

## Product datasheet for **SR312622**

### **MOBKL2B (MOB3B) Human siRNA Oligo Duplex (Locus ID 79817)**

#### **Product data:**

<b>Product Type:</b>	siRNA Oligo Duplexes
<b>Purity:</b>	HPLC purified
<b>Quality Control:</b>	Tested by ESI-MS
<b>Sequences:</b>	Available with shipment
<b>Stability:</b>	One year from date of shipment when stored at -20°C.
<b># of transfections:</b>	Approximately 330 transfections/2nmol in 24-well plate under optimized conditions (final conc. 10 nM).
<b>Note:</b>	Single siRNA duplex (10nmol) can be ordered.
<b>RefSeq:</b>	<a href="#">NM_024761</a>
<b>UniProt ID:</b>	<a href="#">Q86TA1</a>
<b>Synonyms:</b>	C9orf35; MOB1D; MOBKL2B
<b>Components:</b>	MOB3B (Human) - 3 unique 27mer siRNA duplexes - 2 nmol each (Locus ID 79817) Included - SR30004, Trilencer-27 Universal Scrambled Negative Control siRNA Duplex - 2 nmol Included - SR30005, RNase free siRNA Duplex Resuspension Buffer - 2 ml
<b>Summary:</b>	The protein encoded by this gene shares similarity with the yeast Mob1 protein. Yeast Mob1 binds Mps1p, a protein kinase essential for spindle pole body duplication and mitotic checkpoint regulation. This gene is located on the opposite strand as the interferon kappa precursor (IFNK) gene. [provided by RefSeq, Jul 2008]
<b>Performance Guaranteed:</b>	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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