

## **Product datasheet for PH323780**

## OriGene Technologies, Inc.

9620 Medical Center Drive, Ste 200 Rockville, MD 20850, US Phone: +1-888-267-4436 https://www.origene.com techsupport@origene.com EU: info-de@origene.com CN: techsupport@origene.cn

## FADS2 (NM\_004265) Human Mass Spec Standard

**Product data:** 

**Product Type:** Mass Spec Standards

**Description:** FADS2 MS Standard C13 and N15-labeled recombinant protein (NP\_004256)

Species:HumanExpression Host:HEK293

Expression cDNA Clone

RC223780

or AA Sequence: Predicted MW:

52.1 kDa

Protein Sequence: >RC223780 representing NM\_004265

Red=Cloning site Green=Tags(s)

MGKGGNQGEGAAEREVSVPTFSWEEIQKHNLRTDRWLVIDRKVYNITKWSIQHPGGQRVIGHYAGEDATD AFRAFHPDLEFVGKFLKPLLIGELAPEEPSQDHGKNSKITEDFRALRKTAEDMNLFKTNHVFFLLLAHI IALESIAWFTVFYFGNGWIPTLITAFVLATSQAQAGWLQHDYGHLSVYRKPKWNHLVHKFVIGHLKGASA NWWNHRHFQHHAKPNIFHKDPDVNMLHVFVLGEWQPIEYGKKKLKYLPYNHQHEYFFLIGPPLLIPMYFQ YQIIMTMIVHKNWVDLAWAVSYYIRFFITYIPFYGILGALLFLNFIRFLESHWFVWVTQMNHIVMEIDQE AYRDWFSSQLTATCNVEQSFFNDWFSGHLNFQIEHHLFPTMPRHNLHKIAPLVKSLCAKHGIEYQEKPLL

RALLDIIRSLKKSGKLWLDAYLHK

TRTRPLEQKLISEEDLAANDILDYKDDDDKV

Tag: C-Myc/DDK

**Purity:** > 80% as determined by SDS-PAGE and Coomassie blue staining

Concentration: >0.05 µg/µL as determined by microplate BCA method

Labeling Method: Labeled with [U- 13C6, 15N4]-L-Arginine and [U- 13C6, 15N2]-L-Lysine

**Buffer:** 25 mM Tris-HCl, 100 mM glycine, pH 7.3

**Storage:** Store at -80°C. Avoid repeated freeze-thaw cycles.

**Stability:** Stable for 3 months from receipt of products under proper storage and handling conditions.

RefSeq: NP 004256

RefSeq Size: 3149 RefSeq ORF: 1332

Synonyms: D6D; DES6; FADSD6; LLCDL2; SLL0262; TU13



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**Locus ID:** 9415

 UniProt ID:
 O95864

 Cytogenetics:
 11q12.2

**Summary:** The protein encoded by this gene is a member of the fatty acid desaturase (FADS) gene

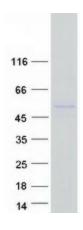
family. Desaturase enzymes regulate unsaturation of fatty acids through the introduction of double bonds between defined carbons of the fatty acyl chain. FADS family members are considered fusion products composed of an N-terminal cytochrome b5-like domain and a C-terminal multiple membrane-spanning desaturase portion, both of which are characterized by conserved histidine motifs. This gene is clustered with family members at 11q12-q13.1; this cluster is thought to have arisen evolutionarily from gene duplication based on its similar exon/intron organization. Alternative splicing results in multiple transcript variants encoding different isoforms. [provided by RefSeq, Jul 2013]

**Protein Families:** Transmembrane

**Protein Pathways:** alpha-Linolenic acid metabolism, Biosynthesis of unsaturated fatty acids, PPAR signaling

pathway

## **Product images:**



Coomassie blue staining of purified FADS2 protein (Cat# [TP323780]). The protein was produced from HEK293T cells transfected with FADS2 cDNA clone (Cat# [RC223780]) using MegaTran 2.0 (Cat# [TT210002]).