

# Product datasheet for TL511756

## Cyp1b1 Mouse shRNA Plasmid (Locus ID 13078)

## **Product data:**

### OriGene Technologies, Inc.

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Product Type:	shRNA Plasmids
Product Name:	Cyp1b1 Mouse shRNA Plasmid (Locus ID 13078)
Locus ID:	13078
Synonyms:	CP1B; P4501b1
Vector:	pGFP-C-shLenti (TR30023)
E. coli Selection:	Chloramphenicol (34 ug/ml)
Mammalian Cell Selection:	Puromycin
Format:	Lentiviral plasmids
Components:	Cyp1b1 - Mouse, 4 unique 29mer shRNA constructs in lentiviral GFP vector(Gene ID = 13078). 5µg purified plasmid DNA per construct 29-mer scrambled shRNA cassette in pGFP-C-shLenti Vector, TR30021, included for free.
RefSeq:	<u>BC050063, NM 009994, NM 009994.1, NM 001364889</u>
UniProt ID:	<u>Q64429</u>



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#### **GRIGENE** Cyp1b1 Mouse shRNA Plasmid (Locus ID 13078) – TL511756

A cytochrome P450 monooxygenase involved in the metabolism of various endogenous Summary: substrates, including fatty acids, steroid hormones and vitamins (By similarity). Mechanistically, uses molecular oxygen inserting one oxygen atom into a substrate, and reducing the second into a water molecule, with two electrons provided by NADPH via cytochrome P450 reductase (NADPH--hemoprotein reductase) (By similarity). Exhibits catalytic activity for the formation of hydroxyestrogens from 17beta-estradiol (E2), namely 2- and 4hydroxy E2 (PubMed:23821647). Metabolizes testosterone and progesterone to B or D ring hydroxylated metabolites (By similarity). May act as a major enzyme for all-trans retinoic acid biosynthesis in extrahepatic tissues. Catalyzes two successive oxidative transformation of alltrans retinol to all-trans retinal and then to the active form all-trans retinoic acid (PubMed:15258110). Catalyzes the epoxidation of double bonds of certain PUFA. Converts arachidonic acid toward epoxyeicosatrienoic acid (EpETrE) regioisomers, 8,9-, 11,12-, and 14,15- EpETrE, that function as lipid mediators in the vascular system (PubMed:15258110). Additionally, displays dehydratase activity toward oxygenated eicosanoids hydroperoxyeicosatetraenoates (HpETEs). This activity is independent of cytochrome P450 reductase, NADPH, and O2 (By similarity). Also involved in the oxidative metabolism of xenobiotics, particularly converting polycyclic aromatic hydrocarbons and heterocyclic aryl amines procarcinogens to DNA-damaging products (By similarity). Plays an important role in retinal vascular development. Under ambient/hyperoxic O2 conditions, promotes angiogenesis and capillary morphogenesis of retinal endothelial cells and pericytes, likely by metabolizing the oxygenated products symptomatic of oxidative stress (PubMed:19005183, PubMed:20032512, PubMed:23568032). Also, contributes to oxidative homeostasis and ultrastructural organization and function of trabecular meshwork tissue through modulation of POSTN expression (PubMed:23979599).[UniProtKB/Swiss-Prot Function] shRNA Design: These shRNA constructs were designed against multiple splice variants at this gene locus. To be certain that your variant of interest is targeted, please contact <u>techsupport@origene.com</u>. If you need a special design or shRNA sequence, please utilize our custom shRNA service. Performance OriGene guarantees that the sequences in the shRNA expression cassettes are verified to **Guaranteed:** correspond to the target gene with 100% identity. One of the four constructs at minimum are guaranteed to produce 70% or more gene expression knock-down provided a minimum

For non-conforming shRNA, requests for replacement product must be made within ninety (90) days from the date of delivery of the shRNA kit. To arrange for a free replacement with newly designed constructs, 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 shRNA control (Western Blot data preferred).

transfection efficiency of 80% is achieved. Western Blot data is recommended over qPCR to evaluate the silencing effect of the shRNA constructs 72 hrs post transfection. To properly assess knockdown, the gene expression level from the included scramble control vector must

be used in comparison with the target-specific shRNA transfected samples.

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