Supplemental Material to:

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Structural characterization of the *Saccharomyces cerevisiae* autophagy regulatory complex Atg17-Atg31-Atg29

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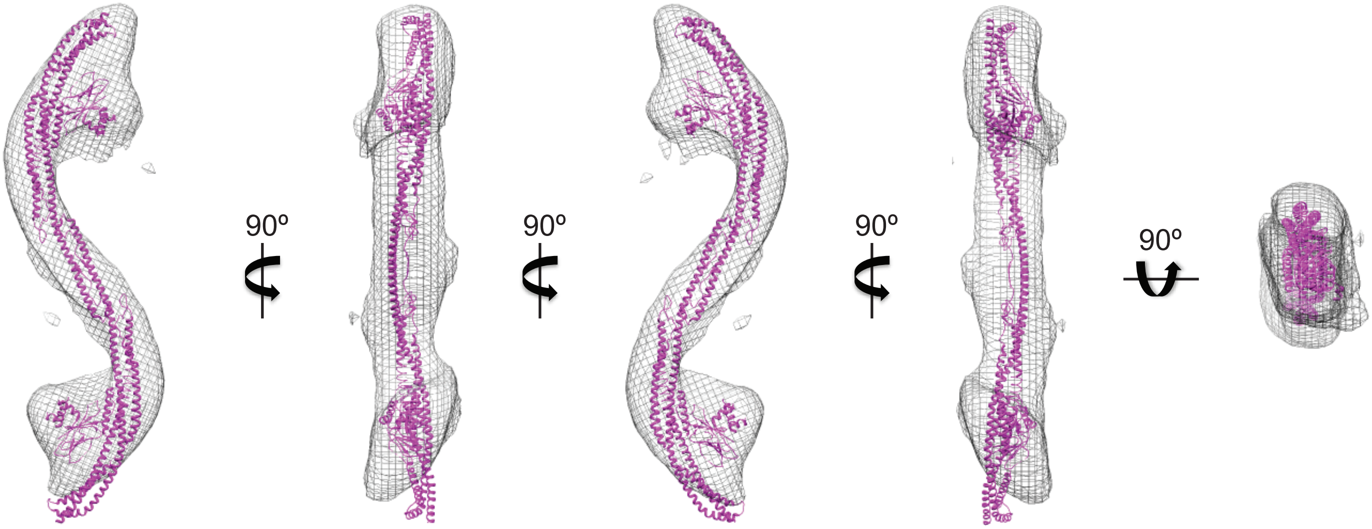
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Figure S1. Docking of the crystal structure of the core Atg17-Atg31-Atg29 complex from *L. thermotolerans* (PDB accession code 4HPQ) into the EM density map of the *S. cerevisiae* complex. Docking was performed using UCSF Chimera and the different panels represent the docked solution viewed in different orientations.

Table S1. Mass spectrometry of TAP purified Atg17-Atg31-Atg29.

Protein	**Number of peptides**	**Coverage by amino acid count (%)**
Atg17 (48.7 kDa)	27	66.43
Atg29 (24.7 kDa)	9	63.38
Atg31 (22.2 kDa)	9	63.78