

## OriGene Technologies, Inc.

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## Product datasheet for TL315168

## Septin 2 (SEPT2) Human shRNA Plasmid Kit (Locus ID 4735)

## **Product data:**

Product Type:	shRNA Plasmids
Product Name:	Septin 2 (SEPT2) Human shRNA Plasmid Kit (Locus ID 4735)
Locus ID:	4735
Synonyms:	DIFF6; hNedd5; NEDD-5; NEDD5; Pnutl3; SEPT2
Vector:	pGFP-C-shLenti (TR30023)
E. coli Selection:	Chloramphenicol (34 ug/ml)
Mammalian Cell Selection:	Puromycin
Format:	Lentiviral plasmids
Components:	SEPT2 - Human, 4 unique 29mer shRNA constructs in lentiviral GFP vector(Gene ID = 4735). 5µg purified plasmid DNA per construct 29-mer scrambled shRNA cassette in pGFP-C-shLenti Vector, TR30021, included for free.
RefSeq:	NM 001008491, NM 001008492, NM 001282972, NM 001282973, NM 004404, NM 006155,   NM 001321029, NM 001321030, NM 001321031, NM 001321032, NM 001321033,   NM 001321034, NM 001321035, NM 001349287, NM 001349288, NM 001349289,   NM 001349290, NM 001349291, NM 001349302, NM 001349304, NM 001349305,   NM 001349306, NM 001349307, NM 001349308, NM 001349309, NM 001349310,   NM 001349311, NM 001349312, NM 001349313, NM 001349314, NM 001349315,   NM 001404.3, NM 001349312, NM 001349313, NM 001349314, NM 001349315,   NM 0014044.3, NM 006155.1, NM 006155.2, NM 00108492.1,   NM 001008492.2, NM 001008491.2, NM 001282973.1, NM 001282972.1, BC014455,   BC014455.1, BC033559, BC040676, BC043180, NM 001008491.3, NM 004404.5 00140404.5
UniProt ID:	<u>Q15019</u>



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	Septin 2 (SEPT2) Human shRNA Plasmid Kit (Locus ID 4735) – TL315168
Summary:	Filament-forming cytoskeletal GTPase. Forms a filamentous structure with SEPTIN12, SEPTIN6, SEPTIN2 and probably SEPTIN4 at the sperm annulus which is required for the structural integrity and motility of the sperm tail during postmeiotic differentiation (PubMed:25588830). Required for normal organization of the actin cytoskeleton. Plays a role in the biogenesis of polarized columnar-shaped epithelium by maintaining polyglutamylated microtubules, thus facilitating efficient vesicle transport, and by impeding MAP4 binding to tubulin. Required for the progression through mitosis. Forms a scaffold at the midplane of the mitotic splindle required to maintain CENPE localization at kinetochores and consequently chromosome congression. During anaphase, may be required for chromosome segregation and spindle elongation. Plays a role in ciliogenesis and collective cell movements. In cilia, required for the integrity of the diffusion barrier at the base of the primary cilium that prevents diffusion of transmembrane proteins between the cilia and plasma membranes: probably acts by regulating the assembly of the tectonic-like complex (also named B9 complex) by localizing TMEM231 protein. May play a role in the internalization of 2 intracellular microbial pathogens, Listeria monocytogenes and Shigella flexneri. [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 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).

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