

Product datasheet for **SC124831**

UBE2D3 (NM_181887) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	UBE2D3 (NM_181887) Human Untagged Clone
Tag:	Tag Free
Symbol:	UBE2D3
Synonyms:	E2(17)KB3; UBC4/5; UBCH5C
Mammalian Cell Selection:	None
Vector:	<u>pCMV6-XL5</u>
E. coli Selection:	Ampicillin (100 ug/mL)
Fully Sequenced ORF:	>NCBI ORF sequence for NM_181887, the custom clone sequence may differ by one or more nucleotides

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ATGGCGCTGAAACGGATTAATAAGGAACTTAGTGATTTGGCCCGTGACCCTCCAGCACAATGTTCTGCAG
GTCCAGTTGGGGATGATATGTTTCATTGGCAAGCCACAATTATGGGACCTAATGACAGCCCATATCAAGG
CGGTGATTCTTTTTGACAATTCATTTTCCTACAGACTACCCCTTCAAACCACCTAAGGTTGCATTTACA
ACAAGAATTTATCATCCAAATATTAACAGTAATGGCAGCATTTGTCTCGATATTCTAAGATCACAGTGGT
CGCCTGCTTTAACAATTTCTAAAGTTCTTTTATCCATTTGTTCACTGCTATGTGATCCAAACCCAGATGA
CCCCCTAGTGCCAGAGATTGCACGGATCTATAAAACAGACAGAGATAAGTACAACAGAATATCTCGGAA
TGGACTCAGAAGTATGCCATGTGA
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5' Read Nucleotide Sequence:	>OriGene 5' read for NM_181887 unedited ATACGACTCACTATAGGGCGGCCGGAATTCGGCACGAGGCACCCACCCCGGATCGCGGC TGTCTTAAGGGACCTGGATTTCATCAGGGGCTCTTCGGGGCCTGTGCGAGTGCTGATCTGC TCCGTTTTTGAAAAGGCGCCTGTGTCTGGCAGAGCTGGTGTGAGACGAGACAATCCTGC CCCGCCCGGGATAATCAAGAGTTTTGGCCGGACCTTGAGCATAACCCGAGAGAGTGA GGAGCCAGACGACAAGCACACACTATGGCGCTGAAACGGATTAATAAGGAACTTAGTGAT TTGGCCCGTGACCTCCAGCACAATGTTCTGCAGGTCCAGTTGGGGATGATATGTTTCAT TGGCAAGCCACAATTATGGGACCTAATGACAGCCATATCAAGGCGGTATTCTTTTTG ACAATTCATTTTTCTACAGACTACCCCTTCAAACCACCTAAGGTTGCATTTACAACAAGA ATTTATCATCAAATATTAACAGTAATGGCAGCATTTGTCTCGATATTCTAAGATCACAG TGGTCGCCTGCTTAACAATTTCTAAAGTTCTTTTATCCATTTGTTCACTGCTATGTGAT CCAAACCCAGATGACCCCTAGTGCCAGAGATTGCACGGATCTATAAACAGACAGAGAT AAGTACAACAGAATATCTCGGAATGGACTCAGAAGTATGCCATGTGATGCTACCTTAAA GTCAGAATAACCTGCATTATAGCTGGAATAAACTNNTAAATACTGTTCTTTTTTGATTT CTTATNCGGCTGCTCCCCTATCAGACTCATTTTTTAATTTATTTTTGGNTTACCTCCTN CANTTCCATGCTCATTGAGAGACTTAAGTCTTCAGCTTGGACATACTGCTTTAGAAGT GTAAGTAGTACAGAGAACAGTGCCAGACTAAATTTTAAAAAATN
Restriction Sites:	NotI-NotI
ACCN:	NM_181887
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:	<u>NM_181887.1</u> , <u>NP_871616.1</u>
RefSeq Size:	2359 bp
RefSeq ORF:	444 bp
Locus ID:	7323
UniProt ID:	<u>P61077</u>
Cytogenetics:	4q24
Protein Pathways:	Ubiquitin mediated proteolysis

Gene Summary:

The modification of proteins with ubiquitin is an important cellular mechanism for targeting abnormal or short-lived proteins for degradation. Ubiquitination involves at least three classes of enzymes: ubiquitin-activating enzymes, or E1s, ubiquitin-conjugating enzymes, or E2s, and ubiquitin-protein ligases, or E3s. This gene encodes a member of the E2 ubiquitin-conjugating enzyme family. This enzyme functions in the ubiquitination of the tumor-suppressor protein p53, which is induced by an E3 ubiquitin-protein ligase. [provided by RefSeq, Jan 2017]

Transcript Variant: This variant (3) differs in the 5' UTR, and encodes the same isoform (1), as compared to variant 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.