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Product datasheet for SC328771

MITF (NM_001184967) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	MITF (NM_001184967) Human Untagged Clone
Tag:	Tag Free
Symbol:	MITF
Synonyms:	bHLHe32; CMM8; COMMAD; MI; WS2; WS2A
Mammalian Cell Selection:	None
Vector:	pCMV6-XL5
E. coli Selection:	Ampicillin (100 ug/mL)
Fully Sequenced ORF:	>OriGene ORF sequence for NM_001184967 edited ATGACATCACGCATCTTGCTACGCCAGCAACTCATGCGTGAGCAGATGCAGGAGCAGGAG CGCAGGGAGCAGCAGCAGAAGCTGCAGGCGGCCCAGTTCATGCAACAGAGAGTGCCCGTG AGTCAGACACCAGCCATAAACGTCAGTGTGCCCACCACCCTTCCCTCTGCCACGCAGGTG CCGATGGAAGTCCTTAAGGTGCAGACCCACCTCGAAAACCCCACCAAGTACCACATACAG CAAGCCCAACGGCAGCAGGTAAAGCAGTACCTTTCTACCACTTTAGCAAATAAACATGCC AACCAAGTCCTGAGCTTGCCATGTCCAAACCAGCCTGGCGATCATGTCATGCCACCGGTG CCGGGGAGCAGCGCACCCAACAGCCCCATGGCTATGCTTACGCTTAACTCCAACTGTGAA AAAGAGGGATTTTATAAGTTTGAAGAGCAAAACAGGGCAGAGAGCGAGTGCCCAGGCATG AACACACATTCACGAGCGTCCTGTATGCAGATGGATGATGTAATCGATGACATCATTAGC CTAGAATCAAGTTATAATGAGGAAATCTTGGGCTTGATGGATCCTGCTTTGCAAATGGCA AATACGTTGCCTGTCTCGGGAAACTTGATTGATCTTTATGGAAACCAAGGTCTGCCCCCA CCAGGCCTCACCATCAGCAACTCCTGTCCAGCCAACCTTCCCAACATAAAAAGGGAGCTC ACAGAGTCTGAAGCAAGAGCACTGGCCAAAGAGAGGCAGAAAAAGGACAATCACAACCTG ATTGAACGAAGAAGAAGATTTAACATAAATGACCGCATTAAAGAACTAGGTACTTTGATT CCCAAGTCAAATGATCCAGACATGCGCTGGAACAAGGGAACCATCTTAAAAGCATCCGTG GACTATATCCGAAAGTTGCAACGAGAACAGCAACGCGCAAAAGAACTTGAAAACCGACAG AAGAAACTGGAGCACGCCAACCGGCATTTGTTGCTCAGAATACAGGAACTTGAAATGCAG GCTCGAGCTCATGGACTTTCCCTTATTCCATCCACGGGTCTCTGCTCTCCAGATTTGGTG AATCGGATCATCAAGCAAGAACCCGTTCTTGAGAACTGCAGCCAAGACCTCCTTCAGCAT CATGCAGACCTAACCTGTACAACAACTCTCGATCTCACGGATGGCACCATCACCTTCAAC AACAACCTCGGAACTGGGACTGAGGCCAACCAAGCCTATAGTGTCCCCACAAAAATGGGA TCCAAACTGGAAGACATCCTGATGGACGACACCCTTTCTCCCGTCGGTGTCACTGATCCA CTCCTTTCCTCAGTGTCCCCCGGAGCTTCCAAAACAAGCAGCCGGAGGAGCAGTATGAGC ATGGAAGAGACGGAGCACACTTGTTAG
Restriction Sites:	Please inquire

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ACCN:	NM_001184967
Insert Size:	1400 bp
OTI Disclaimer:	Our molecular clone sequence data has been matched to the reference identifier above as a point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative RNA splicing form or single nucleotide polymorphism (SNP).
OTI Annotation:	The ORF of this clone has been fully sequenced and found to be a perfect match to NM_001184967.1.
Components:	The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).
Reconstitution Method:	1. Centrifuge at 5,000xg for 5min. 2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA. 3. Close the tube and incubate for 10 minutes at room temperature. 4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom. 5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of shipping when stored at -20°C.
RefSeq:	NM_001184967.1, NP_001171896.1
RefSeq Size:	4685 bp
RefSeq ORF:	1407 bp
Locus ID:	4286
UniProt ID:	O75030
Cytogenetics:	3p13
Protein Families:	Druggable Genome, Transcription Factors
Protein Pathways:	Melanogenesis, Melanoma, Pathways in cancer
Gene Summary:	The protein encoded by this gene is a transcription factor that contains both basic helix-loop-helix and leucine zipper structural features. The encoded protein regulates melanocyte development and is responsible for pigment cell-specific transcription of the melanogenesis enzyme genes. Heterozygous mutations in the this gene cause auditory-pigmentary syndromes, such as Waardenburg syndrome type 2 and Tietz syndrome. [provided by RefSeq, Aug 2017] Transcript Variant: This variant (7) differs in the 5' UTR, lacks a portion of the 5' coding region, and initiates translation at a downstream start codon, compared to variant 1. The encoded isoform (7) is shorter than isoform 1. Sequence Note: This RefSeq record was created from transcript and genomic sequence data to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.

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