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Gene Section

Mini Review

GLI1 (glioma-associated oncogene homolog 1)

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Identity

Other names: GLI; Zinc finger protein GLI1 (gliomaassociated oncogene); Oncogene GLI; Gliomaassociated oncogene homolog 1

HGNC (Hugo): GLI1

Location: 12q13.2-q13.3

Location (base pair): Position 56140200-56152312 on the chromosome 12 genomic sequence.

Local order: Telomeric to the ATF1 gene; centromeric to the OS-9, SAS and CDK4 genes.

Note: GLI1 was the first human member of the Krüppel zinc finger proteins to be identified, and constitutes the archetype of this family of human genes. Other members are GLI2 (2q14) and GLI3 (7p13). GLI4/HKR4 (8q24) was misclassified as member of the human GLI gene family.

DNA/RNA

Description

12 exons, spans approximately 12 kb of genomic DNA in the centromere-to-telomere orientation. The translation initiation codon is located to exon 2, and the stop codon to exon 12.

Transcription

mRNA of 3.6 kb.

Protein

Description

The open reading frame encodes a 1106 amino acid protein, with an estimated molecular weight of approximately 118 kDa. The protein contains five DNA-binding zinc fingers between amino acids 235 and 393 (encoded by exons 7-10), and a transactivating domain constituted by amino acids 1020-1091 (encoded by exon 12).

Expression

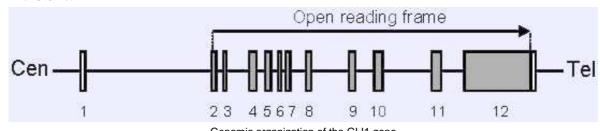
GLI proteins function as direct effectors of sonic hedgehog-signaling during embryogenesis. GLI1 (also GLI2 and GLI3) are therefore likely to be involved in the tissue-specific proliferation of the central nervous system, the zones of polarizing activity in the developing limb, and of the gut. In the adult human, GLI1 expression has been demonstrated in the testes, myometrium and Fallopian tubes.

Localisation

Nuclear. Might be fluctuating between the cytoplasm and the nucleus.

Function

DNA-binding transcription factor.



Genomic organization of the GLI1 gene.

Mutations

Germinal

An abnormal activity of GLI, caused by mutations affecting upstream components of the sonic hedgehogsignaling pathway (sonic hedgehog, patched or smoothened) are associated with developmental disorders.

Somatic

Various tumors of mesenchymal and lymphocytic origin.

Implicated in

Note

Rearrangement and fusion of the GLI1 gene.

Disease

Pericytoma with t(7;12)

Prognosis

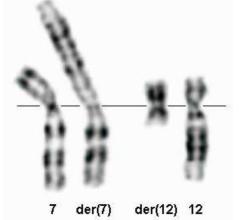
Benign or low-malignant.

Cytogenetics

t(7;12)(p22;q13)

Hybrid/Mutated gene

ACTB-GLI1 fusion gene. The breakpoints reported so far have been located to introns 1, 2 or 3 within the ACTB gene, and to introns 5 or 6 or to exon 7 within the GLI1 gene. Reciprocal GLI1-ACTB gene fusions have also been detected. The breakpoints have been located to introns 5 or 7 within the GLI1 gene, and to intron 3 of the ACTB gene.



Representative G-banded partial karyotype of the t(7;12)(p22;q13).

Abnormal protein

The ACTB-GLI1 fusion protein contains the N-terminal of ACTB and the C-terminal of GLI1, including the DNA-binding zinc finger motifs (encoded by exons 7-10) and transactivating motifs (exon 12).

Oncogenesis

It is suggested that the strong ACTB promoter causes

an overexpression of GLI1 sequences important for transcriptional activation of downstream target genes, akin to the oncogenic mechanisms of the COL1A1-PDGFB fusion gene detected in dermatofibrosarcoma protuberans.

Note

Amplification of the GLI1 gene.

Disease

Glioma, B-cell lymphoma, sarcoma

Prognosis

Depends on tumor type.

Oncogenesis

Overexpression of GL11 sequences. Might be of prognostic importance.

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