

Product datasheet for **RN215899**

Vegfa (NM_001287110) Rat Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: Vegfa (NM_001287110) Rat Untagged Clone
Tag: Tag Free
Symbol: Vegfa
Synonyms: Vegf; VEGF-A; VEGF111; VEGF164; VPF
Vector: pCMV6-Entry (PS100001)
E. coli Selection: Kanamycin (25 ug/mL)
Cell Selection: Neomycin
Fully Sequenced ORF: >RN215899 representing NM_001287110
Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**CGGATCGCC**

ATGAAC**TTTCTGCTCTCTTGGGTGCACTGGACCCTGGCTTTACTGCTGTACCTCCACCATGCCAAGTGGT**
CCCAGGCTGCACCCACGACAGAAGGGGAGCAGAAAGCCCATGAAGTGGTGAAGTTCATGGACGTCTACCA
GCGCAGCTATTGCCGTCCAATTGAGACCCTGGTGGACATCTCCAGGAGTACCCCGATGAGATAGAGTAT
ATCTTCAAGCCGTCTGTGTGCCCTAATGCGGTGTGCGGGCTGCTGCAATGATGAAGCCCTGGAGTGCG
TGCCACGTCGGAGAGCAACGTCACTATGCAGATCATGCGGATCAAACCTCACAAAGCCAGCACATAGG
AGAGATGAGCTTCTGCAGCATAGCAGATGTGAATGCAGACCAAAGAAAGATAGAACAAAGCCAGAAAAA
TGTGACAAGCCAAGGCGG**TGA**

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: SgfI-MluI
ACCN: NM_001287110
Insert Size: 441 bp
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).



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OTI Annotation:	Clone contains native stop codon, and expresses the complete ORF without any c-terminal tag.
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:	<ol style="list-style-type: none">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:	NM_001287110.1 , NP_001274039.1
RefSeq Size:	3342 bp
RefSeq ORF:	441 bp
Locus ID:	83785
UniProt ID:	P16612
Cytogenetics:	9q12
Gene Summary:	<p>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. Alternatively spliced transcript variants encoding different isoforms have been found for this gene. 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 in-frame 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. [provided by RefSeq, Nov 2015]</p> <p>Transcript Variant: This variant (3) lacks two consecutive in-frame exons in the 3' coding region, compared to variant 1. This variant can initiate translation from non-AUG (CUG) site, and also from a downstream, in-frame AUG site. The isoform (8) represented in this RefSeq is derived from the AUG start codon and it is shorter at the N-terminus and lacks an internal segment, compared to isoform 1. Sequence Note: This RefSeq record was created from transcript and genomic sequence data to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.</p>