10320 Camino Santa Fe, Suite G
San Diego, CA 92121
Tel: 858.875.1900 Fax: 858.875.1999

CTCF antibody - N-terminal region
Rabbit Polyclonal Antibody
Catalog # AI16238

Specification

CTCF antibody - N-terminal region - Product Information

Application	**WB, CHIP**
Primary Accession	P49711
Other Accession	NM_006565, NP_006556
Reactivity	**Human, Mouse, Rat, Rabbit, Horse, Bovine, Dog**
Predicted	**Human, Mouse, Rat, Rabbit, Chicken, Horse, Bovine, Dog**
Host	**Rabbit**
Clonality	**Polyclonal**
Calculated MW	**83kDa KDa**

CTCF antibody - N-terminal region - Additional Information

Gene ID 10664

Other Names
Transcriptional repressor CTCF, 11-zinc finger protein, CCCTC-binding factor, CTCFL paralog, CTCF

Format
Liquid. Purified antibody supplied in 1x PBS buffer with 0.09% (w/v) sodium azide and 2% sucrose.

Reconstitution & Storage
Add 50 ul of distilled water. Final anti-CTCF antibody concentration is 1 mg/ml in PBS buffer with 2% sucrose. For longer periods of storage, store at 20°C. Avoid repeat freeze-thaw cycles.

Precautions
CTCF antibody - N-terminal region is for research use only and not for use in diagnostic or therapeutic procedures.

CTCF antibody - N-terminal region - Protein Information

Name CTCF

Function
Chromatin binding factor that binds to DNA sequence specific sites and regulates the 3D structure of chromatin (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:<a

href="http://www.uniprot.org/citations/19322193" target="_blank">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). Plays a critical role in the epigenetic regulation (PubMed:16949368). 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

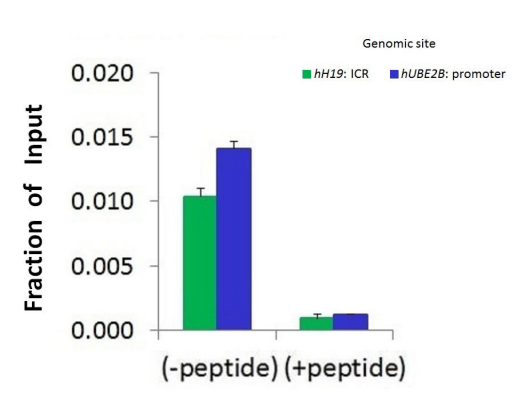
Tissue Location
Ubiquitous. Absent in primary spermatocytes.

CTCF antibody - N-terminal region - Protocols

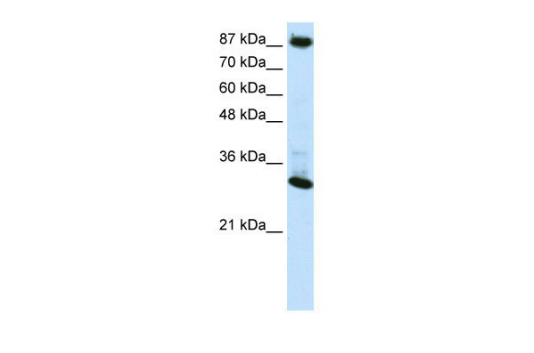
Provided below are standard protocols that you may find useful for product applications.

- Western Blot
- Blocking Peptides
- Dot Blot
- Immunohistochemistry
- Immunofluorescence
- Immunoprecipitation
- Flow Cytomety
- Cell Culture

CTCF antibody - N-terminal region - Images



Chromatin Immunoprecipitation (ChIP) Using CTCF antibody - N-terminal region (AI16238) and HCT116 Cells



WB Suggested Anti-CTCF Antibody Titration: 0.2-1 µg/ml
Positive Control: Transfected 293T

CTCF antibody - N-terminal region - Background

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.

CTCF antibody - N-terminal region - References

Filippova G.N.,et al.Mol. Cell. Biol. 16:2802-2813(1996).
Filippova G.N.,et al.Genes Chromosomes Cancer 22:26-36(1998).
Filippova G.N.,et al.Cancer Res. 62:48-52(2002).
Kalnine N.,et al.Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
Totoki Y.,et al.Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.