* Note: Complete and full testing of this software was not completed due to time restraints, as a result unexpected issues could occur if the instructions are not followed. Additionally, due to a lack of complete testing, inaccurate results may be generated, therefore a healthy skepticism of the results caution may be a good idea.
* These instructions assume you are using spectroscopy.py on Ubuntu (Linux).
* Upload all of the following files to the same folder.
* Make sure you have installed the following software:
  + Python 3.8
    - Command: sudo apt-get install python3.8
  + Python module: scipy
    - Command: pip install scipy
  + Python module: numpy
    - Command: pip install numpy
* Upload a protein prospector tsv file to the folder where spectroscopy.py is
* Command: python3.8 spectroscopy.py
* Enter the protein prospector tsv file name (Note: the file’s name will likely end with “.txt”)
* Enter a peptide sequence or the default peptide sequence will be used, “\*DAEFRHDSGYEVHHQK\*”
* The files that will be generated:
  + fragment-intensities-[current\_date].csv
  + ​​processed-fragment-intensities-[current\_date].csv
  + color-script-[current\_date].txt