Supplementary Table Legends

Table A. Proteins identified in the soluble fraction of bovine chromaffin secretory vesicles.

Identified proteins are listed alphabetically. Proteomic data factors utilized for identification of proteins consisted of peptide sequences determined by tandem mass spectrometry, number of tryptic peptides of the parent protein, protein molecular weight (WT), protein pI (isoelectric point), peptide score, peptide %SPI, peptide pI, fragmentation, and parent charge.

For identification of proteins based on single peptide matches, the peptide MS/MS spectra is illustrated in alphabtical order by protein name that was identified by a single peptide.

Table B. Proteins identified in the membrane fraction of bovine chromaffin secretory vesicles.

Identified proteins are listed alphabetically. Proteomic data factors utilized for identification of proteins consisted of peptide sequences determined by tandem mass spectrometry, number of tryptic peptides of the parent protein, protein molecular weight (WT), protein pI (isoelectric point), peptide score, peptide %SPI, peptide pI, fragmentation, and parent charge.

For identification of proteins based on single peptide matches, the peptide MS/MS spectra is illustrated in alphabtical order by protein name that was identified by a single peptide.

For Table A and B, it is noted that biochemical documentation of such proteins in chromaffin granules by previous studies (for example, endopin (43), cathepsin D (44), cathepsin B (45), and prohormone convertase (46) substantiates such identifications, explained in the manuscript text (methods).