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Gene Section
Mini Review

EPHA7 (EPH receptor A7)

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Identity

Hugo: EPHA7
Other names: EHK3; HEK11
Location: 6q16.1

Probe(s) - Courtesy Mariano Rocchi.

DNA/RNA

Description

The EPHA7 gene maps on chromosome 6q16.1 spanning 178,134 bp. it contains 17 exons, the orientation of the gene is complement.

Transcription

rTanscript of 5,229 bp.

Protein

Description

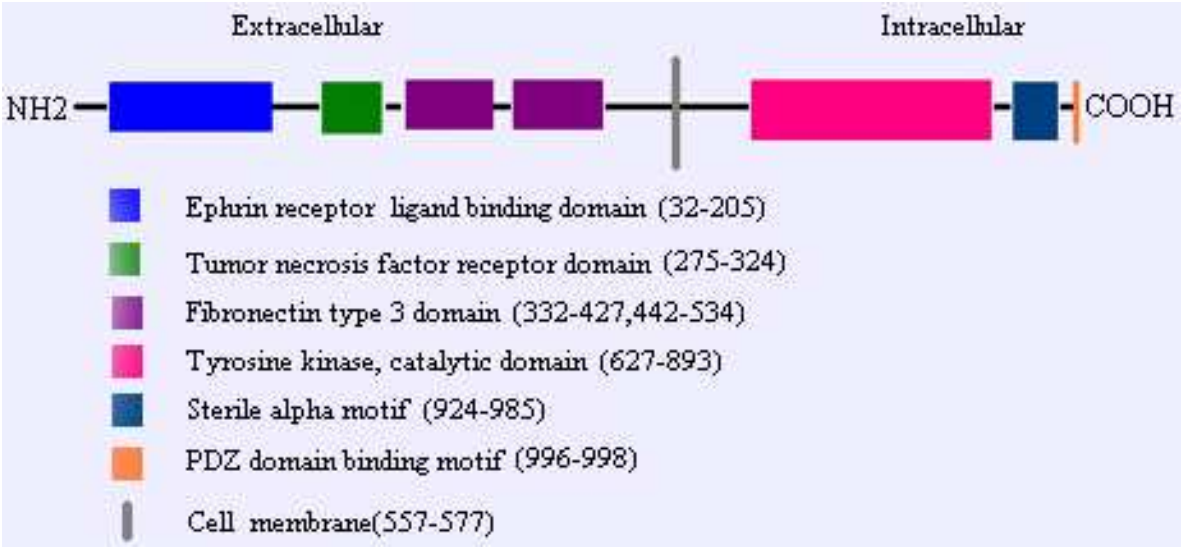
EPHA7 encodes 998 amino acids, theoretical pI is 5.58, theoretical molecular weight is 112 KDa, tyrosine kinase, catalytic domain, sterile alpha motif, 2 fibronectin type 3 domains, ephrin receptor ligand binding domain and tumor necrosis factor receptor domain.

Expression

In brain, skeletal muscle, lung, kidney, liver, colorectum and nerve system.

Localisation

Located in the membrane.



Function

ATP Binding, ephrin receptor activity, nucleotide binding, protein binding, receptor activity, transferase activity.

Homology

Homo sapiens: EPHA5 isoform b [NP_872272] (64%), EPHA5 isoform a [NP_004430] (63%), EPHA4 [NP_004429] (63%), EPHA3 [AAG43576] (63%).

Implicated in

Colorectal cancer

Note: A significant reduction of EphA7 expression in human colorectal cancers was shown using semiquantitative reverse transcription-polymerase chain reaction analysis in 59 colorectal cancer tissues, compared to corresponding normal mucosas (P=0.008), and five colon cancer cell lines. To investigate the mechanism of EphA7 downregulation in colorectal cancer, we examined the methylation status of the 5'CpG island around the translation start site in five colon cancer cell lines using restriction enzymes, methylation-specific PCR, and bisulfite sequencing and found evidence of aberrant methylation. The expression of EphA7 in colon cancer cell lines was restored after treatment with 5-aza-2'-deoxycytidine. Analysis of methylation status in totally 75 tumors compared to clinicopathological parameters revealed that hypermethylation of colorectal cancers was more frequent in male than in female, and in moderately differentiated than in well-differentiated adenocarcinomas. There was a tendency that hypermethylation in rectal cancers was more frequent than in colon cancers. Hypermethylation was also observed in colorectal adenomas. This is the first report describing the downregulation of an Eph family gene in a solid tumor via aberrant 5'CpG island methylation. It provides the evidence that EphA7 gene is involved in human colorectal carcinogenesis.

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