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Product datasheet for RC213959L4V

Macrophage Inflammatory Protein 1 beta (CCL4L2) (NM_001001435) Human Tagged ORF Clone Lentiviral Particle

Product data:

Product Type:	Lentiviral Particles
Product Name:	Macrophage Inflammatory Protein 1 beta (CCL4L2) (NM_001001435) Human Tagged ORF Clone Lentiviral Particle
Symbol:	Macrophage Inflammatory Protein 1 beta
Synonyms:	AT744.2; CCL4L; LAG-1; LAG1; SCYA4L
Mammalian Cell Selection:	Puromycin
Vector:	pLenti-C-mGFP-P2A-Puro (PS100093)
Tag:	mGFP
ACCN:	NM_001001435
ORF Size:	276 bp
ORF Nucleotide Sequence:	`The ORF insert of this clone is exactly the same as(RC213959).`
OTI Disclaimer:	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:	This clone was engineered to express the complete ORF with an expression tag. Expression varies depending on the nature of the gene.
RefSeq:	NM_001001435.2, NP_001001435.1
RefSeq Size:	674 bp
RefSeq ORF:	278 bp
Locus ID:	9560
Cytogenetics:	17q12
Protein Families:	Druggable Genome, Transmembrane

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Protein Pathways:	Chemokine signaling pathway, Cytokine-cytokine receptor interaction, Cytosolic DNA-sensing pathway
MW:	10.1 kDa
Gene Summary:	This gene is one of several cytokine genes that are clustered on the q-arm of chromosome 17. Cytokines are a family of secreted proteins that function in inflammatory and immunoregulatory processes. The protein encoded by this family member is similar to the chemokine (C-C motif) ligand 4 product, which inhibits HIV entry by binding to the cellular receptor CCR5. The copy number of this gene varies among individuals, where most individuals have one to five copies. This gene copy contains a non-consensus splice acceptor site at the 3' terminal exon found in other highly similar gene copies, and it thus uses other alternative splice sites for the 3' terminal exon, resulting in multiple transcript variants. [provided by RefSeq, Apr 2014]