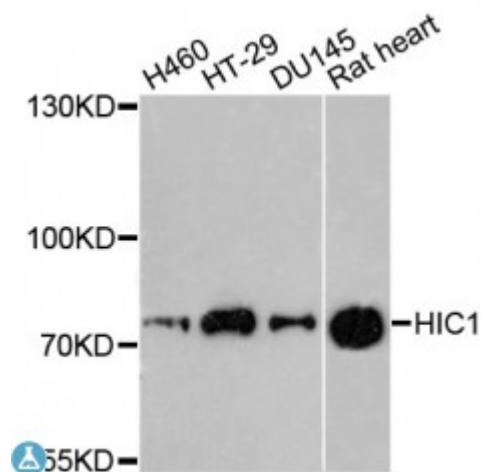


Anti-HIC1 Antibody



Description

This gene functions as a growth regulatory and tumor repressor gene. Hypermethylation or deletion of the region of this gene have been associated with tumors and the contiguous-gene syndrome, Miller-Dieker syndrome. Alternative splicing of this gene results in multiple transcript variants.

Model	STJ116366
Host	Rabbit
Reactivity	Human, Rat
Applications	WB
Immunogen	Recombinant fusion protein containing a sequence corresponding to amino acids 180-430 of human HIC1 (NP_001091672.1).
Gene ID	3090
Gene Symbol	HIC1
Dilution range	WB 1:500 - 1:2000
Tissue Specificity	Ubiquitously expressed with highest levels found in lung, colon, prostate, thymus, testis and ovary, Expression is absent or decreased in many tumor cells
Purification	Affinity purification
Note	For Research Use Only (RUO).
Protein Name	Hypermethylated in cancer 1 protein Hic-1 Zinc finger and BTB domain-containing protein 29

Molecular Weight	76.508 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:4909OMIM:603825Reactome:R-HSA-3232118
Alternative Names	Hypermethylated in cancer 1 protein Hic-1 Zinc finger and BTB domain-containing protein 29
Function	Transcriptional repressor, Recognizes and binds to the consensus sequence '5-[CG]NG[CG]GGGCA[CA]CC-3', May act as a tumor suppressor, May be involved in development of head, face, limbs and ventral body wall, Involved in down-regulation of SIRT1 and thereby is involved in regulation of p53/TP53-dependent apoptotic DNA-damage responses, The specific target gene promoter association seems to be depend on corepressors, such as CTBP1 or CTBP2 and MTA1, The regulation of SIRT1 transcription in response to nutrient deprivation seems to involve CTBP1, In cooperation with MTA1 (indicative for an association with the NuRD complex) represses transcription from CCND1/cyclin-D1 and CDKN1C/p57Kip2 specifically in quiescent cells, Involved in regulation of the Wnt signaling pathway probably by association with TCF7L2 and preventing TCF7L2 and CTNNB1 association with promoters of TCF-responsive genes, Seems to repress transcription from E2F1 and ATOH1 which involves ARID1A, indicative for the participation of a distinct SWI/SNF-type chromatin-remodeling complex, Probably represses transcription from ACKR3, FGFBP1 and EFNA1,
Cellular Localization	Nucleus
Post-translational Modifications	Acetylated on several residues, including Lys-333, Lys-333 is deacetylated by SIRT1,