

**Product Name:** HSP70

**Product Code:** TAP-134

**FOR RESEARCH USE ONLY (RUO)**

**Verified Applications / Usage**

Suitable for studies of ATP-dependent molecular chaperone activity, protein folding/refolding, aggregation suppression, and HSP70-regulated proteostasis.

**Physical Characteristics**

**Species:** Human

**Predicted MW (kDa):** 72 kDa

**Source:** *E. coli* BL21

**Purity:** 90 %

**Tag:** N-His<sub>6</sub>-3C

**Formulation:** 40 mM HEPES, 100 mM NaCl, 10% Glycerol, 2 mM TCEP, 1 mM EDTA, pH 7.6

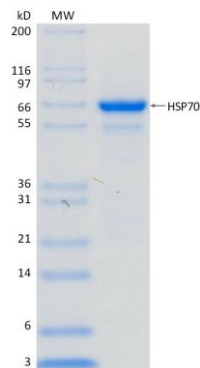
**Shipping:** The product is shipped with dry ice. Upon receipt, store it immediately at the temperature recommended below.

**Stability/Storage:** Use a manual defrost freezer and avoid repeated freeze-thaw cycles. Aliquot and store ≤ -70°C (stable for 24 months from date of receipt).

## Quality Assurance

### Purity & SDS-PAGE

**Protein ID:** Heat shock protein HSP70



2 µg HSP70 run on 4-12% SDS-PAGE gel under reducing conditions, then visualized with Colloidal Coomassie Blue Stain.

### Activity Assay

Verified in Luciferase Refolding Assay.

## Background

### Description

HSP70 is an essential molecular chaperone that regulates protein folding and ubiquitin–proteasome system activity through interactions with co-chaperones and E3 ligases such as CHIP. HSP70 is widely used to study proteostasis, chaperone-mediated ubiquitylation, and targeted protein degradation mechanisms.

**Accession Number:** P0DMV8

**Entrez Gene ID:** HSP70

## Protein Sequence

```
MGHHHHHHSLEVLFGGPGMAKAAAIGIDLGTYSVGVFQHGKVEIIANDQGNRTTPSYVAF
TDTERLIGDAAKNQVALNPQNTVFDKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSY
KGETKAFYP EEISSMVLTKMKEIAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVL
RIINEPTAAAIAYGLDRTGKGERNVLI FDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDF
DNRLVNHVFVEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTS
ITRARFEELCSDLFRSTLEPVEKALRDAKLDKAQIHD LVLVGGSTRIPKVQKLLQDFFNGRDL
NKSINPDEAVAYGA AVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTIPT
KQTQIFTTYSDNQPGVLIQVYEGERAMTKDNNLLGRFELSGIPPAPRGVPQIEVTFDIDANGI
LNV TATDKSTGKANKITITNDKGRLSKEEIERMVQEAEKYKAEDEVQRERVS AKNALESYAFN
MKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLA EKDEF EHKRKELEQVCNPIISGLY
QGAGGPGPGGFGAQQGPKGGSGSGPTIEEVD
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