

## Product datasheet for **RC215899L3V**

### **CARD9 (NM\_052813) Human Tagged ORF Clone Lentiviral Particle**

#### **Product data:**

Product Type:	Lentiviral Particles
Product Name:	CARD9 (NM_052813) Human Tagged ORF Clone Lentiviral Particle
Symbol:	CARD9
Synonyms:	CANDF2; hCARD9
Mammalian Cell Selection:	Puromycin
Vector:	pLenti-C-Myc-DDK-P2A-Puro (PS100092)
Tag:	Myc-DDK
ACCN:	NM_052813
ORF Size:	1608 bp
ORF Nucleotide Sequence:	The ORF insert of this clone is exactly the same as(RC215899).
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_052813.2</a>
RefSeq Size:	2136 bp
RefSeq ORF:	1611 bp
Locus ID:	64170
UniProt ID:	<a href="#">Q9H257</a>
Cytogenetics:	9q34.3
Protein Families:	Druggable Genome
Protein Pathways:	NOD-like receptor signaling pathway



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**MW:** 62.1 kDa

**Gene Summary:** The protein encoded by this gene is a member of the CARD protein family, which is defined by the presence of a characteristic caspase-associated recruitment domain (CARD). CARD is a protein interaction domain known to participate in activation or suppression of CARD containing members of the caspase family, and thus plays an important regulatory role in cell apoptosis. This protein was identified by its selective association with the CARD domain of BCL10, a positive regulator of apoptosis and NF-kappaB activation, and is thought to function as a molecular scaffold for the assembly of a BCL10 signaling complex that activates NF-kappaB. Several alternatively spliced transcript variants have been observed, but their full-length nature is not clearly defined. [provided by RefSeq, Jul 2008]