

Supporting Information

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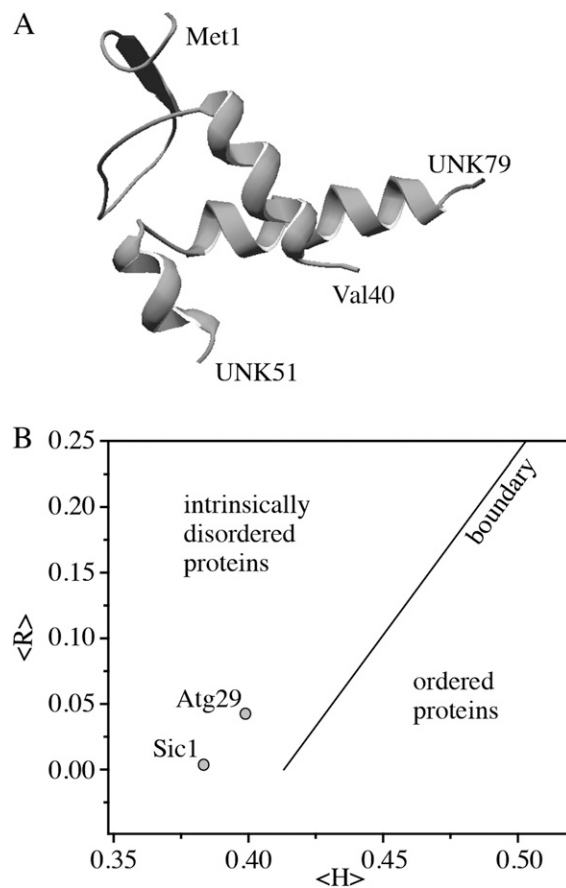


Fig. S1. AuTophagy-related (Atg29) is an intrinsically disordered protein (IDP). (A) Ribbon model of Atg29 [Protein Data Bank (PDB) ID code 4HPQ]. End residues on secondary structure elements are labeled. UNK, unknown. (B) Charge-hydrophobicity (CH) plot shows the mean net charge $\langle R \rangle$ as a function of the mean hydrophobicity $\langle H \rangle$. Solid line marks the boundary that separates ordered (globular) proteins from intrinsically disordered proteins. Plot shows the position of Atg29 relative to the boundary and the position of the recently characterized IDP Sic1 from *Saccharomyces cerevisiae* (1).

1. Brocca S, et al. (2009) Order propensity of an intrinsically disordered protein, the cyclin-dependent-kinase inhibitor Sic1. *Proteins* 76(3):731–746.

Table S1. Strains used in this study

Name	Genotype	Reference
HCY107	YCY123 <i>ATG17-GFP::HIS3</i>	This study
HCY108	YCY131 <i>ATG17-GFP::HIS3</i>	This study
HCY109	SEY6210 <i>atg29Δ::KAN</i>	This study
HCY125	SEY6210 <i>atg17Δ::KAN Atg29-PA::TRP1</i>	This study
HCY129	SEY6210 <i>Atg29-PA::TRP1</i>	This study
KDM1233	SEY6210 <i>atg29Δ::KAN ATG31-GFP::HIS3</i>	This study
KDM1234	SEY6210 <i>ATG17-PA::HIS3</i>	This study
KDM1235	SEY6210 <i>atg29Δ::KAN ATG17-PA::HIS3</i>	This study
KDM1270	SEY6210 <i>atg1Δ::HIS5 atg11Δ::LEU2</i>	This study
KDM1406	TN124 <i>atg11Δ::URA3</i>	This study
KDM1407	TN124 <i>atg29Δ::KAN atg11Δ::URA3</i>	This study
KDM1408	SEY6210 <i>pho13Δ pho8Δ60 atg1Δ::LEU2</i>	This study
KDM1409	SEY6210 <i>pho13Δ pho8Δ60 atg29Δ::HIS5</i>	This study
KDM1410	SEY6210 <i>pho13Δ pho8Δ60 atg1Δ::LEU2 atg29Δ::HIS5</i>	This study
KDM1551	SEY6210 <i>pRPL7b-VC-ATG11::HIS3 ATG17-VN::TRP1</i>	This study
KDM1552	SEY6210 <i>pRPL7b-VC-ATG11::HIS3 ATG29-VN::TRP1</i>	This study
KDM1553	SEY6210 <i>pRPL7b-VC-ATG11::HIS3 ATG31-VN::TRP1</i>	This study
SEY6210	<i>MATα leu2-3,112 ura3-52 his3-Δ200 trp1-Δ901 suc2-Δ9 lys2-801 GAL</i>	(1)
TKY12	SEY6210 <i>atg29Δ::KAN atg1Δ::LEU2</i>	This study
TN124	<i>MATα leu2-3,112 trp1 ura3-52 pho8::pho8Δ60 pho13Δ::LEU2</i>	(2)
WHY1	SEY6210 <i>atg1Δ::HIS5</i>	This study
WLY176	SEY6210 <i>pho13Δ pho8Δ60</i>	This study
YCY123	SEY6210 <i>atg1Δ, 2Δ, 3Δ, 4Δ, 5Δ, 6Δ, 7Δ, 8Δ, 9Δ, 10Δ, 11Δ, 12Δ, 13Δ, 14Δ, 16Δ, 17Δ, 18Δ, 19Δ, 20Δ, 21Δ, 23Δ, 24Δ, 27Δ, 29Δ</i>	(3)
YCY131	SEY6210 <i>atg1Δ, 2Δ, 3Δ, 4Δ, 5Δ, 6Δ, 7Δ, 8Δ, 9Δ, 10Δ, 11Δ, 12Δ, 13Δ, 14Δ, 16Δ, 17Δ, 18Δ, 19Δ, 20Δ, 21Δ, 23Δ, 24Δ, 27Δ, 29Δ, 31Δ::ble</i>	This study
YIY36	TN124 <i>atg29Δ::KAN</i>	This study

- Robinson JS, Klionsky DJ, Banta LM, Emr SD (1988) Protein sorting in *Saccharomyces cerevisiae*: Isolation of mutants defective in the delivery and processing of multiple vacuolar hydrolases. *Mol Cell Biol* 8(11):4936–4948.
- Noda T, Matsuura A, Wada Y, Ohsumi Y (1995) Novel system for monitoring autophagy in the yeast *Saccharomyces cerevisiae*. *Biochem Biophys Res Commun* 210(1):126–132.
- Cao Y, Cheong H, Song H, Klionsky DJ (2008) In vivo reconstitution of autophagy in *Saccharomyces cerevisiae*. *J Cell Biol* 182(4):703–713.