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phospho-CARM1 (Ser228) Rabbit pAb

Catalog # AP98270

Product Information

Application	IHC-P, IHC-F, IF, E
Primary Accession	Q86X55
Other Accession	Q86X55
Predicted	Rat, Pig, Human, Mouse, Horse
Host	Rabbit
Clonality	Polyclonal
Calculated MW	65854
Physical State	Liquid
Immunogen	KLH conjugated Synthesised phosphopeptide derived from human CARM1 around the phosphorylation site of Ser228
Epitope Specificity	VK(p-S)NN
Isotype	IgG
Purity	affinity purified by Protein A
Buffer	0.01M TBS (pH7.4) with 1% BSA, 0.02% Proclin300 and 50% Glycerol.
SIMILARITY	Belongs to the protein arginine N-methyltransferase family.
SUBUNIT	Homodimer (Probable). Interacts with the C-terminus of NCOA2/GRIP1, NCO3/ACTR and NCOA1/SRC1. Part of a complex consisting of CARM1, EP300/P300 and NCOA2/GRIP1. Interacts with FLII, TP53, myogenic factor MEF2, EP300/P300, TRIM24, CREBBP and CTNNB1. Identified in a complex containing CARM1, TRIM24 and NCOA2/GRIP1. Interacts with NCOA3/SRC3. Interacts with SNRPC (By similarity). Interacts with NR1H4. Interacts with RELA. Interacts with HTLV-1 Tax-1.
Post-translational modifications	Auto-methylated on Arg-550. Methylation enhances transcription coactivator activity. Methylation is required for its role in the regulation of pre-mRNA alternative splicing (By similarity). Phosphorylation at Ser-216 interferes with S-adenosyl-L-methionine binding and strongly reduces methyltransferase activity (By similarity). Phosphorylation at Ser-216 is strongly increased during mitosis, and decreases rapidly to a very low, basal level after entry into the G1 phase of the cell cycle. Phosphorylation at Ser-216 may promote location in the cytosol.
Important Note	This product as supplied is intended for research use only, not for use in human, therapeutic or diagnostic applications.
Background Descriptions	The protein encoded by this gene is similar to oxidoreductases, which are enzymes involved in cellular responses to oxidative stresses and irradiation. This gene is induced by the tumor suppressor p53 and is thought to be involved in p53-mediated cell death. It contains a p53 consensus binding site in its promoter region and a downstream pentanucleotide microsatellite sequence. P53 has been shown to transcriptionally activate this gene by interacting with the downstream pentanucleotide microsatellite sequence. The microsatellite is polymorphic, with a varying number of pentanucleotide repeats directly correlated with the extent of transcriptional activation by p53. It has been suggested that the microsatellite polymorphism may be associated with differential susceptibility to cancer. At least two transcript variants encoding the same protein have been found for this gene (from EntrezGene).

Additional Information

Gene ID	10498
Other Names	PRMT4; m9Bei; CARM1_HUMAN; CARM1; Coactivator-associated arginine methyltransferase 1; Protein arginine N-methyltransferase 4; 2.1.1.319; CARM1_MOUSE; CARM1_RAT; coactivator associated arginine methyltransferase 1; CARM1 (phospho-S228); p-CARM1; phospho-CARM1; CARM1 (phospho-Ser228)
Dilution	IHC-P=1:100-500,IHC-F=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	CARM1
Synonyms	PRMT4
Function	Methylates (mono- and asymmetric dimethylation) the guanidino nitrogens of arginyl residues in several proteins involved in DNA packaging, transcription regulation, pre-mRNA splicing, and mRNA stability (PubMed:12237300, PubMed:16497732, PubMed:19405910). Recruited to promoters upon gene activation together with histone acetyltransferases from EP300/P300 and p160 families, methylates histone H3 at 'Arg-17' (H3R17me), forming mainly asymmetric dimethylarginine (H3R17me2a), leading to activation of transcription via chromatin remodeling (PubMed:12237300, PubMed:16497732, PubMed:19405910). During nuclear hormone receptor activation and TCF7L2/TCF4 activation, acts synergically with EP300/P300 and either one of the p160 histone acetyltransferases NCOA1/SRC1, NCOA2/GRIP1 and NCOA3/ACTR or CTNNB1/beta-catenin to activate transcription (By similarity). During myogenic transcriptional activation, acts together with NCOA3/ACTR as a coactivator for MEF2C (By similarity). During monocyte inflammatory stimulation, acts together with EP300/P300 as a coactivator for NF-kappa-B (By similarity). Acts as a coactivator for PPARG, promotes adipocyte differentiation and the accumulation of brown fat tissue (By similarity). Plays a role in the regulation of pre-mRNA alternative splicing by methylation of splicing factors (By similarity). Also seems to be involved in p53/TP53 transcriptional activation (By similarity). Methylates EP300/P300, both at 'Arg-2142', which may loosen its interaction with NCOA2/GRIP1, and at 'Arg-580' and 'Arg-604' in the KIX domain, which impairs its interaction with CREB and inhibits CREB-dependent transcriptional activation (PubMed:15731352). Also methylates arginine residues in RNA-binding proteins PABPC1, ELAVL1 and ELAV4, which may affect their mRNA- stabilizing properties and the half-life of their target mRNAs (By similarity). Acts as a transcriptional coactivator of ACACA/acetyl-CoA carboxylase by enriching H3R17 methylation at its promoter, thereby positively regulating fatty acid synthesis (By similarity). Independently of its methyltransferase activity, involved in replication fork progression: promotes PARP1 recruitment to replication forks, leading to poly-ADP-ribosylation of chromatin at replication forks and reduced fork speed (PubMed:33412112).

Cellular Location	Nucleus. Cytoplasm. Chromosome. Note=Mainly nuclear during the G1, S and G2 phases of the cell cycle (PubMed:19843527). Cytoplasmic during mitosis, after breakup of the nuclear membrane (PubMed:19843527) Localizes to replication forks (PubMed:33412112)
Tissue Location	Overexpressed in prostate adenocarcinomas and high- grade prostatic intraepithelial neoplasia

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