

## Recombinant Human OGG1 cell lysate

Cat. No. OGG1-1246HCL Lot. No. (See product label)

### SPECIFICATION

**Species**

Human

**Description**

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.

**Size**

100 ul

**Storage Buffer**

1X Sample Buffer (50 mM Tris-HCl, 2% SDS, 10% glycerol, 300 mM 2-mercaptoethanol, 0.01% Bromophenol blue)

**Applications**

Western Blot;


### GENE INFORMATION

**Gene Name**


OGG1 8-oxoguanine DNA glycosylase [ Homo sapiens ]

**Official Symbol**

OGG1

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|                            |  |
|----------------------------|--|
| <b>Synonyms</b>            | OGG1; 8-oxoguanine DNA glycosylase; N-glycosylase/DNA lyase; 8 hydroxyguanine DNA glycosylase; HMMH; HOGG1; MUTM; OGG1 type 1d; OGG1 type 1e; OGG1 type 1g; OGG1 type 1h; OGH1; AP lyase; OGG1 type 1f; 8-hydroxyguanine DNA glycosylase; DNA-apurinic or apyrimidinic site lyase;   |
| <b>Gene ID</b>             | <a href="#">4968</a>   |
| <b>mRNA Refseq</b>         | <a href="#">NM_002542</a>  |
| <b>Protein Refseq</b>      | <a href="#">NP_002533</a>  |
| <b>MIM</b>                 | <a href="#">601982</a>   |
| <b>UniProt ID</b>          | <a href="#">O15527</a>   |
| <b>Chromosome Location</b> | 3p26   |
| <b>Pathway</b>             | Base Excision Repair, organism-specific biosystem; Base excision repair, organism-specific biosystem; Base excision repair, conserved biosystem; Base-Excision Repair, AP Site Formation, organism-specific biosystem; Base-free sugar-phosphate removal via the single-nucleotide replacement pathway, organism-specific biosystem; Cleavage of the damaged purine, organism-specific biosystem; DNA Repair, organism-specific biosystem; |
| <b>Function</b>            | damaged DNA binding; endonuclease activity; hydrolase activity, acting on glycosyl bonds; lyase activity; oxidized purine base lesion DNA N-glycosylase activity; protein binding;   |

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