Product Name: HSP70 (E110D)

Product Code: TAP-125

FOR RESEARCH USE ONLY (RUO)

Verified Applications / Usage

Suitable for studies of ATP-dependent molecular chaperone activity, protein folding/refolding, aggregation suppression, and HSP40-regulated proteostasis.

Physical Characteristics

Species: Human

Predicted MW (kDa): 73 kDa

Source: *E. coli* BL21

Purity: 90 %

Tag: N-His_5-3C

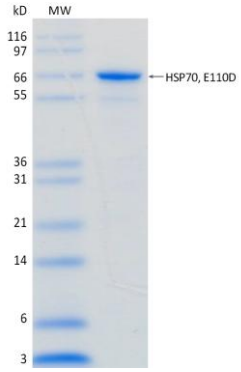
Formulation: 40 mM HEPES, 100 mM NaCl, 10% Glycerol, 1 mM EDTA, 2 mM TCEP, pH 7.6

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



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

Protein ID: Heat shock protein HSP70

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. This product contains the naturally occurring E110D variant within the N-terminal nucleotide-binding domain of HSP70. HSP70 is widely used to study proteostasis, chaperone-mediated ubiquitylation, and targeted protein degradation mechanisms.

Accession Number: P0DMV8

Entrez Gene ID: HSP70

Protein Sequence

MGHHHHHGSLEVLFQGPGMAKAAAIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFT
DTERLIGDAAKNQVALNPQNTVFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYK
GDTKAFYPEEISSMVLTKMKEIAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLR
IINEPTAAAIAYGLDRTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFD
NRLVNHFVEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSI
TRARFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLN
KSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTIPTK
QTQIFTTYSDNQPGVLIQVYEGERAMTKDNNLLGRFELSGIPPAPRGVPQIEVTFDIDANGIL
NVTATDKSTGKANKITITNDKGRLSKEEIERMVQEAEKYKAEDEVQRERVSAKNALESYAFNM
KSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELEQVCNPIISGLYQ
GAGGPGPGGFGAQGPKGGSGSGPTIEEVD