10320 Camino Santa Fe, Suite G
San Diego, CA 92121
Tel: 858.875.1900 Fax: 858.875.1999

ATG7 Rabbit mAb

Catalog # AP75010

Product Information

Application	WB, IHC-P, FC, IP
Primary Accession	O95352
Reactivity	Human
Host	Rabbit
Clonality	Monoclonal Antibody
Isotype	IgG
Conjugate	Unconjugated
Purification	Affinity Purified
Calculated MW	77960

Additional Information

Gene ID	10533
Other Names	ATG7
Dilution	WB~~1:1000-1:5000 IHC-P~~N/A FC~~1:50-1:100 IP~~1:20-1:50
Format	Liquid in 50mM Tris-Glycine(pH 7.4), 0.15M NaCl, 40%Glycerol, 0.01% sodium azide and 0.05% BSA.
Storage	Store at 4°C short term. Aliquot and store at -20°C long term. Avoid freeze/thaw cycles.

Protein Information

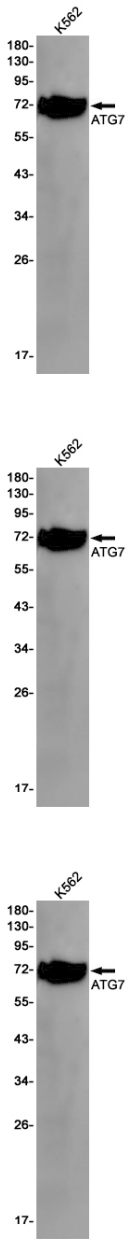
Name	ATG7 (HGNC:16935)
Synonyms	APG7L
Function	E1-like activating enzyme involved in the 2 ubiquitin-like systems required for cytoplasm to vacuole transport (Cvt) and autophagy. Activates ATG12 for its conjugation with ATG5 as well as the ATG8 family proteins for their conjugation with phosphatidylethanolamine. Both systems are needed for the ATG8 association to Cvt vesicles and autophagosomes membranes. Required for autophagic death induced by caspase-8 inhibition. Facilitates LC3-I lipidation with phosphatidylethanolamine to form LC3-II which is found on autophagosomal membranes (PubMed:34161705). Required for mitophagy which contributes to regulate mitochondrial quantity and quality by eliminating the mitochondria to a basal level to fulfill cellular energy requirements and preventing excess ROS production. Modulates p53/TP53 activity to regulate cell cycle and survival during metabolic stress. Also plays a key role in the maintenance of axonal homeostasis, the prevention of axonal

	degeneration, the maintenance of hematopoietic stem cells, the formation of Paneth cell granules, as well as in adipose differentiation. Plays a role in regulating the liver clock and glucose metabolism by mediating the autophagic degradation of CRY1 (clock repressor) in a time-dependent manner (By similarity).
Cellular Location	Cytoplasm. Preautophagosomal structure. Note=Also localizes to discrete punctae along the ciliary axoneme and to the base of the ciliary axoneme
Tissue Location	Widely expressed, especially in kidney, liver, lymph nodes and bone marrow.

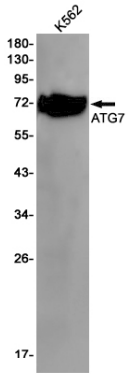
Background

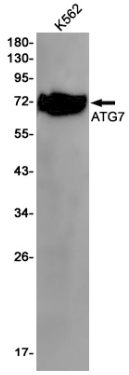
The molecular machinery of autophagy was largely discovered in yeast and referred to as autophagy-related (Atg) genes. Formation of the autophagosome involves a ubiquitin-like conjugation system in which Atg12 is covalently bound to Atg5 and targeted to autophagosome vesicles. This conjugation reaction is mediated by the ubiquitin E1-like enzyme Atg7 and the E2-like enzyme Atg10.

Images



Western blot analysis of ATG7 in K562 lysates using ATG7 antibody.





Please note: All products are 'FOR RESEARCH USE ONLY. NOT FOR USE IN DIAGNOSTIC OR THERAPEUTIC PROCEDURES'.