

Recombinant human Single-strand selective monofunctional uracil DNA glycosylase

Catalog No: #AP71324

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Package Size: #AP71324-1 20ug #AP71324-2 100ug #AP71324-3 1mg

Description

Product Name	Recombinant human Single-strand selective monofunctional uracil DNA glycosylase
Brief Description	Recombinant Protein
Host Species	E.coli
Purification	Greater than 90% as determined by SDS-PAGE.
Immunogen Description	Expression Region:1-177aaSequence Info:Full Length of Isoform 2
Accession No.	Q53HV7
Uniprot	Q53HV7
GeneID	23583;
Calculated MW	35.6 kDa
Tag Info	N-terminal 6xHis-SUMO-tagged
Target Sequence	MPQAFLLGSIHEPAGALMEPQPCPGSLAESFLEEEELRLNAELSQLQFSEPVGIIYNPVEYAWEPHRNYVTRYC QGPKEVLFLGMNPGPFGMAQTGVPFGEVSMVRDWLGIVGPVLTTPQEHPKRPVLGLECPQSEGPRQSMGH EIKSELLMGGCSWIRGKIQCDRVQVRRPGFSSQL
Formulation	Tris-based buffer50% glycerol
Storage	The shelf life is related to many factors, storage state, buffer ingredients, storage temperature and the stability of the protein itself. Generally, the shelf life of liquid form is 6 months at -20°C,-80°C. The shelf life of lyophilized form is 12 months at -20°C,-80°C.Notes:Repeated freezing and thawing is not recommended. Store working aliquots at 4°C for up to one week.

Background

Recognizes base lesions in the genome and initiates base excision DNA repair. Acts as a monofunctional DNA glycosylase specific for uracil (U) residues in DNA with a preference for single-stranded DNA substrates. The activity is greater toward mismatches (U,G) compared to matches (U,A). Excises uracil (U), 5-formyluracil (fU) and uracil derivatives bearing an oxidized group at C5 [5-hydroxyuracil (hoU) and 5-hydroxymethyluracil (hmU)] in ssDNA and dsDNA, but not analogous cytosine derivatives (5-hydroxycytosine and 5-formylcytosine), nor other oxidized bases. The activity is damage-specific and salt-dependent. The substrate preference is the following: ssDNA > dsDNA (G pair) = dsDNA (A pair) at low salt concentration, and dsDNA (G pair) > dsDNA (A pair) > ssDNA at high salt concentration.

References

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) Research Topic: Epigenetics and Nuclear Signaling

Note: This product is for in vitro research use only