

## Product datasheet for **SC306972**

### ST3GAL3 (NM\_174968) Human Untagged Clone


#### Product data:

Product Type:	Expression Plasmids
Product Name:	ST3GAL3 (NM_174968) Human Untagged Clone
Tag:	Tag Free
Symbol:	ST3GAL3
Synonyms:	DEE15; EIEE15; MRT12; SIAT6; ST3GALII; ST3Gal III; ST3GalIII; ST3N
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC306972 representing NM_174968. Blue=Insert sequence Red=Cloning site Green=Tag(s)

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GCTCGTTTGTGAAACCGTCAGAATTTTGTAAACGACTACTATAGGGCGCCGGGAATTCGTCGACTG
GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC
ATGGGACTCTTGGTATTTGTGCGCAATCTGCTGTAGCCCTCTGCCTCTTTCTGGTACTGGGATTTTTG
TATTATTCTGCGTGAAGCTACACTTACTCCAGTGGGAGGAGACTCCAATTCAGTGGTTCTTTCCCTT
GACTCCGCTGGACAAACTAGGCTCAGAGTATGATCGGTTGGGCTTCTCCTGAATCTGGACTCTAAA
CTCTCACCAGGACTCTCTGCACGGTGGTTTTGGCCTTGACTGCATATTGGAATCACCTGGAGAGCCT
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GCATTAGGATTTTTAAAGCTGCCAGGCCTGCTGAATTAGCCACCAAGTACGCAAATTTTCAGAGGGA
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GGTCAAGACAATCTGATCAAAGCCATCTTGTCACTCACCAGAGTACCGCCTGACCCCTGCCTTGGAC
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AAGCTGGTGAAGCTCGCGTCATCACTGATCTAAGCAGTGGCATCTGA
ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
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<b>Restriction Sites:</b>	Sgfl-Mlul
<b>Plasmid Map:</b>	
<b>ACCN:</b>	NM_174968
<b>Insert Size:</b>	1290 bp
<b>OTI Disclaimer:</b>	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).
<b>OTI Annotation:</b>	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.
<b>Components:</b>	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).
<b>Reconstitution Method:</b>	<ol style="list-style-type: none"> <li>1. Centrifuge at 5,000xg for 5min.</li> <li>2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.</li> <li>3. Close the tube and incubate for 10 minutes at room temperature.</li> <li>4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.</li> <li>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.</li> </ol>
<b>RefSeq:</b>	<a href="#">NM_174968.3</a>
<b>RefSeq Size:</b>	2456 bp
<b>RefSeq ORF:</b>	1290 bp
<b>Locus ID:</b>	6487
<b>UniProt ID:</b>	<a href="#">Q11203</a>
<b>Cytogenetics:</b>	1p34.1
<b>Protein Families:</b>	Secreted Protein, Transmembrane
<b>Protein Pathways:</b>	Glycosphingolipid biosynthesis - lacto and neolacto series, Keratan sulfate biosynthesis, Metabolic pathways
<b>MW:</b>	48 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 nonsyndromic 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 (6) utilizes an alternate in-frame splice site compared to variant 1, resulting in an isoform (f, also called B8) that 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.