MTA1 (metastasis-associated gene 1)

Identity

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.

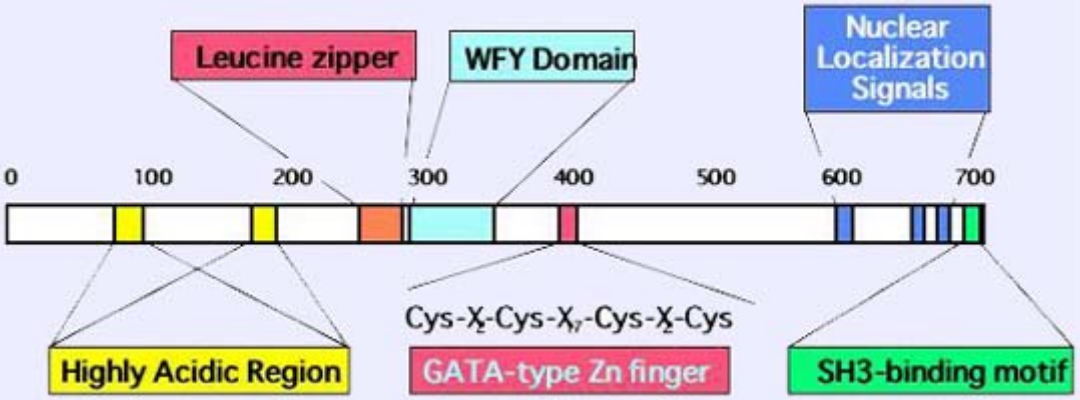
Hugo **MTA1**

Location 14q32.3

DNA/RNA

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

Protein



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.

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.

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.

External links

	Nomenclature
Hugo	MTA1
GDB	MTA1
Entrez_Gene	MTA1 9112 metastasis associated 1
	Cards
Atlas	**MTA1ID41443ch14q32**
GeneCards	MTA1
Ensembl	MTA1
CancerGene	MTA1
Genatlas	MTA1
GeneLynx	MTA1
eGenome	MTA1
euGene	9112
	Genomic and cartography
GoldenPath	MTA1 - 14q32.3 chr14:104957411-105008100 + 14q32.33 (hg17-May_2004)
Ensembl	MTA1 - 14q32.33 [CytoView]
NCBI	Genes Cyto Gene Seq [Map View - NCBI]
OMIM	Disease map [OMIM]
HomoloGene	MTA1
	Gene and transcription
Genbank	AF508978 [SRS] AF508978 [ENTREZ]

Genbank	AW732089 [SRS] AW732089 [ENTREZ]
Genbank	BC006177 [SRS] BC006177 [ENTREZ]
Genbank	BC009443 [SRS] BC009443 [ENTREZ]
Genbank	BX248755 [SRS] BX248755 [ENTREZ]
RefSeq	NM_004689 [SRS] NM_004689 [ENTREZ]
RefSeq	NT_086807 [SRS] NT_086807 [ENTREZ]
AceView	MTA1 AceView - NCBI
TRASER	MTA1 Traser - Stanford
Unigene	Hs.525629 [SRS] Hs.525629 [NCBI] HS525629 [spliceNest]
	Protein : pattern, domain, 3D structure
SwissProt	Q13330 [SRS] Q13330 [EXPASY] Q13330 [INTERPRO]
Prosite	PS51038 BAH [SRS] PS51038 BAH [Expasy]
Prosite	PS00344 GATA_ZN_FINGER_1 [SRS] PS00344 GATA_ZN_FINGER_1 [Expasy]
Prosite	PS50114 GATA_ZN_FINGER_2 [SRS] PS50114 GATA_ZN_FINGER_2 [Expasy]
Prosite	PS50090 MYB_3 [SRS] PS50090 MYB_3 [Expasy]
Interpro	IPR001025 BAH [SRS] IPR001025 BAH [EBI]
Interpro	IPR000949 ELM2 [SRS] IPR000949 ELM2 [EBI]
Interpro	IPR009057 Homeodomain_like [SRS] IPR009057 Homeodomain_like [EBI]
Interpro	IPR001005 Myb_DNA_binding [SRS] IPR001005 Myb_DNA_binding [EBI]
Interpro	IPR001515 Ribosomal_L32E [SRS] IPR001515 Ribosomal_L32E [EBI]
Interpro	IPR000679 Znf_GATA [SRS] IPR000679 Znf_GATA [EBI]
CluSTr	Q13330
Pfam	PF01426 BAH [SRS] PF01426 BAH [Sanger] pfam01426 [NCBI-CDD]
Pfam	PF01448 ELM2 [SRS] PF01448 ELM2 [Sanger] pfam01448 [NCBI-CDD]
Pfam	PF00320 GATA [SRS] PF00320 GATA [Sanger] pfam00320 [NCBI-CDD]
Pfam	PF00249 Myb_DNA-binding [SRS] PF00249 Myb_DNA-binding [Sanger] pfam00249 [NCBI-CDD]
Blocks	Q13330
	Polymorphism : SNP, mutations, diseases
OMIM	603526 [map]
GENECLINICS	603526
SNP	MTA1 [dbSNP-NCBI]
SNP	NM_004689 [SNP-NCI]
SNP	MTA1 [GeneSNPs - Utah] MTA1 [SNP - CSHL] MTA1] [HGBASE - SRS]
	General knowledge

Family Browser	MTA1 [UCSC Family Browser]
SOURCE	NM_004689
SMD	Hs.525629
SAGE	Hs.525629
Amigo	component|nucleus
Amigo	process|regulation of transcription, DNA-dependent
Amigo	process|signal transduction
Amigo	function|transcription factor activity
BIOCARTA	Downregulated of MTA-3 in ER-negative Breast Tumors
PubGene	MTA1
	Other databases
	Probes
Probe	MTA1 Related clones (RZPD - Berlin)
	PubMed
PubMed	**19 Pubmed reference(s) in LocusLink**

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