

Gene Section

Mini Review

LRIG1 (leucine-rich repeats and immunoglobulin-like domains 1)

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Identity

Other names: DKFZp586O1624; LIG-1; LIG1

HGNC (Hugo): LRIG1

Location: 3p14.1

DNA/RNA

Description

Genomic DNA encoding LRIG1 spans a region of 122.89 kilobases on chromosome 3, at 3p14. LRIG1 gene is encoded on the reverse strand.

Transcription

The pre-mRNA comprises 19 exons.
Coding sequence: 4812 bp.

Protein

Description

LRIG1 is a transmembrane cell-surface protein consisting of 1093 amino acids. LRIG1 contains extracellular part containing 15 leucine-rich repeats (LRR) and three C2-type immunoglobulin-like domains, a transmembrane region, and a cytoplasmic tail. LRIG1 can be cut into soluble LRIG1 ectodomain

by proteolytic processing, which also is a functional molecule.

Expression

LRIG1 is expressed ubiquitously in various epithelial cells, endothelial cells, heart, smooth and striated muscles, and in large neurons.

Localisation

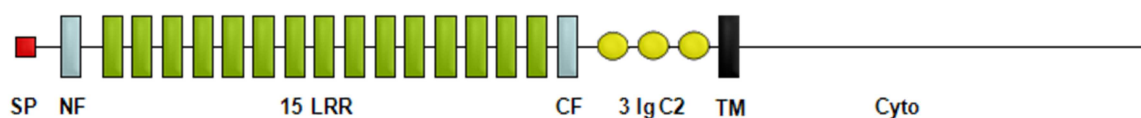
Differential subcellular distribution in a cell type-specific manner.

Function

LRIG1 acts as a suppressor of receptor tyrosine kinases, such as epidermal growth factor receptor (EGFR) family, MET (hepatocyte growth factor receptor), and RET. The interaction of the extracellular LRR domain and immunoglobulin-like domains of LRIG1 with the extracellular parts of the human EGFR results in recruitment of c-Cbl to the cytoplasmic domains, and induction of EGFR degradation. LRIG1 is involved in signal transduction, cell proliferation, cell apoptosis, cell cycle, cell migration, and cell invasion. LRIG1 as a putative tumor suppressor gene often be down-regulated in various human tumors. Soluble ectodomain of LRIG1 protein can modulate EGFR signaling and its growth-promoting activity in a paracrine fashion.



LRIG1 gene. Exons are represented by red boxes (in scale). Exons 1 to 19 are from the 5' to 3' direction.



LRIG1 protein. SP: signal peptide; NF: N-terminal cysteine-rich flanking domain; LRR: leucine-rich repeat; CF: C-terminal cysteine-rich flanking domain; Ig C2: C2-type immunoglobulin-like domains; TM: transmembrane domain; Cyto: cytoplasmic domain.

Implicated in

Ependymoma

Note

Higher cytoplasmic immunoreactivity of LRIG1 correlates with older patient age and higher LRIG1 nuclear immunoreactivity with lower WHO grade.

Prostate cancer

Note

High LRIG1 expression is significantly associated with short overall and prostate cancer-specific survival for 256 Swedish patients analysed. In contrast, in the U.S. series, high LRIG1 expression is significantly associated with longer overall survival.

Renal cell carcinoma (RCC)

Note

LRIG1 expression is generally downregulated in conventional and papillary RCC but not in chromophobic RCC.

Cutaneous squamous cell carcinoma (SCC)

Note

LRIG-1 expression is highest in well-differentiated lesions of cutaneous SCC. LRIG-1 expression intensity of tumor cells is significantly correlated with histologic differentiation of SCC. The SCC patients have significant survival benefits in the high LRIG-1 expression groups compared with low LRIG-1 expression groups.

Breast tumor

Note

LRIG1 protein levels are significantly suppressed in the majority of human breast tumors expressing ErbB2.

Cervical squamous cell carcinoma

Note

LRIG1 appears to be a significant prognosis predictor in early-stage cervical cancer, independent of the other tumor markers.

Astrocytic tumor

Note

Perinuclear staining of LRIG1 is associated with low WHO grade and better survival of the patients.

Psoriasis

Note

In psoriasis, LRIG1 is mostly absent from the cell

surfaces in the spinous layers.

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