

## Product datasheet for **TL301769**

### SEPN1 (SELENON) Human shRNA Plasmid Kit (Locus ID 57190)

#### Product data:

Product Type:	shRNA Plasmids
Product Name:	SEPN1 (SELENON) Human shRNA Plasmid Kit (Locus ID 57190)
Locus ID:	57190
Synonyms:	CFTD; MDRS1; RSMD1; RSS; SELN; SEPN1
Vector:	pGFP-C-shLenti (TR30023)
E. coli Selection:	Chloramphenicol (34 ug/ml)
Mammalian Cell Selection:	Puromycin
Format:	Lentiviral plasmids
Components:	SELENON - Human, 4 unique 29mer shRNA constructs in lentiviral GFP vector(Gene ID = 57190). 5µg purified plasmid DNA per construct 29-mer scrambled shRNA cassette in pGFP-C-shLenti Vector, TR30021, included for free.
RefSeq:	<a href="#">NM_020451</a> , <a href="#">NM_206926</a> , <a href="#">NM_206926.1</a> , <a href="#">NM_020451.1</a> , <a href="#">NM_020451.2</a> , <a href="#">BC005881</a> , <a href="#">BC015638</a> , <a href="#">BC021028</a> , <a href="#">BC033244</a> , <a href="#">BC042154</a> , <a href="#">BC107036</a> , <a href="#">BC156071</a> , <a href="#">NM_206926.2</a> , <a href="#">NM_020451.3</a>
UniProt ID:	<a href="#">Q9NZV5</a>



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**Summary:**

This gene encodes a glycoprotein that is localized in the endoplasmic reticulum. It plays an important role in cell protection against oxidative stress, and in the regulation of redox-related calcium homeostasis. Mutations in this gene are associated with early onset muscle disorders, referred to as SEPN1-related myopathy. SEPN1-related myopathy consists of 4 autosomal recessive disorders, originally thought to be separate entities: rigid spine muscular dystrophy (RSMD1), the classical form of multiminicore disease, desmin related myopathy with Mallory-body like inclusions, and congenital fiber-type disproportion (CFTD). This protein is a selenoprotein, containing the rare amino acid selenocysteine (Sec). Sec is encoded by the UGA codon, which normally signals translation termination. The 3' UTRs of selenoprotein mRNAs contain a conserved stem-loop structure, designated the Sec insertion sequence (SECIS) element, that is necessary for the recognition of UGA as a Sec codon, rather than as a stop signal. A second stop-codon redefinition element (SRE) adjacent to the UGA codon has been identified in this gene (PMID:15791204). SRE is a phylogenetically conserved stem-loop structure that stimulates readthrough at the UGA codon, and augments the Sec insertion efficiency by SECIS. Alternatively spliced transcript variants have been found for this gene. [provided by RefSeq, Dec 2016]

**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](mailto: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](mailto: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).