

Product datasheet for **RC226028L3V**

KLC1 (NM_001130107) Human Tagged ORF Clone Lentiviral Particle

Product data:

Product Type:	Lentiviral Particles
Symbol:	KLC1
Synonyms:	KLC; KNS2; KNS2A
Mammalian Cell Selection:	Puromycin
Vector:	pLenti-C-Myc-DDK-P2A-Puro (PS100092)
Tag:	Myc-DDK
ACCN:	NM_001130107
ORF Size:	1854 bp

ORF Nucleotide Sequence: The ORF insert of this clone is exactly the same as(RC226028).

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.

RefSeq: [NM_001130107.1](#), [NP_001123579.1](#)

RefSeq ORF: 1857 bp

Locus ID: 3831

UniProt ID: [Q07866](#)

Cytogenetics: 14q32.33

Protein Families: Druggable Genome



MW: 69.6 kDa

Gene Summary:

Conventional kinesin is a tetrameric molecule composed of two heavy chains and two light chains, and transports various cargos along microtubules toward their plus ends. The heavy chains provide the motor activity, while the light chains bind to various cargos. This gene encodes a member of the kinesin light chain family. It associates with kinesin heavy chain through an N-terminal domain, and six tetratricopeptide repeat (TPR) motifs are thought to be involved in binding of cargos such as vesicles, mitochondria, and the Golgi complex. Thus, kinesin light chains function as adapter molecules and not motors per se. Although previously named "kinesin 2", this gene is not a member of the kinesin-2 / kinesin heavy chain subfamily of kinesin motor proteins. Extensive alternative splicing produces isoforms with different C-termini that are proposed to bind to different cargos; however, the full-length nature and/or biological validity of most of these variants have not been determined. [provided by RefSeq, Jul 2008]