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# Product datasheet for TR503190

## Stub1 Mouse shRNA Plasmid (Locus ID 56424)

### Product data:

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|---|---|
| **Product Type:** | shRNA Plasmids |
| **Product Name:** | Stub1 Mouse shRNA Plasmid (Locus ID 56424) |
| **Locus ID:** | 56424 |
| **Synonyms:** | 0610033N24Rik; 2210017D18Rik; 2310040B03Rik; AW046544; Chip |
| **Vector:** | pRS (TR20003) |
| **E. coli Selection:** | Ampicillin |
| **Mammalian Cell Selection:** | Puromycin |
| **Format:** | Retroviral plasmids |
| **Components:** | Stub1 - Mouse, 4 unique 29mer shRNA constructs in retroviral untagged vector(Gene ID = 56424). 5µg purified plasmid DNA per construct<br>29-mer scrambled shRNA cassette in pRS Vector, TR30012, included for free. |
| **RefSeq:** | BC027427, BC038939, NM_019719, NM_019719.1, NM_019719.2, NM_019719.3, BC020110, NM_019719.4 |
| **UniProt ID:** | Q9WUD1 |

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**Summary:**

E3 ubiquitin-protein ligase which targets misfolded chaperone substrates towards proteasomal degradation. Collaborates with ATXN3 in the degradation of misfolded chaperone substrates: ATXN3 restricting the length of ubiquitin chain attached to STUB1/CHIP substrates and preventing further chain extension. Ubiquitinates NOS1 in concert with Hsp70 and Hsp40. Modulates the activity of several chaperone complexes, including Hsp70, Hsc70 and Hsp90. Mediates transfer of non-canonical short ubiquitin chains to HSPA8 that have no effect on HSPA8 degradation. Mediates polyubiquitination of DNA polymerase beta (POLB) at 'Lys-41', 'Lys-61' and 'Lys-81', thereby playing a role in base-excision repair: catalyzes polyubiquitination by amplifying the HUWE1/ARF-BP1-dependent monoubiquitination and leading to POLB-degradation by the proteasome. Mediates polyubiquitination of CYP3A4. Ubiquitinates EPHA2 and may regulate the receptor stability and activity through proteasomal degradation. Negatively regulates the suppressive function of regulatory T-cells (Treg) during inflammation by mediating the ubiquitination and degradation of FOXP3 in a HSPA1A/B-dependent manner (PubMed:23973223). Acts as a co-chaperone for HSPA1A and HSPA1B chaperone proteins and promotes ubiquitin-mediated protein degradation. Likely mediates polyubiquitination and downregulates plasma membrane expression of PD-L1/CD274, an immune inhibitory ligand critical for immune tolerance to self and antitumor immunity. Negatively regulates TGF-beta signaling by modulating the basal level of SMAD3 via ubiquitin-mediated degradation (By similarity). May regulate myosin assembly in striated muscles together with UBE4B and VCP/p97 by targeting myosin chaperone UNC45B for proteasomal degradation (By similarity). Mediates ubiquitination of RIPK3 leading to its subsequent proteasome-dependent degradation (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).