

## Product datasheet for SR303216

## OriGene Technologies, Inc.

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## PASD5 (NPAS1) Human siRNA Oligo Duplex (Locus ID 4861)

**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 001321086, NM 002517

**UniProt ID:** 099742

Synonyms: bHLHe11; MOP5; PASD5

Components: NPAS1 (Human) - 3 unique 27mer siRNA duplexes - 2 nmol each (Locus ID 4861)

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

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

The protein encoded by this gene is a member of the basic helix-loop-helix (bHLH)-PAS family **Summary:** 

> of transcription factors. Studies of a related mouse gene suggest that it functions in neurons. The exact function of this gene is unclear, but it may play protective or modulatory roles during late embryogenesis and postnatal development. [provided by RefSeq, Jul 2008]

**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).

