

Product datasheet for TL502087

Snai1 Mouse shRNA Plasmid (Locus ID 20613)

Product data:

OriGene Technologies, Inc.

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| Product Type: | shRNA Plasmids |
|------------------------------|--|
| Product Name: | Snai1 Mouse shRNA Plasmid (Locus ID 20613) |
| Locus ID: | 20613 |
| Synonyms: | Sna; Sna1; Snail; Snail1 |
| Vector: | pGFP-C-shLenti (TR30023) |
| E. coli Selection: | Chloramphenicol (34 ug/ml) |
| Mammalian Cell Selection: | Puromycin |
| Format: | Lentiviral plasmids |
| Components: | Snai1 - Mouse, 4 unique 29mer shRNA constructs in lentiviral GFP vector(Gene ID = 20613). 5µg purified plasmid DNA per construct 29-mer scrambled shRNA cassette in pGFP-C-shLenti Vector, TR30021, included for free. |
| RefSeq: | <u>BC034857, NM 011427, NM 011427.1, NM 011427.2, NM 011427.3</u> |
| UniProt ID: | <u>Q02085</u> |



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GRIGENE Snai1 Mouse shRNA Plasmid (Locus ID 20613) – TL502087

| Summary: | Involved in induction of the epithelial to mesenchymal transition (EMT), formation and maintenance of embryonic mesoderm, growth arrest, survival and cell migration. Binds to 3 E-boxes of the E-cadherin gene promoter and to the promoters of CLDN7 and KRT8 and, in association with histone demethylase KDM1A which it recruits to the promoters, causes a decrease in dimethylated H3K4 levels and represses transcription. Involved in induction of the epithelial to mesenchymal transition (EMT), formation and maintenance of embryonic mesoderm, growth arrest, survival and cell migration. Binds to 3 E-boxes of the E- cadherin/CDH1 gene promoter and to the promoters of CLDN7 and KRT8 and, in association with histone demethylase KDM1A which it recruits to the promoters, causes a decrease in dimethylated H3K4 levels and represses transcription. The N-terminal SNAG domain competes with histone H3 for the same binding site on the histone demethylase complex formed by KDM1A and RCOR1, and thereby inhibits demethylation of histone H3 at 'Lys-4' (in vitro) (By similarity). During EMT, involved with LOXL2 in negatively regulating pericentromeric heterochromatin transcription (PubMed:24239292). SNA11 recruits LOXL2 to pericentromeric regions to oxidize histone H3 and repress transcription which leads to release of heterochromatin component CBX5/HP1A, enabling chromatin reorganization and acquisition of mesenchymal traits (PubMed:24239292). Associates with EGR1 and SP1 to mediate 12-O- tetradecanoylphorbol-13-acetate (TPA)-induced up-regulation of CDKN2B, possibly by binding to the CDKN2B promoter region 5'-TCACA-3'. In addition, may also activate the CDKN2B promoter by itself.[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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