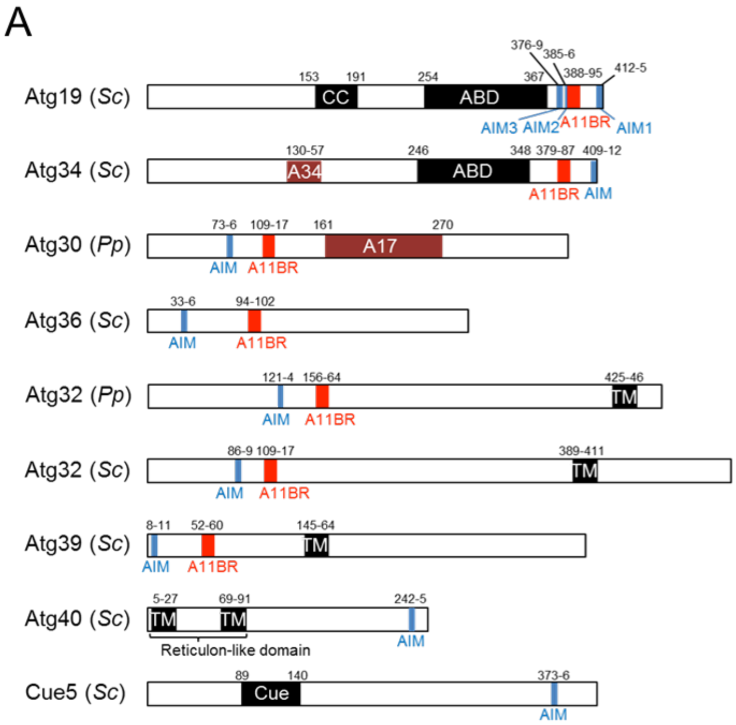
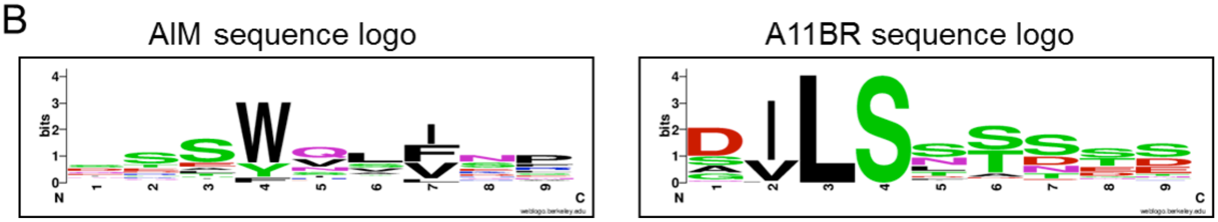


Protein length	Accession n°	AIM	A11BR
415aa	DAA10702	(1)ALTWEEL* (2)DTLPEL (3)QEPFYSFQI	DDSSIISTS
412aa	DAA10701	PFTWEEI*	DESSIMSTP
384aa	CAY70917	NSEWILFSP	DILSSSRRS
293aa	DAA08621	ESLFEVLEL	AILSISSDS
466aa	CAY71556	VTAWQMVHR	SVLSSSEYE
529aa	DAA08407	SGSWQAIQP	SILSSSDTS
398aa	DAA09621	DDHWNLVRL	DVLSNTSSE
256aa	DAA10925	PNDYDFMED	N.D.
411aa	DAA10824	KKKWQPLPP	N.P.



Supplementary Information S1 (Figure): Domain architecture of SARs.

(A) The domain architectures of SARs are shown at the left (drawn roughly to scale). The black boxes indicate domains that bind the cargos (TM: transmembrane domain, Ape1: region that binds aminopeptidase I and Ams1: region that binds mannosidase I). Blue and red boxes indicate regions that bind Atg8 and Atg11, respectively (AIM: Atg8-family interacting motif and A11BR: Atg11-binding region). Brown box shows region required to bind Atg34 (A34) and Atg17 (A17). Protein length, accession number for protein sequence, AIM and A11BR sequences are shown on the right. Atg40 directly binds Atg11, but A11BR is not conserved and the binding region was not determined (N.D.). Cue5 does not interact with Atg11 (N.P.: not present). Red letters in the AIM and A11BR table indicate confirmed phosphosites and blue letters indicate key residues in the AIMs. Asterisks indicate the C-terminal end of the proteins. (B) The AIM and A11BR sequence logos were created using the most divergent sequences of seventeen Atg30, twenty Atg32, seven Atg36 and thirteen Atg39 homologs. Pp, *P. pastoris*; Sc, *S. cerevisiae.*