

Product datasheet for **TR502145**

Srpk1 Mouse shRNA Plasmid (Locus ID 20815)

Product data:

Product Type:	shRNA Plasmids
Product Name:	Srpk1 Mouse shRNA Plasmid (Locus ID 20815)
Locus ID:	20815
Synonyms:	AU017960
Vector:	pRS (TR20003)
E. coli Selection:	Ampicillin
Mammalian Cell Selection:	Puromycin
Format:	Retroviral plasmids
Components:	Srpk1 - Mouse, 4 unique 29mer shRNA constructs in retroviral untagged vector(Gene ID = 20815). 5µg purified plasmid DNA per construct 29-mer scrambled shRNA cassette in pRS Vector, TR30012, included for free.
RefSeq:	BC005707 , BC050761 , NM_016795 , NM_016795.1 , NM_016795.2 , NM_016795.3 , NM_016795.4
UniProt ID:	O70551



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Summary: Serine/arginine-rich protein-specific kinase which specifically phosphorylates its substrates at serine residues located in regions rich in arginine/serine dipeptides, known as RS domains and is involved in the phosphorylation of SR splicing factors and the regulation of splicing. Plays a central role in the regulatory network for splicing, controlling the intranuclear distribution of splicing factors in interphase cells and the reorganization of nuclear speckles during mitosis. Can influence additional steps of mRNA maturation, as well as other cellular activities, such as chromatin reorganization in somatic and sperm cells and cell cycle progression. Phosphorylates SFRS2, ZRSR2, LBR and PRM1. Phosphorylates SRSF1 using a directional (C-terminal to N-terminal) and a dual-track mechanism incorporating both processive phosphorylation (in which the kinase stays attached to the substrate after each round of phosphorylation) and distributive phosphorylation steps (in which the kinase and substrate dissociate after each phosphorylation event). The RS domain of SRSF1 binds first to a docking groove in the large lobe of the kinase domain of SRPK1. This induces certain structural changes in SRPK1 and/or RRM2 domain of SRSF1, allowing RRM2 to bind the kinase and initiate phosphorylation. The cycles continue for several phosphorylation steps in a processive manner (steps 1-8) until the last few phosphorylation steps (approximately steps 9-12). During that time, a mechanical stress induces the unfolding of the beta-4 motif in RRM2, which then docks at the docking groove of SRPK1. This also signals RRM2 to begin to dissociate, which facilitates SRSF1 dissociation after phosphorylation is completed. Can mediate hepatitis B virus (HBV) core protein phosphorylation. It plays a negative role in the regulation of HBV replication through a mechanism not involving the phosphorylation of the core protein but by reducing the packaging efficiency of the pregenomic RNA (pgRNA) without affecting the formation of the viral core particles. Can induce splicing of exon 10 in MAPT/TAU (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 techsupport@origene.com. If you need a special design or shRNA sequence, please utilize our [custom shRNA service](#).

Performance Guaranteed: OriGene guarantees that the sequences in the shRNA expression cassettes are verified to 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 preferred).