

## Product datasheet for **RC224983L4V**

### CENPM (NM\_001110215) Human Tagged ORF Clone Lentiviral Particle

#### Product data:

Product Type:	Lentiviral Particles
Product Name:	CENPM (NM_001110215) Human Tagged ORF Clone Lentiviral Particle
Symbol:	CENPM
Synonyms:	C22orf18; CENP-M; PANE1
Mammalian Cell Selection:	Puromycin
Vector:	pLenti-C-mGFP-P2A-Puro (PS100093)
Tag:	mGFP
ACCN:	NM_001110215
ORF Size:	174 bp
ORF Nucleotide Sequence:	The ORF insert of this clone is exactly the same as(RC224983).
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_001110215.1</a> , <a href="#">NP_001103685.1</a>
RefSeq ORF:	177 bp
Locus ID:	79019
UniProt ID:	<a href="#">Q9NSP4</a>
Cytogenetics:	22q13.2
Protein Families:	Druggable Genome
MW:	6.1 kDa


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**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]