

TRIM21 (5B9) Mouse mAb
Catalog # AP53520**Specification****TRIM21 (5B9) Mouse mAb - Product Information**

| | |
|-------------------|------------------------|
| Application | WB |
| Primary Accession | P19474 |
| Host | Mouse |
| Clonality | Monoclonal Antibody |
| Calculated MW | 54170 |

TRIM21 (5B9) Mouse mAb - Additional Information

Gene ID 6737

Other Names

SSA; RO52; SSA1; RNF81; Ro/SSA

Dilution

WB~~1:1000

TRIM21 (5B9) Mouse mAb - Protein InformationName TRIM21 ([HGNC:11312](#))

Synonyms RNF81, RO52, SSA1

Function

E3 ubiquitin-protein ligase whose activity is dependent on E2 enzymes, UBE2D1, UBE2D2, UBE2E1 and UBE2E2 (PubMed: [16297862](http://www.uniprot.org/citations/16297862) , PubMed: [16316627](http://www.uniprot.org/citations/16316627) , PubMed: [16472766](http://www.uniprot.org/citations/16472766) , PubMed: [16880511](http://www.uniprot.org/citations/16880511) , PubMed: [18022694](http://www.uniprot.org/citations/18022694) , PubMed: [18361920](http://www.uniprot.org/citations/18361920) , PubMed: [18641315](http://www.uniprot.org/citations/18641315) , PubMed: [18845142](http://www.uniprot.org/citations/18845142) , PubMed: [19675099](http://www.uniprot.org/citations/19675099) , PubMed: [26347139](http://www.uniprot.org/citations/26347139)). Forms a ubiquitin ligase complex in cooperation with the E2 UBE2D2 that is used not only for the ubiquitination of USP4 and IKBKB but also for its self-ubiquitination (PubMed: [16880511](http://www.uniprot.org/citations/16880511) , PubMed: [19675099](http://www.uniprot.org/citations/19675099)). Component of cullin-RING-based SCF (SKP1-CUL1-F-box protein) E3 ubiquitin-protein ligase complexes such as SCF(SKP2)-like complexes (PubMed: [16880511](http://www.uniprot.org/citations/16880511)). A TRIM21-containing SCF(SKP2)-like complex is shown to mediate ubiquitination of CDKN1B ('Thr-187' phosphorylated- form), thereby promoting its degradation by the proteasome

(PubMed:16880511). Monoubiquitinates IKBKB that will negatively regulates Tax-induced NF-kappa-B signaling (PubMed:19675099). Negatively regulates IFN-beta production post-pathogen recognition by catalyzing polyubiquitin-mediated degradation of IRF3 (PubMed:18641315). Mediates the ubiquitin-mediated proteasomal degradation of IgG1 heavy chain, which is linked to the VCP-mediated ER-associated degradation (ERAD) pathway (PubMed:18022694). Promotes IRF8 ubiquitination, which enhanced the ability of IRF8 to stimulate cytokine genes transcription in macrophages (By similarity). Plays a role in the regulation of the cell cycle progression (PubMed:16880511). Enhances the decapping activity of DCP2 (PubMed:18361920). Exists as a ribonucleoprotein particle present in all mammalian cells studied and composed of a single polypeptide and one of four small RNA molecules (PubMed:1985094, PubMed:8666824). At least two isoforms are present in nucleated and red blood cells, and tissue specific differences in RO/SSA proteins have been identified (PubMed:8666824). The common feature of these proteins is their ability to bind HY RNAs.2 (PubMed:8666824). Involved in the regulation of innate immunity and the inflammatory response in response to IFNG/IFN-gamma (PubMed:26347139). Organizes autophagic machinery by serving as a platform for the assembly of ULK1, Beclin 1/BECN1 and ATG8 family members and recognizes specific autophagy targets, thus coordinating target recognition with assembly of the autophagic apparatus and initiation of autophagy (PubMed:26347139). Regulates also autophagy through FIP200/RB1CC1 ubiquitination and subsequent decreased protein stability (PubMed:36359729). Represses the innate antiviral response by facilitating the formation of the NMI-IFI35 complex through 'Lys-63'- linked ubiquitination of NMI (PubMed:26342464). During viral infection, promotes cell pyroptosis by mediating 'Lys-6'-linked ubiquitination of ISG12a/IFI27, facilitating its translocation into the mitochondria and subsequent CASP3 activation (PubMed:36426955). When up-regulated through the IFN/JAK/STAT signaling pathway, promotes 'Lys-27'-linked ubiquitination of MAVS, leading to the recruitment of TBK1 and up- regulation of innate immunity (PubMed:29743353). Mediates 'Lys-63'- linked polyubiquitination of G3BP1 in response to heat shock, leading to stress granule disassembly (PubMed:36692217).

Cellular Location

Cytoplasm. Cytoplasmic vesicle, autophagosome. Nucleus. Cytoplasm, P-body. Cytoplasm, Stress granule. Note=Enters the nucleus upon exposure to nitric oxide (PubMed:18361920). Localizes to small dot- or rod-like structures in the cytoplasm, called processing bodies (P-bodies) that are located underneath the plasma membrane and also diffusely in the cytoplasm (PubMed:18361920). They are located along the microtubules and are highly motile in cells (PubMed:18361920). Colocalizes with DCP2 in P-bodies (PubMed:18361920). Localizes to stress granules in response to oxidative stress (PubMed:36692217).

Tissue Location

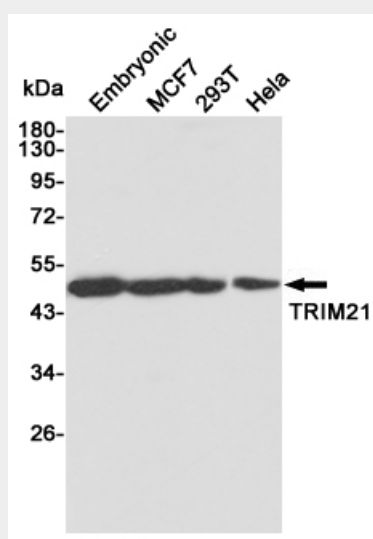
Isoform 1 and isoform 2 are expressed in fetal and adult heart and fetal lung

TRIM21 (5B9) Mouse mAb - Protocols

Provided below are standard protocols that you may find useful for product applications.

- [Western Blot](#)
- [Blocking Peptides](#)
- [Dot Blot](#)
- [Immunohistochemistry](#)
- [Immunofluorescence](#)
- [Immunoprecipitation](#)
- [Flow Cytometry](#)
- [Cell Culture](#)

TRIM21 (5B9) Mouse mAb - Images



Western blot detection of TRIM21 in Embryonic, MCF7, 293T and HeLa cell lysates using TRIM21 mouse mAb (dilution 1:1000). Predicted band size: 50 kDa. Observed band size: 50 kDa.

TRIM21 (5B9) Mouse mAb - Background

Swiss-Prot Acc.P19474. This gene encodes a member of the tripartite motif (TRIM) family. The TRIM motif includes three zinc-binding domains, a RING, a B-box type 1 and a B-box type 2, and a coiled-coil region. The encoded protein is part of the RoSSA ribonucleoprotein, which includes a single polypeptide and one of four small RNA molecules. The RoSSA particle localizes to both the cytoplasm and the nucleus. RoSSA interacts with autoantigens in patients with Sjogren syndrome and systemic lupus erythematosus. Alternatively spliced transcript variants for this gene have been described but the full-length nature of only one has been determined.