

## Product datasheet for SC301031

### VPS24 (CHMP3) (NM\_001005753) Human Untagged Clone

#### Product data:

Product Type:	Expression Plasmids
Product Name:	VPS24 (CHMP3) (NM_001005753) Human Untagged Clone
Tag:	Tag Free
Symbol:	VPS24
Synonyms:	CGI-149; NEDF; VPS24
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC301031 representing NM_001005753. Blue=Insert sequence Red=Cloning site Green=Tag(s)

GCTCGTTTAGTGAACCGTCAGAATTTGTAAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG  
 GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC  
 ATGATCAGGTCAAGGAAGGCTGTGAGCAAGCTGTATGCATCCAAAGCACACATGAAGTCACTGCTCATG  
 GGGATGAAGAACCAGCTCGCGGTCTTGCAGTGGCTGGTTCCTGCAGAAGAGCACAGAAGTGATGAAG  
 GCCATGCAAAGTCTTGTGAAGATTCCAGAGATTGAGGCCACCATGAGGGAGTTGTCCAAAGAAATGATG  
 AAGGCTGGGATCATAGAGGAGATGTTAGAGGACACTTTTGAAGCATGGACGATCAGGAAGAAATGGAG  
 GAAGAAGCAGAAATGAAATTGACAGAATTCTCTTTGAAATTACAGCAGGGGCTTGGGCAAAGCACCC  
 AGTAAAGTGACTGATGCCCTTCCAGAGCCAGAACCTCCAGGAGCGATGGCTGCCTCAGAGGATGAGGAG  
 GAGGAGGAAGAGGCTCTGGAGGCCATGCAGTCCCGGCTGGCCACACTCCGCAGCTAG  
 ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT  
 TACAAGGATGACGACGATAAGGTTAAACGGCCGGC

Restriction Sites:	SgfI-MluI
ACCN:	NM_001005753
Insert Size:	471 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).


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<b>OTI Annotation:</b>	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.
<b>Components:</b>	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).
<b>Reconstitution Method:</b>	<ol style="list-style-type: none"> <li>1. Centrifuge at 5,000xg for 5min.</li> <li>2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.</li> <li>3. Close the tube and incubate for 10 minutes at room temperature.</li> <li>4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.</li> <li>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.</li> </ol>
<b>RefSeq:</b>	<u><a href="#">NM_001005753.2</a></u>
<b>RefSeq Size:</b>	3133 bp
<b>RefSeq ORF:</b>	471 bp
<b>Locus ID:</b>	51652
<b>UniProt ID:</b>	<u><a href="#">Q9Y3E7</a></u>
<b>Cytogenetics:</b>	2p11.2
<b>Protein Pathways:</b>	Endocytosis
<b>MW:</b>	17.3 kDa
<b>Gene Summary:</b>	<p>This gene encodes a protein that sorts transmembrane proteins into lysosomes/vacuoles via the multivesicular body (MVB) pathway. This protein, along with other soluble coiled-coil containing proteins, forms part of the ESCRT-III protein complex that binds to the endosomal membrane and recruits additional cofactors for protein sorting into the MVB. This protein may also co-immunoprecipitate with a member of the IFG-binding protein superfamily. Alternative splicing results in multiple transcript variants. Read-through transcription also exists between this gene and the upstream ring finger protein 103 (RNF103) gene. [provided by RefSeq, Nov 2010]</p> <p>Transcript Variant: This variant (2) lacks an alternate exon in the 5' coding region, compared to variant 1. This results in translation initiation from a downstream start codon and an isoform (2, also known as Vps24beta) that has a shorter N-terminus, compared to isoform 1.</p> <p>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.</p>