

## Product datasheet for RC229002L2V

## OriGene Technologies, Inc.

9620 Medical Center Drive, Ste 200 Rockville, MD 20850, US Phone: +1-888-267-4436 https://www.origene.com techsupport@origene.com EU: info-de@origene.com CN: techsupport@origene.cn

## SETDB2 (NM\_001160308) Human Tagged ORF Clone Lentiviral Particle

**Product data:** 

**Product Type:** Lentiviral Particles

**Product Name:** SETDB2 (NM\_001160308) Human Tagged ORF Clone Lentiviral Particle

Symbol: SETDB2

Synonyms: C13orf4; CLLD8; CLLL8; KMT1F

Mammalian Cell

Selection:

None

**Vector:** pLenti-C-mGFP (PS100071)

Tag: mGFP

**ACCN:** NM\_001160308

ORF Size: 2121 bp

**ORF Nucleotide** 

The ORF insert of this clone is exactly the same as(RC229002).

Sequence:

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.

**RefSeg:** NM 001160308.1

 RefSeq ORF:
 2124 bp

 Locus ID:
 83852

 UniProt ID:
 Q96T68

 Cytogenetics:
 13q14.2

**Protein Families:** Druggable Genome

**Protein Pathways:** Lysine degradation

**MW:** 80.5 kDa







## **Gene Summary:**

This gene encodes a member of a family of proteins that contain a methyl-CpG-binding domain (MBD) and a SET domain and function as histone methyltransferases. This protein is recruited to heterochromatin and plays a role in the regulation of chromosome segregation. This region is commonly deleted in chronic lymphocytic leukemia. Naturally-occuring readthrough transcription occurs from this gene to the downstream PHF11 (PHD finger protein 11) gene. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Mar 2016]