

## Product datasheet for SC335815

### PPP2R5E (NM\_001282182) Human Untagged Clone

#### Product data:

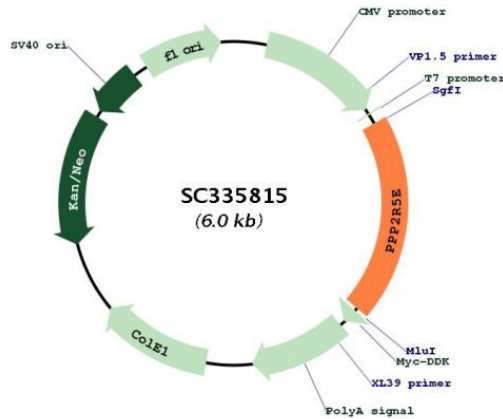
Product Type:	Expression Plasmids
Product Name:	PPP2R5E (NM_001282182) Human Untagged Clone
Tag:	Tag Free
Symbol:	PPP2R5E
Synonyms:	B56E; B56epsilon
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC335815 representing NM_001282182. Blue=Insert sequence Red=Cloning site Green=Tag(s)

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GCTCGTTTGTAGTGAACCGTCAGAATTTTGTAAACGACTACTATAGGGCGCCGGGAATTCGTCGACTG
GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC
ATGGACACGCTATCTGATCTTAAATGAAAGAATACAAGCGCTCCACTCTTAATGAACTGGTGGACTAC
ATTACAATAAGCAGAGGCTGTTTGACAGAGCAGACTTACCCTGAAGTAGTTAGAATGGTATCTTGAAT
ATATTCAGAACTCCCTCCTAGTGACAGCAATGAATTTGATCCAGAAGAAGATGAACCTACCCTTGAG
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GACCCTCGGGAACGGGACTACTTAAAAACAGTCTTACACAGAATTTATGGCAAGTTTCTTGGTCTTAGA
GCATTTATCCGAAAACAGATTAACAATATTTTCTAAGGTTTGTTATGAAACAGAACACTTCAATGGT
GTAGCTGAACTGCTGAAATATTAGGAAGTATTATCAATGGCTTTGCTTTACCTCTTAAGGCAGAACAC
AAACAGTTTCTGGTGAAGTATTGATCCCTTACACACTGTCAGGAGCTTACACTCTTCCATGCACAG
CTGGCATATTGTATAGTACAGTTTCTGGAGAAAGATCCTTCACTCACAGAACCAGTTATTAGGGGGTTA
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GATGTGATTGAACCTTACAATTTGTTAAAATCCAAGAACCTTTGTTTAAACAAATCGCCAAGTGTGA
TCTAGCCCCATTTTCAGGTGGCAGAAAGAGCACTCTATTATTGGAATAATGAATACATCATGAGTTTG
ATAGAAGAAAACCTAACGTCATCCTTCCCATCATGTTTTCCAGCCTTTATAGGATTTCAAAGAACAT
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TTTGACGAGCTGACAGCCACATACAAGTCAGATCGTCAGCGTGAGAAAAAGAAAAGAGGAGCGTGAA
GAATTGTGAAAAAATTGGAGGATCTGGAGTTAAAGAGAGGTCTTAGACGTGATGGAATAATTCCAAT
TAA
ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
```

Restriction Sites: Sgfl-MluI



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**Plasmid Map:**


**ACCN:** NM\_001282182

**Insert Size:** 1176 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).

**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\\_001282182.1](#)

**RefSeq Size:** 3445 bp

**RefSeq ORF:** 1176 bp

**Locus ID:** 5529

**UniProt ID:** [Q16537](#)

**Cytogenetics:** 14q23.2

**Protein Families:** Druggable Genome, Phosphatase

**Protein Pathways:** Oocyte meiosis, Wnt signaling pathway

**MW:** 46.2 kDa

**Gene Summary:** The protein encoded by this gene belongs to the phosphatase 2A regulatory subunit B family. Protein phosphatase 2A is one of the four major Ser/Thr phosphatases, and it is implicated in the negative control of cell growth and division. It consists of a common heteromeric core enzyme, which is composed of a catalytic subunit and a constant regulatory subunit, that associates with a variety of regulatory subunits. The B regulatory subunit might modulate substrate selectivity and catalytic activity. This gene encodes an epsilon isoform of the regulatory subunit B56 subfamily. Multiple transcript variants encoding several different isoforms have been found for this gene. [provided by RefSeq, Aug 2013]

Transcript Variant: This variant (5) contains a distinct 5' UTR and lacks an in-frame portion of the 5' coding region, compared to variant 1. The resulting isoform (c) has a shorter N-terminus compared to isoform a. Variants 4 and 5 both encode the same isoform (c).

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.