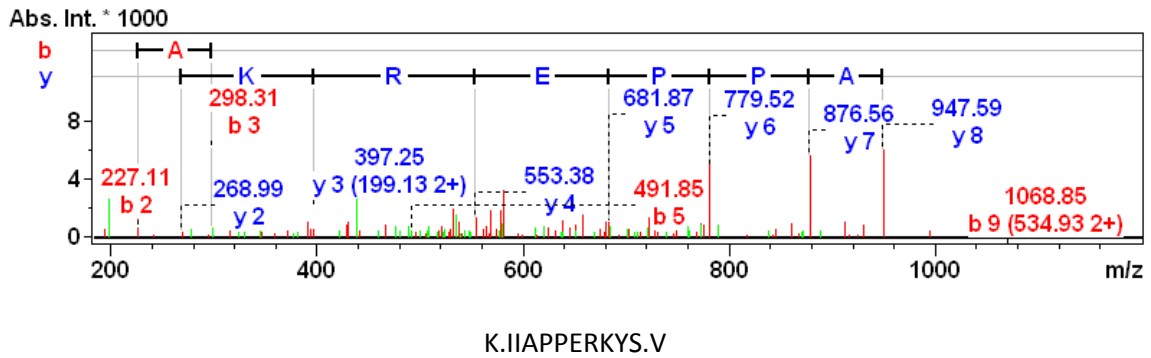
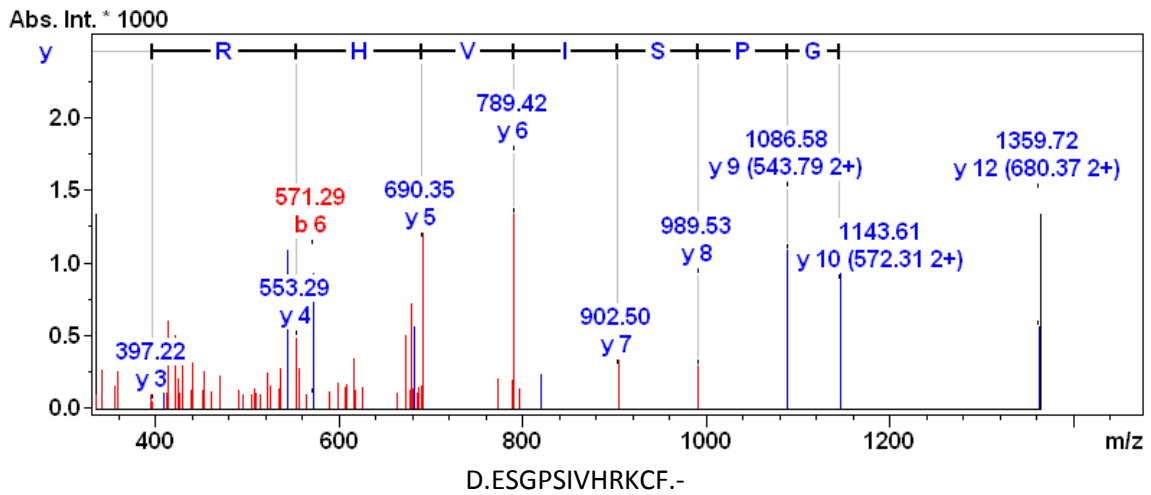
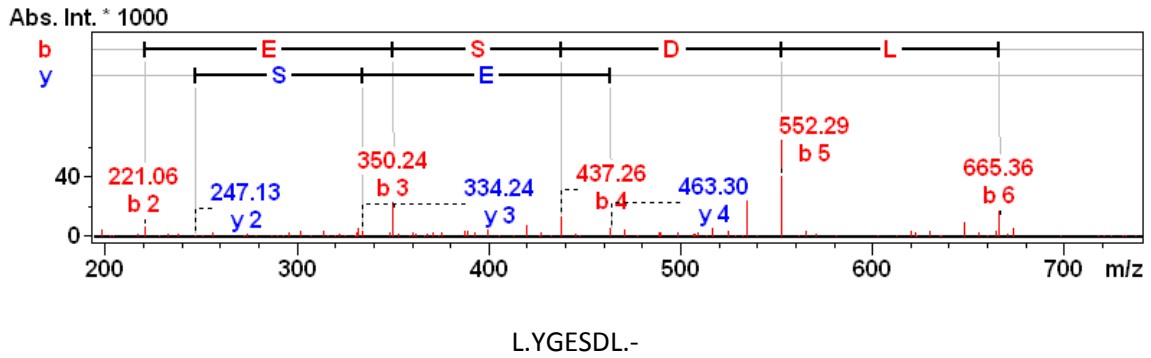


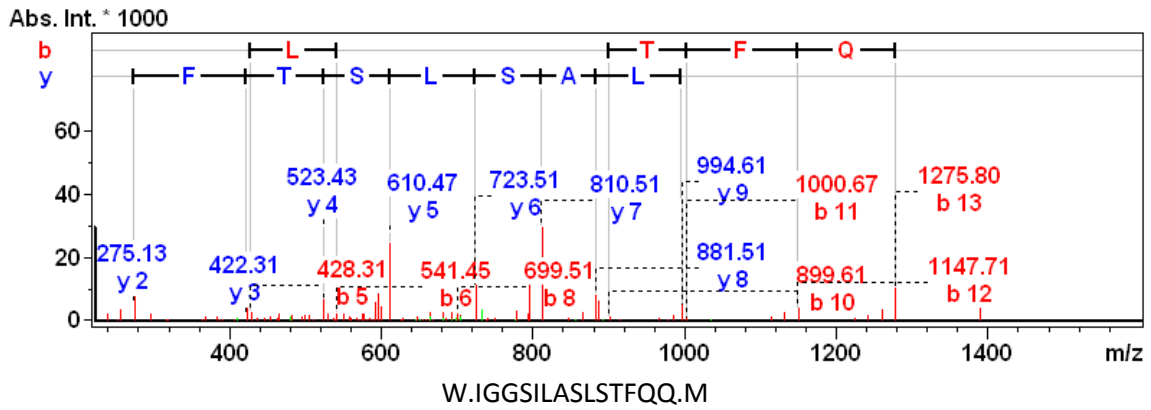
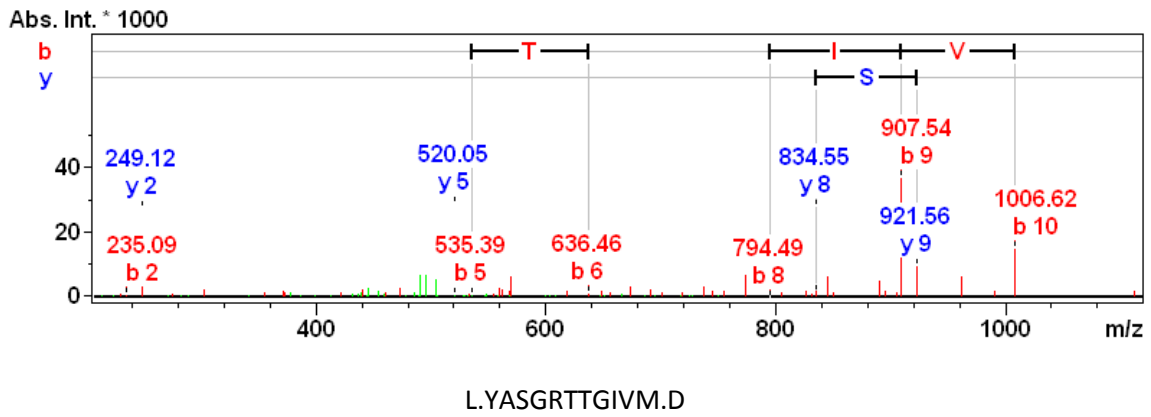
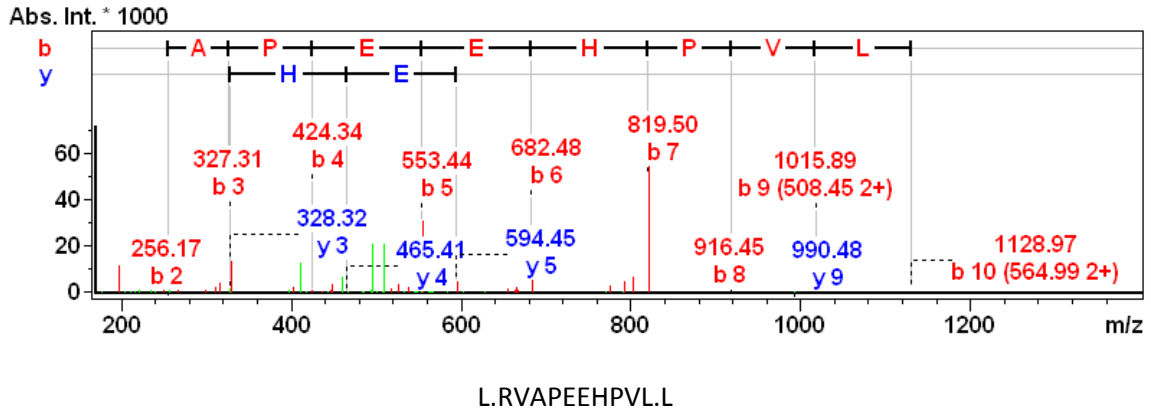
Peptidomic Analyses of Mouse Astrocytic Cell Lines and Rat Primary Cultured Astrocytes

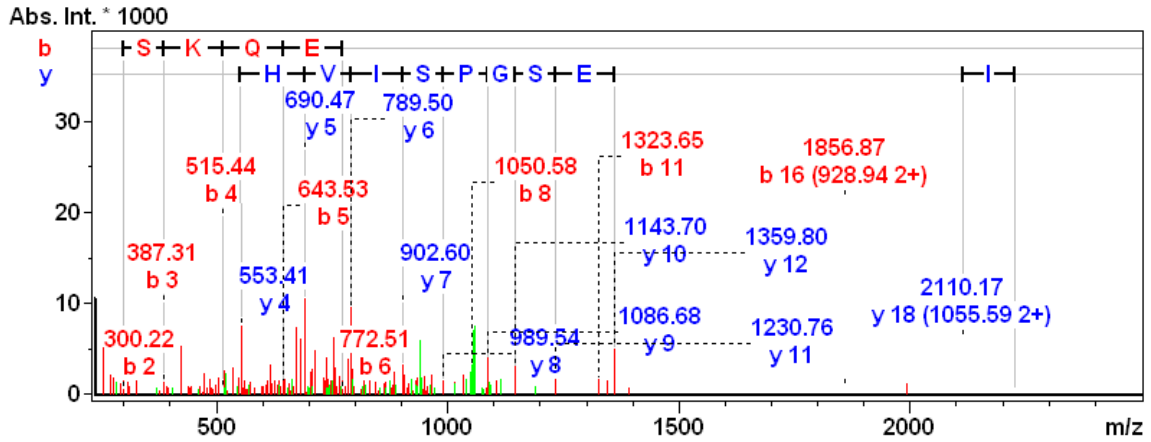
Ping Yin^{1,4}, Ann M. Knolhoff^{1,4}, Harry J. Rosenberg³, Larry J. Millet², Martha U. Gillette²⁻⁴,
Jonathan V. Sweedler^{1,3,4*}

Supporting Information

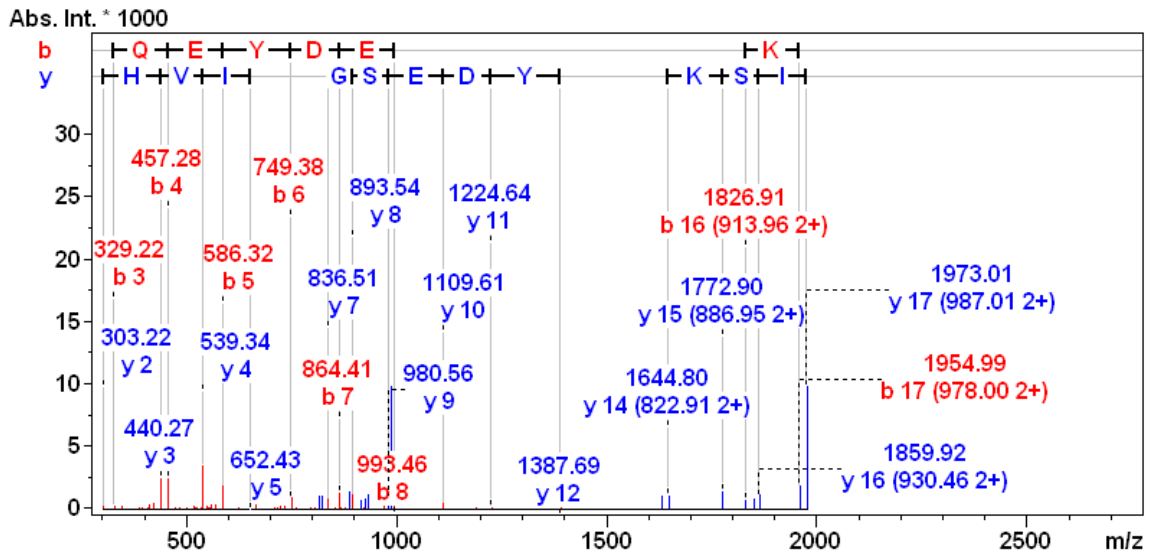
The MS/MS spectra for peptide identifications with the annotations on masses, *b* and *y* ions, and amino acid assignments by BioTools 3.1. The entire peptide sequence is shown under the corresponding MS/MS spectrum. The mass tolerances were set to 0.55 Da for the ESI-IT MS/MS data and 0.05 Da for the ESI-Qq-TOF MS/MS data. Each peptide has either an ion score higher than 30 in the Mascot search or more than three consecutive amino acids assigned within the mass tolerances.



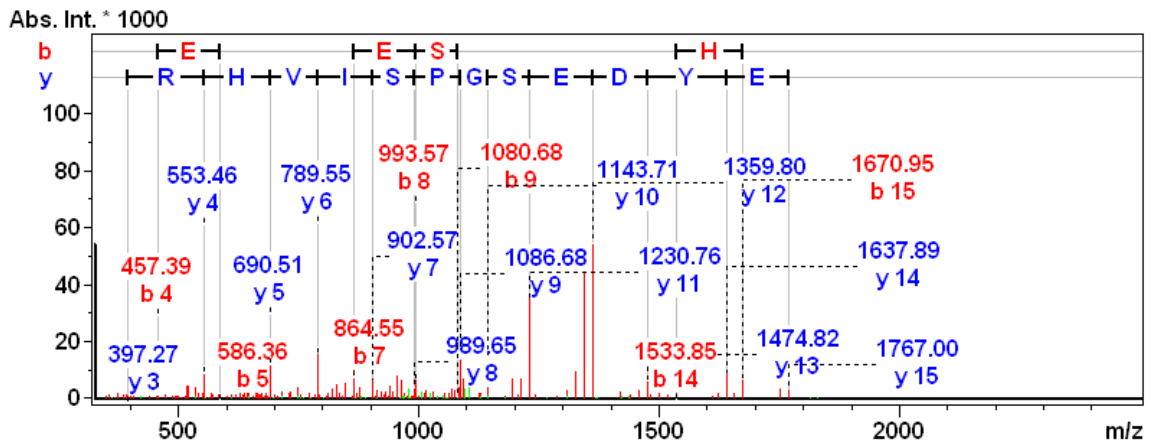




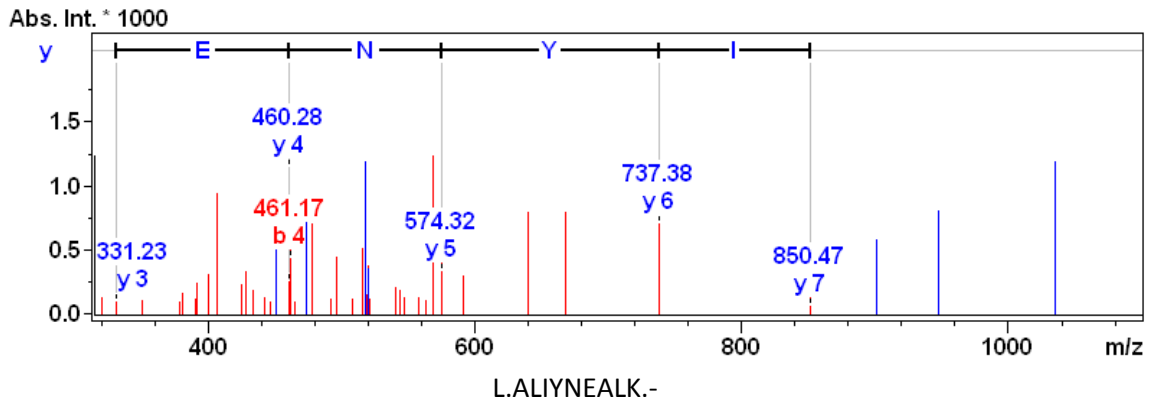
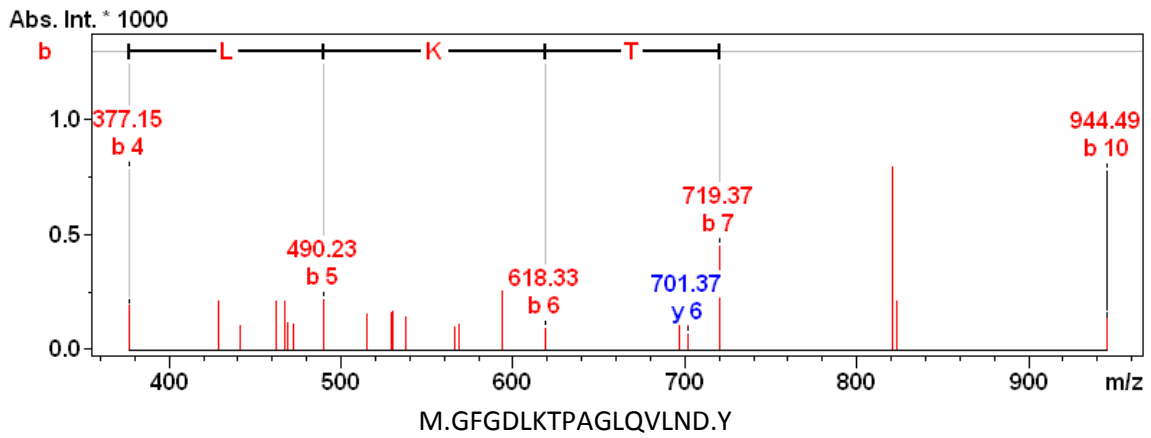
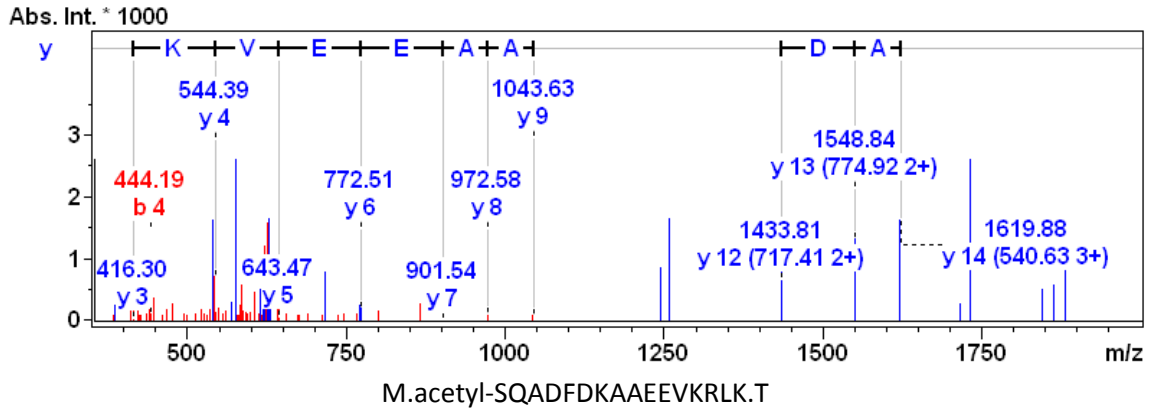
M.WISKQEYDESGPSIVHRKCF.-

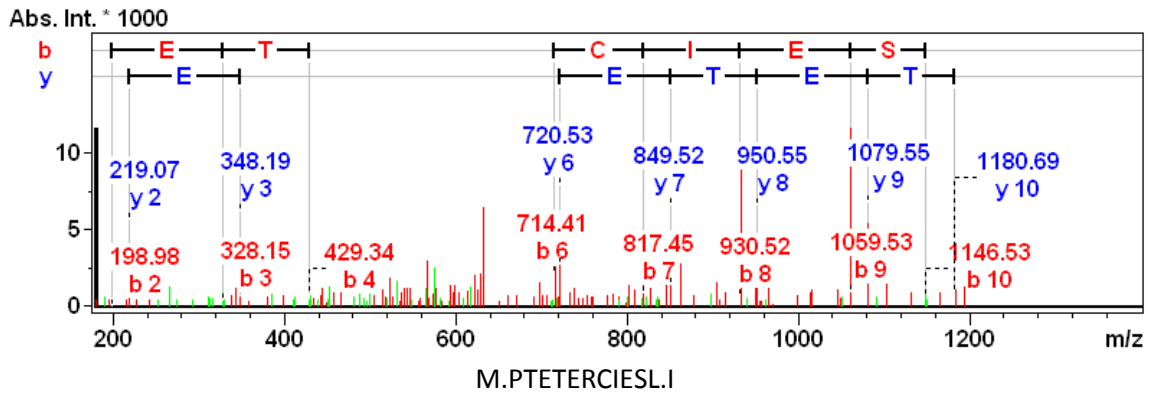
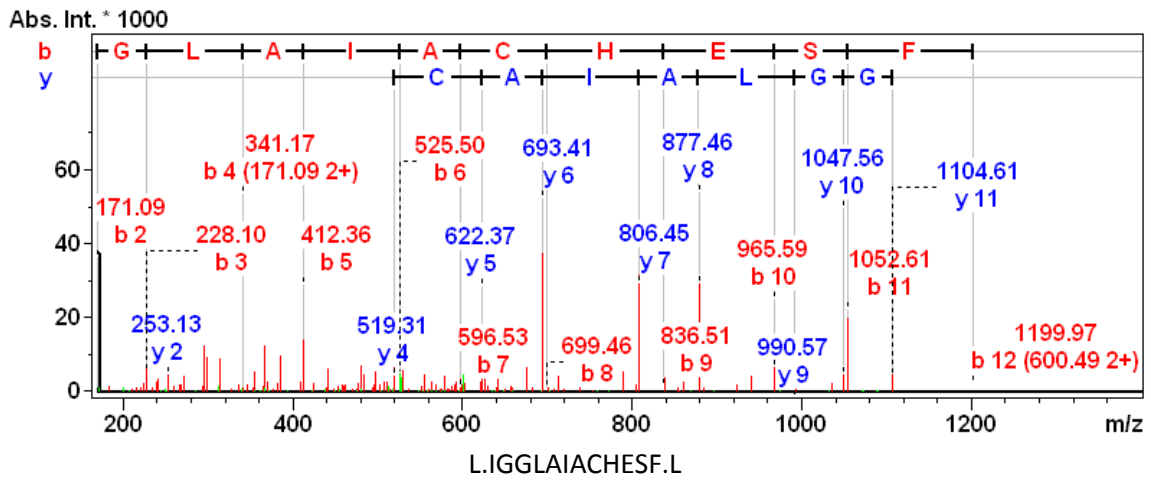
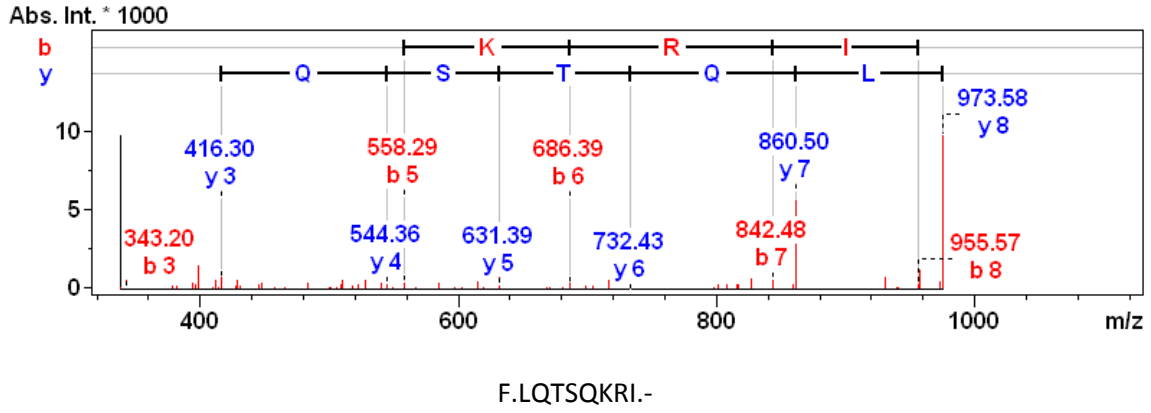


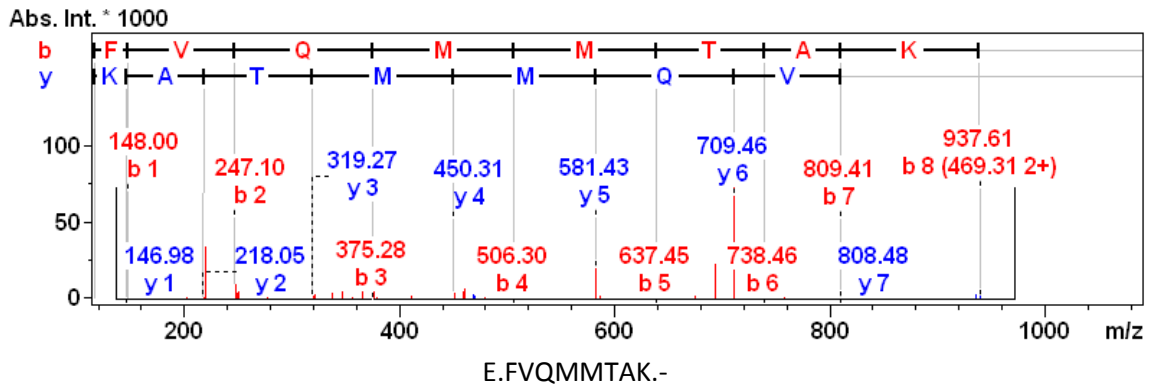
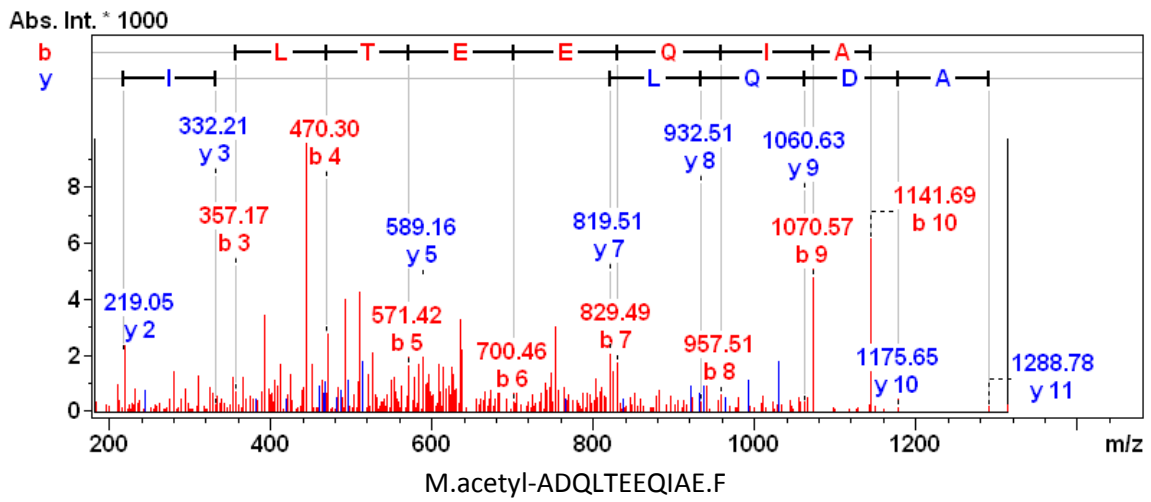
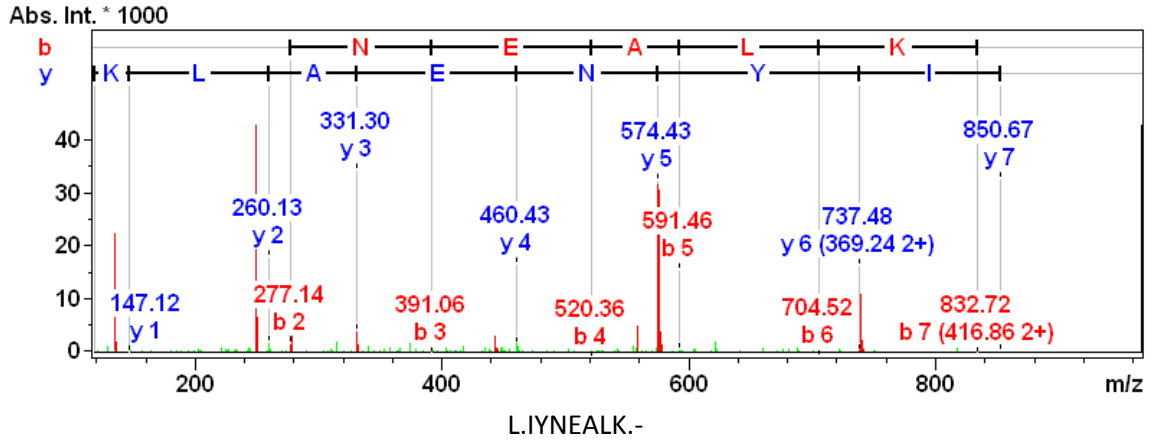
W.ISKQEYDESGPSIVHRK.C

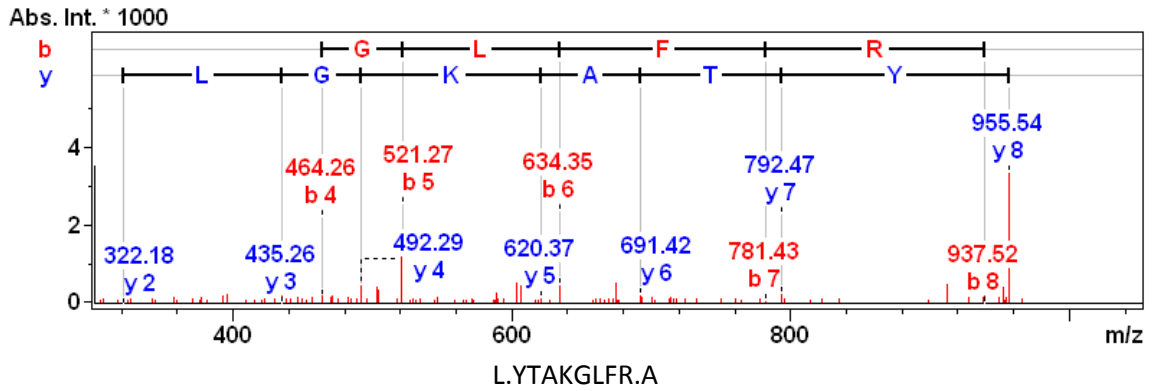
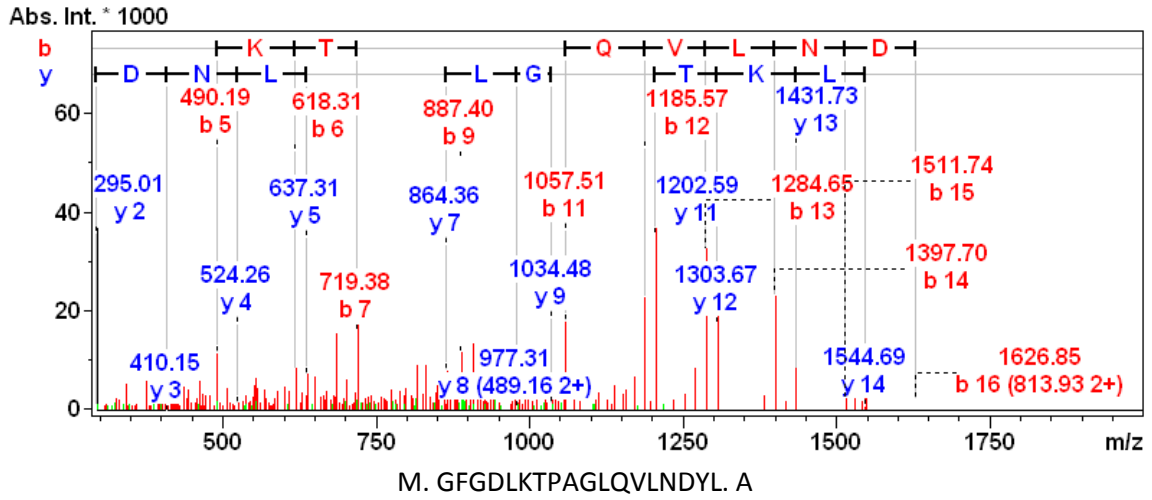
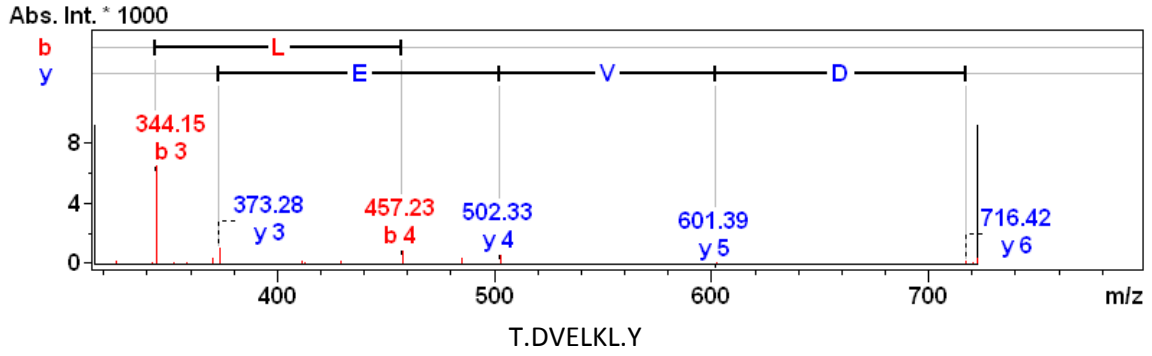


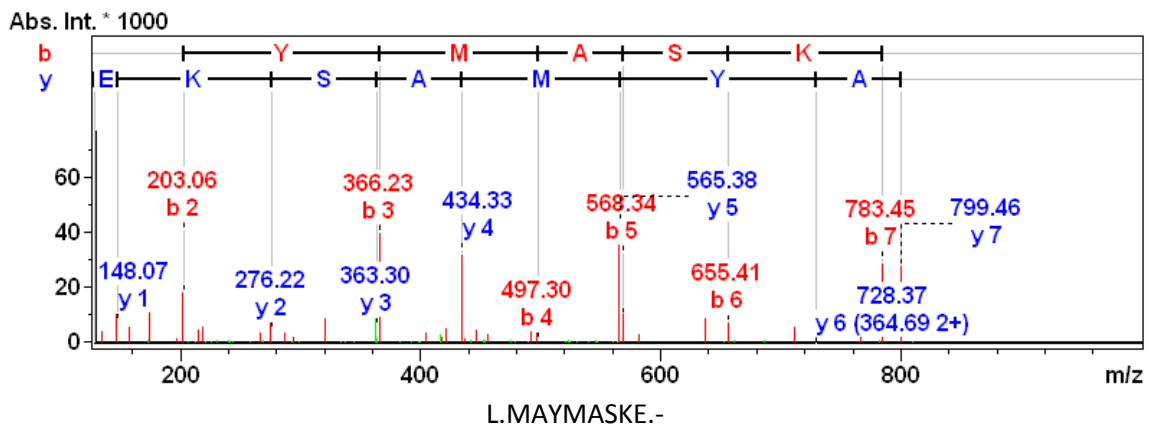
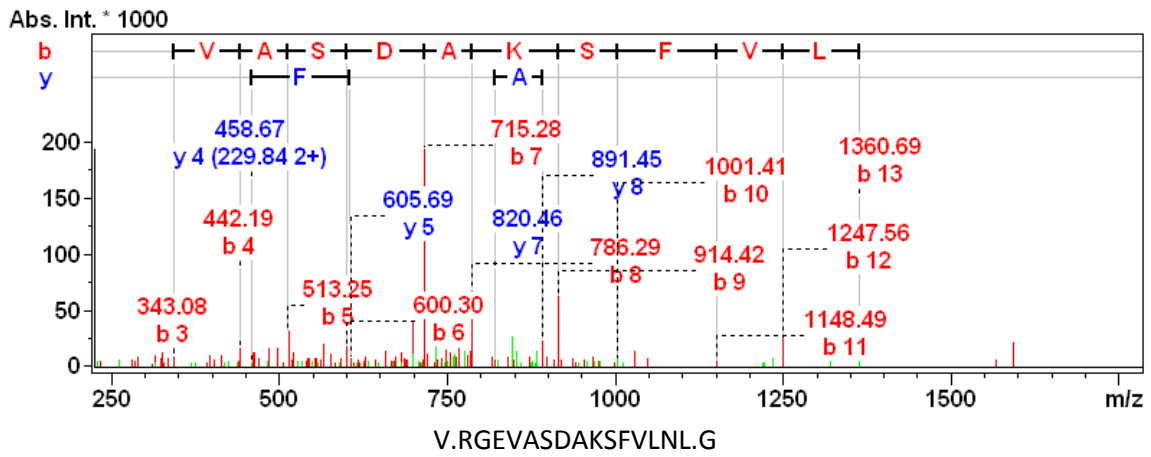
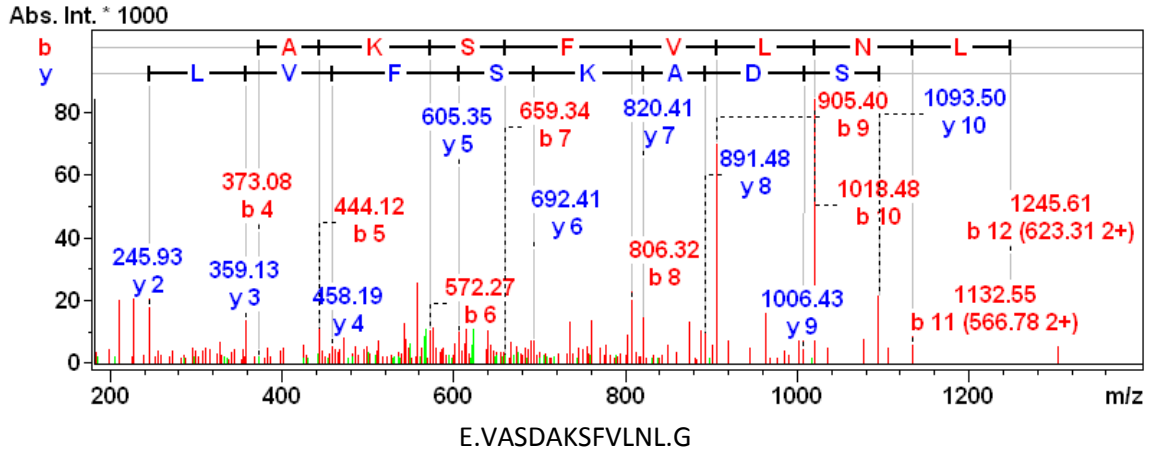
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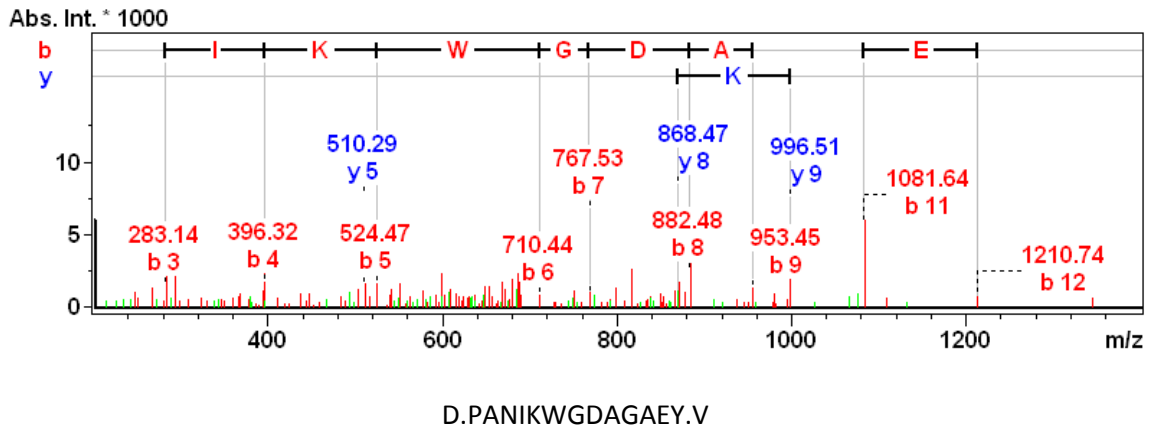
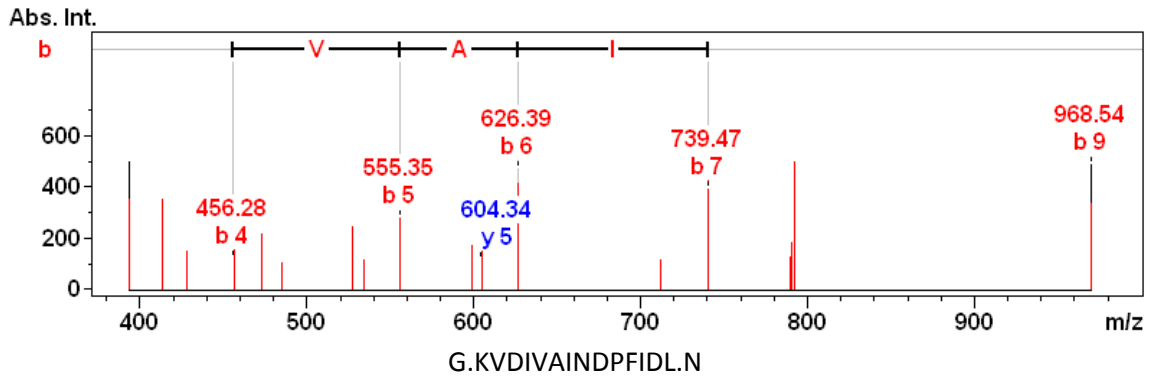
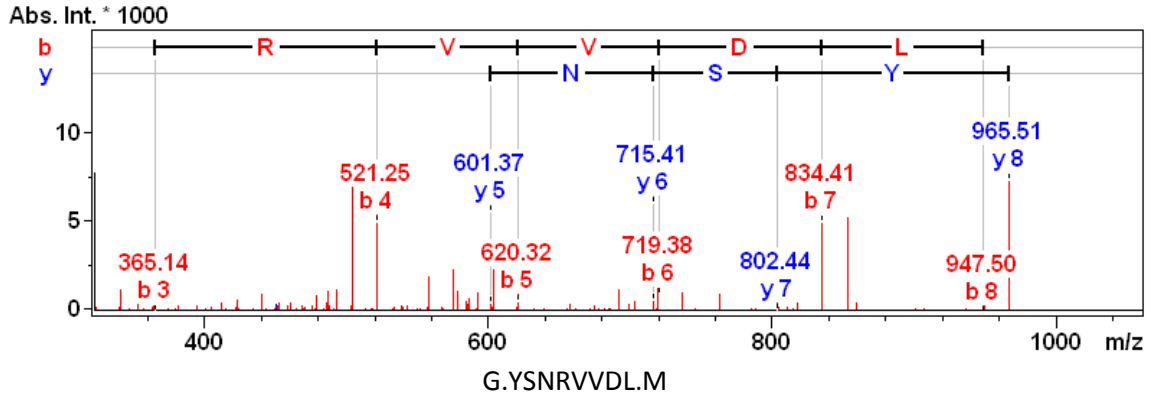


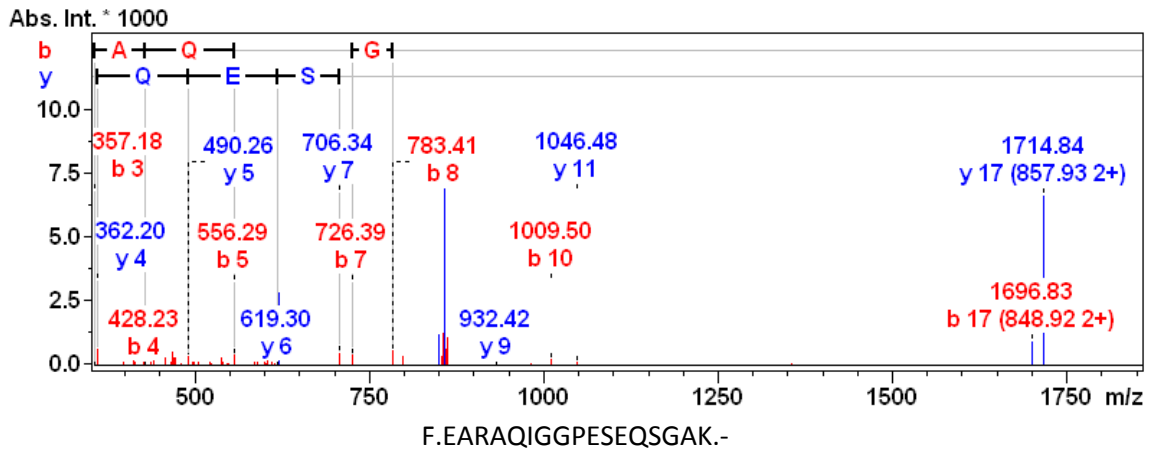
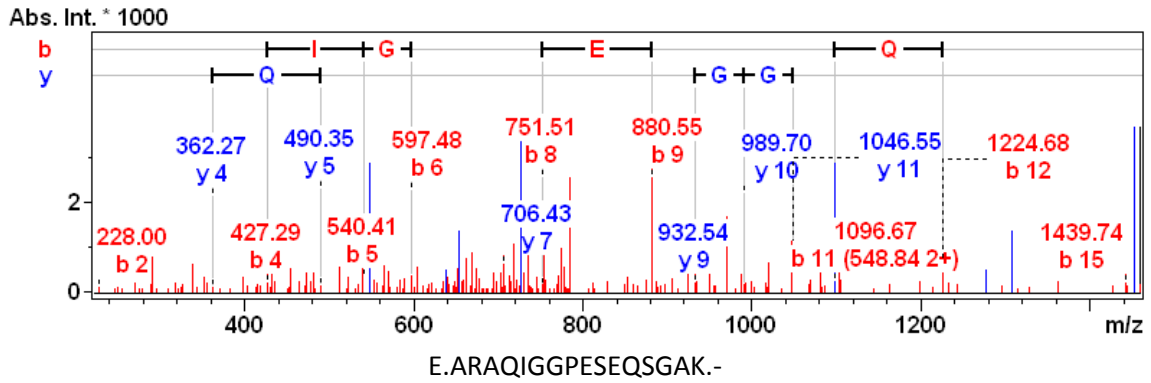
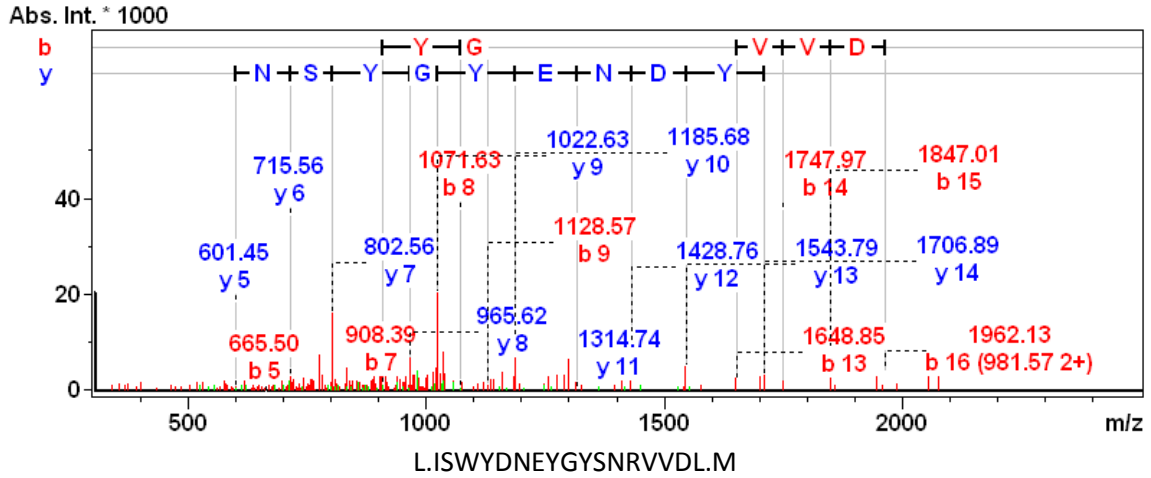


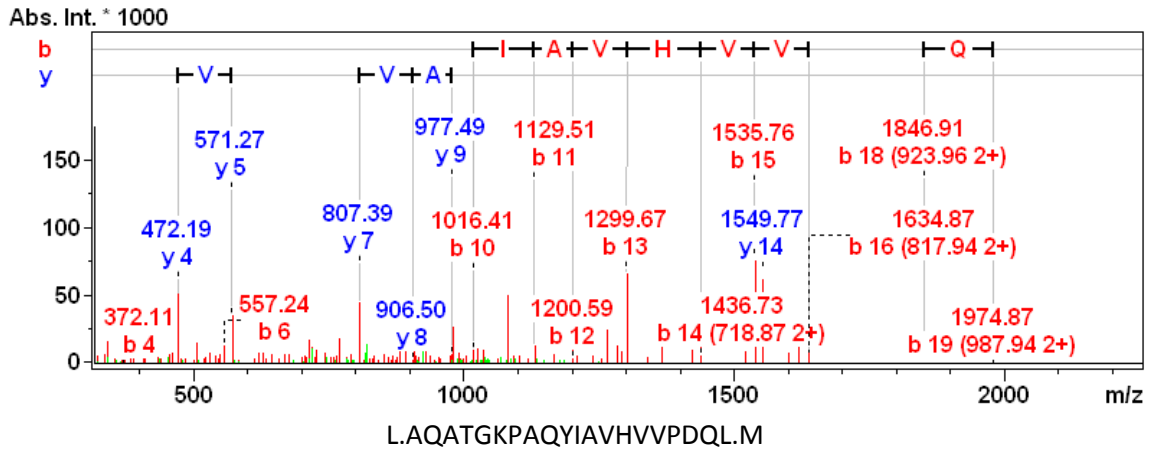
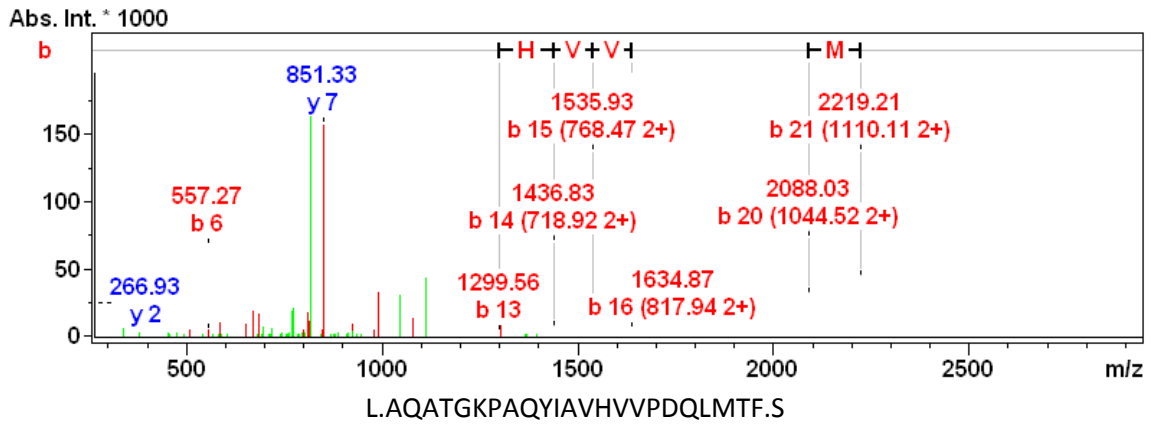
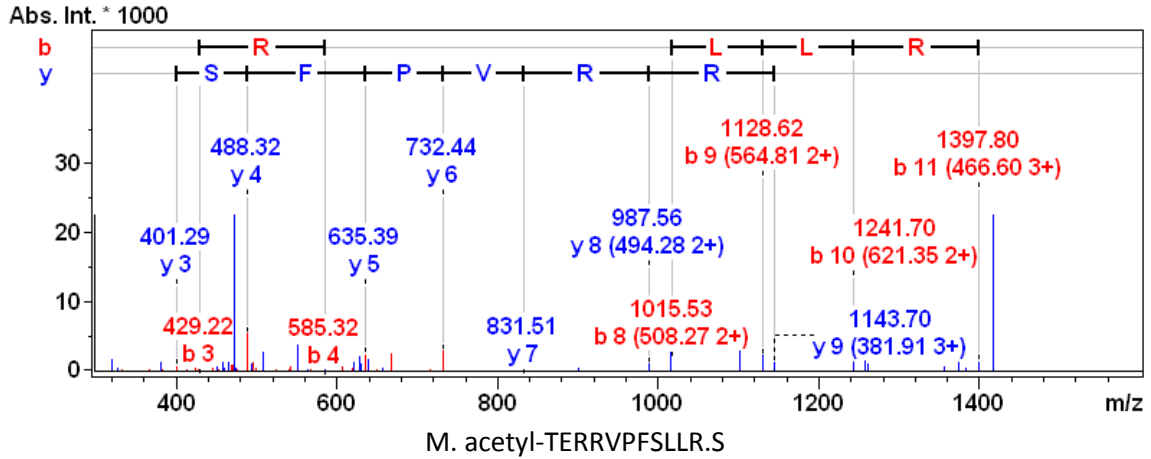


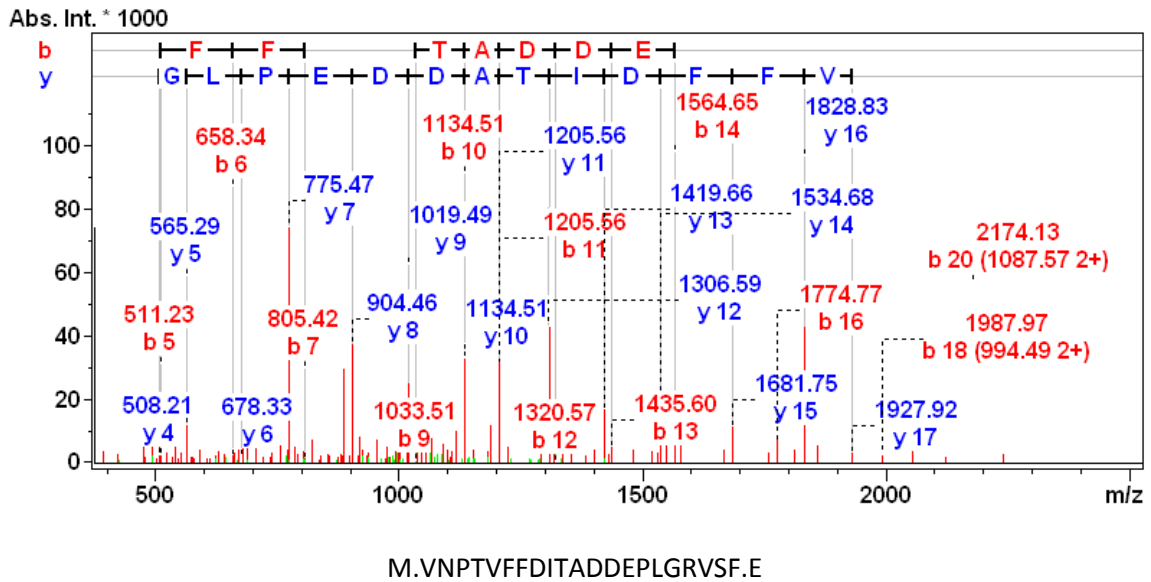
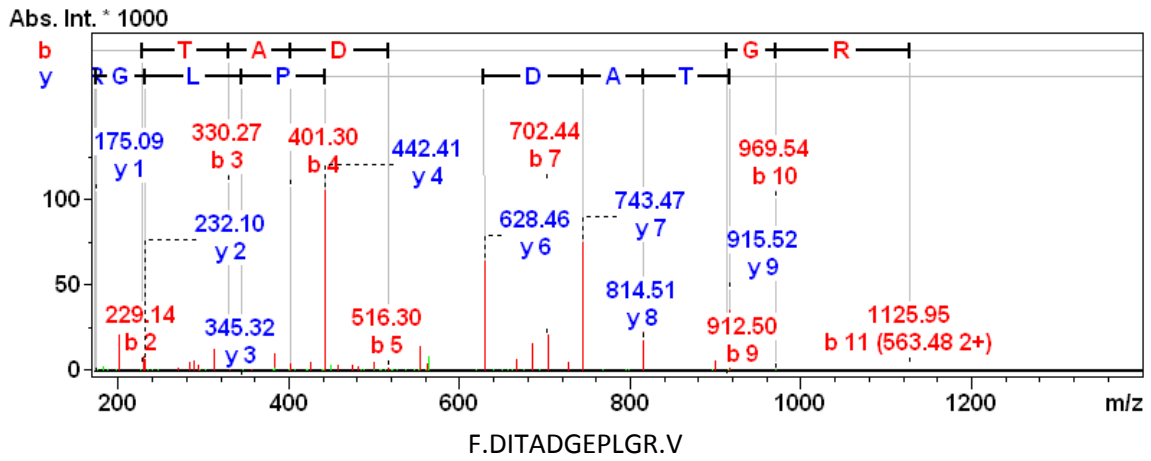
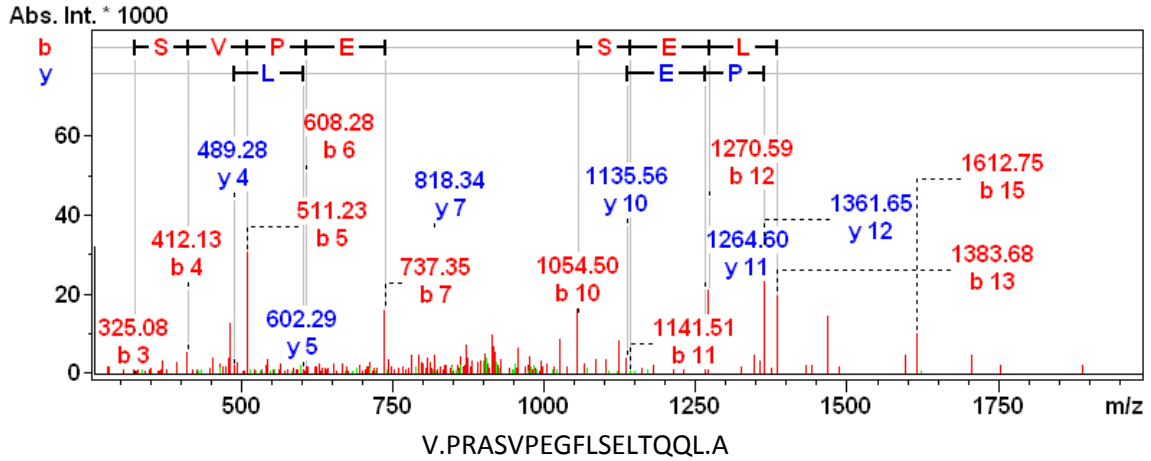


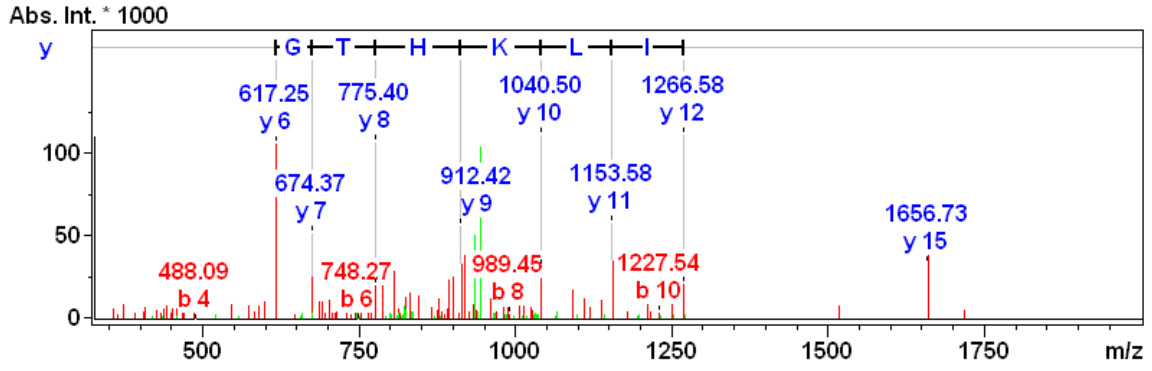




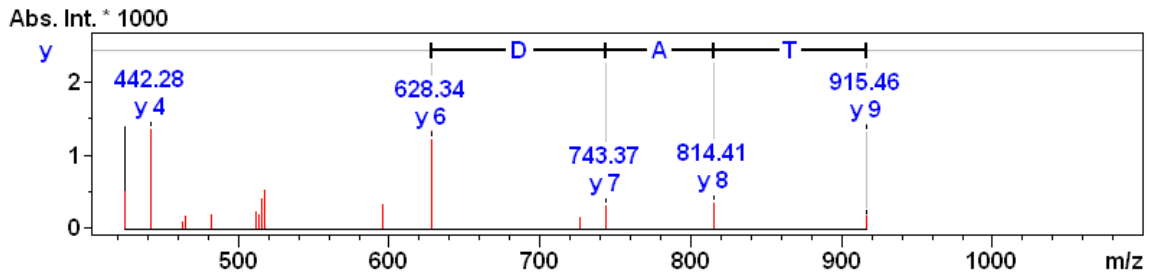




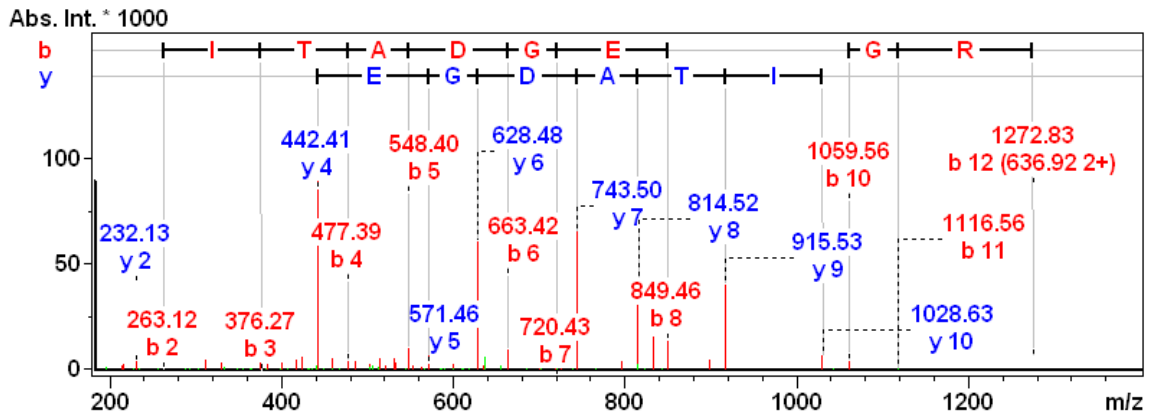




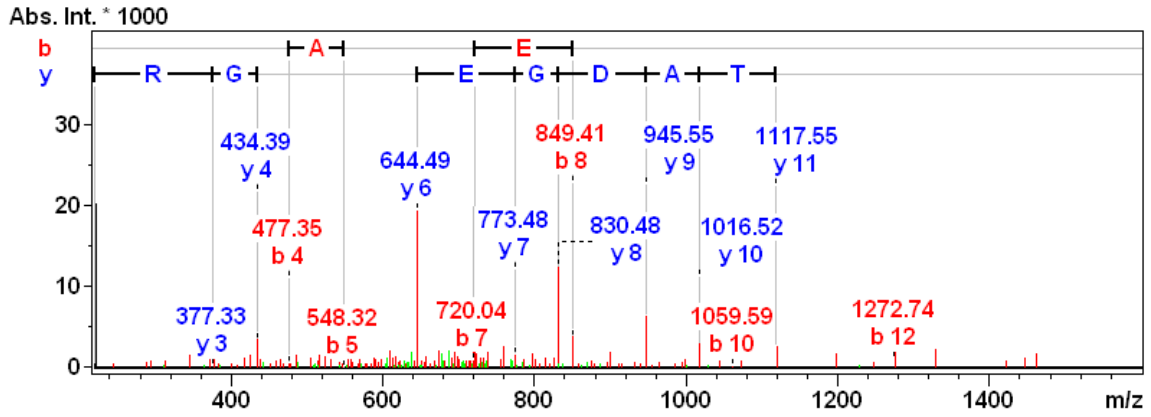
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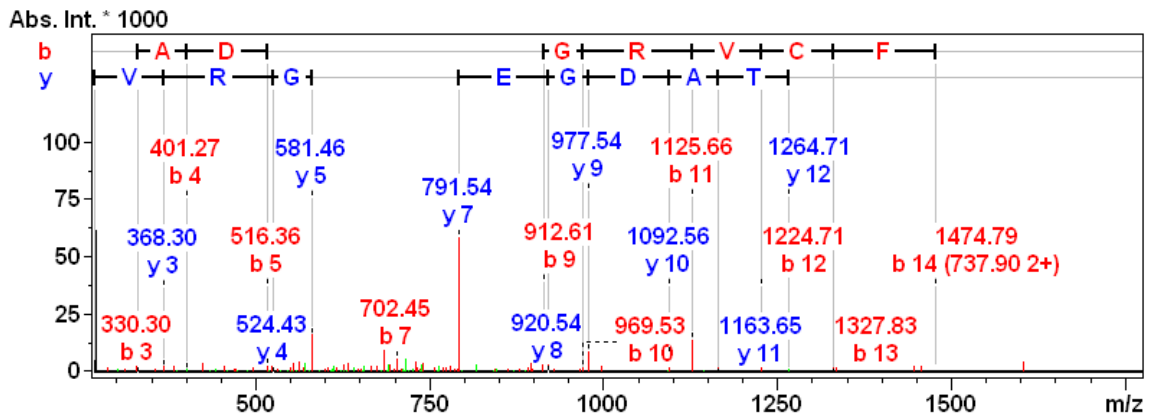
D.ITADGEPLGR.V



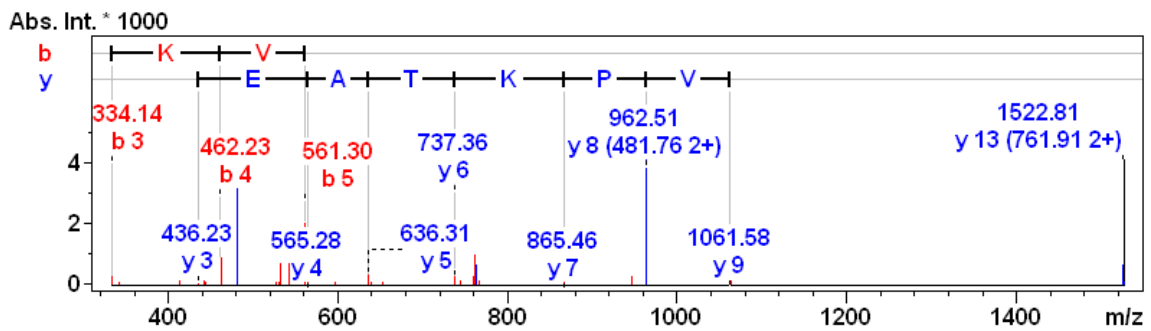
F.FDITADGEPLGR.V



F.FDITADGEPLGRVC.F



F.DITADGEPLGRVCF.E



L.FADKVPKTAENFR.A

