

Product datasheet for **SC203808**

Glutathione S Transferase kappa 1 (GSTK1) (NM_015917) Human 3' UTR Clone

Product data:

Product Type:	3' UTR Clones
Product Name:	Glutathione S Transferase kappa 1 (GSTK1) (NM_015917) Human 3' UTR Clone
Vector:	pMirTarget (PS100062)
Symbol:	GSTK1
Synonyms:	GST; GST13; GST 13-13; GST13-13; GSTK1-1; hGSTK1
ACCN:	NM_015917
Insert Size:	308 bp
Insert Sequence:	>SC203808 3'UTR clone of NM_015917 The sequence shown below is from the reference sequence of NM_015917. The complete sequence of this clone may contain minor differences, such as SNPs. Blue =Stop Codon Red =Cloning site GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAAGCCAAGAAGGGCGGAAAGATCGCCGTG TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC ATACCTCCAGCCGTGAATGCCAGACTTTAAGATTGCCCGGAGGAAGCAAACCTCTTCGTATAAAAAAAGC AGGCCATCTGCTTAACCCTTGGCTCCACCATAAGGCACTGGGACTCGGATTCTCTATCTGATAGAGGT ATTTTCTGTGGCCCTGGGAGCTGTCTGTCTTTCCCTACCCCAAGGATGCCAGGAAGACGTCCACCAT TAGCCATGTGGCAACCTTTACTTCTATGCCTCACAAAGTGCCCTTTCAGAGAGCCCAATTCTGCTTTCCC ACAAAATAAACCTAATGCCATCAGGCAAAACA ACGCGT AAGCGGCCGCGGCATCTAGATTGGAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA CGAGATTCGATTCCACCGCCCTTCTATGAAAGG
Restriction Sites:	Sgfl-MluI
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_015917.3</u>



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Summary: This gene encodes a member of the kappa class of the glutathione transferase superfamily of enzymes that function in cellular detoxification. The encoded protein is localized to the peroxisome and catalyzes the conjugation of glutathione to a wide range of hydrophobic substates facilitating the removal of these compounds from cells. Alternative splicing results in multiple transcript variants.[provided by RefSeq, Jan 2009]

Locus ID: 373156

MW: 11.2