

Product datasheet for **MC225827**

Vma21 (NM_001290780) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Vma21 (NM_001290780) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Vma21
Synonyms:	2610030H06Rik; AI840175
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Restriction Sites:	Sgfl-Mlul
ACCN:	NM_001290780
Insert Size:	405 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:	Clone contains native stop codon, and expresses the complete ORF without any c-terminal tag.
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:	<ol style="list-style-type: none">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_001290780.1 , NP_001277709.1



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RefSeq Size: 4322 bp

RefSeq ORF: 405 bp

Locus ID: 67048

Cytogenetics: X A7.3

Gene Summary: Required for the assembly of the V0 complex of the vacuolar ATPase (V-ATPase) in the endoplasmic reticulum.[UniProtKB/Swiss-Prot Function]
Transcript Variant: This variant (1) encodes the longest isoform (1). Sequence Note: The RefSeq transcript and protein were derived from genomic sequence to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on alignments.