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Gene Section
Mini Review

MTA1 (metastasis-associated gene 1)

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Identity

HGNC (Hugo): MTA1

Location: 14q32.3

Note
MTA1 gene was identified as a novel candidate metastasis-associated gene involved in cancer metastasis by differential cDNA library screening using the 13762NF rat mammary adenocarcinoma metastatic system. Its human homologue, MTA1 was also identified.

DNA/RNA

Transcription

About 2.7 k mRNA; Protein coding region of 714 amino acid residues.

Protein

Description

715 amino acids; about 80 kDa.

Expression

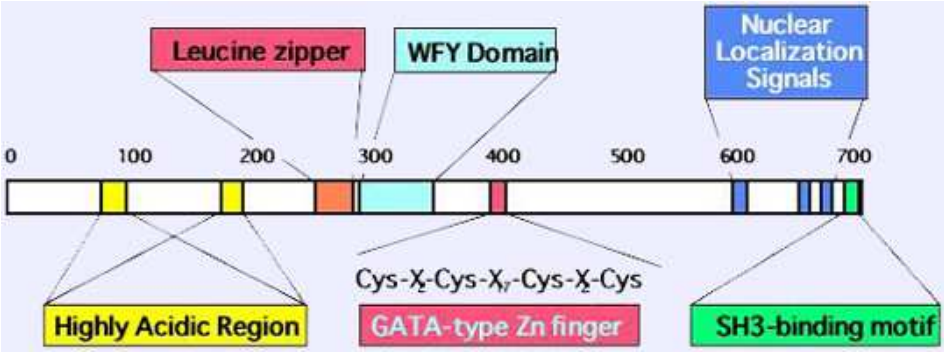
Found in almost all tissues; most abundantly expressed in testis.

Localisation

Nucleus.

Function

MTA1 protein physically interacts with histone deacetylase 1 and is included in a protein nucleosome remodeling complex, NuRD (nucleosome remodeling and histone deacetylation). This protein complex, containing histone deacetylase, plays an important role in histone deacetylation, alteration of chromatin structure and transcriptional control.



Motifs in putative amino acid sequence of MTA1.
A leucine zipper motif and a GATA-type zinc finger motif are found near the mid-portion of the protein. Between them, a SANT domain is found which is homologous to the DNA binding domain of the myb oncogene family. In the amino terminal 200 amino acid residues, there are two highly acidic regions characteristic of the acidic activation domains of many transcription factors. At the carboxyl-terminus is a proline rich stretch whose sequence matches the consensus sequence of the src-homology 3-binding motif. Three putative nuclear localization signals are also present in the sequence.

Homology

MTA2, MTA3.

Implicated in

Disease

Cancer invasion and metastasis as follows:

Overexpression of MTA1 mRNA is correlated with the depth of invasion and lymph node metastasis in gastric and colorectal carcinomas as well as in esophageal carcinomas. The correlation of overexpression of this gene is also reported in lung cancer, thymoma and prostate cancer.

Overexpression of MTA1 protein might be a useful predictor for poor prognosis of human esophageal squamous cell carcinomas.

Forced expression of the MTA1 protein in breast cancer cell line MCF-7 is accompanied by enhancement of the ability of cells to invade an artificial matrix and to grow in an anchorage-independent manner.

Increasing MTA1 expression enhances migration, invasion and anchorage-independent survival of immortalized human keratinocytes.

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