OriGene Technologies, Inc.
9620 Medical Center Drive, Ste 200
Rockville, MD 20850, US
Phone: +1-888-267-4436
https://www.origene.com
techsupport@origene.com
EU: info-de@origene.com
CN: techsupport@origene.cn

Product datasheet for SC330840

ST3GAL3 (NM_001270460) Human Untagged Clone

Product data:

Product Type: Expression Plasmids

Product Name: ST3GAL3 (NM_001270460) Human Untagged Clone

Tag: Tag Free

Symbol: ST3GAL3

Synonyms: DEE15; EIEE15; MRT12; SIAT6; ST3GALII; ST3Gal III; ST3GalIII; ST3N

Vector: pCMV6-Entry (PS100001)

Fully Sequenced ORF:

>SC330840 representing NM_001270460.
Blue=Insert sequence Red=Cloning site Green=Tag(s)

ATGGGACTCTTGGTATTTGTGCGCAATCTGCTGCTAGCCCTCTGCCTCTTTCTGGTACTGGGATTTTTG
TATTATTCTGCGTGGAAGCTACACTTACTCCAGTGGGAGGAGGACTCCAATTCAGTGGTTCTTTCCTTT
GACTCCGCTGGACAAACACTAGGCTCAGAGTATGATCGGTTGGGCTTCCTCCTGAATCTGGACTCTAAA
CTGTTCTCCAAGCCAGCACCCATGTTCCTGGATGACTCCTTTCGCAAGTGGGCTAGAATCCGGGAGTTC
GTGCCGCCTTTTGGGATCAAAGGTCAAGACAATCTGATCAAAGCCATCTTGTCAGTCACCAAAGAGTAC
CGCCTGACCCCTGCCTTGGACAGCCTCCGCTGCCGCCGCTGCATCATCGTGGGCAATGGAGGCGTTCTT
GCCAACAAGTCTCTGGGGTCACGAATTGACGACTATGACATTGTGGTGAGACTGAATTCAGCACCAGTG
AAAGGCTTTGAGAAGGACGTGGGCAGCAAAACGACACTGCGCATCACCTACCCCGAGGGCGCCATGCAG
CGGCCTGAGCAGTACGAGCGCGATTCTCTCTTTGTCCTCGCCGGCTTCAAGTGGCAGGACTTTAAGTGG
TTGAAATACATCGTCTACAAGGAGAGAGTGAGTGCATCGGATGGCTTCTGGAAATCTGTGGCCACTCGA
GTGCCCAAGGAGCCCCCTGAGATTCGAATCCTCAACCCATATTTCATCCAGGAGGCCGCCTTCACCCTC
ATTGGCCTGCCCTTCAACAATGGCCTCATGGGCCGGGGGAACATCCCTACCCTTGGCAGTGTGGCAGTG
ACCATGGCACTACACGGCTGTGACGAGGTGGCAGTCGCAGGATTTGGCTATGACATGAGCACACCCAAC
GCACCCCTGCACTACTATGAGACCGTTCGCATGGCAGCCATCAAAGAGTCCTGGACGCACAATATCCAG
CGAGAGAAAGAGTTTCTGCGGAAGCTGGTGAAAGCTCGCGTCATCACTGATCTAAGCAGTGGCATCTGA

Restriction Sites: SgfI-MluI

ACCN: NM_001270460

Insert Size: 1035 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).

View online »

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:	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:	NM_001270460.1
RefSeq Size:	2201 bp
RefSeq ORF:	1035 bp
Locus ID:	6487
UniProt ID:	Q11203
Cytogenetics:	1p34.1
Protein Families:	Secreted Protein, Transmembrane
Protein Pathways:	Glycosphingolipid biosynthesis - lacto and neolacto series, Keratan sulfate biosynthesis, Metabolic pathways
MW:	38.9 kDa
Gene Summary:	The protein encoded by this gene is a type II membrane protein that catalyzes the transfer of sialic acid from CMP-sialic acid to galactose-containing substrates. The encoded protein is normally found in the Golgi apparatus but can be proteolytically processed to a soluble form. This protein is a member of glycosyltransferase family 29. Mutations in this gene have been associated with a form of autosomal recessive nonsymdromic cognitive disability as well as infantile epileptic encephalopathy. Multiple transcript variants encoding several different isoforms have been found for this gene. [provided by RefSeq, Jul 2017] Transcript Variant: This variant (12) lacks an alternate in-frame exon and uses an alternate in-frame splice site in the 5' coding region compared to variant 1. The resulting isoform (l, also called B4+173) is shorter compared to isoform a. 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.