

Product datasheet for SC206374

GSTM4 (NM_000850) Human 3' UTR Clone

Product data:

OriGene Technologies, Inc.

9620 Medical Center Drive, Ste 200 Rockville, MD 20850, US Phone: +1-888-267-4436 https://www.origene.com techsupport@origene.com EU: info-de@origene.com CN: techsupport@origene.cn

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Product Type:	3' UTR Clones
Product Name:	GSTM4 (NM_000850) Human 3' UTR Clone
Vector:	pMirTarget (PS100062)
Symbol:	GSTM4
Synonyms:	GSTM4-4; GTM4
ACCN:	NM_000850
Insert Size:	476 bp
Insert Sequence:	<pre>>SC206374 3'UTR clone of NM_000850 The sequence shown below is from the reference sequence of NM_000850. The complete sequence of this clone may contain minor differences, such as SNPs. Blue=Stop Codon Red=Cloning site GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC ACAAGGGTGGCTGTCTGGGGCAACAAGTAATGCCTTGAAGGCCAGGAGGTGGGAGTGAGGAGCCCATAC TCAGCCTGCTGCCCAGGCTGTGCAGCGCAGC</pre>
Restriction Sites:	Sgfl-Mlul
OTI Disclaimer:	Our molecular clone sequence data has been matched to the sequence identifier above as a point of reference. Note that the complete sequence of this clone is largely the same as the reference sequence but may contain minor differences , e.g., single nucleotide polymorphisms (SNPs).
Components:	The cDNA clone is shipped in a 2-D bar-coded Matrix tube as 10 ug dried plasmid DNA. The package also includes 100 pmols of both the corresponding 5' and 3' vector primers in separate vials.
RefSeq:	<u>NM 000850.5</u>



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	GSTM4 (NM_000850) Human 3' UTR Clone – SC206374
Summary:	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. Diversification of these genes has occurred in regions encoding substrate-binding domains, as well as in tissue expression patterns, to accommodate an increasing number of foreign compounds. Multiple transcript variants, each encoding a distinct protein isoform, have been identified. [provided by RefSeq, Jul 2008]
Locus ID:	2948
MW:	17

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