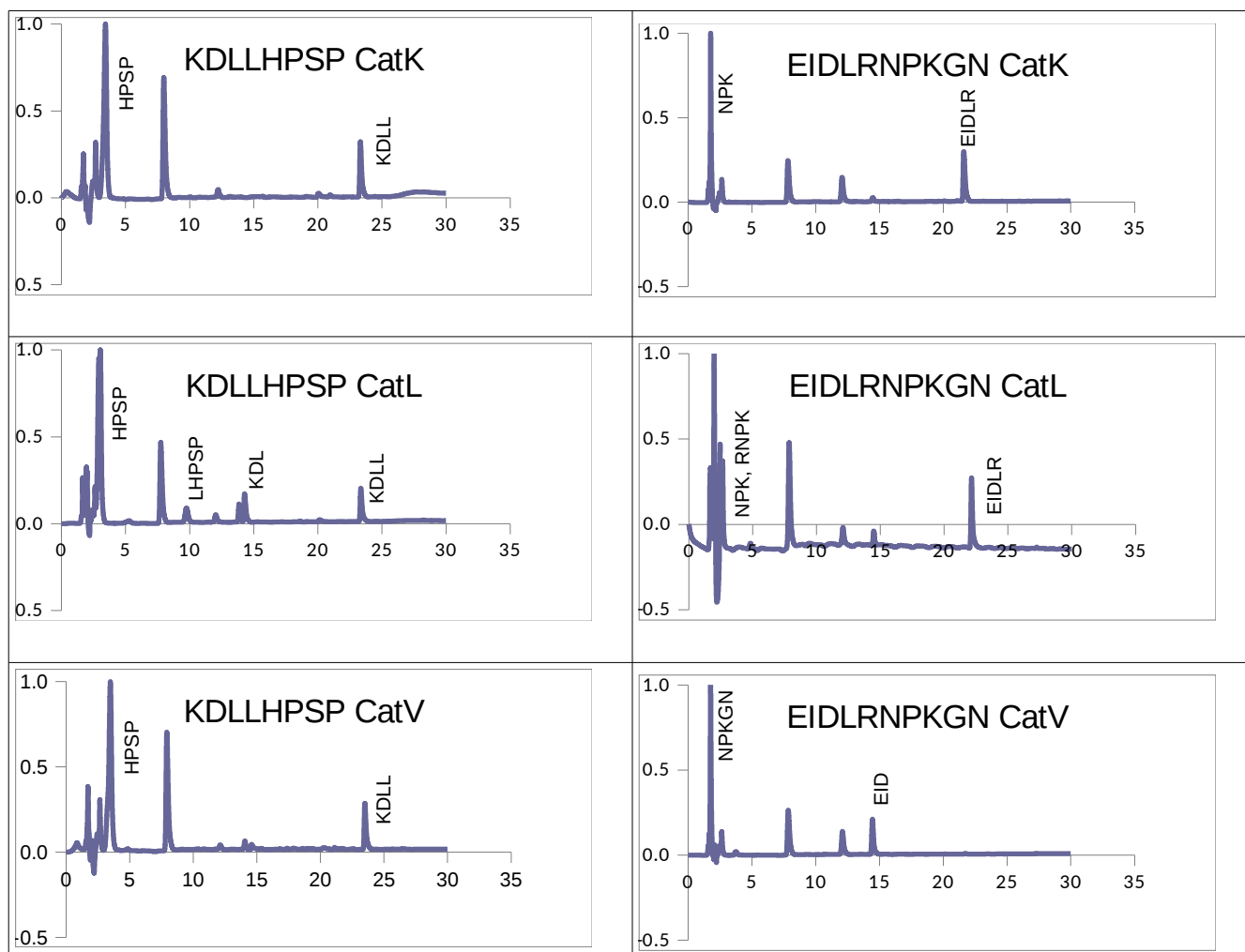
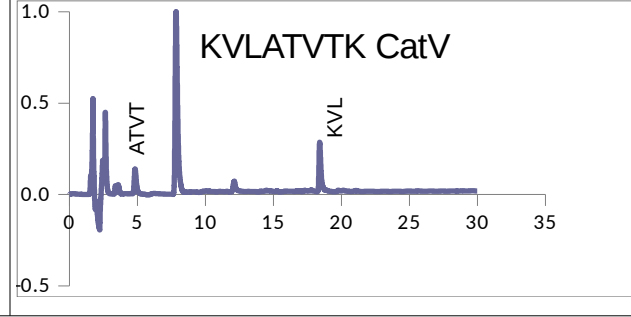
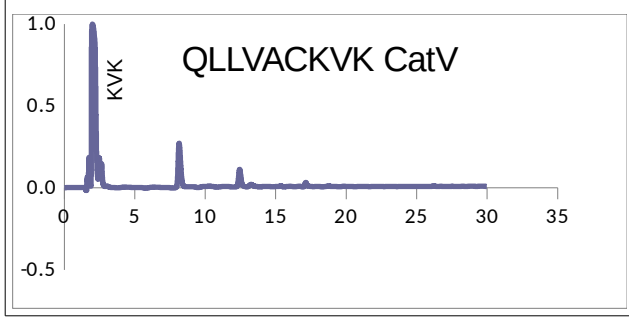
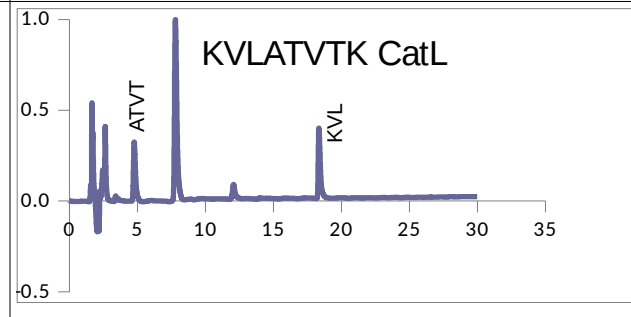
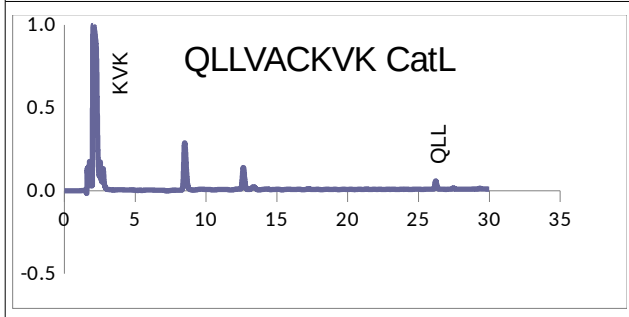
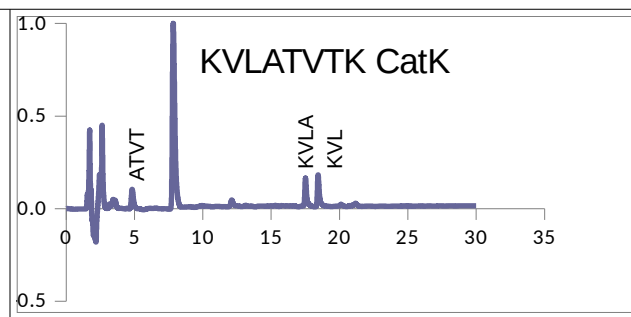
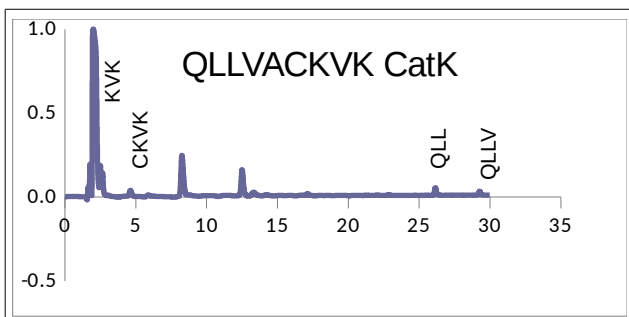
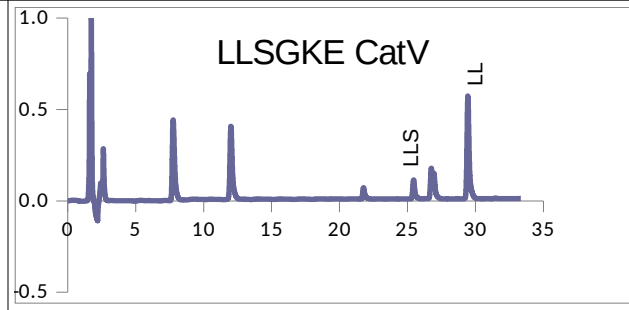
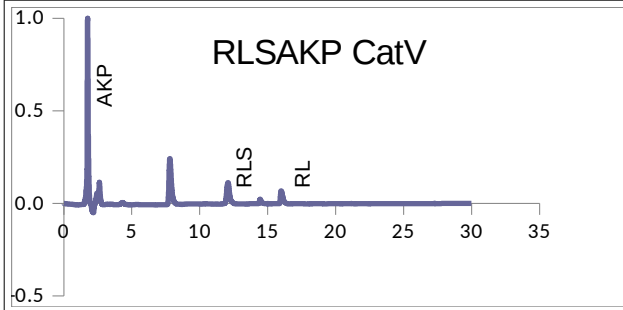
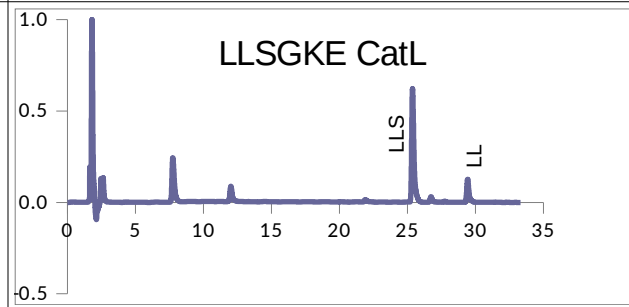
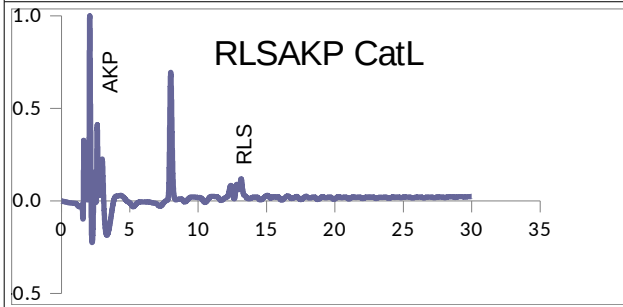
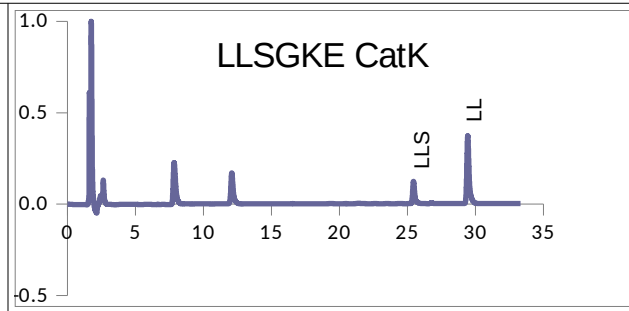
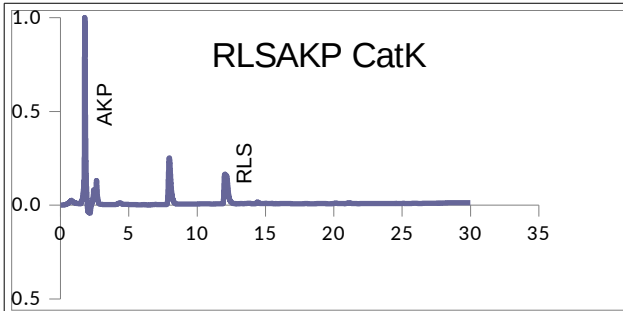


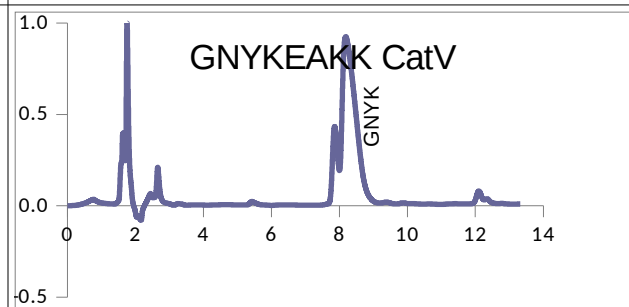
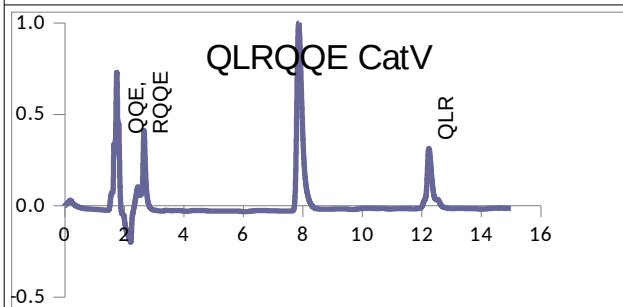
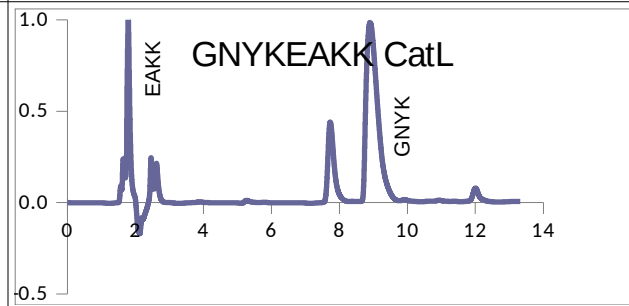
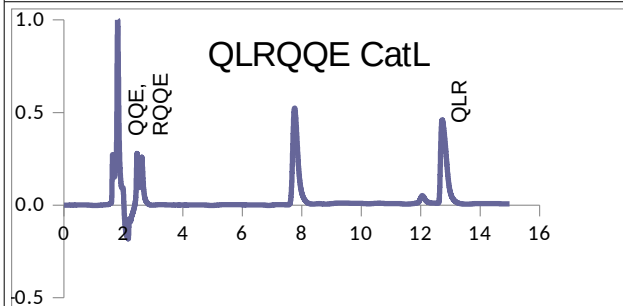
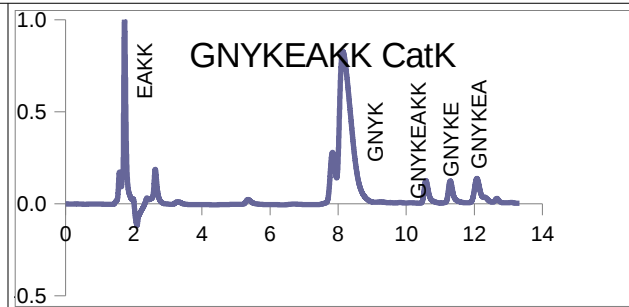
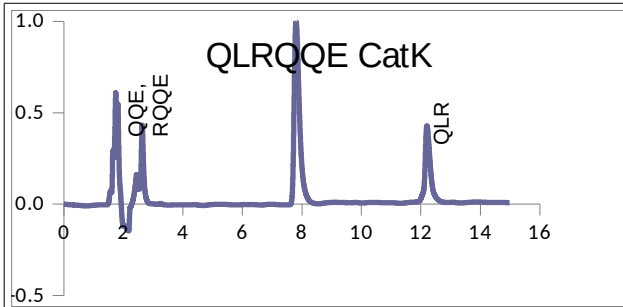
Supplementary Data 4. Peptide cleavage analysis.

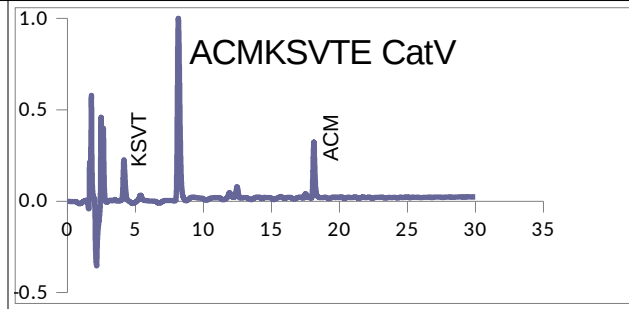
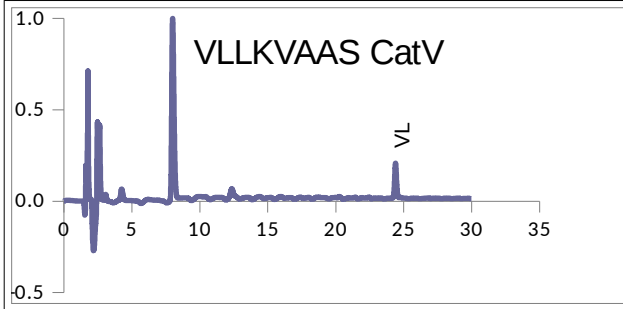
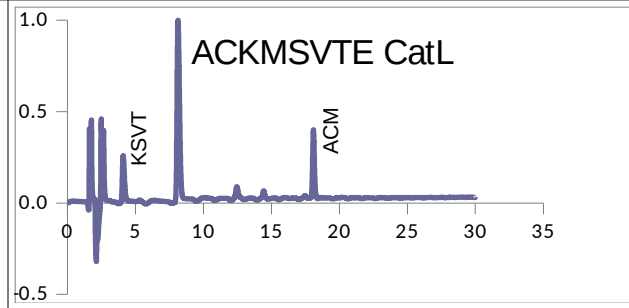
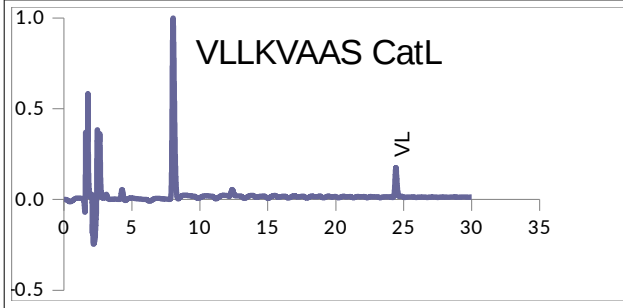
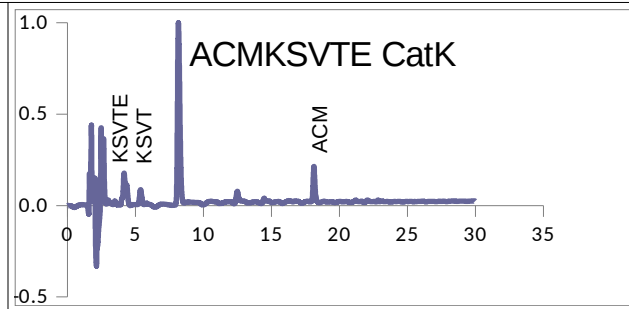
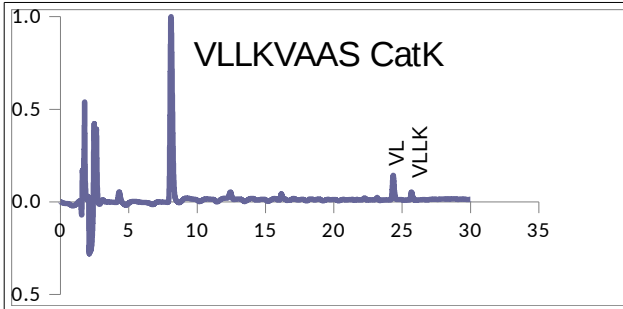
a. Peptide fragment identification. Peptides treated with cathepsins were applied on RP-HPLC. Peaks representing the peptide fragments were captured. Separation was monitored at 214 nm. Y-axis show normalized signal of absorbance at A_{214} and x-axis represent separation time in minutes. Peptide sequences as identified with MALDI-TOF are written on top or next to their corresponding HPLC signal. Characteristics signals at around 8 min and 12 min correspond to buffer component dithiotheritol (DTT) and cathepsin, respectively.

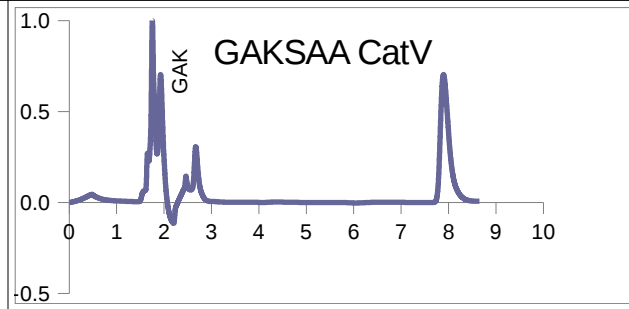
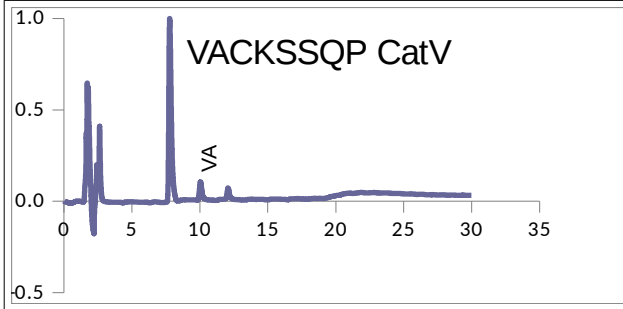
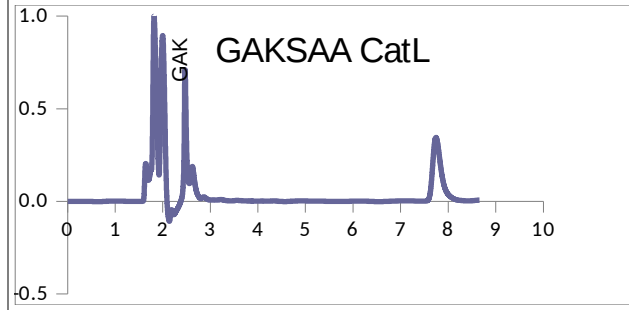
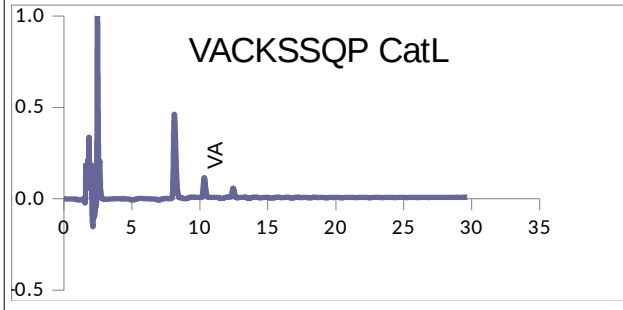
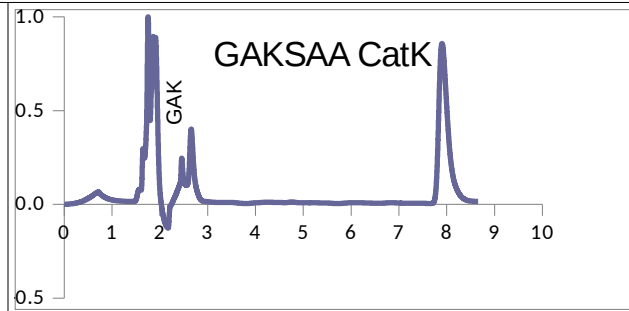
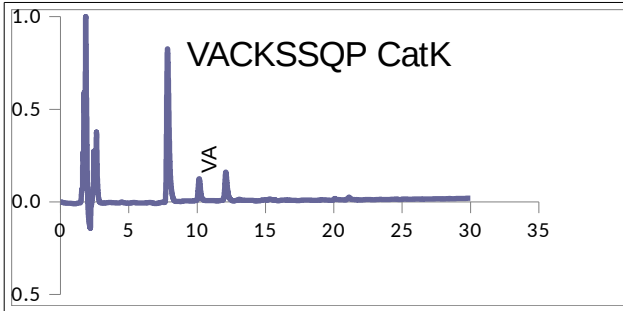


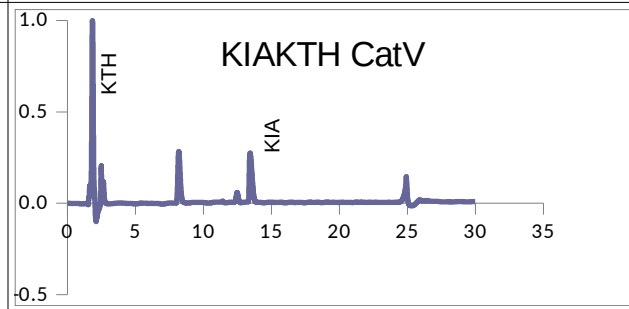
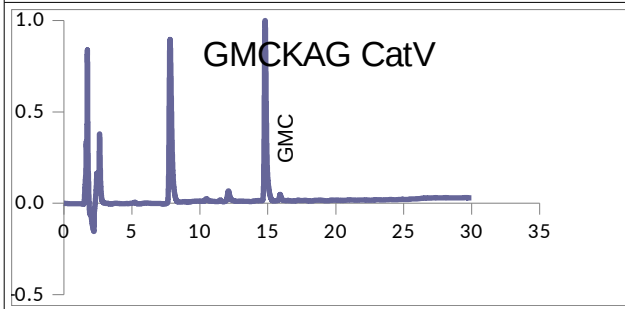
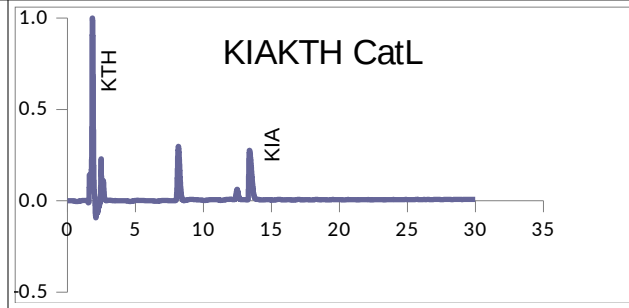
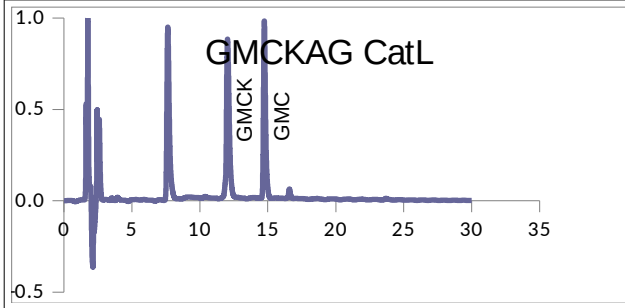
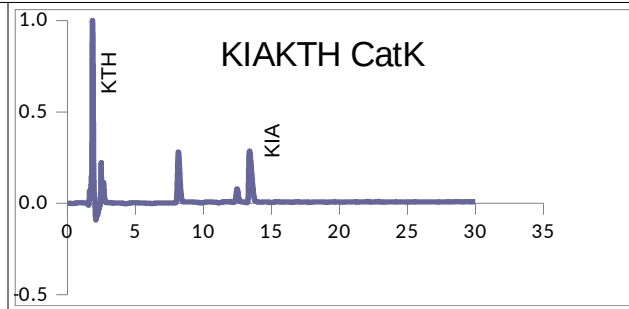
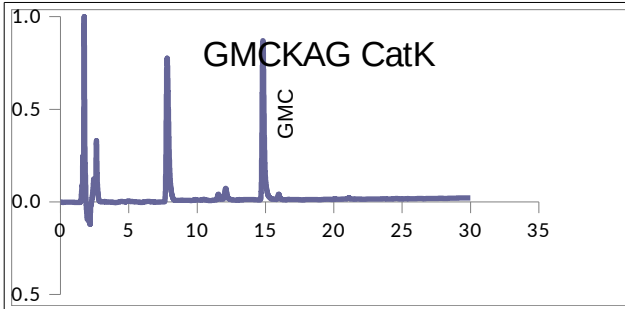


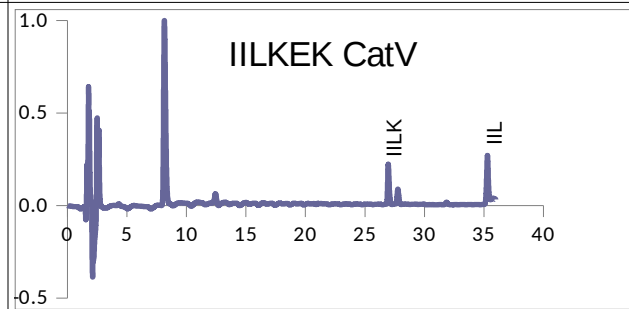
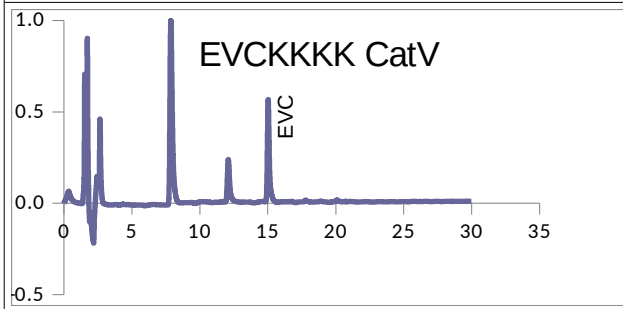
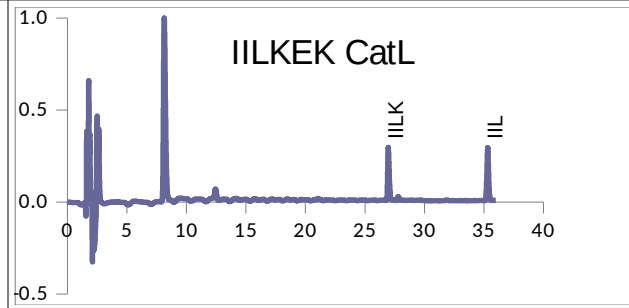
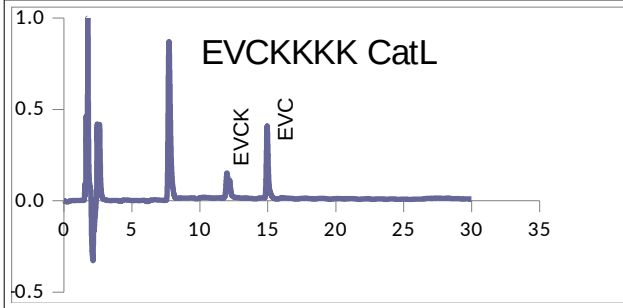
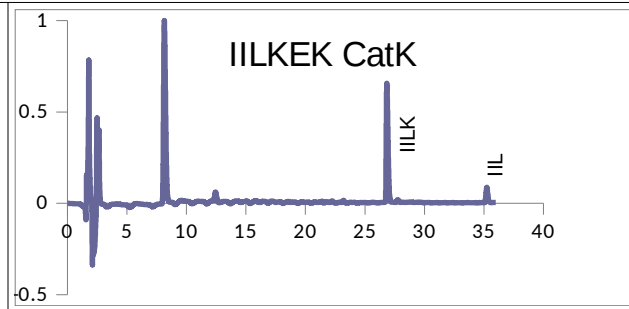
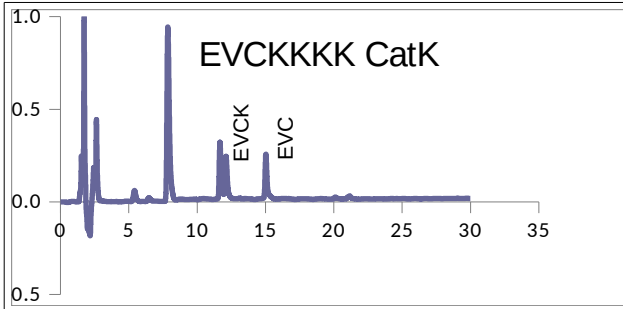


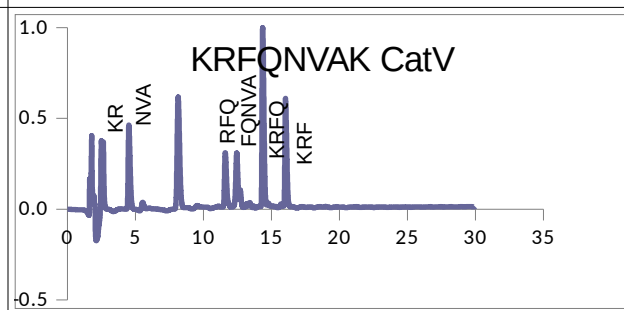
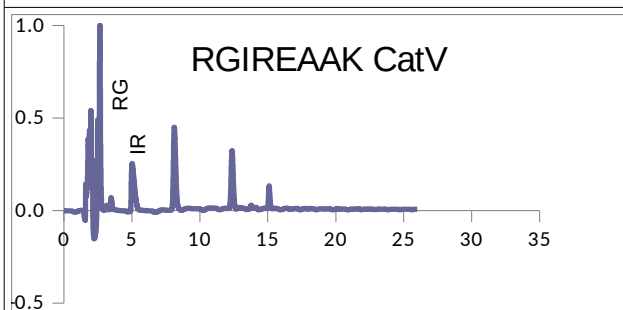
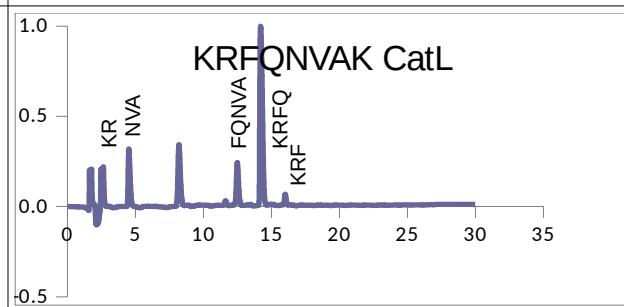
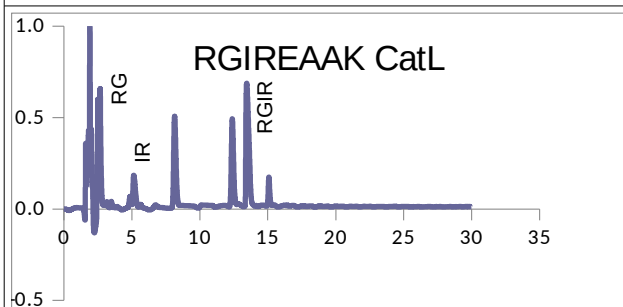
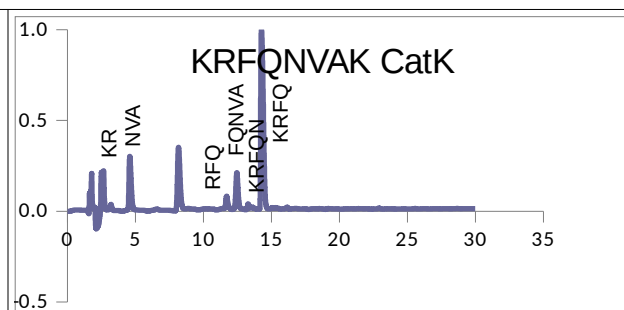
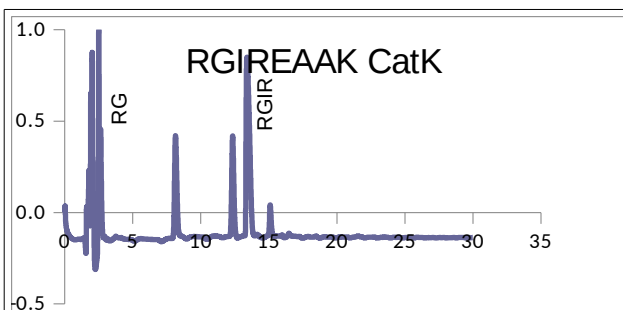


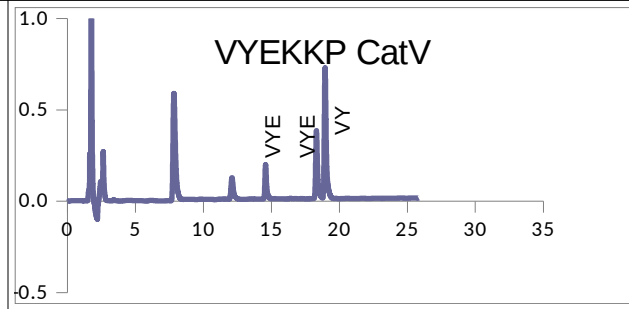
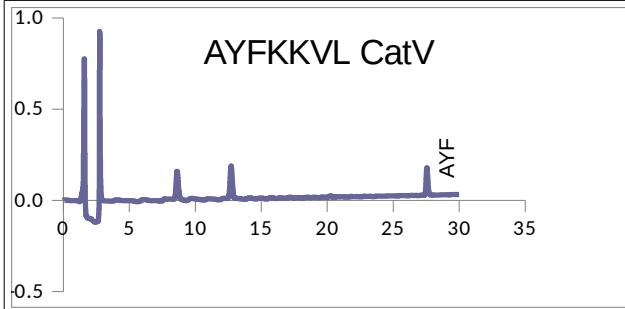
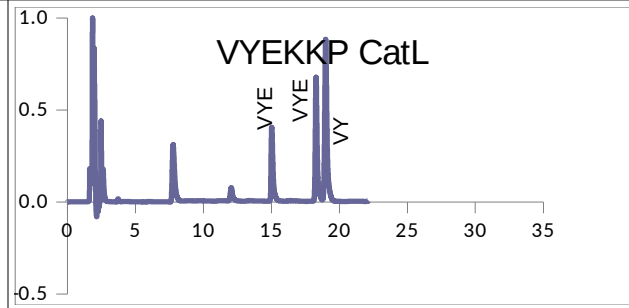
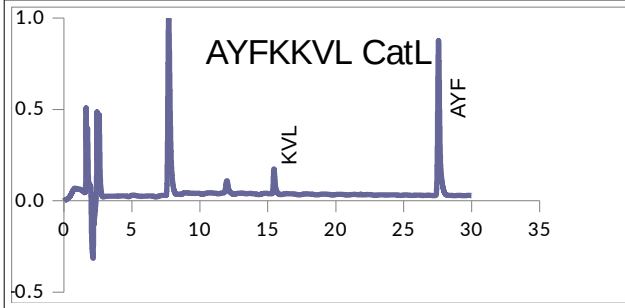
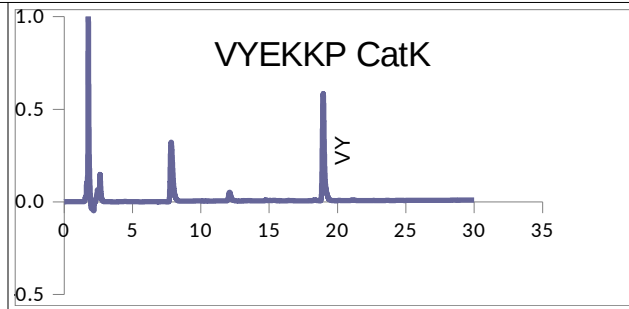
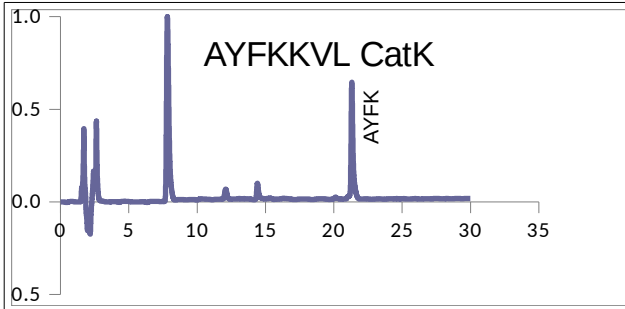


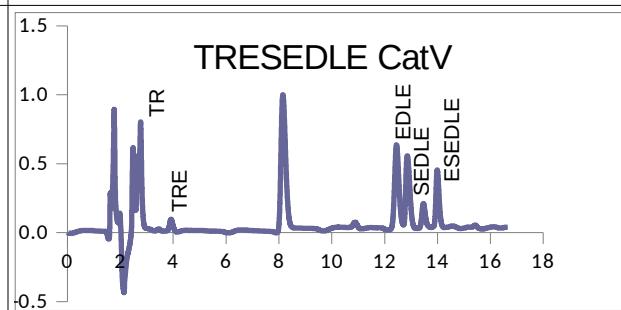
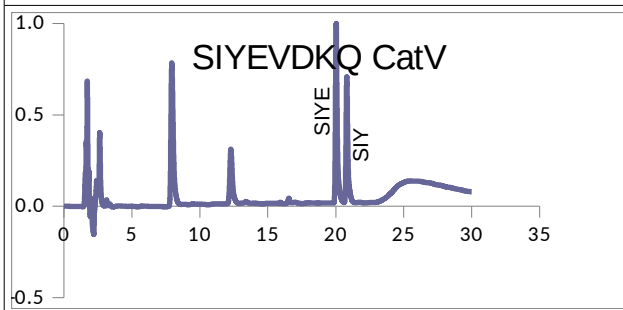
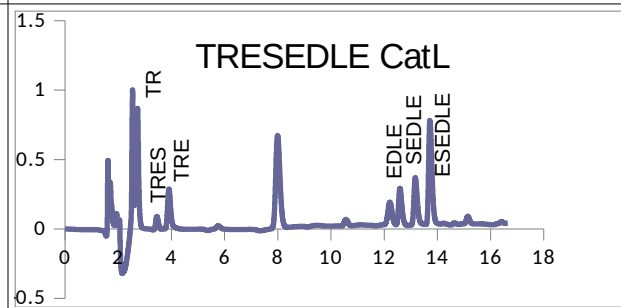
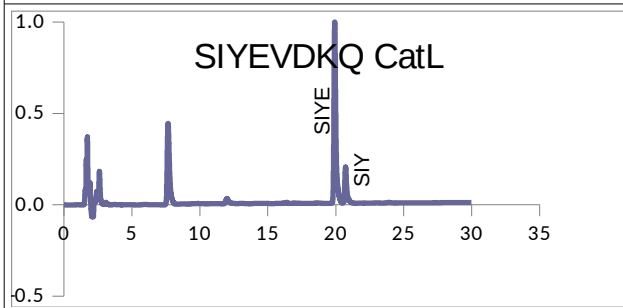
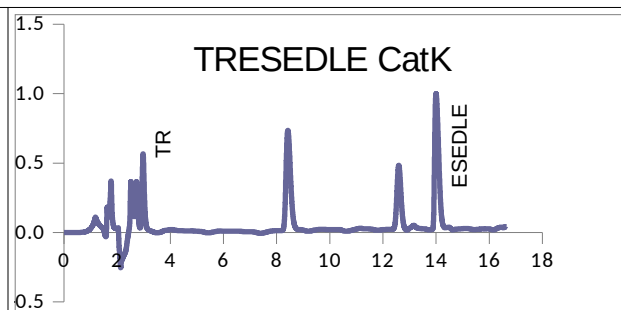
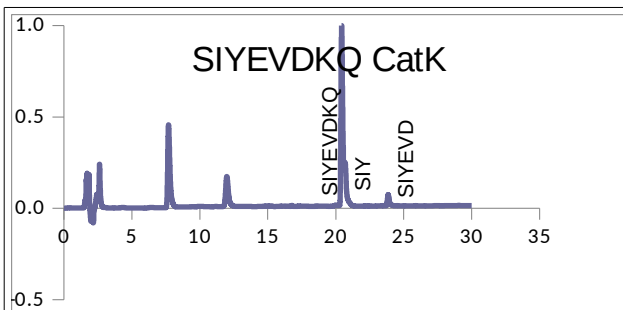


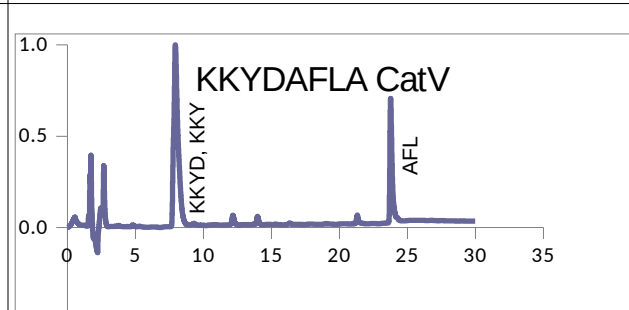
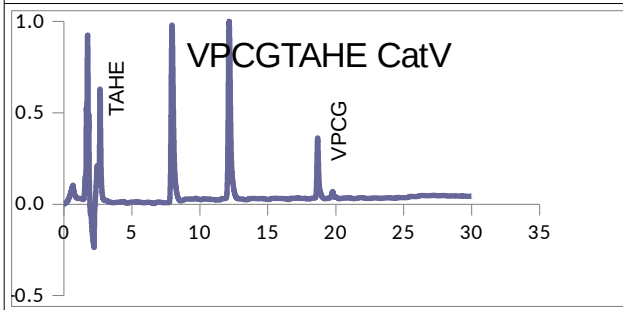
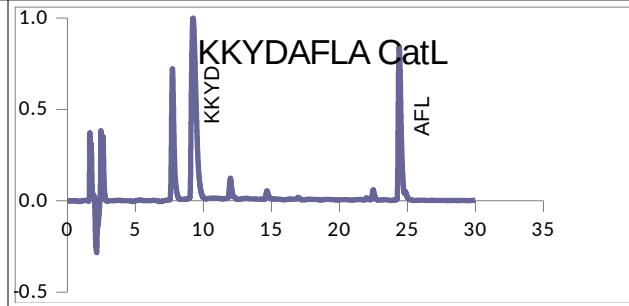
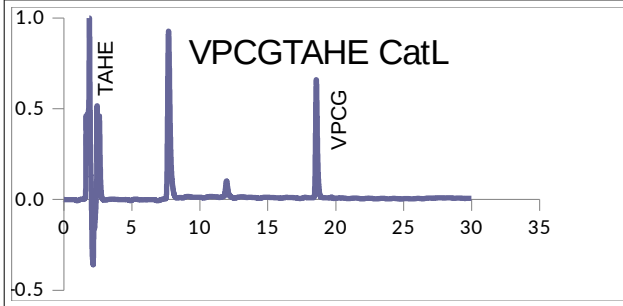
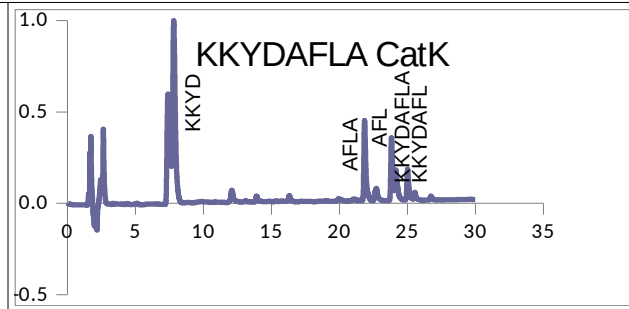
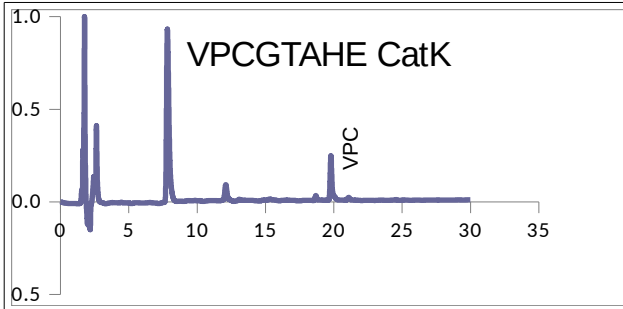


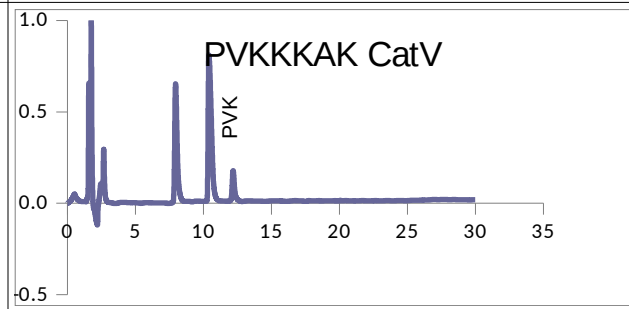
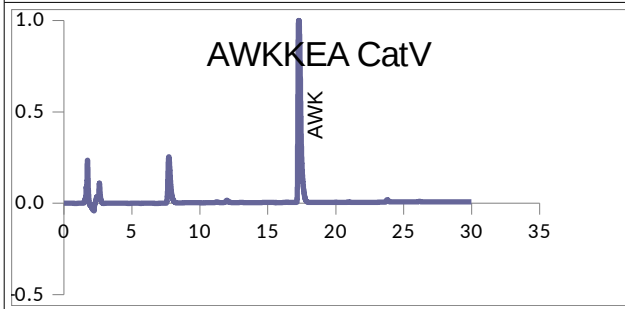
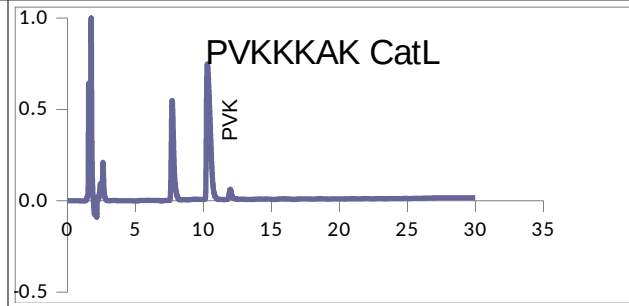
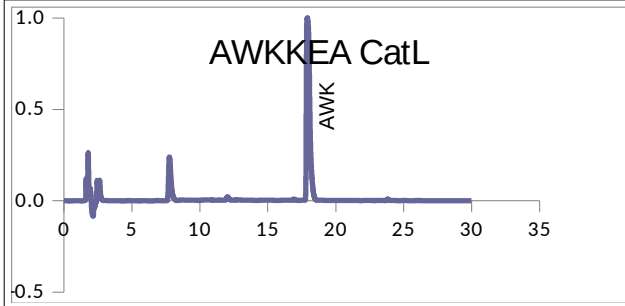
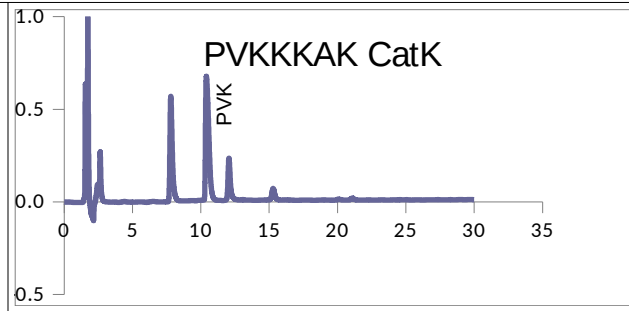
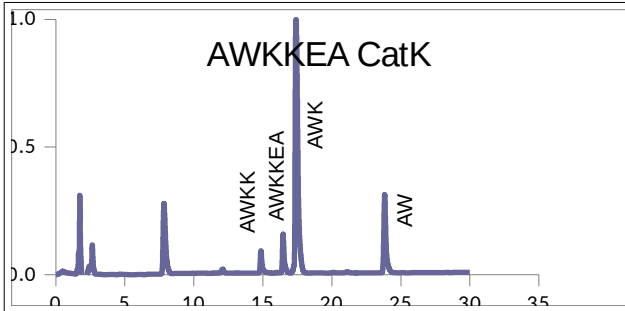


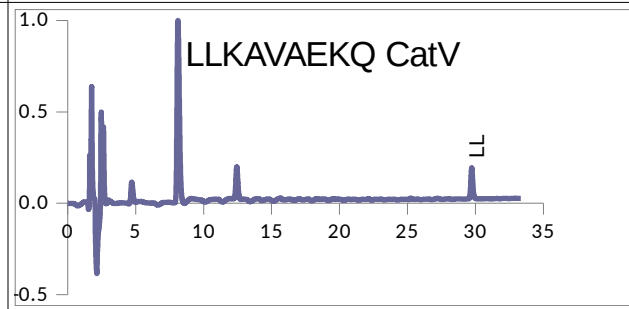
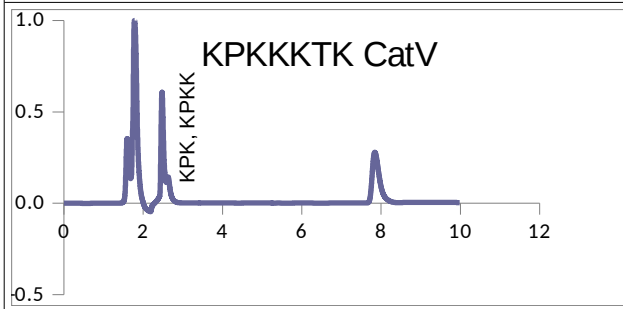
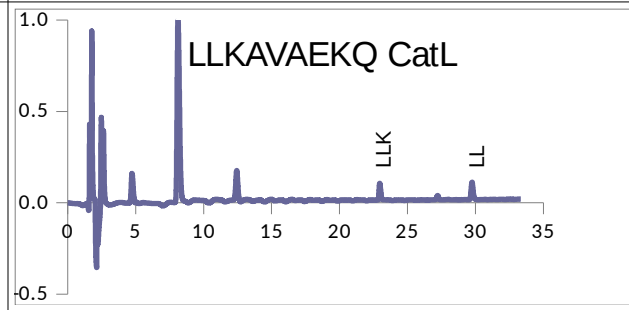
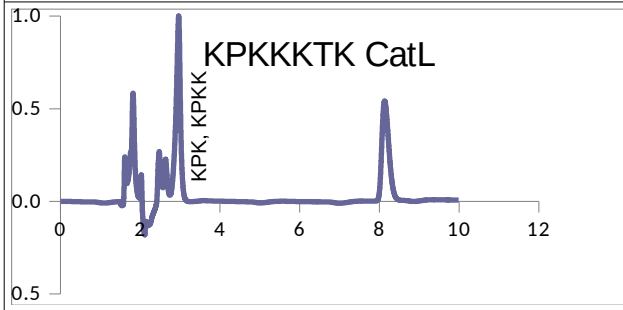
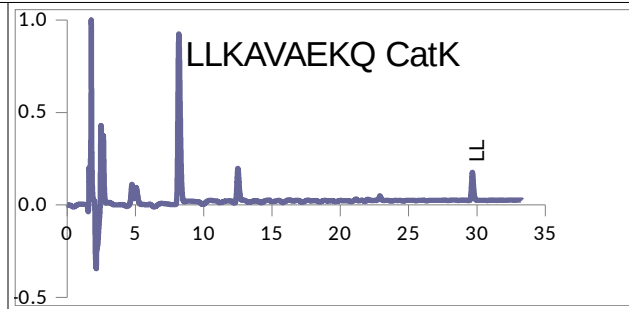
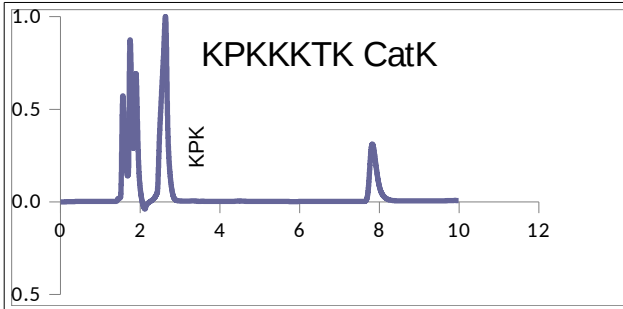












b. Processing of peptides AYFKKVL and KVLATVTK from 5 s–60 min. Peptides treated with cathepsins were applied on RP-HPLC. Peaks representing the peptide fragments were captured. Separation was monitored at 214 nm. Y-axis show signal of absorbance at A_{214} and x-axis represent separation time in minutes. Response at Y-axis is not normalized in order to quantitatively compare fragment signals at different time points. Peptide sequences as identified with MALDI-TOF are written on top or next to their corresponding HPLC signal. Characteristics signals at around 8 min and 12 min correspond to buffer component dithiothreitol (DTT) and cathepsin, respectively. Aliquots were taken after 5 s, 30 s, 2 min, 6 min, 20 min, and 60 min of incubation with cathepsins V and L (both peptides) or K (peptide KVLATVTK).

