

# Product datasheet for SR422799

## Cep162 Mouse siRNA Oligo Duplex (Locus ID 382090)

### **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). Note: Single siRNA duplex (10nmol) can be ordered. **RefSeq:** NM 199316 **UniProt ID:** Q6ZQ06 Synonyms: 4922501C03Rik; mKIAA1009 **Components:** Cep162 (Mouse) - 3 unique 27mer siRNA duplexes - 2 nmol each (Locus ID 382090) Included - SR30004, Trilencer-27 Universal Scrambled Negative Control siRNA Duplex - 2 nmol Included - SR30005, RNAse free siRNA Duplex Resuspension Buffer - 2 ml Required to promote assembly of the transition zone in primary cilia. Acts by specifically Summary: recognizing and binding the axonemal microtubule. Localizes to the distal ends of centrioles before ciliogenesis and directly binds to axonemal microtubule, thereby promoting and restricting transition zone formation specifically at the cilia base. Required to mediate CEP290 association with microtubules (By similarity).[UniProtKB/Swiss-Prot Function]



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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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