

Product datasheet for SC328512

VEGFA (NM 001171622) Human Untagged Clone

Product data:

Product Type: Expression Plasmids

Product Name: VEGFA (NM_001171622) Human Untagged Clone

Tag: Tag Free Symbol: VEGFA

Synonyms: MVCD1; VEGF; VPF

Mammalian Cell

Selection:

Neomycin

Vector:pCMV6-Entry (PS100001)E. coli Selection:Kanamycin (25 ug/mL)

Fully Sequenced ORF: >NCBI ORF sequence for NM_001171622, the custom clone sequence may differ by one or

more nucleotides

Restriction Sites: Sgfl-Mlul

ACCN: NM 001171622



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AGCACAACAAATGTGAATGCAGATGTGACAAGCCGAGGCGG<mark>TGA</mark>



VEGFA (NM_001171622) Human Untagged Clone - SC328512

OTI Disclaimer: Our molecular clone sequence data has been matched to the reference identifier above as a

point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative

RNA splicing form or single nucleotide polymorphism (SNP).

OTI Annotation: This TrueClone is provided through our Custom Cloning Process that includes sub-cloning

into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA.

Components: The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube

containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).

Reconstitution Method: 1. Centrifuge at 5,000xg for 5min.

2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.

3. Close the tube and incubate for 10 minutes at room temperature.

4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid

at the bottom.

5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of

shipping when stored at -20°C.

RefSeq: <u>NM 001171622.1</u>, <u>NP 001165093.1</u>

 RefSeq Size:
 3392 bp

 RefSeq ORF:
 954 bp

 Locus ID:
 7422

 UniProt ID:
 P15692

Cytogenetics:

Protein Families: Druggable Genome, Secreted Protein

6p21.1

Protein Pathways: Bladder cancer, Cytokine-cytokine receptor interaction, Focal adhesion, mTOR signaling

pathway, Pancreatic cancer, Pathways in cancer, Renal cell carcinoma, VEGF signaling pathway



Gene Summary:

This gene is a member of the PDGF/VEGF growth factor family. It encodes a heparin-binding protein, which exists as a disulfide-linked homodimer. This growth factor induces proliferation and migration of vascular endothelial cells, and is essential for both physiological and pathological angiogenesis. Disruption of this gene in mice resulted in abnormal embryonic blood vessel formation. This gene is upregulated in many known tumors and its expression is correlated with tumor stage and progression. Elevated levels of this protein are found in patients with POEMS syndrome, also known as Crow-Fukase syndrome. Allelic variants of this gene have been associated with microvascular complications of diabetes 1 (MVCD1) and atherosclerosis. Alternatively spliced transcript variants encoding different isoforms have been described. There is also evidence for alternative translation initiation from upstream non-AUG (CUG) codons resulting in additional isoforms. A recent study showed that a C-terminally extended isoform is produced by use of an alternative inframe translation termination codon via a stop codon readthrough mechanism, and that this isoform is antiangiogenic. Expression of some isoforms derived from the AUG start codon is regulated by a small upstream open reading frame, which is located within an internal ribosome entry site. The levels of VEGF are increased during infection with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), thus promoting inflammation by facilitating recruitment of inflammatory cells, and by increasing the level of angiopoietin II (Ang II), one of two products of the SARS-CoV-2 binding target, angiotensin-converting enzyme 2 (ACE2). In turn, Ang II facilitates the elevation of VEGF, thus forming a vicious cycle in the release of inflammatory cytokines. [provided by RefSeq, Jun 2020] Transcript Variant: This variant (8) lacks three alternate in-frame exons in the 3' coding region, compared to variant 1. This variant can initiate translation from four non-AUG (CUG) sites, and also from a downstream, in-frame AUG. The isoform (h) represented in this RefSeq is derived from the 5'-most CUG start codon, and is shorter than isoform a. CCDS Note: This CCDS representation starts at an upstream non-AUG (CUG) translation start codon that is supported by conservation data and experimental evidence, including that in PMIDs:11352659, 11563986 and 11731620. Most of the publicly available long mRNAs at this locus do not extend far enough 5' to include the CUG start codon, including DQ229900.1 which supports this variant. However, BC058855.1, several unspliced partial transcripts and the aforementioned publications all support transcription initiation further upstream. Hence, this CCDS representation includes the extended 5' CDS. Alternative translation initiation from a downstream AUG codon (Met-181), which results in a shorter isoform with a predicted signal peptide, has also been shown for this gene. The shorter isoform encoded by this variant is represented by CCDS 55015.1.