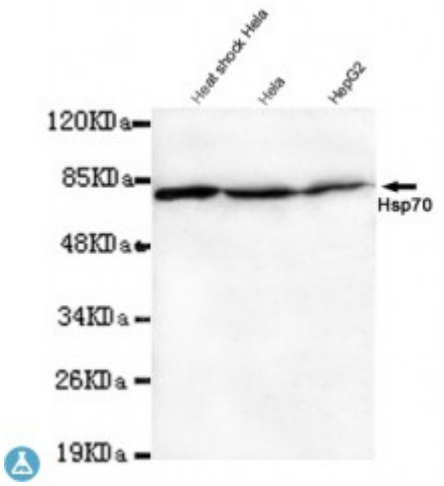
Anti-Hsp70 antibody



Description	Mouse monoclonal to Hsp70.

Model	STJ99062
Host	Mouse
Reactivity	Human
Applications	ELISA, WB
Immunogen	Purified recombinant human Hsp70 (N-term) protein fragments expressed in E.coli.
Immunogen Region	N-term
Gene Symbol	HSPA1A
Dilution range	WB 1:500-2000ELISA 1:10000-20000
Specificity	This antibody detects endogenous levels of Hsp70 (N-term) and does not cross-react with related proteins.
Purification	The antibody was affinity-purified from rabbit antiserum by affinity-chromatography using epitope-specific immunogen.
Clone ID	2D4-F7-C11
Note	For Research Use Only (RUO).
Protein Name	Heat shock 70 kDa protein 1A Heat shock 70 kDa protein 1 HSP70-1 HSP70.1
Molecular Weight	70kDa
Clonality	Monoclonal

Conjugation	Unconjugated
Isotype	IgG1
Formulation	Liquid in PBS containing 50% glycerol, 0.5% BSA and 0.02% sodium azide.
Concentration	1 mg/ml
Storage Instruction	Store at -20°C, and avoid repeat freeze-thaw cycles.
Alternative Names	Heat shock 70 kDa protein 1A Heat shock 70 kDa protein 1 HSP70-1 HSP70.1
Function	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 . (Microbial infection) In case of rotavirus A infection, serves as a post-attachment receptor for the virus to facilitate entry into the cell.
Sequence and Domain Family	The N-terminal nucleotide binding domain (NBD) (also known as the ATPase domain) is responsible for binding and hydrolyzing ATP. The C-terminal substrate-binding domain (SBD) (also known as peptide-binding domain)

	binds to the client/substrate proteins. The two domains are allosterically coupled so that, when ATP is bound to the NBD, the SBD binds relatively weakly to clients. When ADP is bound in the NBD, a conformational change enhances the affinity of the SBD for client proteins.
Cellular Localization	Cytoplasm Nucleus Cytoplasm, cytoskeleton, microtubule organizing center, centrosome. Localized in cytoplasmic mRNP granules containing untranslated mRNAs.
Post-translational Modifications	In response to cellular stress, acetylated at Lys-77 by NA110 and then gradually deacetylated by HDAC4 at later stages. Acetylation enhances its chaperone activity and also determines whether it will function as a chaperone for protein refolding or degradation by controlling its binding to co-chaperones HOPX and STUB1. The acetylated form and the non-acetylated form bind to HOPX and STUB1 respectively. Acetylation also protects cells against various types of cellular stress.