

Product datasheet for **SC303413**

PAX2 (NM_003988) Human Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: PAX2 (NM_003988) Human Untagged Clone
Tag: Tag Free
Symbol: PAX2
Synonyms: FSGS7; PAPRS
Mammalian Cell Selection: None
Vector: pCMV6-XL5
E. coli Selection: Ampicillin (100 ug/mL)

Fully Sequenced ORF: >OriGene sequence for NM_003988 edited
 CCTCCCTTTTCTCCTCAAGTCTGAAGTTGAGTTTGAGAGGCGACACGGCGCGGGCC
 GCGCTGCTCCCGCTCCTCTGCCCTCCCATGGATATGCACTGCAAAGCAGACCCCTTCTCC
 GCGATGACCCAGGGCACGGGGTGTGAACCAGCTCGGGGGGTGTTTGTGAACGCGCG
 CCCTACCCGACGTGGTGAAGCAGCGCATCGTGGAGCTGGCCACCAGGGTGTGCGGCC
 TGTGACATCTCCCGCAGCTGCGGGTCAAGCCAGGCTGTGTGACAAAATCCTGGGCAGG
 TACTACGAGACCGCAGCATCAAGCCGGTGTGATCGGTGGCTCCAAGCCCAAAGTGGCG
 ACGCCCAAAGTGGTGGACAAGATTGCTGAATACAAACGACAGAACCCGACTATGTTCCGC
 TGGGAGATTGAGACCGGCTCCTGGCCGAGGGCATCTGTGACAATGACACAGTCCCAGC
 GTCTCTCCATCAACAGAATCATCCGGACCAAAGTTCAGCAGCCTTCCACCCAACGCCG
 GATGGGGCTGGGACAGGAGTGACCGCCCTGGCCACACCATTGTTCCAGCACGGCTCC
 CCTCCTGTTTCCAGCGCCTCCAATGACCCAGTGGGATCCTACTCCATCAATGGGATCCTG
 GGGATTCTCGCTCCAATGGTGAAGAGGAAACGTGATGAAGATGTGTCTGAGGGCTCA
 GTCCCAATGGAGATTCCCAGAGTGGTGTGGACAGTTTGCAGGACACTTGCAGCTGAC
 ACCTTACCCAGCAGCAGCTGGAAGCTTTGGATCGGGTCTTTGAGCGTCTTCTACCT
 GACGTCTTCCAGGCATCAGAGCAGATCAAATCAGAACAGGGGAACGAGTACTCCCTCCCA
 GCCCTGACCCCTGGGCTTGTGAAGTCAAGTCGAGTCTATCTGCATCCACCAACCCTGAG
 CTGGGCAGCAACGTGTGAGGCACACAGACATACCCAGTTGTGACTGGTCTGTGACATGGCG
 AGCACCCTCTGCCTGGTTACCCCTCAGTGCCTCCACTGGCCAGGGAAGTACCC
 ACCTCCACCCTGGCAGGAATGGTGCCTGAGGCTGCAAGTTGGTCCCTCATCCTCCCTCATG
 AGCAAGCCGGGAGGAAGCTTGCAGAAGTGCCCTTGTGTGCAACCCACTGGAGCGAGT
 TCTCCGGCAACCCGTACAGCCACCCAGTACAGGCCTACAACGAGGCTTGGAGATTCA
 GCAACCCCGCCTTACTAAGTTCCTTATTATTATAGTGCCGCCCCCGGTCCGCCCTG
 CCGCTGCTGCCGTGCCTATGACCGCCACTAGTTAAGGGC

Restriction Sites: Please inquire



[View online »](#)

ACCN:	NM_003988
Insert Size:	1400 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:	The ORF of this clone has been fully sequenced and found to be a perfect match to NM_003988.2.
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_003988.2</u> , <u>NP_003979.2</u>
RefSeq Size:	4290 bp
RefSeq ORF:	1191 bp
Locus ID:	5076
UniProt ID:	<u>Q02962</u>
Cytogenetics:	10q24.31
Protein Families:	Druggable Genome
Gene Summary:	<p>PAX2 encodes paired box gene 2, one of many human homologues of the Drosophila melanogaster gene prd. The central feature of this transcription factor gene family is the conserved DNA-binding paired box domain. PAX2 is believed to be a target of transcriptional suppression by the tumor suppressor gene WT1. Mutations within PAX2 have been shown to result in optic nerve colobomas and renal hypoplasia. Alternative splicing of this gene results in multiple transcript variants. [provided by RefSeq, Dec 2014]</p> <p>Transcript Variant: This variant (c) has multiple differences in the coding region, compared to variant e, one of which results in a translational frameshift. The resulting protein (isoform c) has a distinct C-terminus and is shorter than isoform e. 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>