

## Gene Section

### Mini Review

# FAIM (Fas apoptotic inhibitory molecule)

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## Identity

**Other names:** FAIM1; FLJ10582

**HGNC (Hugo):** FAIM

**Location:** 3q22.3

## DNA/RNA

### Description

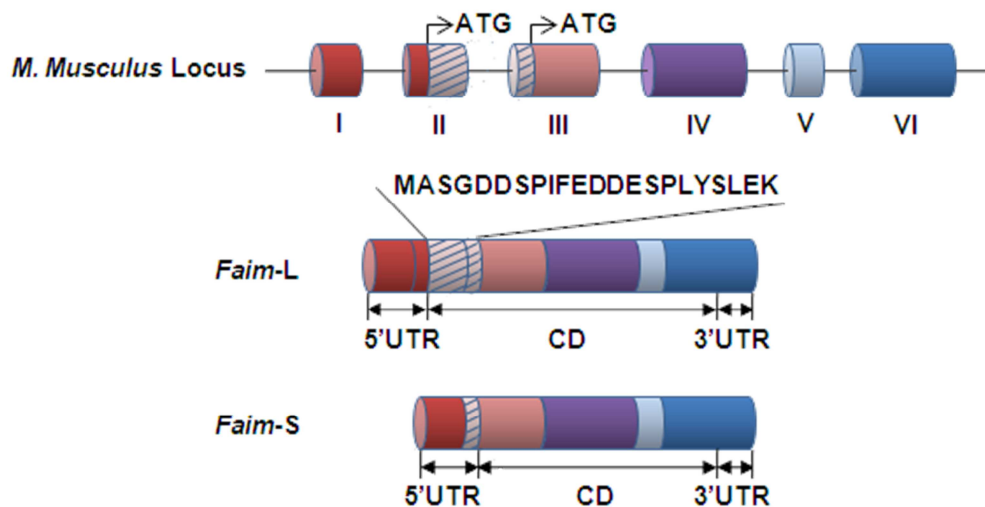
The genomic structure of the FAIM locus gives two alternative splicing results, FAIM-S and FAIM-L,

that share part of the 5'UTR (exon I). Part of the coding sequence in FAIM-L (diagonal bar of exon III) serves as part of the UTR of FAIM-S. The additional 22 amino acid sequence is indicated above the correlating exons (Zhong et al., 2001).

### Transcription

FAIM-S: mRNA size: 1104 nucleotides (nt); coding sequence: 539 nt;

FAIM-L: mRNA size: 1164 nt; coding sequence: 605 nt.

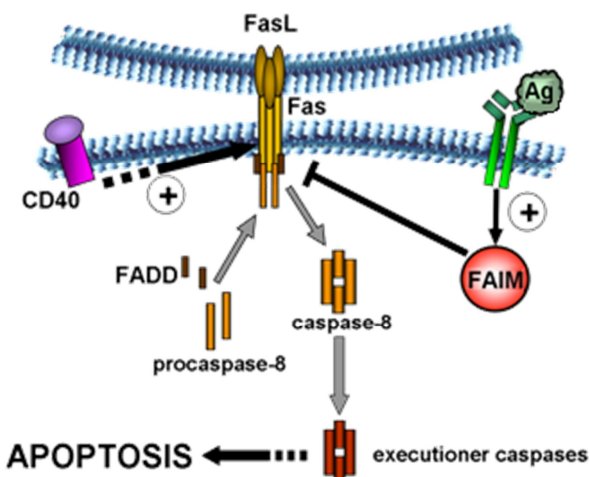


Genomic organization and splice variants of FAIM gene. Schematic representation of the structure of FAIM gene, that contains 4 different transcripts and 6 alternative splice variants but only two resulting proteins have been characterized so far: FAIM-S and FAIM-L (adapted from Zhong et al., 2001).

## Protein

### Note

Signaling pathways controlling cell death and survival are crucial for the normal development and tissue homeostasis. In contrast to most cell types, differentiated cells such as neurons require a highly controlled mechanism that allows survival for the entire life of the organism and protecting it from multitude of stimuli that can affect cellular integrity. Among those stimuli, cell death induction and more precisely, apoptosis induced by the extrinsic pathway mediated by Death Receptors (DRs), has been widely reported in the pathological loss of neurons. Therefore, those proteins that are able to block the apoptotic pathway will play a key role in the protection from neuronal death. Among all the described anti-apoptotic proteins, FAIM, with no homology with a previously known protein, may constitute a new family of proteins that regulate the DR signaling pathway.



Proposed mechanism of FAIM action in B-cells.

### Description

Fas apoptosis inhibitory molecule (FAIM) is a Fas antagonist that was initially characterized by differential display as a gene that is up-regulated in B cells resistant to Fas-mediated cell death and functions as an inhibitor of Fas-induced cell death (Schneider et al., 1999). Shortly after, a new alternative splice variant was described and named FAIM-L. FAIM-S is composed of 179 aminoacids (aa), with stable structure and rich in beta-sheets, and FAIM-L contains 22 additional aa in the N-terminus part of the protein. This extra sequence does not have any particular defined structure.

### Expression

FAIM-S mRNA has been detected in all tissues analyzed so far, whereas FAIM-L has a more restricted pattern of expression, being predominantly expressed in the nervous system and testis. Protein

immunostaining confirmed restricted expression in different areas of the brain.

### Localisation

Both isoforms, FAIM-S and FAIM-L are cytosolic.

### Function

Fas apoptosis inhibitory molecule (FAIM) was first identified as a Fas antagonist in B-cells. The overexpression of FAIM-S, but not FAIM-L, enhances NGF-induced neurite outgrowth in different neuronal populations through activation of the NF- $\kappa$ B pathway. No anti-apoptotic function of FAIM-S has been described in the nervous system (Sole et al., 2004). However, FAIM-L is specifically expressed in neurons and its expression is regulated during development. FAIM-L does not affect neurite outgrowth, nor does it modulate NF- $\kappa$ B activation. However, cells overexpressing FAIM-L are resistant to apoptotic cell death induced by DRs such as Fas or TNFR1. Reduction of endogenous expression shows that endogenous FAIM-L protects primary neurons against DR-induced cell death. FAIM-L normally binds the Fas receptor and prevents its activation. Fas-L binding to Fas induces the release of FAIM-L from Fas, allows the binding of FADD and caspase-8, and leads to apoptosis activation (Segura et al., 2007).

### Homology

FAIM is highly conserved in evolution from *Caenorhabditis elegans* to humans (Rothstein et al., 2000). However, FAIM-L is only conserved in superior vertebrates (Zhong et al., 2001; Segura et al., 2007). There is no homology with previously characterized families of proteins.

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