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Zuschläge

- Mindermengenzuschlag
- Trockeneiszuschlag
- Gefahrgutzuschlag
- Expressversand

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Datasheet

FADS3 (Human) Recombinant Protein (P01)

Catalog Number: H00003995-P01

Regulation Status: For research use only (RUO)

Product Description: Human FADS3 full-length ORF (NP_068373.1, 1 a.a. - 445 a.a.) recombinant protein with GST-tag at N-terminal.

Sequence:

MGGVGEPPREGPAQPGAPLPTFCWEQIRAHQDQPG
DKWLVIERVYDISRWAQRHPGGSRLIGHHGAEDATD
AFRAFHQDLNFVRKFLQPLLIGELAPEEPSQDGPLNAQ
LVEDFRALHQAEDMKLFDASPTFFAFLGHILAMEVL
AWLLIYLLGPGWVPSALAAFILAISQAQSWCLQHDLGH
ASIFKKSWWNHVAQKFVMGQLKGFSAHWWNFRHFQ
HHAKPNIFHKDPDVTVAPVFLGESSVEYGKKRRYLP
YNQQHLYFFLIGPPLLTLVNFEEVENLAYMLVCMQWAD
LLWAASFYARFFLSYLPFYGVPGVLLFFVAVRVLESHW
FVWITQMNHIPPKEIGHEKHRDWVSSQLAATCNVEPSL
FTNWFSGHLNFQIEHHLFPRMPRHNYSRVAPLVKSLC
AKHGLSYEVKPFALTALVDIVRSLKKSQDIWLDAYLHQ

Host: Wheat Germ (in vitro)

Theoretical MW (kDa): 77.5

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]