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Zuschläge

- Mindermengenzuschlag
- Trockeneiszuschlag
- Gefahrgutzuschlag
- Expressversand

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Datasheet

TNK2 (Human) Recombinant Protein (P01)

Catalog Number: H00010188-P01

Regulation Status: For research use only (RUO)

Product Description: Human TNK2 full-length ORF (AAH08884.1, 1 a.a. - 352 a.a.) recombinant protein with GST-tag at N-terminal.

Sequence:

MQPEEGTGWLLELLSEVQLQQYFLRLRDDLNVTRLSH
FEYVKNEDEKIGMGRPGQRRLWEAVKRRKALCKRK
SWMSKVFSGKRLEAEFPPHHSQSTFRKTSPAPGGPA
GEGPLQSLTCLIGEKDLRLLLEKLDGGSFVVRRGEWD
APSGKTVSVAVKCLKPDVLSQPEAMDDFIREVNAMHS
LDHRNLIRLYGVVLTTPMKMVTE LAPLSLLDRLRKHQ
GHFLLGTLSTRYAVQVAEGMGYLESKRFIHRDLAARNLL
LATRDLVKIGDFGLMRALPQNDHYVMQEHRKVPFA
WCAPESLKPPWRDISASSSTQFPHAVPCFPTSLAKLL
LRHSVPASSREIKLVSILC

Host: Wheat Germ (in vitro)

Theoretical MW (kDa): 66.2

Interspecies Antigen Sequence: Mouse (95); Rat (96)

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: 10188

Gene Symbol: TNK2

Gene Alias: ACK, ACK1, FLJ44758, FLJ45547, p21cdc42Hs

Gene Summary: This gene encodes a tyrosine kinase that binds Cdc42Hs in its GTP-bound form and inhibits both the intrinsic and GTPase-activating protein (GAP)-stimulated GTPase activity of Cdc42Hs. This binding is mediated by a unique sequence of 47 amino acids C-terminal to an SH3 domain. The protein may be involved in a regulatory mechanism that sustains the GTP-bound active form of Cdc42Hs and which is directly linked to a tyrosine phosphorylation signal transduction pathway. Several alternatively spliced transcript variants have been identified from this gene, but the full-length nature of only two transcript variants has been determined. [provided by RefSeq]