

Product datasheet for SC325889

HTR3D (NM_001145143) Human Untagged Clone

Product data:

OriGene Technologies, Inc.

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Product Type:	Expression Plasmids
Product Name:	HTR3D (NM_001145143) Human Untagged Clone
Tag:	Tag Free
Symbol:	HTR3D
Synonyms:	5HT3D
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC325889 representing NM_001145143. Blue=Insert sequence <mark>Red</mark> =Cloning site Green=Tag(s)
	GCTCGTTTAGTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC ATGGAAAGAGGCTGGTTCCATGGGAAAGGATTCCTCCTTGGCTTCATCCTCCACCTGCTGCAGAGAT TCACACCTTCAACTGGTGACATCGTTCCTGTGGCTAAATATGTGGAACCCAGATGAATGCGGAGGCATC AAGAAGTCCGGCATGGCAACTGAGAACCTATGGCTTTCAGATGTCTTCATCGAGGAGTCTGTGGATCAG ACACCTGCAGGTCTCATGGCTAGTATGTCAATAGTGAAGGCCACATCAAACACAATAAGCCAATGTGGG TGGTCAGCATCTGCAAACTGGACACCTTCTATTTCCCCTTCCATGGACAGAGGTGAACGCTCTCCTTCA GCCCTTTCACCAACAGGTAACCCGGGCATGGAGAAGGATGTCCAGGAGGTAAAACAATAAAGCCAATGTGGG GCCACTAACCAGTATGAACAAGCGATCTTCCATGTGGCCATCAGGAGGCTTTCAAATACATCACAGA ACCTCATTCAGAACAAGGAGGGAGTGGGTACTGCTGGGTATCCAAAAAAGAACAATAAAGGTGACCGTG GCCACTAACCAGTATGAACAAGCCATCTTCCATGTGGCCATCAGGCGCAGGTGCAGGCCCAGCCCTAC GTGGTAAACTTTCTGGTGCCCCAGTGGCATTCTGATTGCCATCGATGGCCTCAGGTGCAGGCCCAGCCCTAC GTGGTAAACTTTCTGGTGCCCCATTCAAGATGACTGTTCTGCTGGGGCTACAGCGTCTTCCTGCTCATGATG AATGACTTGCTCCCAGCCACTAGCACTTCATCACAGGCTCTCACTAGGCGCAGCGCCGCGCGCG
Restriction Sites:	Sgfl-Mlul

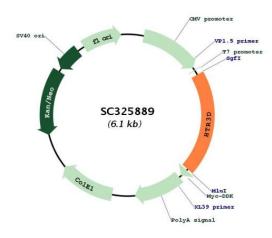


Sgfl-Mlul



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Plasmid Map:



ACCN:	NM_001145143
Insert Size:	1215 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 001145143.1</u>
RefSeq Size:	1609 bp
RefSeq ORF:	1215 bp
Locus ID:	200909
UniProt ID:	<u>Q70Z44</u>
Cytogenetics:	3q27.1

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MATR3D (NM_001145143) Human Untagged Clone – SC325889

Protein Families:	Druggable Genome, Ion Channels: Cys-loop Receptors, Transmembrane
MW:	45.1 kDa
Gene Summary:	The protein encoded this gene belongs to the ligand-gated ion channel receptor superfamily. This gene encodes subunit D of the type 3 receptor for 5-hydroxytryptamine (serotonin), a biogenic hormone that functions as a neurotransmitter, a mitogen and a hormone. This hormone has been linked to neuropsychiatric disorders, including anxiety, depression, and migraine. Serotonin receptors causes fast and depolarizing responses in neurons following activation. The genes encoding subunits C, D and E of this type 3 receptor form a cluster on chromosome 3. Alternatively spliced transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Jul 2009] Transcript Variant: This variant (1) differs in the 5' coding region, compared to variant 3, resulting in an isoform (1) that is shorter than isoform 3. 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.