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 SR310310

ST7L Human siRNA Oligo Duplex (Locus ID 54879)

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:	NM_001308264, NM_017744, NM_138727, NM_138728, NM_138729, NM_139195, NM_139196, NM_198327, NM_198328
UniProt ID:	Q8TDW4
Synonyms:	FAM4B; ST7R; STLR
Components:	ST7L (Human) - 3 unique 27mer siRNA duplexes - 2 nmol each (Locus ID 54879) 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 was identified by its similarity to the ST7 tumor suppressor gene found in the chromosome 7q31 region. This gene is clustered in a tail-to-tail manner with the WNT2B gene in a chromosomal region known to be deleted and rearranged in a variety of cancers. Several transcript variants encoding many different isoforms have been described, but some have not been fully characterized. [provided by RefSeq, Feb 2011]

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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).