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Emp Polyclonal Antibody

Catalog # AP69726

Product Information

Application	WB, IHC-P
Primary Accession	Q7L5Y9
Reactivity	Human, Mouse, Rat
Host	Rabbit
Clonality	Polyclonal
Calculated MW	45287

Additional Information

Gene ID	10296
Other Names	MAEA; EMP; HLC10; PIG5; Macrophage erythroblast attacher; Cell proliferation-inducing gene 5 protein; Erythroblast macrophage protein; Human lung cancer oncogene 10 protein; HLC-10
Dilution	WB~~Western Blot: 1/500 - 1/2000. Immunohistochemistry: 1/100 - 1/300. ELISA: 1/20000. Not yet tested in other applications. IHC-P~~N/A
Format	Liquid in PBS containing 50% glycerol, 0.5% BSA and 0.09% (W/V) sodium azide.
Storage Conditions	-20℃

Protein Information

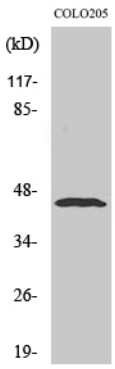
Name	MAEA
Function	Core component of the CTLH E3 ubiquitin-protein ligase complex that selectively accepts ubiquitin from UBE2H and mediates ubiquitination and subsequent proteasomal degradation of the transcription factor HBP1. MAEA and RMND5A are both required for catalytic activity of the CTLH E3 ubiquitin-protein ligase complex (PubMed:29911972). MAEA is required for normal cell proliferation (PubMed:29911972). The CTLH E3 ubiquitin-protein ligase complex is not required for the degradation of enzymes involved in gluconeogenesis, such as FBP1 (PubMed:29911972). Plays a role in erythroblast enucleation during erythrocyte maturation and in the development of mature macrophages (By similarity). Mediates the attachment of erythroid cell to mature macrophages; this MAEA-mediated contact inhibits erythroid cell apoptosis (PubMed:9763581). Participates in erythroblastic island formation, which is the functional unit of definitive erythropoiesis. Associates with F-actin to regulate actin distribution in erythroblasts and macrophages (By similarity). May contribute to nuclear architecture and cells division events (Probable).

Cellular Location	Cytoplasm {ECO:0000250|UniProtKB:Q4VC33}. Nucleus, nucleoplasm. Nucleus matrix. Cell membrane. Cytoplasm, cytoskeleton. Note=Detected in a nuclear, speckled- like pattern (PubMed:16510120). Localized with condensed chromatin at prophase; Detected in nuclear spindle poles at metaphase and in the contractile ring during telophase and cytokinesis (PubMed:16510120) Present in cytoplasm, nuclear matrix and at the cell surface in macrophages; predominantly nuclear in immature macrophages and predominantly detected at the cell surface in mature macrophages Colocalizes with F-actin in macrophages (By similarity) {ECO:0000250|UniProtKB:Q4VC33, ECO:0000269|PubMed:16510120}
Tissue Location	Detected at macrophage membranes (at protein level). Ubiquitous.

Background

Core component of the CTLH E3 ubiquitin-protein ligase complex that selectively accepts ubiquitin from UBE2H and mediates ubiquitination and subsequent proteasomal degradation of the transcription factor HBP1. MAEA and RMND5A are both required for catalytic activity of the CTLH E3 ubiquitin-protein ligase complex (PubMed:29911972). MAEA is required for normal cell proliferation (PubMed:29911972). The CTLH E3 ubiquitin-protein ligase complex is not required for the degradation of enzymes involved in gluconeogenesis, such as FBP1 (PubMed:29911972). Plays a role in erythroblast enucleation during erythrocyte maturation and in the development of mature macrophages (By similarity). Mediates the attachment of erythroid cell to mature macrophages; this MAEA- mediated contact inhibits erythroid cell apoptosis (PubMed:9763581). Participates in erythroblastic island formation, which is the functional unit of definitive erythropoiesis. Associates with F-actin to regulate actin distribution in erythroblasts and macrophages (By similarity). May contribute to nuclear architecture and cells division events (Probable).

Images



Western Blot analysis of various cells using Emp Polyclonal Antibody diluted at 1：500