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Product datasheet for SC119178

GRO alpha (CXCL1) (NM_001511) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	GRO alpha (CXCL1) (NM_001511) Human Untagged Clone
Tag:	Tag Free
Symbol:	GRO alpha
Synonyms:	FSP; GRO1; GROa; MGSA; MGSA-a; NAP-3; SCYB1
Mammalian Cell Selection:	None
Vector:	pCMV6-XL4
E. coli Selection:	Ampicillin (100 ug/mL)
Fully Sequenced ORF:	>OriGene ORF within SC118823 sequence for NM_002089 edited (data generated by NextGen Sequencing) ATGGCCCGCGCCACGCTCTCCGCCGCCCCCAGCAATCCCCGGCTCCTGCGRGTGGCGCTG CTGCTCCTGCTCCTGGTGGCCGCCAGCCGGCGCGCAGCAGGAGCGCCCCTGGCCACTGAA CTGCGCTGCCAGTGCTTGCAGACCCTGCAGGGAATTCACCYCAAGAACATCCAAAGTGTG AACGTGAAGTCCCCCGGACCCCACTGCGCCCAAACCGAAGTCATAGCCACACTCAAGAAT GGGCRGAAAGCTTGYCTCAACCCCGCATCGCCCATGGTTAAGAAAATCATCGAAAAGATG CTGAAAAATGGCAAATCCAACTGA Clone variation with respect to NM_002089.3 51 g=>r;161 t=>y;183 g=>c;245 a=>r;255 t=>y
Restriction Sites:	NotI-NotI
ACCN:	NM_001511
Insert Size:	1100 bp

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OTI Disclaimer:	Due to the inherent nature of this plasmid, standard methods to replicate additional amounts of DNA in E. coli are highly likely to result in mutations and/or rearrangements. Therefore, OriGene does not guarantee the capability to replicate this plasmid DNA. Additional amounts of DNA can be purchased from OriGene with batch-specific, full-sequence verification at a reduced cost. Please contact our customer care team at custsupport@origene.com or by calling 301.340.3188 option 3 for pricing and delivery. The molecular sequence of this clone aligns with the gene accession number as a point of reference only. However, individual transcript sequences of the same gene can differ through naturally occurring variations (e.g. polymorphisms), each with its own valid existence. This clone is substantially in agreement with the reference, but a complete review of all prevailing variants is recommended prior to use. More info
OTI Annotation:	The ORF of this clone has been fully sequenced and found to be a perfect match to NM_001511.1.
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.
Note:	Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um filter is required.
RefSeq:	NM_001511.1, NP_001502.1
RefSeq Size:	1103 bp
RefSeq ORF:	324 bp
Locus ID:	2919
UniProt ID:	P09341
Cytogenetics:	4q13.3
Domains:	IL8
Protein Families:	Druggable Genome, Secreted Protein
Protein Pathways:	Chemokine signaling pathway, Cytokine-cytokine receptor interaction, Epithelial cell signaling in Helicobacter pylori infection, NOD-like receptor signaling pathway

Gene Summary: This antimicrobial gene encodes a member of the CXC subfamily of chemokines. The encoded protein is a secreted growth factor that signals through the G-protein coupled receptor, CXC receptor 2. This protein plays a role in inflammation and as a chemoattractant for neutrophils. Aberrant expression of this protein is associated with the growth and progression of certain tumors. A naturally occurring processed form of this protein has increased chemotactic activity. Alternate splicing results in coding and non-coding variants of this gene. A pseudogene of this gene is found on chromosome 4. [provided by RefSeq, Sep 2014]
Transcript Variant: This variant (1) encodes the functional protein. 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.