Read Me

To use this program, ensure that the HA\_NLGN3\_Developmental\_Mass\_Spec.xlsx needs to be in the same folder as the python files.

1. First please open and run the CreateGeneJson.py. This will create the JSON file which will be written to the same folder.
2. From there please run the DBSCAN\_Cluster.py file. This will open a webpage with the 3D scatter plot.
3. If you can’t access that please open the Biof509 Finalgraph.webarchive