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Product datasheet for SR305249

ZNF214 Human siRNA Oligo Duplex (Locus ID 7761)

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_013249, NM_001354830, NM_001354831, NM_001354832, NM_001354833, NR_148988
UniProt ID:	Q9UL59
Synonyms:	BAZ-1; BAZ1
Components:	ZNF214 (Human) - 3 unique 27mer siRNA duplexes - 2 nmol each (Locus ID 7761) 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 is expressed predominantly in the testis and encodes a zinc finger protein that contains an N-terminal kruppel-associated box A (KRABA) domain and twelve zinc finger domains. This gene is located within one of three regions on chromosome 11p15 associated with Beckwith-Wiedemann syndrome, called Beckwith-Wiedemann syndrome chromosome region-2 (BWSCR2), and is thought to play a role in the etiology of this disease. [provided by RefSeq, Aug 2017]

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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).