

OriGene Technologies, Inc.

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Product datasheet for SC331473

Cytochrome P450 3A4 (CYP3A4) (NM_001202855) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Cytochrome P450 3A4 (CYP3A4) (NM_001202855) Human Untagged Clone
Tag:	Tag Free
Symbol:	Cytochrome P450 3A4
Synonyms:	CP33; CP34; CYP3A; CYP3A3; CYPIIIA3; CYPIIIA4; HLP; NF-25; P450C3; P450PCN1; VDDR3
Vector:	pCMV6-Entry (PS100001)
Fully Sequenced ORF:	<pre>>SC331473 representing NM_001202855. Blue=Insert sequence Red=Cloning site Green=Tag(s)</pre>
	ATGGCTCTCATCCCAGACTTGGCCATGGAAACCTGGCTTCTCCTGGCTGTCAGCCTGGTGCTCCTCTAT CTATATGGAACCCATTCACATGGACTTTTTAAGAAGCTTGGAATTCCAGGGCCCACACCTCTGCCTTTT TTGGGAAATATTTTGTCCTACCATAAGGGCTTTTGTATGTTGACATGGAATGTCATAAAAAGTATGGA AAAGTGTGGGGCTTTTATGATGGTCAACAGCCTGTGCTGGCTACCAGAGTCCTGACATGATCAAAACA GTGCTAGTGAAAGAATGTTATTCTGTCTTCACAAACCGGAGGCCTTTTGGTCCAGTGGGATTTATGAAA AGTGCCATCTCTATAGCTGAGGATGAAGAATGGAAGAATGGAAGAGATTACGATCATTGCTGTCCCAACCTTCAC AGTGGAAAACTCAAGGAGATGGTCCCTATCATTGCCCAGTATGGAGATGTGTGGTGAGAAATCTGAGG CGGGAAAACTCAAGGAGGCTGTCCCTATCATTGCCCAGTATGGAGATGTGTGGTGAGAAATCTGAGG CGGGAAACCAAGGCAAGCCTGTCACCTTGAAAGACGTCTTTGGGGCCTACAGCATGGATGTGAT ACTAGCACATCATTTGGAGTGAACATCGACTCTCTCAACAATCCACAAGACCCCTTTGTGGAAAACACC AAGAAGCTTTTAAGATTTGATTT
Restriction Sites:	Sgfl-Mlul
ACCN:	NM_001202855
Insert Size:	1509 bp



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Cytochrome P450 3A4 (CYP3A4) (NM_001202855) Human Untagged Clone – SC331473	
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:	 Centrifuge at 5,000xg for 5min. Carefully open the tube and add 100ul of sterile water to dissolve the DNA. Close the tube and incubate for 10 minutes at room temperature. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom. 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 001202855.2</u>
RefSeq Size:	2789 bp
RefSeq ORF:	1509 bp
Locus ID:	1576
UniProt ID:	<u>P08684</u>
Cytogenetics:	7q22.1
Protein Families:	Druggable Genome, ES Cell Differentiation/IPS, P450, Transmembrane
Protein Pathways:	Drug metabolism - cytochrome P450, Drug metabolism - other enzymes, Linoleic acid metabolism, Metabolic pathways, Metabolism of xenobiotics by cytochrome P450, Retinol metabolism
MW:	57.3 kDa

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Cytochrome P450 3A4 (CYP3A4) (NM_001202855) Human Untagged Clone – SC331473

Gene Summary: This gene encodes a member of the cytochrome P450 superfamily of enzymes. The cytochrome P450 proteins are monooxygenases that catalyze many reactions involved in drug metabolism and synthesis of cholesterol, steroids and other lipids. This protein localizes to the endoplasmic reticulum and its expression is induced by glucocorticoids and some pharmacological agents. This enzyme is involved in the metabolism of approximately half the drugs in use today, including acetaminophen, codeine, cyclosporin A, diazepam, erythromycin, and chloroquine. The enzyme also metabolizes some steroids and carcinogens. This gene is part of a cluster of cytochrome P450 genes on chromosome 7q21.1. Previously another CYP3A gene, CYP3A3, was thought to exist; however, it is now thought that this sequence represents a transcript variant of CYP3A4. Alternatively spliced transcript variants encoding different isoforms have been identified. [provided by RefSeq, Aug 2020] Transcript Variant: This variant (2) uses an alternate splice site in the CDS compared to variant 1. The resulting isoform (2) is shorter but has the same N- and C-termini compared to isoform 1. Sequence Note: This RefSeg 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.

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