

## Product datasheet for **TR303260**

### MID1 Human shRNA Plasmid Kit (Locus ID 4281)

#### Product data:

Product Type:	shRNA Plasmids
Product Name:	MID1 Human shRNA Plasmid Kit (Locus ID 4281)
Locus ID:	4281
Synonyms:	BBBG1; FXY; GBBB1; MIDIN; OGS1; OS; OSX; RNF59; TRIM18; XPRF; ZNFX
Vector:	pRS (TR20003)
E. coli Selection:	Ampicillin
Mammalian Cell Selection:	Puromycin
Format:	Retroviral plasmids
Components:	MID1 - Human, 4 unique 29mer shRNA constructs in retroviral untagged vector(Gene ID = 4281). 5µg purified plasmid DNA per construct 29-mer scrambled shRNA cassette in pRS Vector, TR30012, included for free.
RefSeq:	<a href="#">NM_000381</a> , <a href="#">NM_001098624</a> , <a href="#">NM_001193277</a> , <a href="#">NM_001193278</a> , <a href="#">NM_001193279</a> , <a href="#">NM_001193280</a> , <a href="#">NM_001193281</a> , <a href="#">NM_033289</a> , <a href="#">NM_033290</a> , <a href="#">NM_033291</a> , <a href="#">NM_001347733</a> , <a href="#">NM_000381.1</a> , <a href="#">NM_000381.2</a> , <a href="#">NM_000381.3</a> , <a href="#">NM_033290.1</a> , <a href="#">NM_033290.2</a> , <a href="#">NM_033290.3</a> , <a href="#">NM_001098624.1</a> , <a href="#">NM_001098624.2</a> , <a href="#">NM_001193281.1</a> , <a href="#">NM_001193280.1</a> , <a href="#">NM_001193279.1</a> , <a href="#">NM_001193278.1</a> , <a href="#">NM_033289.1</a> , <a href="#">NM_001193277.1</a> , <a href="#">NM_033291.1</a> , <a href="#">BC053626</a> , <a href="#">BC053626.1</a> , <a href="#">NM_033290.4</a> , <a href="#">NM_000381.4</a> , <a href="#">NM_033289.2</a>
UniProt ID:	<a href="#">O15344</a>



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<b>Summary:</b>	<p>The protein encoded by this gene is a member of the tripartite motif (TRIM) family, also known as the 'RING-B box-coiled coil' (RBCC) subgroup of RING finger proteins. The TRIM motif includes three zinc-binding domains, a RING, a B-box type 1 and a B-box type 2, and a coiled-coil region. This protein forms homodimers which associate with microtubules in the cytoplasm. The protein is likely involved in the formation of multiprotein structures acting as anchor points to microtubules. Mutations in this gene have been associated with the X-linked form of Opitz syndrome, which is characterized by midline abnormalities such as cleft lip, laryngeal cleft, heart defects, hypospadias, and agenesis of the corpus callosum. This gene was also the first example of a gene subject to X inactivation in human while escaping it in mouse. Alternative promoter use, alternative splicing and alternative polyadenylation result in multiple transcript variants that have different tissue specificities. [provided by RefSeq, Dec 2016]</p>
<b>shRNA Design:</b>	<p>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 <a href="mailto:techsupport@origene.com">techsupport@origene.com</a>. If you need a special design or shRNA sequence, please utilize our <a href="#">custom shRNA service</a>.</p>
<b>Performance Guaranteed:</b>	<p>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.</p> <p>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 <a href="mailto:techsupport@origene.com">techsupport@origene.com</a>. Please provide your data indicating the transfection efficiency and measurement of gene expression knockdown compared to the scrambled shRNA control (Western Blot data preferred).</p>