

## Product datasheet for **TL500343**

### Cdyl Mouse shRNA Plasmid (Locus ID 12593)

#### Product data:

Product Type:	shRNA Plasmids
Product Name:	Cdyl Mouse shRNA Plasmid (Locus ID 12593)
Locus ID:	12593
Synonyms:	AI325931
Vector:	pGFP-C-shLenti (TR30023)
E. coli Selection:	Chloramphenicol (34 ug/ml)
Mammalian Cell Selection:	Puromycin
Format:	Lentiviral plasmids
Components:	Cdyl - Mouse, 4 unique 29mer shRNA constructs in lentiviral GFP vector(Gene ID = 12593). 5µg purified plasmid DNA per construct 29-mer scrambled shRNA cassette in pGFP-C-shLenti Vector, TR30021, included for free.
RefSeq:	<a href="#">BC055103</a> , <a href="#">BC062123</a> , <a href="#">NM_001123386</a> , <a href="#">NM_009881</a> , <a href="#">NM_001123386.1</a> , <a href="#">NM_009881.1</a> , <a href="#">NM_009881.2</a> , <a href="#">NM_009881.3</a>
UniProt ID:	<a href="#">Q9WTK2</a>



[View online »](#)

**Summary:** Isoform 2: Chromatin reader protein that recognizes and binds histone H3 trimethylated at 'Lys-9', dimethylated at 'Lys-27' and trimethylated at 'Lys-27' (H3K9me3, H3K27me2 and H3K27me3, respectively) (PubMed:12947414). Part of multimeric repressive chromatin complexes, where it is required for transmission and restoration of repressive histone marks, thereby preserving the epigenetic landscape (PubMed:12947414). Required for chromatin targeting and maximal enzymatic activity of Polycomb repressive complex 2 (PRC2); acts as a positive regulator of PRC2 activity by bridging the pre-existing histone H3K27me3 and newly recruited PRC2 on neighboring nucleosomes (By similarity). Acts as a corepressor for REST by facilitating histone-lysine N-methyltransferase EHMT2 recruitment and H3K9 dimethylation at REST target genes for repression (By similarity). Involved X chromosome inactivation in females: recruited to Xist RNA-coated X chromosome and facilitates propagation of H3K9me2 by anchoring EHMT2 (PubMed:24144980). Required for neuronal migration during brain development by repressing expression of RHOA (PubMed:28076783). In addition to act as a chromatin reader, acts as a hydro-lyase (By similarity). Shows crotonyl-coA hydratase activity by mediating the conversion of crotonyl-CoA ((2E)-butenoyl-CoA) to beta-hydroxybutyryl-CoA (3-hydroxybutanoyl-CoA), thereby acting as a negative regulator of histone crotonylation (By similarity). Histone crotonylation is required during spermatogenesis; down-regulation of histone crotonylation by CDYL regulates the reactivation of sex chromosome-linked genes in round spermatids and histone replacement in elongating spermatids (PubMed:28803779). May have histone acetyltransferase activity; such activity is however unsure in vivo (PubMed:12072557).[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 [techsupport@origene.com](mailto:techsupport@origene.com). If you need a special design or shRNA sequence, please utilize our [custom shRNA service](#).

**Performance Guaranteed:** OriGene guarantees that the sequences in the shRNA expression cassettes are verified to 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 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.

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](mailto: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).