Product datasheet for SC328516

MAGEA8 (NM_001166400) Human Untagged Clone

Product data:

|	
Product Type:	Expression Plasmids
Product Name:	MAGEA8 (NM_001166400) Human Untagged Clone
Tag:	Tag Free
Symbol:	MAGEA8
Synonyms:	CT1.8; MAGE8
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC328516 representing NM_001166400. Blue=Insert sequence Red=Cloning site Green=Tag(s)

GCTCGTTTAGTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG
GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC
ATGCTTCTTGGGCAGAAGAGTCAGCGCTACAAGGCTGAGGAAGGCCTTCAGGCCCAAGGAGAGGCACCA
GGGCTTATGGATGTGCAGATTCCCACAGCTGAGGAGCAGAAGGCTGCATCCTCCTCCTCTACTCTGATC
ATGGGAACCCTTGAGGAGGTGACTGATTCTGGGTCACCAAGTCCTCCCCAGAGTCCTGAGGGTGCCTCC
TCTTCCCTGACTGTCACCGACAGCACTCTGTGGAGCCAATCCGATGAGGGTTCCAGCAGCAATGAAGAG
GAGGGGCCAAGCACCTCCCCGGACCCAGCTCACCTGGAGTCCCTGTTCCGGGAAGCACTTGATGAGAAA
GTGGCTGAGTTAGTTCGTTTCCTGCTCCGCAAATATCAAATTAAGGAGCCGGTCACAAAGGCAGAAATG
CTTGAGAGTGTCATCAAAAATTACAAGAACCACTTTCCTGATATCTTCAGCAAAGCCTCTGAGTGCATG
CAGGTGATCTTTGGCATTGATGTGAAGGAAGTGGACCCTGCCGGCCACTCCTACATCCTTGTCACCTGC
CTGGGCCTCTCCTATGATGGCCTGCTGGGTGATGATCAGAGTACGCCCAAGACCGGCCTCCTGATAATC
GTCCTGGGCATGATCTTAATGGAGGGCAGCCGCGCCCCGGAGGAGGCAATCTGGGAAGCGTTGAGTGTG
ATGGGGCTGTATGATGGGAGGGAGCACAGTGTCTATTGGAAGCTCAGGAAGCTGCTCACCCAAGAGTGG
GTGCAGGAGAACTACCTGGAGTACCGCCAGGCGCCCGGCAGTGATCCTGTGCGCTACGAGTTCCTGTGG
GGTCCAAGGGCCCTTGCTGAAACCAGCTATGTGAAAGTCCTGGAGCATGTGGTCAGGGTCAATGCAAGA
GTTCGCATTTCCTACCCATCCCTGCATGAAGAGGCTTTGGGAGAGGAGAAAGGAGTTTGA
ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC

Restriction Sites:	SgfI-MluI

View online »

Plasmid Map:
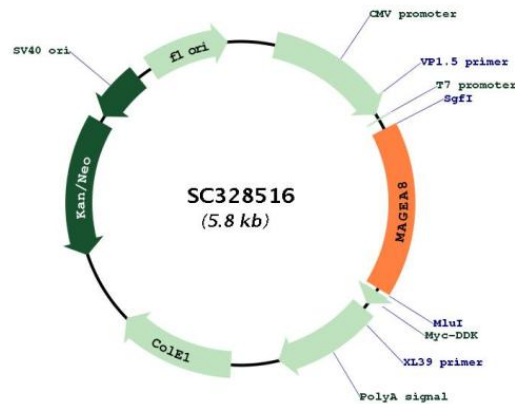
ACCN:	NM_001166400
Insert Size:	957 bp
OTI Disclaimer:	Our molecular clone sequence data has been matched to the reference identifier above as a point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative RNA splicing form or single nucleotide polymorphism (SNP).
OTI Annotation:	This TrueClone is provided through our Custom Cloning Process that includes sub-cloning into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA.
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_001166400.1
RefSeq Size:	2139 bp
RefSeq ORF:	957 bp

Locus ID:	4107
UniProt ID:	P43361
Cytogenetics:	Xq28
MW:	35.2 kDa
Gene Summary:	This gene is a member of the MAGEA gene family. The members of this family encode proteins with 50 to 80% sequence identity to each other. The promoters and first exons of the MAGEA genes show considerable variability, suggesting that the existence of this gene family enables the same function to be expressed under different transcriptional controls. The MAGEA genes are clustered at chromosomal location Xq28. They have been implicated in some hereditary disorders, such as dyskeratosis congenita. Multiple alternatively spliced variants, encoding the same protein, have been identified. [provided by RefSeq, Oct 2009] Transcript Variant: This variant (1) represents the longest transcript. Variants 1, 2 and 3 all encode the same protein. 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.