

Product datasheet for **SC332144**

VIP Receptor 1 (VIPR1) (NM_001251885) Human Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: VIP Receptor 1 (VIPR1) (NM_001251885) Human Untagged Clone
Tag: Tag Free
Symbol: VIP Receptor 1
Synonyms: HVR1; II; PACAP-R-2; PACAP-R2; RDC1; V1RG; VAPC1; VIP-R-1; VIPR; VIRG; VPAC1; VPAC1R; VPCAP1R
Vector: pCMV6-Entry (PS100001)
Fully Sequenced ORF: >SC332144 representing NM_001251885.
 Blue=Insert sequence Red=Cloning site Green=Tag(s)

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ATGCGTGTGGCAGGCTGCAGGAGGAGTGTGACTATGTGCAGATGATCGAGGTGCAGCACAAAGCAGTGC
CTGGAGGAGGCCAGCTGGAGAATGAGACAATAGGCTGCAGCAAGATGTGGGACAACCTCACCTGCTGG
CCAGCCACCCCTCGGGCCAGGTAGTTGTCTTGGCCTGTCCCCTCATCTTCAAGCTCTTCTCCTCCATT
CAAGGCCGCAATGTAAGCCGCAGCTGCACCGACGAAGGCTGGACGCACCTGGAGCCTGGCCCGTACCCC
ATTGCCTGTGGTTTGGATGACAAGGCAGCGAGTTTGGATGAGCAGCAGACCATGTTCTACGGTTCTGTG
AAGACCGCTACACCATTGGCTACGGCCTGTCCCTCGCCACCCTTCTGGTCGCCACAGCTATCCTGAGC
CTGTTCCAGGAAGCTCCACTGCACGCGGAACCTACATCCACATGCACCTCTTCATATCCTTCATCCTGAGG
GCTGCCGCTGTCTTCATCAAAGACTTGGCCCTCTTCGACAGCGGGGAGTCGGACCAGTGCTCCGAGGGC
TCGGTGGGCTGTAAGGCAGCCATGGTCTTTTTCCAATATTGTGTGATGGCTAACTCTTCTGGCTGCTG
GTGGAGGGCCTCTACCTGTACACCCTGCTTGGCCTCTCCTTCTTCTGAGCGGAAGTACTTCTGGGGG
TACATACTCATCGGCTGGGGGTACCCAGCACATTACCATGGTGTGGACCATCGCCAGGATCCATTTT
GAGGATTATGGGTGCTGGGACACCATCAACTCCTCACTGTGGTGGATCATAAAGGGCCCCATCCTCACC
TCCATCTTGGTAAACTTCATCCTGTTTATTTGCATCATCCGAATCCTGCTTCAGAAACTGCGGCCCCCA
GATATCAGGAAGAGTGACAGCAGTCCATACTCAAGGCTAGCCAGGTCCACACTCCTGCTGATCCCCCTG
TTTGGAGTACACTACATCATGTTTCGCCTCTTTCCGGACAATTTAAGCCTGAAGTGAAGTGGTCTTT
GAGCTCGTGGGGTCTTTCCAGGTTTTGTGGTGGCTATCCTCTACTGCTTCCCTCAATGGTGGAGGTG
CAGGCGGAGCTGAGGCGGAAGTGGCGGCCTGGCACCTGCAGGGCGTCTGGGCTGGAACCCCAAATAC
CGGCACCCGTCGGGAGGCAACGCGGCCACGTGCAGCACGCAGGTTTCCATGCTGACCCGCTCAGC
CCAGGTGCCCGCCGCTCCTCCAGCTTCCAAGCCGAAGTCTCCCTGGTCTGA
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Restriction Sites: SgfI-MluI
ACCN: NM_001251885
Insert Size: 1293 bp



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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).
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_001251885.1
RefSeq Size:	2762 bp
RefSeq ORF:	1293 bp
Locus ID:	7433
UniProt ID:	P32241
Cytogenetics:	3p22.1
Protein Families:	Druggable Genome, GPCR, Transmembrane
Protein Pathways:	Neuroactive ligand-receptor interaction
MW:	48.9 kDa
Gene Summary:	<p>This gene encodes a receptor for vasoactive intestinal peptide, a small neuropeptide. Vasoactive intestinal peptide is involved in smooth muscle relaxation, exocrine and endocrine secretion, and water and ion flux in lung and intestinal epithelia. Its actions are effected through integral membrane receptors associated with a guanine nucleotide binding protein which activates adenylate cyclase. Several transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Oct 2011]</p> <p>Transcript Variant: This variant (5) lacks an alternate internal segment in the 5' coding region and uses a downstream start codon, compared to variant 1. The resulting isoform (5z) has a shorter and distinct N-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.</p>