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Lieferung & Zahlungsart

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Zuschläge

- Mindermengenzuschlag
- Trockeneiszuschlag
- Gefahrgutzuschlag
- Expressversand

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Datasheet

OGG1 (Human) Recombinant Protein (P01)

Catalog Number: H00004968-P01

Regulation Status: For research use only (RUO)

Product Description: Human OGG1 full-length ORF (NP_058212.1, 1 a.a. - 324 a.a.) recombinant protein with GST-tag at N-terminal.

Sequence:

MPARALLPRRMGHRTLASTPALWASIPCPRSELRLDL
VLPSSGQSFWRWREQSPAHWVSGVLADQVWTLTQTEEQ
HCTVYRQDKSQASRPTPDELEAVRKYFQLDVTLAQLY
HHWGSVDSHFQEVAKFKQGVRLLRQDPIECLFSFICS
SNNNIARITGMVERLCQAFGPRLIQLDDVTYHGFPSLQ
ALAGPEVEAHLRKLGLGYRARYVSASARAILEEQGGL
AWLQQLRESSYEEAHKALCILPGVGTKVADCICLMALD
KPQAVPVDVHMWHIAQRDYSWHPTTSQAKGSPSQTN
KELGNFFRSLWGPYAGWAQAVSVPRCPP

Host: Wheat Germ (in vitro)

Theoretical MW (kDa): 62.8

Applications: AP, Array, ELISA, WB-Re
(See our web site product page for detailed applications information)

Protocols: See our web site at
<http://www.abnova.com/support/protocols.asp> or product page for detailed protocols

Preparation Method: [in vitro wheat germ expression system](#)

Purification: Glutathione Sepharose 4 Fast Flow

Storage Buffer: 50 mM Tris-HCl, 10 mM reduced Glutathione, pH=8.0 in the elution buffer.

Storage Instruction: Store at -80°C. Aliquot to avoid repeated freezing and thawing.

Entrez GeneID: 4968

Gene Symbol: OGG1

Gene Alias: HMMH, HOGG1, MUTM, OGH1

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]