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Zuschläge

- Mindermengenzuschlag
- Trockeneiszuschlag
- Gefahrgutzuschlag
- Expressversand

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Datasheet

ATP6V1G2 (Human) Recombinant Protein (Q01)

Catalog Number: H00000534-Q01

Regulation Status: For research use only (RUO)

Product Description: Human ATP6V1G2 partial ORF (NP_569730, 41 a.a. - 118 a.a.) recombinant protein with GST-tag at N-terminal.

Sequence:

QMEVEQYRREREHEFQSKQQAAMGSQGNLSAEVEQ
ATTRQVQGMQSSQQRNRERVLAQLLGMVCDVRPQV
HPNYRISA

Host: Wheat Germ (in vitro)

Theoretical MW (kDa): 34.32

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: 534

Gene Symbol: ATP6V1G2

Gene Alias: ATP6G, ATP6G2, NG38, VMA10

Gene Summary: This gene encodes a component of vacuolar ATPase (V-ATPase), a multisubunit enzyme that mediates acidification of intracellular compartments of eukaryotic cells. V-ATPase dependent acidification is necessary for such intracellular processes as protein

sorting, zymogen activation, receptor-mediated endocytosis, and synaptic vesicle proton gradient generation. V-ATPase is composed of a cytosolic V1 domain and a transmembrane V0 domain. The V1 domain consists of three A and three B subunits, two G subunits plus the C, D, E, F, and H subunits. The V1 domain contains the ATP catalytic site. The V0 domain consists of five different subunits: a, c, c', c'', and d. Additional isoforms of many of the V1 and V0 subunit proteins are encoded by multiple genes or alternatively spliced transcript variants. This encoded protein is one of three V1 domain G subunit proteins. This gene had previous gene symbols of ATP6G and ATP6G2. Alternatively spliced transcript variants encoding different isoforms have been described. [provided by RefSeq]