

OriGene Technologies, Inc.

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Product datasheet for SC326947

5 HT 2A (HTR2A) (NM_001165947) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	5 HT 2A (HTR2A) (NM_001165947) Human Untagged Clone
Tag:	Tag Free
Symbol:	5 HT 2A
Synonyms:	5-HT2A; HTR2
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC326947 representing NM_001165947. Blue=Insert sequence <mark>Red=</mark> Cloning site Green=Tag(s)
	GCTCGTTTAGTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC ATGCAGTTTTTGAAGTCAGCAAAACAGAAACAGAAACCAAATTACTATCATATTATGCTGGTGGAAGATCAAGAA GAGGGGACTCTACACCAGTTTAATTACTGTGAGAGATGCAGCGAGTCACAGAATAACAAATGTATCTCA TGTGTGGACCCTGAAGACAAATGGTACCGGTGGCCTCTGCCGAGCAGGCTACGACGACTGGACTTAC CTGGACGTGCTCTTCTCCACGGCCTCCATCATGCACCTCTGCGCAGCAGCTTGGGACCGCTACGTCGCC ATCCAGAATCCCATCCACCACGCCGCTCCAACTCCAGGACCTACGTCGGACCGCTACGTCGC ATCCAGAATCCCATCCACCACGCCGCTTCAACTCCAGGACCTACGGCGCTTCTGGACAGGCTGCTT GGACCATATCAGTAGGTATATCCATGCCAATACCAGTCTTGGGCTACGGGACGATTCGAAAGCTCTT AAGGAGGGGAGTTGCTTACTCGCCGATGATAACTTTGTCCTGATCGGCCTTTTGTGTCAATTTCAT CCCTTAACCATCATGGTGATCACCTACTTTCTAACTATCAAGTCACTCCAGAAAGAA
Restriction Sites:	Søfl-Mlul

Restriction Sites:

Sgfl-Mlul



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GRIGENE 5 HT 2A (HTR2A) (NM_001165947) Human Untagged Clone – SC326947	
ACCN:	NM_001165947
Insert Size:	1164 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	 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 001165947.2</u>
RefSeq Size:	4702 bp
RefSeq ORF:	1164 bp
Locus ID:	3356
UniProt ID:	<u>P28223</u>
Cytogenetics:	13q14.2
Protein Families:	Druggable Genome, GPCR, Transmembrane
Protein Pathways:	Calcium signaling pathway, Gap junction, Neuroactive ligand-receptor interaction
MW:	43.9 kDa

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CRIGENE 5 HT 2A (HTR2A) (NM_001165947) Human Untagged Clone – SC326947

Gene Summary:

This gene encodes one of the receptors for serotonin, a neurotransmitter with many roles. Mutations in this gene are associated with susceptibility to schizophrenia and obsessivecompulsive disorder, and are also associated with response to the antidepressant citalopram in patients with major depressive disorder (MDD). MDD patients who also have a mutation in intron 2 of this gene show a significantly reduced response to citalopram as this antidepressant downregulates expression of this gene. Multiple transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Sep 2009] Transcript Variant: This variant (2) lacks an in-frame exon in the 5' coding region, compared to variant 1, that causes translation initiation at an upstream AUG. The resulting protein (isoform 2) has a distinct N-terminus and is shorter than isoform 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.

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