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Gene Section
Mini Review

CENPF (centromere protein F, 350/400ka (mitosin))

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Identity

Other names: AH antigen; CENF; hcp-1; Mitosin; PRO1779
HGNC (Hugo): CENPF
Location: 1q41
Local order: Chromosome 1, 61,381 bases, 5'- 212,843,155 - 212,904,535 -3': strand (+).

DNA/RNA

Description

The CENPF gene structure consists of twenty exons, ranging from 92 to 3,404 bp, and nineteen introns, ranging from approximately 1 to approximately 10 kb.

Transcription

10,294 bp mRNA; 9630 bp open reading frame.

Pseudogene

No pseudogene.

Protein

Description

The gene encodes a protein associated with the centromere-kinetochore complex, 3210 amino acids (aa), 367594 Da, containing internal repeats, coiled-coil (potential) and NLS (potential).

Expression

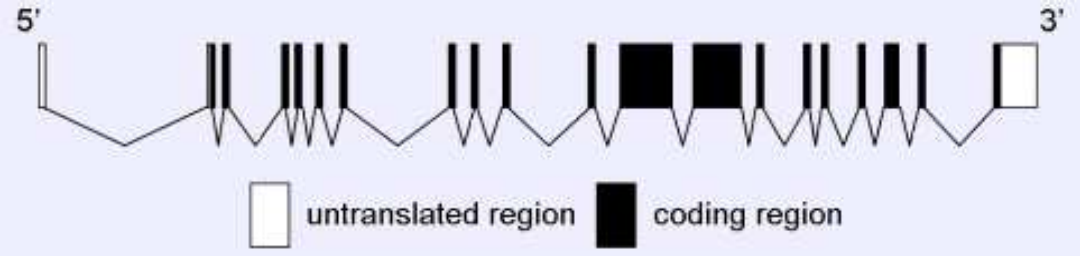
Breast, eye, gastro-intestinal tract, heart, liver, lymph node, ovary, placenta, skin, stomach, testis.

Localisation

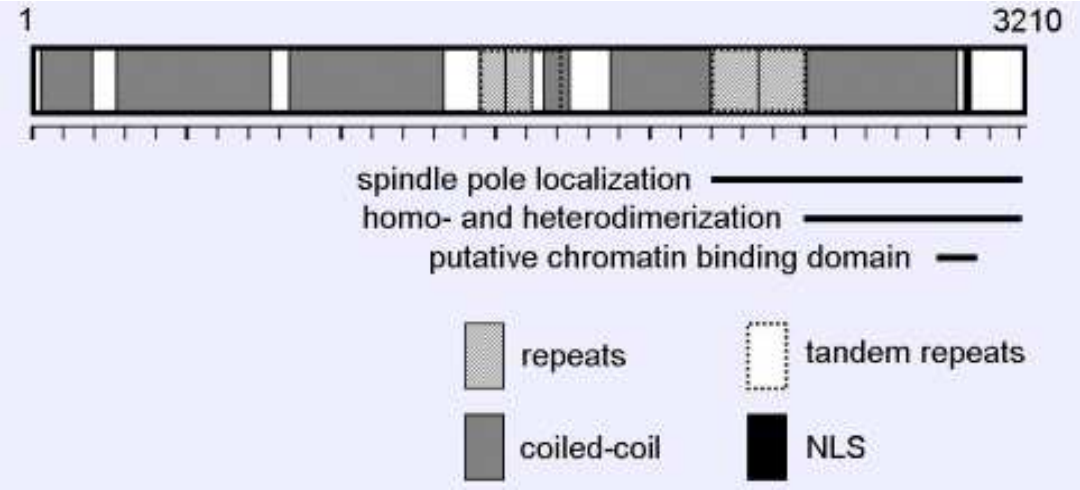
Nucleus matrix, but not in the nucleolus, reorganization to the kinetochore/centromere (coronal surface of the outer plate) and the spindle during mitosis.

Function

CenpF is recruited to kinetochore early in mitosis after recruitment of Bub1 and modulates kinetochore association of certain mitotic proteins including BubR1 for kinetochore assembly.



A schematic diagram of the CENPF gene. The exon numbers are labeled.



A schematics representing the domain structure of full length CENPF. NLS, nuclear localization signal.

CenpF that has a CAAX motif in their C-terminal is target for farnesylation. This modification changes is necessary for CenpF function at the G2/M transition. CenpE and CenpF have a significant role in the antitumor activity of farnesyl transferase inhibitors due to their importance in normal cell division.

Homology

No.

Implicated in

Head and neck squamous cell carcinoma

Disease

CENPF gene amplification and overexpression were observed in head and neck squamous cell carcinoma (HNSCC). Up-regulation of CenpF, especially by gene amplification, suggests the possibility that increased CenpF protein levels could influence tumorigenesis particularly at early stages of tumor development. In addition, over-expression of CenpF is significantly correlated with poor prognosis of HNSCC. CenpF expression is able to use clinically as a proliferation marker in oral epithelia.

Breast cancer

Disease

Over-expression of CENPF mRNA was associated with larger tumor size as well as estrogen receptor (ER) - negative, high grade tumors. CENPF mRNA expression correlated significantly with worse overall survival and a decreased probability of remaining metastasis-free. CenpF expression was also correlated with telomerase activity, cyclin E over-expression, c-Myc amplification and nuclear expression of surviving, indicating that CenpF is a good biomarker for proliferation of breast cancer. ver-expressing In addition, a significant proportion of brest cancer cells over-expressing CENPF were aneuploid, supporting evidence for the relation between CenpF expression and chromosomal instability.

Astrocytic gliomas

Disease

In microarray and real-time RT-PCR analyses, CENPF mRNA levels significantly increased in primary astrocytic gliomas. Interestingly, secondary glioblastomas demonstrated higher CENPF mRNA levels than primary glioblastomas. However, amplification of the gene was not found.

Salivary gland tumor

Disease

CenpF expression was significantly correlated with Ki-67 labeling index in primary malignant salivary gland tumor by immunohistochemical study. In addition, CENPF mRNA level was associated with clinical stage. The data suggests that CenpF expression is a candidate for biomarker of proliferation of salivary tumor.

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