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# **Gene Section**

Mini Review

# KCMF1 (potassium channel modulatory factor 1)

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# Identity

**Other names:** DEBT91; DKFZP434L1021; FIGC; PCMF; ZZZ1

HGNC (Hugo): KCMF1

Location: 2p11.2

# **DNA/RNA**

#### Description

DNA size 87.29 kb, mRNA size 7555 bp, 7 exons.

### Protein

#### Description

381 amino acids; 41.945 kDa protein. KCMF1 protein contains ring finger (Zinc finger, ZZtype) 3-50 (48), zinc finger (C2H2-type) 78-101 (23), nuclear localization signal (NLS) 152-168 (17), and a coiled coil domain 225-257 (33).

Isoforms: Two isoforms that predicted to encode proteins containing the zinc finger domain have been identified; other isoforms are relatively shorter and not well defined.





Isoform bApr07: This partial mRNA is 625 bp long. It is reconstructed from a myeloma cDNA clone. The premessenger RNA has 5 exons and covers 74.08 kb. The predicted partial protein has 208 aa (22.9 kDa, pI 5.8) and a very good coding score (7). It contains one Zinc finger, ZZ-type domain, one zinc finger, C2H2-type domain.

Isoform dApr07: The dApr07 mRNA variant is 431 bp long. It is reconstructed from a testis cDNA clone. The pre-mRNA has 4 exons and covers 12.72 kb. The predicted partial protein has 143 aa (15.7 kDa, pI 7.2) and a very good coding score (5). It contains one zinc finger, C2H2-type domain.

#### Expression

Ubiquitously expressed. High level of expression is in pharynx, thyroid, respiratory tract and larynx; less expressed in female system, uterus and cervix.

#### Localisation

Nuclear.

#### **Function**

KCMF1 is a transcription factor. Basic functions of the KCMF1 gene are (i) early gene up-regulation during growth factor-induced branching tubulogenesis, (ii) ubiquitination through intrinsic E3 ubiquitin ligase activity, and (iii) a possible role in ion channel activity.

#### Homology

The percent identity below represents identity of KCMF1 over an aligned region in UniGene. Pan troglodytes: 97 (Percentage Identity) Canis lupas familiaris: 91 Bos Taurus: 90 Mus musculus: 96 Gallus gallus: 93 Danio rerio: 85.

### Implicated in

# *Ewing's sarcoma family of tumors (ESFT)*

KCMF1 is down regulated by high constitutive CD99 (a cell surface glycoprotein) expression in ESFT. KCMF1 expression is inversely correlated with CD99 expression, as seen in a series of 22 primary ESFT. High CD99 expression levels contribute to the malignant properties of ESFT by promoting growth and migration of tumor cells.

#### Gastric cancer

KCMF1 (also known as FIGC) encode a RING finger protein, has intrinsic E3 ubiquitin ligase activity and promotes ubiquitination. KCMF1 contains a novel C6H2-type RING finger domain at the NH<sub>2</sub>-terminal consensus sequence region,  $CX_2C_{(7-11)}$ CX<sub>2</sub>CX<sub>A5</sub>CX<sub>2</sub>CX<sub>(5-9)</sub> HX (1-3) H (X<sub>A</sub>: acidic residues). Using differential display approach with basic fibroblast growth factor (b-FGF) inducible genes in gastric cancer cells, it was observed that FIGC upregulation in response to bFGF in gastric cancer. This suggests that FIGC might be implicated in gastric carcinogenesis through dysregulation of growth modulator.

## References

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