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PRDM16 Rabbit pAb

Catalog # AP99802

Product Information

Application	IHC-P, IHC-F, IF, E
Primary Accession	Q9HAZ2
Other Accession	Q9HAZ2
Predicted	Human
Host	Rabbit
Clonality	Polyclonal
Calculated MW	140251
Physical State	Liquid
Immunogen	KLH conjugated synthetic peptide derived from human PRDM16
Epitope Specificity	1171-1276/1276
Isotype	IgG
Purity	affinity purified by Protein A
Buffer	0.01M TBS (pH7.4) with 1% BSA, 0.02% Proclin300 and 50% Glycerol.
SIMILARITY	Contains 10 C2H2-type zinc fingers. Contains 1 SET domain.
SUBUNIT	Interacts with CEBPA, CEBPB and CEBPD; the interaction is direct. Interacts with PPARG and PPARA; controls brown adipocytes differentiation. Interacts with CTBP1 and CTBP2; represses the expression of WAT-specific genes. Interacts with PPARGC1A and PPARGC1B; interaction with PPARGC1A or PPARGC1B activates the transcription of BAT-specific gene. Interacts with SMAD3 (By similarity). Interacts with HDAC1, SKI, SMAD2 and SMAD3; the interaction with SKI promotes the recruitment of SMAD3-HDAC1 complex on the promoter of TGF-beta target genes. {ECO:0000250, ECO:0000269|PubMed:19049980}.
DISEASE	Note=A chromosomal aberration involving PRDM16 is found in myelodysplastic syndrome (MDS) and acute myeloid leukemia (AML). Reciprocal translocation t(1;3)(p36;q21). Isoform 4 is specifically expressed in adult T-cell leukemia.
Important Note	This product as supplied is intended for research use only, not for use in human, therapeutic or diagnostic applications.
Background Descriptions	The reciprocal translocation t(1;3)(p36;q21) occurs in a subset of myelodysplastic syndrome (MDS) and acute myeloid leukemia (AML). This gene is located near the 1p36.3 breakpoint and has been shown to be specifically expressed in the t(1:3)(p36,q21)-positive MDS/AML. The protein encoded by this gene is a zinc finger transcription factor and contains an N-terminal PR domain. The translocation results in the overexpression of a truncated version of this protein that lacks the PR domain, which may play an important role in the pathogenesis of MDS and AML. Alternatively spliced transcript variants encoding distinct isoforms have been reported. [provided by RefSeq, Jul 2008]

Additional Information

Gene ID	63976

Other Names	CMD1LL; KMT8F; LVNC8; MEL1; PFM13; PRD16_HUMAN; PRDM16; PR domain zinc finger protein 16; PR domain-containing protein 16; Transcription factor MEL1 (MDS1/EVI1-like gene 1); 2.1.1.367; KIAA1675; PR/SET domain 16; PR domain containing 16; PR domain 16; MDS1/EVI1-like; PR-domain zinc finger protein 16; transcription factor MEL1
Dilution	IHC-P=1:100-500,IHC-F=1:100-500,ICC/IF=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.

Protein Information

Name	PRDM16 {ECO:0000303|PubMed:22939622, ECO:0000312|HGNC:HGNC:14000}
Function	Transcription regulator that acts both as a histone methyltransferase or chromatin adapter, depending on the context (PubMed:12816872). In the cytoplasm, acts as a histone methyltransferase, which catalyzes monomethylation of 'Lys-9' of free histone H3 (H3K9me1) during translation (By similarity). Monomethylated histone H3 is then transported to the nucleus and incorporated into nucleosomes where SUV39H methyltransferases (SUV39H1 and SUV39H2) use it as a substrate to catalyze histone H3 'Lys-9' trimethylation (H3K9me3) (By similarity). Probably one of the primary histone methyltransferases along with MECOM/PRDM3 that direct cytoplasmic H3K9me1 methylation (By similarity). In the nucleus, acts as a key chromatin adapter that mediates differentiation of brown and beige adipocytes, which are specialized in dissipating chemical energy in the form of heat in response to cold or excess feeding (By similarity). Following recruitment to chromatin by PPARG nuclear receptor, promotes differentiation of myoblastic precursors into brown adipose cells (By similarity). Mechanistically, acts by mediating recruitment of (1) EHMT1 histone methyltransferase, thereby inhibiting the expression of white adipose-selective genes or (2) mediator complex, activating genes that are highly expressed in brown adipocytes, such as UCP1, PPARA, and PPARGC1A (By similarity). Also mediates differentiation of beige adipocytes from white adipose cells following recruitment by PPARG (By similarity). In addition to adipocyte differentiation, also involved in tolerance to gut microbiota: following recruitment to chromatin by RORgammaT (RORC) in a subset of antigen-presenting cells, promotes differentiation of peripherally-induced regulatory T-cells (pTreg), which suppress inflammatory responses to commensal microorganisms (By similarity). Also required in adult heart to preserve mitochondrial function and inhibit hypertrophy with advanced age (By similarity). Functions as a repressor of TGF-beta signaling (PubMed:19049980).
Cellular Location	Nucleus. Chromosome {ECO:0000250|UniProtKB:A2A935}. Cytoplasm
Tissue Location	Expressed in uterus and kidney. Expressed in both cardiomyocytes and interstitial cells.

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