

32-5340: Recombinant Human Heat Shock 70kDa protein 9

Alternative Name :

Mortalin,GRP75,MOT2,GSPA9B,PBP74,MOT-2,MTHSP75,Stress-70 protein mitochondrial,75 kDa glucose-regulated protein,GRP 75,Heat shock 70 kDa protein 9,Peptide-binding protein 74,MOT,HSPA9,HSPA9B,CSA,MGC4500.

Description

Source : Escherichia Coli. Recombinant Human HSPA9 produced in E.Coli is a single,non-glycosylated polypeptide chain containing 654 amino acids (47-679) and having a molecular mass of 71 kDa.HSP9A is expressed with a 20 amino acid His tag fused at N-Terminus and purified by proprietary chromatographic techniques. HSPA9 is part of the heat shock protein 70 family which contains both heat-inducible and constitutively expressed members that are also called heat-shock cognate proteins. HSPA9 encodes a heat-shock cognate protein that is involved in the control of cell proliferation and acts as a chaperone. HSPA9 was restricted to chromosome 5, band q31, a region that is often deleted in myeloid leukemias and myelodysplasia (MDS), making it a candidate tumor suppressor gene, which is consistent with the biological function of its murine homologue. HSPA9 supresses nuclear translocation, transcriptional activation, and control of centrosome-duplication functions of p53.

Product Info

Amount : 50 µg

Purification : Greater than 95.0% as determined by SDS-PAGE.

Content : The HSPA9 protein solution contains 20mM Tris-HCl, pH-8, 10% glycerol and 0.5mM DTT.

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 MASEAIKGAV VGIDLTTNS CVAVMGKQA KVLNAEGAR
TTPSVVAF TA DGERLVGMPA KRQAVTNPN TFYATKRLIG RRYDDPEVQK DIKNVPFKIV RASNGDAWVE
AHGKLYSPSQ IGAFVLMKMK ETAENYLGH T AKNVITVPA YFNDSQRQAT KDAGQISGLN VLRVINEPTA
AALAYGLDKS EDKVIAYVDL GGGTFDISIL EIQGVFEVK STNGDTFLGG EDFDQALLRH IVKEFKRETG
VDLT KDNMAL QRVREAAEKA KCELSVVQT DINLPYLTMD SSGPKHLNMK LTRAQFEGIV TDLIRRTIAP
CQKAMQDAEV SKSDIGEVIL VGGMTRMPKV QQTVDLFR APSKAVNPDE AVAIGAAIQG
GVLADGVDV LLLDVTPLSL GIETLGGVFT KLINRNTTIP TKKSQVFSTA ADGQTQVEIK VCQGEREMAG
DNKLLGQFTL IGIPPAPRGV PQIEVTFDID ANGVHVS AK DKGTGREQQI VIQSSGGLSK DDENMVKNA
EKYAEEDRRK KERVEAVNMA EGIIHDTETK MEEFKDQLPA DECNLKEEI SKMRELLARK DSETGENIRQ
AASSLQQASL KLFEMAYKKM ASEREGSGSS GTGEQKEDQK EEKQ.

