

Product datasheet for **SC325580**

GSTM2 (NM_001142368) Human Untagged Clone

Product data:

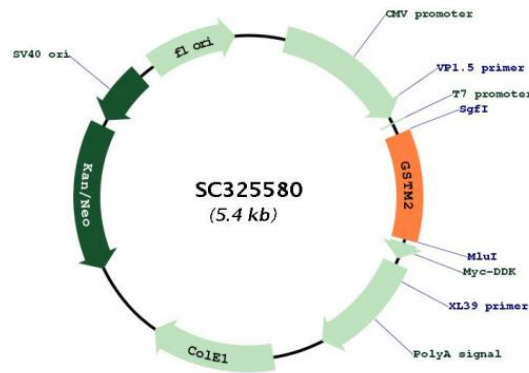
Product Type: Expression Plasmids
Product Name: GSTM2 (NM_001142368) Human Untagged Clone
Tag: Tag Free
Symbol: GSTM2
Synonyms: GST4; GSTM; GSTM2-2; GTHMUS
Mammalian Cell Selection: Neomycin
Vector: pCMV6-Entry (PS100001)
E. coli Selection: Kanamycin (25 ug/mL)
Fully Sequenced ORF: >SC325580 representing NM_001142368.
 Blue=Insert sequence Red=Cloning site Green=Tag(s)

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GCTCGTTTAGTGAACCGTCAGAATTTGTAAACGACTCACTATAGGGCGCCGGGAATTCGTCGACTG
GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC
ATGCCATGACTGGGGTACTGGAACATCCGCGGGCTGGCCATTCCATCCGCCTGCTCCTGGAATAC
ACAGACTCAAGCTACGAGGAAAAGAAGTACACGATGGGGGACGCTCCTGATTATGACAGAAGCCAGTGG
CTGAATGAAAAATCAAGCTGGGCCTGGACTTTCCCAATCTGCCCTACTTGATTGATGGGACTCACAAAG
ATCACCCAGAGCAACGCCATCTGCGGTACATTGCCCGCAAGCACAACTGTGCGGGGAATCAGAAAAG
GAGCAGATTCGCGAAGACATTTGGAGAACCAGTTTATGGACAGCCGTATGCAGCTGGCCAAACTCTGC
TATGACCCAGATTTTGGAAAAGTAAACCAGAATACCTGCAGGCACTCCCTGAAATGCTGAAGCTCTAC
TCACAGTTTCTGGGAAGCAGCCATGGTTTCTTGGGGACAAGATCACCTTTGTGGATTTTCATCGCTTAT
GATGTCCTTGAGAGAAACCAAGTATTTGAGCCAGCTGCCTGGATGCCTTCCCAAACCTGAAGGACTTC
ATCTCCGATTTGAGCATTCTGA
ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
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Restriction Sites: Sgfl-MluI



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Plasmid Map:


ACCN: NM_001142368

Insert Size: 576 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_001142368.1 |
| RefSeq Size: | 1478 bp |
| RefSeq ORF: | 576 bp |
| Locus ID: | 2946 |
| UniProt ID: | P28161 |
| Cytogenetics: | 1p13.3 |
| Protein Pathways: | Drug metabolism - cytochrome P450, Glutathione metabolism, Metabolism of xenobiotics by cytochrome P450 |
| MW: | 22.6 kDa |
| Gene Summary: | <p>Cytosolic and membrane-bound forms of glutathione S-transferase are encoded by two distinct supergene families. At present, eight distinct classes of the soluble cytoplasmic mammalian glutathione S-transferases have been identified: alpha, kappa, mu, omega, pi, sigma, theta and zeta. This gene encodes a glutathione S-transferase that belongs to the mu class. The mu class of enzymes functions in the detoxification of electrophilic compounds, including carcinogens, therapeutic drugs, environmental toxins and products of oxidative stress, by conjugation with glutathione. The genes encoding the mu class of enzymes are organized in a gene cluster on chromosome 1p13.3 and are known to be highly polymorphic. These genetic variations can change an individual's susceptibility to carcinogens and toxins as well as affect the toxicity and efficacy of certain drugs. [provided by RefSeq, Jul 2008]</p> <p>Transcript Variant: This variant (2) uses an alternate splice pattern in the 3' coding region, compared to variant 1. The resulting isoform (2) has a shorter and distinct C-terminus, compared to 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.</p> |