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# SQSTM1/p62 Rabbit mAb

Catalog # AP76880

### **Product Information**

**Application** WB, IHC-P, IHC-F, IP, ICC

Primary Accession <u>Q13501</u>

Reactivity Human, Mouse

**Host** Rabbit

**Clonality** Monoclonal Antibody

Calculated MW 47687

## **Additional Information**

Gene ID 8878

Other Names SQSTM1

**Dilution** WB~~1/500-1/1000 IHC-P~~N/A IHC-F~~N/A IP~~N/A ICC~~N/A

Format 50mM Tris-Glycine(pH 7.4), 0.15M NaCl, 40%Glycerol, 0.01% sodium azide and

0.05% BSA.

### **Protein Information**

Name SQSTM1 {ECO:0000303 | PubMed:16286508,

ECO:0000312 | HGNC:HGNC:11280}

**Function** Molecular adapter required for selective macroautophagy (aggrephagy) by

acting as a bridge between polyubiquitinated proteins and autophagosomes

(PubMed: 15340068, PubMed: 15953362, PubMed: 16286508, PubMed: 17580304, PubMed: 20168092, PubMed: 22017874, PubMed: 22622177, PubMed: 24128730, PubMed: 28404643, PubMed: 29343546, PubMed: 29507397, PubMed: 31857589, PubMed: 33509017, PubMed: 34471133, PubMed: 34893540,

PubMed:<u>35831301</u>, PubMed:<u>37306101</u>, PubMed:<u>37802024</u>). Promotes the recruitment of ubiquitinated cargo proteins to autophagosomes via multiple

domains that bridge proteins and organelles in different steps

(PubMed:16286508, PubMed:20168092, PubMed:22622177, PubMed:24128730, PubMed:28404643, PubMed:29343546,

PubMed: <u>34893540</u>, PubMed: <u>37802024</u>). SQSTM1 first mediates the assembly and removal of ubiquitinated proteins by undergoing liquid-liquid phase separation upon binding to ubiquitinated proteins via its UBA domain, leading to the formation of insoluble cytoplasmic inclusions,

known as p62 bodies (PubMed:<u>15911346</u>, PubMed:<u>20168092</u>, PubMed:<u>22017874</u>, PubMed:<u>24128730</u>, PubMed:<u>29343546</u>,

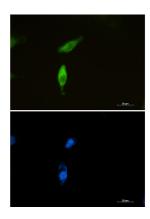
PubMed:<u>29507397</u>, PubMed:<u>31857589</u>, PubMed:<u>37802024</u>). SQSTM1 then interacts with ATG8 family proteins on autophagosomes via its LIR motif,

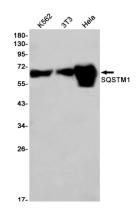
leading to p62 body recruitment to autophagosomes, followed by autophagic clearance of ubiquitinated proteins (PubMed: 16286508, PubMed: 17580304, PubMed:20168092, PubMed:22622177, PubMed:24128730, PubMed:28404643, PubMed:37802024). SQSTM1 is itself degraded along with its ubiquitinated cargos (PubMed: 16286508, PubMed: 17580304, PubMed:37802024). Also required to recruit ubiquitinated proteins to PML bodies in the nucleus (PubMed: 20168092). Also involved in autophagy of peroxisomes (pexophagy) in response to reactive oxygen species (ROS) by acting as a bridge between ubiquitinated PEX5 receptor and autophagosomes (PubMed: 26344566). Acts as an activator of the NFE2L2/NRF2 pathway via interaction with KEAP1: interaction inactivates the BCR(KEAP1) complex by sequestering the complex in inclusion bodies, promoting nuclear accumulation of NFE2L2/NRF2 and subsequent expression of cytoprotective genes (PubMed: 20452972, PubMed: 28380357, PubMed: 33393215, PubMed: 37306101). Promotes relocalization of 'Lys-63'-linked ubiquitinated STING1 to autophagosomes (PubMed: <u>29496741</u>). Involved in endosome organization by retaining vesicles in the perinuclear cloud: following ubiquitination by RNF26, attracts specific vesicle-associated adapters, forming a molecular bridge that restrains cognate vesicles in the perinuclear region and organizes the endosomal pathway for efficient cargo transport (PubMed:27368102, PubMed:33472082). Sequesters tensin TNS2 into cytoplasmic puncta, promoting TNS2 ubiquitination and proteasomal degradation (PubMed:25101860). May regulate the activation of NFKB1 by TNF-alpha, nerve growth factor (NGF) and interleukin-1 (PubMed: 10356400, PubMed: 10747026, PubMed: 11244088, PubMed: 12471037, PubMed: 16079148, PubMed: 19931284). May play a role in titin/TTN downstream signaling in muscle cells (PubMed: 15802564). Adapter that mediates the interaction between TRAF6 and CYLD (By similarity).

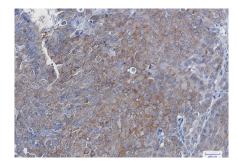
#### **Cellular Location**

Cytoplasmic vesicle, autophagosome. Preautophagosomal structure. Cytoplasm, cytosol. Nucleus, PML body. Late endosome. Lysosome. Nucleus Endoplasmic reticulum. Cytoplasm, myofibril, sarcomere {ECO:0000250|UniProtKB:O08623}. Note=In cardiac muscle, localizes to the sarcomeric band (By similarity). Localizes to cytoplasmic membraneless inclusion bodies, known as p62 bodies, containing polyubiquitinated protein aggregates (PubMed:11786419, PubMed:20357094, PubMed:22017874, PubMed:29343546, PubMed:29507397, PubMed:31857589, PubMed:37306101, PubMed:37802024). In neurodegenerative diseases, detected in Lewy bodies in Parkinson disease, neurofibrillary tangles in Alzheimer disease, and HTT aggregates in Huntington disease (PubMed:15158159). In protein aggregate diseases of the liver, found in large amounts in Mallory bodies of alcoholic and nonalcoholic steatohepatitis, hyaline bodies in hepatocellular carcinoma, and in SERPINA1 aggregates (PubMed:11981755) Enriched in Rosenthal fibers of pilocytic astrocytoma (PubMed:11786419). In the cytoplasm, observed in both membrane-free ubiquitin-containing protein aggregates (sequestosomes) and membranesurrounded autophagosomes (PubMed:15953362, PubMed:17580304) Colocalizes with TRIM13 in the perinuclear endoplasmic reticulum (PubMed:22178386). Co-localizes with TRIM5 in cytoplasmic bodies (PubMed:20357094). When nuclear export is blocked by treatment with leptomycin B, accumulates in PML bodies (PubMed:20168092) {ECO:0000250|UniProtKB:008623, ECO:0000269|PubMed:11786419, ECO:0000269 | PubMed:11981755, ECO:0000269 | PubMed:15158159, ECO:0000269 | PubMed:15953362, ECO:0000269 | PubMed:17580304, ECO:0000269 | PubMed:20168092, ECO:0000269 | PubMed:20357094, ECO:0000269 | PubMed:22017874, ECO:0000269 | PubMed:22178386, ECO:0000269 | PubMed:29343546, ECO:0000269 | PubMed:29507397, ECO:0000269 | PubMed:31857589, ECO:0000269 | PubMed:37306101, ECO:0000269 | PubMed:37802024}

## **Images**







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