

**USER MANUAL for IonStarSPG.R**

The first input into the IonStarStat package is a spectrum report containing a filtered PSM list. This report can be exported conveniently from a number of softwares, e.g. Proteome Discoverer, Scaffold. Here we will demonstrate the use of the IonStarSPG.R spectrum report generator using results obtained from MS-GF+ (database search) and IDPicker (post-search processing).

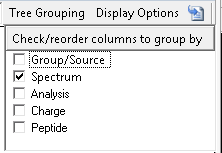
**I. Input files**

*Search results* .tsv files **(Sample name.raw.tsv)** converted from .mzid files using MSGFPlus.jar (-showQValue = 1, -shoeDecoy = 1, -unroll = 1)

*Protein list* .tsv file exported from the Protein View tab of the .idpDB file

*Peptide list* .tsv file exported from the Peptide View tab of the .idpDB file

*Spectrum list* .tsv file exported from the Spectrum View tab of the .idpDB file (Tree grouping = Spectrum)



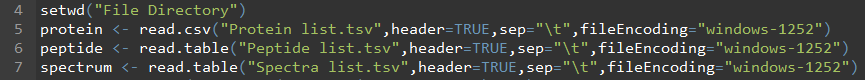
**II. Spectrum report generation with IonStarSPG.R**

*1. Confirm that all input files are located under the same directory.*

*2. Generate spectrum report*

a. Change the input and output file names:

Line 4~7



Line 70



b. Run the script by **Source** function.

c. The output (Spectrum report.csv) contains the filtered PSM from each LC-MS run as follows:

