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BAG6 Polyclonal Antibody

Purified Rabbit Polyclonal Antibody (Pab)
Catalog # AP58702

Product Information

Application	WB, IHC-P, IHC-F, IF, E
Primary Accession	P46379
Reactivity	Rat, Pig, Dog, Bovine
Host	Rabbit
Clonality	Polyclonal
Calculated MW	119409
Physical State	Liquid
Immunogen	KLH conjugated synthetic peptide derived from human BAT3/BAG6
Epitope Specificity	1042-1132/1132
Isotype	IgG
Purity	affinity purified by Protein A
Buffer	0.01M TBS (pH7.4) with 1% BSA, 0.02% Proclin300 and 50% Glycerol.
SUBCELLULAR LOCATION	Cytoplasm, cytosol. Nucleus. Note=The C-terminal fragment generated by caspase-3 is cytoplasmic. Also found in extracellular vesicular exosomes in some tumor cells.
SIMILARITY	Belongs to the protein kinase superfamily. TKL Ser/Thr protein kinase family. Contains 1 death domain. Contains 1 protein kinase domain.
SUBUNIT	Interacts (via RIP homotypic interaction motif) with RIPK3 (via RIP homotypic interaction motif); this interaction induces RIPK1 necroptosis-specific phosphorylation, formation of the necroptosis-inducing complex. Interacts (via the death domain) with TNFRSF6 (via the death domain) and TRADD (via the death domain). Is recruited by TRADD to TNFRSF1A in a TNF-dependent process. Binds RNF216, EGFR, IKBKG, TRAF1, TRAF2 and TRAF3. Interacts with BNLF1. Interacts with SQSTM1 upon TNF-alpha stimulation. May interact with MAVS/IPS1. Interacts with ZFAND5. Interacts with RBCK.
Post-translational modifications	Proteolytically cleaved by caspase-8 during TNF-induced apoptosis. Cleavage abolishes NF-kappa-B activation and enhances pro-apototic signaling through the TRADD-FADD interaction. RIPK1 and RIPK3 undergo reciprocal auto- and trans-phosphorylation. Phosphorylation of Ser-161 by RIPK3 is necessary for the formation of the necroptosis-inducing complex. Ubiquitinated by 'Lys-11'-, 'Lys-48'-, 'Lys-63'- and linear-linked type ubiquitin. Polyubiquitination with 'Lys-63'-linked chains by TRAF2 induces association with the IKK complex. Deubiquitination of 'Lys-63'-linked chains and polyubiquitination with 'Lys-48'-linked chains by TNFAIP3 leads to RIPK1 proteasomal degradation and consequently downregulates TNF-alpha-induced NFkappa-B signaling. Linear polyubiquitinated; the head-to-tail polyubiquitination is mediated by the LUBAC complex. LPS-mediated activation of NF-kappa-B. Also ubiquitinated with 'Lys-11'-linked chains.
Important Note	This product as supplied is intended for research use only, not for use in human, therapeutic or diagnostic applications.
Background Descriptions	Chaperone that plays a key role in various processes such as apoptosis, insertion of tail-anchored (TA) membrane proteins to the endoplasmic reticulum membrane and regulation of chromatin. Acts in part by regulating

stability of proteins and their degradation by the proteasome. Participates in endoplasmic reticulum stress-induced apoptosis via its interaction with AIFM1/AIF by regulating AIFM1/AIF stability and preventing its degradation. Also required during spermatogenesis for synaptonemal complex assembly via its interaction with HSPA2, by inhibiting polyubiquitination and subsequent proteasomal degradation of HSPA2. Required for selective ubiquitin-mediated degradation of defective nascent chain polypeptides by the proteasome. In this context, may play a role in immuno-proteasomes to generate antigenic peptides via targeted degradation, thereby playing a role in antigen presentation in immune response. Key component of the BAG6/BAT3 complex, a cytosolic multiprotein complex involved in the post-translational delivery of tail-anchored (TA) membrane proteins to the endoplasmic reticulum membrane. TA membrane proteins, also named type II transmembrane proteins, contain a single C-terminal transmembrane region. BAG6/BAT3 acts by facilitating TA membrane proteins capture by ASNA1/TRC40: it is recruited to ribosomes synthesizing membrane proteins, interacts with the transmembrane region of newly released TA proteins and transfers them to ASNA1/TRC40 for targeting to the endoplasmic reticulum membrane.

Additional Information

Gene ID	7917
Other Names	Large proline-rich protein BAG6, BAG family molecular chaperone regulator 6, BCL2-associated athanogene 6 {ECO:0000312|HGNC:HGNC:13919}, BAG-6, HLA-B-associated transcript 3, Protein G3, Protein Scythe, BAG6 (HGNC:13919)
Dilution	WB=1:500-2000,IHC-P=1:100-500,IHC-F=1:100-500,IF=1:100-500,ELISA=1:5000-10000
Format	0.01M TBS(pH7.4) with 1% BSA, 0.09% (W/V) sodium azide and 50% Glyce
Storage	Store at -20 °C for one year. Avoid repeated freeze/thaw cycles. When reconstituted in sterile pH 7.4 0.01M PBS or diluent of antibody the antibody is stable for at least two weeks at 2-4 °C.

Protein Information

Name	BAG6 (HGNC:13919)
Function	ATP-independent molecular chaperone preventing the aggregation of misfolded and hydrophobic patches-containing proteins (PubMed:21636303). Functions as part of a cytosolic protein quality control complex, the BAG6/BAT3 complex, which maintains these client proteins in a soluble state and participates in their proper delivery to the endoplasmic reticulum or alternatively can promote their sorting to the proteasome where they undergo degradation (PubMed:20516149, PubMed:21636303, PubMed:21743475, PubMed:28104892). The BAG6/BAT3 complex is involved in the post-translational delivery of tail- anchored/type II transmembrane proteins to the endoplasmic reticulum membrane. Recruited to ribosomes, it interacts with the transmembrane region of newly synthesized tail-anchored proteins and together with SGTA and ASNA1 mediates their delivery to the endoplasmic reticulum (PubMed:20516149, PubMed:20676083, PubMed:25535373, PubMed:28104892). Client proteins that cannot be properly delivered to the endoplasmic reticulum are ubiquitinated by RNF126,

an E3 ubiquitin-protein ligase associated with BAG6 and are sorted to the proteasome (PubMed:24981174, PubMed:27193484, PubMed:28104892). SGTA which prevents the recruitment of RNF126 to BAG6 may negatively regulate the ubiquitination and the proteasomal degradation of client proteins (PubMed:23129660, PubMed:25179605, PubMed:27193484). Similarly, the BAG6/BAT3 complex also functions as a sorting platform for proteins of the secretory pathway that are mislocalized to the cytosol either delivering them to the proteasome for degradation or to the endoplasmic reticulum (PubMed:21743475). The BAG6/BAT3 complex also plays a role in the endoplasmic reticulum-associated degradation (ERAD), a quality control mechanism that eliminates unwanted proteins of the endoplasmic reticulum through their retrotranslocation to the cytosol and their targeting to the proteasome. It maintains these retrotranslocated proteins in an unfolded yet soluble state condition in the cytosol to ensure their proper delivery to the proteasome (PubMed:21636303). BAG6 is also required for selective ubiquitin-mediated degradation of defective nascent chain polypeptides by the proteasome. In this context, it may participate in the production of antigenic peptides and play a role in antigen presentation in immune response (By similarity). BAG6 is also involved in endoplasmic reticulum stress-induced pre- emptive quality control, a mechanism that selectively attenuates the translocation of newly synthesized proteins into the endoplasmic reticulum and reroutes them to the cytosol for proteasomal degradation. BAG6 may ensure the proper degradation of these proteins and thereby protects the endoplasmic reticulum from protein overload upon stress (PubMed:26565908). By inhibiting the polyubiquitination and subsequent proteasomal degradation of HSPA2 it may also play a role in the assembly of the synaptonemal complex during spermatogenesis (By similarity). Also positively regulates apoptosis by interacting with and stabilizing the proapoptotic factor AIFM1 (By similarity). By controlling the steady-state expression of the IGF1R receptor, indirectly regulates the insulin-like growth factor receptor signaling pathway (PubMed:26692333).

Cellular Location

Cytoplasm, cytosol. Nucleus. Secreted, extracellular exosome Note=Normally localized in cytosol and nucleus, it can also be released extracellularly, in exosomes, by tumor and myeloid dendritic cells (PubMed:18055229, PubMed:18852879). Cytoplasmic retention is due to interaction with GET4 (PubMed:29042515).

Tissue Location

Expressed by immature dendritic cells (at protein level).