Supplementary Figure 1. UDMS\textsuperscript{E} peptide fragmentation efficiency is higher than HDMS\textsuperscript{E}. a) Boxplots of the number of matched product ions for rhGH proteolytic peptides, as identified by HDMS\textsuperscript{E} or UDMS\textsuperscript{E} analysis. b) Comparison of peptide high energy spectra acquired by HDMS\textsuperscript{E} and UDMS\textsuperscript{E} modes. Data has been combined over the same retention time window.