

# macro AUTOPHAGY

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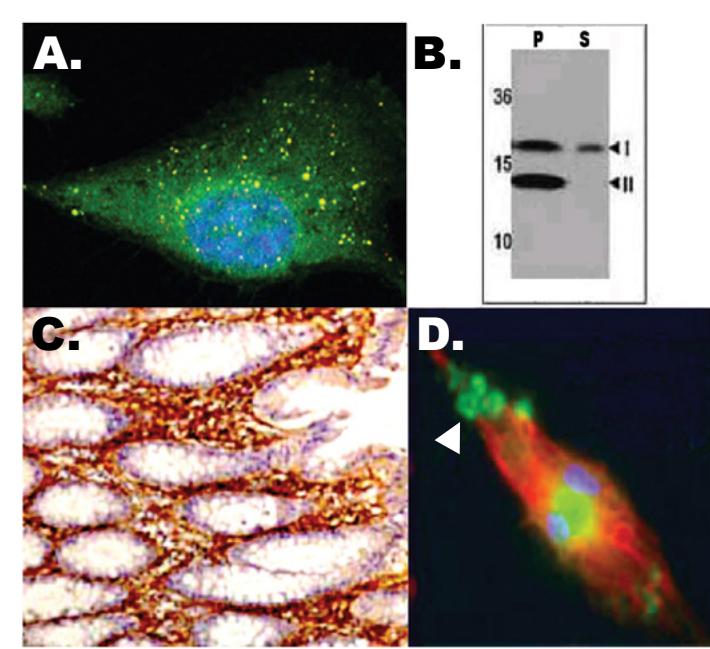
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**Autophagy** is a major self-degradative process in eukaryotic cells, with fundamental roles in cellular and organismal homeostasis. Dysregulation of autophagy has recently been implicated in severe human pathologies such as cancer, neurodegenerative disorders, metabolic and muscular diseases, and viral infections. Structures targeted for autophagic destruction are sequestered into newly emerging double-membrane vesicles called autophagosomes, and delivered for lysosomal degradation. ATG proteins form four main multiprotein complexes: phosphatidylinositol 3-kinase (PI3K) complex, ATG13/ATG1 kinase complex, ATG9 complex, and ubiquitin-like protein conjugation systems. Current research is aimed at understanding how these complexes interact to promote autophagy.

100+ additional Ab  
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Cat#	Target
AM1800a	LC3
AP1801a	LC3
AP1802a	LC3
AP1806a	LC3
AM1818a	Beclin
AP1818b	Beclin
AP2183b	P62
AP1813b	APG7
AP1812a	APG5
AP1812b	APG5
AP1817b	APG16
AP1816a	APG12
AP1820b	GAIP

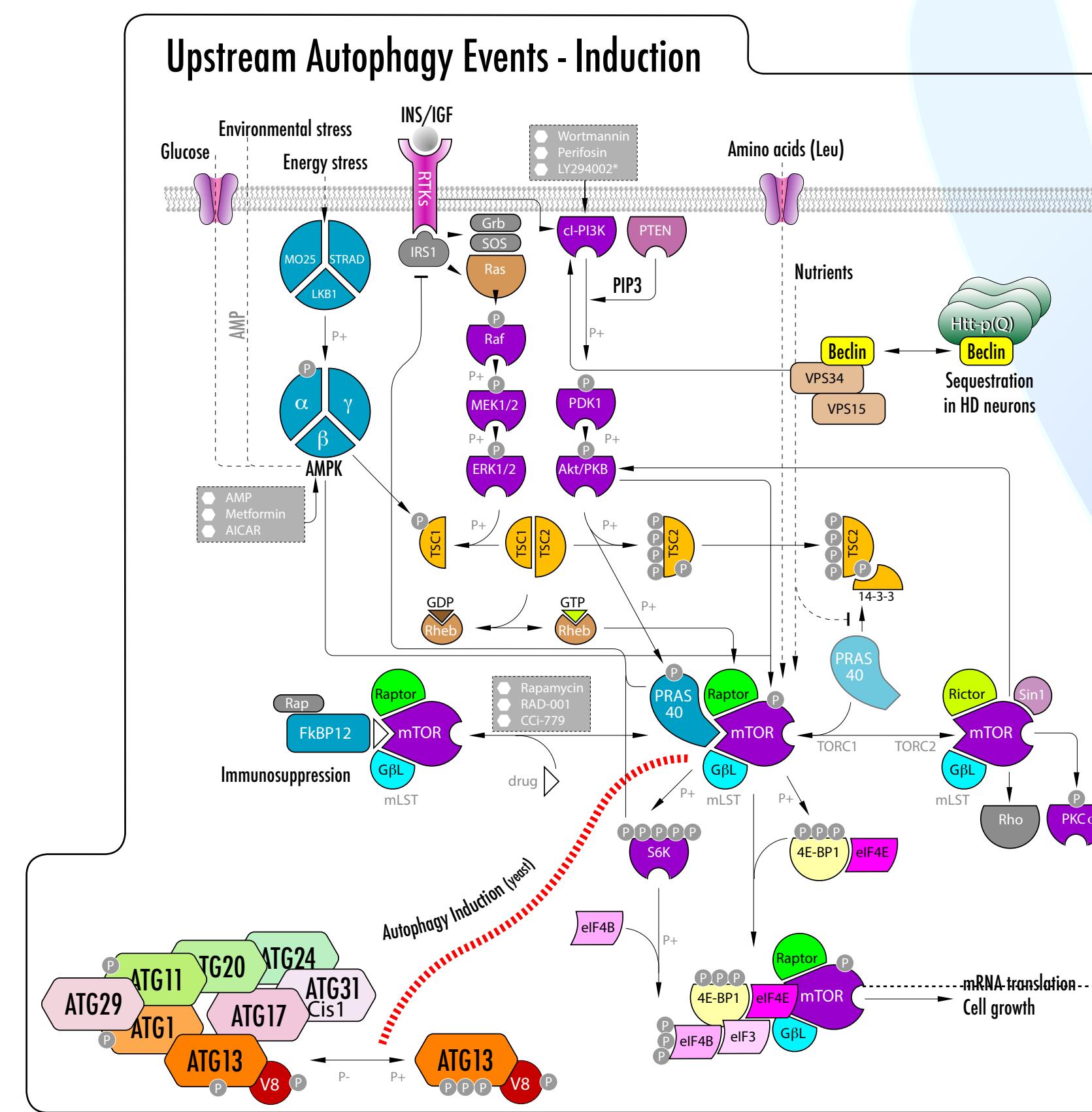
## Autophagy Antibodies



C. Parafomaldehyde-fixed paraffin-embedded biopsy from patient with Crohn disease. Sections incubated with APG16 antibody (Abgent, Cat. # AP1817b).

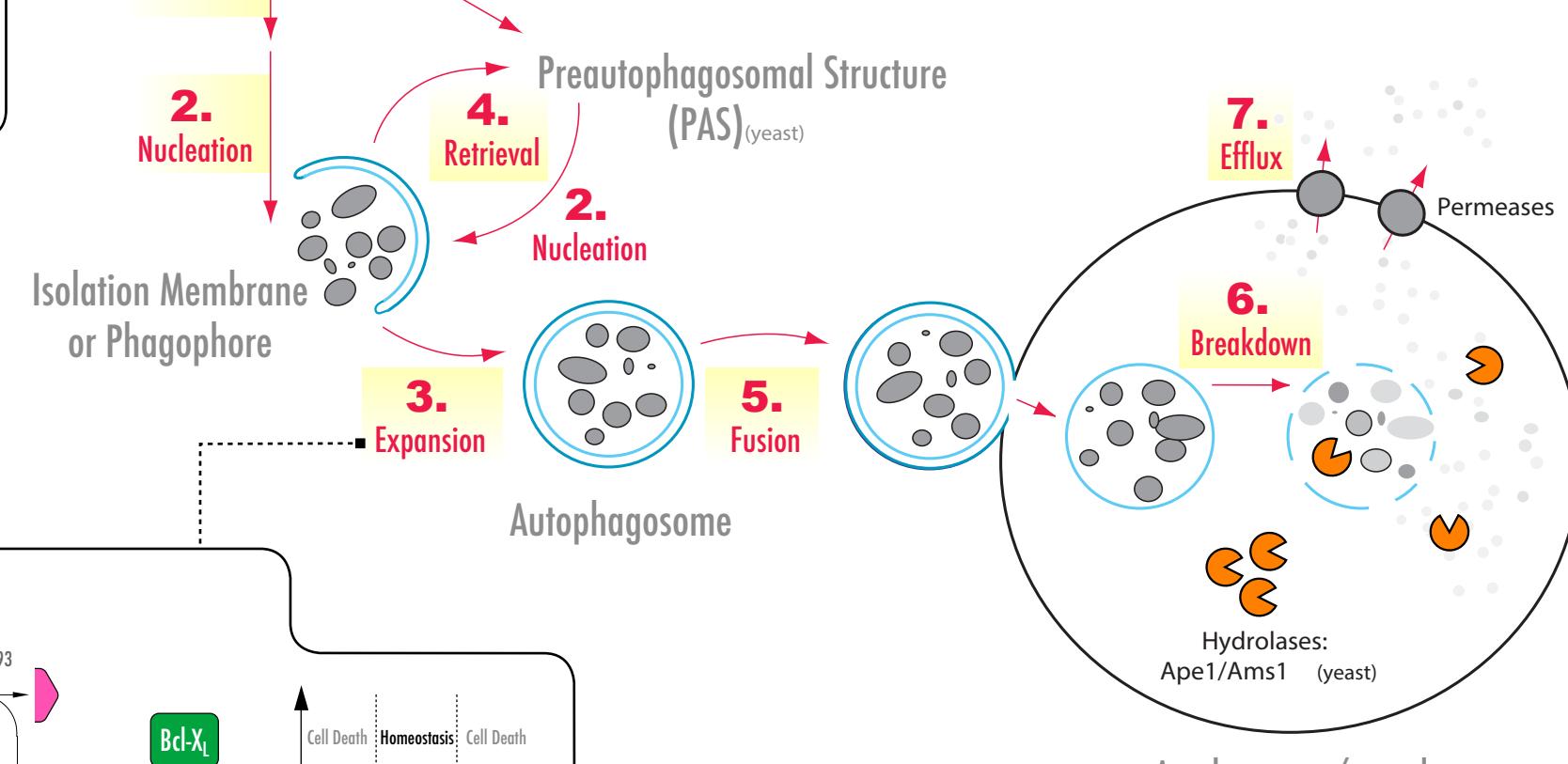
D. Mouse leukemic monocyte macrophage cells treated with U18666A, a drug that causes cholesterol and lipid storage in cells, thereby blocking fusion between late endosomes and lysosomes. LC3 antibody (Abgent, Cat. # AP1806a) detected punctate staining indicative of autophagic vacuole/phagosomal structures.

## Upstream Autophagy Events - Induction

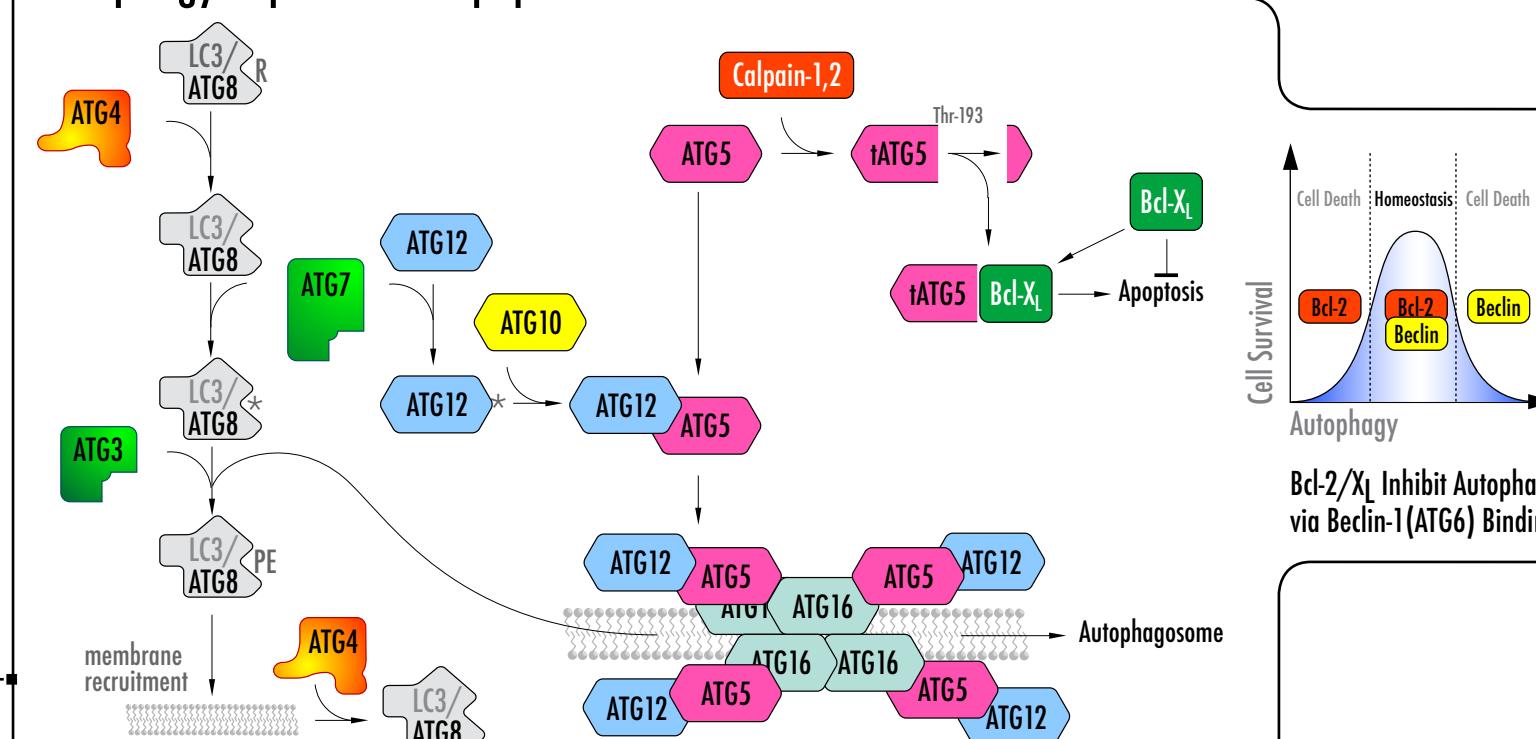


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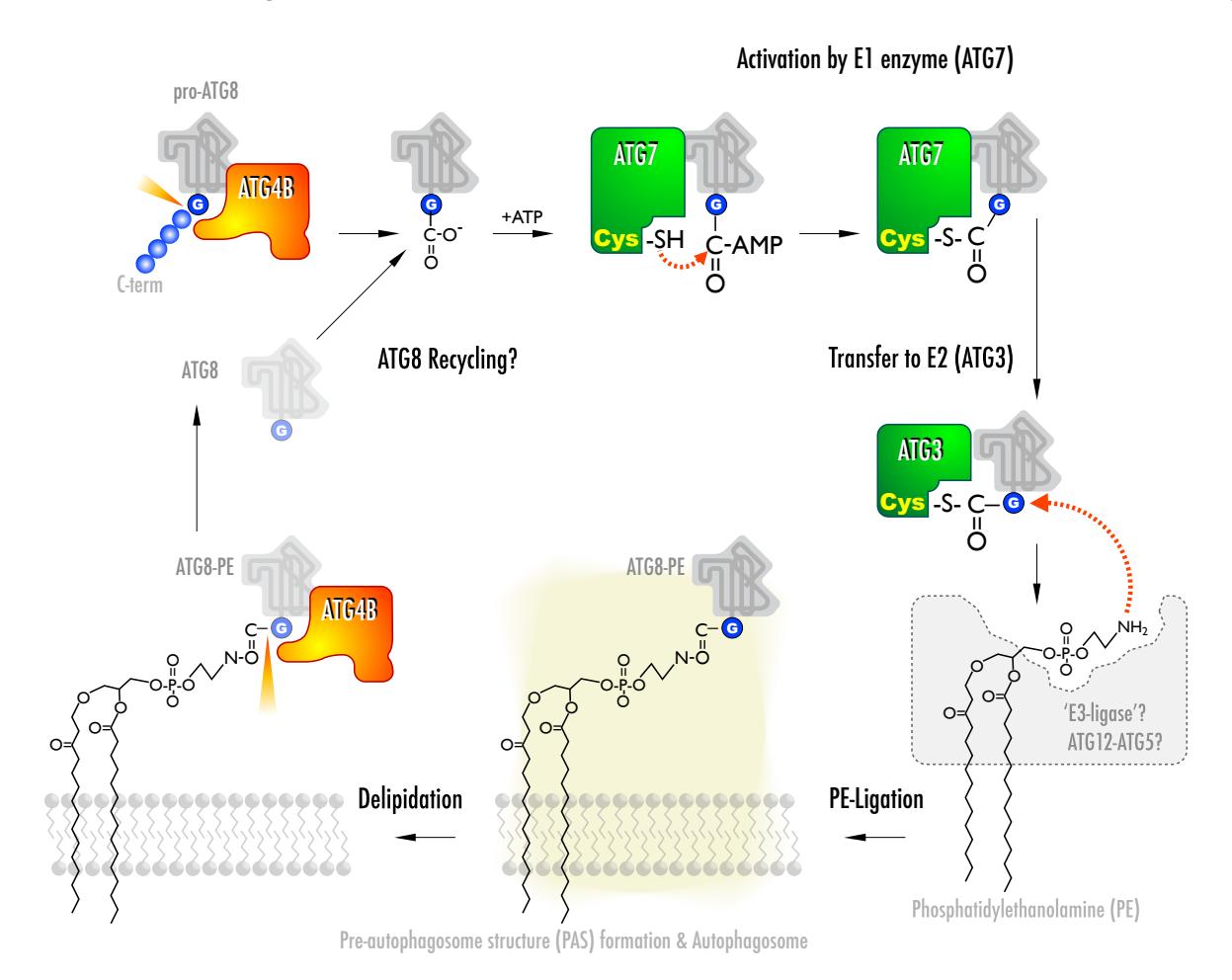
## Autophagy Phases



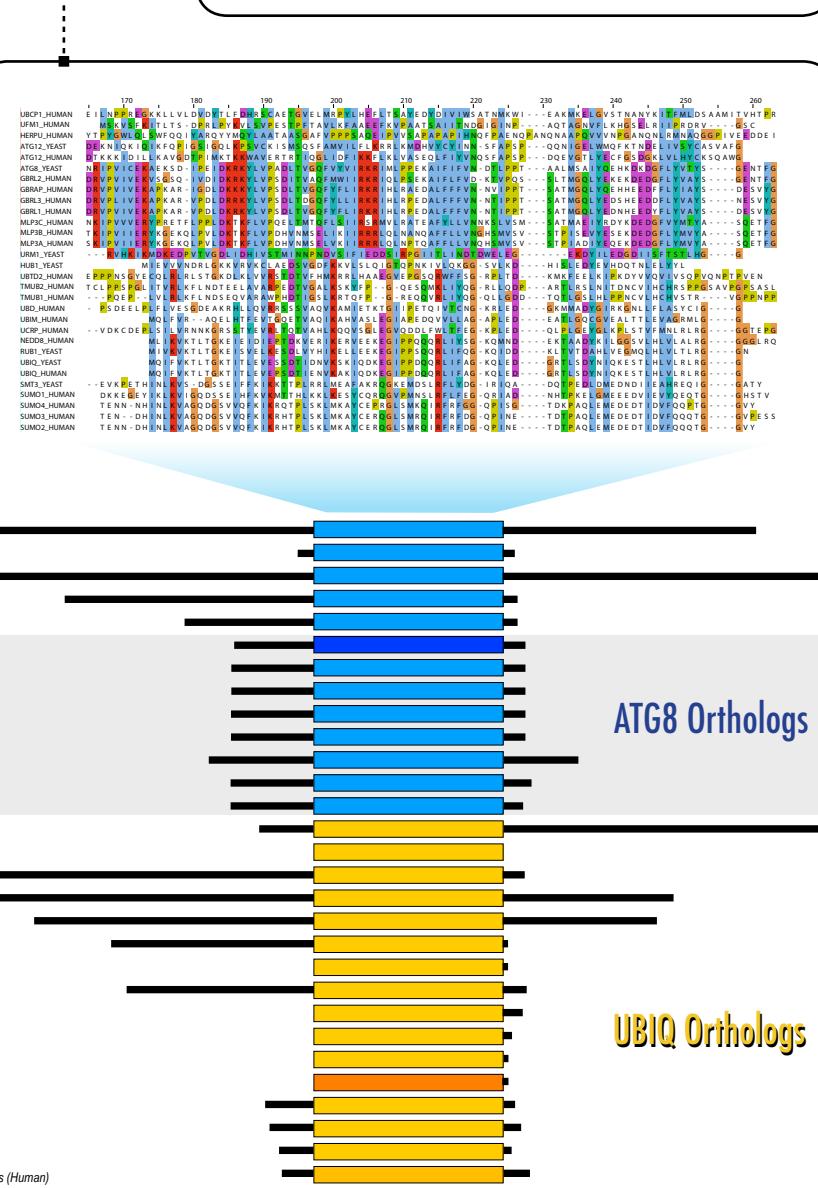
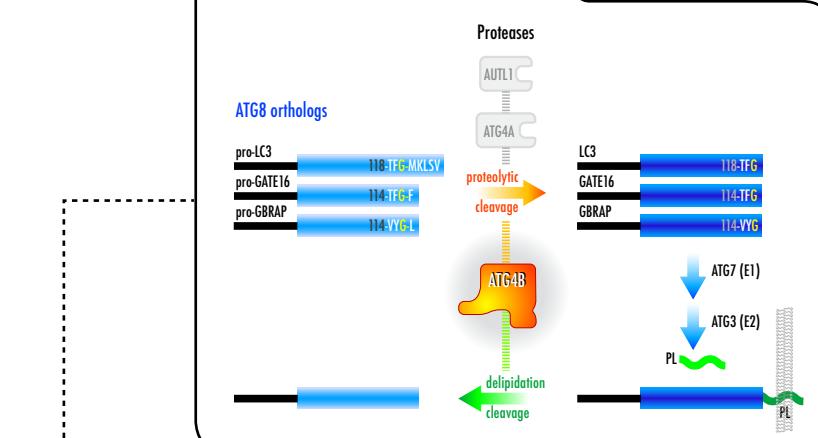
## Autophagy Expansion & Apoptosis



## ATG8 Conjugation Cycle



## ATG4 Dual Protease



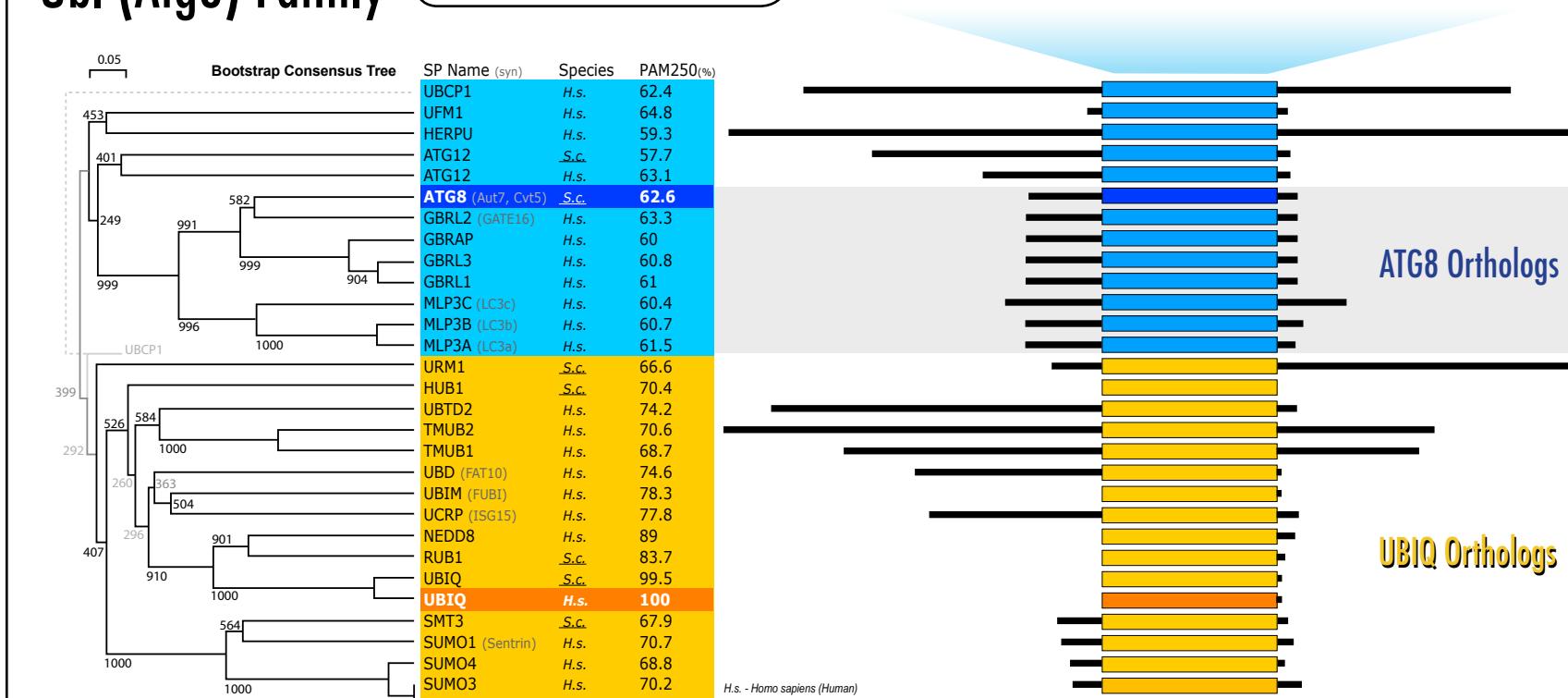
## Abbreviations (Synonyms):

AKT, RAC-alpha serine/threonine-protein kinase (C-AKT, RAC-PK-alpha); PKB, Protein kinase B; AMP, Adenosine monophosphate (5'-adenylic acid); ATP, Adenosine 5'-triphosphate (5'-adenylic acid); PI3K, Phosphatidylinositol 3-kinase; PI3K, Phosphatidylinositol 3-kinase catalytic subunit alpha (PI3K $\alpha$ ); AMPK, 5'-AMP-activated protein kinase catalytic subunit alpha 1 (AMPK $\alpha$ ); ATG4B, Cysteine protease ATG4B (Apoptinin, HAPC4B, AU11); ATG8, Autophagy-related ubiquitin-like modifier (APG8, AUT7, VT5); BCL2, Apoptosis regulator Bcl-2; eIF4B, Eukaryotic translation initiation factor 4B; ERK1, Extracellular signal-regulated kinase 1 (MAPK1, MAPK1, p44MAPK, ERK2, p44ERK, PRK2); FKBP12, Immunoophilin FKBP12.6 (12.6 kDa FKBP, Rotamase 1B, FK506-binding protein 1B, FKBP12.6, FKBP1, FKBP9, OTK4); GBRAP, Gamma-aminobutyric acid receptor-associated protein (GABARAP, MM46); GBR2, Gamma-aminobutyric acid receptor-associated protein-like 2 (GEF-2, FLC3, GATE16); GDP, Guanosine diphosphate (Guanosine 5'-triphosphate); Grb, Growth factor receptor-bound protein; GTP, Guanosine 5'-triphosphate (2'-guanosine 5'-triphosphate); IGF, Insulin growth factor; Htt, Huntington (HD) disease protein; MLP3C, Microtubule-associated protein 1A/1B light chain 3C (Autophagy-related protein LC3); mTOR, Mammalian target of rapamycin (FRAP, RAP1); NEDD8, Neddylin (Ubiquitin-like protein NEDD8); P $\gamma$ , monophosphate; PKC, Protein kinase C; PRAS40, Proline-rich AKT substrate 1 (40 kDa AKT1S1); PP2A, Serine/threonine-protein phosphatase 2A; Raf, RAF proto-oncogene serine/threonine-protein kinase (Raf-1, Raf1); RAPTOR, Regulatory-associated protein of mTOR; Rho, Ras homolog enriched in brain (GTP-binding protein RhoB); SGK, Ribosomal protein S6 kinase alpha-1 (SGK1, p90SGK, RSK-1); SUMO1, Small ubiquitin-related modifier 1 (Sentrin, Ubiquitin-like protein SUMT3, GAP-modifying protein 1, UBL1, P1C1, GMP1); TSC1, Hamartin (Tuberous sclerosis 1 protein); TSC2, tuberin (Tuberous sclerosis 2 protein); UBIQ, Ubiquitin; VPS34, Vacuolar protein sorting-associated protein 15 (GRD8, VAC4, VPL1); VPS15, Vacuolar protein sorting-associated protein 15 (GRD8, VAC4, VPL1).

## References:

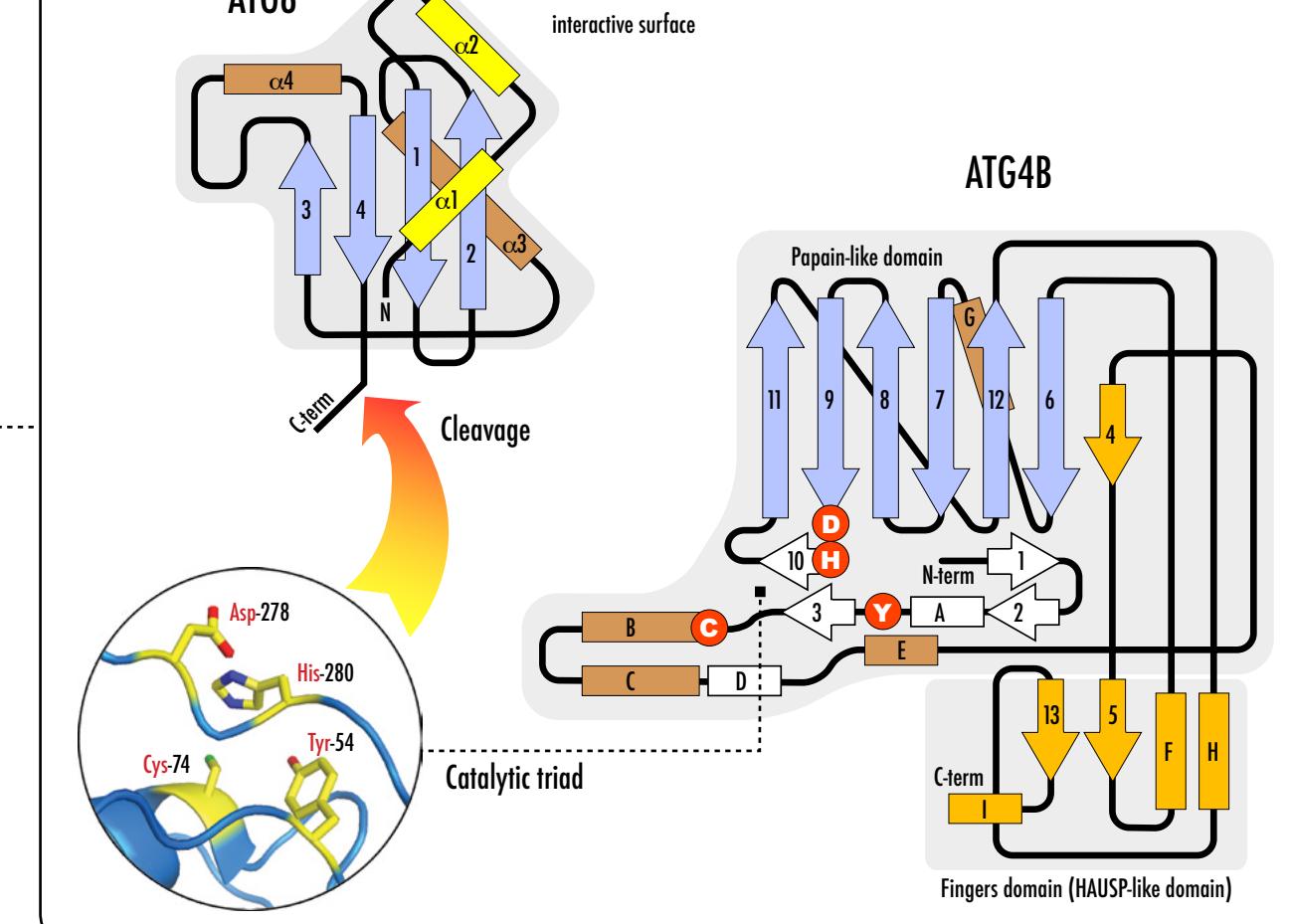
1. De Duve C et al. (1966) *Annu Rev Physiol* 28: 435-492.  
 2. Klionsky DJ & Emr SD (2000) *Science* 290:717-21.  
 3. Cuervo AM (2004) *Trends Cell Biol* 14(7):375-78.  
 4. Levine B & Klionsky DJ (2004) *Dev Cell* 6(4):463-77.  
 5. Klionsky DJ (2005) *J Cell Sci* 118(17):4001-11.  
 6. Hochstrasser M (2000) *Nat Cell Biol* 2(9):E153-7.  
 7. Verschueren M et al. (2006) *Annu Rev Cell Biol* 22:159-80.  
 8. Uhlmann T et al. (2006) *Cell Signal* 18(9):1927-34.  
 9. Hour E et al. (2007) *Nat Cell Biol* 9(2):F4-9.  
 10. Arsham AM & Neufeld TP (2006) *Curr Opin Cell Biol* 18(6):589-97.  
 11. De Virgilio C & Loewen R (2006) *J Biol Chem* 281(14):14761-80.  
 12. Miklosen T et al. (2006) *Biochemical Annu Rev* 42:123-223.  
 13. Proud CG (2004) *DNA Repair (Amst)* 3(8):91-927-34.  
 14. Krymskaya VP (2003) *Cell Signal* 15(6):739-745.  
 15. Regioni F & Klionsky DJ (2002) *Leukemia* 16(1):1-21.  
 16. Furuya N et al. (2005) *Autophagy* 1(1):46-52.  
 17. Konozawa T et al. (2004) *J Biol Chem* 279(19):84529-84539.  
 18. Patingre S et al. (2005) *J Cell Sci* 118(17):4001-11.  
 19. Kumanomidou T et al. (2006) *J Mol Biol* 355(4):612-8.  
 20. Sugawara K et al. (2005) *J Biol Chem* 280(48):40058-65.  
 21. Tondoli J et al. (2004) *J Biol Chem* 279(3):3626-76.  
 22. Yousef S et al. (2006) *Nat Cell Biol* 8(10):1124-32.  
 23. Shibata M et al. (2006) *J Biol Chem* 281(20):14474-85.  
 24. Demarchi F et al. (2007) *Autophagy* 3(3):  
 25. Jones DT et al. (1992) *Comput Appl Biosci* 8(3):725-729.  
 26. Zhourkikh A & Li WH (1993) *Mol Phylogenet Evol* 4(1):44-63.

## Ubl (Atg8) Family



PAM250 (Accepted Point Mutations): Mutational matrix corresponding to a level of evolutionary change, measured by the frequency of substitutions/mutations for proteins, which have diverged 250% (250 mutations per 100 amino acids) [Ref 25].  
 Bootstrap: Is a statistical technique that is widely used to assess confidence limits on phylogenies. It examines the reliability of each interior branch of the phylogenetic tree. If every interior branch length is proved to be positive, the tree is regarded as reliable from a statistical point of view [Ref 26]. The bootstrap values on each interior branch of this tree presented at the above show the number of trees matching on 1,000 possible trees.

## ATG4:ATG8 Cleavage Event



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