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Lieferung & Zahlungsart

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Zuschläge

- Mindermengenzuschlag
- Trockeneiszuschlag
- Gefahrgutzuschlag
- Expressversand

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Datasheet

AGTR1 (Human) Recombinant Protein (Q01)

Catalog Number: H00000185-Q01

Regulation Status: For research use only (RUO)

Product Description: Human AGTR1 partial ORF (AAH22447, 250 a.a. - 359 a.a.) recombinant protein with GST-tag at N-terminal.

Sequence:
FFSWIPHQIFTFLDVLIQLGIIRDCRIADIVDTAMPITICIA YFNNCLNPLFYGFLGKKFKRYFLQLLKYIPPKAKSHSN LSTKMSTLSYRHSDNVSSSTKKPAPCFEVE

Host: Wheat Germ (in vitro)

Theoretical MW (kDa): 37.73

Interspecies Antigen Sequence: Mouse (89); Rat (90)

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: 185

Gene Symbol: AGTR1

Gene Alias: AG2S, AGTR1A, AGTR1B, AT1, AT1B, AT1R, AT2R1, AT2R1A, AT2R1B, HAT1R

Gene Summary: Angiotensin II is a potent vasopressor hormone and a primary regulator of aldosterone secretion. It is an important effector controlling blood pressure and volume in the cardiovascular system. It acts through at least two types of receptors. This gene encodes the type 1 receptor which is thought to mediate the major cardiovascular effects of angiotensin II. This gene may play a role in the generation of reperfusion arrhythmias following restoration of blood flow to ischemic or infarcted myocardium. It was previously thought that a related gene, denoted as AGTR1B, existed; however, it is now believed that there is only one type 1 receptor gene in humans. At least five transcript variants have been described for this gene. Additional variants have been described but their full-length nature has not been determined. The entire coding sequence is contained in the terminal exon and is present in all transcript variants. [provided by RefSeq]