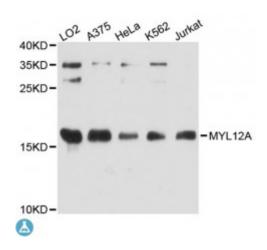


Anti-MYL12A Antibody



Description This gene encodes a nonsarcomeric myosin regulatory light chain. This

protein is activated by phosphorylation and regulates smooth muscle and non-muscle cell contraction. This protein may also be involved in DNA damage repair by sequestering the transcriptional regulator apoptosis-antagonizing transcription factor (AATF)/Che-1 which functions as a repressor of p53-driven apoptosis. Alternate splicing results in multiple transcript variants. A pseudogene of this gene is found on chromosome 8.

Model STJ113619

Host Rabbit
Reactivity Human

Applications WB

Immunogen Recombinant fusion protein containing a sequence corresponding to amino

acids 92-171 of human MYL12A (NP_006462.1).

Gene ID 10627

Gene Symbol MYL12A

Dilution range WB 1:500 - 1:2000

Purification Affinity purification

Note For Research Use Only (RUO).

Protein Name Myosin regulatory light chain 12A Epididymis secretory protein Li 24 HEL-

S-24 MLC-2B Myosin RLC Myosin regulatory light chain 2 nonsarcomeric

Myosin regulatory light chain MRLC3

Molecular Weight 19.794 kDa

Clonality Polyclonal

Conjugation Unconjugated

Isotype IgG

Formulation PBS with 0.02% sodium azide, 50% glycerol, pH7.3.

Storage Instruction Store at -20C. Avoid freeze / thaw cycles.

Database Links HGNC:16701OMIM:609211Reactome:R-HSA-3928664

Alternative Names Myosin regulatory light chain 12A Epididymis secretory protein Li 24 HEL-

S-24 MLC-2B Myosin RLC Myosin regulatory light chain 2 nonsarcomeric

Myosin regulatory light chain MRLC3

Function Myosin regulatory subunit that plays an important role in regulation of both

smooth muscle and nonmuscle cell contractile activity via its phosphorylation,

Implicated in cytokinesis, receptor capping, and cell locomotion,

Post-translational Phosphorylation increases the actin-activated myosin ATPase activity and

thereby regulates the contractile activity, It is required to generate the driving

force in the migration of the cells but not necessary for localization of

myosin-2 at the leading edge,

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Modifications

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