



# SZABO SCANDIC

Part of Europa Biosite

## Produktinformation



Forschungsprodukte & Biochemikalien



Zellkultur & Verbrauchsmaterial



Diagnostik & molekulare Diagnostik



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### Lieferung & Zahlungsart

siehe unsere [Liefer- und Versandbedingungen](#)

### Zuschläge

- Mindermengenzuschlag
- Trockeneiszuschlag
- Gefahrgutzuschlag
- Expressversand

### SZABO-SCANDIC HandelsgmbH

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## Datasheet

### HSD17B10 (Human) Recombinant Protein (Q01)

**Catalog Number:** H00003028-Q01

**Regulation Status:** For research use only (RUO)

**Product Description:** Human HSD17B10 partial ORF ( NP\_004484, 31 a.a. - 128 a.a.) recombinant protein with GST-tag at N-terminal.

**Sequence:**

VGQGASAVLLDLPNSGGEAQAKKLGNNCVFAPADVT  
SEKDVQ TALALAKGKFGFRVDVAVNCAGIAVASKTYNL  
KKGQHTLEDFQRVLDVNLMGTFNV

**Host:** Wheat Germ (in vitro)

**Theoretical MW (kDa):** 36.52

**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:** 3028

**Gene Symbol:** HSD17B10

**Gene Alias:** 17b-HSD10, ABAD, CAMR, DUPXp11.22, ERAB, HADH2, HCD2, MHBD, MRPP2, MRX17, MRX31, MRXS10, SCHAD, SDR5C1

**Gene Summary:** This gene encodes 3-hydroxyacyl-CoA dehydrogenase type II, a member of the short-chain dehydrogenase/reductase superfamily. The gene

product is a mitochondrial protein that catalyzes the oxidation of a wide variety of fatty acids, alcohols, and steroids. The protein has been implicated in the development of Alzheimer's disease, and mutations in the gene are the cause of 2-methyl-3-hydroxybutyryl-CoA dehydrogenase deficiency (MHBD). Several alternatively spliced transcript variants have been identified, but the full-length nature of only two transcript variants has been determined. [provided by RefSeq]