

Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 Recombinant Protein | ATP2A2 recombinant protein

Recombinant Human Sarcoplasmic/endoplasmic reticulum calcium ATPase 2

CATALOG # AAA113752	HOST E Coli or Yeast or Baculovirus or Mammalian Cell
-------------------------------	---

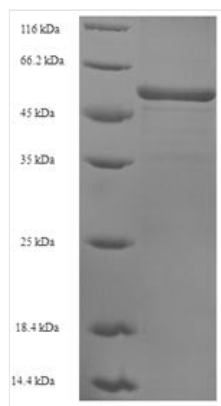
PRODUCT SYNONYMS

Sarcoplasmic/endoplasmic reticulum calcium ATPase 2; Recombinant Human Sarcoplasmic/endoplasmic reticulum calcium ATPase 2; Calcium pump 2; Calcium-transporting ATPase sarcoplasmic reticulum type; slow twitch skeletal muscle isoform; Endoplasmic reticulum class 1/2 Ca(2+) ATPase; ATP2A2 recombinant protein

PRODUCT SPECIFICATIONS

Host	E Coli or Yeast or Baculovirus or Mammalian Cell
Purity/Purification	Greater or equal to 85% purity as determined by SDS-PAGE.
Form/Format	Lyophilized or liquid (Format to be determined during the manufacturing process)
Sequence Positions	314-756aa; Partial
Sequence	VITTCLALGT RRMAKKNAIV RSLPSVETLG CTSVICSDKT GTLTTNQMSV CRMFILDRVE GDTCSLNEFT ITGSTYAPIG EVHKDDKPVN CHQYDGLVEL ATICALCNDS ALDYNEAKGV YEKVGEATET ALTCLVEKMN VFDTELKGLS KIERANACNS VIKQLMKKEF TLEFSRDRKS MSVYCTPNKP SRTSMSKMFV KGAPEGVIDR CTHIRVGSTK VPMTSGVKQK IMSVIREWGS GSDTLRCLAL ATHDNPLRRE EMHLEDSANF IKYETNLTFV GCVGMLDPPR IEVASSVKLC RQAGIRVIMI TGDNKGTAVA ICRRIGIFGQ DEDVTSKAPT GREDELNPS AQRDACLNAR CFARVEPSHK SKIVEFLQSF DEITAMTGDG VNDAPALKKA EIGIAMGSGT AVAKTASEMV LADDNFSTIV AAVEEGRAIY NNM
Preparation and Storage	Store at -20 degree C, for extended storage, conserve at -20 degree C or -80 degree C.

IMAGES



SDS-PAGE

ADDITIONAL INFORMATION

Related Product Information for ATP2A2 recombinant protein	This magnesium-dependent enzyme catalyzes the hydrolysis of ATP coupled with the translocation of calcium from the cytosol to the sarcoplasmic reticulum lumen. Isoform 2 is involved in the regulation of the contraction/relaxation cycle.
--	--

Molecular cloning of cDNAs from human kidney coding for two alternatively spliced products of the cardiac Ca²⁺-ATPase gene. Lytton J., MacLennan D.H.J. *Biol. Chem.* 263:15024-15031(1988) The finished DNA sequence of human chromosome 12. Scherer S.E., Muzny D.M., Buhay C.J., Chen R., Cree A., Ding Y., Dugan-Rocha S., Gill R., Gunaratne P., Harris R.A., Hawes A.C., Hernandez J., Hodgson A.V., Hume J., Jackson A., Khan Z.M., Kovar-Smith C., Lewis L.R., Lozado R.J., Metzker M.L., Milosavljevic A., Miner G.R., Montgomery K.T., Morgan M.B., Nazareth L.V., Scott G., Sodergren E., Song X.-Z., Steffen D., Lovering R.C., Wheeler D.A., Worley K.C., Yuan Y., Zhang Z., Adams C.Q., Ansari-Lari M.A., Ayele M., Brown M.J., Chen G., Chen Z., Clerc-Blankenburg K.P., Davis C., Delgado O., Dinh H.H., Draper H., Gonzalez-Garay M.L., Havlak P., Jackson L.R., Jacob L.S., Kelly S.H., Li L., Li Z., Liu J., Liu W., Lu J., Maheshwari M., Nguyen B.-V., Okwuonu G.O., Pasternak S., Perez L.M., Plopper F.J.H., Santibanez J., Shen H., Tabor P.E., Verduzco D., Waldron L., Wang Q., Williams G.A., Zhang J., Zhou J., Allen C.C., Amin A.G., Anyalebechi V., Bailey M., Barbaria J.A., Bimage K.E., Bryant N.P., Burch P.E., Burkett C.E., Burrell K.L., Calderon E., Cardenas V., Carter K., Casias K., Cavazos I., Cavazos S.R., Ceasar H., Chacko J., Chan S.N., Chavez D., Christopoulos C., Chu J., Cockrell R., Cox C.D., Dang M., Dathorne S.R., David R., Davis C.M., Davy-Carroll L., Deshazo D.R., Donlin J.E., D'Souza L., Eaves K.A., Egan A., Emery-Cohen A.J., Escotto M., Flagg N., Forbes L.D., Gabisi A.M., Garza M., Hamilton C., Henderson N., Hernandez O., Hines S., Hogues M.E., Huang M., Idlebird D.G., Johnson R., Jolivet A., Jones S., Kagan R., King L.M., Leal B., Lebow H., Lee S., LeVan J.M., Lewis L.C., London P., Lorensuhewa L.M., Loulseged H., Lovett D.A., Lucier A., Lucier R.L., Ma J., Madu R.C., Mapua P., Martindale A.D., Martinez E., Massey E., Mawhiney S., Meador M.G., Mendez S., Mercado C., Mercado I.C., Merritt C.E., Miner Z.L., Minja E., Mitchell T., Mohabbat F., Mohabbat K., Montgomery B., Moore N., Morris S., Munidasa M., Ngo R.N., Nguyen N.B., Nickerson E., Nwaokelemeh O.O., Nwokenkwo S., Obregon M., Oguh M., Oragunye N., Oviedo R.J., Parish B.J., Parker D.N., Parrish J., Parks K.L., Paul H.A., Payton B.A., Perez A., Perrin W., Pickens A., Primus E.L., Pu L.-L., Puazo M., Quiles M.M., Quiroz J.B., Rabata D., Reeves K., Ruiz S.J., Shao H., Sisson I., Sonaike T., Sorelle R.P., Sutton A.E., Svatek A.F., Svetz L.A., Tamerisa K.S., Taylor T.R., Teague B., Thomas N., Thorn R.D., Trejos Z.Y., Trevino B.K., Ukegbu O.N., Urban J.B., Vasquez L.I., Vera V.A., Villasana D.M., Wang L., Ward-Moore S., Warren J.T., Wei X., White F., Williamson A.L., Wleczyk R., Wooden H.S., Wooden S.H., Yen J., Yoon L., Yoon V., Zorrilla S.E., Nelson D., Kucheralapati R., Weinstock G., Gibbs R.A. *Nature* 440:346-351(2006) Complete sequencing and characterization of 21,243 full-length human cDNAs. Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S., Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S., Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O., Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S. *Nat. Genet.* 36:40-45(2004) Identification of a new SERCA2 splice variant regulated during monocytic differentiation. Gelebart P., Martin V., Enouf J., Papp B. *Biochem. Biophys. Res. Commun.* 303:676-684(2003) TRAM2 protein interacts with endoplasmic reticulum Ca²⁺ pump Serca2b and is necessary for collagen type I synthesis. Stefanovic B., Stefanovic L., Schnabl B., Bataller R., Brenner D.A. *Mol. Cell. Biol.* 24:1758-1768(2004) Detection of sequence-specific tyrosine nitration of manganese SOD and SERCA in cardiovascular disease and aging. Xu S., Ying J., Jiang B., Guo W., Adachi T., Sharov V., Lazar H., Menzoian J., Knyushko T.V., Bigelow D., Schoeneich C., Cohen R.A. *Am. J. Physiol.* 290:H2220-H2227(2006) Global, in vivo, and site-specific phosphorylation dynamics in signaling networks. Olsen J.V., Blagoev B., Gnäd F., Macek B., Kumar C., Mortensen P., Mann M. *Cell* 127:635-648(2006) Kinase-selective enrichment enables quantitative phosphoproteomics of the kinome across the cell cycle. Daub H., Olsen J.V., Bailein M., Gnäd F., Oppermann F.S., Korner R., Greff Z., Keri G., Stemmann O., Mann M. *Mol. Cell* 31:438-448(2008) A quantitative atlas of mitotic phosphorylation. Dephoure N., Zhou C., Villen J., Beausoleil S.A., Bakalarski C.E., Elledge S.J., Gygi S.P. *Proc. Natl. Acad. Sci. U.S.A.* 105:10762-10767(2008) The anti-apoptotic protein HAX-1 interacts with SERCA2 and regulates its protein levels to promote cell survival. Vafiadaki E., Arvanitis D.A., Pagakis S.N., Papalouka V., Sanoudou D., Kontogianni-Konstantopoulos A., Kraniias E.G. *Mol. Biol. Cell* 20:306-318(2009) Quantitative phosphoproteomic analysis of T cell receptor signaling reveals system-wide modulation of protein-protein interactions. Mayya V., Lundgren D.H., Hwang S.-I., Rezaul K., Wu L., Eng J.K., Rodionov V., Han D.K. *Sci. Signal.* 2:RA46-RA46(2009) Initial characterization of the human central proteome. Burkard T.R., Planyavsky M., Kaupe I., Breitwieser F.P., Buerckstuehmer T., Bennett K.L., Superti-Furga G., Colinge J. *BMC Syst. Biol.* 5:17-17(2011) POST, partner of stromal interaction molecule 1 (STIM1), targets STIM1 to multiple transporters. Krapivinsky G., Krapivinsky L., Stotz S.C., Manasian Y., Clapham D.E. *Proc. Natl. Acad. Sci. U.S.A.* 108:19234-19239(2011) An enzyme assisted RP-RPLC approach for in-depth analysis of human liver phosphoproteome. Bian Y., Song C., Cheng K., Dong M., Wang F., Huang J., Sun D., Wang L., Ye M., Zou H.J. *Proteomics* 96:253-262(2014) Spectrum of novel ATP2A2 mutations in patients with Darier's disease. Sakuntabhai A., Burge S., Monk S., Hovnanian A. *Hum. Mol. Genet.* 8:1611-1619(1999) ATP2A2 mutations in Darier's disease variant cutaneous phenotypes are associated with missense mutations, but neuropsychiatric features are independent of mutation class. Ruiz-Perez V.L., Carter S.A., Healy E.,

NCBI AND UNIPROT INFORMATION

NCBI GI #	4502285
NCBI GeneID	488
NCBI Accession #	NP_001672.1
NCBI GenBank Nucleotide #	NM_001681.3
UniProt Accession #	P16615; P16614; Q86VJ2; A6NDN7; B4DF05
Molecular Weight	52.3 kDa
NCBI Official Full Name	sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform a
NCBI Official Synonym Full Names	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ transporting 2
NCBI Official Symbol	ATP2A2
NCBI Official Synonym Symbols	DD; DAR; ATP2B; SERCA2
NCBI Protein Information	sarcoplasmic/endoplasmic reticulum calcium ATPase 2
UniProt Protein Name	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2
UniProt Gene Name	ATP2A2
UniProt Synonym Gene Names	ATP2B; SERCA2; SR Ca(2+)-ATPase 2
UniProt Entry Name	AT2A2_HUMAN

For Research Use Only. Not for use in diagnostic or therapeutic procedures. Small volumes of product may become entrapped in the seal of the vial during shipment and storage; if necessary, briefly centrifuge the vial on a tabletop centrifuge to dislodge any liquid in the cap.

AAA Biotech | Tel: +1 (619) 604-9440 | Fax: +1 (619) 604-9441 | contact@aaabiotech.com
Online datasheet: <https://www.aaabiotech.com/atp2a2-recombinant-protein-e-coli/113752>