

Recombinant *S. cerevisiae* HSP82 protein ab157058

Description

Product name Recombinant *S. cerevisiae* HSP82 protein

Purity >= 99 % n/a.

Expression system Escherichia coli

Accession **P02829**

Protein length Full length protein

Animal free No

Nature Recombinant

Species *Saccharomyces cerevisiae*

Sequence

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MASETFEFQAEITQLMSLIINTVYSNKEIFLRELISNASDALD
KIRYKSL
SDPKQLETEPDLFIRITPKPEQKVLDIRDSGIGMTKAELINNL
GTIAKSG
TKAFMEALSAGADVSMIGQFVGFYSLFLVADRVQVISKS
NDDEQYWES
NAGGSFTVTLDEVNERIGRGTILRLFLKDDQLEYLEEKRIKE
VIKRHSEF
VAYPIQLVVTKVEVEKEVPIPEEEKKDEEKKDEEKKDEDDK
KPKLEEVDDEE
EEKKPKTKKVKEEVQEI EELNKTPLWTRNPSDITQEEYN
AFYKISNDW
EDPLYVKHFSVEGQLEFRAILFIPKRAPDFDLFESKSKKNNI
KLYVRRVFI
TDEAEDLIPEWLSFVKGVDSEDLPLNLSREMLQQNKIMK
VIRKNIVKKL
IEAFNEIAEDSEQFEKFYSAFSKNIKLGVHEDTQNRAALAK
LLRYNSTKS
VDELTSLTDYVTRMPEHQKNIYITGESLKAVEKSPFLDAL
KAKNFEVLF
LTDPIDEYAFYFTQLKEFEGKTLVDITKDFELEETDEEKAERE
KEIKEYEPL
TKALKEILGDQVEKVVVSYKLLDAPAAIRTGQFGWSANME
RIMKAQALRD
SSMSSYMSSKKTFEISPKSPIIKELKKRVDEGGAQDKTVK
DLTKLLYETA
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LLTSGFSLDEPTSFASRINRLISLGLNIDEDEETETAPEAST
AAPVEEVP ADTEMEEVD

Predicted molecular weight	81 kDa
Amino acids	1 to 709
Tags	His tag N-Terminus
Description	Recombinant <i>S. cerevisiae</i> HSP82 protein

Specifications

Our **Abpromise guarantee** covers the use of **ab157058** in the following tested applications.

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

Applications	Western blot
Form	Liquid
Additional notes	For maximum product recovery after thawing, centrifuge the vial before opening the cap.

Preparation and Storage

Stability and Storage	Shipped at 4°C. Upon delivery aliquot and store at -80°C. Avoid freeze / thaw cycles. Constituent: 1.12% Potassium chloride
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General Info

Relevance	Molecular chaperone that promotes the maturation, structural maintenance and proper regulation of specific target proteins involved in cell cycle control and signal transduction. Undergoes a functional cycle that is linked to its ATPase activity. The nucleotide-free form of the dimer is found in an open conformation in which the N-termini are not dimerized and the complex is ready for client protein binding. Binding of ATP induces large conformational changes, resulting in the formation of a ring-like closed structure in which the N-terminal domains associate intramolecularly with the middle domain and also dimerize with each other, stimulating their intrinsic ATPase activity and acting as a clamp on the substrate. Finally, ATP hydrolysis results in the release of the substrate. This cycle probably induces conformational changes in the client proteins, thereby causing their activation. Interacts dynamically with various co-chaperones that modulate its substrate recognition, ATPase cycle and chaperone function. Required for growth at high temperatures.
Cellular localization	Cytoplasmic

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