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Product datasheet for RC231112L4V

CRISP3 (NM_001190986) Human Tagged ORF Clone Lentiviral Particle

Product data:

Product Type:	Lentiviral Particles
Product Name:	CRISP3 (NM_001190986) Human Tagged ORF Clone Lentiviral Particle
Symbol:	CRISP3
Synonyms:	Aeg2; CRISP-3; CRS3; dJ442L6.3; SGP28
Mammalian Cell Selection:	Puromycin
Vector:	pLenti-C-mGFP-P2A-Puro (PS100093)
Tag:	mGFP
ACCN:	NM_001190986
ORF Size:	804 bp
ORF Nucleotide Sequence:	The ORF insert of this clone is exactly the same as(RC231112).
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_001190986.1
RefSeq ORF:	807 bp
Locus ID:	10321
UniProt ID:	P54108
Cytogenetics:	6p12.3
Protein Families:	Secreted Protein
MW:	30.6 kDa

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Gene Summary: This gene encodes a member of the cysteine-rich secretory protein (CRISP) family within the CRISP, antigen 5 and pathogenesis-related 1 proteins superfamily. The encoded protein has an N-terminal CRISP, antigen 5 and pathogenesis-related 1 proteins domain, a hinge region, and a C-terminal ion channel regulator domain. This protein contains cysteine residues, located in both the N- and C-terminal domains, that form eight disulfide bonds, a distinguishing characteristic of this family. This gene is expressed in the male reproductive tract where it plays a role in sperm function and fertilization, and the female reproductive tract where it plays a role in endometrial receptivity for embryo implantation. This gene is upregulated in certain types of prostate cancer. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Nov 2016]