

Product datasheet for **SC324746**

RPS27A (NM_001135592) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	RPS27A (NM_001135592) Human Untagged Clone
Tag:	Tag Free
Symbol:	RPS27A
Synonyms:	CEP80; HEL112; S27A; UBA80; UBC; UBCEP1; UBCEP80
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC324746 representing NM_001135592. Blue=Insert sequence Red=Cloning site Green=Tag(s)

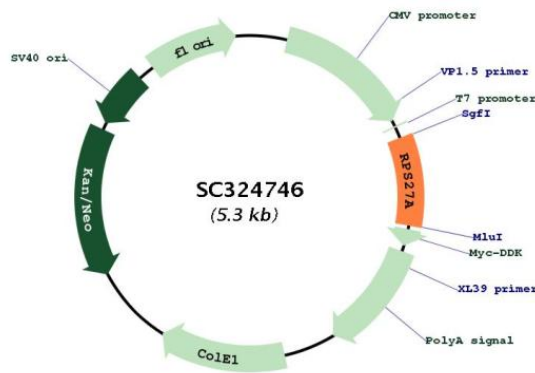
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GCTCGTTTAGTGAACCGTCAGAATTTTGTAAACGACTCACTATAGGGCGCCGGGAATTCGTCGACTG
GATCCGGTACCGAGGAGATCTGCCGCCCGCATCGCC
ATGCAGATTTTCGTGAAAACCTTACGGGGAAGACCATCACCTCGAGTTGAACCTCGGATACGATA
GAAAATGTAAAGGCCAAGATCCAGGATAAGGAAGGAATTCCTCCTGATCAGCAGAGACTGATCTTTGCT
GGCAAGCAGCTGGAAGATGGACGTACTTTGTCTGACTACAATATTCAAAAGGAGTCTACTCTTCATCTT
GTGTTGAGACTTCGTGGTGGTGTCTAAGAAAAGGAAGAAGAAGTCTTACCCACTCCCAAGAAGAATAAG
CACAAGAGAAAAGAAGTTAAGCTGGCTGCCTGAAATATTATAAGGTGGATGAGAATGGCAAATAGT
CGCCTTCGTCGAGAGTGCCCTTCTGATGAATGTGGTGTGGGGTGTATGGCAAGTCACTTTGACAGA
CATTATTGTGGCAAATGTTGTCTGACTTACTGTTTCAACAAACCAGAAGCAAGTAA
ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
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Restriction Sites: Sgfl-Mlul



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Plasmid Map:



ACCN:	NM_001135592
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).
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_001135592.2](#)

RefSeq Size: 970 bp

RefSeq ORF: 471 bp

Locus ID: 6233

UniProt ID: [P62979](#)

Cytogenetics: 2p16.1

Protein Families: Druggable Genome

Protein Pathways: Ribosome

MW: 18 kDa

Gene Summary: Ubiquitin, a highly conserved protein that has a major role in targeting cellular proteins for degradation by the 26S proteasome, is synthesized as a precursor protein consisting of either polyubiquitin chains or a single ubiquitin fused to an unrelated protein. This gene encodes a fusion protein consisting of ubiquitin at the N terminus and ribosomal protein S27a at the C terminus. When expressed in yeast, the protein is post-translationally processed, generating free ubiquitin monomer and ribosomal protein S27a. Ribosomal protein S27a is a component of the 40S subunit of the ribosome and belongs to the S27AE family of ribosomal proteins. It contains C4-type zinc finger domains and is located in the cytoplasm. Pseudogenes derived from this gene are present in the genome. As with ribosomal protein S27a, ribosomal protein L40 is also synthesized as a fusion protein with ubiquitin; similarly, ribosomal protein S30 is synthesized as a fusion protein with the ubiquitin-like protein fubi. Multiple alternatively spliced transcript variants that encode the same proteins have been identified.[provided by RefSeq, Sep 2008]

Transcript Variant: This variant (2) differs in the 5' UTR, compared to variant 1. Variants 1, 2 and 3 encode the same protein. 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.