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Product datasheet for TR304299

G protein alpha S (GNAS) Human shRNA Plasmid Kit (Locus ID 2778)

Product data:

Product Type:	shRNA Plasmids
Product Name:	G protein alpha S (GNAS) Human shRNA Plasmid Kit (Locus ID 2778)
Locus ID:	2778
Synonyms:	AHO; C20orf45; GNAS1; GPSA; GSA; GSP; NESP; PITA3; POH; SCG6; SgVI
Vector:	pRS (TR20003)
E. coli Selection:	Ampicillin
Mammalian Cell Selection:	Puromycin
Format:	Retroviral plasmids
Components:	GNAS - Human, 4 unique 29mer shRNA constructs in retroviral untagged vector(Gene ID = 2778). 5µg purified plasmid DNA per construct 29-mer scrambled shRNA cassette in pRS Vector, TR30012, included for free.
RefSeq:	NM 000516, NM 001077488, NM 001077489, NM 001077490, NM 001309840, NM 001309842, NM 001309861, NM 001309883, NM 016592, NM 080425, NM 080426, NR 003259, NR 132272, NR 132273, NM 016592.1, NM 016592.2, NM 016592.3, NM 000516.1, NM 000516.2, NM 000516.3, NM 000516.4, NM 000516.5, NM 080425.1, NM 080425.2, NM 080425.3, NM 080426.1, NM 080426.2, NM 080426.3, NM 001077489.1, NM 001077489.2, NM 001077489.3, NM 001077490.1, NM 001077490.2, NM 001077488.1, NM 001077488.2, NM 001077488.3, BC002722, BC008855, BC022875, BC036081, BC066923, BC089157, BC104928, BC108315, BM894355, NM 080426.4, NM 001077488.5, NM 001077489.4, NM 016592.5, NM 000516.7
UniProt ID:	<u>Q5JWF2</u>



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CRIGENE G protein alpha S (GNAS) Human shRNA Plasmid Kit (Locus ID 2778) – TR304299

This locus has a highly complex imprinted expression pattern. It gives rise to maternally, Summary: paternally, and biallelically expressed transcripts that are derived from four alternative promoters and 5' exons. Some transcripts contain a differentially methylated region (DMR) at their 5' exons, and this DMR is commonly found in imprinted genes and correlates with transcript expression. An antisense transcript is produced from an overlapping locus on the opposite strand. One of the transcripts produced from this locus, and the antisense transcript, are paternally expressed noncoding RNAs, and may regulate imprinting in this region. In addition, one of the transcripts contains a second overlapping ORF, which encodes a structurally unrelated protein - Alex. Alternative splicing of downstream exons is also observed, which results in different forms of the stimulatory G-protein alpha subunit, a key element of the classical signal transduction pathway linking receptor-ligand interactions with the activation of adenylyl cyclase and a variety of cellular reponses. Multiple transcript variants encoding different isoforms have been found for this gene. Mutations in this gene result in pseudohypoparathyroidism type 1a, pseudohypoparathyroidism type 1b, Albright hereditary osteodystrophy, pseudopseudohypoparathyroidism, McCune-Albright syndrome, progressive osseus heteroplasia, polyostotic fibrous dysplasia of bone, and some pituitary tumors. [provided by RefSeq, Aug 2012]

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.

PerformanceOriGene guarantees that the sequences in the shRNA expression cassettes are verified toGuaranteed: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).

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