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Product datasheet for TR301731

Shugoshin (SGO1) Human shRNA Plasmid Kit (Locus ID 151648)

Product data:

Product Type:	shRNA Plasmids
Product Name:	Shugoshin (SGO1) Human shRNA Plasmid Kit (Locus ID 151648)
Locus ID:	151648
Synonyms:	CAID; NY-BR-85; SGO; SGOL1
Vector:	pRS (TR20003)
E. coli Selection:	Ampicillin
Mammalian Cell Selection:	Puromycin
Format:	Retroviral plasmids
Components:	SGO1 - Human, 4 unique 29mer shRNA constructs in retroviral untagged vector(Gene ID = 151648). 5µg purified plasmid DNA per construct 29-mer scrambled shRNA cassette in pRS Vector, TR30012, included for free.
RefSeq:	NM_001012409, NM_001012410, NM_001012411, NM_001012412, NM_001012413, NM_001199251, NM_001199252, NM_001199253, NM_001199254, NM_001199255, NM_001199256, NM_001199257, NM_138484, NR_131179, NR_131180, NM_138484.1, NM_138484.3, NM_138484.4, NM_001012410.1, NM_001012410.2, NM_001012410.3, NM_001012410.4, NM_001012411.1, NM_001012411.2, NM_001012411.3, NM_001012409.1, NM_001012409.2, NM_001012413.1, NM_001012413.2, NM_001012413.3, NM_001012412.1, NM_001012412.2, NM_001012412.3, NM_001012412.4, NM_001199257.1, NM_001199257.2, NM_001199255.1, NM_001199255.2, NM_001199253.1, NM_001199253.2, NM_001199256.1, NM_001199256.2, NM_001199254.1, NM_001199254.2, NM_001199251.1, NM_001199251.2, NM_001199252.1, NM_001199252.2, BC017867, BC017867.1, BC001339, BC032696, BC039605, BM144963, NM_138484.5, NM_001012410.5, NM_001199251.3, NM_001012412.5, NM_001199252.3, NM_001199254.3, NM_001199257.3, NM_001199256.3
UniProt ID:	Q5FBB7

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Summary:

The protein encoded by this gene is a member of the shugoshin family of proteins. This protein is thought to protect centromeric cohesin from cleavage during mitotic prophase by preventing phosphorylation of a cohesin subunit. Reduced expression of this gene leads to the premature loss of centromeric cohesion, mis-segregation of sister chromatids, and mitotic arrest. Evidence suggests that this protein also protects a small subset of cohesin found along the length of the chromosome arms during mitotic prophase. An isoform lacking exon 6 has been shown to play a role in the cohesion of centrioles (PMID: 16582621 and PMID:18331714). Mutations in this gene have been associated with Chronic Atrial and Intestinal Dysrhythmia (CAID) syndrome, characterized by the co-occurrence of Sick Sinus Syndrome (SSS) and Chronic Intestinal Pseudo-obstruction (CIPO) within the first four decades of life (PMID:25282101). Fibroblast cells from CAID patients exhibited both increased cell proliferation and higher rates of senescence. Pseudogenes of this gene have been found on chromosomes 1 and 7. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Mar 2015]

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).