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Gene Section

Review

CSF1R (colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog)

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Identity

Other names: C-FMS; CD115; CSF-1-R; CSFR; EC 2.7.10.1; FIM2; FMS; c-fms
HGNC (Hugo): CSF1R
Location: 5q32
Local order: The human CSF1R gene is located at the distal end of the q arm of chromosome 5 with telomere to centromere orientation. Proximal flanking genes include CSF2 (GM-CSF) and IL-3 at 5q31.1. Distal flanking genes include PDGFRB at 5q31-q32.

Note
CSF1R (C-FMS) is the human cellular homologue of the retroviral oncogene v-fms. The v-fms oncogene, first identified and isolated by Heisterkamp et al. in 1983, is transduced by the feline sarcoma virus Susan McDonough (SM) and HZ-5 strains, which cause fibrosarcomas in domestic cats. The v-fms oncogene is equivalent to the c-fms gene in its sequence, but has undergone genetic alterations, which constitutively activate the receptor kinase in the absence of its ligand, the colony stimulating factor-1 (CSF1). Infection of mammalian cells with v-fms leads to cell transformation in vitro and in vivo.

DNA/RNA

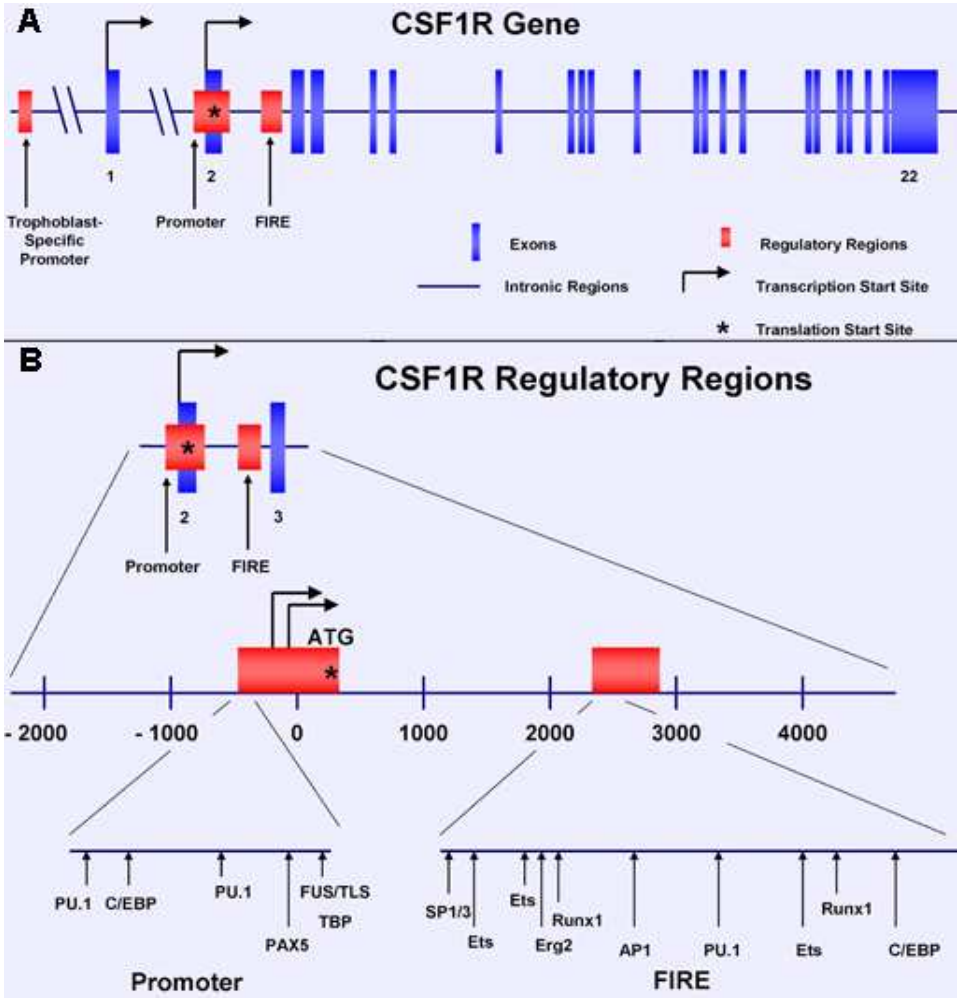
Note
The presence of an anti-sense CSF1R transcript starting within the FIRE region has been reported in mouse macrophages and B cells.

Description

The human CSF1R gene, on the minus strand, spans a region of 60,077 bases (Start: 149,413,051 bp from pter; End: 149,473,128 bp from pter) interrupted by introns ranging from 26kb for intron 1, to a range between 6.3kb to less than 0.1 kb for the other introns. The human CSF1R gene is composed of a total of 22 exons, of which the first exon is non-coding and where the remaining 21 exons (starting with exon 2) encode for the CSF1R protein.
The human CSF1R and mouse Csf1r genomic structures are highly conserved.

Transcription

The 5' end of the human CSF1R gene has 2 alternative transcription start site regions, preceded by two alternative promoters. The transcription of CSF1R mRNA can be initiated at the two independent start sites in a tissue specific manner. The transcription of exon 1 through exon 22 occurs only in placental trophoblasts, and is driven by a trophoblast-specific promoter approximately 20kb upstream of the first exon. The transcript produced is predicted to be approximately 4kb long. In macrophages and a few other tissues (see expression section) transcription of CSF1R occurs only from exon 2 through exon 22 producing a transcript predicted to be approximately 3.9kb in length, which is translated into the CSF1R protein.



A: Genomic structure of the human CSF1R gene.
B: Scheme showing the regulatory regions of the mouse Csf1r gene. The regulatory regions and transcription binding sites within are highly conserved between mouse and human. (Diagram based on Bonifer et al. Frontiers in Bioscience 2008)

The transcription this transcript is under the control of two major regulatory regions, which are highly conserved between human and mouse: the Promoter upstream of exon 2 and the fms-intronic regulatory region (FIRE). Most studies on CSF1R trans-criptional regulation have focused on the mouse gene. However, most of the features of mouse Csf1r are highly conserved in human.

The mouse Csf1r promoter is TATA-less, and drives transcription from multiple sites (known as broad class transcription start sites). This promoter is not GC rich and there are no CpG islands in the vicinity. This promoter contains binding sites for various transcription factors including: PU.1, C/EBP, PAX5, and FUS/TLS-TBP. The mouse FIRE region is located in the second intron, approximately 2kb downstream from the transcription start site. It contains binding sites for a number of transcription factors including: Sp1 / C/EBP. With a few exceptions, the features described for the mouse Csfr1 regulatory regions are highly conserved in human. Specifically, the human CSF1R can be regulated in a hormone dependent fashion via a glucocorticoid response element present in the human CSF1R promoter, but not in the mouse Csf1r promoter.

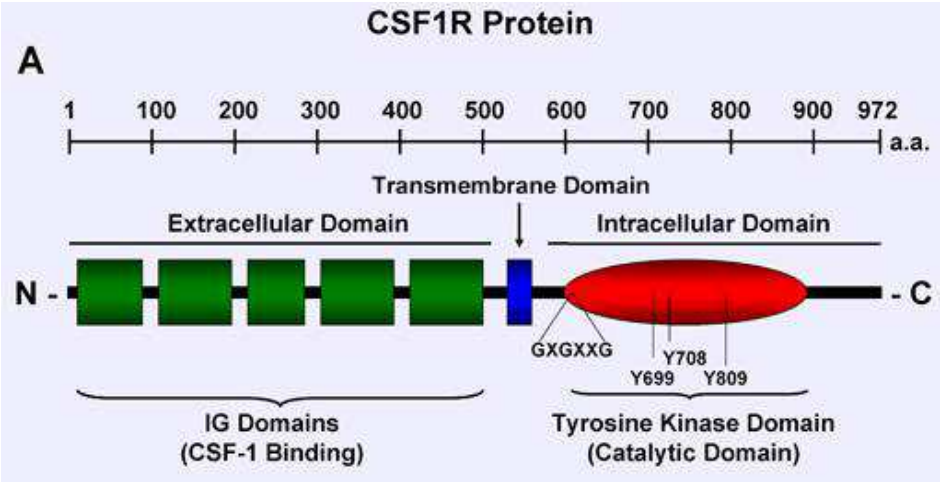
Pseudogene

The first CSF1R intron contains a transcriptionally inactive ribosomal protein L7 processed pseudo-gene that is oriented in the opposite direction of the CSF1R gene itself. This pseudogene is not functional but its sequence is highly conserved across all mammalian species.

Protein

Description

The CSF1R protein consists of 972 amino acids and has a molecular mass of approximately 108 kDa. However due to post-translational modifications,



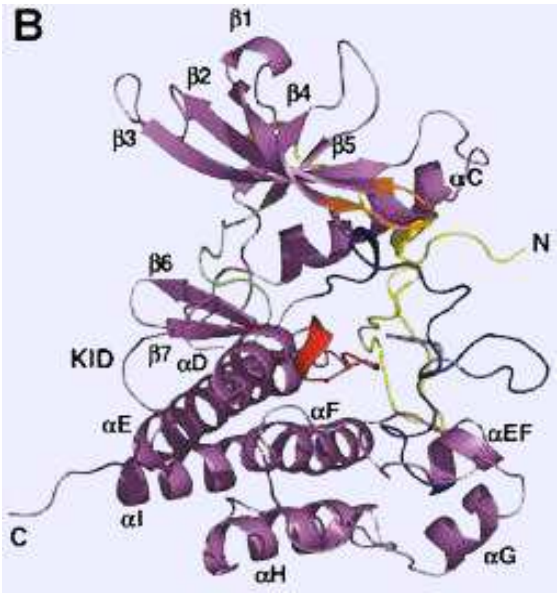
CSF1R Protein Structure. A. Schematic representation of CSF1R protein showing the CSF1-binding IG domains in the extracellular portion, and the tyrosine kinase catalytic domain in the intracellular portion. Phosphorylated tyrosines (Y) are indicated.

which include phosphorylation, glycosylation, and the acquisition of N-linked oligosaccharides, the proteins molecular size increases.

The CSF1R protein also contains a signal peptide and a 512 amino acid N-terminal extracellular segment which contains the ligand binding domain, a hydrophobic 25 amino acid membrane spanning region, and intracellular domain 435 amino acids in length that includes all sequences necessary for tyrosine kinase activity (occurring at tyrosine (Y) Y699 and Y708, as well as Y809). The CSF1R protein contains a glycine-rich signature sequence that is characteristic of kinases, as well as an ATP binding site at lysine (K) K616. The immature intracellular glycoprotein has a molecular mass of 130 kDa after it acquires N-linked oligosaccharides of the high mannose type during co-translational glycosylation. The molecular mass of CSF1R is increased further during intracellular transport to the plasma membrane, where the glycoprotein's N-linked carbohydrates undergo modifications in the Golgi complex, resulting in an increase to 150 kDa molecular mass. There are variations in molecular mass of CSF1R across species due to the differential processing of carbohydrate chains in a species specific manner.

Expression

The major site of CSF1R expression is in macrophages. In hematopoiesis, CSF1R is upregulated during monocytic differentiation, but is downregulated during granulopoiesis. CSF1R is expressed predominantly in committed macrophage precursors (CFU-Ms), monocytes, and tissue macrophages. CSF1R mRNA can be detected granulocytes, but is not translated. CSF1R mRNA/protein expression has been reported also in non-hematopoietic cells such as trophoblasts (where is seems to derive from an alternative transcript including the non-coding exon 1), osteoclasts, smooth muscle cells, and neurons, as well as in female mammary gland epithelium during development and lactation. Expression of CSF1R mRNA/protein has also been reported in breast, ovarian, and endometrial tumors, as well as in hepatocellular carcinomas. CSF1R expression during hematopoiesis is regulated by tissue-specific sets of transcription factors that play a key role in myeloid differentiation. CSF1R is activated in a synergistic manner by the co-expression of the macrophage-specific transcription factor Pu.1 and c-Ets-2. During B-cell lineage restriction and differentiation, the CSF1R gene is repressed by the transcription factor PAX5. It has been shown that PAX5 is required during B-cell differentiation to keep CSF1R in a silent state. It has also been shown that CSF1R can be repressed by Foxp1, a forkhead transcription factor that is in turn regulated by the Beta-2-integrin Mac-1.



CSF1R Protein Structure. B. Diagram of the 2.7 A Crystal Structure of the Autoinhibited Human CSF1R/ kinase Domain (as described in Walter et al. J. Mol. Biol. 2007).

Localisation

CSF1R is located at the cell plasma membrane. Transport of CSF1R from the endoplasmic reticulum (the site of synthesis) to the plasma membrane occurs efficiently with detection of the receptor at the surface within 30 minutes of synthesis.

Function

CSF1R is the receptor for the ligand colony stimulating factor-1 (CSF1). CSF1R is an integral transmembrane glycoprotein that exhibits ligand-induced tyrosine-specific protein kinase activity, which triggers a signaling cascade eventually affecting transcription of CSF1-responsive genes. CSF1R tyrosine phosphorylation is induced upon binding of CSF1, leading to activation of Ras / Erk and class I-A phosphatidylinositol 3-kinase signaling pathways, which in turn activate the signal transducers and activators of transcription (STATs) pathways, specifically STAT1, STAT3, and STAT5. CSF1R activation by CSF1 results in increased growth, proliferation and differentiation.

Homology

Like the CSF1R gene, the CSF1R protein sequence appears to be conserved across Euteleostomi (vertebrates) including: Homo sapiens (Human), Canis lupus familiaris (Dog), Mus musculus (Mouse), Rattus norvegicus (Rat), Gallus gallus (Chicken), and Danio rerio (Zebrafish). CSF1R is a member of the gp140 family of the type I cytokine receptor group and shares a high degree of amino acid sequence homology to platelet-derived growth factor receptor (PDGFRB), specifically in its kinase domain.

Mutations

Germinal

None identified as of yet.

Somatic

Chromosomal abnormalities: A partial deletion of chromosome 5 containing the CSF1R locus has been consistently observed in patients with myelodysplastic syndrome. The CSF1R locus is also affected by the acute megakaryoblastic leukemia-associated translocation t(3;5)(p21;q33) in which the CSF1R gene on chromosome 5 is fused to the RBM6 gene on chromosome 3, resulting in a fusion protein RBM6-CSF1R.

Gene mutations: CSF1R point mutations have been detected mainly in hematopoietic/lymphoid tissue and liver, where they correlate with myelo-dysplastic syndrome and acute myeloid leukemia (AML) and hepatocellular carcinoma, respectively. Specifically, mutations at codons 301 (exon 7) and 969 (exon 22) seem to occur with a higher frequency in both tissues. According to earlier studies these are activating mutations that would play a role in leukemogenesis. However, later studies have failed to find these mutations in AML patients. Additional mutations were discovered in AML patients at codons 245 (exon 6) and 413 (exon 9). However, their contribution to leukemo-genesis is not known. Epi-mutations: Specific fusion proteins resulting from leukemia-associated chromosomal translocations, including the AML1-MTG fusion proteins, result in transcriptional down-regulation of specific AML1 target genes such as CSF1R. AML1-MTG-induced CSF1R downregulation is epigenetic, as it is marked by specific repressive histone changes as well as DNA hypermethylation at the CSF1R regulatory regions. CSF1R epigenetic down-regulation is associated with block of myeloid differentiation and defects in cell proliferation in vitro.

Implicated in

Myelodysplastic syndrome (MDS)

Disease

The human CSF1R gene is consistently lost by partial deletions occurring in chromosome 5 in MDS patients. Moreover, specific deletion of the CSFS1R gene has been detected in as many as 40% of MDS patients.

Acute Myeloid Leukemia (AML)

Disease

Early studies had suggested a link between AML and the presence of CSF1R codon 301 and 969 activating mutations. While there is strong evidence that these mutations have potential transforming activity, recent studies have failed to find these mutations in AML patients. Thus the pathogenic role of CSF1R mutations in leukemogenesis is still controversial.

CSF1R might be involved in leukemia through mechanisms other than gene mutations. CSF1R downregulation has been reported in specific AML subtypes. One of the factors that may lead to CSF1R downregulation is the expression of the AML-associated fusion proteins AML1-MTG8 (AML1-ETO) and AML1-MTG16, derived from the t(8;21) and t(16;21) chromosomal trans-locations, respectively. Specifically, in patients with the t(8;21) translocation, which accounts for approximately 12% of all AML cases, CSF1R down-regulation is marked by epigenetic repressive changes (epi-mutations).

t(3;5)(p21;q33) in Acute Megakaryoblastic Leukemia (AMKL)

Disease

CSF1R has been reported to be affected by the chromosomal translocation t(3;5)(p21;q33) in the AMKL cell line MKPL-1. The fusion protein produced by this translocation, RBM6-CSF1R is found only in the cytoplasm and is constitutively active in the megakaryocyte lineage. The RBM6-CSF1R confers IL-3 independence to the mouse Pro-B cell line BaF3, and induced myelo-proliferative disease in a murine transplant model. The AMKL subtype represents 1% or

less of the cases of AML. It most often occurs in children, and is associated with Down syndrome. The prognosis for AMKL is poor.

Breast Cancer

Disease

58% of all breast carcinomas and 85% of invasive breast carcinomas express higher levels of CSF1R compared to normal resting breast tissue. It has been demonstrated that exogenous expression of CSF1R in untransformed human mammary epithelial cells results in aberrant acinar morpho-genesis, anchorage-independent growth and an invasive phenotype. Expression of CSF1R in breast tumors correlates with increased invasiveness and adverse prognostic features like high histological grade, and an advanced clinical stage of presentation of breast cancer.

Cervical Cancer

Disease

A significant increase in CSF1R expression has been reported in cervical carcinomas as compared to normal cervical tissue. The expression of CSF1R in cervical cancer is usually associated with a more aggressive and invasive disease. It has been suggested that there is an autocrine mode of regulation by CSF1 in this cancer cell type.

Breakpoints

Note

The only breakpoint known for the CSF1R gene can be inferred by the identification of the novel fusion protein RBM6-CSF1R, in which the N-terminal portion of the RBM6 (a.a. 1-36) is fused to the C-terminal portion of CSF1R (a.a. 574-972). This fusion protein is predicated to be produced by the translocation t(3;5)(p21;q33).

References

Heisterkamp N, Groffen J, Stephenson JR. Isolation of v-fms and its human cellular homolog. Virology. 1983 Apr 15;126(1):248-58

Nienhuis AW, Bunn HF, Turner PH, Gopal TV, Nash WG, O'Brien SJ, Sherr CJ. Expression of the human c-fms proto-oncogene in hematopoietic cells and its deletion in the 5q-syndrome. Cell. 1985 Sep;42(2):421-8

Rettenmier CW, Chen JH, Roussel MF, Sherr CJ. The product of the c-fms proto-oncogene: a glycoprotein with associated tyrosine kinase activity. Science. 1985 Apr 19;228(4697):320-2

Sherr CJ, Rettenmier CW, Sacca R, Roussel MF, Look AT, Stanley ER. The c-fms proto-oncogene product is related to the receptor for the mononuclear phagocyte growth factor, CSF-1. Cell. 1985 Jul;41(3):665-76

Rettenmier CW, Sacca R, Furman WL, Roussel MF, Holt JT, Nienhuis AW, Stanley ER, Sherr CJ. Expression of the human c-fms proto-oncogene product (colony-stimulating factor-1 receptor) on peripheral blood mononuclear cells and choriocarcinoma cell lines. J Clin Invest. 1986 Jun;77(6):1740-6

Sherr CJ, Rettenmier CW. The fms gene and the CSF-1 receptor. Cancer Surv. 1986;5(2):221-32

Roussel MF, Dull TJ, Rettenmier CW, Ralph P, Ullrich A, Sherr CJ. Transforming potential of the c-fms proto-oncogene (CSF-1 receptor). Nature. 1987 Feb 5-11;325(6104):549-52

Sherr CJ. The role of the CSF-1 receptor gene (C-fms) in cell transformation. Leukemia. 1988 Dec;2(12 Suppl):132S-142S

Sherr CJ, Roussel MF, Rettenmier CW. Colony-stimulating factor-1 receptor (c-fms). J Cell Biochem. 1988 Nov;38(3):179-87

Weber B, Horiguchi J, Luebbers R, Sherman M, Kufe D. Posttranscriptional stabilization of c-fms mRNA by a labile protein during human monocytic differentiation. Mol Cell Biol. 1989 Feb;9(2):769-75

Sherr CJ. Colony-stimulating factor-1 receptor. Blood. 1990 Jan 1;75(1):1-12

Baiocchi G, Kavanagh JJ, Talpaz M, Wharton JT, Gutterman JU, Kurzrock R. Expression of the macrophage colony-stimulating factor and its receptor in gynecologic malignancies. Cancer. 1991 Feb 15;67(4):990-6

Natazuka T, Matsui T, Ito M, Nakata H, Nakagawa T, Nakamura H, Masaoka T, Isobe T, Nakao Y. Rare point mutation at codon 301 and 969 of FMS/M-CSF receptor in acute myelomonocytic and monocytic leukemia. Leuk Res. 1992;16(5):541-3

Pampfer S, Daiter E, Barad D, Pollard JW. Expression of the colony-stimulating factor-1 receptor (c-fms proto-oncogene product) in the human uterus and placenta. Biol Reprod. 1992 Jan;46(1):48-57

Palmer SE, Dale DC, Livingston RJ, Wijsman EM, Stephens K. Autosomal dominant cyclic hematopoiesis: exclusion of linkage to the major hematopoietic regulatory gene cluster on chromosome 5. Hum Genet. 1994 Feb;93(2):195-7

Zent CS, Mathieu C, Claxton DF, Zhang DE, Tenen DG, Rowley JD, Nucifora G. The chimeric genes AML1/MDS1 and AML1/EAP inhibit AML1B activation at the CSF1R promoter, but only AML1/MDS1 has tumor-promoter properties. Proc Natl Acad Sci U S A. 1996 Feb 6;93(3):1044-8

Hamilton JA. CSF-1 signal transduction. J Leukoc Biol. 1997 Aug;62(2):145-55

Hume DA, Yue X, Ross IL, Favot P, Lichanska A, Ostrowski MC. Regulation of CSF-1 receptor expression. Mol Reprod Dev. 1997 Jan;46(1):46-52; discussion 52-3

Stanley ER, Berg KL, Einstein DB, Lee PS, Pixley FJ, Wang Y, Yeung YG. Biology and action of colony--stimulating factor-1. Mol Reprod Dev. 1997 Jan;46(1):4-10

Wang Y, Berezovska O, Fedoroff S. Expression of colony stimulating factor-1 receptor (CSF-1R) by CNS neurons in mice. J Neurosci Res. 1999 Sep 1;57(5):616-32

Dey A, She H, Kim L, Boruch A, Guris DL, Carlberg K, Sebti SM, Woodley DT, Imamoto A, Li W. Colony-stimulating factor-1 receptor utilizes multiple signaling pathways to induce cyclin D2 expression. Mol Biol Cell. 2000 Nov;11(11):3835-48

Dai XM, Ryan GR, Hapel AJ, Dominguez MG, Russell RG, Kapp S, Sylvestre V, Stanley ER. Targeted disruption of the mouse colony-stimulating factor 1 receptor gene results in osteopetrosis, mononuclear phagocyte deficiency, increased primitive progenitor cell frequencies, and reproductive defects. Blood. 2002 Jan 1;99(1):111-20

Flick MB, Sapi E, Kacinski BM. Hormonal regulation of the c-fms proto-oncogene in breast cancer cells is mediated by a composite glucocorticoid response element. J Cell Biochem. 2002;85(1):10-23

Kascinski B. Expression of CSF-1 and its receptor CSF-1R in non-hematopoietic neoplasms. Cancer Treat Res. 2002;107:285-92

Reilly JT. Class III receptor tyrosine kinases: role in leukaemogenesis. Br J Haematol. 2002 Mar;116(4):744-57

Follows GA, Tagoh H, Lefevre P, Hodge D, Morgan GJ, Bonifer C. Epigenetic consequences of AML1-ETO action at the human c-FMS locus. EMBO J. 2003 Jun 2;22(11):2798-809

Heidenreich O, Krauter J, Riehle H, Hadwiger P, John M, Heil G, Vornlocher HP, Nordheim A. AML1/MTG8 oncogene suppression by small interfering RNAs supports myeloid differentiation of t(8;21)-positive leukemic cells. Blood. 2003 Apr 15;101(8):3157-63

Roussel MF, Sherr CJ. Oncogenic potential of the c-FMS proto-oncogene (CSF-1 receptor). Cell Cycle. 2003 Jan-Feb;2(1):5-6

Barreda DR, Hanington PC, Belosevic M. Regulation of myeloid development and function by colony stimulating factors. Dev Comp Immunol. 2004 May 3;28(5):509-54

Sapi E. The role of CSF-1 in normal physiology of mammary gland and breast cancer: an update. Exp Biol Med (Maywood). 2004 Jan;229(1):1-11

Tagoh H, Schebesta A, Lefevre P, Wilson N, Hume D, Busslinger M, Bonifer C. Epigenetic silencing of the c-fms locus during B-lymphopoiesis occurs in discrete steps and is reversible. EMBO J. 2004 Oct 27;23(21):4275-85

Wrobel CN, Debnath J, Lin E, Beausoleil S, Roussel MF, Brugge JS. Autocrine CSF-1R activation promotes Src-dependent disruption of mammary epithelial architecture. J Cell Biol. 2004 Apr 26;165(2):263-73

Yang DH, Huang W, Cui J, Shu JC, Tang SH, Zhang WJ, Liang JH. The relationship between point mutation and abnormal expression of c-fms oncogene in hepatocellular carcinoma. Hepatobiliary Pancreat Dis Int. 2004 Feb;3(1):86-9

Zapata-Velandia A, Ng SS, Brennan RF, Simonsen NR, Gastanaduy M, Zabaleta J, Lentz JJ, Craver RD, Correa H, Delgado A, Pitts AL, Himel JR, Udall JN Jr, Schmidt-Sommerfeld E, Brown RF, Athas GB, Keats BB, Mannick EE. Association of the T allele of an intronic single nucleotide polymorphism in the colony stimulating factor 1 receptor with Crohn's disease: a case-control study. J Immune Based Ther Vaccines. 2004 May 14;2(1):6

Dewar AL, Cambareri AC, Zannettino AC, Miller BL, Doherty KV, Hughes TP, Lyons AB. Macrophage colony-stimulating factor receptor c-fms is a novel target of imatinib. Blood. 2005 Apr 15;105(8):3127-32

Dewar AL, Zannettino AC, Hughes TP, Lyons AB. Inhibition of c-fms by imatinib: expanding the spectrum of treatment. Cell Cycle. 2005 Jul;4(7):851-3

Follows GA, Tagoh H, Richards SJ, Melnik S, Dickinson H, de Wynter E, Lefevre P, Morgan GJ, Bonifer C. c-FMS chromatin structure and expression in normal and leukaemic myelopoiesis. Oncogene. 2005 May 19;24(22):3643-51

Himes SR, Cronau S, Mulford C, Hume DA. The Runx1 transcription factor controls CSF-1-dependent and -independent growth and survival of macrophages. Oncogene. 2005 Aug 11;24(34):5278-86

Rossetti S, Van Unen L, Touw IP, Hoogeveen AT, Sacchi N. Myeloid maturation block by AML1-MTG16 is associated with Csf1r epigenetic downregulation. Oncogene. 2005 Aug 11;24(34):5325-32

Lee AW, States DJ. Colony-stimulating factor-1 requires PI3-kinase-mediated metabolism for proliferation and survival in myeloid cells. Cell Death Differ. 2006 Nov;13(11):1900-14

Shi C, Simon DI. Integrin signals, transcription factors, and monocyte differentiation. Trends Cardiovasc Med. 2006 Jul;16(5):146-52

Tagoh H, Ingram R, Wilson N, Salvagiotto G, Warren AJ, Clarke D, Busslinger M, Bonifer C. The mechanism of repression of the myeloid-specific c-fms gene by Pax5 during B lineage restriction. EMBO J. 2006 Mar 8;25(5):1070-80

Gu TL, Mercher T, Tyner JW, Goss VL, Walters DK, Cornejo MG, Reeves C, Popova L, Lee K, Heinrich MC, Rush J, Daibata M, Miyoshi I, Gilliland DG, Druker BJ, Polakiewicz RD. A novel fusion of RBM6 to CSF1R in acute megakaryoblastic leukemia. Blood. 2007 Jul 1;110(1):323-33

Herry A, Douet-Guilbert N, Morel F, Le Bris MJ, Morice P, Abgrall JF, Berthou C, De Braekeleer M. Evaluation of chromosome 5 aberrations in complex karyotypes of patients with myeloid disorders reveals their contribution to dicentric and tricentric chromosomes, resulting in the loss of critical 5q regions. Cancer Genet Cytogenet. 2007 Jun;175(2):125-31

Kirma N, Hammes LS, Liu YG, Nair HB, Valente PT, Kumar S, Flowers LC, Tekmal RR. Elevated expression of the oncogene c-fms and its ligand, the macrophage colony-stimulating factor-1, in cervical cancer and the role of transforming growth factor-beta1 in inducing c-fms expression. Cancer Res. 2007 Mar 1;67(5):1918-26

Takeshita S, Faccio R, Chappel J, Zheng L, Feng X, Weber JD, Teitelbaum SL, Ross FP. c-Fms tyrosine 559 is a major mediator of M-CSF-induced proliferation of primary macrophages. J Biol Chem. 2007 Jun 29;282(26):18980-90

Walter M, Lucet IS, Patel O, Broughton SE, Bamert R, Williams NK, Fantino E, Wilks AF, Rossjohn J. The 2.7 A crystal structure of the autoinhibited human c-Fms kinase domain. J Mol Biol. 2007 Mar 30;367(3):839-47

Bonifer C, Hume DA. The transcriptional regulation of the Colony-Stimulating Factor 1 Receptor (csf1r) gene during hematopoiesis. Front Biosci. 2008 Jan 1;13:549-60

Shih LY, Liang DC, Huang CF, Chang YT, Lai CL, Lin TH, Yang CP, Hung IJ, Liu HC, Jaing TH, Wang LY, Yeh TC. Cooperating mutations of receptor tyrosine kinases and Ras genes in childhood core-binding factor acute myeloid leukemia and a comparative analysis on paired diagnosis and relapse samples. Leukemia. 2008 Feb;22(2):303-7

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