

Product datasheet for RC217536L2V

OriGene Technologies, Inc.

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TRIM68 (NM_018073) Human Tagged ORF Clone Lentiviral Particle

Product data:

Product Type: Lentiviral Particles

Product Name: TRIM68 (NM_018073) Human Tagged ORF Clone Lentiviral Particle

Symbol: TRIM68

Synonyms: GC109; RNF137; SS-56; SS56

Mammalian Cell

Selection:

None

Vector: pLenti-C-mGFP (PS100071)

Tag: mGFP

ACCN: NM_018073 **ORF Size:** 1455 bp

ORF Nucleotide

The ORF insert of this clone is exactly the same as(RC217536).

Sequence:

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.

RefSeg: NM 018073.5

 RefSeq Size:
 3321 bp

 RefSeq ORF:
 1458 bp

 Locus ID:
 55128

 UniProt ID:
 Q6AZZ1

 Cytogenetics:
 11p15.4

Domains: zf-B_box, RING, SPRY

Protein Families: Druggable Genome





ORIGENE

MW: 56.1 kDa

Gene Summary:

This gene encodes a member of the tripartite motif-containing protein family, whose members are characterized by a "really interesting new gene" (RING) finger domain, a zinc-binding B-box motif, and a coiled-coil region. Members of this family function as E3 ubiquitin ligases and are involved in a broad range of biological processes. This gene regulates the activation of nuclear receptors, such as androgen receptor, and has been implicated in development of prostate cancer cells, where its expression increases in response to a downregulation of microRNAs. In addition, this gene participates in viral defense regulation as a negative regulator of interferon-beta. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Jan 2015]