Human HSPA1A, Tag Free Protein

HA210756

Product name:	Human HSPA1A, Tag Free
Species reactivity:	Human
Bio-Activity:	Testing in progress.
Protein construction description:	A DNA sequence encoding the human HSPA1A protein (P0DMV8-1) (Met 1-Asp 641) was expressed with tag free.

Background: 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.

Purity:	>90% as determined by SDS-PAGE.
Endotoxin:	Less than 1.0 EU per μg by the LAL method.
Fragment region:	HSPA1A (1-641)
Source:	E.coli
Accession:	P0DMV8-1
Predicted molecular mass:	70.4 kD
Formulation:	Lyophilized from a 0.2 μm filtered solution of PBS, pH7.4, 5% Trehalose, 5% mannitol.
Reconstitution:	Reconstitute at 250 μg/ml in sterile water.
Storage:	Please avoid repeated freeze-thaw cycles. Samples are stable for up to twelve months from date of receipt at -20℃ to -80℃ It is recommended that aliquot the reconstituted solution to minimize freeze-thaw cycles.

Images

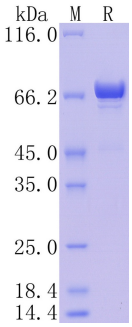

Fig1: Protein on SDS-PAGE under reducing (R) condition.