

## Product datasheet for **RC220299L3V**

### PLEKHM2 (NM\_015164) Human Tagged ORF Clone Lentiviral Particle

#### Product data:

Product Type:	Lentiviral Particles
Product Name:	PLEKHM2 (NM_015164) Human Tagged ORF Clone Lentiviral Particle
Symbol:	PLEKHM2
Synonyms:	SKIP
Mammalian Cell Selection:	Puromycin
Vector:	pLenti-C-Myc-DDK-P2A-Puro (PS100092)
Tag:	Myc-DDK
ACCN:	NM_015164
ORF Size:	3057 bp
ORF Nucleotide Sequence:	The ORF insert of this clone is exactly the same as(RC220299).
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_015164.1</a>
RefSeq Size:	4231 bp
RefSeq ORF:	3060 bp
Locus ID:	23207
UniProt ID:	<a href="#">Q8IWE5</a>
Cytogenetics:	1p36.21
Protein Families:	Druggable Genome
MW:	112.6 kDa



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**Gene Summary:**

This gene encodes a protein that binds the plus-end directed microtubule motor protein kinesin, together with the lysosomal GTPase Arl8, and is required for lysosomes to distribute away from the microtubule-organizing center. The encoded protein belongs to the multisubunit BLOC-one-related complex that regulates lysosome positioning. It binds a Salmonella effector protein called Salmonella induced filament A and is a critical host determinant in Salmonella pathogenesis. It has a domain architecture consisting of an N-terminal RPIP8, UNC-14, and NESCA (RUN) domain that binds kinesin-1 as well as the lysosomal GTPase Arl8, and a C-terminal pleckstrin homology domain that binds the Salmonella induced filament A effector protein. Naturally occurring mutations in this gene lead to abnormal localization of lysosomes, impaired autophagy flux and are associated with recessive dilated cardiomyopathy and left ventricular noncompaction. [provided by RefSeq, Feb 2017]