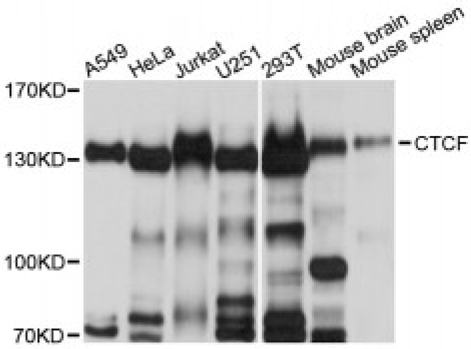
Anti-CTCF Antibody



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. Alternatively spliced transcript variants encoding different isoforms have been found for this gene.

Model	STJ115237
Host	Rabbit
Reactivity	Human, Mouse, Rat
Applications	ChIP, IF, IHC, WB
Immunogen	Recombinant fusion protein containing a sequence corresponding to amino acids 1-260 of human CTCF (NP_006556.1).
Gene ID	10664
Gene Symbol	CTCF
Dilution range	WB 1:1000 - 1:2000 IHC 1:50 - 1:200

	IF 1:50 - 1:200 ChIP 1:50 - 1:200
Tissue Specificity	Ubiquitous, Absent in primary spermatocytes
Purification	Affinity purification
Note	For Research Use Only (RUO).
Protein Name	Transcriptional repressor CTCF 11-zinc finger protein CCCTC-binding factor CTCFL paralog
Molecular Weight	82.785 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:13723OMIM:604167Reactome:R-HSA-5617472
Alternative Names	Transcriptional repressor CTCF 11-zinc finger protein CCCTC-binding factor CTCFL paralog
Function	Chromatin binding factor that binds to DNA sequence specific sites, Involved in transcriptional regulation by binding to chromatin insulators and preventing interaction between promoter and nearby enhancers and silencers, Acts as transcriptional repressor binding to promoters of vertebrate MYC gene and BAG1 gene, Also binds to the PLK and PIM1 promoters, Acts as a transcriptional activator of APP, Regulates APOA1/C3/A4/A5 gene cluster and controls MHC class II gene expression, Plays an essential role in oocyte and preimplantation embryo development by activating or repressing transcription, Seems to act as tumor suppressor, Plays a critical role in the epigenetic regulation, Participates in the allele-specific gene expression at the imprinted IGF2/H19 gene locus, 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, Plays a critical role in gene silencing over considerable distances in the genome, Preferentially interacts with unmethylated DNA, preventing spreading of CpG methylation and maintaining methylation-free zones, Inversely, binding to target sites is prevented by CpG methylation, Plays a important role in chromatin remodeling, Can dimerize when it is bound to different DNA sequences, mediating long-range chromatin looping, Mediates interchromosomal association between IGF2/H19 and WSB1/NF1 and may direct distant DNA segments to a common transcription factory, Causes local loss of histone acetylation and gain of histone methylation in the beta-globin locus, without affecting transcription, When bound to chromatin, it provides an anchor point for nucleosomes positioning, Seems to be essential for homologous X-chromosome pairing, May participate with Tsix in establishing a regulatable epigenetic switch for X chromosome inactivation, May play a role in preventing the propagation of stable methylation at the escape genes from X- inactivation, Involved in sister chromatid cohesion, Associates with both centromeres and chromosomal arms during metaphase and required for cohesin localization to CTCF sites, Regulates asynchronous replication of

	IGF2/H19, Plays a role in the recruitment of CENPE to the pericentromeric/centromeric regions of the chromosome during mitosis ,
Cellular Localization	Nucleus, nucleoplasm,
Post-translational Modifications	Sumoylated on Lys-74 and Lys-689