

Gene Section

Mini Review

CBLb (Cas-Br-M (murine) ecotropic retroviral transforming sequence b)

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Identity

HGNC (Hugo): CBLB

Location: 3q

DNA/RNA

Transcription

Major mRNA species of 4-5 kb and a less prominent species of 6-8 kb; 2946 bp open reading frame.

Protein

Description

982 amino acids; 120 kDa; the overall structure of CBLb is very close to the structure of CBL: the evolutionarily conserved aminoterminal region of CBL is composed of three interacting domains: a four-helix bundle (4H), an EF-hand calcium binding domain, and a divergent SH2 domain; the three domains together form an integrated phosphoprotein recognition module; this aminoterminal region is followed by a central Ring finger with a Cys3HisCys4 motif and an aminoterminal region with multiple proline-rich sequences, a putative leucine zipper and several potential tyrosine phosphorylation sites; two alternatively spliced mRNA code form CBLb proteins lacking the leucine zipper.

Expression

Expression of CBLb was seen in several human adult tissues including lung, spleen and testis but not in human brain, liver, pancreas, salivary gland or skeletal

muscle; expression was also detected in fetal brain and liver, in hematopoietic cell lines and in normal and malignant mammary epithelial cell lines.

Localisation

Cytoplasmic.

Function

Regulation of signal transduction; CBLb has been shown to inhibit c-Jun terminal kinase (JNK) activation mediated by the (VAV oncoprotein and EGF receptor (EGFR) signaling; in contrast, a direct interaction between CBLb and the kinase ZAP-70 induces a positive signal in T cells.

Mutations

Note

No genomic alterations described to date.

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