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CTCF Antibody

Purified Mouse Monoclonal Antibody
Catalog # AO1501a

Product Information

Application	WB, E
Primary Accession	P49711
Reactivity	Human, Monkey
Host	Mouse
Clonality	Monoclonal
Clone Names	1D11
Isotype	IgG1
Calculated MW	82785
Description	This gene is a member of the BORIS + CTCF gene family and encodes a transcriptional regulator protein with 11 highly conserved zinc finger (ZF) domains. This nuclear protein is able to use different combinations of the ZF domains to bind different DNA target sequences and proteins. Depending upon the context of the site, the protein can bind a histone acetyltransferase (HAT)-containing complex and function as a transcriptional activator or bind a histone deacetylase (HDAC)-containing complex and function as a transcriptional repressor. If the protein is bound to a transcriptional insulator element, it can block communication between enhancers and upstream promoters, thereby regulating imprinted expression. Mutations in this gene have been associated with invasive breast cancers, prostate cancers, and Wilms' tumors.Tissue specificity: Ubiquitous. Absent in primary spermatocytes.
Immunogen	Purified recombinant fragment of human CTCF expressed in E. Coli.
Formulation	Ascitic fluid containing 0.03% sodium azide.

Additional Information

Gene ID	10664
Other Names	Transcriptional repressor CTCF, 11-zinc finger protein, CCCTC-binding factor, CTCFL paralog, CTCF
Dilution	WB~~1/500 - 1/2000 E~~N/A
Storage	Maintain refrigerated at 2-8°C for up to 6 months. For long term storage store at -20°C in small aliquots to prevent freeze-thaw cycles.
Precautions	CTCF Antibody is for research use only and not for use in diagnostic or therapeutic procedures.

Protein Information

Name	CTCF
Function	Chromatin binding factor that binds to DNA sequence specific sites and regulates the 3D structure of chromatin (PubMed:16949368, PubMed:18347100, PubMed:18654629, PubMed:19322193). Binds together strands of DNA, thus forming chromatin loops, and anchors DNA to cellular structures, such as the nuclear lamina (PubMed:18347100, PubMed:18654629, PubMed:19322193). Defines the boundaries between active and heterochromatic DNA via binding to chromatin insulators, thereby preventing interaction between promoter and nearby enhancers and silencers (PubMed:18347100, PubMed:18654629, PubMed:19322193). Participates in the allele-specific gene expression at the imprinted IGF2/H19 gene locus (PubMed:16107875, PubMed:16815976, PubMed:17827499). On the maternal allele, binding within the H19 imprinting control region (ICR) mediates maternally inherited higher- order chromatin conformation to restrict enhancer access to IGF2 (By similarity). Mediates interchromosomal association between IGF2/H19 and WSB1/NF1 and may direct distant DNA segments to a common transcription factory (By similarity). Regulates asynchronous replication of IGF2/H19 (By similarity). Plays a critical role in gene silencing over considerable distances in the genome (By similarity). Preferentially interacts with unmethylated DNA, preventing spreading of CpG methylation and maintaining methylation-free zones (PubMed:18413740). Inversely, binding to target sites is prevented by CpG methylation (PubMed:18413740). Plays an important role in chromatin remodeling (PubMed:18413740). Can dimerize when it is bound to different DNA sequences, mediating long-range chromatin looping (PubMed:12191639). Causes local loss of histone acetylation and gain of histone methylation in the beta-globin locus, without affecting transcription (PubMed:12191639). When bound to chromatin, it provides an anchor point for nucleosomes positioning (PubMed:12191639). Seems to be essential for homologous X-chromosome pairing (By similarity). May participate with Tsix in establishing a regulatable epigenetic switch for X chromosome inactivation (PubMed:11743158). May play a role in preventing the propagation of stable methylation at the escape genes from X-inactivation (PubMed:11743158). Involved in sister chromatid cohesion (PubMed:12191639). Associates with both centromeres and chromosomal arms during metaphase and required for cohesin localization to CTCF sites (PubMed:18550811). Plays a role in the recruitment of CENPE to the pericentromeric/centromeric regions of the chromosome during mitosis (PubMed:26321640). Acts as a transcriptional repressor binding to promoters of vertebrate MYC gene and BAG1 gene (PubMed:18413740, PubMed:8649389, PubMed:9591631). Also binds to the PLK and PIM1 promoters (PubMed:12191639). Acts as a transcriptional activator of APP (PubMed:9407128). Regulates APOA1/C3/A4/A5 gene cluster and controls MHC class II gene expression (PubMed:18347100, PubMed:19322193). Plays an essential role in oocyte and preimplantation embryo development by activating or repressing transcription (By similarity). Seems to act as tumor suppressor (PubMed:12191639).
Cellular Location	Nucleus, nucleoplasm. Chromosome. Chromosome, centromere. Note=May translocate to the nucleolus upon cell differentiation. Associates with both centromeres and chromosomal arms during metaphase. Associates with the H19 ICR in mitotic chromosomes. May be preferentially excluded from heterochromatin during interphase
Tissue Location	Ubiquitous. Absent in primary spermatocytes.

References

1. J Mol Med. 2008 Sep;86(9):1057-66. 2. J Exp Med. 2008 Apr 14;205(4):785-98. 3. EMBO J. 2008 Feb 20;27(4):654-66.

Images

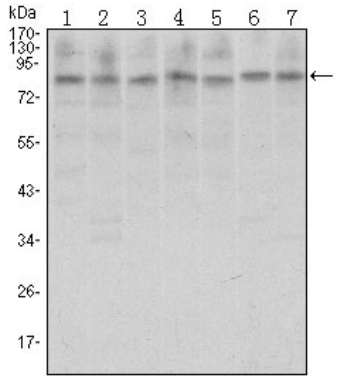

Figure 1: Western blot analysis using CTCF mouse mAb against A31 (1), MCF-7 (2), Hela (3), HCT116 (4), Jurkat (5), NIH/3T3 (6), and Cos7 (7) cell lysate.