

# Product datasheet for MC201802

## Sh3glb1 (NM\_019464) Mouse Untagged Clone

## **Product data:**

#### OriGene Technologies, Inc.

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Product Type:	Expression Plasmids
Product Name:	Sh3glb1 (NM_019464) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Sh3glb1
Synonyms:	AA409932; Al314629; AU015566; Bif-1; mKlAA0491
Mammalian Cell Selection:	Neomycin
Vector:	PCMV6-Kan/Neo (PCMV6KN)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>BC024362 sequence for NM_019464 GCCGTCGCCGCCGCCCGGCGCCCAGCCCGGCGCGCGCGCCGCCGC
<b>Restriction Sites:</b>	Rsrll-Notl



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<b>O</b> RÏGENE S	h3glb1 (NM_019464) Mouse Untagged Clone – MC201802
ACCN:	NM_019464
Insert Size:	1098 bp
OTI Disclaimer:	Due to the inherent nature of this plasmid, standard methods to replicate additional amounts of DNA in E. coli are highly likely to result in mutations and/or rearrangements. Therefore, OriGene does not guarantee the capability to replicate this plasmid DNA. Additional amounts of DNA can be purchased from OriGene with batch-specific, full-sequence verification at a reduced cost. Please contact our customer care team at <u>custsupport@origene.com</u> or by calling 301.340.3188 option 3 for pricing and delivery.
	The molecular sequence of this clone aligns with the gene accession number as a point of reference only. However, individual transcript sequences of the same gene can differ through naturally occurring variations (e.g. polymorphisms), each with its own valid existence. This clone is substantially in agreement with the reference, but a complete review of all prevailing variants is recommended prior to use. <u>More info</u>
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).
Reconstitution Met	<ul> <li>thod: 1. Centrifuge at 5,000xg for 5min.</li> <li>2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.</li> <li>3. Close the tube and incubate for 10 minutes at room temperature.</li> <li>4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.</li> <li>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.</li> </ul>
RefSeq:	BC024362, AAH24362
RefSeq Size:	1579 bp
RefSeq ORF:	1098 bp
Locus ID:	54673
UniProt ID:	<u>Q9]K48</u>
Cytogenetics:	3 H2

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### **GRIGENE** Sh3glb1 (NM\_019464) Mouse Untagged Clone – MC201802

May be required for normal outer mitochondrial membrane dynamics. Required for Gene Summary: coatomer-mediated retrograde transport in certain cells (PubMed:17086176). May recruit other proteins to membranes with high curvature. May promote membrane fusion (By similarity). Involved in activation of caspase-dependent apoptosis by promoting BAX/BAK1 activation (PubMed:16227588). Isoform 1 acts proapoptotic in fibroblasts (PubMed:24523556). Involved in caspase-independent apoptosis during nutrition starvation and involved in the regulation of autophagy. Activates lipid kinase activity of PIK3C3 during autophagy probably by associating with the PI3K complex II (PI3KC3-C2). Associated with PI3KC3-C2 during autophagy may regulate the trafficking of ATG9A from the Golgi complex to the peripheral cytoplasm for the formation of autophagosomes by inducing Golgi membrane tubulation and fragmentation. Involved in regulation of degradative endocytic trafficking and cytokinesis, probably in the context of PI3KC3-C2 (By similarity). Isoform 2 acts antiapoptotic in neuronal cells; involved in maintenance of mitochondrial morphology and promotes neuronal viability (PubMed:24523556).[UniProtKB/Swiss-Prot Function] Transcript Variant: This variant (2) lacks two alternate in-frame exons in the coding region, compared to variant 1. The encoded isoform (2) is shorter, 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.

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