DECODING LIFE: GENOMICS & PROTEOMICS

OriGene Technologies, Inc.
9620 Medical Center Drive, Ste 200
Rockville, MD 20850, US
Phone: +1-888-267-4436
https://www.origene.com
techsupport@origene.com
EU: info-de@origene.com
CN: techsupport@origene.cn

Product datasheet for SC204281

TEX264 (NM_015926) Human 3' UTR Clone

Product data:

Product Type:	3' UTR Clones
Symbol:	TEX264
Synonyms:	ZSIG11
Mammalian Cell Selection:	Neomycin
Vector:	pMirTarget (PS100062)
ACCN:	NM_015926
Insert Size:	337 bp
Insert Sequence:	>SC204281 3’UTR clone of NM_015926 The sequence shown below is from the reference sequence of NM_015926. The complete sequence of this clone may contain minor differences, such as SNPs. Blue=Stop Codon Red=Cloning site GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC CCCACTGCCCCTGAGAAGGGCAAGGAGTAACCCATGGCCTGCACCCTCCTGCAGTGCAGTTGCTGAGGA ACTGAGCAGACTCTCCAGCAGACTCTCCAGCCCTCTTCCTCCTTCCTCTGGGGGAGGAGGGGTTCCTGA GGGACCTGACTTCCCCTGCTCCAGGCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCCAGGG CCAGAGGAGCCAGGGACTATTTTCTGCACCAGCCCCCAGGGCTGCCACCCCTGTTGTGTCTTTTTTTCA GACTCACAGTGGAGCTTCCAGGACCCAGAATAAAGCCAATGATTTACTTGTTTCACCTGGA ACGCGTAAGCGGCCGCGGCATCTAGATTCGAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA CGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGG
Restriction Sites:	SgfI-MluI
OTI Disclaimer:	Our molecular clone sequence data has been matched to the sequence identifier above as a point of reference. Note that the complete sequence of this clone is largely the same as the reference sequence but may contain minor differences , e.g., single nucleotide polymorphisms (SNPs).
Components:	The cDNA clone is shipped in a 2-D bar-coded Matrix tube as 10 ug dried plasmid DNA. The package also includes 100 pmols of both the corresponding 5' and 3' vector primers in separate vials.

View online »

Note:	Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um filter is required.
RefSeq:	NM_015926.6
Summary:	Major reticulophagy (also called ER-phagy) receptor that acts independently of other candidate reticulophagy receptors to remodel subdomains of the endoplasmic reticulum into autophagosomes upon nutrient stress, which then fuse with lysosomes for endoplasmic reticulum turnover (PubMed:31006538, PubMed:31006537). The ATG8-containing isolation membrane (IM) cradles a tubular segment of TEX264-positive ER near a three-way junction, allowing the formation of a synapse of 2 juxtaposed membranes with trans interaction between the TEX264 and ATG8 proteins (PubMed:31006537). Expansion of the IM would extend the capture of ER, possibly through a 'zipper-like' process involving continued trans TEX264-ATG8 interactions, until poorly understood mechanisms lead to the fission of relevant membranes and, ultimately, autophagosomal membrane closure (PubMed:31006537). [UniProtKB/Swiss-Prot Function]
Locus ID:	51368
MW:	12.3