

## Product datasheet for **RC221140L4V**

### Caveolin 3 (CAV3) (NM\_033337) Human Tagged ORF Clone Lentiviral Particle

#### Product data:

Product Type:	Lentiviral Particles
Product Name:	Caveolin 3 (CAV3) (NM_033337) Human Tagged ORF Clone Lentiviral Particle
Symbol:	Caveolin 3
Synonyms:	LGMD1C; LQT9; MPDT; RMD2; VIP-21; VIP21
Mammalian Cell Selection:	Puromycin
Vector:	pLenti-C-mGFP-P2A-Puro (PS100093)
Tag:	mGFP
ACCN:	NM_033337
ORF Size:	453 bp
ORF Nucleotide Sequence:	The ORF insert of this clone is exactly the same as(RC221140).
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. <a href="#">More info</a>
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:	<a href="#">NM_033337.1</a>
RefSeq Size:	1435 bp
RefSeq ORF:	456 bp
Locus ID:	859
UniProt ID:	<a href="#">P56539</a>
Cytogenetics:	3p25.3
Protein Families:	Druggable Genome, Transmembrane
Protein Pathways:	Focal adhesion



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MW: 17.3 kDa

**Gene Summary:** This gene encodes a caveolin family member, which functions as a component of the caveolae plasma membranes found in most cell types. Caveolin proteins are proposed to be scaffolding proteins for organizing and concentrating certain caveolin-interacting molecules. Mutations identified in this gene lead to interference with protein oligomerization or intracellular routing, disrupting caveolae formation and resulting in Limb-Girdle muscular dystrophy type-1C (LGMD-1C), hyperCKemia or rippling muscle disease (RMD). Alternative splicing has been identified for this locus, with inclusion or exclusion of a differentially spliced intron. In addition, transcripts utilize multiple polyA sites and contain two potential translation initiation sites. [provided by RefSeq, Jul 2008]