

Product datasheet for TR302073

RBM24 Human shRNA Plasmid Kit (Locus ID 221662)

Product data:

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

Product Type:	shRNA Plasmids
Product Name:	RBM24 Human shRNA Plasmid Kit (Locus ID 221662)
Locus ID:	221662
Synonyms:	dJ259A10.1; RNPC6
Vector:	pRS (TR20003)
E. coli Selection:	Ampicillin
Mammalian Cell Selection:	Puromycin
Format:	Retroviral plasmids
Components:	RBM24 - Human, 4 unique 29mer shRNA constructs in retroviral untagged vector(Gene ID = 221662). 5µg purified plasmid DNA per construct 29-mer scrambled shRNA cassette in pRS Vector, TR30012, included for free.
RefSeq:	<u>NM 001143941, NM 001143942, NM 153020, NM 153020.1, NM 153020.2, NM 001143941.1, BC104808, BC104808.1, BC018674, BC040928, BC065748, BC104810, NM 001143942.2</u>
UniProt ID:	<u>Q9BX46</u>



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Summary:	Multifunctional RNA-binding protein involved in the regulation of pre-mRNA splicing, mRNA
	stability and mRNA translation important for cell fate decision and differentiation
	(PubMed:20977548, PubMed:24375645, PubMed:29358667, PubMed:29104163). Plays a
	major role in pre-mRNA alternative splicing regulation (PubMed:26990106,
	PubMed:29104163). Mediates preferentially muscle-specific exon inclusion in numerous
	mRNAs important for striated cardiac and skeletal muscle cell differentiation
	(PubMed:29104163). Binds to intronic splicing enhancer (ISE) composed of stretches of GU-
	rich motifs localized in flanking intron of exon that will be included by alternative splicing (By
	similarity). Involved in embryonic stem cell (ESC) transition to cardiac cell differentiation by
	promoting pre-mRNA alternative splicing events of several pluripotency and/or differentiation
	genes (PubMed:26990106). Plays a role in the regulation of mRNA stability
	(PubMed:20977548, PubMed:24356969, PubMed:24375645, PubMed:29104163). Binds to 3'-
	untranslated region (UTR) AU-rich elements in target transcripts, such as CDKN1A and MYOG,
	leading to maintain their stabilities (PubMed:20977548, PubMed:24356969). Involved in
	myogenic differentiation by regulating MYOG levels (PubMed:20977548). Binds to multiple
	regions in the mRNA 3' UTR of TP63 isoform 2, hence inducing its destabilization
	(PubMed:24375645). Promotes also the destabilization of the CHRM2 mRNA via its binding to
	a region in the coding sequence (PubMed:29104163). Plays a role in the regulation of mRNA
	translation (PubMed:29358667). Mediates repression of p53/TP53 mRNA translation through
	its binding to U-rich element in the 3' UTR, hence preventing EIF4E from binding to p53/TP53
	mRNA and translation initiation (PubMed:29358667). Binds to a huge amount of mRNAs
	(PubMed:29104163). Required for embryonic heart development, sarcomer and M-band
	formation in striated muscles (By similarity).[UniProtKB/Swiss-Prot Function]
shRNA Design:	These shRNA constructs were designed against multiple splice variants at this gene locus. To
	be certain that your variant of interest is targeted, please contact <u>techsupport@origene.com</u> .
	If you need a special design or shRNA sequence, please utilize our <u>custom shRNA service</u> .
Performance	OriGene guarantees that the sequences in the shRNA expression cassettes are verified to
Guaranteed:	correspond to the target gene with 100% identity. One of the four constructs at minimum are
	guaranteed to produce 70% or more gene expression knock-down provided a minimum
	transfection efficiency of 80% is achieved. Western Blot data is recommended over qPCR to
	evaluate the silencing effect of the shRNA constructs 72 hrs post transfection. To properly
	assess knockdown, the gene expression level from the included scramble control vector must
	be used in comparison with the target-specific shRNA transfected samples.
	For non-conforming shRNA, requests for replacement product must be made within ninety
	(90) days from the date of delivery of the shRNA kit. To arrange for a free replacement with
	newly designed constructs, please contact Technical Services at techsupport@origene.com.
	Please provide your data indicating the transfection efficiency and measurement of gene
	expression knockdown compared to the scrambled shRNA control (Western Blot data

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preferred).