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Product datasheet for RC200522L4V

OGG1 (NM_002542) Human Tagged ORF Clone Lentiviral Particle

Product data:

Product Type:	Lentiviral Particles
Product Name:	OGG1 (NM_002542) Human Tagged ORF Clone Lentiviral Particle
Symbol:	OGG1
Synonyms:	HMMH; HOGG1; MUTM; OGH1
Mammalian Cell Selection:	Puromycin
Vector:	pLenti-C-mGFP-P2A-Puro (PS100093)
Tag:	mGFP
ACCN:	NM_002542
ORF Size:	1035 bp
ORF Nucleotide Sequence:	The ORF insert of this clone is exactly the same as(RC200522).
OTI Disclaimer:	The molecular sequence of this clone aligns with the gene accession number as a point of reference only. However, individual transcript sequences of the same gene can differ through naturally occurring variations (e.g. polymorphisms), each with its own valid existence. This clone is substantially in agreement with the reference, but a complete review of all prevailing variants is recommended prior to use. More info
OTI Annotation:	This clone was engineered to express the complete ORF with an expression tag. Expression varies depending on the nature of the gene.
RefSeq:	NM_002542.5, NP_002533.1
RefSeq Size:	1652 bp
RefSeq ORF:	1038 bp
Locus ID:	4968
UniProt ID:	O15527
Cytogenetics:	3p25.3
Domains:	HHH, ENDO3c
Protein Families:	Druggable Genome

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Protein Pathways: Base excision repair

MW: 38.8 kDa

Gene 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]