SANTA CRUZ BIOTECHNOLOGY, INC.

ATP5A (C-15): sc-49162

SANTA CRUZ BIOTECHNOLOGY

The Power to Question

BACKGROUND

Mitochondrial ATP synthases (ATPases) transduce the energy contained in membrane electrochemical proton gradients into the energy required for synthesis of high-energy phosphate bonds. ATPases contain two linked complexes: F_1, the hydrophilic catalytic core; and F_0, the membrane-embedded protein channel. F_1 consists of three α chains and three β chains, which are weakly homologous, as well as one γ chain, one δ chain and one ε chain. F_0 consists of three subunits: a, b and c. The α chain of F_1 is a regulatory subunit that contains 509 amino acids. Mitochondrial ATPase α chain (ATP5A) localizes to the mitochondria and catalyzes ATP synthesis.

REFERENCES

1. Walker, J.E., et al. 1985. Primary structure and subunit stoichiometry of F_1-ATPase from bovine mitochondria. J. Mol. Biol. 184: 677-701.
2. Kataoka, H. and Biswas, C. 1991. Nucleotide sequence of a cDNA for the α subunit of human mitochondrial ATP synthase. Biochim. Biophys. Acta 1089: 393-395.
3. Shirakihara, Y., et al. 1997. The crystal structure of the nucleotide-free $\alpha 3/\beta 3$ subcomplex of F_1-ATPase from the thermophilic *Bacillus* PS3 is a symmetric trimer. Structure 5: 825-836.
4. Godbout, R., et al. 1997. Comparative genomic hybridization analysis of Y79 and FISH mapping indicate the amplified human mitochondrial ATP synthase α subunit gene (ATP5A) maps to chromosome 18q12→q21. Cytogenet. Cell. Genet. 77: 253-256.
5. Online Mendelian Inheritance in Man, OMIM™. 2002. Johns Hopkins University, Baltimore, MD. MIM Number: 164360. World Wide Web URL: http://www.ncbi.nlm.nih.gov/omim/

CHROMOSOMAL LOCATION

Genetic locus: ATP5A1 (human) mapping to 18q21.1; Atp5a1 (mouse) mapping to 18 E3.

SOURCE

ATP5A (C-15) is an affinity purified goat polyclonal antibody raised against a peptide mapping near the C-terminus of ATP5A of human origin.

PRODUCT

Each vial contains 200 µg IgG in 1.0 ml of PBS with < 0.1% sodium azide and 0.1% gelatin.

Blocking peptide available for competition studies, sc-49162 P, (100 µg peptide in 0.5 ml PBS containing < 0.1% sodium azide and 0.2% BSA).

STORAGE

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

RESEARCH USE

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

APPLICATIONS

ATP5A (C-15) is recommended for detection of ATP5A of mouse, rat and 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)], immunofluorescence (starting dilution 1:50, dilution range 1:50-1:500) and solid phase ELISA (starting dilution 1:30, dilution range 1:30-1:3000).

ATP5A (C-15) is also recommended for detection of ATP5A in additional species, including bovine and porcine.

Suitable for use as control antibody for ATP5A siRNA (h): sc-60227, ATP5A siRNA (m): sc-60228, ATP5A shRNA Plasmid (h): sc-60227-SH, ATP5A shRNA Plasmid (m): sc-60228-SH, ATP5A shRNA (h) Lentiviral Particles: sc-60227-V and ATP5A shRNA (m) Lentiviral Particles: sc-60228-V.

Molecular Weight (predicted) of ATP5A: 60 kDa.

Molecular Weight (observed) of ATP5A: 51-71 kDa.

Positive Controls: Ramos cell lysate: sc-2216, MDA-MB-231 cell lysate: sc-2232 or MCF7 whole cell lysate: sc-2206.

RECOMMENDED SECONDARY REAGENTS

To ensure optimal results, the following support (secondary) reagents are recommended: 1) Western Blotting: use donkey anti-goat IgG-HRP: sc-2020 (dilution range: 1:2000-1:100,000) or Cruz Marker™ compatible donkey anti-goat IgG-HRP: sc-2033 (dilution range: 1:2000-1:5000), Cruz Marker™ Molecular Weight Standards: sc-2035, TBS Blotto A Blocking Reagent: sc-2333 and Western Blotting Luminol Reagent: sc-2048. 2) Immunoprecipitation: use Protein A/G PLUS-Agarose: sc-2003 (0.5 ml agarose/2.0 ml). 3) Immunofluorescence: use donkey anti-goat IgG-FITC: sc-2024 (dilution range: 1:100-1:400) or donkey anti-goat IgG-TR: sc-2783 (dilution range: 1:100-1:400) with UltraCruz™ Mounting Medium: sc-24941.

SELECT PRODUCT CITATIONS

1. Dong, S., et al. 2009. Discrete molecular states in the brain accompany changing responses to a vocal signal. Proc. Natl. Acad. Sci. USA 106: 11364-11369.
2. Gardmo, C., et al. 2011. Proteomics for the discovery of nuclear bile acid receptor FXR targets. Biochim. Biophys. Acta 1812: 836-841.

PROTOCOLS

See our web site at www.scbt.com or our catalog for detailed protocols and support products.