

Product datasheet for **SR308688**

SLITRK5 Human siRNA Oligo Duplex (Locus ID 26050)

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_015567
UniProt ID:	O94991
Synonyms:	bA364G4.2; LRRC11
Components:	SLITRK5 (Human) - 3 unique 27mer siRNA duplexes - 2 nmol each (Locus ID 26050) Included - SR30004, Trilencer-27 Universal Scrambled Negative Control siRNA Duplex - 2 nmol Included - SR30005, RNase free siRNA Duplex Resuspension Buffer - 2 ml
Summary:	Members of the SLITRK family, such as SLITRK5, are integral membrane proteins with 2 N-terminal leucine-rich repeat (LRR) domains similar to those of SLIT proteins (see SLIT1; MIM 603742). Most SLITRKs, including SLITRK5, also have C-terminal regions that share homology with neurotrophin receptors (see NTRK1; MIM 191315). SLITRKs are expressed predominantly in neural tissues and have neurite-modulating activity (Aruga et al., 2003 [PubMed 14557068]).[supplied by OMIM, Mar 2008]



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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).