

Gene Section

Mini Review

CDC6 (cell division cycle 6 homolog (*S. cerevisiae*))

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Identity

Hugo: CDC6

Other names: CDC18L; cdc6; hCDC6; HsCDC18; HsCDC6; p62

Location: 17q21.3

Local order: centrosome ---- CASC3-RAPGEFL1-WIPF2-CDC6-RARA-TOP2A

DNA/RNA

Accession N°	Transcript length (bp)	Notes
NM_001254	3053	RefSeq
CR598029	1802	mRNA
BC025232	2861	mRNA
HSU77949	2653	mRNA
AF022109	2021	mRNA

Description

The gene starts at 35697672 bp from pter and ends at 35712939 bp from pter. Its size is 15267 bases and its orientation lie at the plus strand.

The 5' promoter region contains putative sites for transcriptional control, including an initiator element, a CHR element, two main binding sites for E2F, a putative Sp1 site, and a CCAAT region. No consensus TATA box is evident. This resembles the organization

of other genes encoding proteins associated with the G1/S transition.

Transcription

The gene has 12 exons. The five putative transcripts (see table below) encode the same product of 560aa. There are about 230 EST sequences.

Pseudogene

There are no known pseudogenes.

Protein

Description

The CDC6 protein or p62 is composed of 560 amino acids with a molecular weight of 62720 Da. The central portion of the protein contains a conserved nucleotide binding/ATPase domain, which classifies it to a large superfamily of ATPases known as "ATPases associated with various cellular activities" (AAA) proteins and specifically to the AAA+ subfamily. The Walker-A motif GXXGXXGK(T/S) (nucleotide binding) of the AAA+ domain spans aa 202-209, while the Walker-B motif D(D/E)XX (nucleotide hydrolysis) spans aa 284-287. The domain contains also a leucine zipper (aa 306-327), and a caspase dependent cleavage site DQL290DS.

The N-terminal domain contains: three consensus phosphorylation sites at serine (S)54, S74 and S106, which are phosphorylated in vivo by CDK-related activity at the G1/S boundary; a putative conserved nuclear localization sequence ((S/T)PXX57R58(L/I)); two putative destruction boxes (D-box (aa 56-64) and KEN box (aa 81-83)), which target CDC6 for proteolysis by APCCDH1 during early G1 or G0, but

not S, G2 or M; and a cyclin binding domain mapped to a Cy-motif (aa 93-100) that is similar to the cyclin binding regions in p21/WAF1/SDI1 and E2F-1.

The C-terminal domain contains: a putative classical nuclear export signal (NES) between residues 462-488 (ILVCSLMLLRQLKI), a caspase dependent cleavage site SEV442DG, and a conserved winged-helix domain (WHD) with unknown function; it possibly mediates protein-protein interactions or a direct interaction with the DNA helix.

Expression

It is expressed in all proliferating cells but not in quiescent or differentiated cells.

Localisation

Even though it was believed at first that p62CDC6 was nuclear during G1 and cytoplasmic during S and G2, lately it has been found that there is an endogenous fraction of the protein that remains chromatin-bound throughout the cell cycle.

Function

- ATP binding
- Chromatin binding
- Nucleoside-triphosphatase activity
- Nucleotide binding
- Protein binding

- Loading factor for MCM2-7: Cdc6/Cdc18 is recruited to replication origins by ORC. Once localized at replication origins, Cdc6 helps to recruit and load MCM factors onto DNA in a process that requires CDC6-mediated ATP hydrolysis. After loading of MCM2-7 on DNA, CDC6 is not necessary for origin firing and dissociates from the complex, through a phosphorylation-dependent procedure. It seems though that CDC6 has additional roles related to S/M checkpoint control. Accumulating evidence suggests that CDC6 is required for proper control of mitotic entry. Deregulation of CDC6 results in mitotic block, aberrant mitotic progression, or apoptosis.

Homology

ORC1

Mutations

Note: No known mutations.

Implicated in

Carcinogenesis

Note: Because of its key role in DNA replication, deregulation of CDC6 could lead to genomic instability fueling the risk for neoplastic transformation. Indeed, CDC6 upregulation has been observed in many cancerous lesions, including brain tumors, non-small cell lung carcinomas, mantle cell lymphomas, and

various cervical neoplasias. Interestingly, in aggressive prostate cancer, CDC6 is downregulated.

CDC6 encompasses certain oncogenic characteristics that manifest themselves when CDC6 expression is deregulated. For example, CDC6 induces DNA replication in quiescent cells, while in certain occasions overexpression of CDC6 leads to DNA overreplication in tumour cells.

While cells have mechanisms to prevent aberrant DNA replication, deregulation of CDC6, or /and its partner in pre-RCs, CDT1 may lead to abrogation of the antitumor barriers of senescence and apoptosis. In addition their stable expression in premalignant papilloma cells lead to transformation of these cells, which upon injection into nude mice produce tumors, an activity that clearly portrays the oncogenic potential of CDC6 deregulation.

Moreover, deregulation of CDC6 may lead to inactivation of the INK4/ARF locus through recruitment of histone deacetylases HDAC1 and HDAC2 and heterochromatinization of the INK4/ARF locus. This locus encodes the tumour suppressor genes p16INK4a, p15INK4b, and ARF, and inactivation of this locus is closely related to cancer.

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