

Product datasheet for **SC328691**

RBMS3 (NM_001177711) Human Untagged Clone

Product data:

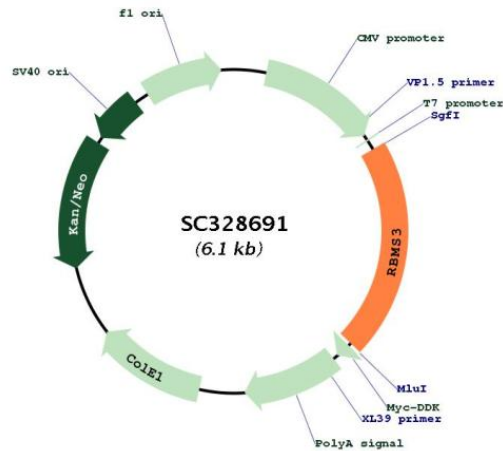
Product Type:	Expression Plasmids
Product Name:	RBMS3 (NM_001177711) Human Untagged Clone
Tag:	Tag Free
Symbol:	RBMS3
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC328691 representing NM_001177711. Blue=Insert sequence Red=Cloning site Green=Tag(s)

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GCTCGTTTAGTGAACCGTCAGAATTTTGTAAACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG
GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC
ATGGGCAAACGCCTGGATCAGCCACAAATGTACCCCAAGTACACTTACTACTATCCTCATTATCTCCAA
ACCAAGCAGTCTATGCACCAGCTCCCCACCCATGGCTCCTCCCAGCCCCAGCACAAACAGCAGCAGC
AACACAGCAGCAACAACAGCAGCGGGGAACAGTTGAGTAAAACCAACCTGTACATTCGAGGCCCTCCA
CCAGGCACCCTGACCAGGACCTAATCAAGCTGTGCCAACCGTATGAAAAATTGTATCTACAAAGGCA
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CCAACAAACCTATACATCTCAAATCTCCCATTTCTATGGATGAGCAGGAGCTTGAGAATATGCTGAAA
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GCCAGAATGGAGTCTACTGAAAAATGTGAAGTGGTAATCAACATTTTAAATGGAAAAATCTGAAAAA
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CAGAATCAAAGCAAATATACCCAGAATGGGAGGCCTTGGCCAGGGAAGGAGAGGCTGGCATGGCTTTG
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CATCCCATGTCAATGCAGCCAGCCAACATGATGGGCCACTGACACAGCAGATGAATCACCTTTCGTTG
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TCCCAGGACACCAGTGGTCAGCAGCAACAGATAGCAGTGGACACATCCAACGAACATGCACCTGCATAT
TCTTACCAACAGTCTAAACCATAA
ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
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Restriction Sites: SgfI-MluI



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Plasmid Map:


ACCN: NM_001177711

Insert Size: 1266 bp

OTI Disclaimer: Our molecular clone sequence data has been matched to the reference identifier above as a point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative RNA splicing form or single nucleotide polymorphism (SNP).

OTI Annotation: This TrueClone is provided through our Custom Cloning Process that includes sub-cloning into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA.

Components: The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).

Reconstitution Method:

1. Centrifuge at 5,000xg for 5min.
2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.
3. Close the tube and incubate for 10 minutes at room temperature.
4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.
5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of shipping when stored at -20°C.

RefSeq: [NM_001177711.1](#)

RefSeq Size: 8186 bp

RefSeq ORF: 1266 bp

Locus ID: 27303

UniProt ID: [Q6XE24](#)

Cytogenetics: 3p24.1

MW: 45.9 kDa

Gene Summary: This gene encodes an RNA-binding protein that belongs to the c-myc gene single-strand binding protein family. These proteins are characterized by the presence of two sets of ribonucleoprotein consensus sequence (RNP-CS) that contain conserved motifs, RNP1 and RNP2, originally described in RNA binding proteins, and required for DNA binding. These proteins have been implicated in such diverse functions as DNA replication, gene transcription, cell cycle progression and apoptosis. The encoded protein was isolated by virtue of its binding to an upstream element of the alpha2(I) collagen promoter. The observation that this protein localizes mostly in the cytoplasm suggests that it may be involved in a cytoplasmic function such as controlling RNA metabolism, rather than transcription. Multiple alternatively spliced transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Apr 2010]

Transcript Variant: This variant (5) lacks an in-frame exon in the coding region, compared to variant 1. The encoded isoform (5) is shorter than isoform 1. Sequence Note: This RefSeq record was created from transcript and genomic sequence data to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.