

Product datasheet for **SR309829**

NIPA (ZC3HC1) Human siRNA Oligo Duplex (Locus ID 51530)

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_001282190 , NM_001282191 , NM_016478 , NM_001363701
UniProt ID:	Q86WB0
Synonyms:	HSPC216; NIPA
Components:	ZC3HC1 (Human) - 3 unique 27mer siRNA duplexes - 2 nmol each (Locus ID 51530) 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 an F-box-containing protein that is a component of an SCF-type E3 ubiquitin ligase complex that regulates the onset of cell division. The G2/M transition in the cell cycle requires the interaction of the proteins cyclin B1 and cyclin-dependent kinase 1. The activated ubiquitin ligase complex targets the protein cyclin B1 for degradation, preventing this transition to mitosis. [provided by RefSeq, Aug 2013]



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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).