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Zuschläge

- Mindermengenzuschlag
- Trockeneiszuschlag
- Gefahrgutzuschlag
- Expressversand

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Datasheet

GOLGA2 (Human) Recombinant Protein (P01)

Catalog Number: H00002801-P01

Regulation Status: For research use only (RUO)

Product Description: Human GOLGA2 full-length ORF (AAH06381.1, 1 a.a. - 345 a.a.) recombinant protein with GST-tag at N-terminal.

Sequence:

MQNDRTTISRALSQNRELKEQLAELQSGFVKLTNENM
EITSALQSEQHVKRELGKKGELQEKLSELKETVELKS
QEAQSLQQQRDQYLGLHQQYVAAYQQLTSEKEVLHN
QLLLQTQLVDQLQQQEAQGKAVAEMARQELQETQER
LEAATQQNQQLRAQLSLMAHPGEGDGLDREEEDEE
EEEEAVAVPQPMPSIPEDLESREAMVAFFNSAVASAE
EEQARLRGQLKEQSVRCRRLAHLASAQKEPEAAAPA
PGTGGDSVCGETHRALQGAMEKLQSRFMEMLQKEA
DLKERPGRVLPVTTPLHSRSCSCFVRCRTPGSAQAW
AATPAFLFFTGLTRMMR

Host: Wheat Germ (in vitro)

Theoretical MW (kDa): 63.58

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: 2801

Gene Symbol: GOLGA2

Gene Alias: GM130, MGC20672

Gene Summary: The Golgi apparatus, which participates in glycosylation and transport of proteins and lipids in the secretory pathway, consists of a series of stacked cisternae (flattened membrane sacs). Interactions between the Golgi and microtubules are thought to be important for the reorganization of the Golgi after it fragments during mitosis. The golgins are a family of proteins, of which the protein encoded by this gene is a member, that are localized to the Golgi. This encoded protein has been postulated to play roles in the stacking of Golgi cisternae and in vesicular transport. Several alternatively spliced transcript variants of this gene have been described, but the full-length nature of these variants has not been determined. [provided by RefSeq]