

## Product datasheet for **RC208097L1V**

### **C2 (NM\_000063) Human Tagged ORF Clone Lentiviral Particle**

#### **Product data:**

Product Type:	Lentiviral Particles
Product Name:	C2 (NM_000063) Human Tagged ORF Clone Lentiviral Particle
Symbol:	C2
Synonyms:	ARMD14; CO2
Mammalian Cell Selection:	None
Vector:	pLenti-C-Myc-DDK (PS100064)
Tag:	Myc-DDK
ACCN:	NM_000063
ORF Size:	2256 bp
ORF Nucleotide Sequence:	The ORF insert of this clone is exactly the same as(RC208097).
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_000063.3</a>
RefSeq Size:	2862 bp
RefSeq ORF:	2259 bp
Locus ID:	717
UniProt ID:	<a href="#">P06681</a>
Cytogenetics:	6p21.33
Domains:	CCP, Tryp_SPc, VWA
Protein Families:	Druggable Genome, Protease, Secreted Protein



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**Protein Pathways:** Complement and coagulation cascades, Systemic lupus erythematosus

**MW:** 83.3 kDa

**Gene Summary:** Component C2 is a serum glycoprotein that functions as part of the classical pathway of the complement system. Activated C1 cleaves C2 into C2a and C2b. The serine proteinase C2a then combines with complement factor 4b to create the C3 or C5 convertase. Deficiency of C2 has been reported to associated with certain autoimmune diseases and SNPs in this gene have been associated with altered susceptibility to age-related macular degeneration. This gene localizes within the class III region of the MHC on the short arm of chromosome 6. Alternative splicing results in multiple transcript variants encoding distinct isoforms. Additional transcript variants have been described in publications but their full-length sequence has not been determined.[provided by RefSeq, Mar 2009]