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Product datasheet for SR309428

TAS2R9 Human siRNA Oligo Duplex (Locus ID 50835)

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_023917
UniProt ID:	Q9NYW1
Synonyms:	T2R9; TRB6
Components:	TAS2R9 (Human) - 3 unique 27mer siRNA duplexes - 2 nmol each (Locus ID 50835) 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 product belongs to the family of candidate taste receptors that are members of the G-protein-coupled receptor superfamily. These proteins are specifically expressed in the taste receptor cells of the tongue and palate epithelia. They are organized in the genome in clusters and are genetically linked to loci that influence bitter perception in mice and humans. In functional expression studies, they respond to bitter tastants. This gene maps to the taste receptor gene cluster on chromosome 12p13. [provided by RefSeq, Jul 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).

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