

Product datasheet for **SC200513**

OGG1 (NM_016820) Human 3' UTR Clone

Product data:

Product Type:	3' UTR Clones
Product Name:	OGG1 (NM_016820) Human 3' UTR Clone
Vector:	pMirTarget (PS100062)
Symbol:	OGG1
Synonyms:	HMMH; HOGG1; MUTM; OGH1
ACCN:	NM_016820
Insert Size:	109 bp
Insert Sequence:	>SC200513 3'UTR clone of NM_016820 The sequence shown below is from the reference sequence of NM_016820. The complete sequence of this clone may contain minor differences, such as SNPs. Blue=Stop Codon Red=Cloning site GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAAGCCAAGAAGGGCGGAAAGATCGCCGTG TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC TGCACAACAAGATGGGGTGGGGGATATTGAGGGAGACAGCGCTAAGGATGGTTTTATCTTCCCTTTATT ACAAGAAGGAACAATAAAATAGAAACATTTGTATGGAAAA ACGCGTAAGCGGCCGCGCATCTAGATTGAAGAAAATGACCGACCAAGCGACGCCAACCTGCCATCA CGAGATTTGATTCCACCGCCGCTTCTATGAAAGG
Restriction Sites:	SgfI-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_016820.4</u>



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Summary:

This gene encodes the enzyme responsible for the excision of 8-oxoguanine, a mutagenic base byproduct which occurs as a result of exposure to reactive oxygen. The action of this enzyme includes lyase activity for chain cleavage. Alternative splicing of the C-terminal region of this gene classifies splice variants into two major groups, type 1 and type 2, depending on the last exon of the sequence. Type 1 alternative splice variants end with exon 7 and type 2 end with exon 8. All variants share the N-terminal region in common, which contains a mitochondrial targeting signal that is essential for mitochondrial localization. Many alternative splice variants for this gene have been described, but the full-length nature for every variant has not been determined. [provided by RefSeq, Aug 2008]

Locus ID:

4968

MW:

4.4