

OriGene Technologies, Inc.

9620 Medical Center Drive, Ste 200 Rockville, MD 20850, US Phone: +1-888-267-4436 https://www.origene.com techsupport@origene.com EU: info-de@origene.com CN: techsupport@origene.cn

Product datasheet for SR313620

MURF1 (TRIM63) Human siRNA Oligo Duplex (Locus ID 84676)

Product data:

Product Type:	siRNA Oligo Duplexes
Purity:	HPLC purified
Quality Control:	Tested by ESI-MS
Sequences:	Available with shipment
Stability:	One year from date of shipment when stored at -20°C.
# of transfections:	Approximately 330 transfections/2nmol in 24-well plate under optimized conditions (final conc. 10 nM).
Note:	Single siRNA duplex (10nmol) can be ordered.
RefSeq:	<u>NM 032588</u>
UniProt ID:	<u>Q969Q1</u>
Synonyms:	IRF; MURF1; MURF2; RNF28; SMRZ
Components:	TRIM63 (Human) - 3 unique 27mer siRNA duplexes - 2 nmol each (Locus ID 84676) Included - SR30004, Trilencer-27 Universal Scrambled Negative Control siRNA Duplex - 2 nmol Included - SR30005, RNAse free siRNA Duplex Resuspension Buffer - 2 ml
Summary:	This gene encodes a member of the RING zinc finger protein family found in striated muscle and iris. The product of this gene is an E3 ubiquitin ligase that localizes to the Z-line and M- line lattices of myofibrils. This protein plays an important role in the atrophy of skeletal and cardiac muscle and is required for the degradation of myosin heavy chain proteins, myosin light chain, myosin binding protein, and for muscle-type creatine kinase. [provided by RefSeq, Feb 2012]



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Performance Guaranteed:	OriGene guarantees that at least two of the three Dicer-Substrate duplexes in the kit will provide at least 70% or more knockdown of the target mRNA when used at 10 nM concentration by quantitative RT-PCR when the TYE-563 fluorescent transfection control duplex (cat# SR30002) indicates that >90% of the cells have been transfected and the HPRT positive control (cat# SR30003) provides 90% knockdown efficiency.
	For non-conforming siRNA, requests for replacement product must be made within ninety (90) days from the date of delivery of the siRNA kit. To arrange for a free replacement with newly designed duplexes, 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 siRNA control (quantitative RT-PCR data required).

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