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Product datasheet for SC303996

ST8SIA5 (NM_013305) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	ST8SIA5 (NM_013305) Human Untagged Clone
Tag:	Tag Free
Symbol:	ST8SIA5
Synonyms:	SIAT8-E; SIAT8E; ST8SiaV
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC303996 representing NM_013305. Blue=Insert sequence Red=Cloning site Green=Tag(s) GCTCGTTTAGTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC ATGCGCTACGCGGACCCCTCGGCCAACCGGGATTTGTTGGGGAGCCGAACTTTGCTCTTCATCTTCATC TGCGCCTTTGCCTTGGTGACCTTGCTGCAACAGATCCTGTATGGCAGGAACTACATTAAGAGGTACTTT GAATTTTATGAGGGGCCTTTTGAATATAACTCCACAAGATGCCTGGAGCTGAGGCACGAAATATTGGAA GTGAAGGTGCTGTCCATGGTGAAGCAGTCAGAGCTGTTCGACAGGTGGAAGAGCCTCCAGATGTGCAAA TGGGCGATGAACATCTCTGAGGCCAACCAGTTCAAGTCTACTCTGTCCAGGTGCTGCAACGCCCCTGCC TTTCTCTTCACCACCCAGAAGAACACTCCCCTGGGGACAAAGCTCAAGTATGAGGTGGACACCAGTGGC ATCTACCACATCAACCAGGAGATCTTCCGCATGTTTCCCAAGGACATGCCCTACTACCGGTCCCAGTTT AAGAAGTGTGCTGTAGTGGGCAACGGAGGCATCTTGAAGAACAGCCGCTGCGGGAGGGAGATCAACAGC GCCGACTTCGTCTTCCGGTGCAACCTGCCCCCCATCTCAGAGAAGTACACCATGGATGTGGGGGTGAAG ACGGATGTGGTCACTGTGAACCCCAGCATCATCACAGAGAGGTTCCACAAGCTGGAGAAGTGGCGGCGG CCGTTCTATCGCGTGCTGCAGGTGTACGAGAACGCGTCGGTGCTGCTGCCTGCCTTCTACAACACGCGC AACACCGACGTGTCCATCCGCGTCAAGTACGTGCTGGACGACTTCGAATCGCCGCAAGCTGTCTACTAC TTCCATCCGCAGTACCTGGTCAACGTGTCGCGCTACTGGCTCAGCCTGGGGGTGCGCGCCAAGCGCATC AGCACCGGCCTCATTCTGGTCACTGCGGCGCTGGAGCTCTGTGAGGAGGTGCACCTCTTTGGCTTCTGG GCCTTCCCCATGAACCCCTCGGGCCTCTACATCACTCACCACTACTATGACAACGTCAAGCCGCGTCCC GGCTTCCACGCCATGCCCTCTGAGATCTTCAACTTCCTGCACTTGCACAGCCGAGGCATCCTCCGCGTG CACACGGGCACCTGCAGCTGCTGCTGA AGCGGACCGACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGAT ATCCTGGATTACAAGGATGACGACGATAAGGTTTAA
Restriction Sites:	SgfI-RsrII

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ACCN:	NM_013305
Insert Size:	1131 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:	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_013305.5
RefSeq Size:	2720 bp
RefSeq ORF:	1131 bp
Locus ID:	29906
UniProt ID:	O15466
Cytogenetics:	18q21.1
Protein Families:	Transmembrane
Protein Pathways:	Glycosphingolipid biosynthesis - ganglio series, Metabolic pathways
MW:	43.9 kDa
Gene Summary:	The protein encoded by this gene is a type II membrane protein that may be present in the Golgi apparatus. The encoded protein, which is a member of glycosyltransferase family 29, may be involved in the synthesis of gangliosides GD1c, GT1a, GQ1b, and GT3 from GD1a, GT1b, GM1b, and GD3, respectively. [provided by RefSeq, Jul 2008] Transcript Variant: This variant (2) lacks an alternate in-frame exon in the 5' coding region compared to variant 1. The encoded isoform (2) 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.