

AATF recombinant protein

Recombinant Human Protein AATF

CATALOG #
AAA81597

HOST
E Coli

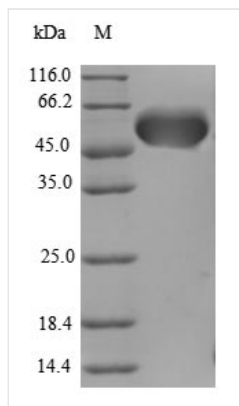
PRODUCT SYNONYMS

AATF; Recombinant Human Protein AATF; Apoptosis-antagonizing transcription factor; Rb-binding protein Che-1; AATF recombinant protein

PRODUCT SPECIFICATIONS

Host	E Coli
Purity/Purification	Greater or equal to 85% purity as determined by SDS-PAGE.
Form/Format	Liquid containing glycerol
Sequence Positions	6-294aa; Partial
Sequence	PLALQLEQLL NPRPSEADPE ADPEEATAAR VIDRFDEGED GEGDFLVVGS IRKLASASLL DTDKRYCGKT TSRKAWNEDH WEQTLPGSSD EEISDEEGSG DEDSEGLGLE EYDEDDLGA EEQECGDHRE SKKSRSHSAK TPGFSVQSI DFEKFTKGMD DLGSSEEEED EESGMEEGDD AEDSQGESEE DRAGDRNSED DGVVMTFSSV KVSEEEVEKGR AVKNQIALWD QLLEGRIKLQ KALLTTNQLP QPDVFPLFKD KGGPEFSSAL KNSHKALKAL LRSLVGLQE
Sequence Length	560
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 AATF recombinant protein

May function as a general inhibitor of the histone deacetylase HDAC1. Binding to the pocket region of RB1 may displace HDAC1 from RB1/E2F complexes, leading to activation of E2F target genes and cell cycle progression. Conversely, displacement of HDAC1 from SP1 bound to the CDKN1A promoter leads to increased expression of this CDK inhibitor and blocks cell cycle progression. Also antagonizes PAWR mediated induction of aberrant amyloid peptide production in Alzheimer disease (presenile and senile dementia), although the molecular basis for this phenomenon has not been described to date.

Product Categories/Family for AATF recombinant protein	Epigenetics and Nuclear Signaling
References	Identification of novel transcription factor-like gene from human intestinal cells.Lindfors K., Halttunen T., Huotari P., Nupponen N., Vihinen M., Visakorpi T., Maki M., Kainulainen H.Biochem. Biophys. Res. Commun. 276:660-666(2000) Identification of a novel partner of RNA polymerase II subunit 11, Che-1, which interacts with and affects the growth suppression function of Rb.Fanciulli M., Bruno T., Di Padova M., De Angelis R., Iezzi S., Iacobini C., Floridi A., Passananti C.FASEB J. 14:904-912(2000) 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) DNA sequence of human chromosome 17 and analysis of rearrangement in the human lineage.Zody M.C., Garber M., Adams D.J., Sharpe T., Harrow J., Lupski J.R., Nicholson C., Searle S.M., Wilming L., Young S.K., Abouelleil A., Allen N.R., Bi W., Bloom T., Borowsky M.L., Bugalter B.E., Butler J., Chang J.L., Chen C.-K., Cook A., Corum B., Cuomo C.A., de Jong P.J., DeCaprio D., Dewar K., FitzGerald M., Gilbert J., Gibson R., Gnerre S., Goldstein S., Grafham D.V., Grocock R., Hafez N., Hagopian D.S., Hart E., Norman C.H., Humphray S., Jaffe D.B., Jones M., Kamal M., Khodiyar V.K., LaButti K., Laird G., Lehoczyk J., Liu X., Lokyitsang T., Loveland J., Lui A., Macdonald P., Major J.E., Matthews L., Mauceli E., McCarroll S.A., Mihalev A.H., Mudge J., Nguyen C., Nicol R., O'Leary S.B., Osoegawa K., Schwartz D.C., Shaw-Smith C., Stankiewicz P., Steward C., Swarbreck D., Venkataraman V., Whittaker C.A., Yang X., Zimmer A.R., Bradley A., Hubbard T., Birren B.W., Rogers J., Lander E.S., Nusbaum C.Nature 440:1045-1049(2006)

NCBI AND UNIPROT INFORMATION

NCBI GI #	7657013
NCBI GeneID	26574
NCBI Accession #	NP_036270.1
NCBI GenBank Nucleotide #	NM_012138.3
UniProt Accession #	Q9NY61; Q9P0A4; Q9UNX5; A6NCJ6; B3KQ26
Molecular Weight	58.8 kDa
NCBI Official Full Name	protein AATF
NCBI Official Synonym Full Names	apoptosis antagonizing transcription factor
NCBI Official Symbol	AATF
NCBI Official Synonym Symbols	DED; BFR2; CHE1; CHE-1
NCBI Protein Information	protein AATF
UniProt Protein Name	Protein AATF
UniProt Gene Name	AATF
UniProt Synonym Gene Names	CHE1; DED

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.

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Online datasheet: <https://www.aaabiotech.com/aatf-recombinant-protein-e-coli/81597>