SANTA CRUZ BIOTECHNOLOGY, INC.

# FADS1 (7-RY13): sc-134337

SANTA CRUZ BIOTECHNOLOGY

*The Power to Question*

## BACKGROUND

Members of the fatty acid desaturase (FADS) family, including FADS1, FADS2 and FADS3, regulate the desaturation of fatty acids by introducing double bonds between defined carbons of fatty acyl chains, thereby playing an essential role in the lipid metabolic pathway. Members of this family share N-terminal cytochrome b5-like domains, C-terminal multiple membrane-spanning desaturase regions and three histidine box motifs. It has been suggested that single nucleotide polymorphisms (SNPs) within the FADS gene cluster may be associated with diseases related to inflammation and immunity processes. FADS1, also known as $\Delta^5$ desaturase or D5D, is a 444 amino acid protein that is abundantly expressed in liver, brain, adrenal gland and heart. Localized to the endoplasmic reticulum where it exists as a multi-pass membrane protein, FADS1 catalyzes the biosynthesis of highly unsaturated fatty acids from linoleic acid and $\alpha$-linolenic acid. Additionally, FADS1 functions to catalyze the desaturation of both dihomo-$\gamma$-linoleic acid (DHGLA) and eicosatetraenoic acid (EA) to produce arachidonic acid (AA) and eicosapentaenoic acid (EPA), respectively.

## REFERENCES


1. Cho, H.P., et al. 1999. Cloning, expression, and fatty acid regulation of the human $\Delta^5$ desaturase. J. Biol. Chem. 274: 37335-37339.
2. Marquardt, A., et al. 2000. cDNA cloning, genomic structure, and chromosomal localization of three members of the human fatty acid desaturase family. Genomics 66: 175-183.
3. Online Mendelian Inheritance in Man, OMIM™. 2002. Johns Hopkins University, Baltimore, MD. MIM Number: 606148. World Wide Web URL: http://www.ncbi.nlm.nih.gov/omim/
4. Schaeffer, L., et al. 2006. Common genetic variants of the FADS1 FADS2 gene cluster and their reconstructed haplotypes are associated with the fatty acid composition in phospholipids. Hum. Mol. Genet. 15: 1745-1756.
5. Dreesen, T.D., et al. 2006. A newly discovered member of the fatty acid desaturase gene family: a non-coding, antisense RNA gene to $\Delta^5$-desaturase. Prostaglandins Leukot. Essent. Fatty Acids 75: 97-106.


## CHROMOSOMAL LOCATION

Genetic locus: FADS1 (human) mapping to 11q12.2.

## SOURCE

FADS1 (7-RY13) is a mouse monoclonal antibody raised against recombinant FADS1 protein of human origin.

## PRODUCT

Each vial contains 100 µg $IgG_{2a}$ kappa light chain in 1.0 ml of PBS with < 0.1% sodium azide and 0.1% gelatin.

## STORAGE

Store at 4° C, **DO NOT FREEZE**. Stable for one year from the date of shipment. Non-hazardous. No MSDS required.

## APPLICATIONS

FADS1 (7-RY13) is recommended for detection of FADS1 of human origin by Western Blotting (starting dilution 1:200, dilution range 1:100-1:1000), immunoprecipitation [1-2 µg per 100-500 µg of total protein (1 ml of cell lysate)] and solid phase ELISA (starting dilution 1:30, dilution range 1:30-1:3000).

Suitable for use as control antibody for FADS1 siRNA (h): sc-96474, FADS1 shRNA Plasmid (h): sc-96474-SH and FADS1 shRNA (h) Lentiviral Particles: sc-96474-V.

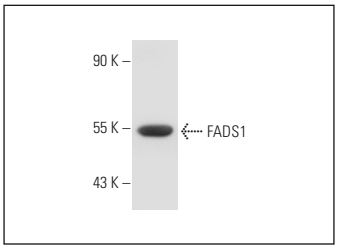
Molecular Weight of FADS1: 52 kDa.

Positive Controls: Jurkat whole cell lysate: sc-2204 or HeLa nuclear extract: sc-2120.

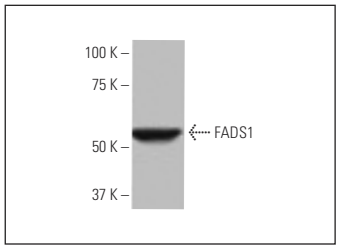
## RECOMMENDED SUPPORT REAGENTS

To ensure optimal results, the following support reagents are recommended: 1) Western Blotting: use m-IgGκ BP-HRP: sc-516102 or m-IgGκ BP-HRP (Cruz Marker): sc-516102-CM (dilution range: 1:1000-1:10000), Cruz Marker™ Molecular Weight Standards: sc-2035, UltraCruz® Blocking Reagent: sc-516214 and Western Blotting Luminol Reagent: sc-2048. 2) Immunoprecipitation: use Protein A/G PLUS-Agarose: sc-2003 (0.5 ml agarose/2.0 ml).

## DATA




FADS1 (7-RY13): sc-134337. Western blot analysis of FADS1 expression in Jurkat whole cell lysate.




FADS1 (7-RY13): sc-134337. Western blot analysis of FADS1 expression in HeLa nuclear extract.

## SELECT PRODUCT CITATIONS


1. Kühn, G., et al. 2018. Resveratrol modulates desaturase expression and fatty acid composition of cultured hepatocytes. Front. Nutr. 5: 106.
2. Tsachaki, M., et al. 2020. Impact of 17β-HSD12, the 3-ketoacyl-CoA reductase of long-chain fatty acid synthesis, on breast cancer cell proliferation and migration. Cell. Mol. Life Sci. 77: 1153-1175.
3. Schindler, M., et al. 2020. Embryonic fatty acid metabolism in diabetic pregnancy: the difference between embryoblasts and trophoblasts. Mol. Hum. Reprod. 26: 837-849.
4. Lee, J.Y., et al. 2020. Polyunsaturated fatty acid biosynthesis pathway determines ferroptosis sensitivity in gastric cancer. Proc. Natl. Acad. Sci. USA 117: 32433-32442.


## RESEARCH USE

For research use only, not for use in diagnostic procedures.