Poly(A)-specific ribonuclease PARN Recombinant Protein | PARN recombinant protein

Recombinant Human Poly(A)-specific ribonuclease PARN

CATALOG #	HOST
AAA115144	**E Coli or Yeast or Baculovirus or Mammalian Cell**

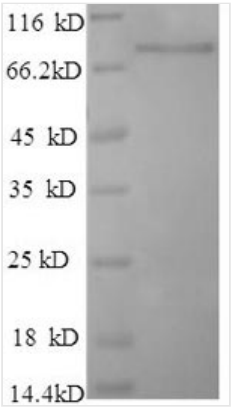
PRODUCT SYNONYMS

Poly(A)-specific ribonuclease PARN; Recombinant Human Poly(A)-specific ribonuclease PARN; Deadenylating nuclease; Deadenylation nuclease; Polyadenylate-specific ribonuclease; PARN 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	1-639aa; Full Length
Sequence	MEIIRSNFKS NLHKVYQAIE EADFFAIDGE FSGISDGPSV SALTNGFDTP EERYQKLKKH SMDFLLFQFG LCTFKYDYTD SKYITKSFNF YVFPKPFNRS SPDVKFVCQS SSIDFLASQG FDFNKVFRNG IPYLNQEEER QLREQYDEKR SQANGAGALS YVSPNTSKCP VTIPEDQKKF IDQVVEKIED LLQSEENKNL DLEPCTGFQR KLIYQTLSWK YPKGIHVETL ETEKKERYIV ISKVDEEERK RREQQKHAKE QEELNDAVGF SRVIHAIANS GKLVIGHNML LDVMHTVHQF YCPLPADLSE FKEMTTCVFP RLLDTKLMAS TQPFKDIINN TSLAELEKRL KETPFNPPKV ESAEGFPSYD TASEQLHEAG YDAYITGLCF ISMANYLGSF LSPPKIHVSA RSKLIEPFFN KLFLMRVMDI PYLNLEGPDL QPKRDHVLHV TFPKEWKTSD LYQLFSAFGN IQISWIDDTS AFVSLSQPEQ VKIAVNTSKY AESYRIQTYA EYMGRKQEEK QIKRKWTEDS WKEADSKRLN PQCIPYTLQN HYYRNNSFTA PSTVGKRNLS PSQEEAGLED GVSGEISDTE LEQTDSCAEP LSEGRKKAKK LKRMKKELSP AGSISKNSPA TLFEVPDTW
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 PARN recombinant protein	3'-exoribonuclease that has a preference for poly(A) tails of mRNAs, thereby efficiently degrading poly(A) tails. Exonucleolytic degradation of the poly(A) tail is often the first step in the decay of eukaryotic mRNAs and is also used to silence certain maternal mRNAs translationally during oocyte maturation and early embryonic development. Interacts with both the 3'-end poly(A) tail and the 5'-end cap structure during degradation, the interaction with the cap structure being required for an efficient degradation of poly(A) tails. Involved in nonsense-mediated mRNA decay, a critical process of selective degradation of mRNAs that contain prature stop codons. Also involved in degradation of inherently unstable mRNAs that contain AU-rich elements (AREs) in their 3'-UTR, possibly via its interaction with KHSRP. Probably mediates the roval of poly(A) tails of AREs mRNAs, which constitutes the first step of destabilization.
Product Categories/Family for PARN recombinant protein	Transcription
References	The deadenylating nuclease (DAN) is involved in poly(A) tail removal during the meiotic maturation of Xenopus oocytes.Koerner C.G., Wormington M., Muckenthaler M., Schneider S., Dehlin E., Wahle E.EMBO J. 17:5427-5437(1998) 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) The sequence and analysis of duplication-rich human chromosome 16.Martin J., Han C., Gordon L.A., Terry A., Prabhakar S., She X., Xie G., Hellsten U., Chan Y.M., Altherr M., Couronne O., Aerts A., Bajorek E., Black S., Blumer H., Branscomb E., Brown N.C., Bruno W.J., Buckingham J.M., Callen D.F., Campbell C.S., Campbell M.L., Campbell E.W., Caoile C., Challacombe J.F., Chasteen L.A., Chertkov O., Chi H.C., Christensen M., Clark L.M., Cohn J.D., Denys M., Detter J.C., Dickson M., Dimitrijevic-Bussod M., Escobar J., Fawcett J.J., Flowers D., Fotopulos D., Glavina T., Gomez M., Gonzales E., Goodstein D., Goodwin L.A., Grady D.L., Grigoriev I., Groza M., Hammon N., Hawkins T., Haydu L., Hildebrand C.E., Huang W., Israni S., Jett J., Jewett P.B., Kadner K., Kimball H., Kobayashi A., Krawczyk M.-C., Leyba T., Longmire J.L., Lopez F., Lou Y., Lowry S., Ludeman T., Manohar C.F., Mark G.A., McMurray K.L., Meincke L.J., Morgan J., Moyzis R.K., Mundt M.O., Munk A.C., Nandkeshwar R.D., Pitluck S., Pollard M., Predki P., Parson-Quintana B., Ramirez L., Rash S., Retterer J., Ricke D.O., Robinson D.L., Rodriguez A., Salamov A., Saunders E.H., Scott D., Shough T., Stallings R.L., Stalvey M., Sutherland R.D., Tapia R., Tesmer J.G., Thayer N., Thompson L.S., Tice H., Torney D.C., Tran-Gyamfi M., Tsai M., Ulanovsky L.E., Ustaszewska A., Vo N., White P.S., Williams A.L., Wills P.L., Wu J.-R., Wu K., Yang J., DeJong P., Bruce D., Doggett N.A., Deaven L., Schmutz J., Grimwood J., Richardson P., Rokhsar D.S., Eichler E.E., Gilna P., Lucas S.M., Myers R.M., Rubin E.M., Pennacchio L.A.Nature 432:988-994(2004)

NCBI AND UNIPROT INFORMATION

NCBI GI #	197333695
NCBI GeneID	5073
NCBI Accession #	NP_001127949.1
NCBI GenBank Nucleotide #	NM_001134477.2
UniProt Accession #	O95453; B2RCB3; B4DDG8; B4DSB0; B4DWR4; B4E1H6
Molecular Weight	75.5 kDa

NCBI Official Full Name	poly(A)-specific ribonuclease PARN isoform 2
NCBI Official Synonym Full Names	poly(A)-specific ribonuclease
NCBI Official Symbol	PARN
NCBI Official Synonym Symbols	DAN; DKCB6; PFBMFT4
NCBI Protein Information	poly(A)-specific ribonuclease PARN
UniProt Protein Name	Poly(A)-specific ribonuclease PARN
UniProt Gene Name	**PARN**
UniProt Synonym Gene Names	DAN
UniProt Entry Name	PARN_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.

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Online datasheet: https://stage.aaabiotech.com/parn-recombinant-protein-e-coli-or-yeast-or-baculovirus-or-mammalian-cell/115144