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Product datasheet for SC302832

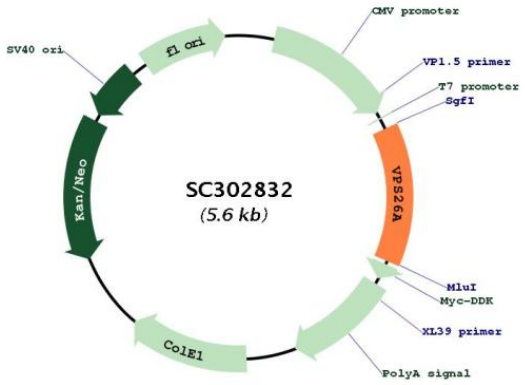
VPS26 (VPS26A) (NM_001035260) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	VPS26 (VPS26A) (NM_001035260) Human Untagged Clone
Tag:	Tag Free
Symbol:	VPS26A
Synonyms:	HB58; Hbeta58; PEP8A; VPS26
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC302832 representing NM_001035260. Blue=Insert sequence Red=Cloning site Green=Tag(s) GCTCGTTTAGTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC ATGAGTTTTCTTGGAGGCTTTTTTGGTCCAATTTGTGAGATCGATATTGTTCTTAATGATGGGGAAACC AGGAAAATGGCAGAAATGAAAACTGAAGATGGCAAAGTAGAAAAACACTATCTCTTCTATGACGGAGAA TCCGTTTCAGGAAAGGTAAACCTAGCCTTTAAGCAACCTGGAAAGAGGCTAGAACACCAAGGAATTAGA ATTGAATTTGTAGGTCAAATTGAACTTTTCAATGACAAGAGTAATACTCATGAATTTGTAAACCTAGTG AAAGAACTAGCCTTACCTGGAGAACTGACTCAGAGCAGAAGTTATGATTTTGAATTTATGCAAGTTGAA AAGCCATATGAATCTTACATCGGTGCCAATGTCCGCTTGAGGTATTTTCTTAAAGTGACAATAGTGAGA AGACTGACAGATTTGGTAAAAGAGTATGATCTTATTGTTCACCAGCTTGCCACCTATCCTGATGTTAAC AACTCTATTAAGATGGAAGTGGGCATTGAAGATTGTCTACATATAGAATTTGAATATAATAAATCAAAG TATCATTTAAAGGATGTGATTGTTGGAAAAATTTACTTCTTATTAGTAAGAATAAAAATACAACATATG GAGTTACAGCTGATCAAAAAAGAGATCACAGGAATTGGACCCAGTACCACAACAGAAACAGAAACAATC GCCAAATATGAAATAATGGATGGTGCACCAGTAAAAGGAGATAATTTTATGGAGAAAAGCTCCTGA ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
Restriction Sites:	SgfI-MluI

View online »

Plasmid Map:



ACCN:	NM_001035260
Insert Size:	756 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_001035260.2

RefSeq Size:	4137 bp
RefSeq ORF:	756 bp
Locus ID:	9559
UniProt ID:	O75436
Cytogenetics:	10q22.1
MW:	28.9 kDa
Gene Summary:	This gene belongs to a group of vacuolar protein sorting (VPS) genes. The encoded protein is a component of a large multimeric complex, termed the retromer complex, involved in retrograde transport of proteins from endosomes to the trans-Golgi network. The close structural similarity between the yeast and human proteins that make up this complex suggests a similarity in function. Expression studies in yeast and mammalian cells indicate that this protein interacts directly with VPS35, which serves as the core of the retromer complex. Alternative splicing results in multiple transcript variants encoding different isoforms. [provided by RefSeq, Jul 2008] Transcript Variant: This variant (2) lacks an exon in the 3' coding region which results in a frameshift and early translation termination, compared to variant 1. The encoded isoform (2) has a shorter and distinct C-terminus, compared to 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.