

## Product datasheet for **RC221881L1V**

### **RUNX1T1 (NM\_175634) Human Tagged ORF Clone Lentiviral Particle**

#### **Product data:**

Product Type:	Lentiviral Particles
Product Name:	RUNX1T1 (NM_175634) Human Tagged ORF Clone Lentiviral Particle
Symbol:	RUNX1T1
Synonyms:	AML1-MTG8; AML1T1; CBFA2T1; CDR; ETO; MTG8; ZMYND2
Mammalian Cell Selection:	None
Vector:	pLenti-C-Myc-DDK (PS100064)
Tag:	Myc-DDK
ACCN:	NM_175634
ORF Size:	1812 bp
ORF Nucleotide Sequence:	The ORF insert of this clone is exactly the same as(RC221881).
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_175634.1</a>
RefSeq Size:	3217 bp
RefSeq ORF:	1815 bp
Locus ID:	862
UniProt ID:	<a href="#">Q06455</a>
Cytogenetics:	8q21.3
Protein Families:	Transcription Factors
Protein Pathways:	Acute myeloid leukemia, Pathways in cancer



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**MW:** 67.4 kDa

**Gene Summary:** This gene encodes a member of the myeloid translocation gene family which interact with DNA-bound transcription factors and recruit a range of corepressors to facilitate transcriptional repression. The t(8;21)(q22;q22) translocation is one of the most frequent karyotypic abnormalities in acute myeloid leukemia. The translocation produces a chimeric gene made up of the 5'-region of the runt-related transcription factor 1 gene fused to the 3'-region of this gene. The chimeric protein is thought to associate with the nuclear corepressor/histone deacetylase complex to block hematopoietic differentiation. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Nov 2010]