

Product datasheet for **MC228082**

Hs6st2 (NM_001290468) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Hs6st2 (NM_001290468) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Hs6st2
Synonyms:	6OST2
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Cell Selection:	Neomycin



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Fully Sequenced ORF: >MC228082 representing NM_001290468
 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
 GCC**CGCATCGCC**

ATGGATGAGAAATCTAACAAGCTGCTGCTGGCTTTGGTATGCTCTTCTATTTGCGGTGATCGTCTCC
 AATACGTGTGCCCGGCACAGAATGCCAGCTCCTCCGCCGTCAGGCGTTACGCTCCCGGTGCCGATCC
 GTACCGCTCGGAGGATGAGAGTTCGGCCAGTTTGTACCCGCTACAATTCAGCCCGCGGATCTCCTG
 CGCAAGGTAGACTTCGACATCAAGGGCGATGACCTGATCGTGTTCTGCACATCCAGAAGACTGGGGCA
 CCCTTTTGGCCGTACCTGGTGCACAACATCCAGCTGGAGCAGCCATGTGAGTGCCCGTGGGGCAGAA
 GAAATGCACTTGCCACCGCCGGTAAGAGGGAGACCTGGCTCTTCTCCAGGTTCTCCACCGCTGGAGC
 TGCGGGTGCATGCCACTGGACCGAGCTACCAGCTGCGTGCCGGCGGTGGTGGATGGCAAGCGCGACG
 CCAGGCTGAGACCTTCCAGGTGGAGATTTTTCAGATTCTAGATGGAACAAGTAAGGATAGATGGGGTTC
 TTCAAACCTCAACTCAGCGCCAACTCTCCATCCTCCACAAAGCCCCGGAGCACATCGAAGAGTGGGAAG
 AACTTCCATTACATTACCATCCTGAGAGACCCAGTGTCACGGTACTTGAGTGAATGGAGGCATGTCCAGA
 GAGGAGCAACTTGAAAGCATCCCTGCACGTCTGTGATGGAAGGCCCCAACTCTGAAGAGCTGCCAG
 CTGCTACACCGGTGATGACTGGTCTGGATGCCCTCTCAAAGAGTTCATGGACTGTCCCTATAATCTGGCC
 AACAACCGCAAGTTCGCATGCTATCTGACCTGACTCTAGTGGGATGCTACAACCTCTGTGCATGCCTG
 AAAAGCAAAGAAACAAAGTCTTCTGAAAAGTGCCAAATCCAATCTGAAGCACATGGCGTCTTTGGCCT
 CACTGAGTTTTCAGCGAAGACCCAGTACCTGTTGAGAAGACCTCAACATGAATTTATCTCGCCGTTT
 ACCCAGTATAATACCCTAGGGCCTCTAGTGTGAGATCAATGAGGAAATCCAAAAGCGTATTGAGGGAC
 TGAATTTCTGGATATGGAGTTGTACAGCTATGCTAAAGACCTTTTCTGCAAAGTATCAGTTTCATGAG
 GCAGAAAAGAACATCAGGATGCCAGGCGGAAGCGTCAGGAGCAACGCAAAATTTCTGAAGGGAAGTTCCTT
 CAGACCCATTTCCAGAGTCAGAGTCAGGGTCAGAGCCAGAGCCAGAGTCCAGGTCAGAATCTGAGTCAGA
 ATCCAAATCCTAACCCAAATCAGAACCTGACTCAGAACCTGAGTCACAATCTGACTCCGAGTTCAAATCC
 CAATTCGACCCAGAGGGAGAACCGGGGAAGTCAGAAGCAGGGCTCAGGCCAGGGACAAGGTGATAGCGGC
 ACCAGCAATGGCACCAATGACTACATAGGGAGCGTAGAGACATGGCG**TAA**

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
 ACAAGGATGACGACGATAAGGTTTAA

- Restriction Sites:** Sgfl-MluI
- ACCN:** NM_001290468
- Insert Size:** 1521 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:** Clone contains native stop codon, and expresses the complete ORF without any c-terminal tag.
- 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_001290468.1](#), [NP_001277397.1](#)

RefSeq Size: 4433 bp

RefSeq ORF: 1521 bp

Locus ID: 50786

UniProt ID: [Q80UW0](#)

Cytogenetics: X A5

Gene Summary: 6-O-sulfation enzyme which catalyzes the transfer of sulfate from 3'-phosphoadenosine 5'-phosphosulfate (PAPS) to position 6 of the N-sulfoglucosamine residue (GlcNS) of heparan sulfate.[UniProtKB/Swiss-Prot Function]
Transcript Variant: This variant (4) differs in the 5' UTR, lacks a portion of the 5' coding region, and initiates translation at a downstream in-frame start codon, compared to variant 1. The encoded isoform (4) has a shorter N-terminus 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.