

Product datasheet for **RC211189L4V**

RGS6 (NM_004296) Human Tagged ORF Clone Lentiviral Particle

Product data:

Product Type:	Lentiviral Particles
Product Name:	RGS6 (NM_004296) Human Tagged ORF Clone Lentiviral Particle
Symbol:	RGS6
Synonyms:	GAP; HA117; S914
Mammalian Cell Selection:	Puromycin
Vector:	pLenti-C-mGFP-P2A-Puro (PS100093)
Tag:	mGFP
ACCN:	NM_004296
ORF Size:	1416 bp
ORF Nucleotide Sequence:	The ORF insert of this clone is exactly the same as(RC211189).
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_004296.3
RefSeq Size:	5750 bp
RefSeq ORF:	1419 bp
Locus ID:	9628
UniProt ID:	P49758
Cytogenetics:	14q24.2
Domains:	RGS, DEP, G-gamma
Protein Families:	Druggable Genome



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MW: 54.4 kDa

Gene Summary: This gene encodes a member of the RGS (regulator of G protein signaling) family of proteins, which are defined by the presence of a RGS domain that confers the GTPase-activating activity of these proteins toward certain G alpha subunits. This protein also belongs to a subfamily of RGS proteins characterized by the presence of DEP and GGL domains, the latter a G beta 5-interacting domain. The RGS proteins negatively regulate G protein signaling, and may modulate neuronal, cardiovascular, lymphocytic activities, and cancer risk. Many alternatively spliced transcript variants encoding different isoforms with long or short N-terminal domains, complete or incomplete GGL domains, and distinct C-terminal domains, have been described for this gene, however, the full-length nature of some of these variants is not known.[provided by RefSeq, Mar 2011]