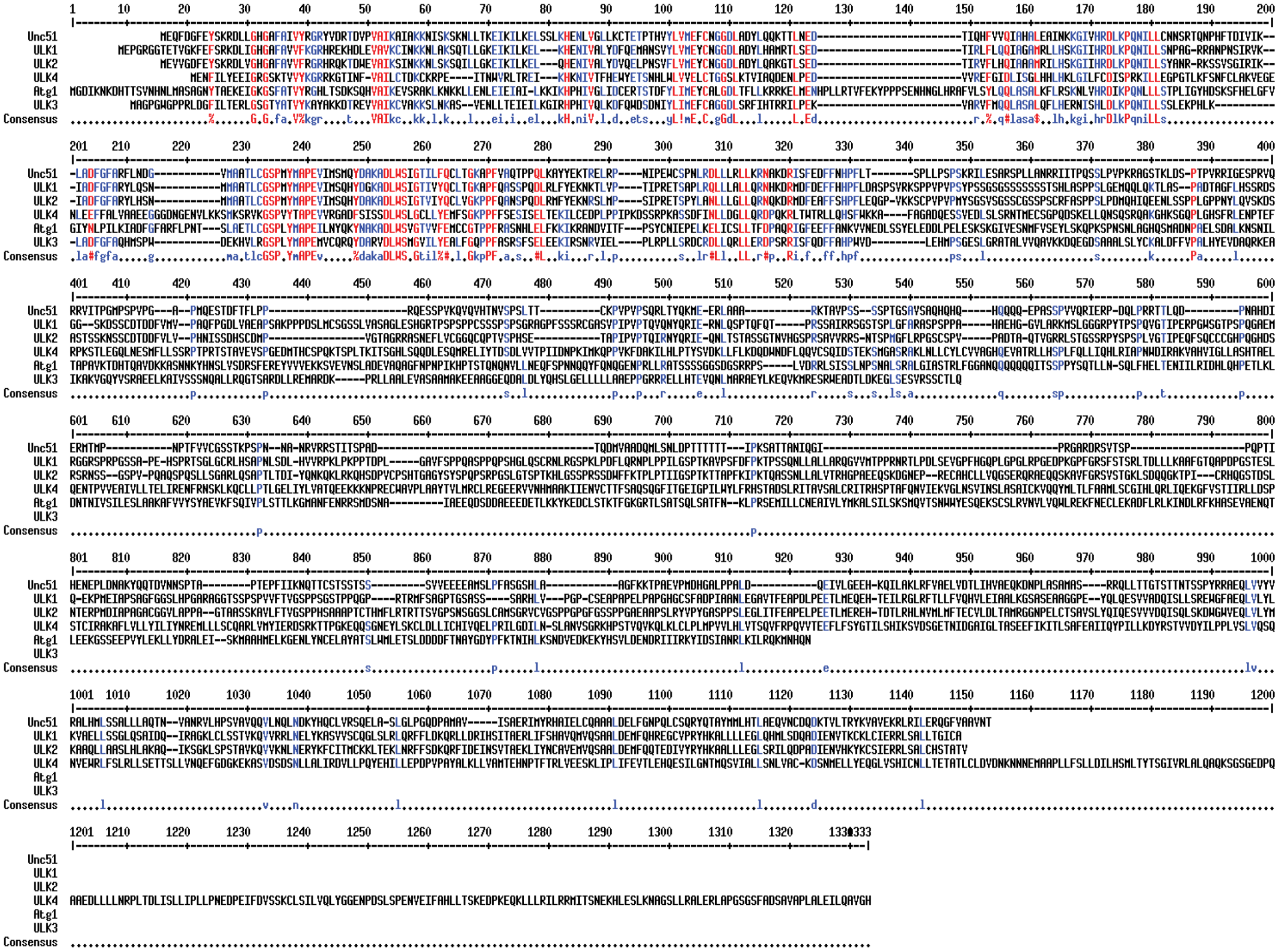

Supplemental Figure 1. Alignment of the amino acid sequences of Atg1 homologues from yeast, C. elegans, and homo sapiens (ULK1, ULK2, ULK3 and ULK4). The software Multalin (F. Corpet (1988). Nucl. Acids Res., 16 (22), 10881-10890) was used.