

## Product datasheet for SR314133

## OriGene Technologies, Inc.

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## **NEK9 Human siRNA Oligo Duplex (Locus ID 91754)**

## **Product data:**

**Product Type:** siRNA Oligo Duplexes

**HPLC** purified **Purity:** 

**Quality Control:** Tested by ESI-MS

Available with shipment **Sequences:** 

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).

Single siRNA duplex (10nmol) can be ordered. Note: RefSeq: NM 001329237, NM 001329238, NM 033116

**UniProt ID:** Q8TD19

Synonyms: APUG; LCCS10; NC; NERCC; NERCC1

Components: NEK9 (Human) - 3 unique 27mer siRNA duplexes - 2 nmol each (Locus ID 91754)

Included - SR30004, Trilencer-27 Universal Scrambled Negative Control siRNA Duplex - 2 nmol

Included - SR30005, RNAse free siRNA Duplex Resuspension Buffer - 2 ml

This gene encodes a member of the NimA (never in mitosis A) family of serine/threonine **Summary:** 

> protein kinases. The encoded protein is activated in mitosis and, in turn, activates other family members during mitosis. This protein also mediates cellular processes that are

essential for interphase progression. [provided by RefSeq, Jul 2016]

**Performance** OriGene guarantees that at least two of the three Dicer-Substrate duplexes in the kit will **Guaranteed:** 

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).

