Recombinant Human HSPA1A Protein (M1-D641), Tag Free

Cat. No. HSPA1A-0701H **Lot. No.** (See product label)

SPECIFICATION

Product Overview	Recombinant Human GG-HSP70(M1-D641 end) Protein was expressed in Insect cell.
Species	Human
Source	Insect Cells
ProteinLength	M1-D641
Description	Molecular chaperone implicated in a wide variety of cellular processes, including protection of the proteome from stress, folding and transport of newly synthesized polypeptides, activation of proteolysis of misfolded proteins and the formation and dissociation of protein complexes. Plays a pivotal role in the protein quality control system, ensuring the correct folding of proteins, the re-folding of misfolded proteins and controlling the targeting of proteins for subsequent degradation. This is achieved through cycles of ATP binding, ATP hydrolysis and ADP release, mediated by co-chaperones. The co-chaperones have been shown to not only regulate different steps of the ATPase cycle, but they also have an individual specificity such that one co-chaperone may promote folding of a substrate while another may promote degradation. The affinity for polypeptides is regulated by its nucleotide bound state. In the ATP-bound form, it has a low affinity for substrate proteins. However, upon hydrolysis of the ATP to ADP, it undergoes a conformational change that increases its affinity for substrate proteins. It goes through repeated cycles of ATP hydrolysis and nucleotide exchange, which permits cycles of substrate binding and release. The co-chaperones are of three types: J-domain co-chaperones such as HSP40s (stimulate

	ATPase hydrolysis by HSP70), the nucleotide exchange factors (NEF) such as BAG1/2/3 (facilitate conversion of HSP70 from the ADP-bound to the ATP-bound state thereby promoting substrate release), and the TPR domain chaperones such as HOPX and STUB1. Maintains protein homeostasis during cellular stress through two opposing mechanisms: protein refolding and degradation. Its acetylation/deacetylation state determines whether it functions in protein refolding or protein degradation by controlling the competitive binding of co-chaperones HOPX and STUB1. During the early stress response, the acetylated form binds to HOPX which assists in chaperone-mediated protein refolding, thereafter, it is deacetylated and binds to ubiquitin ligase STUB1 that promotes ubiquitin-mediated protein degradation. Regulates centrosome integrity during mitosis, and is required for the maintenance of a functional mitotic centrosome that supports the assembly of a bipolar mitotic spindle. Enhances STUB1-mediated SMAD3 ubiquitination and degradation and facilitates STUB1-mediated inhibition of TGF-beta signaling. Essential for STUB1-mediated ubiquitination and degradation of FOXP3 in regulatory T-cells (Treg) during inflammation. Negatively regulates heat shock-induced HSF1 transcriptional activity during the attenuation and recovery phase period of the heat shock response. Involved in the clearance of misfolded PRDM1/Blimp-1 proteins. Sequesters them in the cytoplasm and promotes their association with SYNV1/HRD1, leading to proteasomal degradation.
Form	Liquid
Endotoxin	< 0.01 EU per μg of the protein
Purity	85%
Stability	Samples are stable for up to twelve months from date of receipt at -20 to -80 centigrade.

Storage	Store it under sterile conditions at -20 to -80 centigrade. It is recommended that the protein be aliquoted for optimal storage. Avoid repeated freeze-thaw cycles.
Storage Buffer	Supplied as sterile 50 mM Tris-HCl (pH 7.5), 200 mM NaCl, 5% glycerol, 1mM DTT
Shipping	It is shipped out with blue ice.

GENE INFORMATION

Gene Name	HSPA1A heat shock 70kDa protein 1A [Homo sapiens (human)]
Official Symbol	HSPA1A
Synonyms	HSPA1A; heat shock 70kDa protein 1A; heat shock 70kD protein 1A, HSPA1; heat shock 70 kDa protein 1A/1B; HSP70 1; HSP70-1/HSP70-2; HSP70.1/HSP70.2; heat shock 70kD protein 1A; heat shock-induced protein; heat shock 70 kDa protein 1/2; dnaK-type molecular chaperone HSP70-1; HSP72; HSPA1; HSP70I; HSPA1B; HSP70-1; HSP70-1A; FLJ54303; FLJ54370; FLJ54392; FLJ54408; FLJ75127;
Gene ID	3303
mRNA Refseq	NM_005345
Protein Refseq	NP_005336
MIM	140550
UniProt ID	P0DMV8