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32-5339: Recombinant Human Heat Shock 70kDa Protein-8

Alternative Name : LAP1,HSC54,HSC70,HSC71,HSP1,HSP73,NIP71,HSPA10,MGC29929,MGC131511,HSPA8,Heat shock cognate 71 kDa protein,Heat shock 70 kDa protein 8.

Description

Source : Escherichia Coli. Recombinant Human HSC70 produced in E.Coli is a single, non-glycosylated polypeptide chain containing 666 amino acids (1-646 a.a.) and having a molecular mass of 73.1kDa.HSC70 human recombinant is fused to 20 amino acid His Tag at N-terminus and purified by convential chromatogrpahy techniques. HSPA8 is part of the heat shock protein 70 family which includes both heat-inducible and constitutively expressed proteins (heat-shock cognate proteins). HSPA8 is a heat-shock cognate protein that binds to nascent polypeptides to facilitate correct folding. HSPA8 plays a role as an ATPase in the disassembly of clathrin-coated vesicles through transport of membrane components through the cell. HSPA8 is expressed in colon cancer cells, HSPA8 takes part in reovirus outer capsid disassembly, through membrane penetration, to plan the entering particle for gene expression and replication. serum HSPA8 concentrations are reduced in normal human pregnancy. HSPA8 plays a role in androgen action on dermal papilla cells. HSPA8 is directly linked with Influenza virus matrix protein 1 and thus required for viral production.

Product Info

Amount :	10 µg
Purification :	Greater than 90.0% as determined by SDS-PAGE.
Content :	The HSC70 protein solution contains 20mM Tris, pH-8 & 10% Glycerol.
Storage condition :	Store at 4°C if entire vial will be used within 2-4 weeks. Store, frozen at -20°C for longer periods of time. For long term storage it is recommended to add a carrier protein (0.1% HSA or BSA). Avoid multiple freeze-thaw cycles.
Amino Acid :	MGSSHHHHHH SSGLVPRGSH MSKGPAVGID LGTTYSCVGV FQHGKVEIIA NDQGNRTTPS YVAFTDTERL IGDAAKNQVA MNPTNTVFDA KRLIGRRFDD AVVQSDMKHW PFMVVNDAGR PKVQVEYKGE TKSFYPEEVS SMVLTKMKEI AEAYLGKTVT NAVVTVPAYF NDSQRQATKD AGTIAGLNVL RIINEPTAAA IAYGLDKKVG AERNVLIFDL GGGTFDVSIL TIEDGIFEVK STAGDTHLGG EDFDNRMVNH FIAEFKRKHK KDISENKRAV RRLRTACERA KRTLSSSTQA SIEIDSLYEG IDFYTSITRA RFEELNADLF RGTLDPVEKA LRDAKLDKSQ IHDIVLVGGS TRIPKIQKLL QDFFNGKELN KSINPDEAVA YGAAVQAAIL SGDKSENVQD LLLLDVTPLS LGIETAGGVM TVLIKRNTTI PTKQTQTFTT YSDNQPGVLI QVYEGERAMT KDNNLLGKFE LTGIPPAPRG VPQIEVTFDI DANGILNVSA VDKSTGKENK ITITNDKGRL SKEDIERMVQ EAEKYKAEDE KQRDKVSSKN SLESYAFNMK ATVEDEKLQG KINDEDKQKI LDKCNEIINW LDKNQTAEKE EFEHQQKELE KVCNPIITKL YQSAGGMPGG MPGGFPGGGA PPSGGASSGP TIEEVD.

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