



# SZABO SCANDIC

Part of Europa Biosite

## Produktinformation



Forschungsprodukte & Biochemikalien



Zellkultur & Verbrauchsmaterial



Diagnostik & molekulare Diagnostik



Laborgeräte & Service

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See the following pages for more information!



### Lieferung & Zahlungsart

siehe unsere [Liefer- und Versandbedingungen](#)

### Zuschläge

- Mindermengenzuschlag
- Trockeneiszuschlag
- Gefahrgutzuschlag
- Expressversand

### SZABO-SCANDIC HandelsgmbH

Quellenstraße 110, A-1100 Wien

T. +43(0)1 489 3961-0

F. +43(0)1 489 3961-7

[mail@szabo-scandic.com](mailto:mail@szabo-scandic.com)

[www.szabo-scandic.com](http://www.szabo-scandic.com)

[linkedin.com/company/szaboscandic](https://www.linkedin.com/company/szaboscandic) 

## Datasheet

### FADS3 (Human) Recombinant Protein (Q01)

**Catalog Number:** H00003995-Q01

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

**Product Description:** Human FADS3 partial ORF ( NP\_068373, 16 a.a. - 113 a.a.) recombinant protein with GST-tag at N-terminal.

**Sequence:**

PGAPLPTFCWEQIRAHQPGDKWLVIERVYDISRWA  
QRHPGGSRLIGHHGAEDATDAFRAFHQDLNFVRKFLQ  
PLLIGELAPEEPSQDGPLNAQLVE

**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:** 3995

**Gene Symbol:** FADS3

**Gene Alias:** CYB5RP, LLCDL3

**Gene Summary:** The protein encoded by this gene is a member of the fatty acid desaturase (FADS) gene family. Desaturase enzymes regulate unsaturation of fatty acids through the introduction of double bonds between defined carbons of the fatty acyl chain. FADS

family members are considered fusion products composed of an N-terminal cytochrome b5-like domain and a C-terminal multiple membrane-spanning desaturase portion, both of which are characterized by conserved histidine motifs. This gene is clustered with family members FADS1 and FADS2 at 11q12-q13.1; this cluster is thought to have arisen evolutionarily from gene duplication based on its similar exon/intron organization. [provided by RefSeq]