abcam

Product datasheet

Recombinant human PARP1 protein ab123834

Description

Product name	Recombinant human PARP1 protein
Biological activity	1000 U/vial, specific activity = 20000 U/mg PARP1. 1U=10 fmol ADP-ribose incorporated into 5 µg immobilized histone in 30 min at room temperature. Note: Activity measurements are approximate values.
Purity	> 95 % SDS-PAGE. Affinity purified.
Expression system	Baculovirus
Accession	P09874
Protein length	Full length protein
Animal free	No
Nature	Recombinant
Species	Human
Predicted molecular weight	116 kDa
Amino acids	1 to 1014
Tags	DDDDK tag N-Terminus

Specifications

Our Abpromise guarantee covers the use of **ab123834** in the following tested applications.

The application notes include recommended starting dilutions; optimal dilutions/concentrations should be determined by the end user.

Applications	Functional Studies SDS-PAGE
Form	Lyophilized
Additional notes	STORAGE CONDITIONS: Store reconstituted solution at -70°C. Avoid multiple freeze-thaw cycles. CAUTION: There is loss of PARP1 enzymatic activity upon each free/thaw cycle. It is suggested to aliquot the reconstituted enzyme into multiple tubes and freeze at -70°C. Alternatively, add glycerol at 1:1 vol/vol to the reconstituted PARP1, mix gently by trituration, and store at -20°C (do not store in a frost-free freezer!) for up to 6 months.

Preparation and Storage

Stability and Storage	Shipped at 4°C. Store at -80°C. Constituents: 0.02% DTT, 0.24% Tris, 0.003% EDTA, 1.74% Sodium chloride Contains lyophilization stabilizers. This product is an active protein and may elicit a biological response in vivo, handle with caution.
Reconstitution	Spin tube in a microfuge for 15 sec to sediment lyophilized material. Carefully open the vial and add 100 µL dH_2O. Vortex gently for 20 sec (avoid air bubbles). Let stand for 5 min. Carefully triturate the sample 10-times using a pipetman (avoid air bubbles). Spin briefly in microfuge to consolidate.

General Info

Function	Involved in the base excision repair (BER) pathway, by catalyzing the poly(ADP-ribosyl)ation of a limited number of acceptor proteins involved in chromatin architecture and in DNA metabolism. This modification follows DNA damages and appears as an obligatory step in a detection/signaling pathway leading to the reparation of DNA strand breaks. Mediates the poly(ADP-ribosyl)ation of APLF and CHFR. Positively regulates the transcription of MTUS1 and negatively regulates the transcription of MTUS2/TIP150.
Sequence similarities	Contains 1 BRCT domain. Contains 1 PARP alpha-helical domain. Contains 1 PARP catalytic domain. Contains 2 PARP-type zinc fingers.
Post-translational modifications	Phosphorylated by PRKDC. Phosphorylated upon DNA damage, probably by ATM or ATR. Poly-ADP-ribosylated by PARP2. Poly-ADP-ribosylation mediates the recruitment of CHD1L to DNA damage sites. S-nitrosylated, leading to inhibit transcription regulation activity.
Cellular localization	Nucleus.

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