

## Product datasheet for RC201047L3V

## OriGene Technologies, Inc.

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## **CENPM (NM 024053) Human Tagged ORF Clone Lentiviral Particle**

**Product data:** 

**Product Type: Lentiviral Particles** 

**Product Name:** CENPM (NM 024053) Human Tagged ORF Clone Lentiviral Particle

Symbol:

C22orf18; CENP-M; PANE1 Synonyms:

**Mammalian Cell** 

Selection:

ACCN:

Puromycin

Vector: pLenti-C-Myc-DDK-P2A-Puro (PS100092)

Tag: Myc-DDK NM 024053

**ORF Size:** 540 bp

**ORF Nucleotide** 

OTI Disclaimer:

Sequence:

The ORF insert of this clone is exactly the same as(RC201047).

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 024053.3

RefSeq Size: 947 bp RefSeq ORF: 543 bp Locus ID: 79019 **UniProt ID:** Q9NSP4 Cytogenetics: 22q13.2

**Protein Families:** Druggable Genome

MW: 19.7 kDa







## **Gene Summary:**

The protein encoded by this gene is an inner protein of the kinetochore, the multi-protein complex that binds spindle microtubules to regulate chromosome segregation during cell division. It belongs to the constitutive centromere-associated network protein group, whose members interact with outer kinetochore proteins and help to maintain centromere identity at each cell division cycle. The protein is structurally related to GTPases but cannot bind guanosine triphosphate. A point mutation that affects interaction with another constitutive centromere-associated network protein, CENP-I, impairs kinetochore assembly and chromosome alignment, suggesting that it is required for kinetochore formation. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Jan 2015]