

## Product datasheet for **RC219995L4V**

### splicing factor 1 (SF1) (NM\_004630) Human Tagged ORF Clone Lentiviral Particle

#### Product data:

Product Type:	Lentiviral Particles
Product Name:	splicing factor 1 (SF1) (NM_004630) Human Tagged ORF Clone Lentiviral Particle
Symbol:	splicing factor 1
Synonyms:	BBP; D11S636; MBBP; ZCCHC25; ZFM1; ZNF162
Mammalian Cell Selection:	Puromycin
Vector:	pLenti-C-mGFP-P2A-Puro (PS100093)
Tag:	mGFP
ACCN:	NM_004630
ORF Size:	1917 bp
ORF Nucleotide Sequence:	The ORF insert of this clone is exactly the same as(RC219995).
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_004630.2</a>
RefSeq Size:	3527 bp
RefSeq ORF:	1920 bp
Locus ID:	7536
UniProt ID:	<a href="#">Q15637</a>
Cytogenetics:	11q13.1
Domains:	zf-CCHC, KH
Protein Families:	Transcription Factors



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**MW:** 68.1 kDa

**Gene Summary:** This gene encodes a nuclear pre-mRNA splicing factor. The encoded protein specifically recognizes the intron branch point sequence at the 3' splice site, together with the large subunit of U2 auxiliary factor (U2AF), and is required for the early stages of spliceosome assembly. It also plays a role in nuclear pre-mRNA retention and transcriptional repression. The encoded protein contains an N-terminal U2AF ligand motif, a central hnRNP K homology motif and quaking 2 region which bind a key branch-site adenosine within the branch point sequence, a zinc knuckles domain, and a C-terminal proline-rich domain. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Oct 2016]