

32-5337: Recombinant Human Heat Shock 70kDa protein 5 (19-654 a.a.)

Alternative Name : 78 kDa glucose-regulated protein, GRP-78, Endoplasmic reticulum luminal Ca(2+)-binding protein grp78, Heat shock 70 kDa protein 5, Immunoglobulin heavy chain-binding protein, BiP, HSPA5, GRP78, MIF2, FLJ26106.

Description

Source : Escherichia Coli. HSPA5 (19-654) Human Recombinant produced in E.coli is a single, non-glycosylated polypeptide chain containing 659 amino acids (19-654) and having a molecular mass of 72.9kDa. HSPA5 (19-654) is fused to a 23 amino acid His-tag at N-terminus & purified by proprietary chromatographic techniques. Binding immunoglobulin protein (BiP or HSPA5) is a member of the family of ~70kDa heat shock proteins (HSP 70). HSPA5 is a stress response protein which is induced by agents or conditions that adversely affect endoplasmic reticulum (ER) function. HSPA5 is crucial for the proper glycosylation, folding as well as for the maintenance of cell homeostasis and the prevention of apoptosis.

Product Info

Amount : 20 µg
Purification : Greater than 90% as determined by SDS-PAGE.
Content : The HSPA5 (19-654) solution (1mg/ml) contains 20mM Tris-HCl buffer (pH 8.0), 0.15M NaCl, 1mM DTT and 20% 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 MGSEEDKKE DVGTVVIGIDL GTTYSCVGVF KNGRVEIIAN DQGNRITPSY VAFTPEGERL IGDAAKNQLT SNPENTVFDA KRLIGRTWND PSVQQDIKFL PFKVVEKTK PYIQVDIGGG QTKTFAPEEI SAMVLTKMKE TAEAYLGKKV THAVVTPAY FNDAQRQATK DAGTIAGLNV MRIINEPTAA AIAYGLDKRE GEKNILVFDL GGGTFDVSLL TIDNGVFEVV ATNGDTHLGG EDFDQRVMEH FIKLYKKKTG KDVRKDNRAV QKLRRVEKA KRALSSQHQA RIEIESFYEG EDFSETLTRA KFEELNMDLF RSTMKPVQKV LEDSDLKKS IDEIVLVGGS TRIPKIQQLV KEFFNGKEPS RGINPDEAVA YGAAVQAGVL SGDQDTGDLV LLDVCPLTLG IETVGGVMTK LIPRNTVVPT KKSQIFSTAS DNQPTVTIKV YEGERPLTKD NHLLGTFDLT GIPPAPRGVP QIEVTFEIDV NGILRVTAED KGTGNKNKIT ITNDQNRLLTP EEIERMVNDA EKFAEEDKKL KERIDTRNEL ESYAYSLKNQ IGDKEKLGK LSEDKETME KAVEEKIEWL ESHQDADIED FKAKKKELEE IVQPIISKLY GSAGPPPTGE EDTAEKDEL.

