

Product datasheet for TP527368

Hspa1a (NM_010479) Mouse Recombinant Protein

Product data:

Product Type:	Recombinant Proteins
Description:	Purified recombinant protein of Mouse heat shock protein 1A (Hspa1a), with C-terminal MYC/DDK tag, expressed in HEK293T cells, 20ug
Species:	Mouse
Expression Host:	HEK293T
Expression cDNA Clone or AA Sequence:	>MR227368 representing NM_010479 Red =Cloning site Green =Tags(s)
	<p>MAKNTAIGIDLGTYSYCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALNPQNTVFDA KRLIGRKFGDAVVQSDMKHWPQVNDGDKPKVQVNYKGESRSFFPEEISSMVLTMKKEIAEAYLGHPVT NAVITVPAYFNDSQRQATKDAGVIAGLNVLRINEPTAAAIAYGLDRTGKGERNVLIFDLGGGTFDVSIL TIDDGIFEVKATAGDTHLGGEDFDNRLVSHFVEEFKRKHKKDISQNKRAVRRRLRTACERAKRTLSSSTQA SLEIDSLFEGIDFYTSITRARFEELCSDLFRGTLEPVEKALRDAKMDKAQIHDLVLVGGSTRIPKVQKLL QDFFNGRDLNKSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVM TALIKRNSTI PTKQTQTFTTYSNQPGLVLIQVYGERAMTRDNNLLGRFELSGIPPAPRGVPQIEVTFDIDANGILNVTA TDKTTGKANKITITNDKGRLSKEEIERMVQEAERYKAEDVQRDRVAAKNALESYAFNMKSAVEDEGLKG KLSEADKKKVLDKCQEVISWLDSENTLADKEEFVHKREELERVCSPIISGLYQGAGAPGAGGFGAQAPKGA SGSGPTIEEVD</p> <p>TRTRPLEQKLISEEDLAANDILDYKDDDDKV</p>
Tag:	C-MYC/DDK
Predicted MW:	70.5 kDa
Concentration:	>0.05 µg/µL as determined by microplate BCA method
Purity:	> 80% as determined by SDS-PAGE and Coomassie blue staining
Buffer:	25 mM Tris-HCl, 100 mM glycine, pH 7.3, 10% glycerol
Note:	For testing in cell culture applications, please filter before use. Note that you may experience some loss of protein during the filtration process.
Storage:	Store at -80°C after receiving vials.
Stability:	Stable for 12 months from the date of receipt of the product under proper storage and handling conditions. Avoid repeated freeze-thaw cycles.



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RefSeq:	NP_034609
Locus ID:	193740
UniProt ID:	Q61696
RefSeq Size:	2798
Cytogenetics:	17 18.51 cM
RefSeq ORF:	1923
Synonyms:	hsp68; Hsp70-3; Hsp70.3; hsp70A1; Hsp72
Summary:	<p>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.[UniProtKB/Swiss-Prot Function]</p>