

## Product datasheet for **SC309535**

### **PACE4 (PCSK6) (NM\_138324) Human Untagged Clone**

#### **Product data:**

Product Type:	Expression Plasmids
Product Name:	PACE4 (PCSK6) (NM_138324) Human Untagged Clone
Tag:	Tag Free
Symbol:	PACE4
Synonyms:	PACE4; SPC4
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)



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**Fully Sequenced ORF:** >SC309535 representing NM\_138324.  
 Blue=Insert sequence Red=Cloning site Green=Tag(s)

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GCTCGTTTAGTGAACCGTCAGAATTTTGAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG
GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC
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GAAGGGCAGTGGACCTTGAAATCCAAGATCTGCCATCCAGGTCCGCAACCCGAGAAGCAAGGTGAT
CTTGAGACTCCTGTTGCAATCAACTGACCACAGAAGAGAGGGAACCTGGACTAAAACACGTGTTCCGG
TGGCAGATTGAACAAGAGCTTTGGTAA
ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
  
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**Restriction Sites:** Sgfl-MluI

**ACCN:** NM\_138324

**Insert Size:** 1959 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.

<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>NM_138324.2</u>
<b>RefSeq Size:</b>	3254 bp
<b>RefSeq ORF:</b>	1959 bp
<b>Locus ID:</b>	5046
<b>UniProt ID:</b>	<u>P29122</u>
<b>Cytogenetics:</b>	15q26.3
<b>Protein Families:</b>	Druggable Genome, Protease, Secreted Protein
<b>MW:</b>	71.8 kDa
<b>Gene Summary:</b>	<p>This gene encodes a member of the subtilisin-like proprotein convertase family, which includes proteases that process protein and peptide precursors trafficking through regulated or constitutive branches of the secretory pathway. The encoded protein undergoes an initial autocatalytic processing event in the ER to generate a heterodimer which exits the ER and sorts to the trans-Golgi network where a second autocatalytic event takes place and the catalytic activity is acquired. The encoded protease is constitutively secreted into the extracellular matrix and expressed in many tissues, including neuroendocrine, liver, gut, and brain. This gene encodes one of the seven basic amino acid-specific members which cleave their substrates at single or paired basic residues. Some of its substrates include transforming growth factor beta related proteins, proalbumin, and von Willebrand factor. This gene is thought to play a role in tumor progression and left-right patterning. Alternatively spliced transcript variants encoding different isoforms have been identified. [provided by RefSeq, Feb 2014]</p> <p>Transcript Variant: This variant (4) uses two alternate exons in the 3' coding region and lacks several downstream exons when compared to variant 1. These differences cause a frameshift and thus isoform PACE4C has a distinct C-terminus compared to isoform PACE4-A1. 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>