SANTA CRUZ BIOTECHNOLOGY, INC.

ATP5A (15H4): sc-58613

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.

CHROMOSOMAL LOCATION

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

SOURCE

ATP5A (15H4) is a mouse monoclonal antibody raised against purified ATP5A of bovine origin.

PRODUCT

Each vial contains 100 µg IgG_{2b} 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.

RESEARCH USE

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

PROTOCOLS

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

APPLICATIONS

ATP5A (15H4) 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)] and immunofluorescence (starting dilution 1:50, dilution range 1:50-1:500).

ATP5A (15H4) is also recommended for detection of ATP5A in additional species, including bovine.

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.

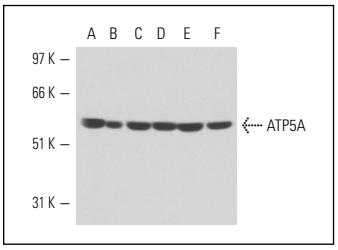
Molecular Weight (observed) of ATP5A: 51-71 kDa.

Positive Controls: Y79 cell lysate: sc-2240, MDA-MB-231 cell lysate: sc-2232 or MCF7 whole cell lysate: sc-2206.

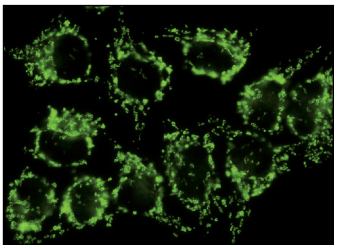
RECOMMENDED SECONDARY REAGENTS

To ensure optimal results, the following support (secondary) reagents are recommended: 1) Western Blotting: use goat anti-mouse IgG-HRP: sc-2005 (dilution range: 1:2000-1:32,000) or Cruz Marker™ compatible goat anti-mouse IgG-HRP: sc-2031 (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 goat anti-mouse IgG-FITC: sc-2010 (dilution range: 1:100-1:400) or goat anti-mouse IgG-TR: sc-2781 (dilution range: 1:100-1:400) with UltraCruz™ Mounting Medium: sc-24941.

DATA



ATP5A (15H4): sc-58613. Western blot analysis of ATP5A expression in Y79 (**A**), MDA-MB-231 (**B**), HUV-EC-C (**C**), MCF7 (**D**), WI 38 (**E**) and ARPE-19 (**F**) whole cell lysates.



ATP5A (15H4): sc-58613. Immunofluorescence staining of methanol-fixed HeLa cells showing cytoplasmic localization.

SELECT PRODUCT CITATIONS

1. Watanabe, Y., et al. 2008. Adherent monomer-misfolded SOD-1. PLoS ONE 3: e3497.
2. Zamorano-León, J.J., et al. 2010. A proteomic approach to determine changes in proteins involved in the myocardial metabolism in left ventricles of spontaneously hypertensive rats. Cell. Physiol. Biochem. 25: 347-358.