

Product datasheet for **SC307073**

SULT1C2 (NM_176825) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	SULT1C2 (NM_176825) Human Untagged Clone
Tag:	Tag Free
Symbol:	SULT1C2
Synonyms:	humSULTC2; ST1C1; ST1C2; SULT1C1
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC307073 representing NM_176825. Blue=Insert sequence Red=Cloning site Green=Tag(s)

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GCTCGTTT TAGTGAACCGTCAGAATTTTGT AATACGACTCACTATAGGGCGCCGGGAATTCGTCGACTG
GATCCGGTACCGAGGAGATCTGCCGCC CGCATCGCC
ATGGCCCTGACCTCAGACCTGGGAAACAGATAAAACTGAAAGAGGTGGAGGGGACCCTCCTGCAGCCT
GCAACTGTGGACAACCTGGAGCCAGATCCAGAGCTTCGAGGCCAAACCAGATGATCTCCTCATCTGCACC
TACCCTAAAGCAGGGACAACGTGGATT CAGGAAATTTGGGATATGATTGAACAGAATGGGGACGTGGAG
AAGTGCCAGCGAGCCATCATCCAACACCCGCATCCTTTTCATTGAGTGGGCTCGGCCACCCCAACCTTCT
GAGACAGGATTTACCATGTTGCCAGGCTGGTCTCAAACCTCCTGAGCTCAAGCAATCCACCTGCCTCA
ACCTCCCAAAGTGCCAAGATTACAGACCTGCTGCCACCGTCTTTCTGGGAAAACAACCTGCAAGTTCTT
TATGTAGCTCGAAATGCCAAAGACTGTATGGTTTCTACTACCATTTCCAAAGGATGAACCACATGCTT
CCTGACCCCTGGTACCTGGGAAGGATATTTTGAACCTTCATCAATGGAAAAGTGGTTTGGGGTTCCTGG
TTTGACCACGTGAAAGGATGGTGGGAGATGAAAGACAGACACCAGATTCTCTTCTTCTATGAGGAC
ATAAAGAGGGACCCAAAGCATGAAATTCGGAAGGTGATGCAGTTCATGGGAAAGAAGGTGGATGAAACA
GTGCTAGATAAAATTTGCCAGGAGACGTCATTTGAGAAAATGAAAGAAAATCCCATGACAAATCGTTCT
ACAGTTTCCAAATCTATCTTGGACCAGTCAATTTCTCCTTCATGAGAAAAGGAAGTGTGGGGGATTGG
AAAAACCACTTCACTGTTGCCAGAATGAGAGGTTTGATGAAATCTATAGAAGAAAGATGGAAGGAACC
TCCATAAACTTCTGCATGGAACTGA
ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
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Restriction Sites:	Sgfl-MluI
ACCN:	NM_176825
Insert Size:	924 bp



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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:	<ol style="list-style-type: none">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_176825.2
RefSeq Size:	2832 bp
RefSeq ORF:	924 bp
Locus ID:	6819
UniProt ID:	O00338
Cytogenetics:	2q12.3
MW:	35.9 kDa
Gene Summary:	<p>Sulfotransferase enzymes catalyze the sulfate conjugation of many hormones, neurotransmitters, drugs, and xenobiotic compounds. These cytosolic enzymes are different in their tissue distributions and substrate specificities. The gene structure (number and length of exons) is similar among family members. This gene encodes a protein that belongs to the SULT1 subfamily, responsible for transferring a sulfo moiety from PAPS to phenol-containing compounds. Two alternatively spliced transcript variants encoding different isoforms have been described for this gene. [provided by RefSeq, Jul 2008]</p> <p>Transcript Variant: This variant (2) contains one alternate in-frame segment and uses a different splice site in an adjacent exon when compared to variant 1. The resulting isoform (b) is longer with a different internal protein sequence when compared to isoform a. Sequence Note: This RefSeq record was created from transcript and genomic sequence data because no single transcript was available for the full length of the gene. The extent of this transcript is supported by transcript alignments and orthologous data.</p>