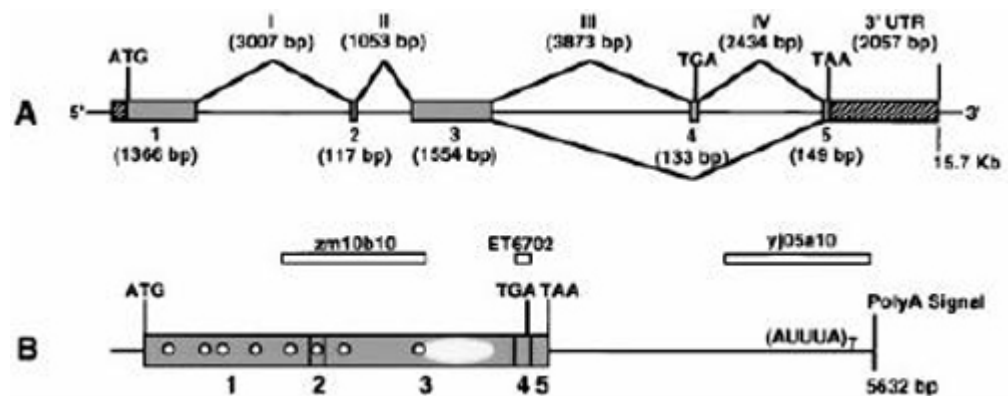


ZNF217

Identity

Other names **13009**
FLJ14031
ZABC1
Hugo [ZNF217](#)
Location 20q13.2

DNA/RNA



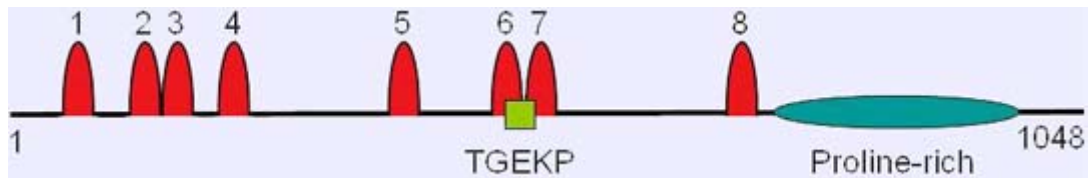
Genomic organization of ZNF217. (A) The genomic organization of the five exons with encoded initiation and termination codons that make up ZNF217. Hatched boxes represent known 5'- and 3'-untranslated regions (UTR) in the cDNA. The sizes of exons and introns appear below and above the map, respectively. (B) The map of the 5632-bp ZNF217 cDNA. Vertical bars represent exon boundaries. The relative positions of the predicted eight C2H2 Kruppel-like zinc finger motifs are indicated by white circles. The position of the proline-rich putative transcription activator domain is shown as a hatched oval. AUUUA motifs are indicated in the 3'-untranslated region. The relative locations of three ESTs are shown in boxes.

Description 5 exons

Transcription Exon 4 encodes a TGA termination codon and is alternatively processed.

Pseudogene None

Protein



Eight C2H2 zinc fingers and a proline-rich domain. Conserved linker sequence, TGEKP, reported to bind DNA with high affinity

Description Full-length ZNF217 cDNAs encode two open reading frames of 1,062 and 1,108 amino acids, due to alternative splicing of exon 4. Each predicted protein has eight C2H2 zinc fingers and a proline-rich domain. Sequence analysis of ZNF217 indicates a strong resemblance to members of the Kruppel-like family of zinc finger proteins. The eight zinc finger domains in ZNF217 are interspersed throughout the ZNF217 sequence and their pattern does not appear to fall into one of the three classes of C2H2 zinc finger proteins; triple-C2H2, multipleadjacent, and separated-paired fingers. The sixth and seventh zinc fingers in ZNF217 are separated by the conserved linker sequence, TGEKP, reported to bind DNA with high affinity. Database analysis indicates that this paired zinc finger region aligns with those in several members of the Delta-EF1/ZFH-1 family of two-handed zinc-finger homeodomain proteins, including Smad-Interacting Protein 1 (SIP-1).

Expression ZNF217 is expressed at low levels in normal tissues.

Localisation Nuclear

Function ZNF217 protein localizes to the nucleus and co-immunoprecipitates with complexes containing the transcriptional corepressors CoREST and CtBP, histone deacetylases [HDAC1](#) and [HDAC2](#), and histone methyltransferases G9a and Eu-HMTase1. This strongly suggests that ZNF217 may function as part of a transcriptional repressor complex.

Implicated in

Entity The findings that ZNF217 can immortalize human mammary epithelial cells, and that its amplification is associated with poor prognosis, suggest that it may play roles in both early and late stage [breast cancer](#). ZNF217 can attenuate apoptotic signals resulting from telomere dysfunction as well as from doxorubicin-induced DNA damage, while silencing ZNF217 with siRNA restores sensitivity to doxorubicin. Moreover, elevated ZNF217 leads to increased phosphorylation of Akt, whereas inhibition of the phosphatidylinositol 3 kinase pathway and Akt phosphorylation decreases ZNF217 protein levels and increases sensitivity to doxorubicin. These results suggest that ZNF217 may promote neoplastic transformation by increasing cell survival during telomeric crisis, and may promote later stages of malignancy by increasing cell survival during chemotherapy.

External links

Nomenclature

Hugo	ZNF217
GDB	ZNF217
Entrez_Gene	ZNF217_7764 zinc finger protein 217

Cards

Atlas	ZNF217ID42875ch20q13
GeneCards	ZNF217
Ensembl	ZNF217
Genatlas	ZNF217
GeneLynx	ZNF217
eGenome	ZNF217
euGene	7764

Genomic and cartography

GoldenPath	ZNF217 - 20q13.2 chr20:51617019-51633043 - 20q13.2 (hg18-Mar_2006)
Ensembl	ZNF217 - 20q13.2 [CytoView]
NCBI	Genes Cyto Gene Seq [Map View - NCBI]
OMIM	Disease map [OMIM]
HomoloGene	ZNF217

Gene and transcription

Genbank	AF041259 [ENTREZ]
Genbank	BC039055 [ENTREZ]
Genbank	BC113427 [ENTREZ]
RefSeq	NM_006526 [SRS] NM_006526 [ENTREZ]
AceView	ZNF217 AceView - NCBI
TRASER	ZNF217 Traser - Stanford
Unigene	Hs.155040 [SRS] Hs.155040 [NCBI] HS155040 [spliceNest]

Protein : pattern, domain, 3D structure

SwissProt	O75362 [SRS] O75362 [EXPASY] O75362 [INTERPRO]
Prosite	PS00028 ZINC FINGER C2H2_1 [SRS] PS00028 ZINC FINGER C2H2_1 [Expasy]
Prosite	PS50157 ZINC FINGER C2H2_2 [SRS] PS50157 ZINC FINGER C2H2_2 [Expasy]
Interpro	IPR007087 Znf_C2H2 [SRS] IPR007087 Znf_C2H2 [EBI]
CluSTr	O75362
Pfam	PF00096 zf-C2H2 [SRS] PF00096 zf-C2H2 [Sanger] pfam00096 [NCBI-CDD]
Smart	SM00355 ZnF_C2H2 [EMBL]
Blocks	O75362

[HPRD](#) [O75362](#)

Protein Interaction databases

[DIP](#) [O75362](#)

[IntAct](#) [O75362](#)

Polymorphism : SNP, mutations, diseases

[OMIM](#) [602967](#) [[map](#)]

[GENECLINICS](#) [602967](#)

[SNP](#) [ZNF217](#) [dbSNP-NCBI]

[SNP](#) [NM_006526](#) [SNP-NCI]

[SNP](#) [ZNF217](#) [GeneSNPs - Utah] [ZNF217](#) [HGBASE - SRS]

[HAPMAP](#) [ZNF217](#) [HAPMAP]

General knowledge

[Family Browser](#) [ZNF217](#) [UCSC Family Browser]

[SOURCE](#) [NM_006526](#)

[SMD](#) [Hs.155040](#)

[SAGE](#) [Hs.155040](#)

[Amigo](#) [transcription factor activity](#)

[Amigo](#) [intracellular](#)

[Amigo](#) [nucleus](#)

[Amigo](#) [regulation of transcription, DNA-dependent](#)

[Amigo](#) [zinc ion binding](#)

[Amigo](#) [metal ion binding](#)

[PubGene](#) [ZNF217](#)

Other databases

Probes

[Probe](#) [ZNF217 Related clones \(RZPD - Berlin\)](#)

PubMed

[PubMed](#) [8 Pubmed reference\(s\) in LocusLink](#)

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Medline [15756435](#)

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Contributor(s)

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URL : <http://AtlasGeneticsOncology.org/Genes/ZNF217ID42875ch20q13.html>

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