0 use only “peptide confidence” filter, no peptide/protein grouping = disabled

Columns to use:

* First scan
* PEP
* Precursor area
* Protein group accession
* Search engine rank
* Xcorr
* Sequence
* Delta M (PPM)
* Intensity

1 sort by rank (up), Xcorr (down), PEP (up), Scan (up), remove duplicates on Scan

2 add intensities to PSMs without precursor area, or “100” to PSMs without both [=if(D2=””,if(E2>0,E2,100),D2]

3 replace cC, mM, yY, copy to next column and replace IL

4 copy seqs and protein accessions to new column, collapse on seqs and countif seqs, sumif deltaM and divide by countif seqs

5 collapse original list with duplicates in seqs and areas and sumif areas

6 (index/match protein accessions) and filter by >1psm, -1.5<deltaM<1.5, VH only

7 combine all injections and map clonotypes and V/J genes

8 calculate R for psm, area and average