

Product datasheet for **SC306294**

GSTM1 (NM_146421) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	GSTM1 (NM_146421) Human Untagged Clone
Tag:	Tag Free
Symbol:	GSTM1
Synonyms:	GST1; GSTM1-1; GSTM1a-1a; GSTM1b-1b; GTH4; GTM1; H-B; MU; MU-1
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC306294 representing NM_146421. Blue=Insert sequence Red=Cloning site Green=Tag(s)

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GCTCGTTT TAGTGAACCGTCAGAATTTTGT AATACGACTCACTATAGGGCGCCGGGAATTCGTCGACTG
GATCCGGTACCGAGGAGATCTGCCGCC CGGATCGCC
ATGCCATGACTGGGGTACTGGGACATCCGCGGGCTGGCCACGCCATCCGCCTGCTCCTGGAATAC
ACAGACTCAAGCTATGAGGAAAAGAAGTACACGATGGGGGACGCTCCTGATTATGACAGAAGCCAGTGG
CTGAATGAAAAATTCAGCTGGGCCTGGACTTCCCAATCTGCCCTACTTGATTGATGGGGCTCACAAG
ATCACCAGAGCAACGCCATCTGTGCTACATTGCCCGCAAGCACAACCTGTGTGGGGAGACAGAAGAG
GAGAAGATTCGTGTGGACATTTGGAGAACCAGACCATGGACAACCATATGCAGCTGGGCATGATCTGC
TACAATCCAGAATTTGAGAACTGAAGCCAAAGTACTTGGAGGAACCTCCCTGAAAAGCTAAAGCTCTAC
TCAGAGTTTCTGGGAAGCGGCCATGGTTTGCAGGAAACAAGGGCTTGGAGAAGATCTCTGCCTACATG
AAGTCCAGCCGCTTCTCCCAAGACCTGTGTTCTCAAAGATGGCTGTCTGGGGCAACAAGTAG
ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGCGC
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Restriction Sites:	Sgfl-Mlul
Plasmid Map:	<input type="checkbox"/>
ACCN:	NM_146421
Insert Size:	546 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).



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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_146421.2
RefSeq Size:	1155 bp
RefSeq ORF:	546 bp
Locus ID:	2944
UniProt ID:	P09488
Cytogenetics:	1p13.3
Protein Families:	Druggable Genome
Protein Pathways:	Drug metabolism - cytochrome P450, Glutathione metabolism, Metabolism of xenobiotics by cytochrome P450
MW:	21.3 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. Null mutations of this class mu gene have been linked with an increase in a number of cancers, likely due to an increased susceptibility to environmental toxins and carcinogens. Multiple protein isoforms are encoded by transcript variants of this gene. [provided by RefSeq, Jul 2008]</p> <p>Transcript Variant: This variant (2) lacks an internal in-frame exon in the coding region, compared to variant 1. The resulting protein (isoform 2) maintains the reading frame but is 37 amino acids shorter than isoform 1.</p>