HSP70/HSPA1A Protein, Human (E110D, His)

Cat. No.:	HY-P701004
Synonyms:	HSP70-1; HSPA1A; HSP72 ; HSPA1; HSX70
Species:	Human
Source:	E. coli
Accession:	P0DMV8-1 (A2-D641, E110D)
Gene ID:	3303
Molecular Weight:	72.2 kDa

PROPERTIES

Appearance	Solution.
Formulation	Supplied as a 0.22μm filtered solution of 25mM Tris, 100mM Glycine, 10% Glycerol, pH 7.4.
Endotoxin Level	<1 EU/μg, determined by LAL method.
Reconsititution	N/A.
Storage & Stability	Stored at -80°C for 1 year. It is stable at -20°C for 3 months after opening. It is recommended to freeze aliquots at -80°C for extended storage. Avoid repeated freeze-thaw cycles.
Shipping	Shipping with dry ice.

DESCRIPTION

Background

HSP70/HSPA1A protein, a molecular chaperone, plays a pivotal role in diverse cellular processes crucial for proteome maintenance. It is involved in protecting the proteome from stress, facilitating the folding and transport of newly synthesized polypeptides, activating the proteolysis of misfolded proteins, and orchestrating the formation and dissociation of protein complexes. Within the protein quality control system, HSP70 ensures the accurate folding of proteins, the re-folding of misfolded counterparts, and control over the targeting of proteins for subsequent degradation. This regulation occurs through cycles of ATP binding, ATP hydrolysis, and ADP release, mediated by co-chaperones. Co-chaperones exhibit specificity, promoting the folding or degradation of substrates. The nucleotide-bound state of HSP70 modulates its affinity for polypeptides, with the ATP-bound form displaying low substrate protein affinity and a conformational change upon ATP hydrolysis to ADP, increasing substrate protein affinity. These cycles of ATP hydrolysis and nucleotide exchange permit repeated cycles of substrate binding and release. Co-chaperones are categorized into three types: J-domain co-chaperones (e.g., HSP40s), nucleotide exchange factors (e.g., BAG1/2/3), and TPR domain chaperones (e.g., HOPX and STUB1). HSP70 maintains protein homeostasis during cellular stress through two opposing mechanisms: protein refolding and degradation, determined by its acetylation/deacetylation state controlling the competitive binding of co-chaperones HOPX and STUB1. During the early stress response, the acetylated form assists in chaperone-mediated protein refolding by binding to HOPX, transitioning to deacetylation and subsequent binding to ubiquitin ligase STUB1 for ubiquitin-mediated protein degradation. Beyond its role in protein homeostasis, HSP70 regulates centrosome integrity during mitosis, essential for

maintaining a functional mitotic centrosome supporting the assembly of a bipolar mitotic spindle. It enhances STUB1-mediated SMAD3 ubiquitination and degradation, facilitating STUB1-mediated inhibition of TGF-beta signaling, and is indispensable for STUB1-mediated ubiquitination and degradation of FOXP3 in regulatory T-cells during inflammation. Negatively regulating heat shock-induced HSF1 transcriptional activity, it is also involved in the clearance of misfolded PRDM1/Blimp-1 proteins, sequestering them in the cytoplasm and promoting their association with SYNV1/HRD1, leading to proteasomal degradation. In the context of microbial infection, particularly rotavirus A infection, HSP70 serves as a post-attachment receptor facilitating the virus's entry into the cell.

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