

Product datasheet for **TG513199**

Rara Mouse shRNA Plasmid (Locus ID 19401)

Product data:

Product Type:	shRNA Plasmids
Product Name:	Rara Mouse shRNA Plasmid (Locus ID 19401)
Locus ID:	19401
Synonyms:	Nr1b1; RAR; RARalpha1
Vector:	pGFP-V-RS (TR30007)
E. coli Selection:	Kanamycin
Mammalian Cell Selection:	Puromycin
Format:	Retroviral plasmids
Components:	Rara - Mouse, 4 unique 29mer shRNA constructs in retroviral GFP vector(Gene ID = 19401). 5µg purified plasmid DNA per construct 29-mer scrambled shRNA cassette in pGFP-V-RS Vector, TR30013, included for free.
RefSeq:	BC010216 , NM_001176528 , NM_001177302 , NM_001177303 , NM_009024 , NM_001177303.1 , NM_009024.1 , NM_009024.2 , NM_001176528.1 , NM_001177302.1 , BC038266 , BC040383 , BC090396 , NM_001361954
UniProt ID:	P11416



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Summary:

Receptor for retinoic acid (PubMed:17205979). Retinoic acid receptors bind as heterodimers to their target response elements in response to their ligands, all-trans or 9-cis retinoic acid, and regulate gene expression in various biological processes (PubMed:17205979). The RXR/RAR heterodimers bind to the retinoic acid response elements (RARE) composed of tandem 5'-AGGTCA-3' sites known as DR1-DR5 (PubMed:17205979). In the absence of ligand, the RXR-RAR heterodimers associate with a multiprotein complex containing transcription corepressors that induce histone deacetylation, chromatin condensation and transcriptional suppression (By similarity). On ligand binding, the corepressors dissociate from the receptors and associate with the coactivators leading to transcriptional activation (PubMed:17205979, PubMed:9230306, PubMed:19078967). Formation of heterocomplex with histone deacetylases might lead to inhibition of RARE DNA element binding and to transcriptional repression (By similarity). Transcriptional activation and RARE DNA element binding might be supported by the transcription factor KLF2 (By similarity). RARA plays an essential role in the regulation of retinoic acid-induced germ cell development during spermatogenesis (PubMed:15901285). Has a role in the survival of early spermatocytes at the beginning prophase of meiosis (PubMed:15901285, PubMed:17905941). In Sertoli cells, may promote the survival and development of early meiotic prophase spermatocytes (PubMed:10660575, PubMed:17905941). In concert with RARG, required for skeletal growth, matrix homeostasis and growth plate function (PubMed:19389355). Together with RXRA, positively regulates microRNA-10a expression, thereby inhibiting the GATA6/VCAM1 signaling response to pulsatile shear stress in vascular endothelial cells (By similarity). In association with HDAC3, HDAC5 and HDAC7 corepressors, plays a role in the repression of microRNA-10a and thereby promotes the inflammatory response (By similarity).[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. 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. Please provide your data indicating the transfection efficiency and measurement of gene expression knockdown compared to the scrambled shRNA control (Western Blot data preferred).