



Supporting Figure 1. Distribution of cellular component gene ontology (GO) terms across three types of modified algal peptides: lysine acetylated peptides, asparagine deamidated peptides, and arginine methylated peptides over the 12-day degradation period. Peptides are from the trypsin-digested (A-C) and naturally-digested fractions (D-F) were compared in this analysis as in all others. Very little selective degradation or preservation was observed across the different modification types. While these three particular modification types were selected because of their implications in degradation, the same indiscriminate degradation scheme is observed for all modifications in the searches (Figure 4).