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Gene Section
Mini Review

CAMTA1 (calmodulin binding transcription activator 1)

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Identity

Other names: KIAA0833

HGNC (Hugo): CAMTA1

Location: 1p36.31

DNA/RNA

Description

The CAMTA1 gene (Henrich and Westermann, 2008) comprises 23 exons (all coding) spanning 984.38 kb of genomic DNA.

Transcription

8442 bp mRNA. Start codon at 208 bp. Stop codon at 5227 bp.

Protein

Description

1673 amino acids; the protein's primary structure contains a nuclear localization signal, two DNA-binding domains (CG-1 and TIG), calmodulin binding motifs (IQ motifs) and ankyrin domains that may mediate protein-protein interactions.

Expression

Although expression of CAMTA1 is found in various organs, highest levels are seen in neuronal tissues (Nagase et al., 1998). In the brain, CAMTA1 levels are highest in the temporal cortex, entorhinal cortex and in the cerebellum (Huentelman et al., 2007).

Localisation

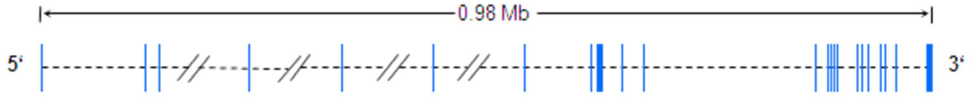
Nucleus.

Function

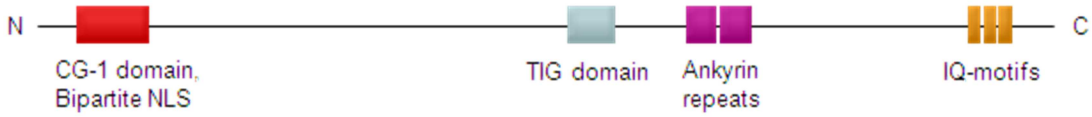
Largely unknown. CAMTA1 has been shown to act as a transcription activator in a reporter expression system (Bouché et al., 2002). Further data on the functional role are scarce. The homolog CAMTA2 is a co-activator of the transcription factor Nkx2-5. This function is inhibited by binding of class II histone deacetylases (Song et al., 2006).

Homology

Members of the CAMTA family are conserved in various eukaryotes including ciliates, plants, nematodes, insects, birds and mammals (Finkler et al., 2007). In human, two homologous CAMTAs are found, CAMTA1 and CAMTA2.



Genomic organization of CAMTA1. Arrows illustrate genomic distance. Exons are represented by vertical blue lines or bars.



Schematic representation of the CAMTA1 protein. Protein domains are indicated by boxes. NLS, nuclear localization signal.

Implicated in

Neuroblastoma

Note

The 1p36 smallest region of overlapping deletion in neuroblastomas spans only 261 kb and pinpoints the CAMTA1 gene (Henrich et al., 2006). In the absence of somatic mutations (Henrich et al., 2007), low CAMTA1 mRNA expression is significantly associated with markers of unfavorable tumor biology and poor neuroblastoma outcome. In multivariate survival analysis, this prognostic value is independent of established risk markers, including 1p deletion (Henrich et al., 2006).

Glioma

Note

CAMTA1 is homozygously deleted in a subset of gliomas (Ichimura et al., 2008) and is the only gene mapping to the smallest region of overlapping heterozygous deletion in this entity (Barbashina et al., 2005).

Colon cancer

Note

In colorectal cancer, loss of a 2 Mb region encompassing CAMTA1 had the strongest impact on survival among all copy number alterations identified by genome-wide copy number analysis (Kim et al., 2006). As in neuroblastoma, low expression of CAMTA1 mRNA is an independent predictor of poor outcome in colorectal cancer (Kim et al., 2006).

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