

Product datasheet for **RN203057**

Snapin (NM_001025648) Rat Untagged Clone

Product data:

| | |
|---------------------------|------------------------------------------------------------------------------------|
| Product Type: | Expression Plasmids |
| Product Name: | Snapin (NM_001025648) Rat Untagged Clone |
| Tag: | Tag Free |
| Symbol: | Snapin |
| Synonyms: | Snapap |
| Mammalian Cell Selection: | Neomycin |
| Vector: | pCMV6-Entry (PS100001) |
| E. coli Selection: | Kanamycin (25 ug/mL) |
| Fully Sequenced ORF: | >RN203057 representing NM_001025648 Red=Cloning site Blue=ORF Orange=Stop codon |

TTTTGTAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**CGATCGCC**

ATGTTGGTTGCACATTTCTCTTTACAGAACTGTGCCGGATCAATGAGGATCAGAAGGTGGCCCTGGATC
TGGACCCCTATGTTAAGAAGCTGCTTAATGCCAGGCGCGAGTTGTCTTGGTCAACAATATTTTACAGAA
TGCACAGGAACGACTAAGGCGTTAAACCACAGTGTGGCCAAGGAAACAGCCCGCAGGAGGCCATGCTG
GATTCAGGAGTTACCCTCCTGGTCTCCAAGCAA**TAA**

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

| | |
|--------------------|--------------|
| Restriction Sites: | Sgfl-MluI |
| ACCN: | NM_001025648 |
| Insert Size: | 249 bp |

OTI Disclaimer: Our molecular clone sequence data has been matched to the reference identifier above as a point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative RNA splicing form or single nucleotide polymorphism (SNP).

Components: The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).



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Reconstitution Method:

1. Centrifuge at 5,000xg for 5min.
2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.
3. Close the tube and incubate for 10 minutes at room temperature.
4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.
5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of shipping when stored at -20°C.

RefSeq: [NM_001025648.1](#), [NP_001020819.1](#)

RefSeq Size: 1636 bp

RefSeq ORF: 249 bp

Locus ID: 295217

Cytogenetics: 2q34

Gene Summary: Component of the BLOC-1 complex, a complex that is required for normal biogenesis of lysosome-related organelles (LRO), such as platelet dense granules and melanosomes. In concert with the AP-3 complex, the BLOC-1 complex is required to target membrane protein cargos into vesicles assembled at cell bodies for delivery into neurites and nerve terminals. The BLOC-1 complex, in association with SNARE proteins, is also proposed to be involved in neurite extension. Plays a role in intracellular vesicle trafficking and synaptic vesicle recycling. May modulate a step between vesicle priming, fusion and calcium-dependent neurotransmitter release through its ability to potentiate the interaction of synaptotagmin with the SNAREs and the plasma-membrane-associated protein SNAP25. Its phosphorylation state influences exocytotic protein interactions and may regulate synaptic vesicle exocytosis. May also have a role in the mechanisms of SNARE-mediated membrane fusion in non-neuronal cells (PubMed:10195194, PubMed:11283605). As part of the BORC complex may play a role in lysosomes movement and localization at the cell periphery. Associated with the cytosolic face of lysosomes, the BORC complex may recruit ARL8B and couple lysosomes to microtubule plus-end-directed kinesin motor (By similarity).[UniProtKB/Swiss-Prot Function] Transcript Variant: This variant (2) contains an additional segment in the 5' region and initiates translation at a downstream start codon compared to variant 1. These differences produce a unique 5' UTR and a protein (isoform 2) with a shorter and distinct N-terminus, compared to isoform 1. Sequence Note: This RefSeq record was created from transcript and genomic sequence data to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.