.01 -
proteinThreshValue 0.01 –enableMsgf true
```

In this example the "`PATH_TO_ProteoAnnotator_test_files`" is "`C:\ProteoAnnotator_test_files`"

Parameter	optional/ mandatory	Explanation
`-prefix`	Optional	A prefix to be attached to the output file names
`-inputGFF_A`	Mandatory	The canonical GFF file
`-inputFasta_A`	Optional if the canonical GFF contains the FASTA	The protein database
`-outputFolder`	Mandatory	The output folder for the analysis
`-spectrum_files`	Mandatory	The MGF file (only one input file currently supported, later builds will incorporate multiple files to be merged).
`-searchParameters`	Mandatory	The search parameters file to be used for the search.
`-inputPredicted`	Optional	The non-canonical gene models, these are a set of GFF/FASTA files. The GFF and FASTA are separated by ';' and the pairs are separated by

		'##'
– peptideThreshValue	Mandatory	Peptide FDR Threshold value
– proteinThreshValue	Mandatory	Protein FDR Threshold value
–enableMsgf	Mandatory	Enable/Disable MSGF+