SANTA CRUZ BIOTECHNOLOGY, INC.

V-ATPase D (D-4): sc-166218

SANTA CRUZ BIOTECHNOLOGY

The Power to Question

BACKGROUND

Vacuolar-type H^+-ATPase (V-ATPase) is a multisubunit enzyme responsible for acidification of eukaryotic intracellular organelles. V-ATPases pump protons against an electrochemical gradient, while F-ATPases reverse the process, thereby synthesizing ATP. A peripheral V_1 domain, which is responsible for ATP hydrolysis and an integral V_0 domain, which is responsible for proton translocation, compose V-ATPase. Nine subunits (A-H) make up the V_1 domain and five subunits (a, d, c, c' and c'') make up the V_0 domain. Like F-ATPase, V-ATPase most likely operates through a rotary mechanism. V-ATPase C is an auxiliary subunit with ubiquitous expression.

REFERENCES

1. Nelson, H., et al. 1990. Molecular cloning of cDNA encoding the C subunit of H^+-ATPase from bovine chromaffin granules. J. Biol. Chem. 265: 20390-20393.
2. van Hille, B., et al. 1993. Cloning and tissue distribution of subunits C, D, and E of the human vacuolar H^+-ATPase. Biochem. Biophys. Res. Commun. 197: 15-21.

CHROMOSOMAL LOCATION

Genetic locus: ATP6V1D (human) mapping to 14q23.3; Atp6v1d (mouse) mapping to 12 C3.

SOURCE

V-ATPase D (D-4) is a mouse monoclonal antibody raised against amino acids 1-243 representing full length V-ATPase D of human origin.

PRODUCT

Each vial contains 200 µg IgG_1 kappa light chain in 1.0 ml of PBS with < 0.1% sodium azide and 0.1% gelatin.

RESEARCH USE

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

APPLICATIONS

V-ATPase D (D-4) is recommended for detection of V-ATPase D of mouse, rat and human origin by Western Blotting (starting dilution 1:100, 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).

Suitable for use as control antibody for V-ATPase D siRNA (h): sc-36791, V-ATPase D siRNA (m): sc-36792, V-ATPase D shRNA Plasmid (h): sc-36791-SH, V-ATPase D shRNA Plasmid (m): sc-36792-SH, V-ATPase D shRNA (h) Lentiviral Particles: sc-36791-V and V-ATPase D shRNA (m) Lentiviral Particles: sc-36792-V.

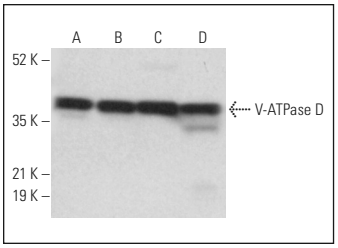
Molecular Weight of V-ATPase D: 38 kDa.

Positive Controls: EOC 20 whole cell lysate: sc-364187, NIH/3T3 whole cell lysate: sc-2210 or HeLa whole cell lysate: sc-2200.

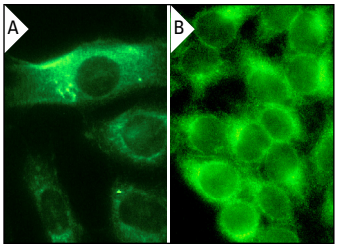
RECOMMENDED SUPPORT REAGENTS

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). 3) Immunofluorescence: use m-IgGκ BP-FITC: sc-516140 or m-IgGκ BP-PE: sc-516141 (dilution range: 1:50-1:200) with UltraCruz® Mounting Medium: sc-24941 or UltraCruz® Hard-set Mounting Medium: sc-359850.

DATA



V-ATPase D (D-4): sc-166218. Western blot analysis of V-ATPase D expression in EOC 20 (**A**), NIH/3T3 (**B**), HeLa (**C**) and T98G (**D**) whole cell lysates.



V-ATPase D (D-4): sc-166218. Immunofluorescence staining of methanol-fixed NIH/3T3 (**A**) and HeLa (**B**) cells showing cytoplasmic localization.

SELECT PRODUCT CITATIONS

1. Cang, C., et al. 2013. mTOR regulates lysosomal ATP-sensitive two-pore Na^+ channels to adapt to metabolic state. Cell 152: 778-790.
2. Liu, B., et al. 2014. Hepatitis B virus X protein inhibits autophagic degradation by impairing lysosomal maturation. Autophagy 10: 416-430.
3. Peng, J., et al. 2014. Atg5 regulates late endosome and lysosome biogenesis. Sci. China Life Sci. 57: 59-68.
4. Jewell, J.L., et al. 2015. Metabolism. Differential regulation of mTORC1 by leucine and glutamine. Science 347: 194-198.
5. Bartlett, J.J., et al. 2016. Doxorubicin impairs cardiomyocyte viability by suppressing transcription factor EB expression and disrupting autophagy. Biochem. J. 473: 3769-3789.
6. Rahman, N., et al. 2016. Soluble adenylyl cyclase is essential for proper lysosomal acidification. J. Gen. Physiol. 148: 325-339.
7. Asrani, K., et al. 2019. mTORC1 feedback to AKT modulates lysosomal biogenesis through MiT/TFE regulation. J. Clin. Invest. 129: 5584-5599.

STORAGE

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

PROTOCOLS

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