

BAG6 Rabbit pAb

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Product Information

Application WB, IHC-P, IHC-F, IF, E

Reactivity Rat, Pig, Mouse, Rabbit, Dog, Horse

Host Rabbit Clonality Polyclonal **Calculated MW** 119 KDa **Physical State** Liquid

Immunogen KLH conjugated synthetic peptide derived from human BAT3/BAG6

1042-1132/1132 **Epitope Specificity**

Isotype IgG

Purity affinity purified by Protein A

Buffer

Cytoplasm, cytosol. Nucleus. Note=The C-terminal fragment generated by SUBCELLULAR LOCATION

caspase-3 is cytoplasmic. Also found in extracellular vesicular exosomes in

0.01M TBS (pH7.4) with 1% BSA, 0.02% Proclin300 and 50% Glycerol.

some tumor cells.

Belongs to the protein kinase superfamily. TKL Ser/Thr protein kinase family. **SIMILARITY**

Contains 1 death domain. Contains 1 protein kinase domain.

Interacts (via RIP homotypic interaction motif) with RIPK3 (via RIP homotypic **SUBUNIT**

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. Deubiguitination of 'Lys-63'-linked chains and polyubiguitination 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.

This product as supplied is intended for research use only, not for use in **Important Note**

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

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

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.

Background

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.

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