**Figure S1.** Crystal structure of human CALR (PDB ID: 3POW). Trp200, Asp201 and Phe202 of the LIR motif (WDPL) are located in the unstructured segment at the beginning of a long (100 amino acid residues) intrinsically disordered region that cannot be seen in the crystal structure. The C terminal IDPR downstream of Leu367 is also missing in the crystal structure. Missing regions are denoted by black dashed lines.

**Figure S2.** PONDR-FIT profiles of autophagy proteins (Atg39, Atg40 and JIP1) that contain an AIM/LIR motif, which is marked in bold in the black box at the corresponding position in the amino acid sequence.

**Figure S3.** YWHA-binding SLiMs in autophagy proteins (BECN1 and ATG9).(**A**) Crystal structure of the BARA domain of BECN1 (in purple) that includes the flexible loop with phosphoserine 295 (pS295), which is part of the YWHA/14-3-3 consensus binding sequence. The light green line shows schematically the IDPR that is upstream of the BARA domain and that contains pS234, which is part of the second YWHA/14-3-3 binding motif in BECN1. Phosphorylation of Ser234 and Ser295 is important for binding of BECN1 to the YWHA/14-3-3 protein that is schematically depicted in teal. (**B**) PONDR-FIT profile of human ATG9. The YWHA/14-3-3 docking motif (RSApSYP) with phosphoserine 761 is highlighted in the black box at the corresponding position in the amino acid sequence.