Supporting Information

Comparative Neuropeptidomic Analysis of Food Intake via a Multi-faceted Mass Spectrometric Approach

Ruibing Chen, Limei Hui, Stephanie S. Cape, Junhua Wang and Lingjun Li*

Department of Chemistry & School of Pharmacy, University of Wisconsin-Madison, 777 Highland Avenue, Madison, WI 53705-2222

Figure S1. Representative mass spectra of reverse formaldehyde labeling of two extract samples from the pericardial organs. (a) The first sample was labeled with H_2-formaldehyde, and the second sample was labeled with D_2-formadehyde. Then the two samples were mixed and analyzed using MALDI-FTMS. (b) The isotopic labeling reagent for each sample was reversed. Similar ratios of peptide peaks were observed. Peaks labeled with H_2-formaldehyde were indicated with open circles, and peaks labeled with D_2-formadehyde were indicated with closed circles.

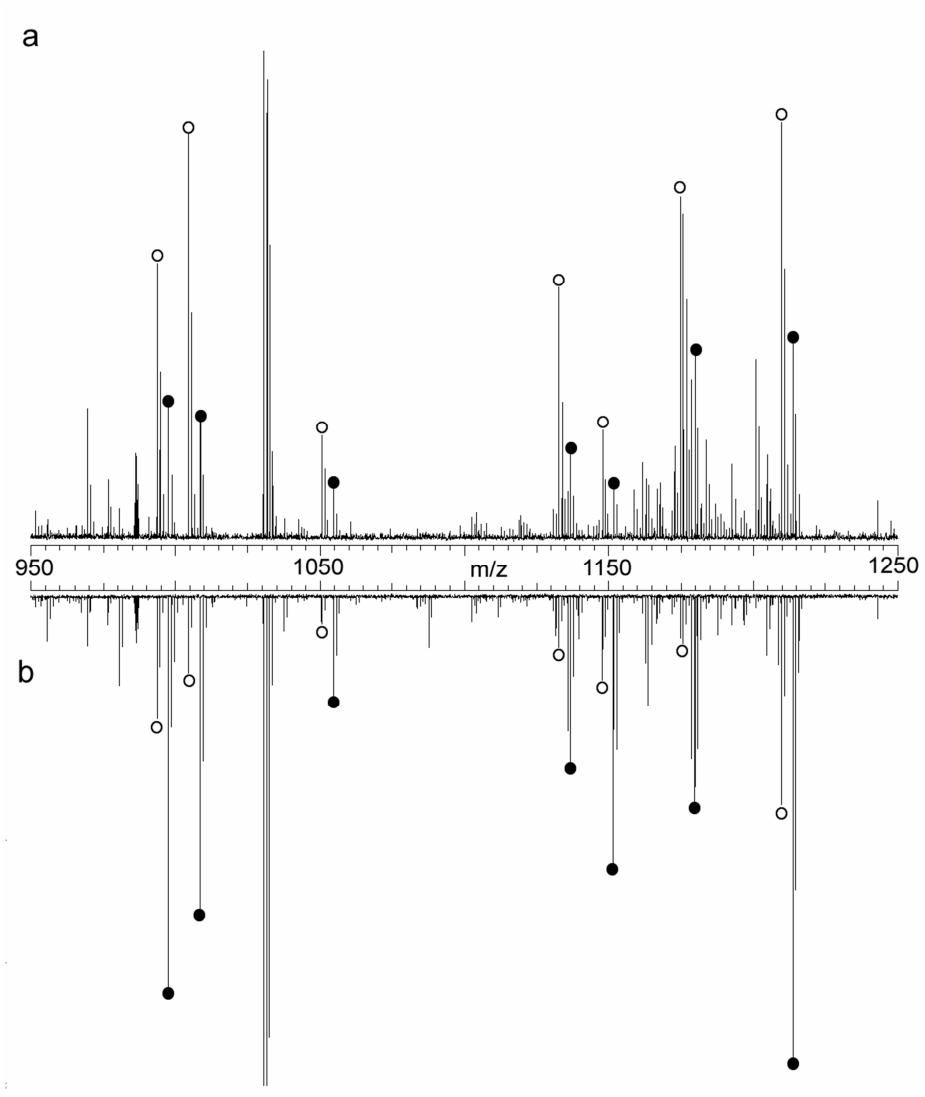
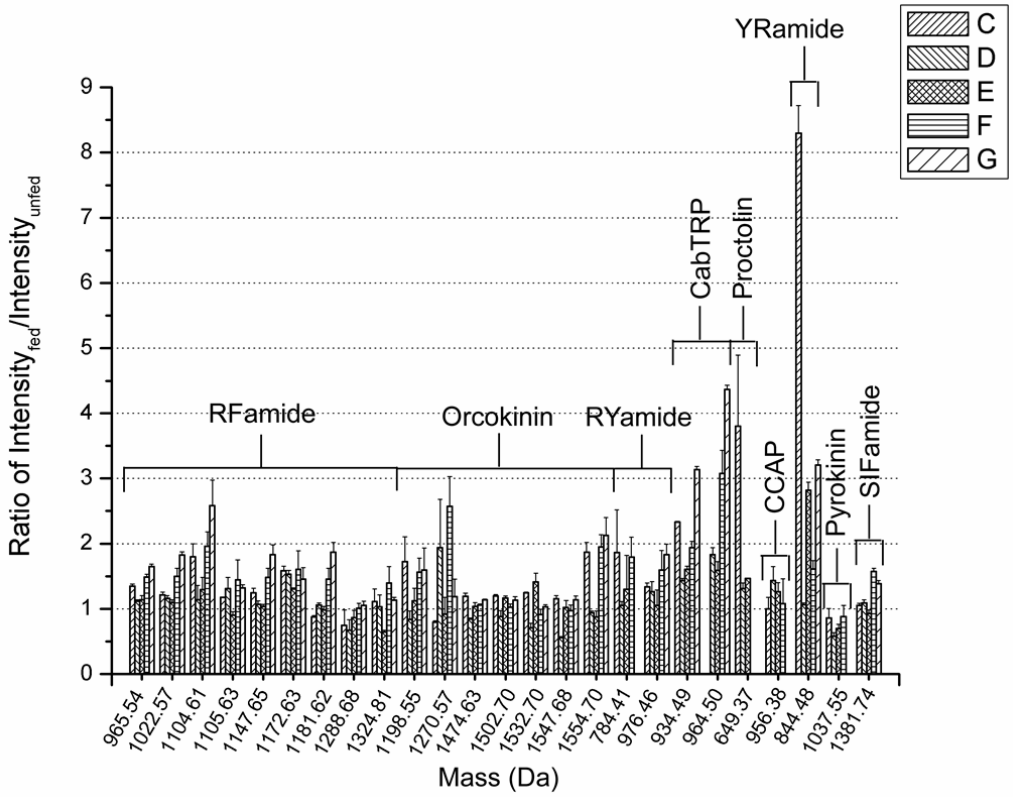
Figure S2. Abundance ratios of 25 neuropeptides in fed crab brain versus unfed crab brain based on five groups of feeding experiments. The masses of each neuropeptide are labeled on the X axis and they are grouped in peptide families. Y axis shows the abundance ratios of each neuropeptide between fed and unfed crabs. The error bars indicate standard deviation of four MS measurements for each sample.